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Integrated mRNA and microRNA transcriptome profiling during Differentiation of Human Nasal Polyp Epithelium reveals an altered Ciliogenesis

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AUTHOR CONTRIBUTIONS

Conceived and designed the experiments, B.C.D., G.F., A.M.A., J.M.; performed the experiments, M.F., B.C.D., J.R.; data analysis, B.C.D., G.F.,C.P., J.M.; contributed reagents/materials, I.A., M.F.; writing paper, B.C.D., G.F. J.M.; provision of study material or patients, I.A., C.P.; final approval of manuscript: C.P., J.M.

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ABSTRACT

Background: Human adult basal stem/progenitor cells (BSCs) obtained from chronic rhinosinusitis with nasal polyps (CRSwNP) when differentiated in an air-liquid interface (ALI) usually provide a pseudostratified airway epithelium with similar abnormalities than original *in vivo* phenotype. However, the intrinsic mechanisms regulating this complex process are not well defined and their understanding could offer potential new therapies for CRSwNP (incurable disease).

Methods: We performed a transcriptome-wide analysis during *in vitro* mucociliary differentiation of human adult BSCs from CRSwNP, compared to those isolated from control nasal mucosa (control-NM), in order to identify which key mRNA and microRNAs are regulating this complex process in pathological and healthy conditions.

Results: A number of genes, miRs, biological processes and pathways were identified during mucociliary differentiation of both CRSwNP and control-NM epithelia and, notably, we have demonstrated for the first time that genetic transcriptional program responsible of ciliogenesis and cilia function is significantly impaired in CRSwNP epithelium, presumably produced by an altered expression of microRNAs, particularly of those miRs belonging to *mir-34* and *mi-449* families.

Conclusions: This study provides for the first time a novel insight into the molecular basis of sinonasal mucociliary differentiation, demonstrating that transcriptome related to ciliogenesis and cilia function is significantly impaired during differentiation of CRSwNP epithelium due to an altered expression of microRNAs.

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KEYWORDS

Air-liquid Interface (ALI) 3D *in vitro* model

Basal stem/progenitor cells (BSCs)

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INTRODUCTION

The upper airways are covered by a pseudo-stratified columnar epithelium containing secretory cells, ciliated and non-ciliated columnar cells and basal stem/progenitor cells (BSCs).[1] Ciliated and goblet cells are actively involved in mucociliary clearance, a critical host defense mechanism, while non-ciliated columnar cells have a structural function. In contrast, BSCs promote the adhesion of columnar epithelium to the basal membrane and constitute a multipotent stem cell population which drives both epithelium homeostasis and its regeneration after injury.[2]

The etiology and pathogenesis of chronic rhinosinusitis (CRS), with (CRSwNP) or without (CRSsNP) nasal polyps, remain still unclear,[3,4] but there is an emerging consensus considering the respiratory epithelium as one of key players.[5] In fact, nasal polyp epithelium is usually damaged (shedding/denudation), showing important defects (defective cilia or epithelial barrier) and abnormal remodeling (goblet or basal cell hyperplasia, metaplasia.[6-9] Airway BSCs could be responsible, at least in part, of all these epithelial abnormalities. Indeed, basal cell hyperplasia is probably produced by an imbalance between proliferation and differentiation, while dysregulation of cell lineage fate in BSCs, or their undifferentiated daughters, might produce goblet cell hyperplasia/metaplasia or squamous metaplasia. Hence, identification of molecular mechanisms underlying the repair and differentiation of healthy/pathological sinonasal BSCs, could offer some potential for the development of new strategies for CRSwNP treatment and could provide a better understanding of their etiology.[10]

Previous studies have demonstrated that BSCs can be easily obtained from upper airways, either from control healthy subjects[11,12] or CRSwNP patients,[12,13] with long-term self-renewal ability, capable of differentiating into the luminal secretory and ciliated cells when cultured in air-liquid interface (ALI) culture. In a previous study,[14] we demonstrated that BSCs were responsible of the reconstitution of both CRSwNP and NM epithelia in ALI cultures, showing for the first time that CRSwNP reconstituted epithelia showed an increased inflammatory function. Moreover, other relevant studies have demonstrated that CRSwNP epithelial cells, cultured and differentiated in ALI, produced CRSwNP restored epithelia with several dysfunctions in epithelial barrier[8,15] or in cilia formation and architecture[7,16] similar to those observed in original epithelia from CRSwNP patients.

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Thus, differences observed between healthy and inflamed 3D *in vitro* models, performed under non-inflammatory *in vitro* controlled conditions, could indicate that adult BSCs retain genetic and/or epigenetic mechanisms determining their fate during mucociliary differentiation.

MicroRNAs (miRs) are short, single-stranded, non-coding RNAs of ~22-nt that act as post-transcriptional regulators of protein-coding gene expression by either inducing degradation of target mRNAs or impairing their translation.[17] MiRs are phylogenetically well conserved in eukaryotic organisms,[18] which implies an important role of miRs in control of many biological processes. Indeed, numerous studies have been revealed that miRs play a central role in development, physiology, and disease, through their tissue-specific or development-specific expression.[17,18] In human airways, miRs are identified as important players in the pathogenesis of many inflammatory diseases including allergy and asthma.[19,20] Identification of miRs underlying the epithelial repair and differentiation in CRSwNP, could lead to the development of novel treatments based on miRs that may represent an alternative and promising approach for nonsteroidal anti-inflammatory treatment, as previously postulated.[21]

Integrated mRNA and miRNA transcriptome analysis makes it possible to perform a systematic screening approach for unraveling which networks of miRs and their potential mRNA targets are regulating biological processes such as mucociliary differentiation, and also for the identification of new miRNA functions.

Thus, the objective of this study was to perform a transcriptome-wide analysis during *in vitro* mucociliary differentiation of human adult BSCs from CRSwNP compared to those isolated from control nasal mucosa (control-NM), in order to identify which key mRNA and miRs are regulating this complex process under pathological and healthy conditions.

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METHODS

Study population

Nasal polyp specimens (n=7) were obtained from patients undergoing endoscopic sinus surgery for chronic rhinosinusitis with nasal polyps (CRSwNP), while control nasal mucosa specimens (n=7) were obtained from inferior turbinates of healthy subjects undergoing septoplasty or partial turbinectomy.

All patients signed informed consent to participate in the study, which was approved by the Ethics Committee for Clinical Research, Hospital Clínic, Universitat de Barcelona (12 of April 2012; 2012\7466).

Characteristics of study population, inclusion and exclusion criteria and ethical issues are displayed in Table S1. Further information provided in Supplemental Experimental Procedures.

Human adult BSC culture and differentiation at the air-liquid interface

Primary cultures of human adult BSCs were obtained from both CRSwNP (CRSwNP-BSCs, n=7) and control nasal (NM-BSCs, n=7) mucosa through the explant method previously outlined,[14] and expanded BSCs transferred to the ALI system to become fully differentiated within 4 weeks. Full details regarding tissue handling, BSC isolation and purity, submerged or ALI culture, and histological characterization by immunofluorescence are provided in Supplemental Experimental Procedures.

mRNA and miR expression microarrays and data analysis

Total RNA, including microRNAs, was isolated from cells at days 0, 14 and 28 of ALI culture. Total RNA (100ng for mRNA, 300ng for miR) was processed for global transcriptional analysis using the Human Genome U219 (gene expression) and miRNA 4.1 Array Plates (miR expression), both purchased by Affymetrix (USA). Statistically significant mRNAs and miRs were determined by using the non-parametric Rank Product test, followed by Benjamini-Hochberg multiple correction to control the false discovery rate (FDR) with a threshold of 1% ($q < 0.01$). Finally, for data analysis, we filtered out the

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differentially expressed mRNAs/miRs from those that were statistically significant, by using Log_2 Ratio (LR) expression greater (upregulated) or lower (downregulated) than 1 for mRNAs (|LR|>1) and 0.6 for miRs (|LR|>0.6). The entire data set of the investigation has been included at the National Center for Biotechnology Information Gene Expression Omnibus (NCBI-GEO), accession number GSE107624. Expression analysis of genes of interest related to epithelial cell phenotypes (Table S2), Gene ontology biological processes (GO_BP) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways determined by functional enrichment analysis were also shown.

Moreover, we matched validated and predicted interaction pairs mRNA/miRNAby using miRTarBase_v7 and TargetScan_v7.2 databases.[22,23] We used stringent parameters to determine mRNA-miRNA correlation interactions (Spearman |rho| > 0.75 and p < 0.01), beingnon-correlated interactions were filtered out. Finally, in order to better visualize these interactions, we generated miR-mRNA networks in Cytoscape.[24] Further information provided in Supplemental Experimental Procedures.

Real time PCR and statistical analysis

In order to confirm data obtained from microarray experiments, mRNA levels were quantified by quantitative real-time PCR (q-PCR). Relative gene expression was determined by comparative Ct method ($2^{-\Delta\Delta Ct}$ method).[25] The details of RNA preparation, genes primer sequences used (Table S3) and real time PCR procedure are described in Supplemental Experimental Procedures.

The statistical analysis of q-PCR results was performed using GraphPad Prism 6. The non-parametric Wilcoxon Signed-Ranks Test was used for paired comparisons (when comparing days 14 and 28 versus day 0, longitudinal analysis), and Mann-Whitney U test was used for between-group comparisons (when comparing CRSwNP vs control-NM at different days, cross-sectional analysis), with statistical significance set at a *P* value of less than 0.05.

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RESULTS

Characterization of BSCs isolated from CRSwNP and control-NM tissues

Human airway BSCs are characterized by the expression of the universal markers TP63 and KRT5, with subpopulations that demonstrate positivity for additional markers including KRT14, PDPN, CD151, NGFR, and ITGA.[2,26] In the current study, BSCs isolated from CRSwNP (CRSwNP-BSCs, n=5) and control-NM (NM-BSCs, n=5) were assessed by immunofluorescence in order to demonstrate their basal cell linage phenotype. The basal cells markers tumor protein p63 (TP63), cytokeratins 5 (KRT5) and 14 (KRT14) were expressed in >85% cells at both passages 0 and 1 (Figures S1 and S2, respectively) in CRSwNP and control-NM cultures, whereas all grown cells were negative for both goblet (MUC5AC) and ciliated (β-Tubulin IV) cell markers (Figures S1 and S2). According to these results, only BSCs were isolated by migration from explants in a similar manner to previous studies performed with endobronchial biopsies from human lower airways.[27,28]

Differentiation of BSCs isolated from CRSwNP and control-NM in ALI culture

In both CRSwNP (n=7) and control-NM (n=7) ALI cultures we observed the mucociliary differentiation from BSCs at day 0 (Figure 1A) to ciliated and goblet cells at day 28 (Figure 1B). At day 0, the majority of confluent cells were BSCs in both ALI cultures (TP63+; NM, 84.0±7.2%; CRSwNP, 74.8±6.4%, Figure 1D), while none of them were ciliated (β-Tub IV$^+$; NM, 0%; CRSwNP, 0%, Figure 1E) or goblet (MUC5AC$^+$; NM, 0%; CRSwNP, 0%, Figure 1F) cells. In contrast, at day 28 of the ALI culture (Figure S3), while TP63+ cells were decreased (NM, 22.5±6.5%; CRSwNP, 18.7±4.3%, $P<0.05$ compared to day 0, Figure 1, B and D), both β-Tub IV$^+$ (NM, 40.3±6.6%; CRSwNP, 43.4±5.9%) and MUC5AC+ (NM, 10.7±1.8%; CRSwNP, 10.2±1.6%) cells were increased ($P<0.05$ compared to day 0, Figure1, E and F). On the other hand, as previously reported,[7,13,15] no significant differences were found in cellular counts when CRSwNP (n=7) was compared to control-NM (n=7) at both days 0 and 28 (Figure 1, D-F).

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Global transcriptional profiling of CRSwNP-BSCs and control-NM-BSCs during mucociliary differentiation

Total RNA was extracted from both cultures at days 0, 14 and 28 of ALI culture and global transcriptional analysis were performed using the Human Genome U219 (gene expression) and miRNA 4.1 Array Plates (miR expression). Microarray data were processed for raw data quality control analysis by using RMA algorithm and then principal component analysis (PCA) was performed for exploratory data analysis. Thus, we observed that samples from day 0 (BSCs monolayer) were clearly separated from those related to days 14 and 28 (pseudostratified epithelium with goblet, ciliated and basal cells) in both CRSwNP and control-NM cultures (Figures S4A and S5A for mRNAs and miRs, respectively).

We determined the DE mRNAs ($q<0.01$, $|LR|>1$) and miRs ($q<0.01$, $|LR|>0.6$) during mucociliary differentiation of both CRSwNP (n=7) and control-NM (n=7) ALI cultures (Tables S1-S14). Thus, in regard to mRNA expression, in control-NM cells we detected 802 upregulated and 739 downregulated DE genes at day 14, and 1,125 upregulated and 761 downregulated DE genes at day 28, compared to day 0 of ALI culture (Table 1, longitudinal analysis); whereas in CRSwNP we identified 684 upregulated and 651 downregulated DE genes at day 14, and 1,129 upregulated and 1,190 downregulated DE genes at day 28, compared to day 0 of ALI culture (Table 1). On the other hand, with respect to microRNAs, in control-NM cells we detected 52 upregulated and 47 downregulated DE miRsat day 14, and 105 upregulated and 43 downregulated DE miRs at day 28, compared to day 0 of ALI culture; while in CRSwNP we identified 143 upregulated and 45 downregulated DE miRs at day 14, and 211 upregulated and 67 downregulated DE miRs at day 28, compared to day 0 of ALI culture (Table 1). Finally, we determined by cross-sectional analysis which mRNAs and miRs were DE between CRSwNP and control-NM (Table 1).

We also created heatmaps with longitudinal DE genes ($q<0.01$, $|LR|>1$) from CRSwNP and NM cells, respecting the sample clustering as much as possible. We found high contrast between gene expression profiles from differentiated CRSwNP and control-NM cells at day 28 when compared to CRSwNP-BSCs and NM-BSCs at day 0 of ALI culture (Figure S4, B and C). These results were similar to the observed in PCA analysis,

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where samples from day 28 were clearly separated from those relative to day 0 (Figure S4A). In addition, heatmap performed with DE miRs (q<0.01, |LR|>0.6) showed big differences in the microRNA expression pattern from CRSwNP compared to control-NM, being both groups naturally clustered by tissue type (Figure S5B).

Since miRs are grouped into families based on targeting properties that normally produce redundant biological functions,[17] we identified which microRNA families were mostly represented during mucociliary differentiation of both CRSwNP and control-NM ALI, taking into account the number of their members expressed at days 14 and 28 (Figure S5, C and D, respectively). Thus, at day 14, we found that some miR families were similarly expressed (*mir-17*, 4DW in CRSwNP vs 4DW in control-NM; *mir-30*, 3UP in CRSwNP vs 2UP in control-NM; Figure S5C), while others families were differentially represented (*mir-378*, 3UP-1DW in CRSwNP vs 0 in control-NM; *mir-449*, 0 UP in CRSwNPvs 4 UP in control-NM;*mir-548*, 2 DW in CRSwNP vs 4 DW in control-NM; Figure S5C). When day 28 was analyzed, we found that some miR families were similarly represented (*mir-17*, 5DW in CRSwNP vs 6DW in control-NM; *mir-188*, 3UP in CRSwNP vs 2UP in control-NM; *mir-449*, 4UP in CRSwNP vs 4UP in control-NM; *mir-548*, 4UP in CRSwNP vs 3UP in control-NM; *mir-8*, 4UP in CRSwNP vs 3UP in control-NM; Figure S5D), while others families were differentially expressed (*mir-30*, 4UP in CRSwNP vs 2UP in control-NM; *mir-34*, 2UP in CRSwNP vs 4UP in control-NM; *mir-378*, 6 in CRSwNP vs 0 in control-NM; Figure S5D).

Genes related to Epithelial Cell Phenotypes during differentiation

By using microarray data (Tables S1-S14), the expression of several genes related to epithelial cell phenotypes (Table S15) was determined during mucociliary differentiation of both CRSwNP (n=7) and NM (n=7) ALI cultures (Table S16). In concordance with cellular counts (Figure 1, D-F), basal cell gene signature was downregulated during differentiation (Figure 2A), while genes relatives to ciliated (Figure 2B) and goblet (Figure 2C) cells were both upregulated, particularly, those related to cilia (Figure 2B). However, we observed that no gene related to ciliogenesis or cilia was upregulated (q<0.01, |LR|>1) in CRSwNP at day 14, while several cilia-related genes were upregulated (q<0.01, |LR|>1) in control-NM (Figure 2B), and, at the same time, a

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number of genes related to basal cells were upregulated (q<0.01, |LR|>1) in CRSwNP compared to NM (Figure 2A). Moreover, cross-sectional analysis showed that 30 cilia-related genes were downregulated (q<0.01, |LR|>1) in fully differentiated CRSwNP compared to NM (Figure 2B). Some of these downregulated genes were components of the axoneme, specifically, elements of outer (DNAH5, DNAH9, DNAI1, DNAI2) and inner (DNAH12, DNALI1, WDR63, WDR78) dynein arms, other relatives to central pair (HYDIN, SPAG6, SPAG17, PCDP1) or radial spoke (RSPH1, RSPH4A, RSPH9), others involved in dynein assembly and docking (DNAAF1, DNAAF3, DYX1C1, ARMC4, DRC1, LRRC6, ZMYND10) or, importantly, master regulators of multiciliogenesis process (FOXJ1, MYB, CCNO).[29]

Experimental validation by quantitative real-time PCR (qPCR)

After differentiation, at days 14 and 28 compared to day 0, mRNA levels of basal cell genes (*TP63*, *KRT5*, *KRT14* and *ITGA6*) were significantly (P<0.05) decreased in control-NM (Figure 2D), with the exception of *PDPN* (not significant, NS), while none of them was decreased in CRSwNP (NS, Figure 2D). However, a significant increase of mRNAs related to goblet (*SCGB1A1*, *AGR2*, *MUC16*, *MUC5AC*, and *MUC5B*) and ciliated (*MCIDAS*, *CCNO*, *MYB*, *RFX3*, and *FOXJ1*) cells was found in both CRSwNP and NM ALI cultures at days 14 and 28 (P<0.05; Figure 2, E and F), indicating mucociliary differentiation.

Furthermore, when cross-sectional analysis was performed, significant differences were found in CRSwNP compared to NM at both days 0 and 28. At day 0, when ALI cultures were mainly composed of BSCs (Figure 1A), we observed a significant downregulated expression of several genes at low mRNA level, such as cilia-related (*MCIDAS*, *CCNO* and *MYB*) and secretory (*SCGB1A1* and *MUC5B*), in CRSwNP compared to NM (P<0.05; Figure 2, E and F). Interestingly, in a previous study from the mice airways,[30] it was also observed that tracheal BSCs express ciliated or secretory cell associated fate determinants (e.g. MYB and NOTCH2), prior to the formation of luminal precursors. Finally, at day 28, in fully differentiated ALI cultures (Figure 2, E and F), we detected a significant decrease on mRNA expression of cilia (*FOXJ1*) and

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goblet/secretory (*SCGB1A1*, *AGR2* and *MUC16*) genes in CRSwNP compared to NM (P<0.05; Figures 1K and 1L).

Functional Enrichment Analysis

By functional enrichment analysis we determined which biological processes (GO_BP) and pathways (KEGG) were significantly (q<0.05) enriched in both CRSwNP and control-NM ALI cultures during differentiation (Tables S17-S23).[31]

1. Gene Ontology Biological Processes

By using *GO_Bubbles*,[32] we identified that cell cycle and cell division biological processes were the most significantly enriched (Top 5, q<0.05) and downregulated (Z-score<0) GO_BP terms in both CRSwNP and control-NM ALI cultures at days 14 (Figure S6, A and B) and 28 (Figure 3, A and C) compared to 0. In contrast, in regard to upregulated GO_BP terms (Top 5, q<0.05, Z-score>0), we found that some biological processes, such as *O-glycan processing, Oxidation-reduction process* and *Antigen processing and presentation*, were commonly enriched in both CRSwNP and control-NM at day 14 (Figure S6, A and B), while those related to cilia were differently enriched in control-NM at day 28 than CRSwNP (Figure 3, A and C). While in differentiated NM most enriched terms (Top 5, q<0.05) were all related to cilia (Figure 3A and Table S18), in differentiated CRSwNP, only one from all upregulated GO_BP terms was related to cilia (Figure 3C and Table S20). In fact, high contrast between NM and CRSwNP ALI cultures is reflected not only in the different number of cilia-related GO_BP terms (12 vs 1 upregulated, respectively), but also in the total number of genes involved in these functions (86 vs 11, respectively) (Tables S18 and S20).

Moreover, we found by cross-sectional analysis that several cilia-related were the most significantly downregulated terms (q<0.05, Z-score<0) in CRSwNP compared to NM at both days 14 and 28 (Figure S6, D and 3E, respectively). On the other hand, at days 0 and 14, we observed that *epidermis development* and *keratinocyte differentiation* were the most significantly upregulated processes (q<0.05, Z-score>0), whereas *wound healing* and *response to hypoxia* were the most downregulated (q<0.05, Z-score<0) in CRSwNP compared to control-NM (Figure S6, C and D).

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Additionally, and in order to better show the differences found in cilia-related GO_BP terms between fully differentiated CRSwNP and NM ALI cultures, we created *GOChord* plots[32] with those enriched terms (q<0.05) but showing all their involved genes as the same time (Figure 3, B, D and F). Thus, we observed again major differences between differentiated control-NM (11 upregulated terms, 120 genes involved, 83% of genes upregulated; Figure 3B and Table 18) and CRSwNP (1 upregulated + 2 downregulated terms, 33 genes involved, 54% of these downregulated, Figure 3D and Table S20). In the same way, we found by cross-sectional analysis at day 28 that 12 cilia-related GO_BP terms were significantly downregulated (q<0.01) in CRSwNP compared to control-NM, with 54 of 55 involved genes downregulated (Figure 3F and Table S23).

2. KEGG Pathways

At days 14 and 28 compared to day 0, we found that some pathways, such as *Type I diabetes mellitus*, *Graft-versus-host disease*, *Rheumatoid arthritis* and *Inflammatory bowel disease*, were commonly enriched (q<0.05) and activated (Z-score>0) in both CRSwNP and control-NM, whereas others, such as *Cell cycle* and *DNA replication*, were commonly inhibited (Z-score<0) (Table 2). Other KEGG paths, such as *Drug metabolism–cytochrome P450*, *Metabolism of xenobiotics by cytochrome P450* or *Metabolic pathways*, were also commonly enriched and activated in both CRSwNP and NM ALI cultures (q<0.05, Z-score>0, Table 2), while others were exclusively activated (Z-score>0) or inhibited (Z-score<0) (Table 2).

mRNA-miRinteraction pairs

Finally, in order to identify which miRs were potentially regulating mRNA expression during differentiation, we obtained interaction pairs of mRNA-miR by matching our miRs and mRNAs datasets with databases composed of validated (miRTarBase_v7) and predicted (TargetScan_v7.2) interactions between miRs and target mRNAs.[22,23] Thus, we generated global networks of mRNA-miRNA interactions for both CRSwNP and control-NM ALI at days 14 (Figure S7) and 28 (Figure 4). In order to identify which of those mRNA-miR pairs were truly significant and inversely correlated in our dataset, a Spearman correlation test was performed taking into account mRNA and miR expression

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values (Spearman |rho| > 0.75 and q < 0.01, Table S24). Those significant mRNA-miR pairs are highlighted in global networks (Figures 4 and S7). For instance, we found a significant inverted correlation between *miR-449a* and *MYC* expression at both days 14 and 28, and between *miR-34c* and *MYC* or *NOTCH1* at day 28, in control-NM but not in CRSwNP ALI (Table S24).

Considering those mir families showing ≥ 2 mRNA-miRs, we found that some families were commonly upregulated (*mir-8*, *mir-30*, *mir-449*) or downregulated (*mir-17*, *mir-10*) in both ALI cultures at days 14 and/or 28. For instance, we observed a prominent role of miRs belonging to the *mir-17* family, which were downregulated during differentiation of both ALI models (Figures 4 and S7). In contrast, we detected a lack of pairs regarding *mir-34* and *mir-449* family members in CRSwNP at day 14 (Figure S7B), although some pairs were latterly found at day 28 (Figure 4B). It is relevant to note that these miRs are significantly downregulated in CRSwNP compared to control-NM (Tables S13 and S14).

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DISCUSSION

In this study we have characterized for the first time the global mRNA and microRNA transcriptome during *in vitro* mucociliary differentiation of human adult BSCs obtained from inflamed (CRSwNP) and healthy (control-NM) upper airway mucosa. We have demonstrated that the genetic transcriptional program responsible for ciliogenesis and cilia function is significantly impaired in CRSwNP epithelium, presumably produced by altered expression of microRNAs, particularly of those miRs belonging to *mir-34* and *mir-449* families.

Previous studies demonstrated that upper airway BSCs, either from control healthy subjects[11,12,14] or CRSwNP patients,[12-14] function as adult tissue multipotent stem cells, capable of differentiating into the luminal secretory and ciliated cells in ALI culture system. We firstly demonstrated that expanded cells from CRSwNP and control-NM explants were BSCs because of the expression of TP63, KRT5 and KRT14 markers,[2,26-28] and due to their differentiation capacity when cultured in ALI system. We showed that basal cells decreased, while secretory and ciliated cells increased during differentiation in both CRSwNP and control-NM ALI cultures. In agreement with previous studies performed with tracheobronchial cells,[33-35] we have demonstrated that basal cell gene signature was downregulated, while goblet and ciliated cell signatures were upregulated during mucociliary differentiation of both CRSwNP and NM ALI cultures.

In the current study, as previously reported,[7,14,16] we did not find any significant differences between CRSwNP and control NM ALI concerning the percentages of the different cell populations during differentiation. However, our findings notably revealed that the transcriptional program responsible for multi-ciliogenesis and cilia architecture/function is significantly impaired in CRSwNP cells *versus* control-NM, at both mRNA and miR levels, and we consider that this may be reflected into functional differences. We have identified a downregulated expression of master regulators genes of multi-ciliogenesis process, such as *MYB*, *CCNO,* and *FOXJ1*,[29,36] as well as many other genes involved in cilia architecture, such as those relatives to axoneme, central pair or radial spoke elements, and dynein assembly/docking. Functional enrichment analysis showed that several biological processes of motile cilium movement or assembly were

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downregulated in CRSwNP. Further experiments are needed to better show the possible impairment in cilia function of CRSwNP cells.

Recent reports have demonstrated that CRSwNP ALI cultures showed cilia impairment[7] or abnormalities in initial steps of ciliogenesis[16] compared to control cells. Li et al. showed that differentiation of CRSwNP cells in ALI produced ciliated cells with remarkable defects in cilia architecture, whereas Lai et al. demonstrated that ciliogenesis is inhibited at initial steps of differentiation by the action of CCP110. Defects in cilia are not only found in CRSwNP ALI cultures. It is well known that sinonasal mucosa from CRS patients, with or without nasal polyposis, have defects in cilia compared with control mucosa[16,37] and impairment of cilia architecture and ciliogenesis is associated to hyperplastic nasal polyp epithelia.[7] Since the *in vitro* model does not include inflammatory components, our results may suggest BSCs from CRSwNP have some kind of genetic/epigenetic background that produces an important fail in the mucociliary differentiation program.

We have demonstrated for the first time that CRSwNP BSCs, compared to control-NM, show a dysregulated miR expression during differentiation and, notably, we identified that some miRs belonging to the *mir-34* and *mir-449* families were significantly reduced in CRSwNP. It has been demonstrated that miRs of the *mir-34* and *mir-449* families are fundamental to trigger multi-ciliogenesis by repressing cell cycle genes[38] and the Notch pathway in the surface of some vertebrate epithelia.[39-41] We found a strong inverted correlation between expression of *miR-449* and *miR-34* with *MYC* and *NOTCH1* in control-NM, at days 14 and/or 28, but not in CRSwNP ALI. The reduced expression of several miRs belonging to *these miR* families in CRSwNP, could be associated with the relevant downregulation of ciliogenesis that we found in CRSwNP compared to control-NM ALI. It has been described that members of *mir-34* and *mir-449* are significantly suppressed in asthma,[42] something that may result in the increase of goblet cells and a decrease of ciliated cells. Because in CRSwNP epithelium is common to find goblet cell hyperplasia and defective cilia,[6,7,9] it would be interesting to investigate if the same epigenetic mechanisms are shared between CRSwNP and asthma diseases.

We also found that most significantly downregulated biological processes/pathways during differentiation of both ALI models were all related to cell cycle, division or proliferation, in agreement with similar previous studies.[33,35] We

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observed in mRNA-miR interaction networks that several genes related to cell cycle, division or proliferation could be notably downregulated in both CRSwNP and control-NM ALI by the action of several miRs, such as those belonging to *mir-30*, *mir-34* and *mir-449* families.[38] It has been described that miRs belonging to cluster *miR-17-92* normally promote proliferation and inhibit differentiation of airway epithelial progenitor cells.[43] We clearly observed a significant downregulation of several members of the *mir-17* family during differentiation of both CRSwNP and control-NM ALI,.

We have also found that other biological processes, such as *O-glycan processing* or *Oxidation-reduction*, which are fundamental for proper function of the respiratory epithelium, were enriched and upregulated during differentiation in both CRSwNP and control-NM. While O-glycan processing is mandatory for the adequate synthesis of glycoproteins, such as mucins,[44] which play a central role in both mucociliary clearance and host defense;[45] oxidation-reduction processes are linked to epithelium homeostasis, i.e., drug/xenobiotic metabolism.[46,47] We also detected that KEGG pathways, such as *Xenobiotic metabolism by cytochrome P450* and *Metabolic pathways*, were commonly activated during differentiation of both CRSwNP and control-NM ALI, as previously reportedin bronchial ALI models.[33-35] We found that several KEGG pathways, such as *Type I diabetes mellitus*, *Graft-versus-host disease*, *Rheumatoid arthritis* and *Inflammatory bowel disease*, were commonly enriched and activated during differentiation in both CRSwNP and control-NM ALI. The enrichment of these pathways seems to be associated to the increased expression of several genes related to *HLA* gene family, particularly those codifying for components of MHC-II, which are related to these autoimmune diseases,[48] although V-type ATPases and Toll like receptors (TLRs) gene families could also be involved. Anyhow, increased expression of *HLA* and *TLR* genes during mucociliary differentiation has also been described in bronchial epithelial cells[33,35] and the increased expression of TLRs could be associated with the development of immune response/host defense functions of the airway epithelium.[49] Recently it has been postulated the possibility that airway epithelial cells have antigen-presenting abilities in specific clinical settings in airway epithelium.[50] We found that some biological processes (e.g. *Antigen processing and presentation*) were among the most significantly enriched in both ALI groups.

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At day 0, before differentiation of both CRSwNP and control-NM ALI cultures, we found that BSCs were expressing low mRNA levels of several genes usually found in differentiated luminal cells, and some of them were downregulated in CRSwNP (*SCGB1A1*, *MUC5B*, *MCIDAS*, *CCNO* and *MYB*). Importantly, in a previous study from the mice airways,[30] using the SO_2 injury model, it was observed that tracheal basal cells express ciliated or secretory cell associated fate determinants, before the formation of luminal precursors. Pardo-Saganta et al. described that steady-state BSCs (~12% of total) expressed low levels of transcription factors usually found in more differentiated cells. Conversely the abundance of BSCs expressing these molecules increased up to ~50% of the total BSC population post injury, and they were observed to proliferate. Our findings showing that BSCs express low levels of mRNAs related to goblet/secretory and ciliated cells may indicate that in our *in vitro* model there is segregation or different subsets of progenitors. It would be interesting to characterize in further studies whether there are different subpopulations between progenitors or if the expression of some genes regulates the lineage commitment of BSCs.

Further *in vitro* or *ex vivo* experiments are required to demonstrate the real action of some miRs on the expression of their targets described in this study. Future studies are also necessary to investigate the role of the genetics of patients/subjects and possible environmental effects on transcriptome and differentiation of BSCs in ALI. In addition, it would be interesting to try to manipulate the expression of these miRs during the differentiation of BSCs because it would allow the development of new therapeutic strategies to repair epithelial defects in CRSwNP. Besides, the possibility to introduce inflammatory and/or anti-inflammatory agents in ALI model could help to a better understanding of miR regulation in CRSwNP epithelium.

In summary, this study provides a novel insight into the molecular basis of sinonasal mucociliary differentiation in both pathological (CRSwNP) and healthy (control-NM) conditions, demonstrating that genetic transcriptional program responsible of ciliogenesis and cilia function is significantly impaired during differentiation of CRSwNP epithelium, presumably produced by an altered expression of microRNAs, particularly of those miRs belonging to *mir-34* and *mi-449* families.

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Table 1. Number of mRNAs and microRNAs differentially expressed in control nasal mucosa (NM) and chronic rhinosinusitis with nasal polyps (CRSwNP) during differentiation in air-liquid interface culture.*

Longitudinal Analysis			
mRNAs	**Contrast**	**mRNAs UP**	**mRNAs DOWN**
Control-NM	0-14	*802*	*739*
	0-28	*1225*	*761*
CRSwNP	0-14	*684*	*651*
	0-28	*1129*	*1190*
microRNAs	**Contrast**	**miRs UP**	**miRsDOWN**
Control-NM	0-14	*52*	*47*
	0-28	*105*	*43*
CRSwNP	0-14	*143*	*45*
	0-28	*211*	*67*
Cross-sectional Analysis			
mRNAs	**Day**	**mRNAs UP**	**mRNAs Down**
CRSwNPvsControl-NM	0	*164*	*234*
	14	*168*	*219*
	28	*32*	*420*
microRNAs	**Day**	**miRs UP**	**miRsDOWN**
CRSwNPvsControl-NM	0	*19*	*28*
	14	*11*	*4*
	28	*3*	*9*

***Differentially expressed mRNAs and microRNAs were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2 Ratio expression greater (upregulated, UP) or lower (downregulated, DOWN) than 1 (| LR | > 1) and 0.6 (| LR | > 0.6) for mRNAs and miRs, respectively; followed by multiple correction using a False Discovery Rate (FDR) threshold of 1% (p-adjusted value or q < 0.01).**

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Table 2. Enriched KEGG pathways in Nasal Polyp (CRSwNP, n=7) and Nasal Mucosa (control-NM, n=7) at days 14 and 28 compared to day 0 of the air-liquid interface (ALI) culture.

		Control-NM		CRSwNP	
KEGG ID	NAME	Z-score 14 vs 0	Z-score 28 vs 0	Z-score 14 vs 0	Z-score 28 vs 0
hsa04940	*Type I Diabetes Mellitus*	2.31	2.67	2.11	2.84
hsa05332	*Graft-versus-Host disease*	1.90	2.31	1.26	2.14
hsa05323	*RheumatoidArthritis*	1.79	1.53	1.41	1.63
hsa05321	*InflammatoryBowelDisease*	1.50	1.81	1.29	2.36
hsa00982	*DrugMetabolism - Cytochrome P450*	3.30	-	3.36	3.58
hsa00980	*Metabolism of Xenobiotics by Cytochrome P450*	2.36	-	2.36	2.56
hsa01100	*MetabolicPathways*	0.97	2.94	-	1.78
hsa05166	*HTLV-1 Infection*	-	0.30	0.67	-0.53
hsa05204	*ChemicalCarcinogenesis*	2.18	-	-	-
hsa00010	*Glycolysis / Gluconeogenesis*	1.29	-	-	-
hsa05416	*Viral Myocarditis*	0.77	1.50	-	-
hsa04145	*Phagosome*	-	-	2.20	1.15
hsa05152	*Tuberculosis*	-	-	1.67	-
hsa05140	*Leishmaniasis*	-	-	1.50	1.61
hsa00561	*GlycerolipidMetabolism*	-	-	1.39	-
hsa04960	*Aldosterone-regulatedSodiumReabsorption*	-	-	-	2.50
hsa05145	*Toxoplasmosis*	-	-	-	1.89
hsa04550	*Signaling Pathways regulating Pluripotency of Stem Cells*	-	-	-	1.62
hsa04110	*Cell Cycle*	-5.49	-4.60	-3.66	-3.90
hsa03030	*DNA Replication*	-3.32	-3.74	-3.16	-4.00
hsa04510	*Focal Adhesion*	-4.64	-	-	-
hsa04512	*ECM-receptor Interaction*	-3.90	-	-	-
hsa04115	*p53 SignalingPathway*	-3.36	-2.50	-	-
hsa04151	*PI3K-Akt SignalingPathway*	-2.60	-	-	-
hsa04012	*ErbBSignalingPathway*	-2.24	-	-	-
hsa00230	*PurineMetabolism*	-	-2.33	-	-

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hsa00240	*PyrimidineMetabolism*	-	-	-	-4.31
hsa04914	*Progesterone-mediatedOocyteMaturation*	-	-	-	-2.13
hsa05205	*Proteoglycans in Cancer*	-	-	-	-1.54

Table is showing KEGG pathways that were enriched(q<0.05) in CRSwNP and NM ALI cultures at both 14and 28 days. KEGG paths showed are separated by z-score values, which represents the overall up/down regulated genes in each term, in both activated (in red) or inhibited (blue) at different days analyzed. Z-score for each pathway was calculated by using microarray data with the differentially expressed genes (q<0.01; | Log_2Ratio | >1).

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FIGURE LEGENDS

Figure 1. Characterization by immunofluorescence of control nasal mucosa (NM, n=7) and chronic rhinosinusitis with nasal polyps (CRSwNP, n=7) ALI cultures. A) Confluent cells stained for tumor protein 63 (TP63+, red), a basal stem/progenitor cell marker, in both control-NM and CRSwNP cultures at day 0 of ALI culture. Cell nuclei stained by DAPI (blue). Scale bar (white) equivalent to 75µm. B) Fully differentiated NM and CRSwNP ALI cultures stained for tumor protein 63 (TP63+, red), ciliated (β-Tub IV+, green) and goblet/secretory (MUC5AC+, red) cell markers at day 28. Scale bar (white) equivalent to 250µm. D-F) Cellular proportions (% from total) of immunoreactive cells for basal (D, TP63+), ciliated (E, β-Tub IV+) and goblet/secretory (F, MUC5AC+) cell markers in CRSwNPandcontrol-NM ALI cultures at both days 0 and 28. *, $P<0.05$ compared to day 0 (Wilcoxon Signed-Ranks Test); NS, not significant, $P>0.05$ compared to control-NM (Mann-Whitney U Test).

Figure 2. Characterization by microarrays and quantitative real-time PCR of control nasal mucosa (NM, n=7) and chronic rhinosinusitis with nasal polyps (CRSwNP, n=7) ALI cultures. A-C) Significant changes ($q<0.05$) of genes related to basal (A), cilia (B) and goblet (C) cells are represented by their Log_2 Ratio (LR) expression values during differentiation at days 14 and 28 compared to day 0 of control-NM (1st and 2nd columns, respectively) and CRSwNP (3rd and 4th columns, respectively) ALI culture; and also when CRSwNP was compared to NM at days 0, 14 and 28 (5th, 6th and 7th columns). D-F) Relative mRNA expression values of several genes related to basal (D), ciliated (E) and goblet (F) cells. Bar graphs indicate mean ± SEM of mRNA relative expression values (% of control) normalized to control-NM at day 0 of ALI culture (100%) for each marker. White bars, control-NM; black bars, CRSwNP values. *, $P<0.05$, compared to each marker at day 28 in same group (Wilcoxon signed rank test); #, $P<0.05$, CRSwNP compared to control-NM at day 0 or 28 (Mann-Whitney test).

Figure 3. Gene Ontology Biological Processes (GO_BP) terms enriched in chronic rhinosinusitis with nasal polyps (CRSwNP, n=7) compared to Nasal Mucosa (NM, n=7) at day 28 of the air-liquid interface (ALI) culture. Enriched GO_BP terms in

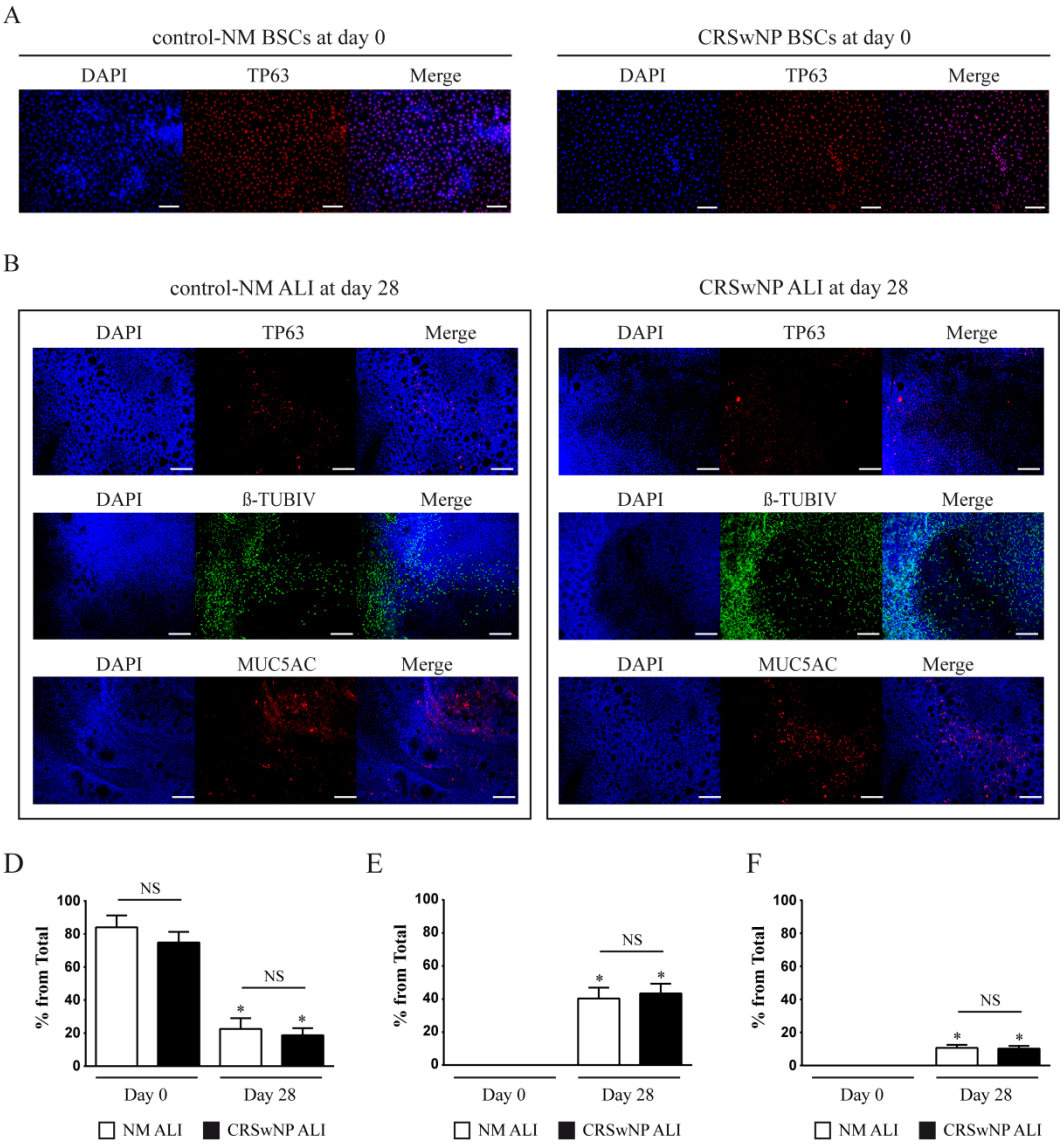
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control-NM (A and B) and CRSwNP (C and D) at day 28 compared to day 0 of ALI culture, and those enriched in CRSwNP compared to NM at day 28 of ALI culture (E and F). A, C, and E) GO_BP terms are displayed by bubbles (area is proportional to the number of genes assigned to each term), separated by on one hand by their statistical significance (-Log adjusted P-values, *Y-axis*) and, on the other, by using their z-score values (*X-axis*) in upregulated (in red, z-score>0) or downregulated (in blue, z-score <0) terms. Downregulated terms, in blue; upregulated terms, in red. B, D, and F) GOChord plots are displaying cilia-related GO_BP_Direct terms (modules on right, see legend for identification of each term) linked to their related genes (on left), which are ordered by Log_2fold change expression (LogFC). Expression data showed come from the microarray analysis ($q<0.01$; $| Log_2Ratio | >1$).

Figure 4. miR-mRNA networks in control nasal mucosa (NM, n=7) and chronic rhinosinusitis with nasal polyps (CRSwNP, n=7) at day 28 of the air-liquid interface (ALI) culture. Networks showing differentially expressed ($q < 0.01$) miRs (diamonds) associated with their potential mRNA targets (hexagons) in control-NM (A) and CRSwNP (B) after 28 days of differentiation. Upregulated and downregulated miRs/mRNAs are showed in red or in blue, respectively, with color intensity depending on Log_2 Ratio expression. Those pairs of miRs and mRNA targets that were significantly correlated ($P < 0.01$, Spearman $\rho > 0.75$) are highlighted in yellow.

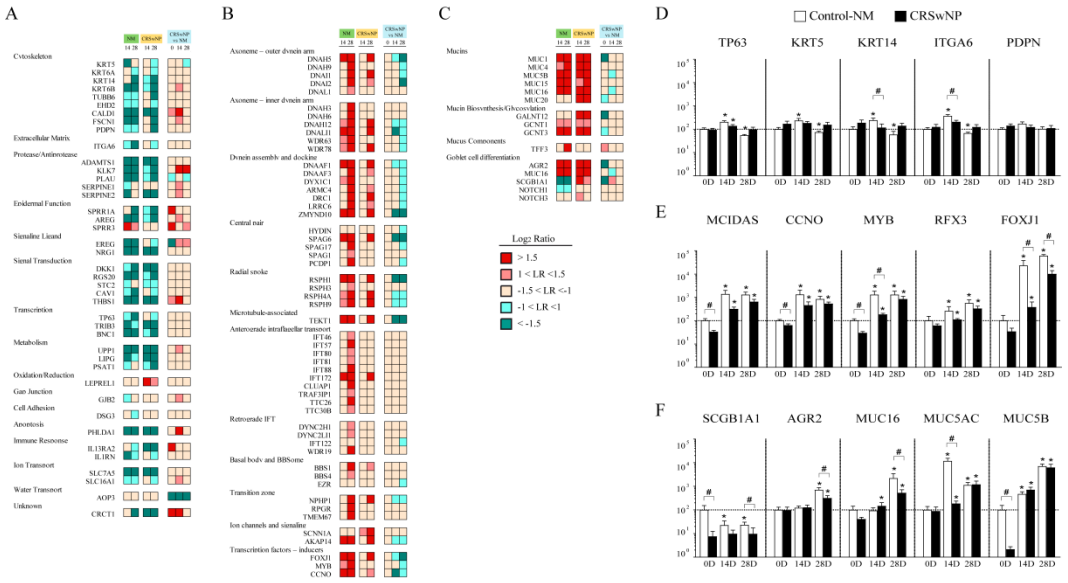
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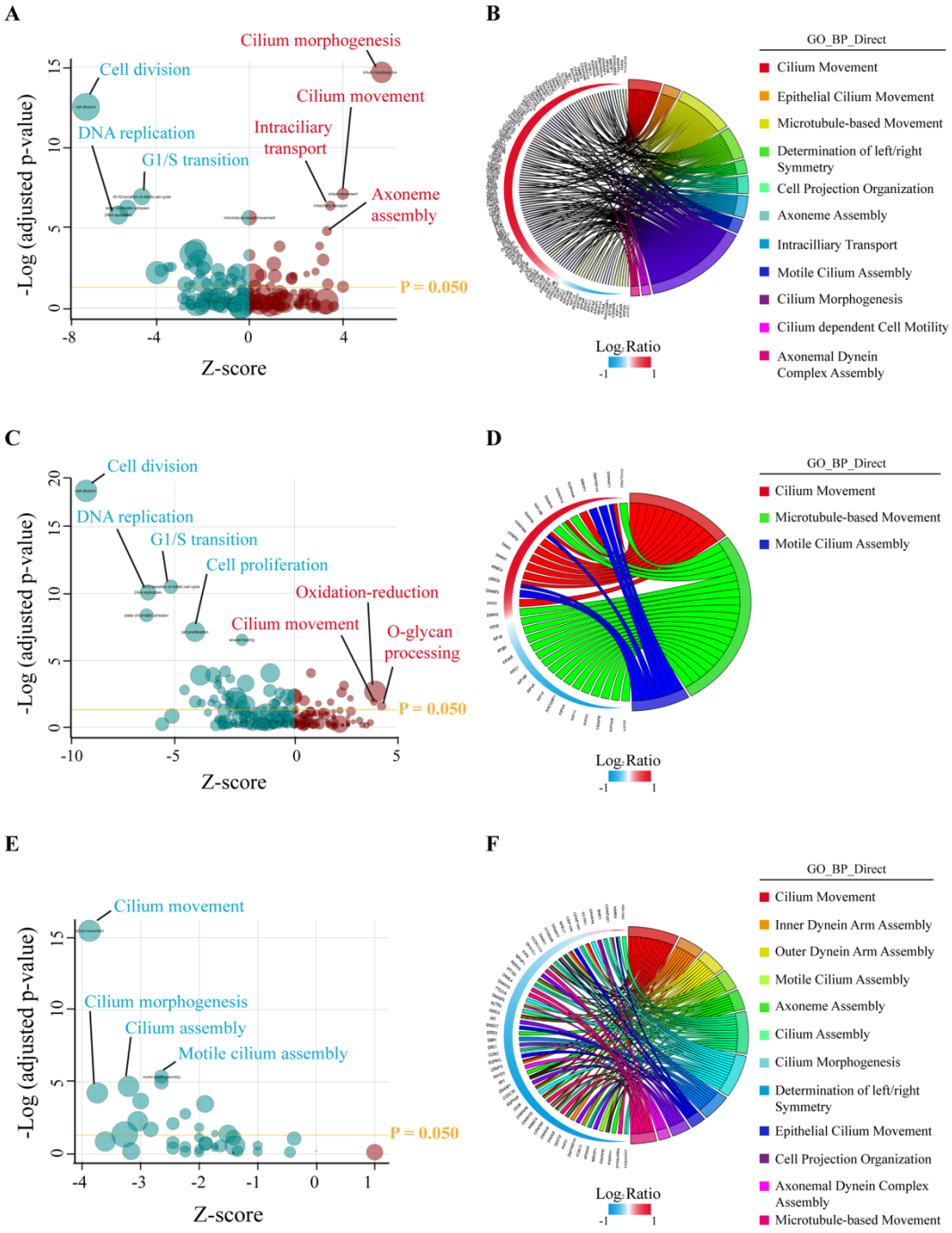


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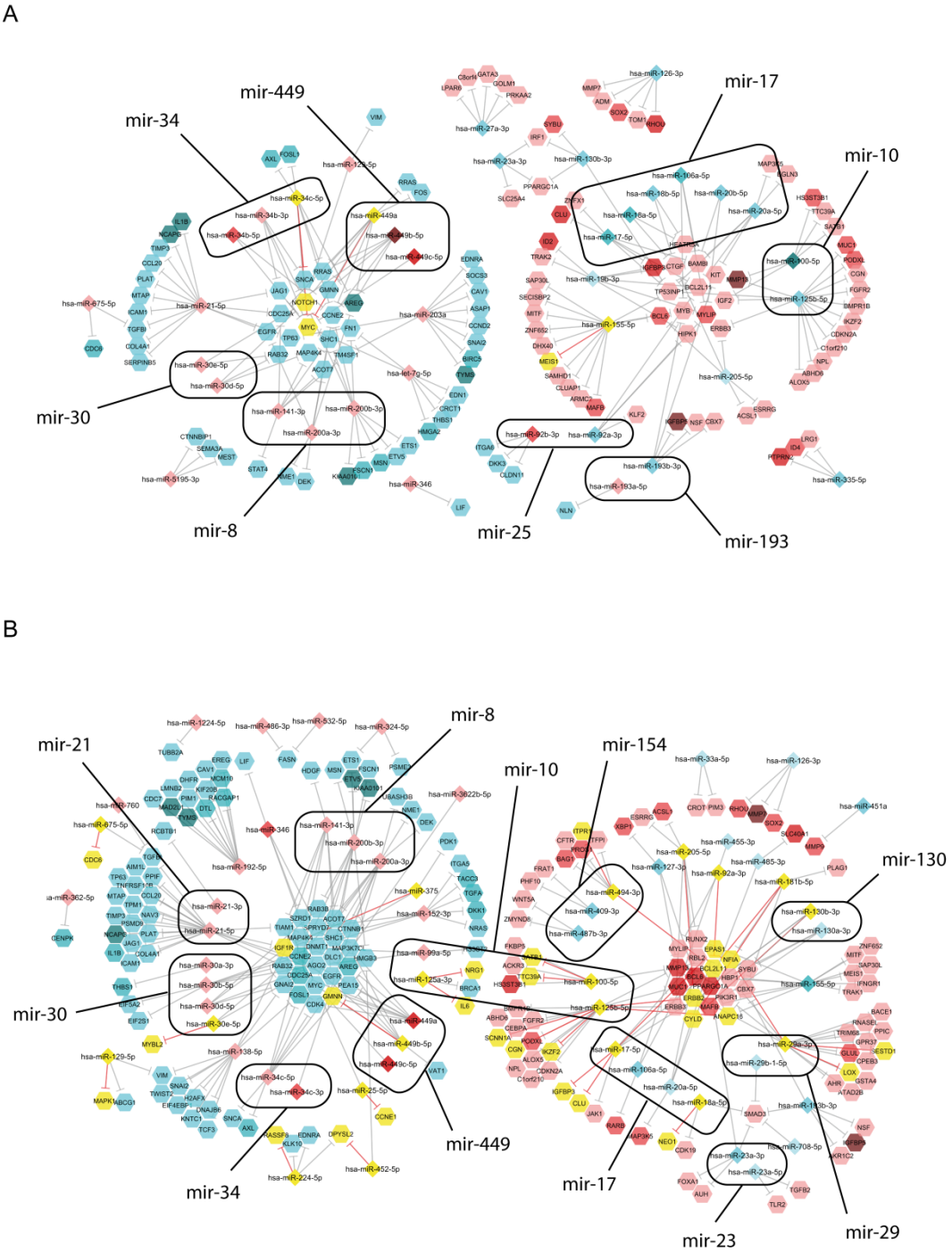
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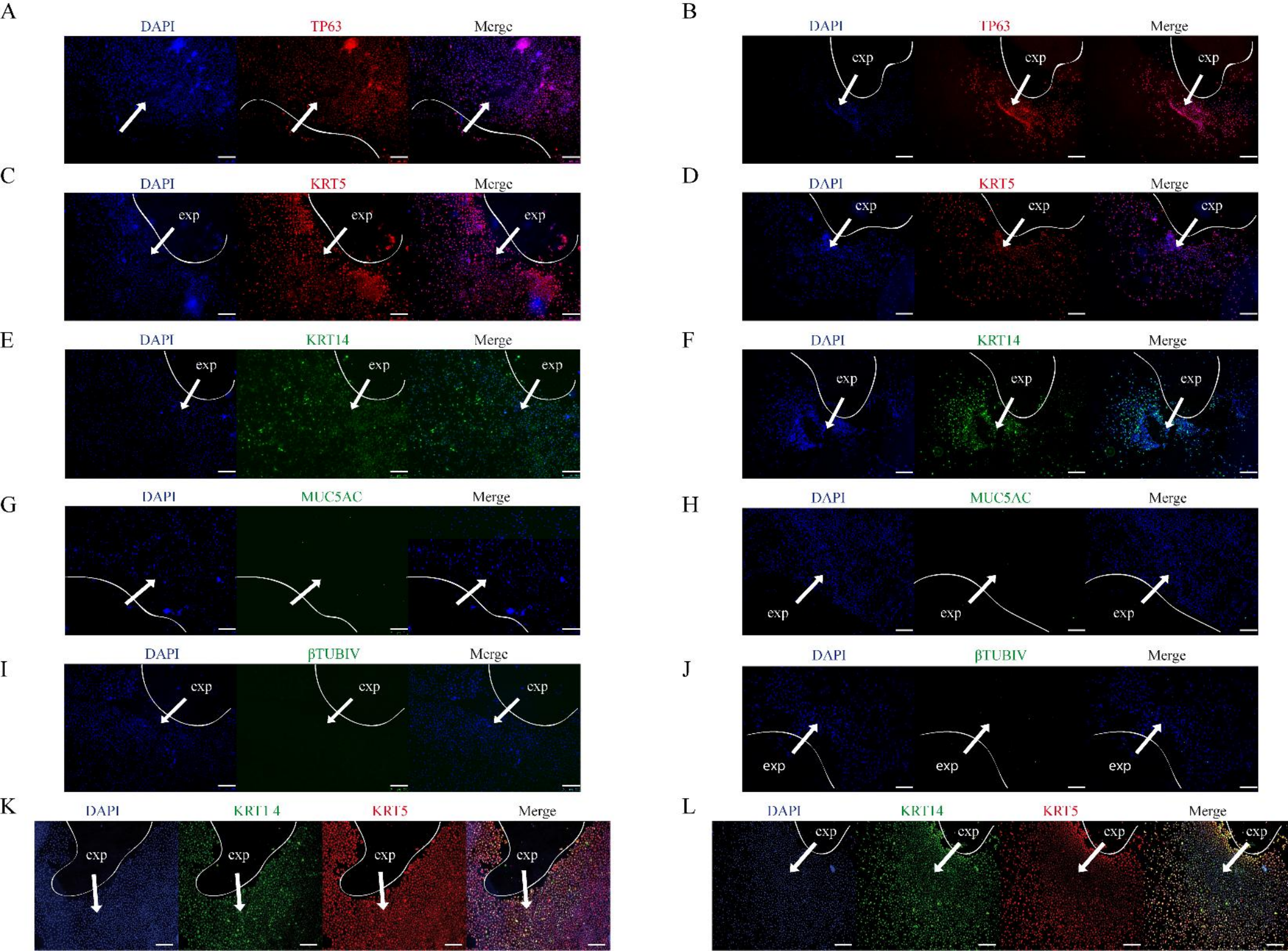
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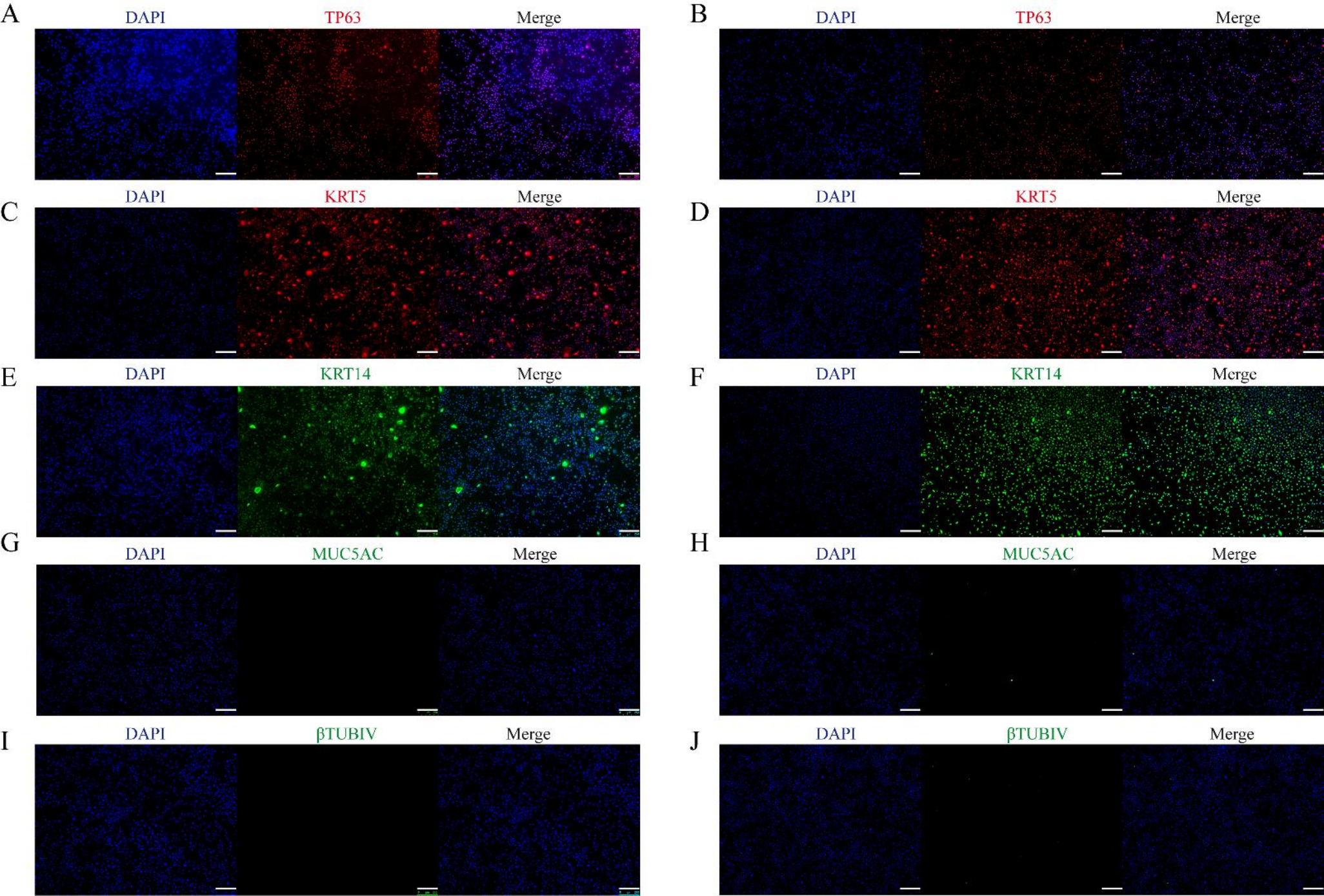
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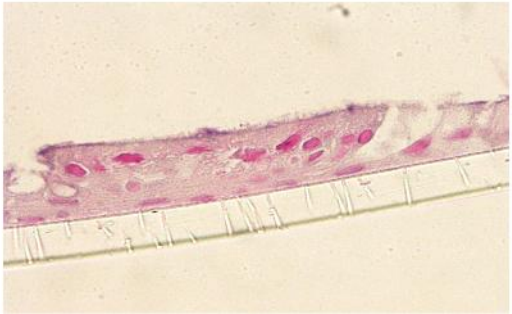

A
DAPI
TP63
Merge
B
DAPI
TP63
Merge
exp
C
DAPI
KRT5
Merge
exp
D
DAPI
KRT5
Merge
exp
E
DAPI
KRT14
Merge
exp
F
DAPI
KRT14
Merge
exp
G
DAPI
MUC5AC
Merge
H
DAPI
MUC5AC
Merge
exp
I
DAPI
βTUBIV
Merge
exp
J
DAPI
βTUBIV
Merge
exp
K
DAPI
KRT14
KRT5
Merge
exp
L
DAPI
KRT14
KRT5
Merge
exp


A
DAPI
TP63
Merge
B
DAPI
TP63
Merge
C
DAPI
KRT5
Merge
D
DAPI
KRT5
Merge
E
DAPI
KRT14
Merge
F
DAPI
KRT14
Merge
G
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DAPI
βTUBIV
Merge

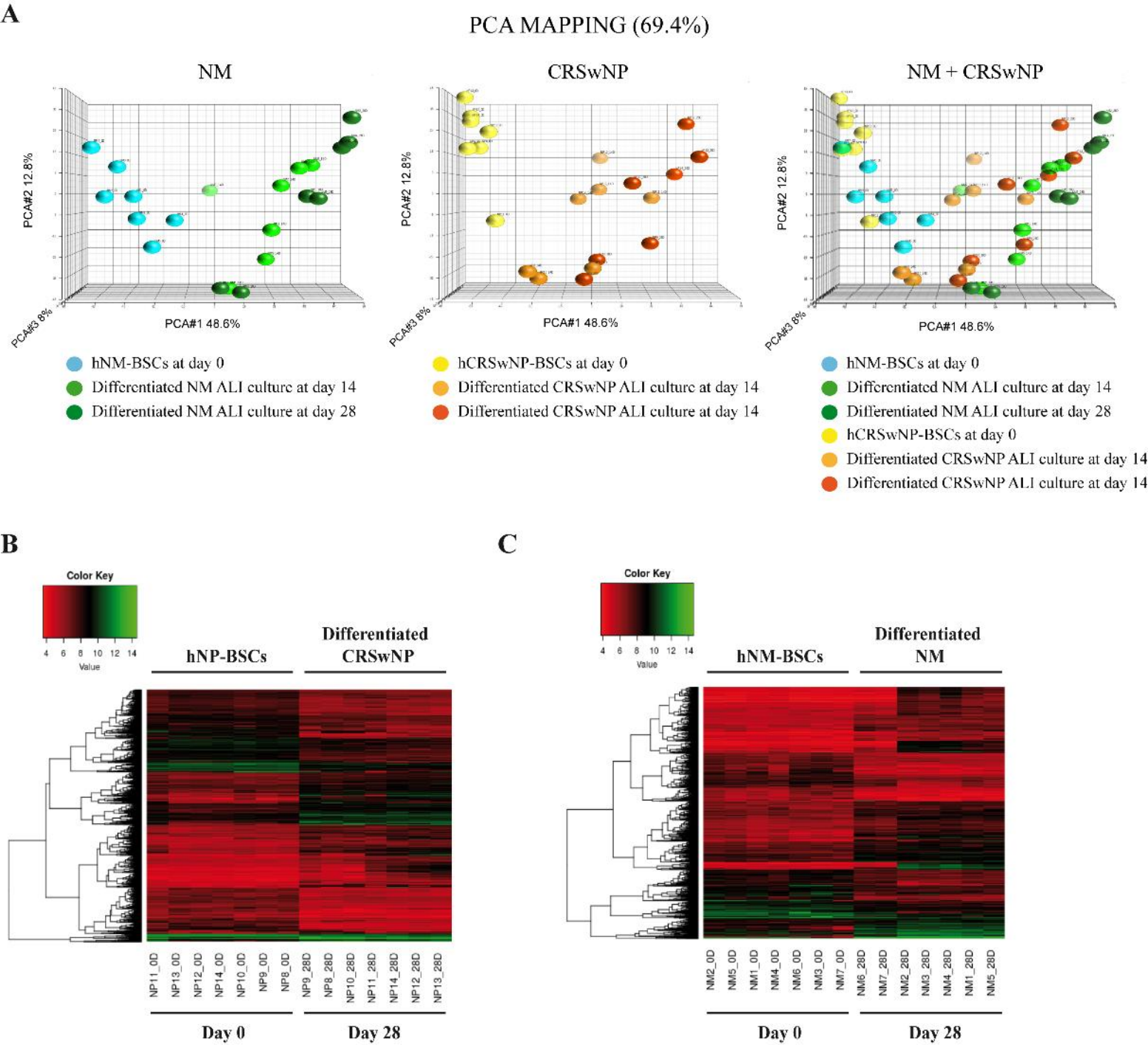
control-NM ALI

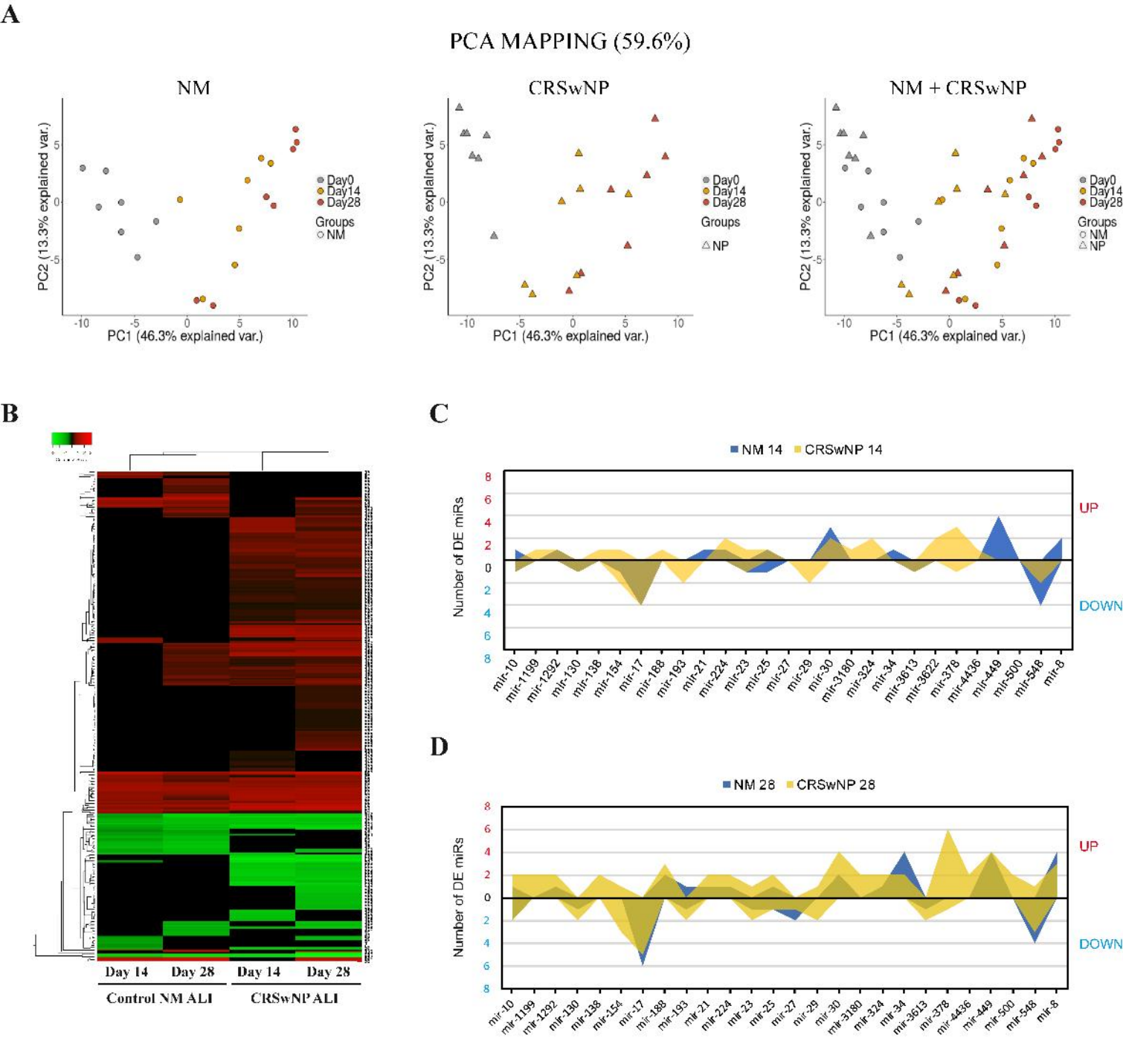
CRSwNP ALI

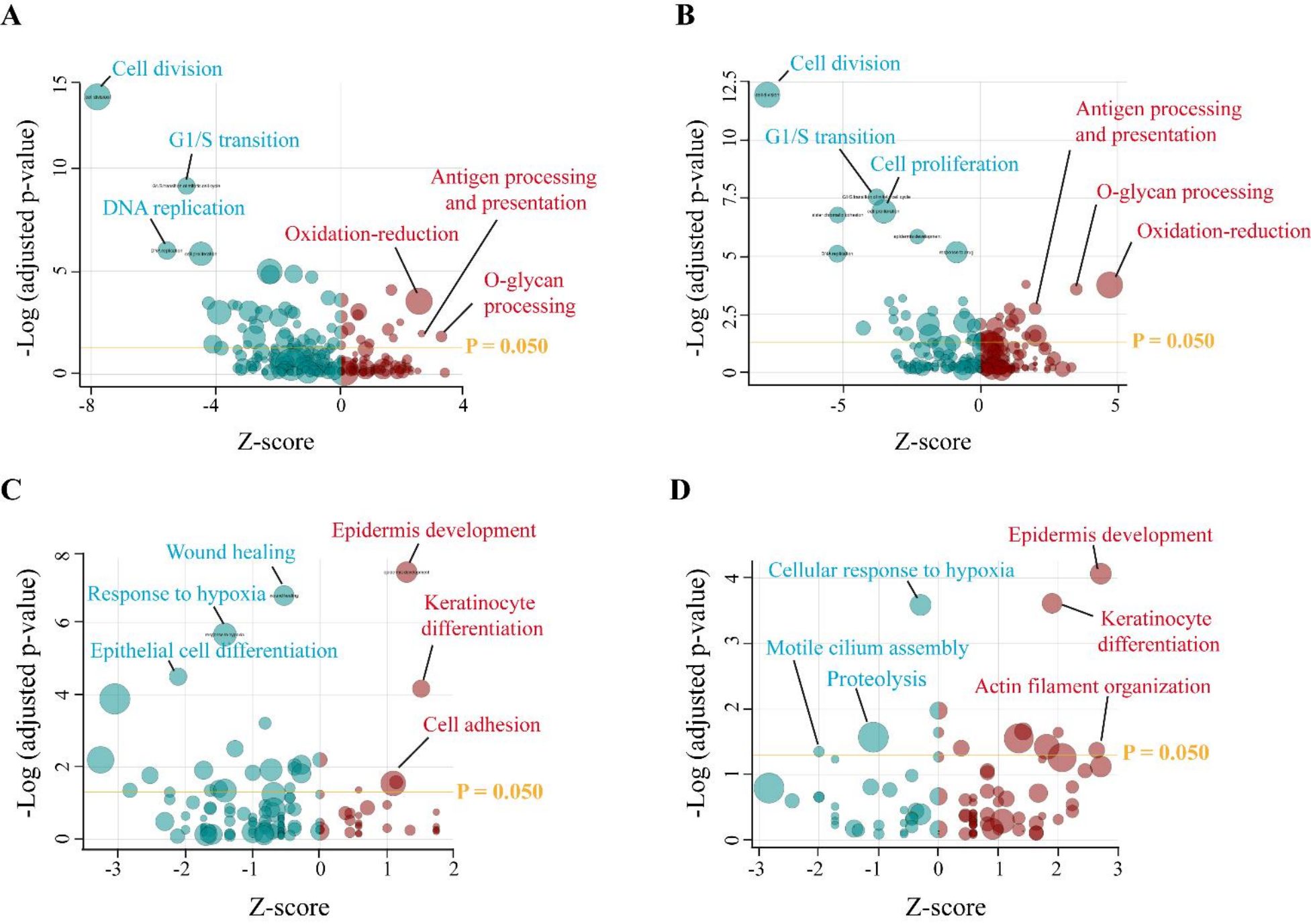
28D

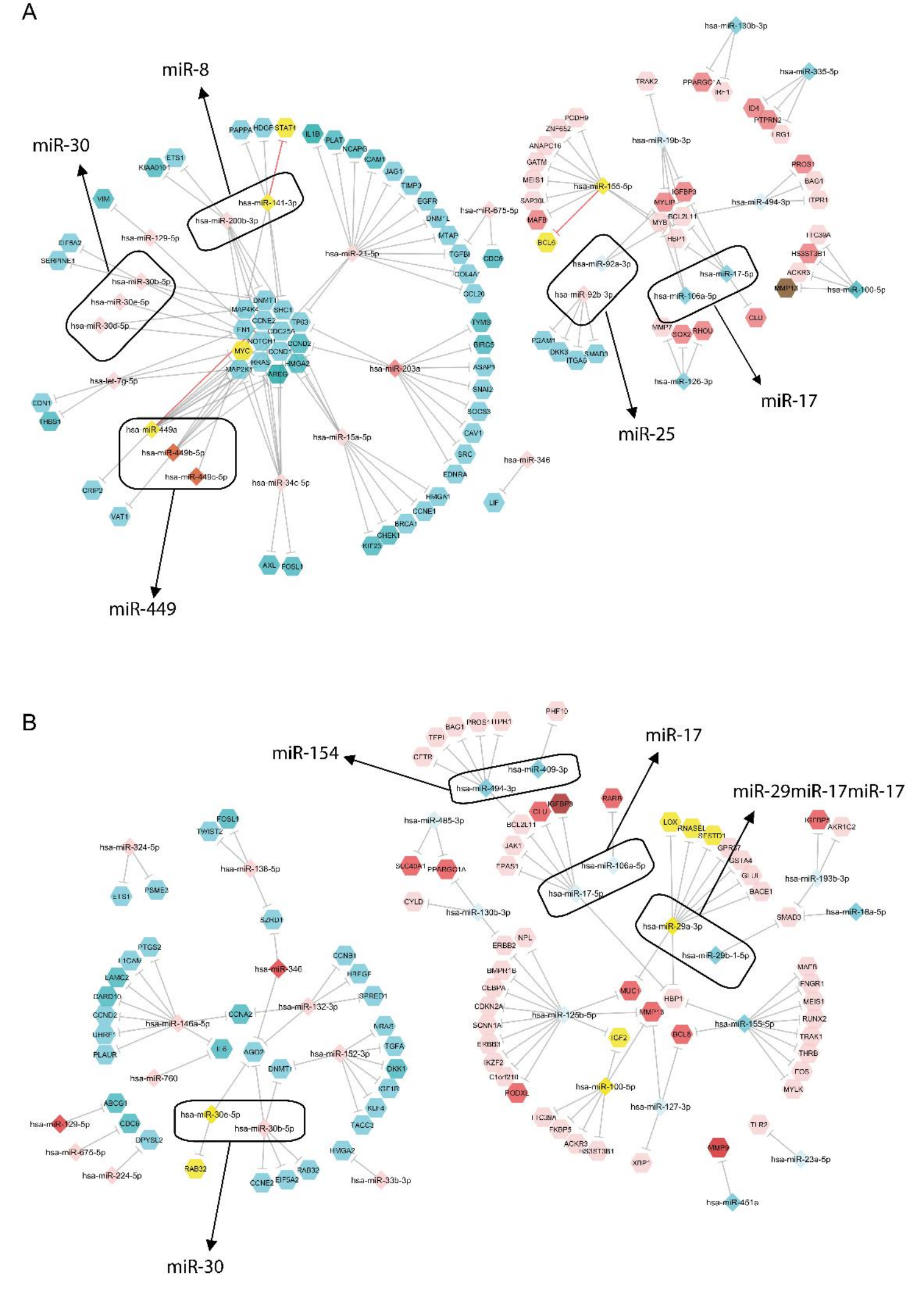





A
PCA MAPPING (69.4%)
NM
CRSwNP
NM + CRSwNP
PCA#2 12.8%
PCA#3 8%
PCA#1 48.6%
hNM-BSCs at day 0
Differentiated NM ALI culture at day 14
Differentiated NM ALI culture at day 28
hCRSwNP-BSCs at day 0
Differentiated CRSwNP ALI culture at day 14
Differentiated CRSwNP ALI culture at day 14
hNM-BSCs at day 0
Differentiated NM ALI culture at day 14
Differentiated NM ALI culture at day 28
hCRSwNP-BSCs at day 0
Differentiated CRSwNP ALI culture at day 14
Differentiated CRSwNP ALI culture at day 14
B
Color Key
4 6 8 10 12 14
Value
hNP-BSCs
Differentiated CRSwNP
NP11_0D
NP13_0D
NP12_0D
NP14_0D
NP10_0D
NP9_0D
NP8_0D
NP9_28D
NP8_28D
NP10_28D
NP11_28D
NP14_28D
NP12_28D
NP13_28D
Day 0
Day 28
C
Color Key
4 6 8 10 12 14
Value
hNM-BSCs
Differentiated NM
NM2_0D
NM5_0D
NM1_0D
NM4_0D
NM6_0D
NM3_0D
NM7_0D
NM6_28D
NM7_28D
NM2_28D
NM3_28D
NM4_28D
NM1_28D
NM5_28D
Day 0
Day 28


A
PCA MAPPING (59.6%)
NM
CRSwNP
NM + CRSwNP
PC2 (13.3% explained var.)
PC1 (46.3% explained var.)
Day0
Day14
Day28
Groups
NM
NP
B
Day 14
Day 28
Day 14
Day 28
Control NM ALI
CRSwNP ALI
C
NM 14
CRSwNP 14
Number of DE miRs
UP
DOWN
mir-10
mir-1199
mir-1292
mir-130
mir-138
mir-154
mir-17
mir-188
mir-193
mir-21
mir-224
mir-23
mir-25
mir-27
mir-29
mir-30
mir-3180
mir-324
mir-34
mir-3613
mir-3622
mir-378
mir-4436
mir-449
mir-500
mir-548
mir-8
D
NM 28
CRSwNP 28
Number of DE miRs
UP
DOWN


A
Cell division
G1/S transition
DNA replication
Antigen processing and presentation
Oxidation-reduction
O-glycan processing
P = 0.050
-Log (adjusted p-value)
Z-score
B
Cell division
G1/S transition
Cell proliferation
Antigen processing and presentation
O-glycan processing
Oxidation-reduction
P = 0.050
-Log (adjusted p-value)
Z-score
C
Epidermis development
Wound healing
Response to hypoxia
Keratinocyte differentiation
Epithelial cell differentiation
Cell adhesion
P = 0.050
-Log (adjusted p-value)
Z-score
D
Epidermis development
Cellular response to hypoxia
Keratinocyte differentiation
Motile cilium assembly
Proteolysis
Actin filament organization
P = 0.050
-Log (adjusted p-value)
Z-score


A
miR-8
miR-30
miR-449
miR-25
miR-17
hsa-miR-130b-3p
hsa-miR-335-5p
hsa-miR-19b-3p
hsa-miR-155-5p
hsa-miR-494-3p
hsa-miR-92a-3p
hsa-miR-92b-3p
hsa-miR-17-5p
hsa-miR-106a-5p
hsa-miR-126-3p
hsa-miR-100-5p
hsa-miR-141-3p
hsa-miR-200b-3p
hsa-miR-675-5p
hsa-miR-21-5p
hsa-miR-129-5p
hsa-miR-30b-5p
hsa-miR-30e-5p
hsa-miR-30d-5p
hsa-miR-203a
hsa-let-7g-5p
hsa-miR-449a
hsa-miR-449b-5p
hsa-miR-449c-5p
hsa-miR-34c-5p
hsa-miR-15a-5p
hsa-miR-346
B
miR-154
miR-17
miR-29miR-17miR-17
hsa-miR-409-3p
hsa-miR-494-3p
hsa-miR-485-3p
hsa-miR-106a-5p
hsa-miR-17-5p
hsa-miR-130b-3p
hsa-miR-29a-3p
hsa-miR-29b-1-5p
hsa-miR-193b-3p
hsa-miR-18a-5p
hsa-miR-324-5p
hsa-miR-138-5p
hsa-miR-346
hsa-miR-132-3p
hsa-miR-146a-5p
hsa-miR-152-3p
hsa-miR-760
hsa-miR-125b-5p
hsa-miR-155-5p
hsa-miR-100-5p
hsa-miR-127-3p
hsa-miR-129-5p
hsa-miR-675-5p
hsa-miR-224-5p
hsa-miR-30e-5p
hsa-miR-30b-5p
hsa-miR-33b-3p
hsa-miR-23a-5p
hsa-miR-451a

Supplemental Information

Supplemental Experimental Procedures

Study population and Ethics

Nasal polyp specimens (n=7) were obtained from patients undergoing endoscopic sinus surgery for CRSwNP. For inclusion, study participants had to have a clinical diagnosis of CRSwNP based on nasal symptoms, presence of nasal polyp by nasal endoscopy, and bilateral sinus opacification detection by computed tomography scan, following EPOS criteria (Fokkens et al., 2012). All included patients had a washout period of 2 weeks for intranasal (INS) and 4 weeks for oral (OCS) corticosteroid treatment. They did not receive previous biological treatments. Patients with bronchial asthma, aspirin intolerance or cystic fibrosis were excluded from the study (Table S25).

Control nasal mucosa specimens (n=7) were obtained from inferior turbinates of healthy subjects undergoing septoplasty or partial turbinectomy. All subjects had negative skin prick test to common allergens, without bronchial asthma or aspirin intolerance (Table S25).

All patients signed informed consent to participate in the study, which was approved by our institution's Scientific and Ethics Committee: Ethics Committee for Clinical Research, Hospital Clínic, Universitat de Barcelona; date on which approval was given: 12/04/2012; document number of approval: 2012\7466.

Fresh tissue specimens were processed for different purposes: epithelial cell isolation, culture and differentiation in air-liquid interface cultures (ALI), immunofluorescence technique (IF) for histological/cellular characterization; microarrays, and quantitative real time polymerase chain reaction (qRT-PCR).

Tissue handling and epithelial BSC isolation from the explant culture

Tissue specimens handling and primary cultures of human adult BSCs were obtained through the explant method as previously outlined (de Borja et al., 2014).

Tissue specimens were surgically removed and immediately transported to laboratory in sterile growth medium composed of BEBM™ (Bronchial Epithelial Cell Basal Medium; Clonetics©, Lonza Group Ltd, Switzerland) supplemented with Epidermal Growth Factor (25ng/ml), Hydrocortisone (0.5µg/ml), Epinephrine (0.5µg/ml), Transferrin (10µg/ml), Insulin (5µg/ml), Triiodothyronine (6.5µg/ml), all-trans retinoic acid (50nM), Bovine Pituitary Extract (52µg/ml), Gentamicin (30µg/ml), and Amphotericin B (15ng/ml), all included in the SingleQuots™ Kit purchased by Clonetics© (Lonza), with the exception of human recombinant epidermal growth factor and all-trans retinoic acid that were purchased by Sigma-Aldrich Co (St. Louis, MO, USA).

Primary cultures of human CRSwNP and control nasal epithelial cells were obtained through the explant method as previously outlined (de Borja et al., 2014). Briefly, tissue explants were carefully dissected away from the mucosal surface of tissue specimens by using sterile surgical material. Size of explants obtained was of approximately 20-30 mm^2. Small explants were washed three times with fresh, sterile media, in order to remove blood and mucous when was present. Then, tissue explants were plated on 6-well plates coated with rat tail collagen type I (Sigma-Aldrich), always orientated with the epithelial layer to be in contact with the collagen-coated culture plates. A single drop of growth medium was added directly on to the tissue to allow the tissue to adhere to the plate. Once the tissue was adherent, more media was added

slowly (in order not to dislodge the tissue). Explant culture was performed in a 5% CO_2 humidified atmosphere at 37ºC, with the culture media being changed daily. Epithelial cell growth from explants usually started from day 2 to day 3. When 70-80% of confluence was reached, cells were trypsinized using the Subculture Reagent Pack (Lonza). These cells were then cultured in 6-well plates coated with collagen type I using growth media. The culture was performed in a 5% CO_2-humidified atmosphere at 37°C and the media was changed every 48h during the submerged culture for approximately 7 days.

To demonstrate the purity of epithelial BSCs obtained from both CRSwNP mucosa (CRSwNP-BSCs, n=7) and control nasal mucosa (NM-BSCs, n=7), tissue explants were also cultured in chamber slides and cell phenotype analysis was assessed by immunofluorescence before (passage 0) and after (passage 1) trypsinization. Briefly, cells were fixed in 4% paraformaldehyde for 15 minutes, and processed for immunofluorescent detection of universal basal (TP63, KRT5, KRT14), goblet (MUC5AC) and ciliated (β-Tub IV) cell markers (stained BSCs at passage 0, Figure S1;co-expression of both KRT14 and KRT5 in BSCs at passage 0, Figure S1, K and L; and stained BSCs at passage 1, Figure S2).

Mucociliary differentiation of CRSwNP-BSCs and control NM-BSCs in the Air-Liquid Interface (ALI) culture system

After reaching 80-90% of confluence in the submerged culture, epithelial cells were subcultured and seeded at a density of $5x10^4$ cells/cm^2 onto 0.33 cm^2 inserts with polyethylene terephthalate (PET) transparent membranes for growth of attachment-dependent cells without matrix (0.4µm pore size, 24-well, Millipore, Billerica, MA, USA) and incubated at 37°C supplemented with 5% CO_2. Cells were submerged in differentiation media composed of 50% DMEM (Lonza) in BEBM™ supplemented with Epidermal Growth Factor (0.5ng/ml), Hydrocortisone (0.5µg/ml), Epinephrine (0.5µg/ml), Transferrin (10µg/ml), Insulin (5µg/ml), Triiodothyronine (6.5µg/ml), all-trans retinoic acid (50nM), Bovine Pituitary Extract (52µg/ml), Gentamicin (30µg/ml), and Amphotericin B (15ng/ml) for the first 7 days.

Cells were then cultured for differentiation for a further 28 days with the apical surface exposed to air (ALI cultures). Throughout the culture period cells were maintained at 37°C in a 5% CO_2 incubator with media changes every 48 hours.

Histological characterization by immunofluorescence

Mucociliary differentiation was evaluated by immunofluorescence at days 0 and 28 of ALI culture, corresponding to an initial step (day 0, monolayer of undifferentiated cells) and final step (day 28, mature pseudostratified differentiated epithelium). To characterize the mucociliary differentiation of CRSwNP-BSCs (n=7) and control NM-BSCs (n=7) in ALI culture, cells were fixed at different days (0 and 28) with 4% paraformaldehyde during 15 min at room temperature. For immunofluorescent detection, the cells were permeabilized with 0.2% Triton X-100 (Sigma-Aldrich Co.) in phosphate buffered saline, pH 7.4 (PBS, Sigma-Aldrich Co.), at room temperature, and then blocked with 6% goat serum (Sigma-Aldrich Co.) for 60 minutes to prevent unspecific binding. Incubation overnight at 4ºC with primary antibodies, including rabbit monoclonal anti-TP63 (Clone EPR5701, ab124762, Abcam) and mouse monoclonal anti-cytokeratins 5 and 14 (PA5-29670 and MA1-06323, respectively, Sigma) for basal stem/progenitors cells, anti-MUC5AC (Clone 45M1, MS-145, Thermo Fisher Scientific, Waltham, MA, USA) for goblet cells and mouse monoclonal anti-β-Tubulin IV (clone ONS.1A6, T7941, Sigma- Aldrich) for ciliated cells.Negative controls were performed by omitting the primary antibody and using a negative control serum of the same isotype. Alexa Fluor® 488 Goat Anti-Mouse IgG (H+L, green channel), Alexa Fluor® 594 Goat Anti-Mouse IgG (H+L, red channel), and Alexa Fluor® 594 Donkey Anti-rabbit IgG

(H+L, red channel) were used as the secondary antibodies (Invitrogen, Life Technologies Ltd, UK). The samples were counterstained with DAPI to identify cell nuclei (blue channel), and the slides were cover-slipped with ProLong® Gold Antifade Reagent (Invitrogen, Life Technologies Ltd, UK). Finally, slides were examined with the Leica DMI6000 B inverted microscope (Leica Microsystems, Germany).

Total and positive cells were counted in three wells (5 fields from different areas of each well at 400x magnification) from different CRSwNP (n= 7) and control-NM (NM, n =7) cultures at the days 0 and 28 of ALI. The results were subsequently averaged and % from total was calculated for each marker.

RNA extraction

Total RNA, including small RNAs (e.g. microRNAs), was isolated from cells using the miRNeasy Mini Kit from Qiagen (Valencia, CA, USA). Briefly, cells were lysed with Qiazollysis buffer (Qiagen), with cells from three inserts pooled for each time point, followed by passage through a Qiashredder column (Qiagen). Total RNA was extracted via RNeasy mini spin columns. All incubation and washing steps were performed following the manufacturer's instructions.

RNA integrity was determined by assessing an aliquot of each RNA sample on an Agilent Bioanalyzer (Agilent Technologies, Palo Alto, CA, USA). Thus, only those RNA samples with a RNA Integrity Number greater than 8 (RIN > 8) were used in later experiments. Total RNA concentration was determined using a NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA). The purified total RNA was stored at -80ºC until all time points were collected.

Gene and miRexpression microarrays

Total RNA (100ng for mRNA, 300ng for miR) was processed for global transcriptional analysis using theHuman Genome U219 (gene expression) and miRNA 4.1 Array Plates (miR expression), following the manufacturer's directions (both microarrays were purchased by Affymetrix,Santa Clara, CA, USA).The Human Genome U219 Array Plate is comprised of more than 530,000 probes covering more than 36,000 transcripts and variants, which represent more than 20,000 genes mapped through UniGene or via RefSeq annotation. On the other hand, miRNA 4.1 Array is designed to interrogate all mature miRNA sequences in miRBase Release 21, covering 2,578 mature miRs. The entire data set of the investigation has been included at the National Center for Biotechnology Information Gene ExpressionOmnibus (NCBI GEO; http://www.ncbi.nlm.nih.gov/projects/geo/index.cgi), accession number GSE107624.

Microarray data analysis

Microarray data (Affymetrix.celfiles) were processed for raw data quality control analysis by using Robust Multichip Analysis (RMA) algorithm, which perform background correction, probe-level normalization, and probe-set summary. Principal Components Analysis (PCA) statistical procedure was also used for exploratory data analysis (grade of separation between sample groups or homogeneity within each group, see Figure S3). PCA figures were created with Partek® Genomics Suite software, version 7.0, 2018 (Partek Inc., St. Louis, MO, USA).

After normality test exploration, statistically significant mRNAs and miRs were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/), followed by Benjamini-Hochberg multiple correction to control the false discovery rate (FDR) with a threshold of 1% ($q < 0.01$). Finally, for data analysis, we filtered out the differentially expressed mRNAs/miRs from those that were statistically significant, by using Log_2 Ratio (LR) expression greater (upregulated) or lower (downregulated) than 1 for mRNAs ($|LR|>1$, equivalent to fold change > 2 and

fold change < 0.5) and 0.6 for miRs (|LR|>0.6, equivalent to fold change > 1.5 and fold change < 0.7).

We also created heatmaps and Venn diagrams in order to show contrast between ALI groups and to determine DE genes that were over or under expressed in different conditions and time points, respectively. While heatmaps were created by using Partek® Genomics Suite software, version 7.0, 2018 (Partek Inc., St. Louis, MO, USA), the Venn diagrams were created thanks to Venny 2.1 (Oliveros, J.C. 2007-2015,*Venny. An interactive tool for comparing lists with Venn's diagrams*. http://bioinfogp.cnb.csic.es/tools/venny/index.html).

Functional enrichment analysis was done using Database for Annotation, Visualization and Integrated Discovery (DAVID, version 6.8, recently updated in Oct. 2016, https://david.ncifcrf.gov/home.jsp) using a False Discovery Rate (FDR) threshold of 5% (q<0.05). DAVID provides many information extracted from several functional annotation tools, but we only focused in the following main categories: Gene Ontology (GO), particularly, we attended to biological processes related terms (GO_BP_Direct), and KEGG (Kyoto Encyclopedia of Genes and Genomes) pathways database. GO terms and pathways were ranked based on their Fisher Exact probability adjusted-value (FDR=5%, q<0.05) from the enrichment analysis to identify which processes and pathways showed significant overrepresentation.

In addition, enriched Gene Ontology and KEGG pathways terms were visualized using R package GOplot (Walter et al. 2015). Thanks to GOplot, we generated GOBubble figures, where different enriched terms are represented by circles (area of the displayed circles is proportional to the number of genes assigned to each term) and they are separated by their statistical significance (adjusted *P*-values) and Z-score value, which represents the overall up/down regulated genes in each term (Z-score = [up-down] / √number of involved genes in term; up and down are the number of assigned genes upregulated [LR>1] in the data or downregulated [LR<-1], respectively). Thus, GO and KEGG terms were then divided in upregulated (Z-score >0) or downregulated (Z-score <0).

Additionally, we also created GOChord figures, which display the relationship between enriched terms and a list of their related genes, considering the fold change (FC) expression of the genes (Log_2FC). GOChrod figures were produced with GOplot tool, although GOChrod plotting function is based on the *Circos* plots designed by Martin Krzywinski (http://mkweb.bcgsc.ca/). In addition, we also characterized the expression of different genes of interest, related to epithelial cell phenotypes (basal, goblet and ciliated cells) or functions (host defense, epithelial repair, adaptive immune response), in both longitudinal (days 14 and 28 vs day 0) and cross-sectional (CRSwNPvs NM ALI at days 0, 14 and 28) analysis.

Moreover, we matched validated and predicted interaction pairs mRNA/miRNAby using miRTarBase_v7 (for experimentally validated interactions, Chou et al., 2018) and TargetScan_v7.2 (for predicted interactions, Agarwal et al. 2015) databases. We used stringent parameters to determine mRNA/miRNA correlation interactions (Spearman |rho| > 0.75 and q < 0.01), being non-correlated interactions were filtered out. Pairs only contained up or downregulated mRNAsor miRNAs of our study, the rest were filtered out. We focused on opposite differential expression between mRNAs and miRNAs. Finally, in order to better visualize these interactions, we generated miR-mRNA networks in Cytoscape.

Real Time PCR

To verify and validate data obtained from microarrays analysis, quantitative real-time PCR (q-PCR) was performed to quantify changes produced on mRNA expression of 15 key genes (Table S26) during differentiation of CRSwNP (n=7) and NM (n=7) ALI cultures. Some of selected genes were relative to basal cell phenotype (TP63, KRT5, KRT14, ITGA6, PDPN), while other markers were representative of

goblet/secretory cells (SCGB1A1, AGR2, MUC5AC, MUC16 and MUC5B) or related to cilia formation and/or ciliated cells (MCIDAS, CCNO, MYB, RFX3, FOXJ1).

In order to perform mRNAq-PCR technique, RNA samples were reverse transcribed to cDNA using the High Capacity cDNA RT kit (Applied Biosystems, Rockville, MD, USA). Quantitative amplification of cDNA was performed using the SYBR®*Premix Ex Taq*™ *(*TliRNaseH Plus) kit from Takara Bio Inc. (Kusatsu-shi, Japan) and oligo primers purchased by Metabion International AG (Munich, Germany). Primer sequences details can be found in supplementary data (Table S26). Gene expression levels were normalized by geometric mean of multiple reference genes (GAPDH, b-act and HSP90AA1). All real-time PCR assays were performed on a ViiA™ 7 Real-Time PCR System (Thermo Fisher Scientific). Relative gene expression was determined by comparative CT method ($2^{-\Delta\Delta Ct}$ method, Schmittgen T.D. and Livak K.J. 2008).

Statistical Analysis of Real Time PCR results

The statistical analysis of real time PCR results was performed using Graph Pad Prism 6. The nonparametric Wilcoxon Signed-Ranks Test was used for paired comparisons (when comparing days 14 and 28 versus day 0, longitudinal analysis), and Mann-Whitney U test was used for between-group comparisons (when comparing CRSwNPvs control NM at different days, cross-sectional analysis).

Supplemental References

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Supplemental Data Items

Figure S1

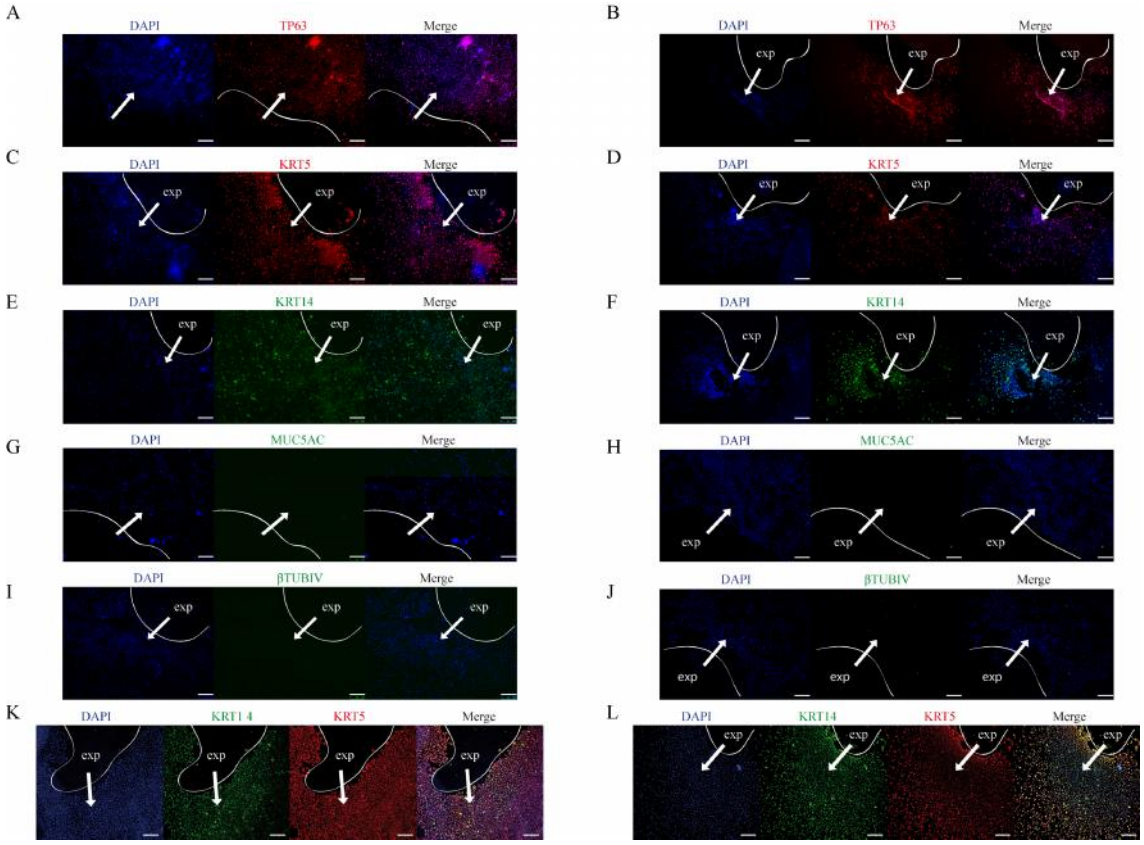


Figure S1. Characterization by immunofluorescence of epithelial basal stem/progenitor cells (BSCs) isolated from mucosa explants excised from control subjects (NM, n=5) or patients with chronic rhinosinusitiswith nasal polyps (CRSwNP, n=5). Pictures are showing BSCs migrated from NM (left column) or CRSwNP (right column) tissue explants to collagen surface of the cell culture chambers (passage 0). BSCs are positively stained for basal stem/progenitor cell markers, such as tumor protein 63 (A-B, TP63, in red), cytokeratins 5 (C-D, KRT5, in red) and cytokeratin 14 (E-F, KRT14, in green); while they are negatively stained for goblet/secretory (G-H, mucin 5AC, MUC5AC, in green) and ciliated (I-J, β-Tub IV in green) cell markers in an immunofluorescence assay. Co-staining for KTR5 and KRT14 in both control NM and CRSwNPare showed in panels K-L, respectively. Cell nuclei are stained by DAPI (blue). Tissue explant location (Exp, in white) and direction of cell migration (arrows, in white) are also showed. Scale bar (white) for all panels equivalent to 250μm, except for panels K-L where is equivalent to 100μm.

Figure S2

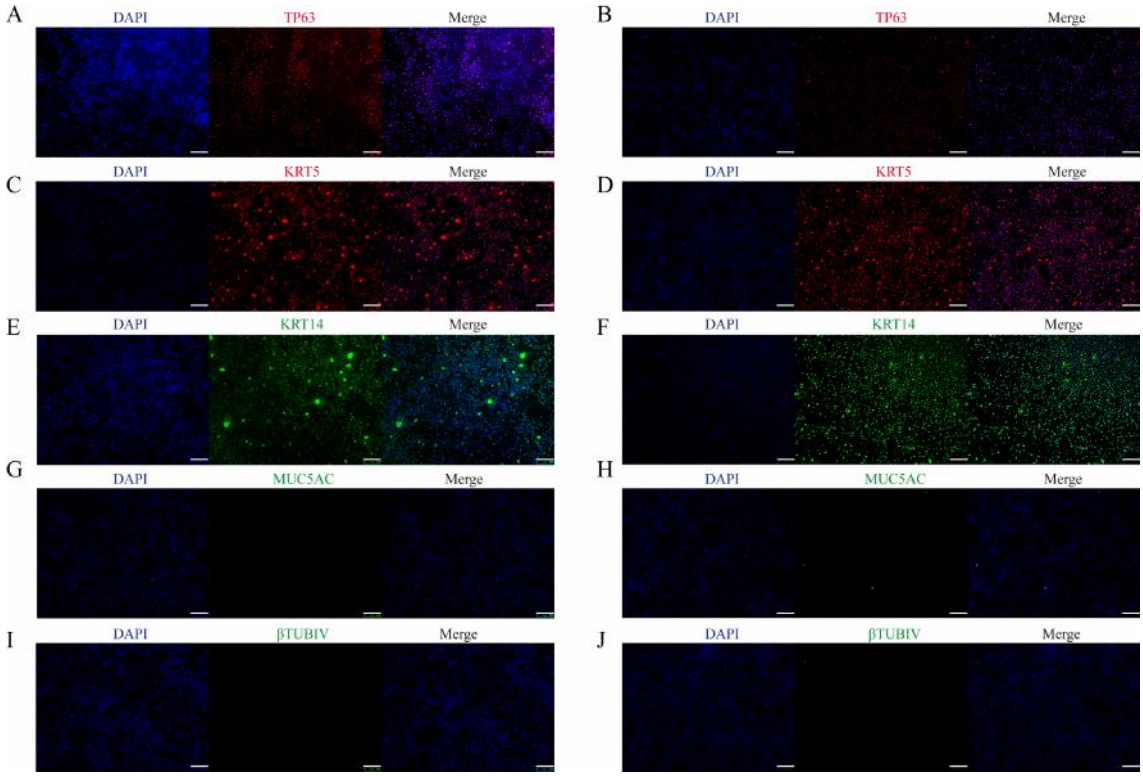


Figure S2. Characterization by immunofluorescence of subcultured epithelial basal stem/progenitor cells (BSCs) isolated from control subjects (NM, n=5) and patients with chronic rhinosinusitis with nasal polyps (CRSwNP, n=5) at passage 1. Pictures are showing BSCs, extracted from both control NM (left column) and CRSwNP (right column), after onetrypsinization (passage 1). BSCs are positively stained for basal stem/progenitor cell markers, such as tumor protein 63 (A-B, TP63, in red), cytokeratins 5 (C-D, KRT5, in red) and cytokeratin 14 (E-F, KRT14, in green); while they are negatively stained for goblet/secretory (G-H, mucin 5AC, MUC5AC, in green) and ciliated (I-J, β-Tub IV in green) cell markers in an immunofluorescence assay. Cell nuclei are stained by DAPI (blue). Scale bar (white) for all panels equivalent to 250µm.

Figure S3

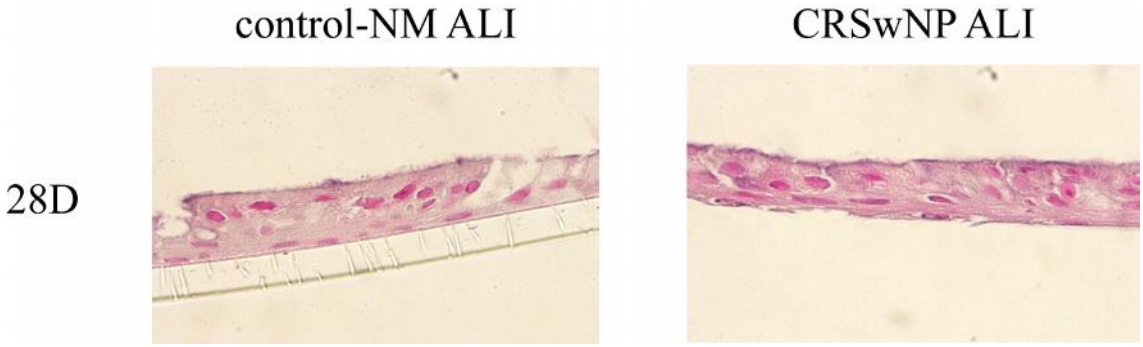


Figure S3. Representative immunohistochemical images of fully differentiated (day 28) cultures from both control-NM and CRSwNP. Pictures are showing control-NM and CRSwNP ALI at day 28 stained with hematoxilin-eosin (final magnification x1000, oil-immersion).

Figure S4

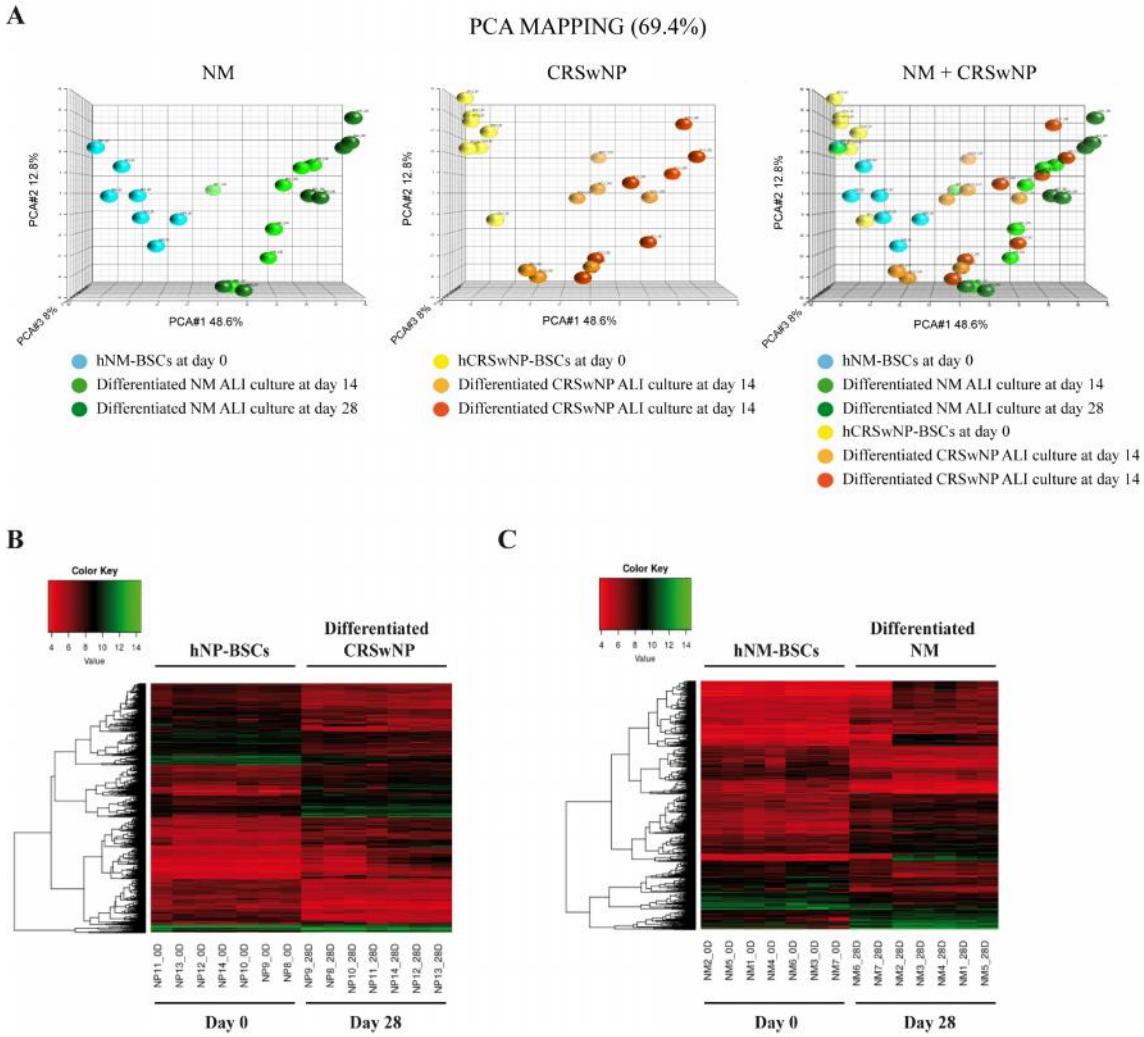


Figure S4. Visualization of the principal component analysis (PCA)and heatmaps relatives to global mRNA expression analysis performed by microarrays in control nasal mucosa (NM, n=7) and chronic rhinosinusitis with nasal polyps (CRSwNP, n=7) air-liquid interface (ALI) cultures. A) PCA boxes are showing data from control NM and CRSwNP ALI cultures at days 0, when cultures are monolayers of basal stem/progenitor cells (BSCs), and at days 14 and 28, when differentiated airway epithelia are reconstituted in ALI cultures. Input database: 49.386 probes sets.B-C) Heatmaps with longitudinal DE mRNAs ($q<0.05$, $|Log_2Ratio| >1$) from CRSwNP and NM ALI.Data showed are relative to cultures at day 0, composed of monolayer of basal stem/progenitor cells from CRSwNP (CRSwNP-BSCs) or NM (hNM-BSCs), and at day 28, corresponding to fully differentiated ALI cultures. Heatmaps were generated respecting the sample clustering as much as possible.

Figure S5

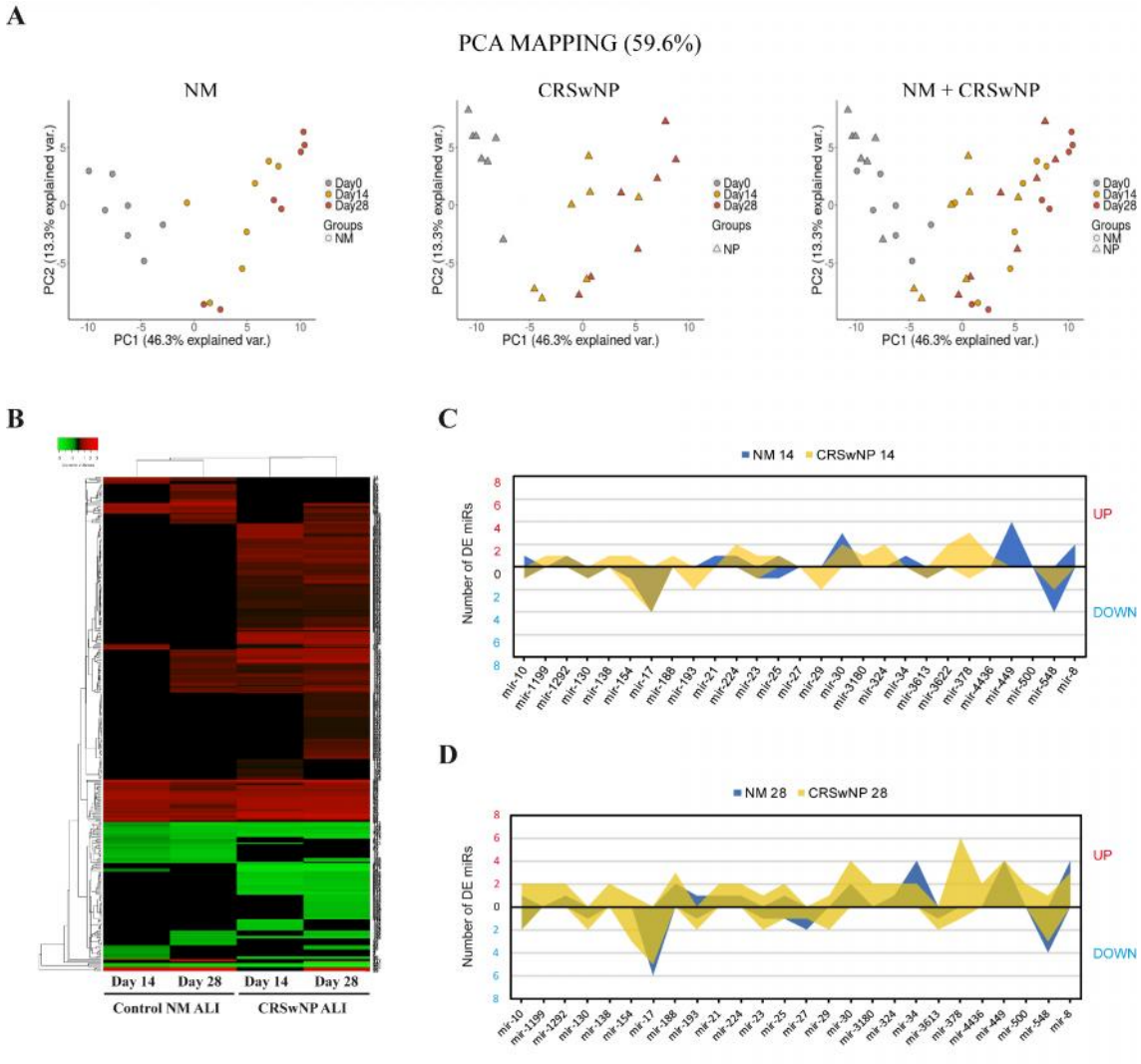


Figure S5. Visualization of the principal component analysis (PCA), heatmaps and miR families, relatives to global microRNA expression analysis performed by microarrays in control nasal mucosa (NM, n=7) and chronic rhinosinusitis withnasal polyps (CRSwNP, n=7) air-liquid interface (ALI) cultures. A) PCA boxes are showing miRdata from control NM and CRSwNP ALI cultures at days 0, when cultures are monolayers of basal stem/progenitor cells (BSCs), and at days 14 and 28, when differentiated airway epithelia are reconstituted in ALI cultures. Input database: 2,578 mature miRNAprobes. B)Heatmap with longitudinal DE miRNAs ($q<0.01$, $|\ Log_2Ratio\ | > 0.6$) from CRSwNP and control NM ALI. Data showed are relative to cultures at day 0. Heatmaps were generated respecting the sample clustering as much as possible. C-D) Graphs showing the number of miRs of the main mir families that were DE ($q < 0.01$) and upregulated/downregulated ($|LR| > 0.6$) in control NM (in blue) and CRSwNP (in yellow) after 14 (C) and 28 (D) days of differentiation in ALI, compared to day 0.

Figure S6

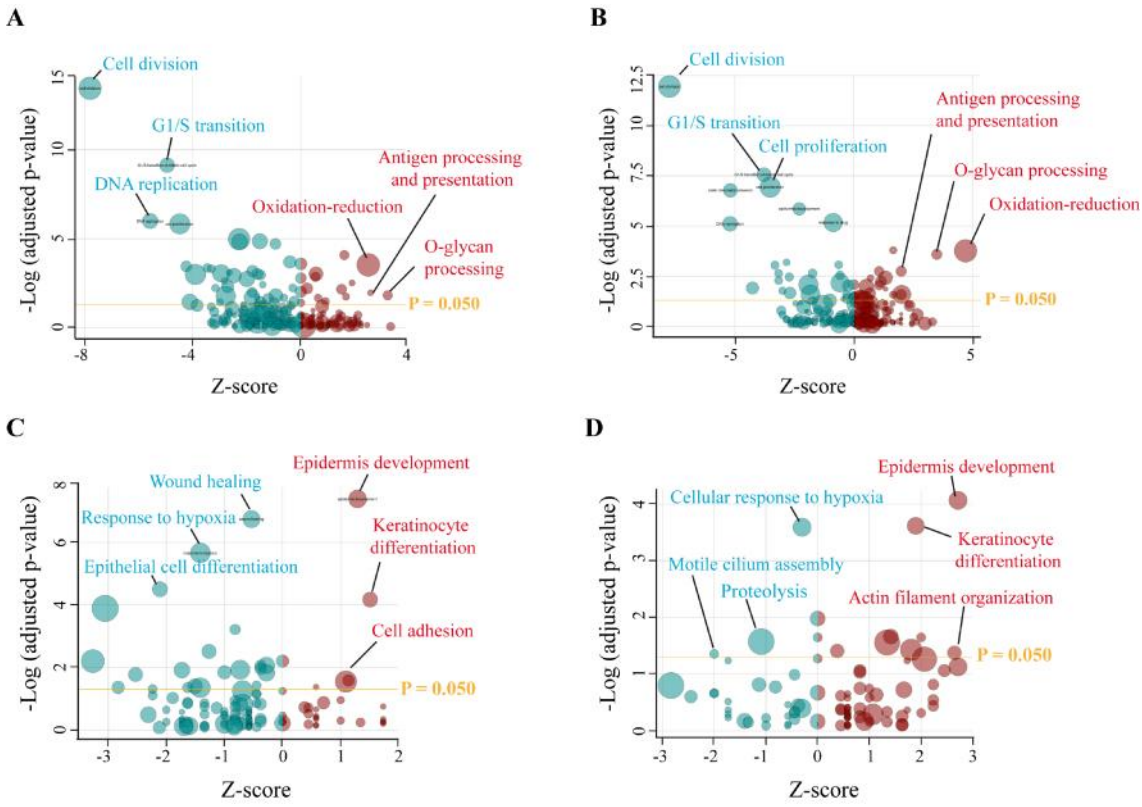


Figure S6. GOBubbles displaying gene ontology biological processes (GO_BP_Direct) terms enriched in control nasal nucosa (NM, n=7) and chronic rhinosinusitis withnasal polyp (CRSwNP, n=7) air-liquid interface (ALI) cultures at day 14compared to day 0 (A and B, respectively),andin CRSwNP compared to NM at days 0 (C) and 14 (D).GO_BP terms are displayed by bubbles (area is proportional to the number of genes assigned to each term), separated by on one hand by their statistical significance (-Log adjusted P-values, Y-axis) and, on the other, by using their z-score values (X-axis) in upregulated (in red, z-score >0) or downregulated (in blue, z-score <0) terms. The names of GO_BP are indicating most significant up or downregulated terms.

Figure S7

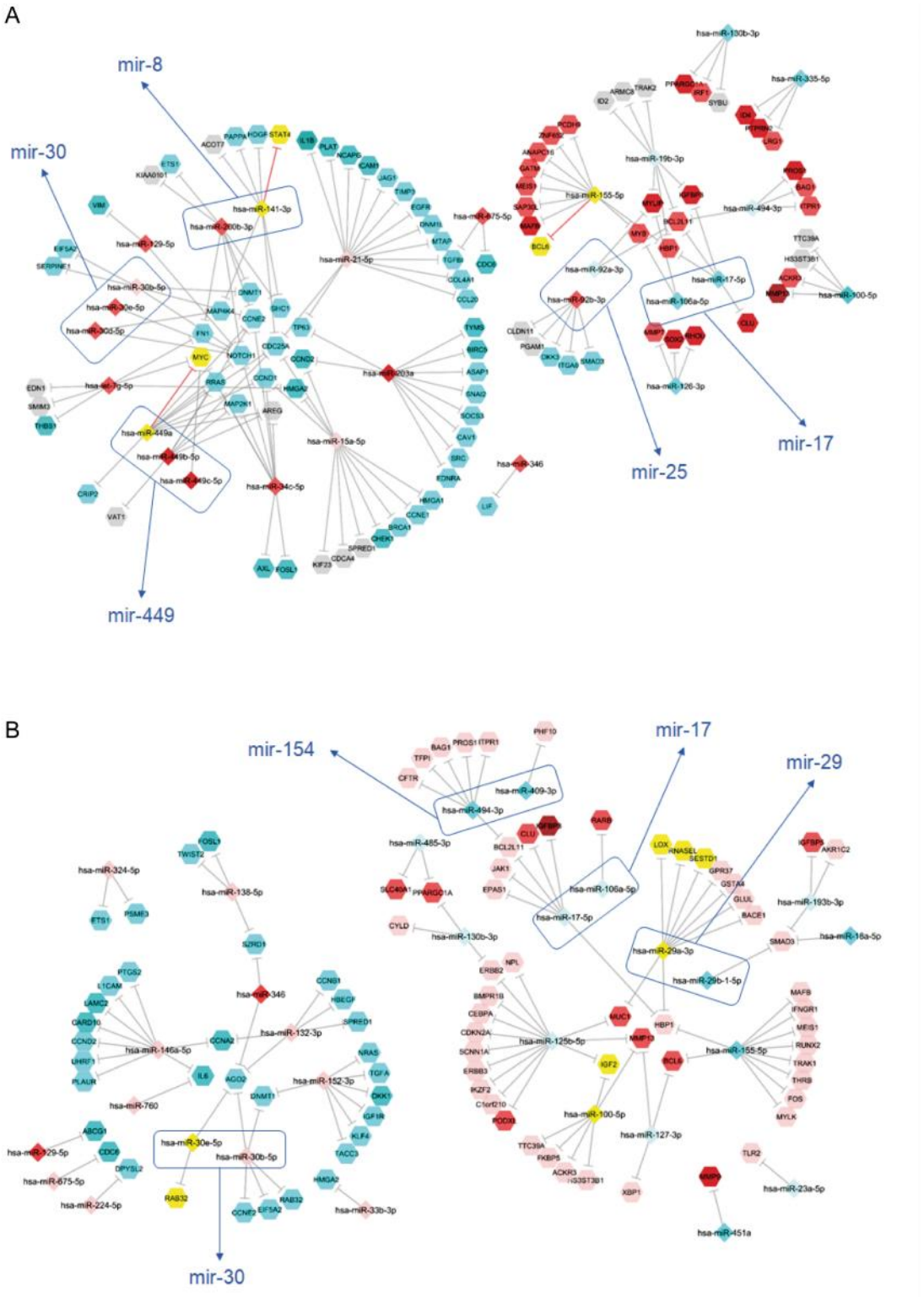


Figure S7. miR-mRNA networks in control nasal mucosa (NM, n=7) and chronic rhinosinusitis withnasal polyp (CRSwNP, n=7) at day 14 of the air-liquid interface (ALI) culture. Networks showing differentially expressed (q < 0.01) miRs (diamonds) associated with their potential mRNA targets (hexagons) in control NM (A) andCRSwNP (B) after 14 days of differentiation.Upregulated and downregulatedmiRs/mRNAs are showed in red or in blue, respectively,with color intensity depending on Log_2 Ratio expression. Those pairs of miRs and mRNA targets that were significantly correlated (P < 0.01, Spearman ρ > 0.75) are highlighted in yellow.

Tables

TABLE S1. Differentially expressed mRNAs in control NM air-liquid interface culture after 14 days of differentiation compared to day 0 (monolayer of hNM-BSCs).*

UPREGULATED mRNAs (802)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log2Ratio**	**Fold Change**
11720917_a_at	BPIFB1	*BPI fold containing family B member 1*	6.8505	115.4006
11719818_at	PIP	*prolactin induced protein*	5.7014	52.0353
11723642_a_at	BPIFA1	*BPI fold containing family A member 1*	5.3468	40.6963
11758196_s_at	IGFBP5	*insulin like growth factor binding protein 5*	5.2189	37.2432
11724085_at	DAPL1	*death associated protein like 1*	5.0396	32.8898
11730779_at	ADH1C	*Alcohol Dehydrogenase 1C (Class I), Gamma Polypeptide*	4.7924	27.7114
11743003_a_at	CYP4B1	*cytochrome P450 family 4 subfamily B member 1*	4.5999	24.2501
11722994_s_at	ADH1A	*Alcohol Dehydrogenase 1A (Class I), Alpha Polypeptide*	4.5497	23.4200
11736917_at	LYPD2	*LY6/PLAUR domain containing 2*	4.5166	22.8895
11758272_at	SLC34A2	*solute carrier family 34 member 2*	4.3512	20.4103
11724692_a_at	CAPN13	*calpain 13*	4.3501	20.3946
11744484_s_at	HLA-DRA	*major histocompatibility complex, class II, DR alpha*	4.3080	19.8083
11729297_at	MMP13	*matrix metallopeptidase 13*	4.0446	16.5022
11754354_s_at	PROM1	*prominin 1*	4.0329	16.3695
11752548_a_at	ALDH1A1	*aldehyde dehydrogenase 1 family member A1*	3.8626	14.5461
11732460_a_at	PLEKHS1	*pleckstrin homology domain containing S1*	3.8322	14.2435
11727698_a_at	VMO1	*vitelline membrane outer layer 1 homolog*	3.8239	14.1611
11748034_a_at	CMAHP	*cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene*	3.7866	13.8001
11726981_a_at	CP	*ceruloplasmin*	3.7549	13.5005
11726434_at	CHL1	*cell adhesion molecule L1 like*	3.6915	12.9195
11744104_a_at	TMC5	*transmembrane channel like 5*	3.6902	12.9082
11755588_a_at	SLC5A5	*solute carrier family 5 member 5*	3.6748	12.7711
11723524_at	AGR3	*anterior gradient 3, protein disulphide isomerase family member*	3.6576	12.6199
11717820_a_at	SLC4A4	*solute carrier family 4 member 4*	3.6518	12.5693
11715994_x_at	ID2	*inhibitor of DNA binding 2, HLH protein*	3.6455	12.5143
11723925_a_at	KRT13	*keratin 13*	3.6105	12.2143
11757612_a_at	ASRGL1	*asparaginase like 1*	3.5785	11.9467
11751769_a_at	LOC100287413	*uncharacterized LOC100287413*	3.5660	11.8433
11726303_a_at	MFSD4A	*major facilitator superfamily domain containing 4A*	3.5510	11.7210
11755202_a_at	VTCN1	*V-set domain containing T cell activation inhibitor 1*	3.5325	11.5713
11716109_a_at	PIGR	*polymeric immunoglobulin receptor*	3.4947	11.2726
11755403_a_at	CHST9	*carbohydrate sulfotransferase 9*	3.4249	10.7397
11737634_a_at	UGT2A1	*UDP glucuronosyltransferase family 2 member A1 complex locus*	3.4162	10.6750
11715343_at	MUC16	*mucin 16, cell surface associated*	3.3456	10.1653
11754650_a_at	ATP10B	*ATPase Phospholipid Transporting 10B (Putative)*	3.3377	10.1101
11721895_	GAS1	*growth arrest specific 1*	3.3148	9.9505

x_at				
11758952_at	AGR2	*anterior gradient 2, protein disulphide isomerase family member*	3.2963	9.8239
11744556_x_at	CYP2B7P	*cytochrome P450 family 2 subfamily B member 7, pseudogene*	3.2677	9.6308
11739916_a_at	SERPINB11	*Serpin Family B Member 11 (Gene/Pseudogene)*	3.2536	9.5372
11721531_a_at	AQP5	*aquaporin 5*	3.2212	9.3258
11719538_at	BBOX1	*gamma-butyrobetaine hydroxylase 1*	3.2176	9.3023
11716489_a_at	STATH	*statherin*	3.1801	9.0639
11729770_at	BPIFA2	*BPI fold containing family A member 2*	3.1566	8.9173
11728753_at	ADH7	*Alcohol Dehydrogenase 7 (Class IV), Mu Or Sigma Polypeptide*	3.1557	8.9120
11756098_a_at	SYTL5	*synaptotagmin like 5*	3.1456	8.8498
11723441_a_at	EPHA4	*EPH receptor A4*	3.1355	8.7876
11744063_a_at	MUC5B	*mucin 5B, oligomeric mucus/gel-forming*	3.1076	8.6196
11731657_s_at	VAV3	*vav guanine nucleotide exchange factor 3*	3.0720	8.4091
11727966_a_at	MSMB	*microseminoprotein beta*	3.0520	8.2935
11740755_a_at	LYNX1	*Ly6/neurotoxin 1*	3.0175	8.0976
11755748_s_at	PLAC8	*placenta specific 8*	2.9978	7.9880
11720349_at	ROPN1L	*rhophilin associated tail protein 1 like*	2.9701	7.8361
11734503_x_at	ALOX15	*arachidonate 15-lipoxygenase*	2.9509	7.7324
11718213_a_at	SLC27A2	*solute carrier family 27 member 2*	2.9485	7.7195
11725562_at	C20orf85	*chromosome 20 open reading frame 85*	2.9237	7.5878
11744378_a_at	KRT4	*keratin 4*	2.9158	7.5467
11721898_at	FAM3D	*family with sequence similarity 3 member D*	2.9131	7.5326
11718722_at	PSCA	*prostate stem cell antigen*	2.8970	7.4486
11721539_at	RAB15	*RAB15, member RAS oncogene family*	2.8612	7.2660
11757645_s_at	FIBIN	*Fin Bud Initiation Factor Homolog (Zebrafish)*	2.8572	7.2462
11758225_s_at	IQGAP2	*IQ motif containing GTPase activating protein 2*	2.8567	7.2436
11723163_s_at	NR3C2	*nuclear receptor subfamily 3 group C member 2*	2.8564	7.2421
11730245_a_at	FMO2	*flavin containing monooxygenase 2*	2.8501	7.2106
11726124_at	TCN1	*transcobalamin 1*	2.8501	7.2104
11724762_a_at	DEPTOR	*DEP domain containing MTOR-interacting protein*	2.8495	7.2073
11722838_a_at	GABRP	*gamma-aminobutyric acid type A receptor pi subunit*	2.8409	7.1645
11722054_a_at	CYP4X1	*cytochrome P450 family 4 subfamily X member 1*	2.7751	6.8450
11757570_s_at	PRR15	*proline rich 15*	2.7732	6.8362
11733474_at	SOX21	*SRY-box 21*	2.7485	6.7204
11715788_a_at	SLC40A1	*solute carrier family 40 member 1*	2.7467	6.7117
11724703_a_at	ELF5	*E74 like ETS transcription factor 5*	2.7321	6.6441
11733934_a_at	PIFO	*primary cilia formation*	2.7167	6.5738
11757815_s_at	METTL7A	*methyltransferase like 7A*	2.7082	6.5352
11724875_a_at	CD36	*CD36 molecule*	2.7062	6.5262
11739044_s_at	SLC15A2	*solute carrier family 15 member 2*	2.7013	6.5039
11752737_a_at	CLEC7A	*C-type lectin domain family 7 member A*	2.6944	6.4729
11721688_at	ID4	*inhibitor of DNA binding 4, HLH protein*	2.6750	6.3864

11717595_s_at	ELF3	*E74 like ETS transcription factor 3*	2.6514	6.2829
11721175_at	RARRES1	*retinoic acid receptor responder 1*	2.6415	6.2399
11721318_at	PARM1	*prostate androgen-regulated mucin-like protein 1*	2.6408	6.2368
11744374_x_at	HLA-DRB1	*major histocompatibility complex, class II, DR beta 1*	2.6393	6.2302
11718790_at	HES6	*hes family bHLH transcription factor 6*	2.6173	6.1359
11721572_at	C10orf99	*chromosome 10 open reading frame 99*	2.6105	6.1072
11731433_a_at	SELENOP	*selenoprotein P*	2.5937	6.0364
11716401_a_at	SELENBP1	*selenium binding protein 1*	2.5787	5.9741
11758474_s_at	COLCA1	*colorectal cancer associated 1*	2.5771	5.9673
11755226_s_at	KLHDC7A	*kelch domain containing 7A*	2.5768	5.9662
11721135_s_at	IGFBP3	*insulin like growth factor binding protein 3*	2.5699	5.9377
11715708_s_at	MB	*myoglobin*	2.5639	5.9129
11716532_a_at	EGFL6	*EGF like domain multiple 6*	2.5470	5.8443
11723878_a_at	ATP7B	*ATPase copper transporting beta*	2.5441	5.8326
11751078_s_at	CYP2F1	*cytochrome P450 family 2 subfamily F member 1*	2.5212	5.7406
11728239_at	RRAGD	*Ras related GTP binding D*	2.5139	5.7117
11727906_at	MMP10	*matrix metallopeptidase 10*	2.5021	5.6650
11719554_at	CTSS	*cathepsin S*	2.4942	5.6340
11756191_a_at	MAN1C1	*mannosidase alpha class 1C member 1*	2.4910	5.6215
11724516_s_at	GPD1L	*glycerol-3-phosphate dehydrogenase 1-like*	2.4846	5.5966
11754295_a_at	FAM107B	*family with sequence similarity 107 member B*	2.4805	5.5809
11717575_at	PPP1R3C	*protein phosphatase 1 regulatory subunit 3C*	2.4730	5.5521
11742251_s_at	CYP2A6	*cytochrome P450 family 2 subfamily A member 6*	2.4672	5.5296
11734525_a_at	C11orf88	*chromosome 11 open reading frame 88*	2.4659	5.5246
11720243_x_at	TCN2	*transcobalamin 2*	2.4633	5.5146
11748750_a_at	GPNMB	*glycoprotein nmb*	2.4595	5.5003
11717885_a_at	CCDC3	*coiled-coil domain containing 3*	2.4507	5.4670
11754627_s_at	RAB37	*RAB37, member RAS oncogene family*	2.4456	5.4474
11720372_at	TESC	*tescalcin*	2.4394	5.4240
11720713_a_at	KCNE3	*potassium voltage-gated channel subfamily E regulatory subunit 3*	2.4374	5.4168
11734939_a_at	SLC16A9	*solute carrier family 16 member 9*	2.4359	5.4109
11722242_at	TSPAN12	*tetraspanin 12*	2.4281	5.3819
11757798_s_at	MAFB	*MAF bZIP transcription factor B*	2.4250	5.3702
11719265_a_at	MLPH	*melanophilin*	2.4233	5.3639
11728771_a_at	CLCA4	*chloride channel accessory 4*	2.4230	5.3629
11754601_s_at	LOC100130872	*uncharacterized LOC100130872*	2.4188	5.3473
11754421_a_at	VSIG2	*V-set and immunoglobulin domain containing 2*	2.4160	5.3368
11724219_x_at	GSTA1	*glutathione S-transferase alpha 1*	2.4150	5.3331
11717720_a_at	ST6GAL1	*ST6 beta-galactoside alpha-2,6-sialyltransferase 1*	2.4121	5.3224
11720993_at	SOX2	*SRY-box 2*	2.4020	5.2854
11732500_a_at	FAM3B	*family with sequence similarity 3 member B*	2.3985	5.2725
11759642_x_at	HLA-DRB1	*major histocompatibility complex, class II, DR beta 1*	2.3959	5.2631

11729439_a_at	CAPSL	*calcyphosine like*	2.3946	5.2583
11729920_at	BBOF1	*basal body orientation factor 1*	2.3932	5.2532
11744596_a_at	LYPD6B	*LY6/PLAUR domain containing 6B*	2.3708	5.1722
11745989_a_at	HLA-DMA	*major histocompatibility complex, class II, DM alpha*	2.3691	5.1662
11731606_at	SCIN	*scinderin*	2.3584	5.1281
11717417_s_at	RHOU	*ras homolog family member U*	2.3282	5.0219
11720134_s_at	PROS1	*Protein S (Alpha)*	2.3258	5.0136
11726916_at	SLCO4C1	*solute carrier organic anion transporter family member 4C1*	2.3204	4.9948
11755020_a_at	SLC46A3	*solute carrier family 46 member 3*	2.3137	4.9716
11731248_a_at	TMEM116	*transmembrane protein 116*	2.3118	4.9650
11724258_a_at	MUC15	*mucin 15, cell surface associated*	2.3061	4.9454
11728727_at	CEACAM7	*carcinoembryonic antigen related cell adhesion molecule 7*	2.2980	4.9178
11732910_x_at	FAM183A	*family with sequence similarity 183 member A*	2.2971	4.9148
11722863_at	SCGB2A1	*secretoglobin family 2A member 1*	2.2886	4.8858
11721430_a_at	SYBU	*syntabulin*	2.2564	4.7781
11732833_a_at	C9orf135	*chromosome 9 open reading frame 135*	2.2524	4.7646
11720139_a_at	VSTM2L	*V-set and transmembrane domain containing 2 like*	2.2494	4.7550
11736855_a_at	ATP6V1C2	*ATPase H+ transporting V1 subunit C2*	2.2431	4.7340
11756547_a_at	CLU	*clusterin*	2.2413	4.7283
11730044_a_at	C9orf24	*chromosome 9 open reading frame 24*	2.2322	4.6984
11758134_s_at	PPM1H	*protein phosphatase, Mg2+/Mn2+ dependent 1H*	2.2309	4.6944
11718754_at	CAPN5	*calpain 5*	2.2277	4.6838
11756881_a_at	LOC101926951	*uncharacterized LOC101926951*	2.2231	4.6688
11715763_a_at	PODXL	*podocalyxin like*	2.2084	4.6217
11719658_a_at	TF	*transferrin*	2.2068	4.6165
11725922_a_at	CLIC6	*chloride intracellular channel 6*	2.2065	4.6154
11753973_x_at	MUC1	*mucin 1, cell surface associated*	2.1935	4.5742
11729976_a_at	PTPRN2	*protein tyrosine phosphatase, receptor type N2*	2.1901	4.5635
11738435_x_at	CD74	*CD74 molecule*	2.1576	4.4618
11763989_at	LOC101927057	*uncharacterized LOC101927057*	2.1433	4.4178
11727239_a_at	C4orf19	*chromosome 4 open reading frame 19*	2.1406	4.4096
11763594_a_at	HS3ST3B1	*heparan sulfate-glucosamine 3-sulfotransferase 3B1*	2.1360	4.3954
11719843_a_at	ABI3BP	*ABI family member 3 binding protein*	2.1324	4.3846
11731722_a_at	ALDH3B1	*aldehyde dehydrogenase 3 family member B1*	2.1283	4.3720
11727146_at	GPR160	*G protein-coupled receptor 160*	2.1222	4.3537
11744240_at	SNTN	*sentan, cilia apical structure protein*	2.1212	4.3507
11757972_s_at	MYLIP	*myosin regulatory light chain interacting protein*	2.1123	4.3237
11732240_a_at	SLITRK6	*SLIT and NTRK like family member 6*	2.1119	4.3227
11759322_at	BCL6	*B-cell CLL/lymphoma 6*	2.1046	4.3008
11742730_a_at	CAPS	*calcyphosine*	2.1017	4.2920
11732959_a_at	SPRR3	*small proline rich protein 3*	2.0991	4.2844
11728523_a_at	MYCL	*v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog*	2.0983	4.2819

11727734_at	CFAP126	*cilia and flagella associated protein 126*	2.0975	4.2797
11758586_s_at	GGT6	*gamma-glutamyltransferase 6*	2.0968	4.2776
11721887_a_at	CRYM	*crystallin mu*	2.0928	4.2657
11723194_x_at	HLA-DQB1	*major histocompatibility complex, class II, DQ beta 1*	2.0894	4.2556
11715490_s_at	AMY1A	*Amylase, Alpha 1A (Salivary)*	2.0882	4.2522
11739725_a_at	TC2N	*tandem C2 domains, nuclear*	2.0880	4.2515
11720901_a_at	GRAMD1C	*GRAM domain containing 1C*	2.0769	4.2190
11754316_a_at	PIK3R3	*phosphoinositide-3-kinase regulatory subunit 3*	2.0667	4.1893
11716308_s_at	CYBRD1	*cytochrome b reductase 1*	2.0634	4.1797
11718432_a_at	SASH1	*SAM and SH3 domain containing 1*	2.0589	4.1668
11719767_a_at	TPPP3	*tubulin polymerization promoting protein family member 3*	2.0425	4.1195
11737141_a_at	RSPH1	*radial spoke head 1 homolog*	2.0420	4.1183
11743071_a_at	LPAR6	*lysophosphatidic acid receptor 6*	2.0381	4.1071
11725691_a_at	VWA5A	*von Willebrand factor A domain containing 5A*	2.0375	4.1052
11722157_a_at	CCNO	*cyclin O*	2.0309	4.0865
11758468_s_at	TSHZ2	*teashirt zinc finger homeobox 2*	2.0267	4.0746
11736144_at	ENPP4	*Ectonucleotide Pyrophosphatase/Phosphodiesterase 4 (Putative)*	2.0222	4.0621
11744138_at	CAMK1D	*calcium/calmodulin dependent protein kinase ID*	2.0208	4.0580
11723063_a_at	GCHFR	*GTP cyclohydrolase I feedback regulator*	2.0203	4.0566
11731538_a_at	ADGRF1	*adhesion G protein-coupled receptor F1*	2.0155	4.0432
11723404_at	PPARGC1A	*PPARG coactivator 1 alpha*	2.0138	4.0384
11719444_s_at	PTPRZ1	*protein tyrosine phosphatase, receptor type Z1*	2.0112	4.0311
11730265_x_at	CCDC69	*coiled-coil domain containing 69*	2.0074	4.0207
11727921_a_at	TEKT1	*tektin 1*	2.0055	4.0154
11725625_s_at	ACE2	*angiotensin I converting enzyme 2*	2.0040	4.0111
11722070_a_at	CHPT1	*choline phosphotransferase 1*	2.0023	4.0065
11730881_a_at	NEBL	*nebulette*	2.0000	4.0001
11758544_s_at	RDH10	*Retinol Dehydrogenase 10*	1.9781	3.9397
11716974_a_at	PDK4	*pyruvate dehydrogenase kinase 4*	1.9754	3.9325
11727995_a_at	SPINK5	*serine peptidase inhibitor, Kazal type 5*	1.9639	3.9012
11726576_x_at	CYP2A6	*cytochrome P450 family 2 subfamily A member 6*	1.9628	3.8982
11744086_a_at	PRR15L	*proline rich 15 like*	1.9619	3.8958
11729025_a_at	ILDR1	*immunoglobulin like domain containing receptor 1*	1.9598	3.8902
11724795_at	ZG16B	*zymogen granule protein 16B*	1.9524	3.8702
11758221_s_at	ARRDC3	*arrestin domain containing 3*	1.9476	3.8572
11764261_s_at	TMPRSS11A	*transmembrane protease, serine 11A*	1.9408	3.8391
11726051_a_at	FMO3	*flavin containing monooxygenase 3*	1.9401	3.8373
11729453_s_at	CYP2B6	*cytochrome P450 family 2 subfamily B member 6*	1.9379	3.8316
11746662_a_at	ARMC3	*armadillo repeat containing 3*	1.9277	3.8044
11715931_s_at	SGK1	*serum/glucocorticoid regulated kinase 1*	1.9274	3.8036
11742816_a_at	FAM13A	*family with sequence similarity 13 member A*	1.9254	3.7985
11726283_s_at	ENPP5	*Ectonucleotide Pyrophosphatase/Phosphodiesterase 5 (Putative)*	1.9216	3.7883

11724109_a_at	C9orf116	*chromosome 9 open reading frame 116*	1.9203	3.7850
11754735_s_at	ABCA13	*ATP binding cassette subfamily A member 13*	1.9146	3.7700
11755640_s_at	RALGPS1	*Ral GEF with PH domain and SH3 binding motif 1*	1.9096	3.7570
11730927_x_at	FUT2	*fucosyltransferase 2*	1.9076	3.7519
11758595_at	NBEA	*neurobeachin*	1.9042	3.7431
11721704_a_at	CRIP1	*cysteine rich protein 1*	1.9018	3.7367
11725632_at	NR4A2	*nuclear receptor subfamily 4 group A member 2*	1.8989	3.7293
11723899_a_at	DHRS9	*dehydrogenase/reductase 9*	1.8946	3.7181
11737088_at	TLL1	*tolloid like 1*	1.8920	3.7114
11721460_s_at	TAPBPL	*TAP binding protein like*	1.8915	3.7101
11736369_at	MBOAT1	*membrane bound O-acyltransferase domain containing 1*	1.8862	3.6966
11725223_at	SNTB1	*syntrophin beta 1*	1.8777	3.6748
11740438_a_at	FUT6	*fucosyltransferase 6*	1.8759	3.6704
11754640_a_at	EPHX2	*epoxide hydrolase 2*	1.8733	3.6636
11733359_a_at	CFAP45	*cilia and flagella associated protein 45*	1.8691	3.6531
11752106_x_at	CEACAM5	*carcinoembryonic antigen related cell adhesion molecule 5*	1.8649	3.6425
11737992_s_at	GPR37	*G protein-coupled receptor 37*	1.8647	3.6418
11756097_s_at	ZMYND10	*zinc finger MYND-type containing 10*	1.8618	3.6345
11724589_s_at	MMP12	*matrix metallopeptidase 12*	1.8604	3.6310
11718919_a_at	ATP6V1B1	*ATPase H+ transporting V1 subunit B1*	1.8540	3.6151
11739882_a_at	GLIS3	*GLIS family zinc finger 3*	1.8518	3.6095
11754888_a_at	ADSSL1	*adenylosuccinate synthase like 1*	1.8508	3.6071
11722743_a_at	TLE2	*transducin like enhancer of split 2*	1.8497	3.6043
11756495_a_at	SPAG6	*sperm associated antigen 6*	1.8464	3.5959
11739351_a_at	AMOT	*angiomotin*	1.8438	3.5896
11755010_s_at	POC1B-GALNT4	*POC1B-GALNT4 readthrough*	1.8429	3.5874
11764077_s_at	EDIL3	*EGF like repeats and discoidin domains 3*	1.8410	3.5826
11743595_at	C5orf49	*chromosome 5 open reading frame 49*	1.8313	3.5586
11723703_s_at	ABHD5	*abhydrolase domain containing 5*	1.8311	3.5582
11734359_a_at	RNASEL	*ribonuclease L*	1.8256	3.5445
11724394_at	KIAA1211L	*KIAA1211 like*	1.8196	3.5299
11719692_a_at	RARRES3	*retinoic acid receptor responder 3*	1.8094	3.5050
11724528_a_at	GCNT3	*Glucosaminyl (N-Acetyl) Transferase 3, Mucin Type*	1.8066	3.4981
11728200_a_at	LOX	*lysyl oxidase*	1.8065	3.4979
11730469_s_at	LMO2	*LIM domain only 2*	1.8048	3.4938
11757882_x_at	GSTA1	*glutathione S-transferase alpha 1*	1.7943	3.4684
11721759_a_at	ASAP3	*ArfGAP with SH3 domain, ankyrin repeat and PH domain 3*	1.7904	3.4590
11735523_a_at	FAM47E	*family with sequence similarity 47 member E*	1.7884	3.4543
11730214_at	DUOX2	*dual oxidase 2*	1.7790	3.4318
11718287_at	UBL3	*ubiquitin like 3*	1.7758	3.4242
11719321_a_at	DNALI1	*dynein axonemal light intermediate chain 1*	1.7717	3.4146
11718481_s_at	CFI	*complement factor I*	1.7676	3.4048

11732657_a_at	CYP26A1	*cytochrome P450 family 26 subfamily A member 1*	1.7674	3.4045
11725450_a_at	TMEM45B	*transmembrane protein 45B*	1.7646	3.3979
11721657_at	LMO4	*LIM domain only 4*	1.7617	3.3909
11734214_a_at	MPP7	*membrane palmitoylated protein 7*	1.7605	3.3881
11758070_s_at	PBX1	*PBX homeobox 1*	1.7586	3.3838
11722756_at	TMEM37	*transmembrane protein 37*	1.7554	3.3763
11721141_x_at	TCEA3	*transcription elongation factor A3*	1.7548	3.3748
11723367_a_at	RAB26	*RAB26, member RAS oncogene family*	1.7536	3.3719
11737857_a_at	DNAAF1	*dynein axonemal assembly factor 1*	1.7524	3.3693
11733011_x_at	SLC44A4	*solute carrier family 44 member 4*	1.7503	3.3643
11720007_a_at	STEAP4	*STEAP4 metalloreductase*	1.7477	3.3582
11731779_a_at	C11orf70	*chromosome 11 open reading frame 70*	1.7433	3.3481
11727198_a_at	PCDHAC2	*protocadherin alpha subfamily C, 2*	1.7394	3.3390
11729061_a_at	DNAH5	*dynein axonemal heavy chain 5*	1.7363	3.3317
11718448_at	SH3BGRL2	*SH3 domain binding glutamate rich protein like 2*	1.7350	3.3288
11719447_s_at	GBP2	*guanylate binding protein 2*	1.7282	3.3131
11743921_at	TMEM125	*transmembrane protein 125*	1.7264	3.3089
11753734_x_at	WFDC2	*WAP four-disulfide core domain 2*	1.7236	3.3026
11723007_a_at	DYX1C1-CCPG1	*DYX1C1-CCPG1 Readthrough (NMD Candidate)*	1.7233	3.3020
11756588_a_at	ST6GALNAC1	*ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1*	1.7152	3.2835
11752060_x_at	ERN2	*endoplasmic reticulum to nucleus signaling 2*	1.7115	3.2750
11718302_at	HSD11B2	*hydroxysteroid 11-beta dehydrogenase 2*	1.7113	3.2746
11728953_a_at	ADGRV1	*adhesion G protein-coupled receptor V1*	1.7110	3.2738
11731286_at	EDN2	*endothelin 2*	1.7088	3.2688
11725863_a_at	FAM13B	*family with sequence similarity 13 member B*	1.7071	3.2650
11727241_at	WNT4	*Wnt family member 4*	1.7024	3.2545
11735084_s_at	FREM2	*FRAS1 related extracellular matrix protein 2*	1.7023	3.2543
11729364_at	PRKAA2	*protein kinase AMP-activated catalytic subunit alpha 2*	1.7018	3.2530
11729137_at	UGT2B7	*UDP glucuronosyltransferase family 2 member B7*	1.6995	3.2478
11721957_at	YPEL2	*yippee like 2*	1.6992	3.2472
11759343_x_at	FMN1	*formin 1*	1.6977	3.2438
11721993_at	SLC6A6	*solute carrier family 6 member 6*	1.6975	3.2433
11735570_a_at	SORBS2	*sorbin and SH3 domain containing 2*	1.6971	3.2424

11718780_a_at	**SSBP2**	***single stranded DNA binding protein 2***	**1.6963**	**3.2407**
11728342_at	**DCLK1**	***doublecortin like kinase 1***	**1.6956**	**3.2391**
11718766_at	**PRSS23**	***protease, serine 23***	**1.6930**	**3.2333**
11725368_at	**LRG1**	***leucine rich alpha-2-glycoprotein 1***	**1.6921**	**3.2313**
11726693_s_at	**ANGPT1**	***angiopoietin 1***	**1.6911**	**3.2291**
11728954_a_at	**KITLG**	***KIT ligand***	**1.6862**	**3.2181**
11721619_at	**FOXJ1**	***forkhead box J1***	**1.6839**	**3.2129**
11763193_at	**GDPD1**	***glycerophosphodiester phosphodiesterase domain containing 1***	**1.6815**	**3.2077**
11729972_at	**CYP4Z1**	***cytochrome P450 family 4 subfamily Z member 1***	**1.6728**	**3.1884**
11724667_s_at	**ENPP3**	***ectonucleotide pyrophosphatase/phosphodiesterase 3***	**1.6726**	**3.1878**
11743577_s_at	**CPE**	***carboxypeptidase E***	**1.6718**	**3.1861**
11715165_at	**DNAJC12**	***DnaJ Heat Shock Protein Family (Hsp40) Member C12***	**1.6705**	**3.1833**
11727702_at	**C9orf152**	***chromosome 9 open reading frame 152***	**1.6704**	**3.1831**
11760254_at	**IFI44**	***interferon induced protein 44***	**1.6689**	**3.1798**
11746749_a_at	**ZBBX**	***zinc finger B-box domain containing***	**1.6673**	**3.1761**
11724796_at	**DDIT4L**	***DNA damage inducible transcript 4 like***	**1.6649**	**3.1710**
11730971_a_at	**CYP4F12**	***cytochrome P450 family 4 subfamily F member 12***	**1.6642**	**3.1693**

11730632_a_at	**OCA2**	***OCA2 melanosomal transmembrane protein***	**1.6623**	**3.1651**
11744508_a_at	**CCDC146**	***coiled-coil domain containing 146***	**1.6593**	**3.1587**
11721267_s_at	**TMPRSS4**	***transmembrane protease, serine 4***	**1.6583**	**3.1564**
11729692_a_at	**SERPINB3**	***serpin family B member 3***	**1.6579**	**3.1556**
11727302_a_at	**TMEM71**	***transmembrane protein 71***	**1.6568**	**3.1532**
11730035_at	**FMO4**	***flavin containing monooxygenase 4***	**1.6555**	**3.1504**
11758460_s_at	**FAAH2**	***fatty acid amide hydrolase 2***	**1.6542**	**3.1474**
11756793_a_at	**VNN2**	***vanin 2***	**1.6538**	**3.1467**
11730801_at	**CXCL6**	***C-X-C motif chemokine ligand 6***	**1.6504**	**3.1392**
11727918_s_at	**MUC20**	***mucin 20, cell surface associated***	**1.6462**	**3.1301**
11728288_a_at	**KRT15**	***keratin 15***	**1.6445**	**3.1263**
11728981_at	**ERICH5**	***glutamate rich 5***	**1.6434**	**3.1241**
11740868_a_at	**LDLRAD1**	***low density lipoprotein receptor class A domain containing 1***	**1.6421**	**3.1212**
11729128_at	**CPA4**	***carboxypeptidase A4***	**1.6419**	**3.1208**
11717440_a_at	**EPS8**	***epidermal growth factor receptor pathway substrate 8***	**1.6388**	**3.1141**
11724063_s_at	**FA2H**	***fatty acid 2-hydroxylase***	**1.6301**	**3.0953**
11721412_a_at	**BSPRY**	***B-box and SPRY domain containing***	**1.6262**	**3.0869**

11750836_a_at	**EFHC1**	***EF-hand domain containing 1***	**1.6253**	**3.0851**
11722507_a_at	**CLIC5**	***chloride intracellular channel 5***	**1.6200**	**3.0738**
11715222_at	**MAGI3**	***membrane associated guanylate kinase, WW and PDZ domain containing 3***	**1.6162**	**3.0657**
11734578_a_at	**CFH**	***complement factor H***	**1.6070**	**3.0461**
11732337_x_at	**BCAS1**	***breast carcinoma amplified sequence 1***	**1.5975**	**3.0261**
11755310_s_at	**ACOT2**	***acyl-CoA thioesterase 2***	**1.5947**	**3.0203**
11736050_s_at	**FAM229B**	***family with sequence similarity 229 member B***	**1.5929**	**3.0165**
11725980_at	**CFD**	***complement factor D***	**1.5884**	**3.0071**
11755109_a_at	**CYFIP2**	***cytoplasmic FMR1 interacting protein 2***	**1.5852**	**3.0005**
11755787_s_at	**TCTN1**	***tectonic family member 1***	**1.5809**	**2.9916**
11731817_s_at	**RAB17**	***RAB17, member RAS oncogene family***	**1.5797**	**2.9890**
11726412_s_at	**ZBTB7C**	***zinc finger and BTB domain containing 7C***	**1.5785**	**2.9866**
11722862_x_at	**TRIM2**	***tripartite motif containing 2***	**1.5785**	**2.9865**
11732468_at	**ATP12A**	***ATPase H+/K+ transporting non-gastric alpha2 subunit***	**1.5762**	**2.9818**
11755362_a_at	**IFT172**	***intraflagellar transport 172***	**1.5738**	**2.9768**
11720064_a_at	**GLIPR2**	***GLI pathogenesis related 2***	**1.5727**	**2.9746**
11748865_a_at	**TMEM139**	***transmembrane protein 139***	**1.5710**	**2.9711**

11715583_s_at	**HLA-DPA1**	***major histocompatibility complex, class II, DP alpha 1***	**1.5709**	**2.9708**
11716127_a_at	**BAG1**	***BCL2 associated athanogene 1***	**1.5682**	**2.9654**
11721025_a_at	**TRAPPC6A**	***trafficking protein particle complex 6A***	**1.5662**	**2.9613**
11757824_s_at	**RGL1**	***ral guanine nucleotide dissociation stimulator like 1***	**1.5636**	**2.9560**
11729832_s_at	**CLDN8**	***claudin 8***	**1.5626**	**2.9538**
11734176_a_at	**CFAP52**	***cilia and flagella associated protein 52***	**1.5582**	**2.9449**
11725790_at	**DPYD**	***dihydropyrimidine dehydrogenase***	**1.5580**	**2.9445**
11723961_s_at	**PTN**	***pleiotrophin***	**1.5563**	**2.9410**
11732580_a_at	**ME3**	***malic enzyme 3***	**1.5544**	**2.9371**
11746995_a_at	**NPL**	***N-acetylneuraminate pyruvate lyase***	**1.5504**	**2.9289**
11728701_a_at	**CD55**	***CD55 Molecule (Cromer Blood Group)***	**1.5467**	**2.9214**
11730623_at	**DSEL**	***dermatan sulfate epimerase-like***	**1.5463**	**2.9207**
11717465_s_at	**LXN**	***latexin***	**1.5458**	**2.9197**
11758028_s_at	**FOXQ1**	***forkhead box Q1***	**1.5437**	**2.9155**
11747167_x_at	**ADH1B**	***Alcohol Dehydrogenase 1B (Class I), Beta Polypeptide***	**1.5435**	**2.9151**
11729455_x_at	**CYP2B6**	***cytochrome P450 family 2 subfamily B member 6***	**1.5431**	**2.9141**
11757390_s_at	**KLHL24**	***kelch like family member 24***	**1.5419**	**2.9118**

11730338_a_at	**SMAD6**	***SMAD family member 6***	**1.5407**	**2.9093**
11729693_at	**SERPINB3**	***serpin family B member 3***	**1.5393**	**2.9066**
11742224_a_at	**CDC20B**	***cell division cycle 20B***	**1.5356**	**2.8991**
11756684_a_at	**DYNLRB2**	***dynein light chain roadblock-type 2***	**1.5352**	**2.8983**
11745074_a_at	**GSTA4**	***glutathione S-transferase alpha 4***	**1.5300**	**2.8878**
11758064_s_at	**MIR4683**	***microRNA 4683***	**1.5275**	**2.8829**
11730250_a_at	**LNX1**	***ligand of numb-protein X 1***	**1.5213**	**2.8705**
11727538_at	**NME5**	***NME/NM23 family member 5***	**1.5205**	**2.8690**
11734893_s_at	**SOBP**	***sine oculis binding protein homolog***	**1.5195**	**2.8669**
11747376_s_at	**CCPG1**	***cell cycle progression 1***	**1.5186**	**2.8652**
11736238_a_at	**ABCA5**	***ATP binding cassette subfamily A member 5***	**1.5155**	**2.8590**
11764253_s_at	**IFITM10**	***interferon induced transmembrane protein 10***	**1.5136**	**2.8553**
11721445_x_at	**ERBB3**	***erb-b2 receptor tyrosine kinase 3***	**1.5090**	**2.8462**
11731755_a_at	**SYTL2**	***synaptotagmin like 2***	**1.5068**	**2.8417**
11723641_a_at	**FUCA1**	***fucosidase, alpha-L- 1, tissue***	**1.5057**	**2.8397**
11723585_a_at	**SMPDL3A**	***sphingomyelin phosphodiesterase acid like 3A***	**1.5050**	**2.8383**
11759546_a_at	**CXXC5**	***CXXC finger protein 5***	**1.5036**	**2.8354**

11725676_a_at	**RORA**	***RAR related orphan receptor A***	**1.5028**	**2.8339**
11727754_a_at	**PLA2G4A**	***phospholipase A2 group IVA***	**1.5023**	**2.8329**
11756274_a_at	**ALDH1L1**	***aldehyde dehydrogenase 1 family member L1***	**1.5022**	**2.8328**
11721700_a_at	**RERG**	***RAS like estrogen regulated growth inhibitor***	**1.5001**	**2.8287**
11722348_a_at	**REPS2**	***RALBP1 associated Eps domain containing 2***	**1.4996**	**2.8277**
11754164_a_at	**BCL2L15**	***BCL2 like 15***	**1.4990**	**2.8264**
11716210_at	**CITED2**	***Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2***	**1.4967**	**2.8220**
11735674_a_at	**AKAP14**	***A-kinase anchoring protein 14***	**1.4958**	**2.8203**
11725758_at	**ISL1**	***ISL LIM homeobox 1***	**1.4951**	**2.8189**
11725662_a_at	**SLC16A14**	***solute carrier family 16 member 14***	**1.4945**	**2.8176**
11737557_at	**AMTN**	***amelotin***	**1.4944**	**2.8174**
11729400_at	**PCP4L1**	***Purkinje cell protein 4 like 1***	**1.4942**	**2.8170**
11740580_at	**ASAH1**	***N-acylsphingosine amidohydrolase 1***	**1.4901**	**2.8091**
11720146_a_at	**DAPK1**	***death associated protein kinase 1***	**1.4894**	**2.8078**
11725892_a_at	**PLEKHH1**	***pleckstrin homology, MyTH4 and FERM domain containing H1***	**1.4891**	**2.8072**
11726159_a_at	**IQCG**	***IQ motif containing G***	**1.4886**	**2.8061**
11758673_s_at	**SORD**	***sorbitol dehydrogenase***	**1.4863**	**2.8017**

11727416_a_at	**CRYL1**	***crystallin lambda 1***	**1.4842**	**2.7977**
11722884_at	**CREBRF**	***CREB3 regulatory factor***	**1.4804**	**2.7902**
11717929_s_at	**FOLR1**	***folate receptor 1***	**1.4749**	**2.7797**
11753810_a_at	**CCL5**	***C-C motif chemokine ligand 5***	**1.4715**	**2.7731**
11725522_at	**MESP1**	***mesoderm posterior bHLH transcription factor 1***	**1.4714**	**2.7729**
11750527_s_at	**HLA-DQA1**	***major histocompatibility complex, class II, DQ alpha 1***	**1.4713**	**2.7727**
11743657_x_at	**HPGD**	***hydroxyprostaglandin dehydrogenase 15-***	**1.4707**	**2.7715**
11716694_at	**TSPAN6**	***tetraspanin 6***	**1.4694**	**2.7690**
11736285_a_at	**CHKA**	***choline kinase alpha***	**1.4688**	**2.7680**
11758013_s_at	**C8orf4**	***chromosome 8 open reading frame 4***	**1.4657**	**2.7619**
11721368_at	**CRLF1**	***cytokine receptor like factor 1***	**1.4630**	**2.7568**
11742709_s_at	**P4HTM**	***prolyl 4-hydroxylase, transmembrane***	**1.4627**	**2.7563**
11754461_s_at	**UCP2**	***uncoupling protein 2***	**1.4626**	**2.7561**
11724372_at	**ANXA10**	***annexin A10***	**1.4626**	**2.7560**
11734013_a_at	**BMP4**	***bone morphogenetic protein 4***	**1.4595**	**2.7501**
11755050_s_at	**PLCB4**	***phospholipase C beta 4***	**1.4550**	**2.7416**
11720678_a_at	**CREB3L1**	***cAMP responsive element binding protein 3 like 1***	**1.4540**	**2.7397**

11726682_a_at	**MEIS1**	***Meis homeobox 1***	**1.4540**	**2.7397**
11726535_a_at	**MORN5**	***MORN repeat containing 5***	**1.4514**	**2.7348**
11718651_at	**TMTC1**	***transmembrane and tetratricopeptide repeat containing 1***	**1.4505**	**2.7331**
11756356_a_at	**FAM81B**	***family with sequence similarity 81 member B***	**1.4504**	**2.7329**
11743321_at	**CTSO**	***cathepsin O***	**1.4483**	**2.7289**
11717742_a_at	**GPRC5C**	***G protein-coupled receptor class C group 5 member C***	**1.4464**	**2.7252**
11755110_a_at	**LRIG1**	***leucine rich repeats and immunoglobulin like domains 1***	**1.4449**	**2.7225**
11720088_x_at	**NUCB2**	***nucleobindin 2***	**1.4447**	**2.7221**
11734552_a_at	**CX3CL1**	***C-X3-C motif chemokine ligand 1***	**1.4417**	**2.7165**
11735717_a_at	**ZNF226**	***zinc finger protein 226***	**1.4414**	**2.7158**
11756342_s_at	**GDA**	***guanine deaminase***	**1.4389**	**2.7112**
11722658_at	**CXCL17**	***C-X-C motif chemokine ligand 17***	**1.4386**	**2.7105**
11745830_a_at	**ALAD**	***aminolevulinate dehydratase***	**1.4357**	**2.7052**
11726430_at	**HSPB2-C11orf52**	***HSPB2-C11orf52 Readthrough (NMD Candidate)***	**1.4353**	**2.7043**
11759191_at	**NIPAL2**	***NIPA like domain containing 2***	**1.4321**	**2.6983**
11715462_x_at	**LYZ**	***lysozyme***	**1.4316**	**2.6975**
11752898_a_at	**PPIL6**	***peptidylprolyl isomerase like 6***	**1.4292**	**2.6930**

11730699_at	**LOC100652777**	***group 10 secretory phospholipase A2-like***	**1.4290**	**2.6926**
11727296_s_at	**TGFB3**	***transforming growth factor beta 3***	**1.4263**	**2.6875**
11744581_a_at	**KHDRBS3**	***KH RNA binding domain containing, signal transduction associated 3***	**1.4255**	**2.6860**
11722820_at	**GGT7**	***gamma-glutamyltransferase 7***	**1.4254**	**2.6859**
11724321_s_at	**C11orf54**	***chromosome 11 open reading frame 54***	**1.4186**	**2.6733**
11719148_a_at	**ARRDC2**	***arrestin domain containing 2***	**1.4164**	**2.6692**
11730944_a_at	**CCDC65**	***coiled-coil domain containing 65***	**1.4161**	**2.6687**
11720283_at	**JMY**	***junction mediating and regulatory protein, p53 cofactor***	**1.4138**	**2.6643**
11756888_a_at	**TFCP2L1**	***transcription factor CP2 like 1***	**1.4135**	**2.6638**
11754806_s_at	**CADPS2**	***calcium dependent secretion activator 2***	**1.4132**	**2.6633**
11718078_a_at	**BCL2L11**	***BCL2 like 11***	**1.4122**	**2.6614**
11718025_at	**IL1R1**	***interleukin 1 receptor type 1***	**1.4122**	**2.6614**
11744866_x_at	**CEL**	***carboxyl ester lipase***	**1.4102**	**2.6577**
11725249_at	**LY75**	***lymphocyte antigen 75***	**1.4096**	**2.6566**
11730066_s_at	**MAPK10**	***mitogen-activated protein kinase 10***	**1.4093**	**2.6560**
11724068_at	**PELI2**	***pellino E3 ubiquitin protein ligase family member 2***	**1.4059**	**2.6499**
11718435_a_at	**NPNT**	***nephronectin***	**1.4015**	**2.6417**

11731271_a_at	**MGAM**	***maltase-glucoamylase***	**1.4012**	**2.6413**
11721491_a_at	**FBP1**	***fructose-bisphosphatase 1***	**1.4004**	**2.6398**
11744282_at	**PLBD1**	***phospholipase B domain containing 1***	**1.3973**	**2.6340**
11727336_at	**SAMD12**	***sterile alpha motif domain containing 12***	**1.3888**	**2.6186**
11741659_a_at	**CDH26**	***cadherin 26***	**1.3863**	**2.6141**
11742497_x_at	**SSX6**	***SSX family member 6, pseudogene***	**1.3859**	**2.6134**
11725841_at	**ZSCAN16**	***zinc finger and SCAN domain containing 16***	**1.3852**	**2.6120**
11754681_s_at	**HLA-DMB**	***major histocompatibility complex, class II, DM beta***	**1.3804**	**2.6034**
11730395_x_at	**ZNF552**	***zinc finger protein 552***	**1.3797**	**2.6021**
11740586_a_at	**PTGFR**	***prostaglandin F receptor***	**1.3793**	**2.6014**
11759103_at	**CYP4F3**	***cytochrome P450 family 4 subfamily F member 3***	**1.3790**	**2.6009**
11734857_at	**ERO1B**	***endoplasmic reticulum oxidoreductase 1 beta***	**1.3766**	**2.5966**
11721614_a_at	**KIT**	***KIT proto-oncogene receptor tyrosine kinase***	**1.3762**	**2.5959**
11742423_a_at	**STEAP2**	***STEAP2 metalloreductase***	**1.3759**	**2.5953**
11734614_a_at	**GABRE**	***gamma-aminobutyric acid type A receptor epsilon subunit***	**1.3745**	**2.5927**
11737644_a_at	**RNF183**	***ring finger protein 183***	**1.3745**	**2.5927**
11750630_s_at	**MAP3K5**	***mitogen-activated protein kinase 5***	**1.3690**	**2.5829**

11741221_a_at	**COLCA2**	***colorectal cancer associated 2***	**1.3685**	**2.5820**
11730527_a_at	**DAPK2**	***death associated protein kinase 2***	**1.3674**	**2.5800**
11730037_at	**DEGS2**	***delta 4-desaturase, sphingolipid 2***	**1.3651**	**2.5760**
11730549_a_at	**IKZF2**	***IKAROS family zinc finger 2***	**1.3636**	**2.5733**
11723946_a_at	**ACSL5**	***acyl-CoA synthetize long-chain family member 5***	**1.3604**	**2.5675**
11715290_s_at	**CLDN3**	***claudin 3***	**1.3599**	**2.5666**
11723885_at	**NATD1**	***N-acetyltransferase domain containing 1***	**1.3592**	**2.5655**
11733545_x_at	**NWD1**	***NACHT and WD repeat domain containing 1***	**1.3536**	**2.5555**
11755450_a_at	**ZNF608**	***zinc finger protein 608***	**1.3524**	**2.5533**
11730509_s_at	**ABCC5**	***ATP binding cassette subfamily C member 5***	**1.3502**	**2.5495**
11728507_at	**LY96**	***lymphocyte antigen 96***	**1.3465**	**2.5429**
11723824_s_at	**MYO5C**	***myosin VC***	**1.3430**	**2.5367**
11756524_a_at	**RBBP9**	***RB binding protein 9, serine hydrolase***	**1.3410**	**2.5333**
11722283_at	**CA11**	***carbonic anhydrase 11***	**1.3409**	**2.5331**
11727238_at	**UST**	***uronyl 2-sulfotransferase***	**1.3407**	**2.5327**
11758382_s_at	**ABCC9**	***ATP binding cassette subfamily C member 9***	**1.3395**	**2.5306**
11729079_s_at	**ESRRG**	***estrogen related receptor gamma***	**1.3394**	**2.5305**

11724953_a_at	**PDIK1L**	***PDLIM1 interacting kinase 1 like***	**1.3387**	**2.5292**
11720650_a_at	**DUSP23**	***dual specificity phosphatase 23***	**1.3329**	**2.5191**
11742763_a_at	**FAM214A**	***family with sequence similarity 214 member A***	**1.3328**	**2.5189**
11734103_a_at	**FGGY**	***FGGY carbohydrate kinase domain containing***	**1.3321**	**2.5177**
11722310_a_at	**TMC4**	***transmembrane channel like 4***	**1.3267**	**2.5082**
11724157_x_at	**SULT1E1**	***sulfotransferase family 1E member 1***	**1.3238**	**2.5033**
11744760_s_at	**TSLP**	***thymic stromal lymphopoietin***	**1.3224**	**2.5009**
11731200_a_at	**TLR5**	***toll like receptor 5***	**1.3222**	**2.5005**
11725137_x_at	**SYNGR1**	***synaptogyrin 1***	**1.3218**	**2.4997**
11746264_a_at	**PLPP1**	***phospholipid phosphatase 1***	**1.3198**	**2.4964**
11749140_a_at	**RCBTB2**	***RCC1 and BTB domain containing protein 2***	**1.3189**	**2.4948**
11721030_a_at	**PIP5K1B**	***phosphatidylinositol-4-phosphate 5-kinase type 1 beta***	**1.3185**	**2.4940**
11744307_a_at	**TTC39A**	***tetratricopeptide repeat domain 39A***	**1.3167**	**2.4910**
11735488_a_at	**CASC1**	***cancer susceptibility candidate 1***	**1.3162**	**2.4901**
11726030_x_at	**UPK1B**	***uroplakin 1B***	**1.3161**	**2.4900**
11758988_at	**SYT17**	***synaptotagmin 17***	**1.3141**	**2.4864**
11729459_x_at	**BNIPL**	***BCL2 interacting protein like***	**1.3117**	**2.4824**

11737067_a_at	**TGM5**	***transglutaminase 5***	**1.3067**	**2.4738**
11738149_a_at	**TOX3**	***TOX high mobility group box family member 3***	**1.3060**	**2.4725**
11740394_a_at	**FGFR2**	***fibroblast growth factor receptor 2***	**1.3056**	**2.4718**
11729575_a_at	**XBP1**	***X-box binding protein 1***	**1.3033**	**2.4679**
11727158_a_at	**STRBP**	***spermatid perinuclear RNA binding protein***	**1.3017**	**2.4652**
11729395_s_at	**HECTD2**	***HECT domain E3 ubiquitin protein ligase 2***	**1.2982**	**2.4593**
11720331_at	**SELENOM**	***selenoprotein M***	**1.2957**	**2.4550**
11758224_s_at	**CCDC80**	***coiled-coil domain containing 80***	**1.2942**	**2.4524**
11739375_at	**SYT7**	***synaptotagmin 7***	**1.2937**	**2.4515**
11731126_at	**GXYLT2**	***glucoside xylosyltransferase 2***	**1.2925**	**2.4496**
11732444_a_at	**RBPMS**	***RNA binding protein with multiple splicing***	**1.2911**	**2.4471**
11719521_at	**SEMA5A**	***semaphorin 5A***	**1.2906**	**2.4463**
11734506_a_at	**MECOM**	***MDS1 and EVI1 complex locus***	**1.2898**	**2.4449**
11721780_a_at	**LLGL2**	***LLGL2, scribble cell polarity complex component***	**1.2886**	**2.4429**
11743226_at	**CCDC160**	***coiled-coil domain containing 160***	**1.2881**	**2.4420**
11719544_a_at	**MSLN**	***mesothelin***	**1.2829**	**2.4332**
11744430_a_at	**KIF9**	***kinesin family member 9***	**1.2824**	**2.4325**

11722614_a_at	**CYP2J2**	***cytochrome P450 family 2 subfamily J member 2***	**1.2805**	**2.4292**
11736745_a_at	**ZBTB20**	***zinc finger and BTB domain containing 20***	**1.2799**	**2.4282**
11756271_a_at	**FANK1**	***fibronectin type III and ankyrin repeat domains 1***	**1.2794**	**2.4273**
11727440_at	**LOXL4**	***lysyl oxidase like 4***	**1.2774**	**2.4240**
11755724_a_at	**MLF1**	***myeloid leukemia factor 1***	**1.2739**	**2.4182**
11729679_a_at	**PCDHB14**	***protocadherin beta 14***	**1.2717**	**2.4145**
11763485_a_at	**#N/A**	***#N/A***	**1.2717**	**2.4144**
11756702_a_at	**CYP39A1**	***cytochrome P450 family 39 subfamily A member 1***	**1.2701**	**2.4117**
11729333_at	**PADI1**	***peptidyl arginine deiminase 1***	**1.2657**	**2.4045**
11731030_at	**BICDL2**	***BICD family like cargo adaptor 2***	**1.2652**	**2.4036**
11724673_a_at	**BCKDHB**	***branched chain keto acid dehydrogenase E1 subunit beta***	**1.2627**	**2.3994**
11760972_x_at	**SPACA9**	***sperm acrosome associated 9***	**1.2627**	**2.3994**
11730261_a_at	**PRKAR2B**	***protein kinase cAMP-dependent type II regulatory subunit beta***	**1.2612**	**2.3970**
11722307_at	**GLCE**	***glucuronic acid epimerase***	**1.2609**	**2.3965**
11728363_s_at	**IL20RA**	***interleukin 20 receptor subunit alpha***	**1.2605**	**2.3958**
11743952_a_at	**CFAP206**	***cilia and flagella associated protein 206***	**1.2600**	**2.3950**
11732678_a_at	**DNAH12**	***dynein axonemal heavy chain 12***	**1.2595**	**2.3941**

11742865_a_at	**TJP3**	***tight junction protein 3***	**1.2588**	**2.3930**
11743405_a_at	**SMIM14**	***small integral membrane protein 14***	**1.2577**	**2.3911**
11751973_x_at	**LZTS3**	***leucine zipper tumor suppressor family member 3***	**1.2576**	**2.3910**
11745292_a_at	**C22orf15**	***chromosome 22 open reading frame 15***	**1.2576**	**2.3910**
11756677_a_at	**CYB5D2**	***cytochrome b5 domain containing 2***	**1.2559**	**2.3882**
11743943_a_at	**RSPH4A**	***radial spoke head 4 homolog A***	**1.2553**	**2.3872**
11742669_s_at	**HIST4H4**	***histone cluster 4 H4***	**1.2545**	**2.3858**
11718789_x_at	**ZNF302**	***zinc finger protein 302***	**1.2544**	**2.3856**
11733852_at	**EGLN3**	***egl-9 family hypoxia inducible factor 3***	**1.2522**	**2.3821**
11716814_s_at	**GATM**	***glycine amidinotransferase***	**1.2519**	**2.3815**
11726054_a_at	**MUC4**	***mucin 4, cell surface associated***	**1.2501**	**2.3785**
11719202_a_at	**MORN2**	***MORN repeat containing 2***	**1.2497**	**2.3779**
11727722_a_at	**MYB**	***MYB proto-oncogene, transcription factor***	**1.2470**	**2.3735**
11740223_x_at	**LRRC26**	***leucine rich repeat containing 26***	**1.2438**	**2.3682**
11722524_s_at	**TMCO4**	***transmembrane and coiled-coil domains 4***	**1.2429**	**2.3668**
11743072_a_at	**FBXO34**	***F-box protein 34***	**1.2423**	**2.3657**
11758637_x_at	**AMY1A**	***Amylase, Alpha 1A (Salivary)***	**1.2414**	**2.3642**

11757928_s_at	**TMEM178A**	***transmembrane protein 178A***	**1.2376**	**2.3581**
11743949_s_at	**FRAT1**	***frequently rearranged in advanced T-cell lymphomas 1***	**1.2348**	**2.3535**
11734334_at	**LINC01559**	***long intergenic non-protein coding RNA 1559***	**1.2348**	**2.3535**
11726470_s_at	**PLS1**	***plastin 1***	**1.2341**	**2.3524**
11739493_at	**MGAT4A**	***Mannosyl (A-1,3-)-Glycoprotein Beta-1,4-N-Acetylglucosaminyltransferase, Isozyme A***	**1.2327**	**2.3500**
11719785_s_at	**B4GALT4**	***beta-1,4-galactosyltransferase 4***	**1.2308**	**2.3469**
11754776_x_at	**CCDC74A**	***coiled-coil domain containing 74A***	**1.2290**	**2.3441**
11726892_a_at	**SLC51A**	***solute carrier family 51 alpha subunit***	**1.2280**	**2.3425**
11732060_a_at	**LEMD1**	***LEM domain containing 1***	**1.2280**	**2.3425**
11727983_a_at	**LRRC46**	***leucine rich repeat containing 46***	**1.2276**	**2.3418**
11739849_x_at	**UPK3BL**	***uroplakin 3B-like***	**1.2268**	**2.3405**
11757504_a_at	**DDAH1**	***dimethylarginine dimethylaminohydrolase 1***	**1.2248**	**2.3373**
11725518_at	**FRAT2**	***frequently rearranged in advanced T-cell lymphomas 2***	**1.2245**	**2.3368**
11740000_a_at	**CPEB3**	***cytoplasmic polyadenylation element binding protein 3***	**1.2240**	**2.3360**
11734530_x_at	**HLA-F**	***major histocompatibility complex, class I, F***	**1.2238**	**2.3356**
11759039_at	**SVIP**	***small VCP interacting protein***	**1.2224**	**2.3333**
11758377_s_at	**TLR1**	***toll like receptor 1***	**1.2216**	**2.3320**

11720106_a_at	**SLC26A2**	***solute carrier family 26 member 2***	**1.2215**	**2.3319**
11721352_at	**SLC1A1**	***solute carrier family 1 member 1***	**1.2214**	**2.3317**
11748981_a_at	**NAT1**	***N-acetyltransferase 1***	**1.2206**	**2.3305**
11728085_s_at	**BMPR1B**	***bone morphogenetic protein receptor type 1B***	**1.2205**	**2.3302**
11751905_a_at	**NID1**	***nidogen 1***	**1.2193**	**2.3284**
11742912_a_at	**GAREM1**	***GRB2 associated regulator of MAPK1 subtype 1***	**1.2177**	**2.3257**
11755873_a_at	**ACSS1**	***acyl-CoA synthetase short-chain family member 1***	**1.2176**	**2.3256**
11724983_at	**PCDH7**	***protocadherin 7***	**1.2163**	**2.3235**
11743794_a_at	**CFAP69**	***cilia and flagella associated protein 69***	**1.2153**	**2.3219**
11728482_a_at	**ZNF181**	***zinc finger protein 181***	**1.2104**	**2.3140**
11758027_s_at	**HOOK1**	***hook microtubule tethering protein 1***	**1.2086**	**2.3112**
11733530_at	**C1RL**	***complement C1r subcomponent like***	**1.2076**	**2.3095**
11755425_a_at	**FAM179B**	***family with sequence similarity 179 member B***	**1.2076**	**2.3095**
11756891_a_at	**ZNF12**	***zinc finger protein 12***	**1.2073**	**2.3090**
11740361_s_at	**FOXN3**	***forkhead box N3***	**1.2053**	**2.3059**
11726360_a_at	**ALDH3A1**	***aldehyde dehydrogenase 3 family member A1***	**1.2034**	**2.3028**
11730465_at	**KCNJ2**	***potassium voltage-gated channel subfamily J member 2***	**1.2027**	**2.3017**

11738185_s_at	**PDE8B**	***phosphodiesterase 8B***	**1.2022**	**2.3009**
11729100_a_at	**CFAP70**	***cilia and flagella associated protein 70***	**1.1991**	**2.2959**
11715558_a_at	**TMEM59**	***transmembrane protein 59***	**1.1972**	**2.2930**
11724051_at	**TRIM68**	***tripartite motif containing 68***	**1.1959**	**2.2909**
11759572_a_at	**STAU2**	***staufen double-stranded RNA binding protein 2***	**1.1959**	**2.2908**
11721417_at	**SCNN1B**	***sodium channel epithelial 1 beta subunit***	**1.1957**	**2.2905**
11733622_x_at	**NCMAP**	***non-compact myelin associated protein***	**1.1947**	**2.2890**
11735637_a_at	**LRRC23**	***leucine rich repeat containing 23***	**1.1940**	**2.2879**
11754306_a_at	**MCCC1**	***methylcrotonoyl-CoA carboxylase 1***	**1.1931**	**2.2864**
11753939_x_at	**PSMB10**	***proteasome subunit beta 10***	**1.1921**	**2.2849**
11717614_at	**KIF13B**	***kinesin family member 13B***	**1.1892**	**2.2803**
11725559_a_at	**ZNF112**	***zinc finger protein 112***	**1.1892**	**2.2802**
11755831_a_at	**WDR63**	***WD repeat domain 63***	**1.1889**	**2.2798**
11740239_a_at	**CFAP161**	***cilia and flagella associated protein 161***	**1.1875**	**2.2776**
11756469_x_at	**UPK3BL**	***uroplakin 3B-like***	**1.1874**	**2.2774**
11743286_at	**DTX4**	***deltex E3 ubiquitin ligase 4***	**1.1870**	**2.2768**
11726113_a_at	**FAM46B**	***family with sequence similarity 46 member B***	**1.1866**	**2.2762**

11731681_a_at	**KATNAL2**	***katanin catalytic subunit A1 like 2***	**1.1856**	**2.2746**
11723785_s_at	**LIMCH1**	***LIM and calponin homology domains 1***	**1.1843**	**2.2725**
11730073_at	**CNTN3**	***contactin 3***	**1.1824**	**2.2695**
11721665_a_at	**PLA2G16**	***phospholipase A2 group XVI***	**1.1818**	**2.2686**
11755121_x_at	**OSCP1**	***organic solute carrier partner 1***	**1.1808**	**2.2670**
11756059_a_at	**CXCL14**	***C-X-C motif chemokine ligand 14***	**1.1793**	**2.2647**
11723604_a_at	**INPP5J**	***inositol polyphosphate-5-phosphatase J***	**1.1792**	**2.2645**
11758993_at	**TRIM52**	***tripartite motif containing 52***	**1.1787**	**2.2638**
11718563_a_at	**ANKRD10**	***ankyrin repeat domain 10***	**1.1772**	**2.2613**
11731617_x_at	**SIDT1**	***SID1 transmembrane family member 1***	**1.1761**	**2.2597**
11752942_s_at	**DBP**	***D-box binding PAR bZIP transcription factor***	**1.1750**	**2.2580**
11763271_at	**PEX11A**	***peroxisomal biogenesis factor 11 alpha***	**1.1747**	**2.2575**
11723954_s_at	**CLINT1**	***clathrin interactor 1***	**1.1676**	**2.2463**
11721758_at	**TMEM47**	***transmembrane protein 47***	**1.1674**	**2.2460**
11727007_at	**SORT1**	***sortilin 1***	**1.1642**	**2.2411**
11723176_s_at	**PLEKHA6**	***pleckstrin homology domain containing A6***	**1.1634**	**2.2398**
11755903_x_at	**N4BP2L1**	***NEDD4 binding protein 2 like 1***	**1.1629**	**2.2391**

11744051_at	**TSPAN1**	***tetraspanin 1***	**1.1616**	**2.2371**
11722132_a_at	**MGAT3**	***Mannosyl (Beta-1,4-)-Glycoprotein Beta-1,4-N-Acetylglucosaminyltransferase***	**1.1615**	**2.2369**
11754624_a_at	**CYB5A**	***cytochrome b5 type A***	**1.1608**	**2.2358**
11721433_a_at	**CRBN**	***cereblon***	**1.1605**	**2.2354**
11742736_at	**MCEE**	***methylmalonyl-CoA epimerase***	**1.1595**	**2.2338**
11718169_a_at	**AZGP1**	***alpha-2-glycoprotein 1, zinc-binding***	**1.1594**	**2.2336**
11740115_a_at	**CGN**	***cingulin***	**1.1593**	**2.2335**
11724985_a_at	**EXPH5**	***exophilin 5***	**1.1593**	**2.2335**
11741447_s_at	**RNASE4**	***ribonuclease A family member 4***	**1.1587**	**2.2326**
11759299_s_at	**ARMC8**	***armadillo repeat containing 8***	**1.1584**	**2.2321**
11725494_at	**RSPH9**	***radial spoke head 9 homolog***	**1.1579**	**2.2314**
11737805_a_at	**TMPRSS11D**	***transmembrane protease, serine 11D***	**1.1542**	**2.2256**
11735271_a_at	**GCNT1**	***Glucosaminyl (N-Acetyl) Transferase 1, Core 2***	**1.1538**	**2.2250**
11744130_a_at	**VGLL1**	***vestigial like family member 1***	**1.1526**	**2.2231**
11723161_a_at	**ZNF776**	***zinc finger protein 776***	**1.1517**	**2.2218**
11758166_s_at	**ANOS1**	***anosmin 1***	**1.1498**	**2.2189**
11719307_a_at	**RASSF4**	***Ras association domain family member 4***	**1.1492**	**2.2179**

11740224_a_at	**CHST4**	***carbohydrate sulfotransferase 4***	**1.1490**	**2.2176**
11728163_a_at	**HSD17B3**	***hydroxysteroid 17-beta dehydrogenase 3***	**1.1487**	**2.2171**
11744031_at	**MMP7**	***matrix metallopeptidase 7***	**1.1473**	**2.2150**
11720865_a_at	**IFT27**	***intraflagellar transport 27***	**1.1462**	**2.2133**
11744615_s_at	**KLHDC9**	***kelch domain containing 9***	**1.1460**	**2.2130**
11721788_at	**C1orf226**	***chromosome 1 open reading frame 226***	**1.1454**	**2.2121**
11739527_a_at	**SECTM1**	***secreted and transmembrane 1***	**1.1443**	**2.2104**
11718617_a_at	**DNAJA4**	***DnaJ Heat Shock Protein Family (Hsp40) Member A4***	**1.1429**	**2.2083**
11723325_a_at	**KCNQ1**	***potassium voltage-gated channel subfamily Q member 1***	**1.1412**	**2.2057**
11759611_at	**SMIM11A**	***small integral membrane protein 11A***	**1.1401**	**2.2040**
11740995_x_at	**GLUL**	***glutamate-ammonia ligase***	**1.1372**	**2.1995**
11724620_a_at	**WDR78**	***WD repeat domain 78***	**1.1367**	**2.1987**
11743774_a_at	**LZTFL1**	***leucine zipper transcription factor like 1***	**1.1344**	**2.1953**
11715739_s_at	**PLPP3**	***phospholipid phosphatase 3***	**1.1343**	**2.1951**
11729130_at	**ANAPC16**	***anaphase promoting complex subunit 16***	**1.1327**	**2.1927**
11728388_at	**TSPAN2**	***tetraspanin 2***	**1.1278**	**2.1852**
11717993_at	**CBX7**	***chromobox 7***	**1.1275**	**2.1848**

11736801_a_at	**PLAG1**	***PLAG1 zinc finger***	**1.1271**	**2.1842**
11728530_a_at	**BLNK**	***B-cell linker***	**1.1266**	**2.1835**
11743730_at	**TNFSF10**	***tumor necrosis factor superfamily member 10***	**1.1260**	**2.1825**
11744132_at	**SECISBP2L**	***SECIS binding protein 2 like***	**1.1248**	**2.1807**
11735610_a_at	**RPS6KA5**	***ribosomal protein S6 kinase A5***	**1.1243**	**2.1800**
11755679_a_at	**CATSPERB**	***cation channel sperm associated auxiliary subunit beta***	**1.1242**	**2.1798**
11758736_at	**PSMC2**	***proteasome 26S subunit, ATPase 2***	**1.1235**	**2.1787**
11745723_a_at	**MALAT1**	***Metastasis Associated Lung Adenocarcinoma Transcript 1 (Non-Protein Coding)***	**1.1227**	**2.1776**
11733069_at	**WDR5B**	***WD repeat domain 5B***	**1.1223**	**2.1770**
11725035_s_at	**LMBRD1**	***LMBR1 domain containing 1***	**1.1215**	**2.1757**
11724691_at	**RIBC2**	***RIB43A domain with coiled-coils 2***	**1.1209**	**2.1748**
11727147_at	**ZNF564**	***zinc finger protein 564***	**1.1202**	**2.1737**
11720124_at	**SRD5A3**	***steroid 5 alpha-reductase 3***	**1.1182**	**2.1708**
11726384_at	**FRY**	***FRY microtubule binding protein***	**1.1168**	**2.1687**
11716302_s_at	**ACSL1**	***acyl-CoA synthetase long-chain family member 1***	**1.1167**	**2.1685**
11754914_x_at	**PGAP3**	***post-GPI attachment to proteins 3***	**1.1160**	**2.1675**
11729998_a_at	**B3GNT7**	***UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7***	**1.1147**	**2.1655**

11728055_at	**GHR**	***growth hormone receptor***	**1.1139**	**2.1643**
11739564_s_at	**ITPR1**	***inositol 1,4,5-trisphosphate receptor type 1***	**1.1133**	**2.1634**
11732569_at	**SLCO1B3**	***solute carrier organic anion transporter family member 1B3***	**1.1125**	**2.1622**
11732516_a_at	**CERS4**	***ceramide synthase 4***	**1.1120**	**2.1614**
11755220_a_at	**C17orf97**	***chromosome 17 open reading frame 97***	**1.1114**	**2.1606**
11720834_a_at	**APIP**	***APAF1 interacting protein***	**1.1088**	**2.1566**
11732920_a_at	**FOXN4**	***forkhead box N4***	**1.1088**	**2.1566**
11720196_at	**CIPC**	***CLOCK interacting pacemaker***	**1.1087**	**2.1565**
11764116_s_at	**LOC102724364**	***vesicle-trafficking protein SEC22b-like***	**1.1074**	**2.1545**
11719353_s_at	**GCC2**	***GRIP and coiled-coil domain containing 2***	**1.1034**	**2.1486**
11715617_a_at	**RNF130**	***ring finger protein 130***	**1.1028**	**2.1477**
11730133_s_at	**ICK**	***intestinal cell kinase***	**1.1027**	**2.1475**
11730802_at	**CRNN**	***cornulin***	**1.1016**	**2.1459**
11737215_a_at	**CRACR2B**	***calcium release activated channel regulator 2B***	**1.1002**	**2.1438**
11735839_at	**STX19**	***syntaxin 19***	**1.0997**	**2.1431**
11719025_a_at	**ZNF652**	***zinc finger protein 652***	**1.0990**	**2.1421**
11757333_s_at	**NUDT4**	***nudix hydrolase 4***	**1.0986**	**2.1415**

11719584_s_at	**CNNM3**	***cyclin and CBS domain divalent metal cation transport mediator 3***	**1.0978**	**2.1403**
11739734_a_at	**CPEB4**	***cytoplasmic polyadenylation element binding protein 4***	**1.0978**	**2.1403**
11723876_at	**KCNK5**	***potassium two pore domain channel subfamily K member 5***	**1.0970**	**2.1391**
11718927_a_at	**ARID5B**	***AT-rich interaction domain 5B***	**1.0968**	**2.1388**
11733725_a_at	**CFB**	***complement factor B***	**1.0967**	**2.1386**
11720481_s_at	**ABCD3**	***ATP binding cassette subfamily D member 3***	**1.0964**	**2.1382**
11722485_a_at	**ALG11**	***ALG11, alpha-1,2-mannosyltransferase***	**1.0944**	**2.1352**
11758110_s_at	**SIX1**	***SIX homeobox 1***	**1.0925**	**2.1325**
11716823_s_at	**BDH2**	***3-hydroxybutyrate dehydrogenase, type 2***	**1.0921**	**2.1318**
11727113_at	**EGF**	***epidermal growth factor***	**1.0901**	**2.1289**
11727377_a_at	**TBC1D15**	***TBC1 domain family member 15***	**1.0879**	**2.1257**
11734141_at	**GK5**	***Glycerol Kinase 5 (Putative)***	**1.0877**	**2.1254**
11730439_a_at	**AKAP9**	***A-kinase anchoring protein 9***	**1.0864**	**2.1234**
11725890_s_at	**ABCC6**	***ATP binding cassette subfamily C member 6***	**1.0849**	**2.1212**
11736257_at	**PRKCE**	***protein kinase C epsilon***	**1.0847**	**2.1209**
11728483_at	**ZNF181**	***zinc finger protein 181***	**1.0846**	**2.1208**
11756146_x_at	**S100A4**	***S100 calcium binding protein A4***	**1.0846**	**2.1208**

11726055_at	**B3GALT4**	***beta-1,3-galactosyltransferase 4***	**1.0845**	**2.1206**
11752501_a_at	**ACKR3**	***atypical chemokine receptor 3***	**1.0843**	**2.1204**
11764283_s_at	**PNISR**	***PNN interacting serine and arginine rich protein***	**1.0841**	**2.1201**
11755814_a_at	**CFAP43**	***cilia and flagella associated protein 43***	**1.0839**	**2.1198**
11742683_x_at	**HIST1H1C**	***histone cluster 1 H1 family member c***	**1.0832**	**2.1187**
11753966_a_at	**ZNF204P**	***zinc finger protein 204, pseudogene***	**1.0791**	**2.1127**
11720503_a_at	**ALDH3A2**	***aldehyde dehydrogenase 3 family member A2***	**1.0789**	**2.1124**
11725849_s_at	**SENP7**	***SUMO1/sentrin specific peptidase 7***	**1.0785**	**2.1119**
11724296_a_at	**BMP7**	***bone morphogenetic protein 7***	**1.0755**	**2.1075**
11755349_a_at	**GDPD3**	***glycerophosphodiester phosphodiesterase domain containing 3***	**1.0742**	**2.1055**
11721413_at	**MBTD1**	***mbt domain containing 1***	**1.0733**	**2.1042**
11720717_a_at	**FGF13**	***fibroblast growth factor 13***	**1.0723**	**2.1028**
11717348_a_at	**ADD3**	***adducin 3***	**1.0710**	**2.1009**
11723786_a_at	**ZNF766**	***zinc finger protein 766***	**1.0704**	**2.1000**
11742046_a_at	**PCMTD2**	***Protein-L-Isoaspartate (D-Aspartate) O-Methyltransferase Domain Containing 2***	**1.0703**	**2.0999**
11726443_a_at	**KCTD6**	***potassium channel tetramerization domain containing 6***	**1.0685**	**2.0972**
11739762_a_at	**CLDN10**	***claudin 10***	**1.0685**	**2.0972**

11733432_at	**AK7**	***adenylate kinase 7***	**1.0682**	**2.0968**
11724940_x_at	**CDHR3**	***cadherin related family member 3***	**1.0676**	**2.0960**
11759674_a_at	**CAPS2**	***calcyphosine 2***	**1.0669**	**2.0949**
11741192_a_at	**RBKS**	***ribokinase***	**1.0652**	**2.0925**
11741276_s_at	**TMEM144**	***transmembrane protein 144***	**1.0644**	**2.0913**
11719432_at	**KIAA0513**	***KIAA0513***	**1.0630**	**2.0893**
11732414_a_at	**LRRC8B**	***leucine rich repeat containing 8 family member B***	**1.0624**	**2.0884**
11718523_s_at	**ANTXR1**	***anthrax toxin receptor 1***	**1.0618**	**2.0875**
11721978_a_at	**PLCE1**	***phospholipase C epsilon 1***	**1.0615**	**2.0871**
11732261_a_at	**RRAGB**	***Ras related GTP binding B***	**1.0605**	**2.0856**
11759895_at	**PCDH9**	***protocadherin 9***	**1.0601**	**2.0851**
11735212_at	**STYK1**	***serine/threonine/tyrosine kinase 1***	**1.0600**	**2.0850**
11715722_a_at	**GOLM1**	***golgi membrane protein 1***	**1.0598**	**2.0846**
11758955_at	**LGALS8**	***galectin 8***	**1.0586**	**2.0829**
11728177_a_at	**DYX1C1**	***dyslexia susceptibility 1 candidate 1***	**1.0569**	**2.0805**
11726152_a_at	**ZBTB21**	***zinc finger and BTB domain containing 21***	**1.0552**	**2.0780**
11756809_a_at	**EFHC2**	***EF-hand domain containing 2***	**1.0544**	**2.0769**

11731874_x_at	**MIA2**	***melanoma inhibitory activity 2***	**1.0533**	**2.0753**
11732674_at	**C1orf53**	***chromosome 1 open reading frame 53***	**1.0526**	**2.0743**
11724367_a_at	**SEMA6D**	***semaphorin 6D***	**1.0525**	**2.0741**
11734752_a_at	**ARHGAP24**	***Rho GTPase activating protein 24***	**1.0508**	**2.0717**
11724588_a_at	**ANKRD35**	***ankyrin repeat domain 35***	**1.0498**	**2.0702**
11737546_at	**ZNF648**	***zinc finger protein 648***	**1.0480**	**2.0676**
11735478_a_at	**CHST6**	***carbohydrate sulfotransferase 6***	**1.0470**	**2.0662**
11730455_a_at	**SLC35A3**	***solute carrier family 35 member A3***	**1.0457**	**2.0644**
11717522_at	**TMEM50B**	***transmembrane protein 50B***	**1.0431**	**2.0607**
11733877_s_at	**LMO7**	***LIM domain 7***	**1.0426**	**2.0600**
11755525_a_at	**ATOH8**	***atonal bHLH transcription factor 8***	**1.0415**	**2.0583**
11732589_a_at	**ZNF467**	***zinc finger protein 467***	**1.0404**	**2.0568**
11716698_s_at	**HBP1**	***HMG-box transcription factor 1***	**1.0401**	**2.0564**
11722325_a_at	**ZNF84**	***zinc finger protein 84***	**1.0398**	**2.0560**
11756604_a_at	**PCDHB2**	***protocadherin beta 2***	**1.0387**	**2.0544**
11743025_at	**ATP7A**	***ATPase copper transporting alpha***	**1.0382**	**2.0537**
11727286_a_at	**ZSCAN31**	***zinc finger and SCAN domain containing 31***	**1.0382**	**2.0536**

11757896_s_at	**RSRP1**	***arginine and serine rich protein 1***	**1.0382**	**2.0536**
11758582_s_at	**SIX4**	***SIX homeobox 4***	**1.0360**	**2.0506**
11759623_at	**C11orf71**	***chromosome 11 open reading frame 71***	**1.0358**	**2.0502**
11758385_s_at	**HEY2**	***hes related family bHLH transcription factor with YRPW motif 2***	**1.0356**	**2.0500**
11756316_a_at	**CHI3L1**	***chitinase 3 like 1***	**1.0351**	**2.0492**
11723221_a_at	**EXOC6**	***exocyst complex component 6***	**1.0346**	**2.0485**
11721480_s_at	**GOLPH3L**	***golgi phosphoprotein 3 like***	**1.0344**	**2.0483**
11721974_a_at	**SUOX**	***sulfite oxidase***	**1.0331**	**2.0464**
11724374_at	**BATF**	***basic leucine zipper ATF-like transcription factor***	**1.0331**	**2.0464**
11728939_at	**RASEF**	***RAS and EF-hand domain containing***	**1.0325**	**2.0455**
11734144_s_at	**LRRC37A2**	***leucine rich repeat containing 37 member A2***	**1.0324**	**2.0454**
11737330_at	**ZNF345**	***zinc finger protein 345***	**1.0322**	**2.0452**
11744517_a_at	**SLC2A10**	***solute carrier family 2 member 10***	**1.0321**	**2.0450**
11717496_a_at	**IMPA2**	***inositol monophosphatase 2***	**1.0282**	**2.0395**
11727164_at	**ACVR2A**	***activin A receptor type 2A***	**1.0281**	**2.0393**
11740832_at	**PLEKHG7**	***pleckstrin homology and RhoGEF domain containing G7***	**1.0279**	**2.0391**
11730855_a_at	**HMGN3**	***high mobility group nucleosomal binding domain 3***	**1.0272**	**2.0381**

11720367_a_at	**TMEM2**	***transmembrane protein 2***	**1.0258**	**2.0361**
11718272_a_at	**TAX1BP1**	***Tax1 binding protein 1***	**1.0250**	**2.0349**
11716485_at	**STK38**	***serine/threonine kinase 38***	**1.0239**	**2.0334**
11728145_a_at	**SHC2**	***SHC adaptor protein 2***	**1.0239**	**2.0334**
11735119_x_at	**NBR1**	***NBR1, autophagy cargo receptor***	**1.0236**	**2.0330**
11717774_a_at	**PLEKHB1**	***pleckstrin homology domain containing B1***	**1.0236**	**2.0330**
11716734_at	**IRF1**	***interferon regulatory factor 1***	**1.0235**	**2.0328**
11729252_a_at	**SLC44A3**	***solute carrier family 44 member 3***	**1.0225**	**2.0315**
11744453_s_at	**TMBIM4**	***transmembrane BAX inhibitor motif containing 4***	**1.0223**	**2.0311**
11742725_s_at	**ELF2**	***E74 like ETS transcription factor 2***	**1.0221**	**2.0309**
11741124_a_at	**SAR1B**	***secretion associated Ras related GTPase 1B***	**1.0220**	**2.0308**
11729258_at	**MNS1**	***meiosis specific nuclear structural 1***	**1.0213**	**2.0297**
11737812_a_at	**NNT**	***nicotinamide nucleotide transhydrogenase***	**1.0193**	**2.0270**
11720377_s_at	**SAP30L**	***SAP30 like***	**1.0187**	**2.0261**
11715466_at	**ARHGDIB**	***Rho GDP dissociation inhibitor beta***	**1.0184**	**2.0257**
11718824_at	**IGIP**	***IgA inducing protein***	**1.0181**	**2.0252**
11727500_at	**ALDH3B2**	***aldehyde dehydrogenase 3 family member B2***	**1.0176**	**2.0246**

11733385_a_at	**TMEM182**	***transmembrane protein 182***	**1.0167**	**2.0233**
11716784_at	**TRAK2**	***trafficking kinesin protein 2***	**1.0166**	**2.0232**
11736422_s_at	**POSTN**	***periostin***	**1.0150**	**2.0209**
11732326_x_at	**PBLD**	***phenazine biosynthesis like protein domain containing***	**1.0133**	**2.0185**
11733742_a_at	**DCXR**	***dicarbonyl and L-xylulose reductase***	**1.0129**	**2.0179**
11743197_at	**TLR4**	***toll like receptor 4***	**1.0129**	**2.0179**
11716937_a_at	**NUPR1**	***nuclear protein 1, transcriptional regulator***	**1.0114**	**2.0159**
11732773_at	**CCDC57**	***coiled-coil domain containing 57***	**1.0113**	**2.0157**
11723329_a_at	**GSN**	***gelsolin***	**1.0112**	**2.0156**
11725644_at	**TET2**	***tet methylcytosine dioxygenase 2***	**1.0109**	**2.0151**
11721217_s_at	**TMEM106B**	***transmembrane protein 106B***	**1.0107**	**2.0149**
11716972_s_at	**NSF**	***N-ethylmaleimide sensitive factor, vesicle fusing ATPase***	**1.0105**	**2.0146**
11732689_s_at	**TTC14**	***tetratricopeptide repeat domain 14***	**1.0095**	**2.0132**
11720518_a_at	**TACC2**	***transforming acidic coiled-coil containing protein 2***	**1.0090**	**2.0125**
11728488_a_at	**NRXN3**	***neurexin 3***	**1.0089**	**2.0124**
11743716_a_at	**BRWD1**	***bromodomain and WD repeat domain containing 1***	**1.0086**	**2.0120**
11726258_at	**RNF141**	***ring finger protein 141***	**1.0084**	**2.0117**

11757483_s_at	VWA1	*von Willebrand factor A domain containing 1*	1.0078	2.0108
11742685_a_at	LAMP2	*lysosomal associated membrane protein 2*	1.0072	2.0100
11736744_x_at	C1orf168	*chromosome 1 open reading frame 168*	1.0056	2.0078
11724022_a_at	TRIM13	*tripartite motif containing 13*	1.0046	2.0064
11739942_s_at	SEPSECS	*Sep (O-Phosphoserine) TRNA:Sec (Selenocysteine) TRNA Synthase*	1.0042	2.0058
11720743_x_at	CROT	*carnitine O-octanoyltransferase*	1.0025	2.0035
11733013_at	PEX2	*peroxisomal biogenesis factor 2*	1.0025	2.0034
11716464_at	SIAE	*sialic acid acetylesterase*	1.0025	2.0034
11736747_x_at	ADAM28	*ADAM metallopeptidase domain 28*	1.0016	2.0022
11736159_a_at	MPPE1	*metallophosphoesterase 1*	1.0013	2.0018
11719004_at	ANKH	*ANKH inorganic pyrophosphate transport regulator*	1.0004	2.0005
11733804_at	AMN	*amnion associated transmembrane protein*	1.0002	2.0003
11726310_at	GLRB	*glycine receptor beta*	1.0002	2.0003
11754808_s_at	CPAMD8	*C3 and PZP like, alpha-2-macroglobulin domain containing 8*	1.0002	2.0003
DOWNREGULATED mRNAs (739)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log2Ratio**	**Fold Change**
11717355_a_at	FEZ1	*fasciculation and elongation protein zeta 1*	-3.8997	0.0670
11738511_at	DEFB4B	*defensin beta 4B*	-3.5598	0.0848
11758672_s_at	UCHL1	*ubiquitin C-terminal hydrolase L1*	-3.5295	0.0866
11757698_s_at	MIG7	*mig-7*	-3.4675	0.0904
11735693_x_at	SPRR2E	*small proline rich protein 2E*	-3.4643	0.0906
11729712_at	SPRR2A	*small proline rich protein 2A*	-3.4375	0.0923
11751020_a_at	RHCG	*Rh family C glycoprotein*	-3.3452	0.0984
11715524_a_at	COTL1	*coactosin like F-actin binding protein 1*	-3.3162	0.1004

11721307_at	PHLDA1	*pleckstrin homology like domain family A member 1*	-3.2919	0.1021
11725703_a_at	KLK6	*kallikrein related peptidase 6*	-3.2723	0.1035
11719916_at	IL1B	*interleukin 1 beta*	-3.0710	0.1190
11755207_a_at	NT5E	*5'-nucleotidase ecto*	-3.0493	0.1208
11754662_s_at	ADAMTS1	*ADAM metallopeptidase with thrombospondin type 1 motif 1*	-3.0350	0.1220
11729265_at	SPRR2D	*small proline rich protein 2D*	-3.0093	0.1242
11726909_at	ZBED2	*zinc finger BED-type containing 2*	-3.0035	0.1247
11754360_a_at	RRM2	*ribonucleotide reductase regulatory subunit M2*	-2.9669	0.1279
11715562_x_at	SCD	*stearoyl-CoA desaturase*	-2.9613	0.1284
11737798_a_at	PROCR	*protein C receptor*	-2.9490	0.1295
11737324_x_at	LAMC2	*laminin subunit gamma 2*	-2.9280	0.1314
11758478_s_at	CDCA7	*cell division cycle associated 7*	-2.9225	0.1319
11729243_s_at	FBN2	*fibrillin 2*	-2.9073	0.1333
11733957_x_at	SPRR2F	*small proline rich protein 2F*	-2.9073	0.1333
11728715_at	CXCL5	*C-X-C motif chemokine ligand 5*	-2.8997	0.1340
11717481_s_at	FKBP10	*FK506 binding protein 10*	-2.8932	0.1346
11753008_a_at	IL36G	*interleukin 36, gamma*	-2.8562	0.1381
11758261_s_at	CEP55	*centrosomal protein 55*	-2.7939	0.1442
11732719_at	EREG	*epiregulin*	-2.7919	0.1444
11720020_x_at	RTEL1-TNFRSF6B	*RTEL1-TNFRSF6B Readthrough (NMD Candidate)*	-2.7829	0.1453
11715306_s_at	AREG	*amphiregulin*	-2.7642	0.1472
11720970_at	TOP2A	*Topoisomerase (DNA) II Alpha*	-2.7563	0.1480
11751805_a_at	TYMS	*thymidylate synthetase*	-2.7341	0.1503
11733695_a_at	UBE2C	*ubiquitin conjugating enzyme E2 C*	-2.7160	0.1522
11722572_at	CCNA2	*cyclin A2*	-2.6971	0.1542
11724032_a_at	FST	*follistatin*	-2.6785	0.1562
11752670_a_at	MIR1908	*microRNA 1908*	-2.6739	0.1567
11716358_s_at	PRC1	*protein regulator of cytokinesis 1*	-2.6666	0.1575
11758125_s_at	DEPDC1B	*DEP domain containing 1B*	-2.6295	0.1616
11739061_at	SLC7A5	*solute carrier family 7 member 5*	-2.6242	0.1622
11757783_s_at	VCAN	*versican*	-2.5986	0.1651
11724478_s_at	FOSL1	*FOS like 1, AP-1 transcription factor subunit*	-2.5960	0.1654
11750598_s_at	TPX2	*TPX2, microtubule nucleation factor*	-2.5916	0.1659
11743721_at	LGALS1	*galectin 1*	-2.5743	0.1679
11723804_a_at	AKAP12	*A-kinase anchoring protein 12*	-2.5718	0.1682
11721143_a_at	MKI67	*marker of proliferation Ki-67*	-2.5666	0.1688
11717154_a_at	PLAU	*plasminogen activator, urokinase*	-2.5547	0.1702
11717566_at	EMP1	*epithelial membrane protein 1*	-2.5023	0.1765
11723298_s_at	AKAP2	*A-kinase anchoring protein 2*	-2.4982	0.1770
11747399_x_at	PLAT	*plasminogen activator, tissue type*	-2.4901	0.1780
11724459_x_at	MIR6756	*microRNA 6756*	-2.4763	0.1797
11753255_a_at	KLK7	*kallikrein related peptidase 7*	-2.4755	0.1798

11721092_a_at	**THBS1**	***thrombospondin 1***	**-2.4604**	**0.1817**
11729579_at	**CDH13**	***cadherin 13***	**-2.4525**	**0.1827**
11723939_a_at	**CCNB1**	***cyclin B1***	**-2.4391**	**0.1844**
11740656_a_at	**HMGA2**	***high mobility group AT-hook 2***	**-2.4305**	**0.1855**
11760935_x_at	**KRT6B**	***keratin 6B***	**-2.4074**	**0.1885**
11745464_x_at	**CDKN3**	***cyclin dependent kinase inhibitor 3***	**-2.3868**	**0.1912**
11740957_x_at	**SLC2A6**	***solute carrier family 2 member 6***	**-2.3823**	**0.1918**
11731394_a_at	**VIM**	***vimentin***	**-2.3823**	**0.1918**
11719898_s_at	**HBEGF**	***heparin binding EGF like growth factor***	**-2.3651**	**0.1941**
11756918_a_at	**KIF23**	***kinesin family member 23***	**-2.3651**	**0.1941**
11755200_a_at	**DCBLD2**	***discoidin, CUB and LCCL domain containing 2***	**-2.3599**	**0.1948**
11719197_at	**CCND2**	***cyclin D2***	**-2.3540**	**0.1956**
11751116_a_at	**ACTN1**	***actinin alpha 1***	**-2.3408**	**0.1974**
11728404_at	**SHCBP1**	***SHC binding and spindle associated 1***	**-2.3212**	**0.2001**
11718127_at	**TK1**	***thymidine kinase 1***	**-2.3004**	**0.2030**
11725749_a_at	**GAL**	***galanin and GMAP prepropeptide***	**-2.2990**	**0.2032**
11742735_a_at	**NUSAP1**	***nucleolar and spindle associated protein 1***	**-2.2884**	**0.2047**
11718005_a_at	**CDC25B**	***cell division cycle 25B***	**-2.2765**	**0.2064**
11743252_a_at	**CALD1**	***caldesmon 1***	**-2.2653**	**0.2080**
11728863_at	**GINS1**	***GINS complex subunit 1***	**-2.2550**	**0.2095**
11718832_a_at	**LOXL2**	***lysyl oxidase like 2***	**-2.2406**	**0.2116**
11746880_x_at	**FLNA**	***filamin A***	**-2.2351**	**0.2124**
11730096_a_at	**BCL2A1**	***BCL2 related protein A1***	**-2.2270**	**0.2136**
11753830_a_at	**MLLT11**	***myeloid/lymphoid or mixed-lineage leukemia; translocated to, 11***	**-2.2243**	**0.2140**
11745948_a_at	**CHEK1**	***checkpoint kinase 1***	**-2.2243**	**0.2140**
11715491_s_at	**FSCN1**	***fascin actin-bundling protein 1***	**-2.2236**	**0.2141**
11725198_at	**IL1A**	***interleukin 1 alpha***	**-2.2196**	**0.2147**
11745722_x_at	**FHL1**	***four and a half LIM domains 1***	**-2.2176**	**0.2150**
11742832_a_at	**ASPM**	***abnormal spindle microtubule assembly***	**-2.2142**	**0.2155**
11755046_a_at	**SPHK1**	***sphingosine kinase 1***	**-2.2096**	**0.2162**
11724888_a_at	**CARD10**	***caspase recruitment domain family member 10***	**-2.1976**	**0.2180**
11733115_a_at	**CA2**	***carbonic anhydrase 2***	**-2.1917**	**0.2189**
11717163_s_at	**CDC20**	***cell division cycle 20***	**-2.1857**	**0.2198**
11744425_a_at	**KIAA0101**	***KIAA0101***	**-2.1851**	**0.2199**
11716793_a_at	**CCNB2**	***cyclin B2***	**-2.1844**	**0.2200**
11745377_x_at	**PTRF**	***polymerase I and transcript release factor***	**-2.1766**	**0.2212**
11732997_a_at	**MCM6**	***minichromosome maintenance complex component 6***	**-2.1766**	**0.2212**
11720528_at	**LTBP2**	***latent transforming growth factor beta binding protein 2***	**-2.1733**	**0.2217**
11733864_a_at	**BIRC5**	***baculoviral IAP repeat containing 5***	**-2.1675**	**0.2226**
11724139_s_at	**SACS**	***sacsin molecular chaperone***	**-2.1629**	**0.2233**
11722826_a_at	**NCAPG**	***non-SMC condensin I complex subunit G***	**-2.1629**	**0.2233**
11747820_x_at	**UPP1**	***uridine phosphorylase 1***	**-2.1591**	**0.2239**

11722839_at	LYAR	*Ly1 antibody reactive*	-2.1475	0.2257
11723104_at	GNB4	*G protein subunit beta 4*	-2.1380	0.2272
11715716_at	MSN	*moesin*	-2.1272	0.2289
11754074_s_at	G0S2	*G0/G1 switch 2*	-2.1272	0.2289
11731526_s_at	TRIP13	*thyroid hormone receptor interactor 13*	-2.1266	0.2290
11754593_x_at	TUBB3	*tubulin beta 3 class III*	-2.1253	0.2292
11728135_at	NIPAL4	*NIPA like domain containing 4*	-2.1228	0.2296
11739328_x_at	CENPH	*centromere protein H*	-2.1153	0.2308
11733884_a_at	DEPDC1	*DEP domain containing 1*	-2.1103	0.2316
11725155_at	FJX1	*four jointed box 1*	-2.1090	0.2318
11741376_a_at	LRP8	*LDL receptor related protein 8*	-2.1016	0.2330
11723151_s_at	SUGCT	*succinyl-CoA:glutarate-CoA transferase*	-2.0948	0.2341
11718290_a_at	FXYD5	*FXYD domain containing ion transport regulator 5*	-2.0899	0.2349
11725459_s_at	S100A7A	*S100 calcium binding protein A7A*	-2.0813	0.2363
11716587_at	AXL	*AXL receptor tyrosine kinase*	-2.0643	0.2391
11722367_a_at	DLGAP5	*DLG associated protein 5*	-2.0607	0.2397
11744263_s_at	RAC2	*Ras-Related C3 Botulinum Toxin Substrate 2 (Rho Family, Small GTP Binding Protein Rac2)*	-2.0499	0.2415
11744435_a_at	DUSP6	*dual specificity phosphatase 6*	-2.0487	0.2417
11725460_x_at	S100A7	*S100 calcium binding protein A7*	-2.0439	0.2425
11733465_at	XDH	*xanthine dehydrogenase*	-2.0416	0.2429
11727215_a_at	NRG1	*neuregulin 1*	-2.0410	0.2430
11723192_a_at	UHRF1	*ubiquitin like with PHD and ring finger domains 1*	-2.0398	0.2432
11746931_a_at	INHBA	*inhibin beta A subunit*	-2.0368	0.2437
11743065_at	CDC6	*cell division cycle 6*	-2.0309	0.2447
11745868_a_at	KIF2C	*kinesin family member 2C*	-2.0250	0.2457
11763367_at	NABP1	*nucleic acid binding protein 1*	-2.0239	0.2459
11715803_a_at	ANXA6	*annexin A6*	-2.0221	0.2462
11732999_a_at	ICAM1	*intercellular adhesion molecule 1*	-2.0157	0.2473
11755252_a_at	AMIGO2	*adhesion molecule with Ig like domain 2*	-2.0087	0.2485
11723499_a_at	PCSK9	*proprotein convertase subtilisin/kexin type 9*	-2.0081	0.2486
11721068_a_at	FHOD3	*formin homology 2 domain containing 3*	-2.0075	0.2487
11715915_a_at	CD44	*CD44 Molecule (Indian Blood Group)*	-2.0075	0.2487
11721842_a_at	GLIPR1	*GLI pathogenesis related 1*	-2.0069	0.2488
11723010_a_at	KIF20A	*kinesin family member 20A*	-2.0069	0.2488
11727455_x_at	SCGB1A1	*secretoglobin family 1A member 1*	-2.0064	0.2489
11757940_at	PGF	*placental growth factor*	-2.0064	0.2489
11720203_a_at	AURKB	*aurora kinase B*	-2.0023	0.2496
11718943_a_at	AURKA	*aurora kinase A*	-1.9896	0.2518
11723950_a_at	PBK	*PDZ binding kinase*	-1.9822	0.2531
11743513_a_at	GINS2	*GINS complex subunit 2*	-1.9817	0.2532
11718183_at	CDCA5	*cell division cycle associated 5*	-1.9692	0.2554
11750723_x_at	MICB	*MHC class I polypeptide-related sequence B*	-1.9635	0.2564

11737184_at	SAA2	*serum amyloid A2*	-1.9602	0.2570
11758529_s_at	CENPA	*centromere protein A*	-1.9585	0.2573
11725274_s_at	RGS20	*regulator of G-protein signaling 20*	-1.9568	0.2576
11752515_a_at	ODC1	*ornithine decarboxylase 1*	-1.9529	0.2583
11719262_a_at	SMTN	*smoothelin*	-1.9506	0.2587
11719849_s_at	UBE2S	*ubiquitin conjugating enzyme E2 S*	-1.9473	0.2593
11722880_a_at	PHF19	*PHD finger protein 19*	-1.9462	0.2595
11745929_a_at	AHCY	*adenosylhomocysteinase*	-1.9429	0.2601
11728054_a_at	DIAPH3	*diaphanous related formin 3*	-1.9335	0.2618
11758089_s_at	HMMR	*hyaluronan mediated motility receptor*	-1.9296	0.2625
11743530_a_at	CENPK	*centromere protein K*	-1.9219	0.2639
11733442_x_at	SAA1	*serum amyloid A1*	-1.9138	0.2654
11751993_a_at	JAG1	*jagged 1*	-1.9110	0.2659
11748136_a_at	MAD2L1	*MAD2 mitotic arrest deficient-like 1 (yest)*	-1.9094	0.2662
11754313_s_at	ARL4C	*ADP ribosylation factor like GTPase 4C*	-1.9089	0.2663
11720794_a_at	SRPX	*sushi repeat containing protein, X-linked*	-1.9073	0.2666
11759429_a_at	KLF7	*Kruppel like factor 7*	-1.8965	0.2686
11723435_s_at	TTK	*TTK protein kinase*	-1.8911	0.2696
11754676_a_at	CENPE	*centromere protein E*	-1.8751	0.2726
11751206_s_at	RAB3GAP2	*RAB3 GTPase activating non-catalytic protein subunit 2*	-1.8730	0.2730
11758136_s_at	SLC35G2	*solute carrier family 35 member G2*	-1.8720	0.2732
11758619_s_at	LIF	*leukemia inhibitory factor*	-1.8693	0.2737
11743296_a_at	CENPF	*centromere protein F*	-1.8693	0.2737
11753704_a_at	STMN1	*stathmin 1*	-1.8683	0.2739
11724562_x_at	RHOF	*ras homolog family member F, filopodia associated*	-1.8678	0.2740
11724464_a_at	ANLN	*anillin actin binding protein*	-1.8678	0.2740
11749650_x_at	A2ML1	*alpha-2-macroglobulin like 1*	-1.8656	0.2744
11739536_x_at	FN1	*fibronectin 1*	-1.8630	0.2749
11745958_a_at	CD99	*CD99 molecule*	-1.8620	0.2751
11719032_a_at	FADS3	*fatty acid desaturase 3*	-1.8614	0.2752
11723829_s_at	ANO1	*anoctamin 1*	-1.8552	0.2764
11715437_at	TIMP3	*TIMP metallopeptidase inhibitor 3*	-1.8448	0.2784
11759328_at	KNL1	*kinetochore scaffold 1*	-1.8303	0.2812
11725945_x_at	TINAGL1	*tubulointerstitial nephritis antigen like 1*	-1.8247	0.2823
11751983_a_at	EGFR	*epidermal growth factor receptor*	-1.8181	0.2836
11727504_at	SOX7	*SRY-box 7*	-1.8160	0.2840
11715452_s_at	COL4A2	*collagen type IV alpha 2 chain*	-1.8069	0.2858
11755103_a_at	CDA	*cytidine deaminase*	-1.8054	0.2861
11753356_x_at	TUBB	*tubulin beta class I*	-1.8004	0.2871
11721256_a_at	CCND1	*cyclin D1*	-1.7989	0.2874
11719811_a_at	TRIB3	*tribbles pseudokinase 3*	-1.7964	0.2879
11746438_a_at	SHMT2	*serine hydroxymethyltransferase 2*	-1.7934	0.2885

11729263_x_at	**SERPINB9**	***serpin family B member 9***	**-1.7854**	**0.2901**
11716094_a_at	**KLF6**	***Kruppel like factor 6***	**-1.7834**	**0.2905**
11728024_a_at	**KLK5**	***kallikrein related peptidase 5***	**-1.7804**	**0.2911**
11723487_a_at	**LAMB1**	***laminin subunit beta 1***	**-1.7784**	**0.2915**
11725469_at	**LIPG**	***lipase G, endothelial type***	**-1.7774**	**0.2917**
11757789_a_at	**EPB41L2**	***erythrocyte membrane protein band 4.1 like 2***	**-1.7760**	**0.2920**
11755466_a_at	**CDCA2**	***cell division cycle associated 2***	**-1.7760**	**0.2920**
11750141_a_at	**CTPS1**	***CTP synthase 1***	**-1.7651**	**0.2942**
11722122_at	**CYP27B1**	***cytochrome P450 family 27 subfamily B member 1***	**-1.7637**	**0.2945**
11752047_a_at	**FERMT1**	***fermitin family member 1***	**-1.7637**	**0.2945**
11726757_s_at	**CDC25A**	***cell division cycle 25A***	**-1.7602**	**0.2952**
11746471_s_at	**MAP4K4**	***mitogen-activated protein kinase 4***	**-1.7558**	**0.2961**
11750186_a_at	**ALDH1A3**	***aldehyde dehydrogenase 1 family member A3***	**-1.7510**	**0.2971**
11720353_s_at	**ETV5**	***ETS variant 5***	**-1.7505**	**0.2972**
11758938_x_at	**SAA2-SAA4**	***SAA2-SAA4 readthrough***	**-1.7500**	**0.2973**
11727364_s_at	**SHC1**	***SHC adaptor protein 1***	**-1.7456**	**0.2982**
11716630_a_at	**ANGPTL4**	***angiopoietin like 4***	**-1.7456**	**0.2982**
11727489_a_at	**KIF11**	***kinesin family member 11***	**-1.7399**	**0.2994**
11744005_at	**PHLDA2**	***pleckstrin homology like domain family A member 2***	**-1.7317**	**0.3011**
11743169_a_at	**LPXN**	***leupaxin***	**-1.7288**	**0.3017**
11747361_x_at	**HMGA1**	***high mobility group AT-hook 1***	**-1.7269**	**0.3021**
11720647_a_at	**BUB1B**	***BUB1 mitotic checkpoint serine/threonine kinase B***	**-1.7259**	**0.3023**
11763188_a_at	**SNX5**	***sorting nexin 5***	**-1.7245**	**0.3026**
11724978_a_at	**ITGB4**	***integrin subunit beta 4***	**-1.7245**	**0.3026**
11755281_a_at	**TGFBI**	***transforming growth factor beta induced***	**-1.7245**	**0.3026**
11716638_s_at	**COL4A1**	***collagen type IV alpha 1 chain***	**-1.7236**	**0.3028**
11738997_s_at	**DPYSL2**	***dihydropyrimidinase like 2***	**-1.7207**	**0.3034**
11723883_at	**SOWAHC**	***sosondowah ankyrin repeat domain family member C***	**-1.7174**	**0.3041**
11756882_a_at	**RTTN**	***rotatin***	**-1.7160**	**0.3044**
11727837_at	**ORC6**	***origin recognition complex subunit 6***	**-1.7150**	**0.3046**
11718297_a_at	**TACC3**	***transforming acidic coiled-coil containing protein 3***	**-1.7145**	**0.3047**
11723591_at	**LRRC8C**	***leucine rich repeat containing 8 family member C***	**-1.7141**	**0.3048**
11743160_a_at	**HJURP**	***Holliday junction recognition protein***	**-1.7070**	**0.3063**
11729422_a_at	**POPDC3**	***popeye domain containing 3***	**-1.7065**	**0.3064**
11715951_s_at	**KCTD12**	***potassium channel tetramerization domain containing 12***	**-1.7042**	**0.3069**
11719699_a_at	**CDC45**	***cell division cycle 45***	**-1.7027**	**0.3072**
11724828_at	**CCL20**	***C-C motif chemokine ligand 20***	**-1.6999**	**0.3078**
11744286_s_at	**CBS**	***cystathionine-beta-synthase***	**-1.6953**	**0.3088**
11758222_s_at	**SLC20A1**	***solute carrier family 20 member 1***	**-1.6873**	**0.3105**
11745843_a_at	**CDK1**	***cyclin dependent kinase 1***	**-1.6790**	**0.3123**
11720566_at	**BCAT1**	***branched chain amino acid transaminase 1***	**-1.6716**	**0.3139**
11717055_a_at	**CORO1C**	***coronin 1C***	**-1.6666**	**0.3150**

11723274_a_at	SLC35F2	*solute carrier family 35 member F2*	-1.6657	0.3152
11718404_at	RFC3	*replication factor C subunit 3*	-1.6602	0.3164
11756952_a_at	TKT	*transketolase*	-1.6597	0.3165
11719194_a_at	DFNA5	*DFNA5, deafness associated tumor suppressor*	-1.6547	0.3176
11753619_s_at	EIF5AL1	*eukaryotic translation initiation factor 5A-like 1*	-1.6547	0.3176
11756790_a_at	ITGA3	*integrin subunit alpha 3*	-1.6538	0.3178
11733876_x_at	SMC4	*structural maintenance of chromosomes 4*	-1.6529	0.3180
11723414_a_at	CNN2	*calponin 2*	-1.6493	0.3188
11746875_x_at	GNAI2	*G protein subunit alpha i2*	-1.6448	0.3198
11726779_a_at	IKBIP	*IKBKB interacting protein*	-1.6430	0.3202
11747230_a_at	BUB1	*BUB1 mitotic checkpoint serine/threonine kinase*	-1.6416	0.3205
11726023_a_at	EDN1	*endothelin 1*	-1.6416	0.3205
11740722_a_at	IL1RN	*interleukin 1 receptor antagonist*	-1.6407	0.3207
11720448_at	SOX9	*SRY-box 9*	-1.6389	0.3211
11718204_a_at	REC8	*REC8 meiotic recombination protein*	-1.6317	0.3227
11740744_x_at	TPM2	*tropomyosin 2 (beta)*	-1.6304	0.3230
11751389_s_at	FEN1	*flap structure-specific endonuclease 1*	-1.6299	0.3231
11748045_x_at	LDLR	*low density lipoprotein receptor*	-1.6259	0.3240
11741015_a_at	CDCA8	*cell division cycle associated 8*	-1.6233	0.3246
11757022_x_at	TFPI2	*tissue factor pathway inhibitor 2*	-1.6215	0.3250
11734701_a_at	DKK3	*dickkopf WNT signaling pathway inhibitor 3*	-1.6162	0.3262
11739654_at	TNFRSF10A	*TNF receptor superfamily member 10a*	-1.6153	0.3264
11737223_a_at	ARTN	*artemin*	-1.6140	0.3267
11736810_at	RPL27A	*ribosomal protein L27a*	-1.6122	0.3271
11719824_at	ZAK	*sterile alpha motif and leucine zipper containing kinase AZK*	-1.6100	0.3276
11728233_a_at	CLDN1	*claudin 1*	-1.6091	0.3278
11754375_s_at	SNX10	*sorting nexin 10*	-1.6047	0.3288
11756358_a_at	PLK3	*polo like kinase 3*	-1.6021	0.3294
11732756_a_at	ELAVL2	*ELAV like RNA binding protein 2*	-1.6021	0.3294
11737852_s_at	PPP1R18	*protein phosphatase 1 regulatory subunit 18*	-1.6016	0.3295
11723747_a_at	FAM64A	*family with sequence similarity 64 member A*	-1.5951	0.3310
11719586_a_at	TAGLN3	*transgelin 3*	-1.5929	0.3315
11727937_x_at	MSANTD3	*Myb/SANT DNA binding domain containing 3*	-1.5834	0.3337
11735400_a_at	BNC1	*basonuclin 1*	-1.5812	0.3342
11756626_s_at	ZWINT	*ZW10 interacting kinetochore protein*	-1.5760	0.3354
11730264_a_at	FAM83D	*family with sequence similarity 83 member D*	-1.5730	0.3361
11728894_at	HES2	*hes family bHLH transcription factor 2*	-1.5722	0.3363
11722327_at	PGBD5	*piggyBac transposable element derived 5*	-1.5722	0.3363
11744034_a_at	VASP	*vasodilator-stimulated phosphoprotein*	-1.5709	0.3366
11727543_at	OIP5	*Opa interacting protein 5*	-1.5705	0.3367
11752905_a_at	MCM7	*minichromosome maintenance complex component 7*	-1.5705	0.3367
11717743_a_at	ACOT7	*acyl-CoA thioesterase 7*	-1.5688	0.3371

11747334_a_at	**DDX39A**	***DExD-box helicase 39A***	**-1.5683**	**0.3372**
11759496_at	**CHST11**	***carbohydrate sulfotransferase 11***	**-1.5666**	**0.3376**
11756412_a_at	**NT5DC2**	***5'-nucleotidase domain containing 2***	**-1.5645**	**0.3381**
11716494_a_at	**MAP4**	***microtubule associated protein 4***	**-1.5560**	**0.3401**
11754318_at	**SSH1**	***slingshot protein phosphatase 1***	**-1.5471**	**0.3422**
11718283_a_at	**EIF4EBP1**	***eukaryotic translation initiation factor 4E binding protein 1***	**-1.5441**	**0.3429**
11756666_x_at	**MCM2**	***minichromosome maintenance complex component 2***	**-1.5441**	**0.3429**
11754939_x_at	**FADS2**	***fatty acid desaturase 2***	**-1.5433**	**0.3431**
11726302_a_at	**DTL**	***denticleless E3 ubiquitin protein ligase homolog***	**-1.5433**	**0.3431**
11721854_a_at	**NCAPH**	***non-SMC condensin I complex subunit H***	**-1.5433**	**0.3431**
11750040_a_at	**ANXA5**	***annexin A5***	**-1.5408**	**0.3437**
11723225_a_at	**CLDN11**	***claudin 11***	**-1.5391**	**0.3441**
11717388_x_at	**SEPT11**	***septin 11***	**-1.5383**	**0.3443**
11736670_a_at	**MCM4**	***minichromosome maintenance complex component 4***	**-1.5370**	**0.3446**
11749461_a_at	**CDH11**	***cadherin 11***	**-1.5357**	**0.3449**
11738052_at	**MRGPRX3**	***MAS related GPR family member X3***	**-1.5349**	**0.3451**
11725049_s_at	**ARHGDIA**	***Rho GDP dissociation inhibitor alpha***	**-1.5337**	**0.3454**
11728303_at	**TGFA**	***transforming growth factor alpha***	**-1.5316**	**0.3459**
11755032_s_at	**ASAP1**	***ArfGAP with SH3 domain, ankyrin repeat and PH domain 1***	**-1.5274**	**0.3469**
11747039_x_at	**EHD1**	***EH domain containing 1***	**-1.5270**	**0.3470**
11716171_s_at	**LMNB2**	***lamin B2***	**-1.5241**	**0.3477**
11721828_x_at	**ZWILCH**	***zwilch kinetochore protein***	**-1.5241**	**0.3477**
11744047_a_at	**MAP1B**	***microtubule associated protein 1B***	**-1.5212**	**0.3484**
11739856_s_at	**TENM2**	***teneurin transmembrane protein 2***	**-1.5162**	**0.3496**
11725825_a_at	**GJB3**	***gap junction protein beta 3***	**-1.5158**	**0.3497**
11752051_a_at	**MYH9**	***myosin heavy chain 9***	**-1.5158**	**0.3497**
11751723_a_at	**KRT5**	***keratin 5***	**-1.5154**	**0.3498**
11744746_x_at	**TNIP1**	***TNFAIP3 interacting protein 1***	**-1.5137**	**0.3502**
11747427_a_at	**SEC14L2**	***SEC14 like lipid binding 2***	**-1.5068**	**0.3519**
11717863_a_at	**DUSP5**	***dual specificity phosphatase 5***	**-1.5059**	**0.3521**
11731602_at	**TMEM154**	***transmembrane protein 154***	**-1.5059**	**0.3521**
11716322_s_at	**PRKCDBP**	***protein kinase C delta binding protein***	**-1.5055**	**0.3522**
11718399_s_at	**TGM2**	***transglutaminase 2***	**-1.5051**	**0.3523**
11741680_a_at	**SERPINE2**	***serpin family E member 2***	**-1.5031**	**0.3528**
11727784_x_at	**TPM4**	***tropomyosin 4***	**-1.4978**	**0.3541**
11745198_s_at	**CDCA4**	***cell division cycle associated 4***	**-1.4974**	**0.3542**
11756121_a_at	**DUSP7**	***dual specificity phosphatase 7***	**-1.4957**	**0.3546**
11740062_a_at	**SIGMAR1**	***sigma non-opioid intracellular receptor 1***	**-1.4937**	**0.3551**
11743922_at	**NUDT11**	***nudix hydrolase 11***	**-1.4880**	**0.3565**
11749410_x_at	**DMKN**	***dermokine***	**-1.4876**	**0.3566**
11757458_s_at	**LRRC8A**	***leucine rich repeat containing 8 family member A***	**-1.4856**	**0.3571**
11746283_s_at	**KRTAP2-3**	***keratin associated protein 2-3***	**-1.4844**	**0.3574**

11743675_x_at	ABL2	*ABL proto-oncogene 2, non-receptor tyrosine kinase*	-1.4836	0.3576
11746856_a_at	SERPINE1	*serpin family E member 1*	-1.4836	0.3576
11739809_at	TMEM156	*transmembrane protein 156*	-1.4832	0.3577
11722069_a_at	SKA1	*spindle and kinetochore associated complex subunit 1*	-1.4828	0.3578
11716847_a_at	SLC43A3	*solute carrier family 43 member 3*	-1.4779	0.3590
11743373_a_at	KNSTRN	*kinetochore localized astrin/SPAG5 binding protein*	-1.4771	0.3592
11742890_at	MND1	*meiotic nuclear divisions 1*	-1.4735	0.3601
11737197_s_at	KIF4A	*kinesin family member 4A*	-1.4719	0.3605
11736596_s_at	GINS4	*GINS complex subunit 4*	-1.4683	0.3614
11744218_at	SNAI2	*snail family transcriptional repressor 2*	-1.4675	0.3616
11718141_at	DKK1	*dickkopf WNT signaling pathway inhibitor 1*	-1.4632	0.3627
11725641_at	EFHD2	*EF-hand domain family member D2*	-1.4612	0.3632
11730170_a_at	GPX3	*glutathione peroxidase 3*	-1.4592	0.3637
11739524_a_at	MPRIP	*myosin phosphatase Rho interacting protein*	-1.4552	0.3647
11736405_a_at	DNMT1	*DNA methyltransferase 1*	-1.4525	0.3654
11737413_at	MICALCL	*MICAL C-terminal like*	-1.4505	0.3659
11720620_s_at	ACLY	*ATP citrate lyase*	-1.4489	0.3663
11747634_a_at	PYGB	*phosphorylase, glycogen; brain*	-1.4477	0.3666
11717812_a_at	KIF3C	*kinesin family member 3C*	-1.4473	0.3667
11756230_a_at	FLNB	*filamin B*	-1.4469	0.3668
11720403_at	EFNB2	*ephrin B2*	-1.4414	0.3682
11739910_a_at	ELOVL6	*ELOVL fatty acid elongase 6*	-1.4403	0.3685
11746588_a_at	ALDH1B1	*aldehyde dehydrogenase 1 family member B1*	-1.4399	0.3686
11717521_x_at	PTTG3P	*pituitary tumor-transforming 3, pseudogene*	-1.4387	0.3689
11718140_a_at	EMP3	*epithelial membrane protein 3*	-1.4383	0.3690
11722931_a_at	GART	*phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase*	-1.4375	0.3692
11721345_at	PLEK2	*pleckstrin 2*	-1.4371	0.3693
11728415_s_at	POMZP3	*POM121 and ZP3 fusion*	-1.4332	0.3703
11720562_a_at	PLXNA2	*plexin A2*	-1.4328	0.3704
11715703_s_at	ITGA5	*integrin subunit alpha 5*	-1.4301	0.3711
11732329_a_at	MAP7D1	*MAP7 domain containing 1*	-1.4301	0.3711
11756298_a_at	SNRPA	*small nuclear ribonucleoprotein polypeptide A*	-1.4290	0.3714
11748763_a_at	EEF2	*eukaryotic translation elongation factor 2*	-1.4290	0.3714
11726441_a_at	ERCC6L	*ERCC excision repair 6 like, spindle assembly checkpoint helicase*	-1.4228	0.3730
11730235_a_at	MYADM	*myeloid associated differentiation marker*	-1.4200	0.3737
11754959_a_at	AK4	*adenylate kinase 4*	-1.4200	0.3737
11727731_at	RASGEF1A	*RasGEF domain family member 1A*	-1.4181	0.3742
11736931_s_at	FAM72C	*family with sequence similarity 72 member C*	-1.4162	0.3747
11753459_x_at	HNRNPA1	*heterogeneous nuclear ribonucleoprotein A1*	-1.4154	0.3749
11749098_a_at	CAPRIN2	*caprin family member 2*	-1.4108	0.3761
11725788_a_at	CENPN	*centromere protein N*	-1.4085	0.3767
11726717_at	C1orf74	*chromosome 1 open reading frame 74*	-1.4077	0.3769

11729514_a_at	CSF3	*colony stimulating factor 3*	-1.4051	0.3776
11739204_a_at	TTL	*tubulin tyrosine ligase*	-1.4043	0.3778
11724407_s_at	CCNE1	*cyclin E1*	-1.4035	0.3780
11726433_a_at	OSBPL3	*oxysterol binding protein like 3*	-1.4032	0.3781
11719173_s_at	PAICS	*phosphoribosylaminoimidazole carboxylase; phosphoribosylaminoimidazolesuccinocarboxamide synthase*	-1.4028	0.3782
11725842_a_at	PIF1	*PIF1 5'-to-3' DNA helicase*	-1.3982	0.3794
11715926_s_at	PLEC	*plectin*	-1.3967	0.3798
11752302_a_at	LAMB3	*laminin subunit beta 3*	-1.3948	0.3803
11746650_a_at	ACER3	*alkaline ceramidase 3*	-1.3937	0.3806
11744274_at	NDC80	*NDC80, kinetochore complex component*	-1.3914	0.3812
11725588_a_at	CBLC	*Cbl proto-oncogene C*	-1.3857	0.3827
11724209_a_at	KIFC1	*kinesin family member C1*	-1.3857	0.3827
11748995_a_at	MYO1C	*myosin IC*	-1.3812	0.3839
11753645_a_at	CFL1	*cofilin 1*	-1.3793	0.3844
11740991_a_at	TSPAN4	*tetraspanin 4*	-1.3786	0.3846
11725110_a_at	NDE1	*nudE neurodevelopment protein 1*	-1.3759	0.3853
11716132_a_at	FSTL3	*follistatin like 3*	-1.3759	0.3853
11717731_at	SQLE	*squalene epoxidase*	-1.3759	0.3853
11729063_a_at	PDGFA	*platelet derived growth factor subunit A*	-1.3756	0.3854
11721563_a_at	MELK	*maternal embryonic leucine zipper kinase*	-1.3744	0.3857
11719218_at	SOCS3	*suppressor of cytokine signaling 3*	-1.3737	0.3859
11757152_s_at	MIR1304	*microRNA 1304*	-1.3737	0.3859
11716262_a_at	AP2B1	*adaptor related protein complex 2 beta 1 subunit*	-1.3733	0.3860
11755219_a_at	THBD	*thrombomodulin*	-1.3730	0.3861
11717909_at	IGFBP6	*insulin like growth factor binding protein 6*	-1.3707	0.3867
11722121_a_at	PC	*pyruvate carboxylase*	-1.3703	0.3868
11752113_a_at	INPP4B	*inositol polyphosphate-4-phosphatase type II B*	-1.3692	0.3871
11743467_at	MIR664B	*microRNA 664b*	-1.3685	0.3873
11748025_s_at	GJB2	*gap junction protein beta 2*	-1.3681	0.3874
11730875_a_at	FANCI	*Fanconi anemia complementation group I*	-1.3670	0.3877
11723616_a_at	PLTP	*phospholipid transfer protein*	-1.3666	0.3878
11726536_at	CYP1A1	*cytochrome P450 family 1 subfamily A member 1*	-1.3666	0.3878
11722300_a_at	ETS1	*ETS proto-oncogene 1, transcription factor*	-1.3651	0.3882
11718634_a_at	KIF1B	*kinesin family member 1B*	-1.3636	0.3886
11719179_a_at	PVR	*poliovirus receptor*	-1.3625	0.3889
11760037_a_at	GLS	*glutaminase*	-1.3614	0.3892
11755006_x_at	BCAR3	*breast cancer anti-estrogen resistance 3*	-1.3607	0.3894
11720400_at	NCS1	*neuronal calcium sensor 1*	-1.3607	0.3894
11720154_at	NRIP1	*nuclear receptor interacting protein 1*	-1.3559	0.3907
11744272_a_at	NCAPD2	*non-SMC condensin I complex subunit D2*	-1.3559	0.3907
11743314_a_at	FASN	*fatty acid synthase*	-1.3525	0.3916
11736687_a_at	FGF5	*fibroblast growth factor 5*	-1.3522	0.3917

11730374_a_at	FYB	*FYN binding protein*	-1.3507	0.3921
11728410_a_at	INO80C	*INO80 complex subunit C*	-1.3503	0.3922
11734177_a_at	SLC2A9	*solute carrier family 2 member 9*	-1.3503	0.3922
11744519_a_at	POLE2	*DNA polymerase epsilon 2, accessory subunit*	-1.3503	0.3922
11736029_a_at	ITGA6	*integrin subunit alpha 6*	-1.3496	0.3924
11728731_s_at	DSCC1	*DNA replication and sister chromatid cohesion 1*	-1.3478	0.3929
11742992_s_at	PSAT1	*phosphoserine aminotransferase 1*	-1.3474	0.3930
11747935_a_at	TNC	*tenascin C*	-1.3470	0.3931
11742184_a_at	LAMA3	*laminin subunit alpha 3*	-1.3463	0.3933
11728203_a_at	PHGDH	*phosphoglycerate dehydrogenase*	-1.3437	0.3940
11717617_a_at	PXN	*paxillin*	-1.3415	0.3946
11739144_a_at	SKP2	*S-phase kinase associated protein 2*	-1.3375	0.3957
11743063_x_at	PLAUR	*plasminogen activator, urokinase receptor*	-1.3364	0.3960
11750045_x_at	TPM3	*tropomyosin 3*	-1.3353	0.3963
11756393_x_at	CORO1A	*coronin 1A*	-1.3335	0.3968
11723389_a_at	C16orf74	*chromosome 16 open reading frame 74*	-1.3324	0.3971
11716150_a_at	PMEPA1	*prostate transmembrane protein, androgen induced 1*	-1.3313	0.3974
11758266_s_at	PSMD2	*proteasome 26S subunit, non-ATPase 2*	-1.3313	0.3974
11720047_a_at	ARMCX1	*armadillo repeat containing, X-linked 1*	-1.3284	0.3982
11723188_s_at	ADAM19	*ADAM metallopeptidase domain 19*	-1.3284	0.3982
11729158_at	UBE2T	*ubiquitin conjugating enzyme E2 T*	-1.3277	0.3984
11756409_a_at	BLM	*Bloom syndrome RecQ like helicase*	-1.3252	0.3991
11725705_a_at	AMOTL1	*angiomotin like 1*	-1.3252	0.3991
11720163_at	VEGFC	*vascular endothelial growth factor C*	-1.3248	0.3992
11751185_a_at	SMAD3	*SMAD family member 3*	-1.3226	0.3998
11745021_a_at	MYC	*v-myc avian myelocytomatosis viral oncogene homolog*	-1.3201	0.4005
11744764_s_at	WHSC1	*Wolf-Hirschhorn syndrome candidate 1*	-1.3201	0.4005
11729834_at	EIF5A2	*eukaryotic translation initiation factor 5A2*	-1.3155	0.4018
11723998_at	SPC25	*SPC25, NDC80 kinetochore complex component*	-1.3151	0.4019
11736367_a_at	MCM10	*minichromosome maintenance 10 replication initiation factor*	-1.3147	0.4020
11736329_a_at	ACOT9	*acyl-CoA thioesterase 9*	-1.3137	0.4023
11726286_a_at	WARS	*tryptophanyl-tRNA synthetase*	-1.3129	0.4025
11725987_a_at	MMP14	*matrix metallopeptidase 14*	-1.3097	0.4034
11729749_at	SAA2-SAA4	*SAA2-SAA4 readthrough*	-1.3086	0.4037
11719067_s_at	EIF2S3	*eukaryotic translation initiation factor 2 subunit gamma*	-1.3065	0.4043
11715728_a_at	ITGB1	*integrin subunit beta 1*	-1.3065	0.4043
11750438_x_at	PGAM1	*phosphoglycerate mutase 1*	-1.3037	0.4051
11733126_a_at	PRIM1	*Primase (DNA) Subunit 1*	-1.3019	0.4056
11741132_a_at	TP63	*tumor protein p63*	-1.3004	0.4060
11724285_at	FRMD4A	*FERM domain containing 4A*	-1.2997	0.4062
11725525_at	DSG2	*desmoglein 2*	-1.2987	0.4065
11752617_a_at	MIR6884	*microRNA 6884*	-1.2973	0.4069

11723326_at	CA9	*carbonic anhydrase 9*	-1.2951	0.4075
11763856_a_at	HOMER3	*homer scaffolding protein 3*	-1.2934	0.4080
11743546_a_at	MYO1B	*myosin IB*	-1.2930	0.4081
11754810_a_at	ITGB5	*integrin subunit beta 5*	-1.2927	0.4082
11715572_a_at	CLSTN1	*calsyntenin 1*	-1.2927	0.4082
11721554_a_at	COLGALT1	*Collagen Beta(1-O)Galactosyltransferase 1*	-1.2916	0.4085
11743602_a_at	RRM1	*ribonucleotide reductase catalytic subunit M1*	-1.2916	0.4085
11728161_at	WNT7A	*Wnt family member 7A*	-1.2902	0.4089
11743448_s_at	BICD2	*BICD cargo adaptor 2*	-1.2902	0.4089
11724152_a_at	TNS4	*tensin 4*	-1.2895	0.4091
11734724_a_at	IRF6	*interferon regulatory factor 6*	-1.2856	0.4102
11717291_a_at	MAP2K1	*mitogen-activated protein kinase 1*	-1.2845	0.4105
11719227_x_at	KCNN4	*potassium calcium-activated channel subfamily N member 4*	-1.2838	0.4107
11720928_at	SRM	*spermidine synthase*	-1.2838	0.4107
11749656_a_at	ARHGAP11A	*Rho GTPase activating protein 11A*	-1.2831	0.4109
11749478_a_at	MCM3	*minichromosome maintenance complex component 3*	-1.2828	0.4110
11752165_s_at	PKM	*pyruvate kinase, muscle*	-1.2828	0.4110
11745181_a_at	NAA15	*N(Alpha)-Acetyltransferase 15, NatA Auxiliary Subunit*	-1.2786	0.4122
11734825_at	SPRED1	*sprouty related EVH1 domain containing 1*	-1.2782	0.4123
11715919_a_at	SH3BGRL3	*SH3 domain binding glutamate rich protein like 3*	-1.2754	0.4131
11716872_a_at	ADCY3	*adenylate cyclase 3*	-1.2751	0.4132
11743190_s_at	RAD51AP1	*RAD51 associated protein 1*	-1.2747	0.4133
11717436_a_at	CDCA7L	*cell division cycle associated 7 like*	-1.2744	0.4134
11736047_a_at	ANTXR2	*anthrax toxin receptor 2*	-1.2740	0.4135
11719899_at	C11orf96	*chromosome 11 open reading frame 96*	-1.2723	0.4140
11733828_x_at	SNORD88C	*small nucleolar RNA, C/D box 88C*	-1.2706	0.4145
11725630_a_at	EIF3B	*eukaryotic translation initiation factor 3 subunit B*	-1.2702	0.4146
11757117_at	SNORA64	*small nucleolar RNA, H/ACA box 64*	-1.2678	0.4153
11727324_at	NAGS	*N-acetylglutamate synthase*	-1.2674	0.4154
11753856_a_at	CKS2	*CDC28 protein kinase regulatory subunit 2*	-1.2633	0.4166
11716631_s_at	SERPINB2	*serpin family B member 2*	-1.2622	0.4169
11757013_x_at	CAV1	*caveolin 1*	-1.2619	0.4170
11725065_a_at	TCOF1	*treacle ribosome biogenesis factor 1*	-1.2598	0.4176
11745571_a_at	CENPA	*centromere protein A*	-1.2584	0.4180
11748808_a_at	ARID3B	*AT-rich interaction domain 3B*	-1.2581	0.4181
11716126_x_at	ZYX	*zyxin*	-1.2570	0.4184
11747298_a_at	S100A16	*S100 calcium binding protein A16*	-1.2570	0.4184
11752673_x_at	LMNA	*lamin A/C*	-1.2564	0.4186
11747072_s_at	TUBB6	*tubulin beta 6 class V*	-1.2546	0.4191
11735234_a_at	SLC38A5	*solute carrier family 38 member 5*	-1.2529	0.4196
11724207_x_at	MAD1L1	*MAD1 mitotic arrest deficient like 1*	-1.2522	0.4198
11722193_a_at	C12orf75	*chromosome 12 open reading frame 75*	-1.2512	0.4201

11725441_a_at	FOXM1	*forkhead box M1*	-1.2509	0.4202
11742904_s_at	BAG2	*BCL2 associated athanogene 2*	-1.2505	0.4203
11749316_a_at	SURF4	*surfeit 4*	-1.2495	0.4206
11744604_at	ERVMER34-1	*endogenous retrovirus group MER34 member 1*	-1.2491	0.4207
11749379_a_at	UXS1	*UDP-glucuronate decarboxylase 1*	-1.2474	0.4212
11746395_x_at	NRCAM	*neuronal cell adhesion molecule*	-1.2471	0.4213
11728524_a_at	SPOCD1	*SPOC domain containing 1*	-1.2461	0.4216
11754579_at	PAPPA	*pappalysin 1*	-1.2457	0.4217
11733320_a_at	HRAS	*HRas proto-oncogene, GTPase*	-1.2457	0.4217
11749094_a_at	DSE	*dermatan sulfate epimerase*	-1.2454	0.4218
11717409_at	SH2B3	*SH2B adaptor protein 3*	-1.2450	0.4219
11743596_a_at	PTPRE	*protein tyrosine phosphatase, receptor type E*	-1.2440	0.4222
11748355_a_at	SLC16A1	*solute carrier family 16 member 1*	-1.2433	0.4224
11725832_s_at	OTUB2	*OTU deubiquitinase, ubiquitin aldehyde binding 2*	-1.2416	0.4229
11751527_s_at	WDR1	*WD repeat domain 1*	-1.2413	0.4230
11734618_a_at	ALOX15B	*arachidonate 15-lipoxygenase, type B*	-1.2375	0.4241
11749491_a_at	PLOD1	*procollagen-lysine,2-oxoglutarate 5-dioxygenase 1*	-1.2368	0.4243
11725714_a_at	RPS14	*ribosomal protein S14*	-1.2355	0.4247
11718548_x_at	ILF3	*interleukin enhancer binding factor 3*	-1.2355	0.4247
11721615_a_at	THEMIS2	*thymocyte selection associated family member 2*	-1.2351	0.4248
11757631_s_at	VGLL3	*vestigial like family member 3*	-1.2348	0.4249
11757313_s_at	VAT1	*vesicle amine transport 1*	-1.2331	0.4254
11744103_at	TLCD1	*TLC domain containing 1*	-1.2328	0.4255
11755024_a_at	MYEOV	*myeloma overexpressed*	-1.2324	0.4256
11716288_s_at	ESYT1	*extended synaptotagmin 1*	-1.2304	0.4262
11747460_x_at	TAGLN2	*transgelin 2*	-1.2270	0.4272
11754573_a_at	LPIN1	*lipin 1*	-1.2267	0.4273
11745543_x_at	AJUBA	*ajuba LIM protein*	-1.2257	0.4276
11748672_x_at	POLR1E	*RNA polymerase I subunit E*	-1.2253	0.4277
11717461_a_at	NSUN2	*NOP2/Sun RNA methyltransferase family member 2*	-1.2250	0.4278
11736440_at	INF2	*inverted formin, FH2 and WH2 domain containing*	-1.2243	0.4280
11750554_a_at	NEDD4	*neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase*	-1.2236	0.4282
11738069_a_at	HAS3	*hyaluronan synthase 3*	-1.2216	0.4288
11725347_a_at	TFDP1	*transcription factor Dp-1*	-1.2189	0.4296
11719258_at	TICAM1	*toll like receptor adaptor molecule 1*	-1.2186	0.4297
11752435_s_at	EXT2	*exostosin glycosyltransferase 2*	-1.2176	0.4300
11746200_s_at	EHD2	*EH domain containing 2*	-1.2146	0.4309
11738062_x_at	S100A7A	*S100 calcium binding protein A7A*	-1.2146	0.4309
11755100_a_at	COL16A1	*collagen type XVI alpha 1 chain*	-1.2139	0.4311
11731101_at	MELTF	*melanotransferrin*	-1.2129	0.4314
11724405_at	NDUFC2-KCTD14	*NDUFC2-KCTD14 readthrough*	-1.2122	0.4316
11758536_s_at	KCTD15	*potassium channel tetramerization domain containing 15*	-1.2122	0.4316

11726887_a_at	**SOX15**	***SRY-box 15***	**-1.2112**	**0.4319**
11727968_at	**ESCO2**	***establishment of sister chromatid cohesion N-acetyltransferase 2***	**-1.2099**	**0.4323**
11753435_x_at	**SLC3A2**	***solute carrier family 3 member 2***	**-1.2089**	**0.4326**
11733240_at	**IRAK2**	***interleukin 1 receptor associated kinase 2***	**-1.2086**	**0.4327**
11723136_x_at	**SRC**	***SRC proto-oncogene, non-receptor tyrosine kinase***	**-1.2079**	**0.4329**
11741779_s_at	**HSD11B1**	***hydroxysteroid 11-beta dehydrogenase 1***	**-1.2069**	**0.4332**
11718119_s_at	**CFL2**	***cofilin 2***	**-1.2069**	**0.4332**

11754822_x_at	**TDP1**	***tyrosyl-DNA phosphodiesterase 1***	**-1.2049**	**0.4338**
11716987_a_at	**HMGCS1**	***3-hydroxy-3-methylglutaryl-CoA synthase 1***	**-1.2049**	**0.4338**
11724735_a_at	**PDPN**	***podoplanin***	**-1.2046**	**0.4339**
11717349_a_at	**RBP1**	***retinol binding protein 1***	**-1.2042**	**0.4340**
11718076_at	**MAPKAPK3**	***mitogen-activated protein kinase-activated protein kinase 3***	**-1.2032**	**0.4343**
11756303_a_at	**SH3TC1**	***SH3 domain and tetratricopeptide repeats 1***	**-1.2026**	**0.4345**
11758165_s_at	**MRTO4**	***MRT4 homolog, ribosome maturation factor***	**-1.2012**	**0.4349**
11734865_a_at	**PSMC3IP**	***PSMC3 interacting protein***	**-1.2009**	**0.4350**
11722867_at	**CDCP1**	***CUB domain containing protein 1***	**-1.2002**	**0.4352**
11728840_at	**TMCC3**	***transmembrane and coiled-coil domain family 3***	**-1.1986**	**0.4357**
11723051_at	**FGFBP1**	***fibroblast growth factor binding protein 1***	**-1.1986**	**0.4357**
11723226_at	**SGCB**	***sarcoglycan beta***	**-1.1983**	**0.4358**
11732818_at	**TMEM171**	***transmembrane protein 171***	**-1.1973**	**0.4361**
11742945_a_at	**MIR6733**	***microRNA 6733***	**-1.1963**	**0.4364**
11760209_a_at	**RPL37A**	***ribosomal protein L37a***	**-1.1959**	**0.4365**
11722442_a_at	**NUF2**	***NUF2, NDC80 kinetochore complex component***	**-1.1953**	**0.4367**
11763556_at	**EIF4A1**	***eukaryotic translation initiation factor 4A1***	**-1.1940**	**0.4371**

11758149_s_at	**RACGAP1**	***Rac GTPase activating protein 1***	**-1.1936**	**0.4372**
11755424_a_at	**HMOX2**	***heme oxygenase 2***	**-1.1917**	**0.4378**
11745020_a_at	**TNFRSF12A**	***TNF receptor superfamily member 12A***	**-1.1907**	**0.4381**
11738203_x_at	**IMPDH1**	***inosine monophosphate dehydrogenase 1***	**-1.1903**	**0.4382**
11718262_a_at	**ERF**	***ETS2 repressor factor***	**-1.1894**	**0.4385**
11717444_at	**BYSL**	***bystin like***	**-1.1880**	**0.4389**
11748128_a_at	**SLC25A32**	***solute carrier family 25 member 32***	**-1.1877**	**0.4390**
11756471_a_at	**MFSD2A**	***major facilitator superfamily domain containing 2A***	**-1.1874**	**0.4391**
11746367_a_at	**CSE1L**	***chromosome segregation 1 like***	**-1.1867**	**0.4393**
11720493_s_at	**MOB3A**	***MOB kinase activator 3A***	**-1.1851**	**0.4398**
11718788_a_at	**ADA**	***adenosine deaminase***	**-1.1834**	**0.4403**
11717161_at	**RRAS**	***Related RAS Viral (R-Ras) Oncogene Homolog***	**-1.1834**	**0.4403**
11747589_a_at	**GOT2**	***glutamic-oxaloacetic transaminase 2***	**-1.1828**	**0.4405**
11744559_a_at	**SLC25A37**	***solute carrier family 25 member 37***	**-1.1818**	**0.4408**
11724249_a_at	**SLC39A8**	***solute carrier family 39 member 8***	**-1.1772**	**0.4422**
11720967_a_at	**GPSM2**	***G-protein signaling modulator 2***	**-1.1769**	**0.4423**
11735576_a_at	**LETM2**	***leucine zipper and EF-hand containing transmembrane protein 2***	**-1.1769**	**0.4423**

11718260_at	**NOTCH1**	***notch 1***	**-1.1763**	**0.4425**
11725910_a_at	**COL4A6**	***collagen type IV alpha 6 chain***	**-1.1753**	**0.4428**
11738887_s_at	**MICA**	***MHC class I polypeptide-related sequence A***	**-1.1753**	**0.4428**
11758151_s_at	**RNASEH2A**	***ribonuclease H2 subunit A***	**-1.1753**	**0.4428**
11727092_x_at	**IL18**	***interleukin 18***	**-1.1743**	**0.4431**
11750026_a_at	**DNM1L**	***dynamin 1 like***	**-1.1714**	**0.4440**
11750175_s_at	**SVILP1**	***supervillin pseudogene 1***	**-1.1710**	**0.4441**
11745877_x_at	**HDGF**	***hepatoma-derived growth factor***	**-1.1710**	**0.4441**
11717165_a_at	**RANGAP1**	***Ran GTPase activating protein 1***	**-1.1707**	**0.4442**
11728300_at	**CCNE2**	***cyclin E2***	**-1.1704**	**0.4443**
11717341_at	**PTGFRN**	***prostaglandin F2 receptor inhibitor***	**-1.1704**	**0.4443**
11719777_at	**NDST1**	***N-deacetylase and N-sulfotransferase 1***	**-1.1684**	**0.4449**
11750029_a_at	**EIF4H**	***eukaryotic translation initiation factor 4H***	**-1.1681**	**0.4450**
11759176_at	**GTSE1**	***G2 and S-phase expressed 1***	**-1.1652**	**0.4459**
11719391_a_at	**PRKDC**	***protein kinase, DNA-activated, catalytic polypeptide***	**-1.1652**	**0.4459**
11743916_a_at	**NPC1**	***NPC intracellular cholesterol transporter 1***	**-1.1649**	**0.4460**
11740312_at	**HAS2**	***hyaluronan synthase 2***	**-1.1639**	**0.4463**

11715431_a_at	**MIR6513**	***microRNA 6513***	**-1.1639**	**0.4463**
11721421_s_at	**RAP1GAP2**	***RAP1 GTPase activating protein 2***	**-1.1633**	**0.4465**
11718295_a_at	**SEMA4B**	***semaphorin 4B***	**-1.1629**	**0.4466**
11715698_a_at	**NOLC1**	***nucleolar and coiled-body phosphoprotein 1***	**-1.1607**	**0.4473**
11720494_a_at	**CTNNAL1**	***catenin alpha like 1***	**-1.1600**	**0.4475**
11758679_s_at	**MIR1292**	***microRNA 1292***	**-1.1588**	**0.4479**
11736240_a_at	**AAED1**	***AhpC/TSA antioxidant enzyme domain containing 1***	**-1.1575**	**0.4483**
11746116_a_at	**PINX1**	***PIN2/TERF1 interacting, telomerase inhibitor 1***	**-1.1575**	**0.4483**
11737787_at	**SHISA5**	***shisa family member 5***	**-1.1552**	**0.4490**
11727063_a_at	**MIR3658**	***microRNA 3658***	**-1.1542**	**0.4493**
11716919_a_at	**MIR7110**	***microRNA 7110***	**-1.1533**	**0.4496**
11728984_a_at	**LOC100996643**	***monofunctional C1-tetrahydrofolate synthase, mitochondrial-like***	**-1.1530**	**0.4497**
11723682_at	**ALYREF**	***Aly/REF export factor***	**-1.1530**	**0.4497**
11743536_at	**VRK1**	***vaccinia related kinase 1***	**-1.1523**	**0.4499**
11760436_a_at	**DST**	***dystonin***	**-1.1523**	**0.4499**
11751557_s_at	**MED27**	***mediator complex subunit 27***	**-1.1507**	**0.4504**
11743808_a_at	**DHCR7**	***7-dehydrocholesterol reductase***	**-1.1498**	**0.4507**

11736083_x_at	**GTSE1**	***G2 and S-phase expressed 1***	**-1.1491**	**0.4509**
11718980_a_at	**YKT6**	***YKT6 V-SNARE Homolog (S. Cerevisiae)***	**-1.1491**	**0.4509**
11724357_a_at	**MYO5A**	***myosin VA***	**-1.1459**	**0.4519**
11718578_a_at	**GSTM3**	***glutathione S-transferase mu 3***	**-1.1456**	**0.4520**
11744297_a_at	**RMI2**	***RecQ mediated genome instability 2***	**-1.1453**	**0.4521**
11721208_at	**IFFO2**	***intermediate filament family orphan 2***	**-1.1453**	**0.4521**
11729227_a_at	**GRK5**	***G protein-coupled receptor kinase 5***	**-1.1440**	**0.4525**
11741650_a_at	**LRP12**	***LDL receptor related protein 12***	**-1.1437**	**0.4526**
11722352_s_at	**ACTA2**	***actin, alpha 2, smooth muscle, aorta***	**-1.1418**	**0.4532**
11727081_a_at	**TIPIN**	***TIMELESS interacting protein***	**-1.1415**	**0.4533**
11724147_at	**RAB38**	***RAB38, member RAS oncogene family***	**-1.1415**	**0.4533**
11716665_s_at	**GDF15**	***growth differentiation factor 15***	**-1.1386**	**0.4542**
11756810_a_at	**MFAP2**	***microfibrillar associated protein 2***	**-1.1386**	**0.4542**
11757751_s_at	**NRP1**	***neuropilin 1***	**-1.1386**	**0.4542**
11741012_a_at	**MSMO1**	***methylsterol monooxygenase 1***	**-1.1386**	**0.4542**
11745234_a_at	**HACD4**	***3-hydroxyacyl-CoA dehydratase 4***	**-1.1376**	**0.4545**
11727269_at	**S100A3**	***S100 calcium binding protein A3***	**-1.1373**	**0.4546**

11756747_a_at	**RBMS2**	***RNA binding motif single stranded interacting protein 2***	**-1.1373**	**0.4546**
11726559_s_at	**LCP1**	***lymphocyte cytosolic protein 1***	**-1.1351**	**0.4553**
11728076_at	**HDAC9**	***histone deacetylase 9***	**-1.1348**	**0.4554**
11755689_x_at	**NCLN**	***nicalin***	**-1.1338**	**0.4557**
11715893_s_at	**IFI27**	***interferon alpha inducible protein 27***	**-1.1335**	**0.4558**
11715430_a_at	**AKR1B1**	***aldo-keto reductase family 1 member B***	**-1.1310**	**0.4566**
11756784_x_at	**NCAPG2**	***non-SMC condensin II complex subunit G2***	**-1.1300**	**0.4569**
11724810_at	**CBL**	***Cbl proto-oncogene***	**-1.1291**	**0.4572**
11728843_a_at	**PROSER2**	***proline and serine rich 2***	**-1.1288**	**0.4573**
11758396_s_at	**POLR3G**	***RNA polymerase III subunit G***	**-1.1275**	**0.4577**
11716667_a_at	**MTHFD1**	***methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltetrahydrofolate synthetase 1***	**-1.1275**	**0.4577**
11717321_at	**OAF**	***out at first homolog***	**-1.1269**	**0.4579**
11740349_at	**RNASE7**	***ribonuclease A family member 7***	**-1.1269**	**0.4579**
11747408_x_at	**FBLIM1**	***filamin binding LIM protein 1***	**-1.1250**	**0.4585**
11718531_a_at	**CAD**	***carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase***	**-1.1250**	**0.4585**
11736035_a_at	**EXOSC2**	***exosome component 2***	**-1.1250**	**0.4585**
11720319_at	**SPAG5**	***sperm associated antigen 5***	**-1.1244**	**0.4587**

11759656_a_at	**KLHL7**	***kelch like family member 7***	**-1.1234**	**0.4590**
11722691_at	**AVEN**	***apoptosis and caspase activation inhibitor***	**-1.1225**	**0.4593**
11721767_s_at	**ATAD3A**	***ATPase family, AAA domain containing 3A***	**-1.1206**	**0.4599**
11726116_at	**MTAP**	***methylthioadenosine phosphorylase***	**-1.1181**	**0.4607**
11755028_a_at	**DENND1A**	***DENN domain containing 1A***	**-1.1175**	**0.4609**
11727658_s_at	**KLK10**	***kallikrein related peptidase 10***	**-1.1172**	**0.4610**
11753254_a_at	**SGO2**	***shugoshin 2***	**-1.1156**	**0.4615**
11718400_a_at	**PNP**	***purine nucleoside phosphorylase***	**-1.1128**	**0.4624**
11759151_at	**SPC24**	***SPC24, NDC80 kinetochore complex component***	**-1.1125**	**0.4625**
11720226_s_at	**TBC1D1**	***TBC1 domain family member 1***	**-1.1122**	**0.4626**
11721622_a_at	**KATNAL1**	***katanin catalytic subunit A1 like 1***	**-1.1122**	**0.4626**
11754344_s_at	**SPRY4**	***sprouty RTK signaling antagonist 4***	**-1.1119**	**0.4627**
11725117_a_at	**NLN**	***neurolysin***	**-1.1100**	**0.4633**
11755618_a_at	**ALDH4A1**	***aldehyde dehydrogenase 4 family member A1***	**-1.1084**	**0.4638**
11722413_a_at	**SLC7A1**	***solute carrier family 7 member 1***	**-1.1084**	**0.4638**
11717155_a_at	**NME1**	***NME/NM23 nucleoside diphosphate kinase 1***	**-1.1047**	**0.4650**
11740375_a_at	**RGS10**	***regulator of G-protein signaling 10***	**-1.1041**	**0.4652**

11739483_a_at	**CCDC88A**	***coiled-coil domain containing 88A***	**-1.1016**	**0.4660**
11725192_at	**TTPAL**	***alpha tocopherol transfer protein like***	**-1.1001**	**0.4665**
11715913_s_at	**EFNB1**	***ephrin B1***	**-1.0994**	**0.4667**
11728538_a_at	**MCC**	***mutated in colorectal cancers***	**-1.0988**	**0.4669**
11719860_a_at	**SLC2A4RG**	***SLC2A4 regulator***	**-1.0954**	**0.4680**
11743084_s_at	**BNIP3**	***BCL2 interacting protein 3***	**-1.0951**	**0.4681**
11719686_a_at	**MICAL1**	***microtubule associated monooxygenase, calponin and LIM domain containing 1***	**-1.0939**	**0.4685**
11728558_a_at	**HSF2BP**	***heat shock transcription factor 2 binding protein***	**-1.0917**	**0.4692**
11754243_a_at	**H2AFX**	***H2A histone family member X***	**-1.0905**	**0.4696**
11718802_a_at	**PSRC1**	***proline and serine rich coiled-coil 1***	**-1.0899**	**0.4698**
11729887_at	**HACD1**	***3-hydroxyacyl-CoA dehydratase 1***	**-1.0896**	**0.4699**
11734713_s_at	**DBF4**	***DBF4 zinc finger***	**-1.0887**	**0.4702**
11756522_a_at	**SCARB1**	***scavenger receptor class B member 1***	**-1.0880**	**0.4704**
11758629_s_at	**SPTBN1**	***spectrin beta, non-erythrocytic 1***	**-1.0874**	**0.4706**
11737097_a_at	**DSC2**	***desmocollin 2***	**-1.0853**	**0.4713**
11745424_a_at	**SMC2**	***structural maintenance of chromosomes 2***	**-1.0853**	**0.4713**
11726724_a_at	**CKAP2L**	***cytoskeleton associated protein 2 like***	**-1.0847**	**0.4715**

11746103_a_at	**DTD1**	***D-tyrosyl-tRNA deacylase 1***	**-1.0841**	**0.4717**
11756289_x_at	**CCM2**	***CCM2 scaffolding protein***	**-1.0828**	**0.4721**
11721806_a_at	**EMC1**	***ER membrane protein complex subunit 1***	**-1.0798**	**0.4731**
11719719_at	**LAD1**	***ladinin 1***	**-1.0789**	**0.4734**
11754630_a_at	**MLKL**	***mixed lineage kinase domain like***	**-1.0767**	**0.4741**
11742775_a_at	**GPR161**	***G protein-coupled receptor 161***	**-1.0761**	**0.4743**
11719598_s_at	**CDCA3**	***cell division cycle associated 3***	**-1.0749**	**0.4747**
11746242_a_at	**ARNTL2**	***aryl hydrocarbon receptor nuclear translocator like 2***	**-1.0740**	**0.4750**
11747671_x_at	**CRIP2**	***cysteine rich protein 2***	**-1.0710**	**0.4760**
11724948_at	**CITED4**	***Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 4***	**-1.0707**	**0.4761**
11757855_a_at	**GARS**	***glycyl-tRNA synthetase***	**-1.0704**	**0.4762**
11722120_a_at	**KNTC1**	***kinetochore associated 1***	**-1.0695**	**0.4765**
11718715_a_at	**B4GALT2**	***beta-1,4-galactosyltransferase 2***	**-1.0688**	**0.4767**
11733215_a_at	**STAT4**	***signal transducer and activator of transcription 4***	**-1.0685**	**0.4768**
11755027_a_at	**TGFB1I1**	***transforming growth factor beta 1 induced transcript 1***	**-1.0682**	**0.4769**
11723446_s_at	**TMEM132A**	***transmembrane protein 132A***	**-1.0679**	**0.4770**
11728469_a_at	**BTBD11**	***BTB domain containing 11***	**-1.0670**	**0.4773**

11749354_x_at	**WDR41**	***WD repeat domain 41***	**-1.0670**	**0.4773**
11732078_a_at	**EVA1A**	***eva-1 homolog A, regulator of programmed cell death***	**-1.0667**	**0.4774**
11728749_a_at	**TCF19**	***transcription factor 19***	**-1.0655**	**0.4778**
11725052_a_at	**TOP1MT**	***Topoisomerase (DNA) I, Mitochondrial***	**-1.0646**	**0.4781**
11719980_a_at	**FMNL2**	***formin like 2***	**-1.0646**	**0.4781**
11734557_a_at	**GALNT5**	***polypeptide N-acetylgalactosaminyltransferase 5***	**-1.0637**	**0.4784**
11731880_at	**NLRP1**	***NLR family pyrin domain containing 1***	**-1.0619**	**0.4790**
11730754_s_at	**AGPAT5**	***1-acylglycerol-3-phosphate O-acyltransferase 5***	**-1.0607**	**0.4794**
11751426_a_at	**IL33**	***interleukin 33***	**-1.0601**	**0.4796**
11743965_s_at	**CERCAM**	***cerebral endothelial cell adhesion molecule***	**-1.0598**	**0.4797**
11719488_at	**EDNRA**	***endothelin receptor type A***	**-1.0592**	**0.4799**
11719732_at	**TIGAR**	***TP53 induced glycolysis regulatory phosphatase***	**-1.0589**	**0.4800**
11719830_a_at	**ERCC1**	***ERCC excision repair 1, endonuclease non-catalytic subunit***	**-1.0580**	**0.4803**
11731653_a_at	**IVL**	***involucrin***	**-1.0574**	**0.4805**
11724963_s_at	**FBXO5**	***F-box protein 5***	**-1.0574**	**0.4805**
11751629_a_at	**ASF1B**	***anti-silencing function 1B histone chaperone***	**-1.0565**	**0.4808**
11743687_s_at	**HMGB2**	***high mobility group box 2***	**-1.0547**	**0.4814**

11723697_s_at	**FLI1**	***Fli-1 proto-oncogene, ETS transcription factor***	**-1.0544**	**0.4815**
11717576_a_at	**SFN**	***stratifin***	**-1.0535**	**0.4818**
11753670_a_at	**AP1S3**	***adaptor related protein complex 1 sigma 3 subunit***	**-1.0532**	**0.4819**
11719587_a_at	**MICALL1**	***MICAL like 1***	**-1.0529**	**0.4820**
11744317_x_at	**BRCA1**	***BRCA1, DNA repair associated***	**-1.0529**	**0.4820**
11752782_a_at	**DDHD2**	***DDHD domain containing 2***	**-1.0499**	**0.4830**
11734142_a_at	**METTL8**	***methyltransferase like 8***	**-1.0484**	**0.4835**
11723256_a_at	**PKMYT1**	***protein kinase, membrane associated tyrosine/threonine 1***	**-1.0484**	**0.4835**
11734841_a_at	**RAD51**	***RAD51 recombinase***	**-1.0460**	**0.4843**
11736570_a_at	**SLC39A14**	***solute carrier family 39 member 14***	**-1.0454**	**0.4845**
11717656_a_at	**SPRED2**	***sprouty related EVH1 domain containing 2***	**-1.0436**	**0.4851**
11731899_s_at	**PPAT**	***phosphoribosyl pyrophosphate amidotransferase***	**-1.0436**	**0.4851**
11722406_at	**PFKFB4**	***6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4***	**-1.0410**	**0.4860**
11753706_a_at	**CALM1**	***calmodulin 1***	**-1.0374**	**0.4872**
11758249_s_at	**FDPS**	***farnesyl diphosphate synthase***	**-1.0365**	**0.4875**
11744345_x_at	**TUBA1B**	***tubulin alpha 1b***	**-1.0356**	**0.4878**
11734495_a_at	**GRB10**	***growth factor receptor bound protein 10***	**-1.0342**	**0.4883**

11754652_a_at	**ECI2**	***enoyl-CoA delta isomerase 2***	**-1.0336**	**0.4885**
11721435_at	**STC2**	***stanniocalcin 2***	**-1.0333**	**0.4886**
11752940_a_at	**EGR1**	***early growth response 1***	**-1.0327**	**0.4888**
11741819_a_at	**TGM1**	***transglutaminase 1***	**-1.0324**	**0.4889**
11716642_s_at	**DTYMK**	***deoxythymidylate kinase***	**-1.0318**	**0.4891**
11721070_a_at	**DEF8**	***differentially expressed in FDCP 8 homolog***	**-1.0318**	**0.4891**
11720241_at	**KIF4A**	***kinesin family member 4A***	**-1.0315**	**0.4892**
11722600_x_at	**P3H4**	***Prolyl 3-Hydroxylase Family Member 4 (Non-Enzymatic)***	**-1.0312**	**0.4893**
11755929_a_at	**THOP1**	***thimet oligopeptidase 1***	**-1.0297**	**0.4898**
11716450_s_at	**RFTN1**	***raftlin, lipid raft linker 1***	**-1.0291**	**0.4900**
11724462_x_at	**ALDOC**	***aldolase, fructose-bisphosphate C***	**-1.0271**	**0.4907**
11731992_x_at	**TROAP**	***trophinin associated protein***	**-1.0262**	**0.4910**
11758106_at	**NRM**	***Nurim (Nuclear Envelope Membrane Protein)***	**-1.0253**	**0.4913**
11757036_x_at	**SAC3D1**	***SAC3 domain containing 1***	**-1.0247**	**0.4915**
11732533_a_at	**LMNB1**	***lamin B1***	**-1.0244**	**0.4916**
11727536_x_at	**CCNF**	***cyclin F***	**-1.0241**	**0.4917**
11727879_s_at	**CHAF1A**	***chromatin assembly factor 1 subunit A***	**-1.0177**	**0.4939**

11757018_a_at	**COL12A1**	***collagen type XII alpha 1 chain***	**-1.0168**	**0.4942**
11750301_x_at	**FAM92A**	***family with sequence similarity 92 member A***	**-1.0165**	**0.4943**
11732494_at	**AUNIP**	***aurora kinase A and ninein interacting protein***	**-1.0165**	**0.4943**
11717937_at	**SMIM3**	***small integral membrane protein 3***	**-1.0162**	**0.4944**
11728062_a_at	**SH3BP1**	***SH3 domain binding protein 1***	**-1.0145**	**0.4950**
11722379_at	**GNG11**	***G protein subunit gamma 11***	**-1.0130**	**0.4955**
11728101_at	**ZNF367**	***zinc finger protein 367***	**-1.0125**	**0.4957**
11741126_s_at	**SLFN11**	***schlafen family member 11***	**-1.0125**	**0.4957**
11736054_a_at	**CELF1**	***CUGBP, Elav-like family member 1***	**-1.0125**	**0.4957**
11740068_at	**CCDC8**	***coiled-coil domain containing 8***	**-1.0119**	**0.4959**
11721908_at	**SGPP1**	***sphingosine-1-phosphate phosphatase 1***	**-1.0101**	**0.4965**
11720550_a_at	**NCAPD3**	***non-SMC condensin II complex subunit D3***	**-1.0087**	**0.4970**
11756456_a_at	**TWNK**	***twinkle mtDNA helicase***	**-1.0064**	**0.4978**
11746009_a_at	**ACAT2**	***acetyl-CoA acetyltransferase 2***	**-1.0061**	**0.4979**
11735167_x_at	**RFC2**	***replication factor C subunit 2***	**-1.0058**	**0.4980**
11731168_at	**IGFL1**	***IGF like family member 1***	**-1.0029**	**0.4990**

***Differentially expressed mRNAs were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ([Log_2Ratio > 1] or [Log_2Ratio < -1] for both upregulated or downregulated mRNAs, respectively),**

followed by multiple correction using a False Discovery Rate (FDR) threshold of 1% (p-adjusted value or q < 0.01).

TABLE S2. Differentially expressed mRNAs in control NM air-liquid interface culture after 28 days of differentiation compared to day 0 (monolayer of hNM-BSCs).*

UPREGULATED mRNAs (1225)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11720917_a_at	BPIFB1	*BPI fold containing family B member 1*	7.6725	204.0071
11719818_at	PIP	*prolactin induced protein*	6.0507	66.2873
11758196_s_at	IGFBP5	*insulin like growth factor binding protein 5*	5.9124	60.2277
11743003_a_at	CYP4B1	*cytochrome P450 family 4 subfamily B member 1*	5.8172	56.3848
11723642_a_at	BPIFA1	*BPI fold containing family A member 1*	5.5831	47.9396
11754354_s_at	PROM1	*prominin 1*	5.4916	44.9927
11723524_at	AGR3	*anterior gradient 3, protein disulphide isomerase family member*	5.4615	44.0628
11730780_x_at	ADH1C	*Alcohol Dehydrogenase 1C (Class I), Gamma Polypeptide*	5.3503	40.7950
11725562_at	C20orf85	*chromosome 20 open reading frame 85*	5.3364	40.4045
11763989_at	LOC101927057	*uncharacterized LOC101927057*	5.2437	37.8878
11722994_s_at	ADH1A	*Alcohol Dehydrogenase 1A (Class I), Alpha Polypeptide*	5.1825	36.3157
11720349_at	ROPN1L	*rhophilin associated tail protein 1 like*	5.1189	34.7484
11744484_s_at	HLA-DRA	*major histocompatibility complex, class II, DR alpha*	5.0579	33.3107
11733934_a_at	PIFO	*primary cilia formation*	4.9889	31.7556
11730044_a_at	C9orf24	*chromosome 9 open reading frame 24*	4.9108	30.0808
11744240_at	SNTN	*sentan, cilia apical structure protein*	4.8993	29.8421
11724692_a_at	CAPN13	*calpain 13*	4.8664	29.1701
11729439_a_at	CAPSL	*calcyphosine like*	4.8244	28.3331
11758272_at	SLC34A2	*solute carrier family 34 member 2*	4.5723	23.7908
11736917_at	LYPD2	*LY6/PLAUR domain containing 2*	4.5348	23.1799
11732833_a_at	C9orf135	*chromosome 9 open reading frame 135*	4.4833	22.3666
11719767_a_at	TPPP3	*tubulin polymerization promoting protein family member 3*	4.4776	22.2793
11734525_a_at	C11orf88	*chromosome 11 open reading frame 88*	4.4755	22.2462
11729297_at	MMP13	*matrix metallopeptidase 13*	4.4071	21.2164
11755588_a_at	SLC5A5	*solute carrier family 5 member 5*	4.3715	20.6991
11744104_a_at	TMC5	*transmembrane channel like 5*	4.3532	20.4376
11737141_a_at	RSPH1	*radial spoke head 1 homolog*	4.3414	20.2711
11732910_x_at	FAM183A	*family with sequence similarity 183 member A*	4.2917	19.5858
11727734_at	CFAP126	*cilia and flagella associated protein 126*	4.2582	19.1354
11755403_a_at	CHST9	*carbohydrate sulfotransferase 9*	4.2492	19.0172
11727698_a_at	VMO1	*vitelline membrane outer layer 1 homolog*	4.2297	18.7616
11756684_a_at	DYNLRB2	*dynein light chain roadblock-type 2*	4.2136	18.5536
11743044_a_at	ALDH1A1	*aldehyde dehydrogenase 1 family member A1*	4.1873	18.2178
11757612_a_at	ASRGL1	*asparaginase like 1*	4.1700	18.0009
11746749_a_at	ZBBX	*zinc finger B-box domain containing*	4.1534	17.7951
11742730_a_at	CAPS	*calcyphosine*	4.1388	17.6161
11729920_at	BBOF1	*basal body orientation factor 1*	4.1336	17.5527

11737634_a_at	UGT2A1	*UDP glucuronosyltransferase family 2 member A1 complex locus*	4.1144	17.3206
11740996_a_at	SPAG6	*sperm associated antigen 6*	4.0856	16.9784
11739916_a_at	SERPINB11	*Serpin Family B Member 11 (Gene/Pseudogene)*	4.0798	16.9095
11724085_at	DAPL1	*death associated protein like 1*	4.0764	16.8706
11726434_at	CHL1	*cell adhesion molecule L1 like*	4.0677	16.7691
11732460_a_at	PLEKHS1	*pleckstrin homology domain containing S1*	4.0568	16.6427
11722863_at	SCGB2A1	*secretoglobin family 2A member 1*	4.0523	16.5902
11721704_a_at	CRIP1	*cysteine rich protein 1*	4.0455	16.5129
11751769_a_at	LOC100287413	*uncharacterized LOC100287413*	4.0373	16.4190
11737857_a_at	DNAAF1	*dynein axonemal assembly factor 1*	3.9872	15.8587
11743595_at	C5orf49	*chromosome 5 open reading frame 49*	3.9857	15.8425
11734503_x_at	ALOX15	*arachidonate 15-lipoxygenase*	3.9806	15.7865
11746662_a_at	ARMC3	*armadillo repeat containing 3*	3.9565	15.5249
11727921_a_at	TEKT1	*tektin 1*	3.9277	15.2183
11734176_a_at	CFAP52	*cilia and flagella associated protein 52*	3.9170	15.1057
11750860_a_at	CMAHP	*cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene*	3.9167	15.1026
11726981_a_at	CP	*ceruloplasmin*	3.9098	15.0307
11716109_a_at	PIGR	*polymeric immunoglobulin receptor*	3.8762	14.6847
11735523_a_at	FAM47E	*family with sequence similarity 47 member E*	3.8630	14.5509
11756356_a_at	FAM81B	*family with sequence similarity 81 member B*	3.8377	14.2980
11726063_a_at	C2orf40	*chromosome 2 open reading frame 40*	3.7925	13.8562
11724109_a_at	C9orf116	*chromosome 9 open reading frame 116*	3.7905	13.8370
11726535_a_at	MORN5	*MORN repeat containing 5*	3.7835	13.7700
11744374_x_at	HLA-DRB1	*major histocompatibility complex, class II, DR beta 1*	3.7599	13.5467
11756097_s_at	ZMYND10	*zinc finger MYND-type containing 10*	3.7421	13.3805
11733359_a_at	CFAP45	*cilia and flagella associated protein 45*	3.7166	13.1465
11757882_x_at	GSTA1	*glutathione S-transferase alpha 1*	3.7067	13.0569
11726303_a_at	MFSD4A	*major facilitator superfamily domain containing 4A*	3.6913	12.9178
11715343_at	MUC16	*mucin 16, cell surface associated*	3.6359	12.4314
11718213_a_at	SLC27A2	*solute carrier family 27 member 2*	3.5986	12.1138
11735674_a_at	AKAP14	*A-kinase anchoring protein 14*	3.5976	12.1055
11726159_a_at	IQCG	*IQ motif containing G*	3.5699	11.8750
11719321_a_at	DNALI1	*dynein axonemal light intermediate chain 1*	3.5660	11.8430
11759642_x_at	HLA-DRB1	*major histocompatibility complex, class II, DR beta 1*	3.5586	11.7828
11744063_a_at	MUC5B	*mucin 5B, oligomeric mucus/gel-forming*	3.5343	11.5859
11729770_at	BPIFA2	*BPI fold containing family A member 2*	3.5069	11.3682
11729061_a_at	DNAH5	*dynein axonemal heavy chain 5*	3.5049	11.3522
11723097_a_at	VTCN1	*V-set domain containing T cell activation inhibitor 1*	3.4900	11.2353
11744556_x_at	CYP2B7P	*cytochrome P450 family 2 subfamily B member 7, pseudogene*	3.4875	11.2159
11717820_a_at	SLC4A4	*solute carrier family 4 member 4*	3.4820	11.1732
11744588_a_at	CCDC17	*coiled-coil domain containing 17*	3.4743	11.1137
11730944_a_at	CCDC65	*coiled-coil domain containing 65*	3.4740	11.1115

11724620_a_at	WDR78	*WD repeat domain 78*	3.4600	11.0041
11740755_a_at	LYNX1	*Ly6/neurotoxin 1*	3.4591	10.9977
11752898_a_at	PPIL6	*peptidylprolyl isomerase like 6*	3.4505	10.9318
11747755_a_at	KRT13	*keratin 13*	3.4495	10.9247
11758225_s_at	IQGAP2	*IQ motif containing GTPase activating protein 2*	3.4468	10.9039
11755748_s_at	PLAC8	*placenta specific 8*	3.4460	10.8981
11743943_a_at	RSPH4A	*radial spoke head 4 homolog A*	3.4320	10.7926
11735488_a_at	CASC1	*cancer susceptibility candidate 1*	3.4191	10.6970
11758952_at	AGR2	*anterior gradient 2, protein disulphide isomerase family member*	3.3842	10.4414
11717417_s_at	RHOU	*ras homolog family member U*	3.3739	10.3669
11754650_a_at	ATP10B	*ATPase Phospholipid Transporting 10B (Putative)*	3.3719	10.3528
11715112_at	ERICH3	*glutamate rich 3*	3.3555	10.2352
11755226_s_at	KLHDC7A	*kelch domain containing 7A*	3.3427	10.1453
11721619_at	FOXJ1	*forkhead box J1*	3.3054	9.8861
11731779_a_at	C11orf70	*chromosome 11 open reading frame 70*	3.2925	9.7983
11732678_a_at	DNAH12	*dynein axonemal heavy chain 12*	3.2873	9.7626
11733545_x_at	NWD1	*NACHT and WD repeat domain containing 1*	3.2687	9.6380
11727966_a_at	MSMB	*microseminoprotein beta*	3.2526	9.5311
11750836_a_at	EFHC1	*EF-hand domain containing 1*	3.2524	9.5295
11726233_a_at	DRC3	*dynein regulatory complex subunit 3*	3.2522	9.5279
11724219_x_at	GSTA1	*glutathione S-transferase alpha 1*	3.2495	9.5106
11716489_a_at	STATH	*statherin*	3.2490	9.5073
11723194_x_at	HLA-DQB1	*major histocompatibility complex, class II, DQ beta 1*	3.2472	9.4954
11735643_a_at	RARRES1	*retinoic acid receptor responder 1*	3.2470	9.4941
11757570_s_at	PRR15	*proline rich 15*	3.2456	9.4850
11743952_a_at	CFAP206	*cilia and flagella associated protein 206*	3.2435	9.4709
11742251_s_at	CYP2A6	*cytochrome P450 family 2 subfamily A member 6*	3.2304	9.3856
11735637_a_at	LRRC23	*leucine rich repeat containing 23*	3.2124	9.2692
11723912_at	MS4A8	*membrane spanning 4-domains A8*	3.2060	9.2278
11731855_at	C10orf107	*chromosome 10 open reading frame 107*	3.1956	9.1613
11729073_a_at	TSPAN19	*tetraspanin 19*	3.1900	9.1261
11729976_a_at	PTPRN2	*protein tyrosine phosphatase, receptor type N2*	3.1783	9.0526
11735169_at	C6orf118	*chromosome 6 open reading frame 118*	3.1708	9.0057
11721895_x_at	GAS1	*growth arrest specific 1*	3.1698	8.9990
11740868_a_at	LDLRAD1	*low density lipoprotein receptor class A domain containing 1*	3.1566	8.9172
11727983_a_at	LRRC46	*leucine rich repeat containing 46*	3.1565	8.9165
11731273_a_at	KCNE1	*potassium voltage-gated channel subfamily E regulatory subunit 1*	3.1555	8.9105
11715490_s_at	AMY1A	*Amylase, Alpha 1A (Salivary)*	3.1530	8.8952
11727538_at	NME5	*NME/NM23 family member 5*	3.1464	8.8546
11756547_a_at	CLU	*clusterin*	3.1453	8.8475
11718790_at	HES6	*hes family bHLH transcription factor 6*	3.1446	8.8435
11718722_at	PSCA	*prostate stem cell antigen*	3.1410	8.8214

11720713_a_at	KCNE3	*potassium voltage-gated channel subfamily E regulatory subunit 3*	3.1384	8.8057
11724940_x_at	CDHR3	*cadherin related family member 3*	3.1170	8.6761
11758504_s_at	FAM216B	*family with sequence similarity 216 member B*	3.1141	8.6583
11722255_a_at	RRAD	*RRAD, Ras related glycolysis inhibitor and calcium channel regulator*	3.1066	8.6136
11715994_x_at	ID2	*inhibitor of DNA binding 2, HLH protein*	3.1044	8.6001
11756098_a_at	SYTL5	*synaptotagmin like 5*	3.1017	8.5840
11754238_a_at	DYDC2	*DPY30 domain containing 2*	3.1011	8.5808
11732082_s_at	STOML3	*stomatin like 3*	3.0815	8.4649
11751078_s_at	CYP2F1	*cytochrome P450 family 2 subfamily F member 1*	3.0741	8.4218
11727906_at	MMP10	*matrix metallopeptidase 10*	3.0719	8.4086
11733761_at	TMEM190	*transmembrane protein 190*	3.0665	8.3775
11755544_a_at	EFHB	*EF-hand domain family member B*	3.0646	8.3664
11720372_at	TESC	*tescalcin*	3.0635	8.3601
11749589_x_at	CTSS	*cathepsin S*	3.0590	8.3341
11724394_at	KIAA1211L	*KIAA1211 like*	3.0521	8.2942
11721539_at	RAB15	*RAB15, member RAS oncogene family*	3.0444	8.2500
11755831_a_at	WDR63	*WD repeat domain 63*	3.0394	8.2214
11729503_at	CFAP53	*cilia and flagella associated protein 53*	3.0379	8.2128
11749912_x_at	IGFBP3	*insulin like growth factor binding protein 3*	3.0361	8.2025
11721531_a_at	AQP5	*aquaporin 5*	3.0249	8.1391
11725494_at	RSPH9	*radial spoke head 9 homolog*	3.0242	8.1355
11721318_at	PARM1	*prostate androgen-regulated mucin-like protein 1*	3.0239	8.1337
11736050_s_at	FAM229B	*family with sequence similarity 229 member B*	3.0137	8.0762
11729031_a_at	C1orf194	*chromosome 1 open reading frame 194*	3.0106	8.0590
11757815_s_at	METTL7A	*methyltransferase like 7A*	3.0061	8.0340
11740239_a_at	CFAP161	*cilia and flagella associated protein 161*	3.0051	8.0285
11733432_at	AK7	*adenylate kinase 7*	3.0034	8.0190
11717595_s_at	ELF3	*E74 like ETS transcription factor 3*	2.9925	7.9583
11745292_a_at	C22orf15	*chromosome 22 open reading frame 15*	2.9813	7.8971
11733607_a_at	LRRC34	*leucine rich repeat containing 34*	2.9745	7.8601
11747509_a_at	FAM107B	*family with sequence similarity 107 member B*	2.9677	7.8229
11756809_a_at	EFHC2	*EF-hand domain containing 2*	2.9596	7.7793
11760972_x_at	SPACA9	*sperm acrosome associated 9*	2.9533	7.7451
11729100_a_at	CFAP70	*cilia and flagella associated protein 70*	2.9532	7.7449
11756688_x_at	EFCAB1	*EF-hand calcium binding domain 1*	2.9508	7.7316
11732552_a_at	ENKUR	*enkurin, TRPC channel interacting protein*	2.9453	7.7025
11729258_at	MNS1	*meiosis specific nuclear structural 1*	2.9391	7.6692
11724762_a_at	DEPTOR	*DEP domain containing MTOR-interacting protein*	2.9290	7.6158
11731924_a_at	KCNRG	*potassium channel regulator*	2.9218	7.5777
11727185_at	DRC1	*dynein regulatory complex subunit 1*	2.9190	7.5634
11728239_at	RRAGD	*Ras related GTP binding D*	2.9174	7.5548
11732856_at	CDHR4	*cadherin related family member 4*	2.9120	7.5266

11716401_a_at	SELENBP1	*selenium binding protein 1*	2.9113	7.5231
11735858_a_at	RIIAD1	*Regulatory Subunit Of Type II PKA R-Subunit (RIIa) Domain Containing 1*	2.9103	7.5179
11756191_a_at	MAN1C1	*mannosidase alpha class 1C member 1*	2.9071	7.5012
11718066_a_at	TCTN1	*tectonic family member 1*	2.9027	7.4783
11755814_a_at	CFAP43	*cilia and flagella associated protein 43*	2.9026	7.4777
11729418_a_at	TEKT2	*tektin 2*	2.9021	7.4750
11721898_at	FAM3D	*family with sequence similarity 3 member D*	2.8998	7.4630
11724454_at	SLC22A4	*solute carrier family 22 member 4*	2.8974	7.4507
11736948_at	TEX26	*testis expressed 26*	2.8925	7.4256
11739440_a_at	KRT4	*keratin 4*	2.8881	7.4027
11738435_x_at	CD74	*CD74 molecule*	2.8673	7.2968
11756783_a_at	TF	*transferrin*	2.8611	7.2658
11733164_a_at	TTC29	*tetratricopeptide repeat domain 29*	2.8525	7.2227
11722838_a_at	GABRP	*gamma-aminobutyric acid type A receptor pi subunit*	2.8486	7.2028
11731722_a_at	ALDH3B1	*aldehyde dehydrogenase 3 family member B1*	2.8423	7.1717
11721887_a_at	CRYM	*crystallin mu*	2.8403	7.1616
11753938_a_at	FAM166B	*family with sequence similarity 166 member B*	2.8146	7.0353
11731341_a_at	AGBL2	*ATP/GTP binding protein like 2*	2.8055	6.9909
11730661_a_at	CCDC78	*coiled-coil domain containing 78*	2.7998	6.9636
11725922_a_at	CLIC6	*chloride intracellular channel 6*	2.7996	6.9627
11752531_a_at	MDH1B	*malate dehydrogenase 1B*	2.7976	6.9526
11754627_s_at	RAB37	*RAB37, member RAS oncogene family*	2.7859	6.8967
11758474_s_at	COLCA1	*colorectal cancer associated 1*	2.7851	6.8928
11721630_at	MAFB	*MAF bZIP transcription factor B*	2.7667	6.8057
11728727_at	CEACAM7	*carcinoembryonic antigen related cell adhesion molecule 7*	2.7521	6.7369
11728981_at	ERICH5	*glutamate rich 5*	2.7438	6.6983
11717575_at	PPP1R3C	*protein phosphatase 1 regulatory subunit 3C*	2.7427	6.6932
11752737_a_at	CLEC7A	*C-type lectin domain family 7 member A*	2.7340	6.6532
11739532_a_at	DAW1	*dynein assembly factor with WD repeats 1*	2.7338	6.6520
11727957_a_at	DNAI1	*dynein axonemal intermediate chain 1*	2.7336	6.6512
11717720_a_at	ST6GAL1	*ST6 beta-galactoside alpha-2,6-sialyltransferase 1*	2.7320	6.6439
11755724_a_at	MLF1	*myeloid leukemia factor 1*	2.7215	6.5956
11720139_a_at	VSTM2L	*V-set and transmembrane domain containing 2 like*	2.7205	6.5912
11732500_a_at	FAM3B	*family with sequence similarity 3 member B*	2.7205	6.5910
11724691_at	RIBC2	*RIB43A domain with coiled-coils 2*	2.7136	6.5595
11727664_x_at	STOX1	*storkhead box 1*	2.7108	6.5467
11726124_at	TCN1	*transcobalamin 1*	2.7101	6.5438
11722054_a_at	CYP4X1	*cytochrome P450 family 4 subfamily X member 1*	2.7084	6.5361
11732932_at	SAXO2	*stabilizer of axonemal microtubules 2*	2.7032	6.5123
11730456_at	CCDC96	*coiled-coil domain containing 96*	2.7029	6.5113
11719202_a_at	MORN2	*MORN repeat containing 2*	2.6975	6.4866
11755087_a_at	C4orf47	*chromosome 4 open reading frame 47*	2.6897	6.4517

11752329_a_at	DNAI2	*dynein axonemal intermediate chain 2*	2.6889	6.4483
11724017_a_at	OSCP1	*organic solute carrier partner 1*	2.6826	6.4199
11728177_a_at	DYX1C1	*dyslexia susceptibility 1 candidate 1*	2.6795	6.4065
11723163_s_at	NR3C2	*nuclear receptor subfamily 3 group C member 2*	2.6743	6.3832
11736144_at	ENPP4	*Ectonucleotide Pyrophosphatase/Phosphodiesterase 4 (Putative)*	2.6701	6.3648
11744508_a_at	CCDC146	*coiled-coil domain containing 146*	2.6653	6.3434
11739351_a_at	AMOT	*angiomotin*	2.6644	6.3397
11748500_a_at	ENPP5	*Ectonucleotide Pyrophosphatase/Phosphodiesterase 5 (Putative)*	2.6631	6.3341
11727667_at	DNAH7	*dynein axonemal heavy chain 7*	2.6582	6.3125
11741477_a_at	NPHP1	*nephrocystin 1*	2.6576	6.3099
11750733_x_at	SLC44A4	*solute carrier family 44 member 4*	2.6545	6.2961
11753718_a_at	LRTOMT	*leucine rich transmembrane and O-methyltransferase domain containing*	2.6529	6.2892
11719538_at	BBOX1	*gamma-butyrobetaine hydroxylase 1*	2.6516	6.2838
11715788_a_at	SLC40A1	*solute carrier family 40 member 1*	2.6455	6.2573
11729682_a_at	TMEM231	*transmembrane protein 231*	2.6447	6.2537
11743089_a_at	LRRC6	*leucine rich repeat containing 6*	2.6331	6.2036
11743800_a_at	DNAH2	*dynein axonemal heavy chain 2*	2.6272	6.1781
11759102_at	UBXN10	*UBX domain protein 10*	2.6207	6.1504
11753973_x_at	MUC1	*mucin 1, cell surface associated*	2.6185	6.1409
11724589_s_at	MMP12	*matrix metallopeptidase 12*	2.6160	6.1303
11731050_at	CEP126	*centrosomal protein 126*	2.6126	6.1161
11745989_a_at	HLA-DMA	*major histocompatibility complex, class II, DM alpha*	2.6106	6.1076
11715709_x_at	MB	*myoglobin*	2.6030	6.0755
11724988_a_at	CCDC113	*coiled-coil domain containing 113*	2.6030	6.0753
11720901_a_at	GRAMD1C	*GRAM domain containing 1C*	2.5961	6.0463
11724842_a_at	ARMC4	*armadillo repeat containing 4*	2.5897	6.0197
11754461_s_at	UCP2	*uncoupling protein 2*	2.5821	5.9881
11724381_at	FAM65B	*family with sequence similarity 65 member B*	2.5749	5.9581
11721638_s_at	CES1	*carboxylesterase 1*	2.5743	5.9557
11723441_a_at	EPHA4	*EPH receptor A4*	2.5734	5.9523
11733636_at	FAM92B	*family with sequence similarity 92 member B*	2.5733	5.9516
11727239_a_at	C4orf19	*chromosome 4 open reading frame 19*	2.5720	5.9462
11723878_a_at	ATP7B	*ATPase copper transporting beta*	2.5678	5.9292
11740438_a_at	FUT6	*fucosyltransferase 6*	2.5669	5.9255
11733330_at	CCDC170	*coiled-coil domain containing 170*	2.5660	5.9217
11755362_a_at	IFT172	*intraflagellar transport 172*	2.5659	5.9211
11722157_a_at	CCNO	*cyclin O*	2.5623	5.9065
11727166_a_at	FBXO15	*F-box protein 15*	2.5604	5.8989
11744137_a_at	CAMK1D	*calcium/calmodulin dependent protein kinase ID*	2.5564	5.8823
11758134_s_at	PPM1H	*protein phosphatase, Mg2+/Mn2+ dependent 1H*	2.5500	5.8562
11747692_a_at	IQUB	*IQ motif and ubiquitin domain containing*	2.5439	5.8316
11715583_s_at	HLA-DPA1	*major histocompatibility complex, class II, DP alpha 1*	2.5419	5.8234

11739044_s_at	SLC15A2	*solute carrier family 15 member 2*	2.5385	5.8097
11755742_a_at	ADH7	*Alcohol Dehydrogenase 7 (Class IV), Mu Or Sigma Polypeptide*	2.5377	5.8066
11725691_a_at	VWA5A	*von Willebrand factor A domain containing 5A*	2.5359	5.7995
11718754_at	CAPN5	*calpain 5*	2.5314	5.7815
11719265_a_at	MLPH	*melanophilin*	2.5254	5.7575
11733474_at	SOX21	*SRY-box 21*	2.5239	5.7512
11735554_at	PPP1R42	*protein phosphatase 1 regulatory subunit 42*	2.5182	5.7287
11763594_a_at	HS3ST3B1	*heparan sulfate-glucosamine 3-sulfotransferase 3B1*	2.5099	5.6957
11726576_x_at	CYP2A6	*cytochrome P450 family 2 subfamily A member 6*	2.5075	5.6864
11743794_a_at	CFAP69	*cilia and flagella associated protein 69*	2.5055	5.6783
11730699_at	LOC100652777	*group 10 secretory phospholipase A2-like*	2.5038	5.6719
11731248_a_at	TMEM116	*transmembrane protein 116*	2.4964	5.6428
11743799_a_at	SPAG17	*sperm associated antigen 17*	2.4949	5.6369
11737637_a_at	CFAP77	*cilia and flagella associated protein 77*	2.4914	5.6233
11730633_at	MAK	*male germ cell associated kinase*	2.4910	5.6217
11724258_a_at	MUC15	*mucin 15, cell surface associated*	2.4892	5.6148
11736861_at	PIH1D3	*PIH1 domain containing 3*	2.4812	5.5835
11715763_a_at	PODXL	*podocalyxin like*	2.4739	5.5554
11727146_at	GPR160	*G protein-coupled receptor 160*	2.4726	5.5504
11745295_a_at	ANKRD66	*ankyrin repeat domain 66*	2.4682	5.5335
11731433_a_at	SELENOP	*selenoprotein P*	2.4616	5.5081
11719843_a_at	ABI3BP	*ABI family member 3 binding protein*	2.4601	5.5027
11755367_s_at	DNAAF3	*dynein axonemal assembly factor 3*	2.4509	5.4674
11732287_at	DZIP3	*DAZ interacting zinc finger protein 3*	2.4507	5.4670
11722507_a_at	CLIC5	*chloride intracellular channel 5*	2.4506	5.4663
11755020_a_at	SLC46A3	*solute carrier family 46 member 3*	2.4468	5.4519
11749250_a_at	ZMYND12	*zinc finger MYND-type containing 12*	2.4385	5.4206
11721430_a_at	SYBU	*syntabulin*	2.4383	5.4201
11755609_a_at	HYDIN2	*HYDIN2, Axonemal Central Pair Apparatus Protein (Pseudogene)*	2.4366	5.4138
11744430_a_at	KIF9	*kinesin family member 9*	2.4321	5.3966
11724875_a_at	CD36	*CD36 molecule*	2.4313	5.3938
11756271_a_at	FANK1	*fibronectin type III and ankyrin repeat domains 1*	2.4179	5.3438
11754601_s_at	LOC100130872	*uncharacterized LOC100130872*	2.4176	5.3429
11730265_x_at	CCDC69	*coiled-coil domain containing 69*	2.4161	5.3372
11755220_a_at	C17orf97	*chromosome 17 open reading frame 97*	2.4120	5.3222
11754316_a_at	PIK3R3	*phosphoinositide-3-kinase regulatory subunit 3*	2.4071	5.3039
11720993_at	SOX2	*SRY-box 2*	2.4027	5.2880
11730214_at	DUOX2	*dual oxidase 2*	2.3931	5.2529
11721736_s_at	TNFRSF19	*TNF receptor superfamily member 19*	2.3862	5.2278
11742709_s_at	P4HTM	*prolyl 4-hydroxylase, transmembrane*	2.3841	5.2203
11732657_a_at	CYP26A1	*cytochrome P450 family 26 subfamily A member 1*	2.3835	5.2181
11732954_at	CCDC153	*coiled-coil domain containing 153*	2.3832	5.2168

11731945_a_at	WDR38	*WD repeat domain 38*	2.3816	5.2113
11756956_a_at	SPEF1	*sperm flagellar 1*	2.3749	5.1870
11720134_s_at	PROS1	*Protein S (Alpha)*	2.3747	5.1862
11763360_a_at	VSIG2	*V-set and immunoglobulin domain containing 2*	2.3719	5.1761
11737564_a_at	CCDC74A	*coiled-coil domain containing 74A*	2.3716	5.1753
11733903_a_at	SPATA4	*spermatogenesis associated 4*	2.3699	5.1691
11729042_a_at	DLEC1	*deleted in lung and esophageal cancer 1*	2.3695	5.1675
11744920_a_at	ODF3B	*outer dense fiber of sperm tails 3B*	2.3683	5.1632
11746354_a_at	C1orf158	*chromosome 1 open reading frame 158*	2.3624	5.1423
11730245_a_at	FMO2	*flavin containing monooxygenase 2*	2.3595	5.1320
11754776_x_at	CCDC74A	*coiled-coil domain containing 74A*	2.3595	5.1318
11738656_a_at	PACRG	*PARK2 coregulated*	2.3594	5.1316
11728854_at	CCDC173	*coiled-coil domain containing 173*	2.3569	5.1227
11759674_a_at	CAPS2	*calcyphosine 2*	2.3491	5.0952
11754735_s_at	ABCA13	*ATP binding cassette subfamily A member 13*	2.3433	5.0746
11729453_s_at	CYP2B6	*cytochrome P450 family 2 subfamily B member 6*	2.3372	5.0533
11720243_x_at	TCN2	*transcobalamin 2*	2.3344	5.0434
11717465_s_at	LXN	*latexin*	2.3260	5.0141
11756399_x_at	CCDC189	*coiled-coil domain containing 189*	2.3185	4.9880
11750205_a_at	BCAS1	*breast carcinoma amplified sequence 1*	2.3160	4.9794
11730976_a_at	NSUN7	*NOP2/Sun RNA methyltransferase family member 7*	2.3155	4.9779
11731681_a_at	KATNAL2	*katanin catalytic subunit A1 like 2*	2.3043	4.9392
11726051_a_at	FMO3	*flavin containing monooxygenase 3*	2.3021	4.9318
11732022_a_at	TTC25	*tetratricopeptide repeat domain 25*	2.3020	4.9313
11731660_a_at	VWA3B	*von Willebrand factor A domain containing 3B*	2.2975	4.9161
11758468_s_at	TSHZ2	*teashirt zinc finger homeobox 2*	2.2962	4.9116
11732634_a_at	TSGA10	*testis specific 10*	2.2946	4.9063
11719692_a_at	RARRES3	*retinoic acid receptor responder 3*	2.2920	4.8974
11724914_at	SPATA18	*spermatogenesis associated 18*	2.2809	4.8598
11725223_at	SNTB1	*syntrophin beta 1*	2.2785	4.8517
11734396_at	HRASLS2	*HRAS like suppressor 2*	2.2741	4.8371
11744086_a_at	PRR15L	*proline rich 15 like*	2.2735	4.8348
11757615_a_at	MAP6	*microtubule associated protein 6*	2.2714	4.8278
11736369_at	MBOAT1	*membrane bound O-acyltransferase domain containing 1*	2.2699	4.8230
11718617_a_at	DNAJA4	*DnaJ Heat Shock Protein Family (Hsp40) Member A4*	2.2684	4.8178
11730801_at	CXCL6	*C-X-C motif chemokine ligand 6*	2.2677	4.8156
11730785_a_at	TTC21A	*tetratricopeptide repeat domain 21A*	2.2594	4.7878
11720064_a_at	GLIPR2	*GLI pathogenesis related 2*	2.2573	4.7808
11763973_a_at	CFAP157	*cilia and flagella associated protein 157*	2.2572	4.7805
11758637_x_at	AMY1A	*Amylase, Alpha 1A (Salivary)*	2.2544	4.7715
11729554_at	CFAP73	*cilia and flagella associated protein 73*	2.2542	4.7706
11724667_s_at	ENPP3	*ectonucleotide pyrophosphatase/phosphodiesterase 3*	2.2519	4.7632

11734013_a_at	BMP4	*bone morphogenetic protein 4*	2.2516	4.7621
11725908_at	LRRC10B	*leucine rich repeat containing 10B*	2.2498	4.7561
11758595_at	NBEA	*neurobeachin*	2.2453	4.7414
11717774_a_at	PLEKHB1	*pleckstrin homology domain containing B1*	2.2453	4.7412
11743226_at	CCDC160	*coiled-coil domain containing 160*	2.2363	4.7120
11759322_at	BCL6	*B-cell CLL/lymphoma 6*	2.2357	4.7099
11754734_a_at	ATP6V1C2	*ATPase H+ transporting V1 subunit C2*	2.2299	4.6910
11739882_a_at	GLIS3	*GLIS family zinc finger 3*	2.2274	4.6829
11759187_at	TNFAIP8L1	*TNF alpha induced protein 8 like 1*	2.2173	4.6503
11725912_a_at	ERBB4	*erb-b2 receptor tyrosine kinase 4*	2.2132	4.6371
11715290_s_at	CLDN3	*claudin 3*	2.2131	4.6368
11756539_a_at	TCTEX1D1	*Tctex1 domain containing 1*	2.2008	4.5975
11739610_a_at	CALML4	*calmodulin like 4*	2.1956	4.5807
11743921_at	TMEM125	*transmembrane protein 125*	2.1955	4.5804
11739039_x_at	CEACAM5	*carcinoembryonic antigen related cell adhesion molecule 5*	2.1926	4.5712
11724515_a_at	GPD1L	*glycerol-3-phosphate dehydrogenase 1-like*	2.1875	4.5553
11750527_s_at	HLA-DQA1	*major histocompatibility complex, class II, DQ alpha 1*	2.1874	4.5549
11744615_s_at	KLHDC9	*kelch domain containing 9*	2.1748	4.5152
11734939_a_at	SLC16A9	*solute carrier family 16 member 9*	2.1730	4.5095
11722242_at	TSPAN12	*tetraspanin 12*	2.1644	4.4828
11735381_a_at	MAP3K19	*mitogen-activated protein kinase 19*	2.1595	4.4677
11744596_a_at	LYPD6B	*LY6/PLAUR domain containing 6B*	2.1539	4.4504
11731817_s_at	RAB17	*RAB17, member RAS oncogene family*	2.1528	4.4469
11715462_x_at	LYZ	*lysozyme*	2.1438	4.4192
11755640_s_at	RALGPS1	*Ral GEF with PH domain and SH3 binding motif 1*	2.1431	4.4172
11732851_at	CCDC60	*coiled-coil domain containing 60*	2.1419	4.4134
11742224_a_at	CDC20B	*cell division cycle 20B*	2.1383	4.4023
11728342_at	DCLK1	*doublecortin like kinase 1*	2.1370	4.3984
11727116_a_at	PLA1A	*phospholipase A1 member A*	2.1367	4.3974
11732751_a_at	CC2D2A	*coiled-coil and C2 domain containing 2A*	2.1307	4.3794
11738255_x_at	C7orf57	*chromosome 7 open reading frame 57*	2.1296	4.3759
11726430_at	HSPB2-C11orf52	*HSPB2-C11orf52 Readthrough (NMD Candidate)*	2.1266	4.3668
11730881_a_at	NEBL	*nebulette*	2.1234	4.3572
11758221_s_at	ARRDC3	*arrestin domain containing 3*	2.1229	4.3557
11739725_a_at	TC2N	*tandem C2 domains, nuclear*	2.1211	4.3502
11731538_a_at	ADGRF1	*adhesion G protein-coupled receptor F1*	2.1172	4.3384
11725587_a_at	RAB36	*RAB36, member RAS oncogene family*	2.1058	4.3045
11732523_a_at	TMEM232	*transmembrane protein 232*	2.1053	4.3029
11741768_a_at	VNN2	*vanin 2*	2.1039	4.2986
11721688_at	ID4	*inhibitor of DNA binding 4, HLH protein*	2.1032	4.2965
11754888_a_at	ADSSL1	*adenylosuccinate synthase like 1*	2.0965	4.2766
11715263_at	SPEF2	*sperm flagellar 2*	2.0928	4.2658

11729025_a_at	ILDR1	*immunoglobulin like domain containing receptor 1*	2.0903	4.2584
11723899_a_at	DHRS9	*dehydrogenase/reductase 9*	2.0838	4.2393
11749717_a_at	RP1	*RP1, Axonemal Microtubule Associated*	2.0838	4.2391
11737557_at	AMTN	*amelotin*	2.0831	4.2371
11724703_a_at	ELF5	*E74 like ETS transcription factor 5*	2.0759	4.2161
11724264_a_at	IFT22	*intraflagellar transport 22*	2.0745	4.2119
11755558_a_at	DRC7	*dynein regulatory complex subunit 7*	2.0681	4.1932
11752544_a_at	GPNMB	*glycoprotein nmb*	2.0658	4.1867
11724795_at	ZG16B	*zymogen granule protein 16B*	2.0631	4.1788
11740326_x_at	SORBS2	*sorbin and SH3 domain containing 2*	2.0580	4.1640
11718919_a_at	ATP6V1B1	*ATPase H+ transporting V1 subunit B1*	2.0572	4.1618
11743570_s_at	EML1	*echinoderm microtubule associated protein like 1*	2.0538	4.1519
11741192_a_at	RBKS	*ribokinase*	2.0530	4.1496
11727918_s_at	MUC20	*mucin 20, cell surface associated*	2.0497	4.1403
11756588_a_at	ST6GALNAC1	*ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1*	2.0496	4.1398
11756624_x_at	RABL2A	*RAB, member of RAS oncogene family-like 2A*	2.0493	4.1390
11737207_at	C1orf189	*chromosome 1 open reading frame 189*	2.0470	4.1326
11757824_s_at	RGL1	*ral guanine nucleotide dissociation stimulator like 1*	2.0468	4.1320
11753873_a_at	BCL2L15	*BCL2 like 15*	2.0464	4.1307
11718433_a_at	SASH1	*SAM and SH3 domain containing 1*	2.0457	4.1288
11741956_a_at	LRRIQ1	*leucine rich repeats and IQ motif containing 1*	2.0364	4.1023
11721993_at	SLC6A6	*solute carrier family 6 member 6*	2.0348	4.0977
11757972_s_at	MYLIP	*myosin regulatory light chain interacting protein*	2.0335	4.0941
11742483_a_at	CCDC190	*coiled-coil domain containing 190*	2.0306	4.0857
11728479_x_at	CCDC181	*coiled-coil domain containing 181*	2.0291	4.0815
11758586_s_at	GGT6	*gamma-glutamyltransferase 6*	2.0247	4.0691
11744051_at	TSPAN1	*tetraspanin 1*	2.0202	4.0563
11756018_a_at	C4orf22	*chromosome 4 open reading frame 22*	2.0168	4.0468
11728523_a_at	MYCL	*v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog*	2.0142	4.0395
11743773_s_at	LZTFL1	*leucine zipper transcription factor like 1*	2.0111	4.0308
11744226_a_at	SPA17	*sperm autoantigenic protein 17*	2.0110	4.0307
11757504_a_at	DDAH1	*dimethylarginine dimethylaminohydrolase 1*	2.0102	4.0283
11730037_at	DEGS2	*delta 4-desaturase, sphingolipid 2*	2.0067	4.0187
11757913_x_at	TUBA1A	*tubulin alpha 1a*	2.0055	4.0153
11716875_at	GON7	*GON7, KEOPS complex subunit homolog*	2.0045	4.0126
11732748_at	DNAH6	*dynein axonemal heavy chain 6*	2.0026	4.0073
11732240_a_at	SLITRK6	*SLIT and NTRK like family member 6*	2.0021	4.0059
11728561_a_at	TSNAXIP1	*translin associated factor X interacting protein 1*	2.0005	4.0015
11755109_a_at	CYFIP2	*cytoplasmic FMR1 interacting protein 2*	1.9956	3.9879
11756881_a_at	LOC101926951	*uncharacterized LOC101926951*	1.9903	3.9732
11728953_a_at	ADGRV1	*adhesion G protein-coupled receptor V1*	1.9806	3.9467
11755425_a_at	FAM179B	*family with sequence similarity 179 member B*	1.9755	3.9327

11764253_s_at	IFITM10	*interferon induced transmembrane protein 10*	1.9644	3.9024
11733042_at	SLC7A2	*solute carrier family 7 member 2*	1.9622	3.8965
11718287_at	UBL3	*ubiquitin like 3*	1.9574	3.8836
11743043_a_at	FBLN5	*fibulin 5*	1.9568	3.8821
11756342_s_at	GDA	*guanine deaminase*	1.9561	3.8801
11721944_x_at	RABL2B	*RAB, member of RAS oncogene family-like 2B*	1.9537	3.8738
11739797_a_at	RFX2	*regulatory factor X2*	1.9468	3.8553
11748066_s_at	LRRC49	*leucine rich repeat containing 49*	1.9385	3.8332
11736285_a_at	CHKA	*choline kinase alpha*	1.9320	3.8159
11749583_a_at	FUT2	*fucosyltransferase 2*	1.9304	3.8115
11717339_s_at	SORD	*sorbitol dehydrogenase*	1.9264	3.8011
11725249_at	LY75	*lymphocyte antigen 75*	1.9242	3.7952
11742263_a_at	SPAG8	*sperm associated antigen 8*	1.9144	3.7696
11734274_a_at	VWA3A	*von Willebrand factor A domain containing 3A*	1.9140	3.7686
11734893_s_at	SOBP	*sine oculis binding protein homolog*	1.9134	3.7670
11723007_a_at	DYX1C1-CCPG1	*DYX1C1-CCPG1 Readthrough (NMD Candidate)*	1.9126	3.7649
11726521_a_at	SPATA17	*spermatogenesis associated 17*	1.9117	3.7626
11731606_at	SCIN	*scinderin*	1.9115	3.7620
11737992_s_at	GPR37	*G protein-coupled receptor 37*	1.9102	3.7586
11751459_x_at	LRG1	*leucine rich alpha-2-glycoprotein 1*	1.9102	3.7585
11715147_at	MAATS1	*MYCBP associated and testis expressed 1*	1.9094	3.7565
11728847_a_at	FAM179A	*family with sequence similarity 179 member A*	1.9043	3.7434
11727722_a_at	MYB	*MYB proto-oncogene, transcription factor*	1.9037	3.7416
11726119_at	RPGR	*retinitis pigmentosa GTPase regulator*	1.9025	3.7386
11717440_a_at	EPS8	*epidermal growth factor receptor pathway substrate 8*	1.9004	3.7332
11724528_a_at	GCNT3	*Glucosaminyl (N-Acetyl) Transferase 3, Mucin Type*	1.8933	3.7149
11715165_at	DNAJC12	*DnaJ Heat Shock Protein Family (Hsp40) Member C12*	1.8912	3.7095
11757928_s_at	TMEM178A	*transmembrane protein 178A*	1.8892	3.7043
11759343_x_at	FMN1	*formin 1*	1.8871	3.6988
11759602_a_at	RSRP1	*arginine and serine rich protein 1*	1.8865	3.6974
11754222_a_at	CFAP221	*cilia and flagella associated protein 221*	1.8861	3.6964
11737088_at	TLL1	*tolloid like 1*	1.8858	3.6957
11753734_x_at	WFDC2	*WAP four-disulfide core domain 2*	1.8833	3.6891
11728604_at	RSPH14	*radial spoke head 14 homolog*	1.8814	3.6844
11758544_s_at	RDH10	*Retinol Dehydrogenase 10*	1.8810	3.6834
11757645_s_at	FIBIN	*Fin Bud Initiation Factor Homolog (Zebrafish)*	1.8788	3.6776
11727198_a_at	PCDHAC2	*protocadherin alpha subfamily C, 2*	1.8784	3.6767
11722383_a_at	MDM1	*Mdm1 nuclear protein*	1.8749	3.6677
11721700_a_at	RERG	*RAS like estrogen regulated growth inhibitor*	1.8683	3.6511
11716974_a_at	PDK4	*pyruvate dehydrogenase kinase 4*	1.8673	3.6485
11727180_a_at	PHTF1	*putative homeodomain transcription factor 1*	1.8632	3.6382
11722743_a_at	TLE2	*transducin like enhancer of split 2*	1.8626	3.6366

11718448_at	SH3BGRL2	*SH3 domain binding glutamate rich protein like 2*	1.8573	3.6234
11730066_s_at	MAPK10	*mitogen-activated protein kinase 10*	1.8551	3.6178
11727572_s_at	KLHL6	*kelch like family member 6*	1.8540	3.6149
11723404_at	PPARGC1A	*PPARG coactivator 1 alpha*	1.8522	3.6104
11722534_at	RPRM	*reprimo, TP53 dependent G2 arrest mediator candidate*	1.8494	3.6035
11735478_a_at	CHST6	*carbohydrate sulfotransferase 6*	1.8484	3.6011
11725450_a_at	TMEM45B	*transmembrane protein 45B*	1.8433	3.5883
11721759_a_at	ASAP3	*ArfGAP with SH3 domain, ankyrin repeat and PH domain 3*	1.8426	3.5865
11720865_a_at	IFT27	*intraflagellar transport 27*	1.8422	3.5856
11726916_at	SLCO4C1	*solute carrier organic anion transporter family member 4C1*	1.8417	3.5842
11728116_at	DNAH10	*dynein axonemal heavy chain 10*	1.8415	3.5838
11742816_a_at	FAM13A	*family with sequence similarity 13 member A*	1.8407	3.5819
11728200_a_at	LOX	*lysyl oxidase*	1.8308	3.5574
11734373_a_at	CSPP1	*centrosome and spindle pole associated protein 1*	1.8305	3.5565
11725625_s_at	ACE2	*angiotensin I converting enzyme 2*	1.8264	3.5465
11731547_a_at	TMEM67	*transmembrane protein 67*	1.8253	3.5438
11721460_s_at	TAPBPL	*TAP binding protein like*	1.8217	3.5350
11720088_x_at	NUCB2	*nucleobindin 2*	1.8211	3.5335
11755671_a_at	SYTL2	*synaptotagmin like 2*	1.8181	3.5261
11738640_a_at	EFCAB12	*EF-hand calcium binding domain 12*	1.8152	3.5190
11718766_at	PRSS23	*protease, serine 23*	1.8099	3.5063
11718481_s_at	CFI	*complement factor I*	1.8074	3.5001
11752060_x_at	ERN2	*endoplasmic reticulum to nucleus signaling 2*	1.8058	3.4963
11763291_a_at	CFAP65	*cilia and flagella associated protein 65*	1.8048	3.4937
11745282_a_at	AK9	*adenylate kinase 9*	1.8020	3.4871
11750736_a_at	STEAP4	*STEAP4 metalloreductase*	1.8020	3.4870
11731956_at	CFAP100	*cilia and flagella associated protein 100*	1.8005	3.4835
11722712_x_at	PPOX	*protoporphyrinogen oxidase*	1.7959	3.4724
11716210_at	CITED2	*Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2*	1.7939	3.4674
11758064_s_at	MIR4683	*microRNA 4683*	1.7933	3.4660
11756074_a_at	MMP7	*matrix metallopeptidase 7*	1.7913	3.4612
11754475_a_at	IQCK	*IQ motif containing K*	1.7902	3.4587
11731984_at	CERKL	*ceramide kinase like*	1.7900	3.4581
11729455_x_at	CYP2B6	*cytochrome P450 family 2 subfamily B member 6*	1.7889	3.4555
11722310_a_at	TMC4	*transmembrane channel like 4*	1.7858	3.4480
11734144_s_at	LRRC37A2	*leucine rich repeat containing 37 member A2*	1.7848	3.4458
11738185_s_at	PDE8B	*phosphodiesterase 8B*	1.7835	3.4427
11716532_a_at	EGFL6	*EGF like domain multiple 6*	1.7814	3.4375
11727296_s_at	TGFB3	*transforming growth factor beta 3*	1.7804	3.4353
11727702_at	C9orf152	*chromosome 9 open reading frame 152*	1.7798	3.4339
11724866_a_at	SCGB3A1	*secretoglobin family 3A member 1*	1.7721	3.4156
11718169_a_at	AZGP1	*alpha-2-glycoprotein 1, zinc-binding*	1.7702	3.4110

11718302_at	HSD11B2	*hydroxysteroid 11-beta dehydrogenase 2*	1.7679	3.4056
11738889_at	IQCD	*IQ motif containing D*	1.7618	3.3913
11734103_a_at	FGGY	*FGGY carbohydrate kinase domain containing*	1.7586	3.3838
11721665_a_at	PLA2G16	*phospholipase A2 group XVI*	1.7575	3.3811
11722070_a_at	CHPT1	*choline phosphotransferase 1*	1.7573	3.3807
11734334_at	LINC01559	*long intergenic non-protein coding RNA 1559*	1.7551	3.3756
11743575_a_at	CCDC180	*coiled-coil domain containing 180*	1.7542	3.3734
11757005_a_at	FUCA1	*fucosidase, alpha-L- 1, tissue*	1.7503	3.3644
11727007_at	SORT1	*sortilin 1*	1.7464	3.3552
11726360_a_at	ALDH3A1	*aldehyde dehydrogenase 3 family member A1*	1.7449	3.3518
11724779_at	PGM2L1	*phosphoglucomutase 2 like 1*	1.7433	3.3481
11747526_a_at	TSPAN6	*tetraspanin 6*	1.7429	3.3471
11730259_a_at	ZC2HC1C	*zinc finger C2HC-type containing 1C*	1.7382	3.3361
11731657_s_at	VAV3	*vav guanine nucleotide exchange factor 3*	1.7378	3.3353
11748865_a_at	TMEM139	*transmembrane protein 139*	1.7370	3.3335
11719381_a_at	PSENEN	*presenilin enhancer gamma-secretase subunit*	1.7369	3.3331
11755050_s_at	PLCB4	*phospholipase C beta 4*	1.7336	3.3255
11721411_a_at	BSPRY	*B-box and SPRY domain containing*	1.7319	3.3217
11723876_at	KCNK5	*potassium two pore domain channel subfamily K member 5*	1.7317	3.3212
11758657_s_at	PKIG	*CAMP-Dependent Protein Kinase Inhibitor Gamma*	1.7292	3.3154
11721030_a_at	PIP5K1B	*phosphatidylinositol-4-phosphate 5-kinase type 1 beta*	1.7291	3.3152
11726479_a_at	MX2	*MX dynamin like GTPase 2*	1.7154	3.2839
11728379_at	EFCAB2	*EF-hand calcium binding domain 2*	1.7152	3.2835
11734359_a_at	RNASEL	*ribonuclease L*	1.7151	3.2832
11725758_at	ISL1	*ISL LIM homeobox 1*	1.7065	3.2637
11722820_at	GGT7	*gamma-glutamyltransferase 7*	1.7058	3.2621
11740038_s_at	ANKRD36	*ankyrin repeat domain 36*	1.7056	3.2616
11730467_at	NTN1	*netrin 1*	1.7053	3.2610
11747474_a_at	NR4A2	*nuclear receptor subfamily 4 group A member 2*	1.7022	3.2540
11722756_at	TMEM37	*transmembrane protein 37*	1.7010	3.2512
11716127_a_at	BAG1	*BCL2 associated athanogene 1*	1.6992	3.2471
11750791_a_at	NEK11	*NIMA related kinase 11*	1.6964	3.2409
11729365_at	PRKAA2	*protein kinase AMP-activated catalytic subunit alpha 2*	1.6959	3.2397
11747234_a_at	DTHD1	*death domain containing 1*	1.6957	3.2393
11728829_at	INHBB	*inhibin beta B subunit*	1.6944	3.2364
11718506_at	TFF3	*trefoil factor 3*	1.6932	3.2338
11722862_x_at	TRIM2	*tripartite motif containing 2*	1.6931	3.2335
11715722_a_at	GOLM1	*golgi membrane protein 1*	1.6925	3.2321
11754987_x_at	C21orf58	*chromosome 21 open reading frame 58*	1.6920	3.2311
11723063_a_at	GCHFR	*GTP cyclohydrolase I feedback regulator*	1.6909	3.2285
11730936_s_at	AKNA	*AT-hook transcription factor*	1.6892	3.2248
11754640_a_at	EPHX2	*epoxide hydrolase 2*	1.6880	3.2222

11756604_a_at	PCDHB2	*protocadherin beta 2*	1.6879	3.2219
11731286_at	EDN2	*endothelin 2*	1.6877	3.2215
11727030_s_at	MAP1A	*microtubule associated protein 1A*	1.6866	3.2189
11758988_at	SYT17	*synaptotagmin 17*	1.6864	3.2185
11728388_at	TSPAN2	*tetraspanin 2*	1.6863	3.2184
11716167_a_at	MX1	*MX dynamin like GTPase 1*	1.6862	3.2180
11721988_at	CCDC191	*coiled-coil domain containing 191*	1.6845	3.2144
11740586_a_at	PTGFR	*prostaglandin F receptor*	1.6835	3.2120
11746280_a_at	SYTL3	*synaptotagmin like 3*	1.6835	3.2120
11733675_x_at	WDR49	*WD repeat domain 49*	1.6819	3.2086
11721758_at	TMEM47	*transmembrane protein 47*	1.6804	3.2052
11722884_at	CREBRF	*CREB3 regulatory factor*	1.6791	3.2022
11726412_s_at	ZBTB7C	*zinc finger and BTB domain containing 7C*	1.6770	3.1977
11718025_at	IL1R1	*interleukin 1 receptor type 1*	1.6752	3.1936
11726213_x_at	CCL15	*C-C motif chemokine ligand 15*	1.6746	3.1922
11735099_a_at	C2orf73	*chromosome 2 open reading frame 73*	1.6735	3.1898
11736239_a_at	ABCA5	*ATP binding cassette subfamily A member 5*	1.6728	3.1884
11735752_a_at	CXXC5	*CXXC finger protein 5*	1.6701	3.1823
11764077_s_at	EDIL3	*EGF like repeats and discoidin domains 3*	1.6687	3.1792
11725000_at	DUOXA2	*dual oxidase maturation factor 2*	1.6684	3.1787
11720158_a_at	WDR19	*WD repeat domain 19*	1.6674	3.1764
11719453_a_at	BBS1	*Bardet-Biedl syndrome 1*	1.6665	3.1745
11757724_x_at	HNRNPUL2-BSCL2	*HNRNPUL2-BSCL2 Readthrough (NMD Candidate)*	1.6637	3.1682
11731617_x_at	SIDT1	*SID1 transmembrane family member 1*	1.6621	3.1648
11730261_a_at	PRKAR2B	*protein kinase cAMP-dependent type II regulatory subunit beta*	1.6596	3.1592
11754491_a_at	C16orf46	*chromosome 16 open reading frame 46*	1.6552	3.1496
11734149_x_at	PRRT3	*proline rich transmembrane protein 3*	1.6532	3.1453
11743321_at	CTSO	*cathepsin O*	1.6531	3.1450
11737644_a_at	RNF183	*ring finger protein 183*	1.6530	3.1448
11757752_s_at	STK36	*serine/threonine kinase 36*	1.6491	3.1364
11759623_at	C11orf71	*chromosome 11 open reading frame 71*	1.6485	3.1350
11748981_a_at	NAT1	*N-acetyltransferase 1*	1.6468	3.1314
11735883_a_at	DNAH9	*dynein axonemal heavy chain 9*	1.6465	3.1307
11742833_a_at	FAM149A	*family with sequence similarity 149 member A*	1.6446	3.1267
11720678_a_at	CREB3L1	*cAMP responsive element binding protein 3 like 1*	1.6441	3.1256
11734552_a_at	CX3CL1	*C-X3-C motif chemokine ligand 1*	1.6427	3.1226
11729545_a_at	DZANK1	*double zinc ribbon and ankyrin repeat domains 1*	1.6417	3.1204
11723703_s_at	ABHD5	*abhydrolase domain containing 5*	1.6399	3.1165
11740000_a_at	CPEB3	*cytoplasmic polyadenylation element binding protein 3*	1.6381	3.1126
11723824_s_at	MYO5C	*myosin VC*	1.6375	3.1112
11731126_at	GXYLT2	*glucoside xylosyltransferase 2*	1.6369	3.1100
11721445_x_at	ERBB3	*erb-b2 receptor tyrosine kinase 3*	1.6363	3.1087

11721368_at	CRLF1	*cytokine receptor like factor 1*	1.6361	3.1082
11754603_a_at	DUSP18	*dual specificity phosphatase 18*	1.6356	3.1071
11729137_at	UGT2B7	*UDP glucuronosyltransferase family 2 member B7*	1.6339	3.1036
11720290_at	IQCE	*IQ motif containing E*	1.6308	3.0969
11720146_a_at	DAPK1	*death associated protein kinase 1*	1.6305	3.0962
11763193_at	GDPD1	*glycerophosphodiester phosphodiesterase domain containing 1*	1.6273	3.0894
11727997_a_at	MYEF2	*myelin expression factor 2*	1.6269	3.0885
11758582_s_at	SIX4	*SIX homeobox 4*	1.6269	3.0884
11723885_at	NATD1	*N-acetyltransferase domain containing 1*	1.6243	3.0829
11723367_a_at	RAB26	*RAB26, member RAS oncogene family*	1.6234	3.0809
11734242_x_at	KIF19	*kinesin family member 19*	1.6223	3.0786
11756888_a_at	TFCP2L1	*transcription factor CP2 like 1*	1.6217	3.0774
11741221_a_at	COLCA2	*colorectal cancer associated 2*	1.6210	3.0758
11729693_at	SERPINB3	*serpin family B member 3*	1.6207	3.0753
11725856_a_at	DNAH1	*dynein axonemal heavy chain 1*	1.6202	3.0741
11760254_at	IFI44	*interferon induced protein 44*	1.6198	3.0734
11742865_a_at	TJP3	*tight junction protein 3*	1.6196	3.0730
11727881_at	BBS12	*Bardet-Biedl syndrome 12*	1.6194	3.0724
11729575_a_at	XBP1	*X-box binding protein 1*	1.6185	3.0705
11721957_at	YPEL2	*yippee like 2*	1.6183	3.0701
11732580_a_at	ME3	*malic enzyme 3*	1.6176	3.0686
11722348_a_at	REPS2	*RALBP1 associated Eps domain containing 2*	1.6173	3.0679
11740104_at	APOBEC4	*apolipoprotein B mRNA editing enzyme catalytic polypeptide like 4*	1.6171	3.0675
11743951_a_at	ZNF214	*zinc finger protein 214*	1.6154	3.0640
11721491_a_at	FBP1	*fructose-bisphosphatase 1*	1.6124	3.0575
11721917_a_at	ANKRD37	*ankyrin repeat domain 37*	1.6116	3.0559
11742669_s_at	HIST4H4	*histone cluster 4 H4*	1.6079	3.0481
11729998_a_at	B3GNT7	*UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7*	1.6074	3.0470
11732516_a_at	CERS4	*ceramide synthase 4*	1.6066	3.0453
11724080_x_at	COL21A1	*collagen type XXI alpha 1 chain*	1.6042	3.0402
11729692_a_at	SERPINB3	*serpin family B member 3*	1.6022	3.0360
11755010_s_at	POC1B-GALNT4	*POC1B-GALNT4 readthrough*	1.6011	3.0338
11761330_x_at	NME9	*NME/NM23 family member 9*	1.5981	3.0274
11732667_x_at	RSPH10B	*radial spoke head 10 homolog B*	1.5974	3.0260
11738149_a_at	TOX3	*TOX high mobility group box family member 3*	1.5941	3.0190
11749355_a_at	CFB	*complement factor B*	1.5934	3.0177
11721780_a_at	LLGL2	*LLGL2, scribble cell polarity complex component*	1.5931	3.0169
11733612_s_at	DOCK8	*dedicator of cytokinesis 8*	1.5930	3.0167
11743200_a_at	ARMC2	*armadillo repeat containing 2*	1.5929	3.0166
11732468_at	ATP12A	*ATPase H+/K+ transporting non-gastric alpha2 subunit*	1.5902	3.0109
11729079_s_at	ESRRG	*estrogen related receptor gamma*	1.5882	3.0068
11730972_x_at	CYP4F12	*cytochrome P450 family 4 subfamily F member 12*	1.5877	3.0056

11724400_a_at	ENKD1	*enkurin domain containing 1*	1.5872	3.0046
11739375_at	SYT7	*synaptotagmin 7*	1.5868	3.0038
11754681_s_at	HLA-DMB	*major histocompatibility complex, class II, DM beta*	1.5866	3.0034
11729089_a_at	C1orf87	*chromosome 1 open reading frame 87*	1.5865	3.0033
11715441_a_at	CTGF	*connective tissue growth factor*	1.5859	3.0019
11755174_a_at	CGN	*cingulin*	1.5853	3.0008
11721267_s_at	TMPRSS4	*transmembrane protease, serine 4*	1.5830	2.9959
11736257_at	PRKCE	*protein kinase C epsilon*	1.5814	2.9927
11758651_s_at	SH3GL3	*SH3 domain containing GRB2 like 3, endophilin A3*	1.5812	2.9922
11729972_at	CYP4Z1	*cytochrome P450 family 4 subfamily Z member 1*	1.5809	2.9915
11752254_a_at	DNAH3	*dynein axonemal heavy chain 3*	1.5752	2.9798
11740832_at	PLEKHG7	*pleckstrin homology and RhoGEF domain containing G7*	1.5733	2.9759
11725863_a_at	FAM13B	*family with sequence similarity 13 member B*	1.5727	2.9747
11723716_a_at	CYB5D1	*cytochrome b5 domain containing 1*	1.5727	2.9747
11717111_a_at	REPIN1	*replication initiator 1*	1.5722	2.9735
11752398_a_at	C1orf228	*chromosome 1 open reading frame 228*	1.5709	2.9708
11728446_a_at	PLCH1	*phospholipase C eta 1*	1.5686	2.9661
11747167_x_at	ADH1B	*Alcohol Dehydrogenase 1B (Class I), Beta Polypeptide*	1.5679	2.9648
11755084_x_at	CD55	*CD55 Molecule (Cromer Blood Group)*	1.5675	2.9639
11726054_a_at	MUC4	*mucin 4, cell surface associated*	1.5674	2.9638
11729128_at	CPA4	*carboxypeptidase A4*	1.5634	2.9554
11754411_a_at	CLUAP1	*clusterin associated protein 1*	1.5585	2.9455
11743657_x_at	HPGD	*hydroxyprostaglandin dehydrogenase 15-*	1.5579	2.9442
11731271_a_at	MGAM	*maltase-glucoamylase*	1.5507	2.9296
11731030_at	BICDL2	*BICD family like cargo adaptor 2*	1.5497	2.9276
11728858_at	CEP19	*centrosomal protein 19*	1.5495	2.9271
11725596_a_at	ZDHHC23	*zinc finger DHHC-type containing 23*	1.5475	2.9231
11722658_at	CXCL17	*C-X-C motif chemokine ligand 17*	1.5461	2.9202
11749510_a_at	SAMHD1	*SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1*	1.5460	2.9201
11725892_a_at	PLEKHH1	*pleckstrin homology, MyTH4 and FERM domain containing H1*	1.5450	2.9180
11757444_a_at	EGLN3	*egl-9 family hypoxia inducible factor 3*	1.5435	2.9150
11728939_at	RASEF	*RAS and EF-hand domain containing*	1.5407	2.9094
11735530_a_at	PIH1D2	*PIH1 domain containing 2*	1.5404	2.9088
11719353_s_at	GCC2	*GRIP and coiled-coil domain containing 2*	1.5396	2.9072
11758460_s_at	FAAH2	*fatty acid amide hydrolase 2*	1.5396	2.9071
11720196_at	CIPC	*CLOCK interacting pacemaker*	1.5390	2.9060
11734214_a_at	MPP7	*membrane palmitoylated protein 7*	1.5389	2.9057
11735084_s_at	FREM2	*FRAS1 related extracellular matrix protein 2*	1.5388	2.9056
11728363_s_at	IL20RA	*interleukin 20 receptor subunit alpha*	1.5372	2.9024
11725890_s_at	ABCC6	*ATP binding cassette subfamily C member 6*	1.5356	2.8991
11724022_a_at	TRIM13	*tripartite motif containing 13*	1.5352	2.8982
11729420_a_at	TTC26	*tetratricopeptide repeat domain 26*	1.5351	2.8980

11741659_a_at	CDH26	*cadherin 26*	1.5335	2.8949
11736719_at	ZNF474	*zinc finger protein 474*	1.5333	2.8945
11728326_a_at	TTC30A	*tetratricopeptide repeat domain 30A*	1.5330	2.8939
11729890_at	ZFP3	*ZFP3 zinc finger protein*	1.5286	2.8850
11716308_s_at	CYBRD1	*cytochrome b reductase 1*	1.5280	2.8839
11732917_at	DZIP1L	*DAZ interacting zinc finger protein 1 like*	1.5257	2.8792
11718876_at	DNER	*delta/notch like EGF repeat containing*	1.5254	2.8786
11735717_a_at	ZNF226	*zinc finger protein 226*	1.5253	2.8784
11753179_s_at	FAM134B	*family with sequence similarity 134 member B*	1.5242	2.8763
11724051_at	TRIM68	*tripartite motif containing 68*	1.5228	2.8735
11717885_a_at	CCDC3	*coiled-coil domain containing 3*	1.5225	2.8729
11730035_at	FMO4	*flavin containing monooxygenase 4*	1.5217	2.8713
11721788_at	C1orf226	*chromosome 1 open reading frame 226*	1.5217	2.8712
11755873_a_at	ACSS1	*acyl-CoA synthetase short-chain family member 1*	1.5215	2.8708
11737749_a_at	SGK1	*serum/glucocorticoid regulated kinase 1*	1.5210	2.8698
11729679_a_at	PCDHB14	*protocadherin beta 14*	1.5189	2.8658
11736745_a_at	ZBTB20	*zinc finger and BTB domain containing 20*	1.5168	2.8616
11756274_a_at	ALDH1L1	*aldehyde dehydrogenase 1 family member L1*	1.5166	2.8612
11721726_a_at	IFT88	*intraflagellar transport 88*	1.5147	2.8574
11736113_at	ARHGAP18	*Rho GTPase activating protein 18*	1.5124	2.8528
11731145_a_at	SYNE1	*spectrin repeat containing nuclear envelope protein 1*	1.5120	2.8521
11727995_a_at	SPINK5	*serine peptidase inhibitor, Kazal type 5*	1.5107	2.8494
11731440_a_at	IFT57	*intraflagellar transport 57*	1.5086	2.8454
11730250_a_at	LNX1	*ligand of numb-protein X 1*	1.5082	2.8445
11732966_a_at	MIA	*melanoma inhibitory activity*	1.5067	2.8416
11721657_at	LMO4	*LIM domain only 4*	1.5065	2.8412
11727754_a_at	PLA2G4A	*phospholipase A2 group IVA*	1.5058	2.8398
11737119_a_at	NEK10	*NIMA related kinase 10*	1.5040	2.8363
11743405_a_at	SMIM14	*small integral membrane protein 14*	1.5039	2.8361
11744307_a_at	TTC39A	*tetratricopeptide repeat domain 39A*	1.5027	2.8338
11733637_a_at	MORN3	*MORN repeat containing 3*	1.5021	2.8326
11724157_x_at	SULT1E1	*sulfotransferase family 1E member 1*	1.5019	2.8321
11749398_a_at	B9D1	*B9 domain containing 1*	1.5019	2.8321
11717929_s_at	FOLR1	*folate receptor 1*	1.4992	2.8269
11732444_a_at	RBPMS	*RNA binding protein with multiple splicing*	1.4991	2.8266
11725522_at	MESP1	*mesoderm posterior bHLH transcription factor 1*	1.4952	2.8190
11727241_at	WNT4	*Wnt family member 4*	1.4945	2.8177
11730465_at	KCNJ2	*potassium voltage-gated channel subfamily J member 2*	1.4936	2.8159
11740320_at	CFAP47	*Cilia And Flagella Associated Protein 47*	1.4916	2.8121
11723585_a_at	SMPDL3A	*sphingomyelin phosphodiesterase acid like 3A*	1.4912	2.8112
11759039_at	SVIP	*small VCP interacting protein*	1.4871	2.8032
11725697_at	TRIM56	*tripartite motif containing 56*	1.4869	2.8028

11725941_at	WNT7B	*Wnt family member 7B*	1.4846	2.7983
11730469_s_at	LMO2	*LIM domain only 2*	1.4840	2.7973
11742683_x_at	HIST1H1C	*histone cluster 1 H1 family member c*	1.4830	2.7953
11729030_a_at	SPATS1	*spermatogenesis associated serine rich 1*	1.4826	2.7945
11727158_a_at	STRBP	*spermatid perinuclear RNA binding protein*	1.4814	2.7922
11751791_a_at	CCDC80	*coiled-coil domain containing 80*	1.4797	2.7889
11716399_at	TP53INP2	*tumor protein p53 inducible nuclear protein 2*	1.4796	2.7887
11736901_at	ANKRD45	*ankyrin repeat domain 45*	1.4769	2.7835
11730338_a_at	SMAD6	*SMAD family member 6*	1.4765	2.7827
11722523_a_at	TMCO4	*transmembrane and coiled-coil domains 4*	1.4697	2.7697
11719148_a_at	ARRDC2	*arrestin domain containing 2*	1.4693	2.7688
11729395_s_at	HECTD2	*HECT domain E3 ubiquitin protein ligase 2*	1.4679	2.7661
11724909_a_at	TMPRSS2	*transmembrane protease, serine 2*	1.4661	2.7628
11717093_at	TCTA	*T-cell leukemia translocation altered*	1.4659	2.7623
11718523_s_at	ANTXR1	*anthrax toxin receptor 1*	1.4649	2.7605
11757390_s_at	KLHL24	*kelch like family member 24*	1.4639	2.7585
11715222_at	MAGI3	*membrane associated guanylate kinase, WW and PDZ domain containing 3*	1.4628	2.7565
11755310_s_at	ACOT2	*acyl-CoA thioesterase 2*	1.4620	2.7549
11722614_a_at	CYP2J2	*cytochrome P450 family 2 subfamily J member 2*	1.4613	2.7535
11723946_a_at	ACSL5	*acyl-CoA synthetase long-chain family member 5*	1.4578	2.7469
11725474_a_at	MAP3K5	*mitogen-activated protein kinase 5*	1.4560	2.7435
11721025_a_at	TRAPPC6A	*trafficking protein particle complex 6A*	1.4534	2.7385
11744495_a_at	IFT46	*intraflagellar transport 46*	1.4519	2.7356
11732326_x_at	PBLD	*phenazine biosynthesis like protein domain containing*	1.4506	2.7332
11721601_s_at	ZBTB18	*zinc finger and BTB domain containing 18*	1.4466	2.7256
11744130_a_at	VGLL1	*vestigial like family member 1*	1.4460	2.7246
11717418_at	DNAL1	*dynein axonemal light chain 1*	1.4456	2.7238
11721322_at	UNC93B1	*Unc-93 Homolog B1 (C. Elegans)*	1.4430	2.7189
11717090_a_at	HIST2H2BE	*histone cluster 2 H2B family member e*	1.4419	2.7168
11724626_a_at	IFT74	*intraflagellar transport 74*	1.4403	2.7138
11736970_at	TMEM213	*transmembrane protein 213*	1.4400	2.7132
11756702_a_at	CYP39A1	*cytochrome P450 family 39 subfamily A member 1*	1.4378	2.7090
11724063_s_at	FA2H	*fatty acid 2-hydroxylase*	1.4376	2.7087
11726384_at	FRY	*FRY microtubule binding protein*	1.4371	2.7077
11742497_x_at	SSX6	*SSX family member 6, pseudogene*	1.4284	2.6915
11747376_s_at	CCPG1	*cell cycle progression 1*	1.4270	2.6888
11736323_a_at	BAIAP3	*BAI1 associated protein 3*	1.4266	2.6882
11723396_at	B9D2	*B9 protein domain 2*	1.4241	2.6835
11750031_a_at	CRYL1	*crystallin lambda 1*	1.4235	2.6824
11730527_a_at	DAPK2	*death associated protein kinase 2*	1.4228	2.6811
11733592_x_at	LCA5	*LCA5, lebercilin*	1.4221	2.6797
11724848_a_at	DIXDC1	*DIX domain containing 1*	1.4219	2.6793

11731200_a_at	TLR5	*toll like receptor 5*	1.4182	2.6726
11758110_s_at	SIX1	*SIX homeobox 1*	1.4162	2.6689
11734454_a_at	WFDC3	*WAP four-disulfide core domain 3*	1.4162	2.6689
11727238_at	UST	*uronyl 2-sulfotransferase*	1.4149	2.6664
11740580_at	ASAH1	*N-acylsphingosine amidohydrolase 1*	1.4147	2.6660
11731436_at	CETN2	*centrin 2*	1.4133	2.6635
11744029_a_at	BBS4	*Bardet-Biedl syndrome 4*	1.4112	2.6596
11724985_a_at	EXPH5	*exophilin 5*	1.4100	2.6574
11757307_s_at	CTSD	*cathepsin D*	1.4072	2.6522
11739493_at	MGAT4A	*Mannosyl (Alpha-1,3-)-Glycoprotein Beta-1,4-N-Acetylglucosaminyltransferase, Isozyme A*	1.4057	2.6494
11724612_a_at	DYRK2	*dual specificity tyrosine phosphorylation regulated kinase 2*	1.4016	2.6420
11720651_x_at	DUSP23	*dual specificity phosphatase 23*	1.4011	2.6410
11735423_a_at	PPP1R36	*protein phosphatase 1 regulatory subunit 36*	1.4004	2.6398
11716114_x_at	POR	*cytochrome p450 oxidoreductase*	1.3993	2.6377
11740105_x_at	TMEM17	*transmembrane protein 17*	1.3968	2.6332
11744164_a_at	VRK3	*vaccinia related kinase 3*	1.3965	2.6327
11732502_a_at	ICA1L	*islet cell autoantigen 1 like*	1.3929	2.6261
11732959_a_at	SPRR3	*small proline rich protein 3*	1.3925	2.6253
11723325_a_at	KCNQ1	*potassium voltage-gated channel subfamily Q member 1*	1.3918	2.6240
11727336_at	SAMD12	*sterile alpha motif domain containing 12*	1.3915	2.6236
11718824_at	IGIP	*IgA inducing protein*	1.3850	2.6117
11724321_s_at	C11orf54	*chromosome 11 open reading frame 54*	1.3837	2.6094
11724374_at	BATF	*basic leucine zipper ATF-like transcription factor*	1.3830	2.6081
11733622_x_at	NCMAP	*non-compact myelin associated protein*	1.3816	2.6056
11718651_at	TMTC1	*transmembrane and tetratricopeptide repeat containing 1*	1.3772	2.5976
11730623_at	DSEL	*dermatan sulfate epimerase-like*	1.3767	2.5968
11739521_at	ST8SIA4	*ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4*	1.3767	2.5968
11755110_a_at	LRIG1	*leucine rich repeats and immunoglobulin like domains 1*	1.3766	2.5965
11752232_a_at	ECT2L	*epithelial cell transforming 2 like*	1.3765	2.5963
11747341_a_at	ARL6	*ADP ribosylation factor like GTPase 6*	1.3758	2.5952
11728164_a_at	EPPIN-WFDC6	*EPPIN-WFDC6 readthrough*	1.3732	2.5904
11740409_a_at	FGFR2	*fibroblast growth factor receptor 2*	1.3721	2.5885
11727670_s_at	ROPN1B	*rhophilin associated tail protein 1B*	1.3718	2.5880
11734055_a_at	CFAP61	*cilia and flagella associated protein 61*	1.3717	2.5877
11728954_a_at	KITLG	*KIT ligand*	1.3713	2.5871
11744282_at	PLBD1	*phospholipase B domain containing 1*	1.3713	2.5871
11732397_a_at	IFT80	*intraflagellar transport 80*	1.3712	2.5868
11745050_a_at	ALCAM	*activated leukocyte cell adhesion molecule*	1.3707	2.5860
11756096_a_at	SLC25A4	*solute carrier family 25 member 4*	1.3704	2.5855
11725805_a_at	ZNF606	*zinc finger protein 606*	1.3702	2.5851
11743129_at	SORL1	*sortilin related receptor 1*	1.3698	2.5843
11744581_a_at	KHDRBS3	*KH RNA binding domain containing, signal transduction associated 3*	1.3696	2.5840

11743286_at	**DTX4**	***deltex E3 ubiquitin ligase 4***	**1.3688**	**2.5825**
11727256_a_at	**ZNF625-ZNF20**	***ZNF625-ZNF20 Readthrough (NMD Candidate)***	**1.3687**	**2.5824**
11722132_a_at	**MGAT3**	***Mannosyl (Beta-1,4-)-Glycoprotein Beta-1,4-N-Acetylglucosaminyltransferase***	**1.3684**	**2.5819**
11736221_a_at	**FAM187A**	***family with sequence similarity 187 member A***	**1.3671**	**2.5795**
11723961_s_at	**PTN**	***pleiotrophin***	**1.3666**	**2.5787**
11719521_at	**SEMA5A**	***semaphorin 5A***	**1.3666**	**2.5786**
11752263_a_at	**FHAD1**	***forkhead associated phosphopeptide binding domain 1***	**1.3659**	**2.5773**
11757871_s_at	**PBX1**	***PBX homeobox 1***	**1.3657**	**2.5771**
11744866_x_at	**CEL**	***carboxyl ester lipase***	**1.3636**	**2.5732**
11754371_a_at	**FAM102A**	***family with sequence similarity 102 member A***	**1.3609**	**2.5685**
11726310_at	**GLRB**	***glycine receptor beta***	**1.3587**	**2.5646**
11744132_at	**SECISBP2L**	***SECIS binding protein 2 like***	**1.3578**	**2.5629**
11756745_a_at	**FAM214A**	***family with sequence similarity 214 member A***	**1.3530**	**2.5545**
11749150_a_at	**ABCD3**	***ATP binding cassette subfamily D member 3***	**1.3517**	**2.5522**
11722871_a_at	**DYNC2H1**	***dynein cytoplasmic 2 heavy chain 1***	**1.3510**	**2.5509**
11757336_s_at	**LIMCH1**	***LIM and calponin homology domains 1***	**1.3509**	**2.5507**
11725980_at	**CFD**	***complement factor D***	**1.3504**	**2.5498**
11740420_s_at	**SPAG1**	***sperm associated antigen 1***	**1.3499**	**2.5490**
11745242_a_at	**TNFRSF21**	***TNF receptor superfamily member 21***	**1.3498**	**2.5487**
11756648_a_at	**SLC25A14**	***solute carrier family 25 member 14***	**1.3496**	**2.5485**
11726682_a_at	**MEIS1**	***Meis homeobox 1***	**1.3492**	**2.5477**
11720331_at	**SELENOM**	***selenoprotein M***	**1.3491**	**2.5476**

11728488_a_at	**NRXN3**	***neurexin 3***	**1.3483**	**2.5461**
11735970_a_at	**DNAJB13**	***DnaJ Heat Shock Protein Family (Hsp40) Member B13***	**1.3467**	**2.5433**
11720106_a_at	**SLC26A2**	***solute carrier family 26 member 2***	**1.3432**	**2.5371**
11758377_s_at	**TLR1**	***toll like receptor 1***	**1.3432**	**2.5371**
11741044_a_at	**PLS1**	***plastin 1***	**1.3425**	**2.5359**
11716937_a_at	**NUPR1**	***nuclear protein 1, transcriptional regulator***	**1.3414**	**2.5340**
11734262_a_at	**AK8**	***adenylate kinase 8***	**1.3406**	**2.5325**
11731762_s_at	**RPS6KA2**	***ribosomal protein S6 kinase A2***	**1.3379**	**2.5279**
11754806_s_at	**CADPS2**	***calcium dependent secretion activator 2***	**1.3372**	**2.5266**
11740223_x_at	**LRRC26**	***leucine rich repeat containing 26***	**1.3363**	**2.5251**
11748622_s_at	**CTSA**	***cathepsin A***	**1.3362**	**2.5249**
11757929_s_at	**RALGAPA2**	***Ral GTPase activating protein catalytic alpha subunit 2***	**1.3362**	**2.5248**
11718078_a_at	**BCL2L11**	***BCL2 like 11***	**1.3358**	**2.5242**
11719544_a_at	**MSLN**	***mesothelin***	**1.3346**	**2.5221**
11722909_a_at	**GATS**	***GATS, stromal antigen 3 opposite strand***	**1.3342**	**2.5213**
11731095_x_at	**TRAF3IP1**	***TRAF3 interacting protein 1***	**1.3335**	**2.5201**
11745830_a_at	**ALAD**	***aminolevulinate dehydratase***	**1.3295**	**2.5132**

11748896_s_at	**ACKR4**	***atypical chemokine receptor 4***	**1.3289**	**2.5121**
11721352_at	**SLC1A1**	***solute carrier family 1 member 1***	**1.3281**	**2.5108**
11755547_a_at	**STK33**	***serine/threonine kinase 33***	**1.3272**	**2.5092**
11724195_at	**MIR1282**	***microRNA 1282***	**1.3264**	**2.5077**
11721711_at	**SHROOM3**	***shroom family member 3***	**1.3262**	**2.5075**
11717993_at	**CBX7**	***chromobox 7***	**1.3261**	**2.5073**
11732432_a_at	**GK**	***glycerol kinase***	**1.3258**	**2.5068**
11717742_a_at	**GPRC5C**	***G protein-coupled receptor class C group 5 member C***	**1.3253**	**2.5058**
11728771_a_at	**CLCA4**	***chloride channel accessory 4***	**1.3250**	**2.5053**
11737848_a_at	**RSPH3**	***radial spoke 3 homolog***	**1.3248**	**2.5050**
11724322_a_at	**CST6**	***cystatin E/M***	**1.3239**	**2.5034**
11718435_a_at	**NPNT**	***nephronectin***	**1.3231**	**2.5021**
11733069_at	**WDR5B**	***WD repeat domain 5B***	**1.3219**	**2.4999**
11754864_a_at	**LRRC71**	***leucine rich repeat containing 71***	**1.3211**	**2.4985**
11745555_a_at	**C11orf74**	***chromosome 11 open reading frame 74***	**1.3208**	**2.4981**
11716641_x_at	**PSMB10**	***proteasome subunit beta 10***	**1.3203**	**2.4972**
11718780_a_at	**SSBP2**	***single stranded DNA binding protein 2***	**1.3202**	**2.4970**

11723128_a_at	**HERC6**	***HECT and RLD domain containing E3 ubiquitin protein ligase family member 6***	**1.3192**	**2.4952**
11727440_at	**LOXL4**	***lysyl oxidase like 4***	**1.3168**	**2.4912**
11759918_at	**SPATA6**	***spermatogenesis associated 6***	**1.3148**	**2.4876**
11753966_a_at	**ZNF204P**	***zinc finger protein 204, pseudogene***	**1.3125**	**2.4838**
11745361_a_at	**CRNDE**	***Colorectal Neoplasia Differentially Expressed (Non-Protein Coding)***	**1.3121**	**2.4830**
11738201_a_at	**EYA2**	***EYA transcriptional coactivator and phosphatase 2***	**1.3112**	**2.4814**
11736244_s_at	**HIST1H2AC**	***histone cluster 1 H2A family member c***	**1.3105**	**2.4803**
11730700_a_at	**C11orf49**	***chromosome 11 open reading frame 49***	**1.3084**	**2.4767**
11758993_at	**TRIM52**	***tripartite motif containing 52***	**1.3068**	**2.4740**
11743949_s_at	**FRAT1**	***frequently rearranged in advanced T-cell lymphomas 1***	**1.3066**	**2.4736**
11721199_a_at	**IFT122**	***intraflagellar transport 122***	**1.3056**	**2.4718**
11731197_a_at	**PRR5L**	***proline rich 5 like***	**1.3047**	**2.4703**
11729154_x_at	**CEACAM6**	***carcinoembryonic antigen related cell adhesion molecule 6***	**1.3039**	**2.4690**
11738402_a_at	**WDPCP**	***WD repeat containing planar cell polarity effector***	**1.3024**	**2.4664**
11724796_at	**DDIT4L**	***DNA damage inducible transcript 4 like***	**1.3019**	**2.4656**
11718610_at	**TP53INP1**	***tumor protein p53 inducible nuclear protein 1***	**1.3017**	**2.4652**
11724609_x_at	**FUZ**	***fuzzy planar cell polarity protein***	**1.3015**	**2.4649**

11746264_a_at	**PLPP1**	***phospholipid phosphatase 1***	**1.3007**	**2.4635**
11723955_a_at	**CLINT1**	***clathrin interactor 1***	**1.2994**	**2.4612**
11725841_at	**ZSCAN16**	***zinc finger and SCAN domain containing 16***	**1.2994**	**2.4612**
11763271_at	**PEX11A**	***peroxisomal biogenesis factor 11 alpha***	**1.2988**	**2.4602**
11723329_a_at	**GSN**	***gelsolin***	**1.2978**	**2.4586**
11756677_a_at	**CYB5D2**	***cytochrome b5 domain containing 2***	**1.2972**	**2.4575**
11750762_a_at	**DHX40**	***DEAH-box helicase 40***	**1.2965**	**2.4564**
11751393_a_at	**PIK3IP1**	***phosphoinositide-3-kinase interacting protein 1***	**1.2963**	**2.4559**
11721978_a_at	**PLCE1**	***phospholipase C epsilon 1***	**1.2951**	**2.4540**
11731296_a_at	**SPATA6L**	***spermatogenesis associated 6 like***	**1.2937**	**2.4516**
11721147_at	**SYNGR1**	***synaptogyrin 1***	**1.2932**	**2.4507**
11722325_a_at	**ZNF84**	***zinc finger protein 84***	**1.2928**	**2.4500**
11736098_a_at	**CDK20**	***cyclin dependent kinase 20***	**1.2914**	**2.4476**
11731325_a_at	**CAPN8**	***calpain 8***	**1.2898**	**2.4449**
11721118_a_at	**ANKHD1-EIF4EBP3**	***ANKHD1-EIF4EBP3 readthrough***	**1.2896**	**2.4446**
11739734_a_at	**CPEB4**	***cytoplasmic polyadenylation element binding protein 4***	**1.2889**	**2.4434**
11756059_a_at	**CXCL14**	***C-X-C motif chemokine ligand 14***	**1.2881**	**2.4421**

11734534_s_at	**MFSD6**	***major facilitator superfamily domain containing 6***	**1.2880**	**2.4419**
11743704_x_at	**ABHD11**	***abhydrolase domain containing 11***	**1.2877**	**2.4414**
11739787_a_at	**IGF2**	***insulin like growth factor 2***	**1.2872**	**2.4406**
11730073_at	**CNTN3**	***contactin 3***	**1.2862**	**2.4389**
11740224_a_at	**CHST4**	***carbohydrate sulfotransferase 4***	**1.2860**	**2.4385**
11743197_at	**TLR4**	***toll like receptor 4***	**1.2849**	**2.4367**
11756524_a_at	**RBBP9**	***RB binding protein 9, serine hydrolase***	**1.2835**	**2.4343**
11750303_x_at	**B3GALT5-AS1**	***B3GALT5 antisense RNA 1***	**1.2801**	**2.4286**
11757333_s_at	**NUDT4**	***nudix hydrolase 4***	**1.2791**	**2.4268**
11728603_a_at	**CLDN23**	***claudin 23***	**1.2777**	**2.4245**
11727563_at	**PCDHB5**	***protocadherin beta 5***	**1.2766**	**2.4227**
11743161_x_at	**HILPDA**	***hypoxia inducible lipid droplet associated***	**1.2765**	**2.4225**
11717614_at	**KIF13B**	***kinesin family member 13B***	**1.2752**	**2.4203**
11759097_a_at	**ZNF703**	***zinc finger protein 703***	**1.2751**	**2.4201**
11730439_a_at	**AKAP9**	***A-kinase anchoring protein 9***	**1.2746**	**2.4194**
11730855_a_at	**HMGN3**	***high mobility group nucleosomal binding domain 3***	**1.2738**	**2.4179**
11747097_a_at	**RIBC1**	***RIB43A domain with coiled-coils 1***	**1.2733**	**2.4171**

11732920_a_at	**FOXN4**	***forkhead box N4***	**1.2730**	**2.4167**
11728085_s_at	**BMPR1B**	***bone morphogenetic protein receptor type 1B***	**1.2699**	**2.4114**
11715347_s_at	**HBB**	***hemoglobin subunit beta***	**1.2696**	**2.4110**
11732135_a_at	**COQ8A**	***coenzyme Q8A***	**1.2672**	**2.4069**
11732926_a_at	**VNN3**	***vanin 3***	**1.2620**	**2.3983**
11744846_a_at	**LCA5L**	***LCA5L, lebercilin like***	**1.2607**	**2.3962**
11723424_at	**IFNAR1**	***interferon alpha and beta receptor subunit 1***	**1.2601**	**2.3951**
11755376_a_at	**TTC12**	***tetratricopeptide repeat domain 12***	**1.2598**	**2.3947**
11717370_at	**ARSD**	***arylsulfatase D***	**1.2580**	**2.3916**
11731962_a_at	**ZNF709**	***zinc finger protein 709***	**1.2566**	**2.3893**
11757607_s_at	**SUSD4**	***sushi domain containing 4***	**1.2565**	**2.3892**
11742458_a_at	**C2orf81**	***chromosome 2 open reading frame 81***	**1.2562**	**2.3886**
11725875_at	**WDR66**	***WD repeat domain 66***	**1.2551**	**2.3869**
11751783_a_at	**MFSD1**	***major facilitator superfamily domain containing 1***	**1.2531**	**2.3836**
11734506_a_at	**MECOM**	***MDS1 and EVI1 complex locus***	**1.2524**	**2.3823**
11742423_a_at	**STEAP2**	***STEAP2 metalloreductase***	**1.2508**	**2.3798**
11716485_at	**STK38**	***serine/threonine kinase 38***	**1.2496**	**2.3778**

11741276_s_at	**TMEM144**	***transmembrane protein 144***	**1.2491**	**2.3770**
11726892_a_at	**SLC51A**	***solute carrier family 51 alpha subunit***	**1.2486**	**2.3761**
11740841_a_at	**NFIA**	***nuclear factor I A***	**1.2480**	**2.3752**
11725240_at	**RTP4**	***receptor transporter protein 4***	**1.2477**	**2.3746**
11720518_a_at	**TACC2**	***transforming acidic coiled-coil containing protein 2***	**1.2468**	**2.3732**
11731124_at	**FBXO36**	***F-box protein 36***	**1.2450**	**2.3702**
11725559_a_at	**ZNF112**	***zinc finger protein 112***	**1.2448**	**2.3698**
11716169_at	**CCDC28A**	***coiled-coil domain containing 28A***	**1.2437**	**2.3681**
11729222_a_at	**GATA3**	***GATA binding protein 3***	**1.2437**	**2.3681**
11725229_s_at	**HEATR5A**	***HEAT repeat containing 5A***	**1.2434**	**2.3676**
11762566_at	**BTC**	***betacellulin***	**1.2433**	**2.3674**
11757194_a_at	**LMLN**	***leishmanolysin like peptidase***	**1.2429**	**2.3668**
11722239_a_at	**HIPK1**	***homeodomain interacting protein kinase 1***	**1.2425**	**2.3660**
11763307_s_at	**NFATC2**	***nuclear factor of activated T-cells 2***	**1.2420**	**2.3653**
11723851_x_at	**ODF2L**	***outer dense fiber of sperm tails 2 like***	**1.2411**	**2.3638**
11730133_s_at	**ICK**	***intestinal cell kinase***	**1.2395**	**2.3611**
11726769_a_at	**XAF1**	***XIAP associated factor 1***	**1.2393**	**2.3608**

11726557_a_at	**GSDMB**	***gasdermin B***	**1.2379**	**2.3585**
11735715_a_at	**IFT81**	***intraflagellar transport 81***	**1.2376**	**2.3580**
11740751_a_at	**ZNF688**	***zinc finger protein 688***	**1.2374**	**2.3578**
11721454_a_at	**SERPINA1**	***serpin family A member 1***	**1.2361**	**2.3556**
11734578_a_at	**CFH**	***complement factor H***	**1.2356**	**2.3548**
11717934_at	**DNAL4**	***dynein axonemal light chain 4***	**1.2352**	**2.3541**
11725262_a_at	**WDR60**	***WD repeat domain 60***	**1.2338**	**2.3519**
11758955_at	**LGALS8**	***galectin 8***	**1.2336**	**2.3516**
11757618_a_at	**IFT43**	***intraflagellar transport 43***	**1.2333**	**2.3511**
11730737_a_at	**SCCPDH**	***Saccharopine Dehydrogenase (Putative)***	**1.2318**	**2.3486**
11730395_x_at	**ZNF552**	***zinc finger protein 552***	**1.2309**	**2.3471**
11734141_at	**GK5**	***Glycerol Kinase 5 (Putative)***	**1.2300**	**2.3457**
11735479_x_at	**CCDC125**	***coiled-coil domain containing 125***	**1.2296**	**2.3450**
11715558_a_at	**TMEM59**	***transmembrane protein 59***	**1.2285**	**2.3433**
11724455_a_at	**ZDHHC1**	***zinc finger DHHC-type containing 1***	**1.2273**	**2.3413**
11723772_at	**SMPD2**	***sphingomyelin phosphodiesterase 2***	**1.2272**	**2.3411**
11724452_a_at	**PATZ1**	***POZ/BTB and AT hook containing zinc finger 1***	**1.2248**	**2.3372**

11758027_s_at	**HOOK1**	***hook microtubule tethering protein 1***	**1.2240**	**2.3360**
11734857_at	**ERO1B**	***endoplasmic reticulum oxidoreductase 1 beta***	**1.2221**	**2.3329**
11725662_a_at	**SLC16A14**	***solute carrier family 16 member 14***	**1.2214**	**2.3317**
11744233_at	**FZD8**	***frizzled class receptor 8***	**1.2213**	**2.3315**
11751136_a_at	**CCDC30**	***coiled-coil domain containing 30***	**1.2202**	**2.3298**
11731691_at	**TTC30B**	***tetratricopeptide repeat domain 30B***	**1.2201**	**2.3296**
11744828_a_at	**CLK1**	***CDC like kinase 1***	**1.2198**	**2.3292**
11734530_x_at	**HLA-F**	***major histocompatibility complex, class I, F***	**1.2187**	**2.3273**
11719432_at	**KIAA0513**	***KIAA0513***	**1.2186**	**2.3272**
11754624_a_at	**CYB5A**	***cytochrome b5 type A***	**1.2165**	**2.3239**
11756570_a_at	**TMEM50B**	***transmembrane protein 50B***	**1.2150**	**2.3214**
11750652_a_at	**FRK**	***fyn related Src family tyrosine kinase***	**1.2149**	**2.3213**
11742124_a_at	**CACNG6**	***calcium voltage-gated channel auxiliary subunit gamma 6***	**1.2149**	**2.3212**
11720124_at	**SRD5A3**	***steroid 5 alpha-reductase 3***	**1.2141**	**2.3199**
11720283_at	**JMY**	***junction mediating and regulatory protein, p53 cofactor***	**1.2128**	**2.3179**
11726456_at	**MYO5B**	***myosin VB***	**1.2124**	**2.3172**
11724588_a_at	**ANKRD35**	***ankyrin repeat domain 35***	**1.2106**	**2.3143**

11739564_s_at	**ITPR1**	***inositol 1,4,5-trisphosphate receptor type 1***	**1.2095**	**2.3126**
11737215_a_at	**CRACR2B**	***calcium release activated channel regulator 2B***	**1.2093**	**2.3123**
11740854_a_at	**SLC6A20**	***solute carrier family 6 member 20***	**1.2092**	**2.3121**
11722514_a_at	**IDNK**	***IDNK, gluconokinase***	**1.2076**	**2.3095**
11751616_a_at	**LACTB2**	***lactamase beta 2***	**1.2070**	**2.3086**
11720367_a_at	**TMEM2**	***transmembrane protein 2***	**1.2061**	**2.3071**
11732343_at	**ZNF33A**	***zinc finger protein 33A***	**1.2053**	**2.3059**
11736599_a_at	**DLG3**	***discs large MAGUK scaffold protein 3***	**1.2053**	**2.3058**
11719122_at	**DPCD**	***Deleted In Primary Ciliary Dyskinesia Homolog (Mouse)***	**1.2051**	**2.3056**
11719785_s_at	**B4GALT4**	***beta-1,4-galactosyltransferase 4***	**1.2026**	**2.3015**
11726904_a_at	**COBL**	***cordon-bleu WH2 repeat protein***	**1.2022**	**2.3009**
11742912_a_at	**GAREM1**	***GRB2 associated regulator of MAPK1 subtype 1***	**1.1993**	**2.2963**
11720649_a_at	**FBXW9**	***F-box and WD repeat domain containing 9***	**1.1982**	**2.2945**
11734902_a_at	**CYP4V2**	***cytochrome P450 family 4 subfamily V member 2***	**1.1972**	**2.2930**
11723550_a_at	**ABHD6**	***abhydrolase domain containing 6***	**1.1963**	**2.2915**
11755333_a_at	**NFX1**	***nuclear transcription factor, X-box binding 1***	**1.1956**	**2.2904**
11716734_at	**IRF1**	***interferon regulatory factor 1***	**1.1956**	**2.2904**

11741065_a_at	**EPHX1**	***epoxide hydrolase 1***	**1.1945**	**2.2886**
11725676_a_at	**RORA**	***RAR related orphan receptor A***	**1.1914**	**2.2837**
11755450_a_at	**ZNF608**	***zinc finger protein 608***	**1.1908**	**2.2828**
11738850_a_at	**BCL2L14**	***BCL2 like 14***	**1.1900**	**2.2816**
11716406_x_at	**LGALS9**	***galectin 9***	**1.1887**	**2.2794**
11743576_at	**CPE**	***carboxypeptidase E***	**1.1880**	**2.2784**
11739294_a_at	**SLC29A3**	***solute carrier family 29 member 3***	**1.1851**	**2.2738**
11751973_x_at	**LZTS3**	***leucine zipper tumor suppressor family member 3***	**1.1847**	**2.2731**
11720936_a_at	**CACFD1**	***calcium channel flower domain containing 1***	**1.1841**	**2.2722**
11721026_a_at	**OCEL1**	***occludin/ELL domain containing 1***	**1.1836**	**2.2714**
11745124_a_at	**BDH1**	***3-hydroxybutyrate dehydrogenase, type 1***	**1.1835**	**2.2712**
11741041_x_at	**DPP7**	***dipeptidyl peptidase 7***	**1.1819**	**2.2688**
11733257_x_at	**CFAP36**	***cilia and flagella associated protein 36***	**1.1817**	**2.2684**
11746995_a_at	**NPL**	***N-acetylneuraminate pyruvate lyase***	**1.1811**	**2.2675**
11728525_at	**C11orf63**	***chromosome 11 open reading frame 63***	**1.1811**	**2.2675**
11726509_at	**SMPD3**	***sphingomyelin phosphodiesterase 3***	**1.1804**	**2.2664**
11716871_at	**GAA**	***glucosidase alpha, acid***	**1.1802**	**2.2661**

11739716_at	**KIAA0556**	***KIAA0556***	**1.1796**	**2.2652**
11755705_a_at	**SMIM5**	***small integral membrane protein 5***	**1.1784**	**2.2633**
11724277_a_at	**SLC35C1**	***solute carrier family 35 member C1***	**1.1782**	**2.2630**
11743711_a_at	**C22orf23**	***chromosome 22 open reading frame 23***	**1.1781**	**2.2628**
11717661_a_at	**PPP1R16B**	***protein phosphatase 1 regulatory subunit 16B***	**1.1779**	**2.2624**
11760894_s_at	**SRSF5**	***serine and arginine rich splicing factor 5***	**1.1772**	**2.2614**
11721783_a_at	**SLC9A8**	***solute carrier family 9 member A8***	**1.1749**	**2.2577**
11756316_a_at	**CHI3L1**	***chitinase 3 like 1***	**1.1738**	**2.2560**
11755583_a_at	**FAM161A**	***family with sequence similarity 161 member A***	**1.1736**	**2.2557**
11721480_s_at	**GOLPH3L**	***golgi phosphoprotein 3 like***	**1.1727**	**2.2543**
11754284_s_at	**CYB561**	***cytochrome b561***	**1.1715**	**2.2524**
11729333_at	**PADI1**	***peptidyl arginine deiminase 1***	**1.1690**	**2.2486**
11729605_a_at	**ATL1**	***atlastin GTPase 1***	**1.1675**	**2.2462**
11722283_at	**CA11**	***carbonic anhydrase 11***	**1.1661**	**2.2440**
11754106_a_at	**EFNA1**	***ephrin A1***	**1.1656**	**2.2432**
11729006_at	**OVOL2**	***ovo like zinc finger 2***	**1.1654**	**2.2429**
11758723_at	**IDH2**	***Isocitrate Dehydrogenase (NADP(+)) 2, Mitochondrial***	**1.1650**	**2.2423**

11754306_a_at	**MCCC1**	***methylcrotonoyl-CoA carboxylase 1***	**1.1636**	**2.2401**
11730166_a_at	**C11orf16**	***chromosome 11 open reading frame 16***	**1.1634**	**2.2399**
11743723_a_at	**GALC**	***galactosylceramidase***	**1.1632**	**2.2396**
11736744_x_at	**C1orf168**	***chromosome 1 open reading frame 168***	**1.1622**	**2.2380**
11741447_s_at	**RNASE4**	***ribonuclease A family member 4***	**1.1616**	**2.2371**
11717691_a_at	**ANKRD13A**	***ankyrin repeat domain 13A***	**1.1616**	**2.2370**
11758755_at	**MPC2**	***mitochondrial pyruvate carrier 2***	**1.1615**	**2.2369**
11720815_a_at	**BAALC**	***brain and acute leukemia, cytoplasmic***	**1.1605**	**2.2353**
11756891_a_at	**ZNF12**	***zinc finger protein 12***	**1.1603**	**2.2350**
11753531_s_at	**ZNF428**	***zinc finger protein 428***	**1.1601**	**2.2348**
11724068_at	**PELI2**	***pellino E3 ubiquitin protein ligase family member 2***	**1.1599**	**2.2344**
11730651_a_at	**SYTL4**	***synaptotagmin like 4***	**1.1576**	**2.2308**
11718789_x_at	**ZNF302**	***zinc finger protein 302***	**1.1574**	**2.2305**
11732414_a_at	**LRRC8B**	***leucine rich repeat containing 8 family member B***	**1.1537**	**2.2249**
11715617_a_at	**RNF130**	***ring finger protein 130***	**1.1534**	**2.2244**
11745189_a_at	**APOL1**	***apolipoprotein L1***	**1.1530**	**2.2237**
11758013_s_at	**C8orf4**	***chromosome 8 open reading frame 4***	**1.1529**	**2.2236**

11728008_x_at	**FUT3**	***Fucosyltransferase 3 (Lewis Blood Group)***	**1.1503**	**2.2196**
11722969_s_at	**TRPV4**	***transient receptor potential cation channel subfamily V member 4***	**1.1500**	**2.2191**
11754610_a_at	**FICD**	***FIC domain containing***	**1.1483**	**2.2165**
11718130_s_at	**OLFM4**	***olfactomedin 4***	**1.1467**	**2.2141**
11753994_a_at	**IQCB1**	***IQ motif containing B1***	**1.1455**	**2.2123**
11723843_a_at	**ADGB**	***androglobin***	**1.1447**	**2.2110**
11717338_a_at	**CUX1**	***cut like homeobox 1***	**1.1441**	**2.2101**
11730805_a_at	**BCAS3**	***BCAS3, microtubule associated cell migration factor***	**1.1437**	**2.2094**
11732232_x_at	**ORAI2**	***ORAI calcium release-activated calcium modulator 2***	**1.1432**	**2.2087**
11764173_s_at	**TMEM183B**	***transmembrane protein 183B***	**1.1425**	**2.2077**
11721897_a_at	**DHX58**	***DExH-box helicase 58***	**1.1420**	**2.2068**
11721614_a_at	**KIT**	***KIT proto-oncogene receptor tyrosine kinase***	**1.1417**	**2.2064**
11748779_a_at	**ABHD16A**	***abhydrolase domain containing 16A***	**1.1411**	**2.2055**
11728599_a_at	**PHOSPHO2**	***phosphatase, orphan 2***	**1.1403**	**2.2043**
11727898_a_at	**CLMN**	***calmin***	**1.1399**	**2.2036**
11736056_x_at	**BORCS7**	***BLOC-1 related complex subunit 7***	**1.1391**	**2.2024**
11747233_a_at	**KBTBD7**	***kelch repeat and BTB domain containing 7***	**1.1374**	**2.1998**

11727147_at	**ZNF564**	***zinc finger protein 564***	**1.1368**	**2.1990**
11725252_at	**FAM120C**	***family with sequence similarity 120C***	**1.1359**	**2.1976**
11723903_at	**PLEKHG1**	***pleckstrin homology and RhoGEF domain containing G1***	**1.1359**	**2.1976**
11726055_at	**B3GALT4**	***beta-1,3-galactosyltransferase 4***	**1.1357**	**2.1973**
11728507_at	**LY96**	***lymphocyte antigen 96***	**1.1356**	**2.1971**
11758634_s_at	**CASZ1**	***castor zinc finger 1***	**1.1338**	**2.1943**
11716484_at	**UNC119B**	***unc-119 lipid binding chaperone B***	**1.1336**	**2.1941**
11755886_a_at	**C5orf42**	***chromosome 5 open reading frame 42***	**1.1323**	**2.1921**
11732389_a_at	**DYNC2LI1**	***dynein cytoplasmic 2 light intermediate chain 1***	**1.1321**	**2.1918**
11718563_a_at	**ANKRD10**	***ankyrin repeat domain 10***	**1.1305**	**2.1893**
11719584_s_at	**CNNM3**	***cyclin and CBS domain divalent metal cation transport mediator 3***	**1.1297**	**2.1882**
11728145_a_at	**SHC2**	***SHC adaptor protein 2***	**1.1293**	**2.1876**
11759320_at	**MPZL3**	***myelin protein zero like 3***	**1.1290**	**2.1870**
11724953_a_at	**PDIK1L**	***PDLIM1 interacting kinase 1 like***	**1.1288**	**2.1867**
11716784_at	**TRAK2**	***trafficking kinesin protein 2***	**1.1286**	**2.1865**
11729400_at	**PCP4L1**	***Purkinje cell protein 4 like 1***	**1.1272**	**2.1844**
11733530_at	**C1RL**	***complement C1r subcomponent like***	**1.1272**	**2.1843**

11754686_a_at	**LRRC56**	***leucine rich repeat containing 56***	**1.1251**	**2.1811**
11744179_x_at	**TM7SF2**	***transmembrane 7 superfamily member 2***	**1.1245**	**2.1802**
11720393_at	**RAB11FIP4**	***RAB11 family interacting protein 4***	**1.1238**	**2.1792**
11743071_a_at	**LPAR6**	***lysophosphatidic acid receptor 6***	**1.1229**	**2.1779**
11717190_s_at	**TXNIP**	***thioredoxin interacting protein***	**1.1211**	**2.1752**
11743072_a_at	**FBXO34**	***F-box protein 34***	**1.1208**	**2.1747**
11732773_at	**CCDC57**	***coiled-coil domain containing 57***	**1.1206**	**2.1744**
11755838_a_at	**PCDHB13**	***protocadherin beta 13***	**1.1202**	**2.1738**
11745585_a_at	**CCT6B**	***chaperonin containing TCP1 subunit 6B***	**1.1199**	**2.1733**
11730549_a_at	**IKZF2**	***IKAROS family zinc finger 2***	**1.1194**	**2.1726**
11761126_at	**ZNF396**	***zinc finger protein 396***	**1.1185**	**2.1712**
11735178_a_at	**C4orf33**	***chromosome 4 open reading frame 33***	**1.1184**	**2.1710**
11728482_a_at	**ZNF181**	***zinc finger protein 181***	**1.1164**	**2.1681**
11753034_a_at	**ZNFX1**	***zinc finger NFX1-type containing 1***	**1.1162**	**2.1677**
11733535_a_at	**NUDT7**	***nudix hydrolase 7***	**1.1160**	**2.1675**
11758023_x_at	**GABARAPL1**	***GABA type A receptor associated protein like 1***	**1.1157**	**2.1670**
11743265_a_at	**ENSA**	***endosulfine alpha***	**1.1149**	**2.1658**

11729832_s_at	**CLDN8**	***claudin 8***	**1.1124**	**2.1620**
11745723_a_at	**MALAT1**	***Metastasis Associated Lung Adenocarcinoma Transcript 1 (Non-Protein Coding)***	**1.1123**	**2.1619**
11759191_at	**NIPAL2**	***NIPA like domain containing 2***	**1.1119**	**2.1613**
11733923_a_at	**CROT**	***carnitine O-octanoyltransferase***	**1.1114**	**2.1605**
11739527_a_at	**SECTM1**	***secreted and transmembrane 1***	**1.1106**	**2.1593**
11758028_s_at	**FOXQ1**	***forkhead box Q1***	**1.1089**	**2.1568**
11721108_at	**ZNF627**	***zinc finger protein 627***	**1.1076**	**2.1548**
11746462_a_at	**LMO7**	***LIM domain 7***	**1.1065**	**2.1533**
11746595_a_at	**PCM1**	***pericentriolar material 1***	**1.1041**	**2.1496**
11736909_at	**C1orf210**	***chromosome 1 open reading frame 210***	**1.1037**	**2.1491**
11753618_a_at	**ADM**	***adrenomedullin***	**1.1031**	**2.1482**
11729459_x_at	**BNIPL**	***BCL2 interacting protein like***	**1.1025**	**2.1473**
11743730_at	**TNFSF10**	***tumor necrosis factor superfamily member 10***	**1.1025**	**2.1472**
11748541_s_at	**PRADC1**	***protease associated domain containing 1***	**1.1010**	**2.1450**
11735690_s_at	**PTPMT1**	***protein tyrosine phosphatase, mitochondrial 1***	**1.0983**	**2.1410**
11716316_x_at	**CYTH2**	***cytohesin 2***	**1.0962**	**2.1379**
11721890_s_at	**ADGRL1**	***adhesion G protein-coupled receptor L1***	**1.0954**	**2.1367**

11732550_at	**PTGER2**	***prostaglandin E receptor 2***	**1.0949**	**2.1360**
11717582_a_at	**RGCC**	***regulator of cell cycle***	**1.0948**	**2.1359**
11725894_at	**TXLNB**	***taxilin beta***	**1.0946**	**2.1356**
11737028_at	**OTX1**	***orthodenticle homeobox 1***	**1.0939**	**2.1345**
11733091_a_at	**TSPAN8**	***tetraspanin 8***	**1.0939**	**2.1345**
11721206_x_at	**ANK3**	***ankyrin 3***	**1.0933**	**2.1336**
11753199_x_at	**SMARCA2**	***SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2***	**1.0882**	**2.1261**
11724920_a_at	**EFCAB7**	***EF-hand calcium binding domain 7***	**1.0879**	**2.1256**
11736159_a_at	**MPPE1**	***metallophosphoesterase 1***	**1.0877**	**2.1253**
11762406_s_at	**GBP2**	***guanylate binding protein 2***	**1.0873**	**2.1247**
11729430_at	**CCDC121**	***coiled-coil domain containing 121***	**1.0864**	**2.1234**
11724372_at	**ANXA10**	***annexin A10***	**1.0855**	**2.1221**
11721417_at	**SCNN1B**	***sodium channel epithelial 1 beta subunit***	**1.0839**	**2.1198**
11723516_a_at	**CAB39L**	***calcium binding protein 39 like***	**1.0836**	**2.1193**
11745281_at	**LOC100287896**	***uncharacterized LOC100287896***	**1.0835**	**2.1191**
11725688_x_at	**RHPN2**	***rhophilin Rho GTPase binding protein 2***	**1.0829**	**2.1183**
11718293_a_at	**CDKN2A**	***cyclin dependent kinase inhibitor 2A***	**1.0811**	**2.1156**

11719683_a_at	**MPC1**	***mitochondrial pyruvate carrier 1***	**1.0780**	**2.1111**
11716823_s_at	**BDH2**	***3-hydroxybutyrate dehydrogenase, type 2***	**1.0775**	**2.1104**
11730175_at	**C4orf3**	***chromosome 4 open reading frame 3***	**1.0764**	**2.1087**
11727302_a_at	**TMEM71**	***transmembrane protein 71***	**1.0760**	**2.1082**
11755839_x_at	**ARFGEF3**	***ARFGEF family member 3***	**1.0752**	**2.1070**
11746240_a_at	**RWDD2A**	***RWD domain containing 2A***	**1.0751**	**2.1069**
11719224_s_at	**COQ10A**	***coenzyme Q10A***	**1.0742**	**2.1056**
11719829_a_at	**SLC26A11**	***solute carrier family 26 member 11***	**1.0732**	**2.1041**
11745879_a_at	**SARAF**	***store-operated calcium entry associated regulatory factor***	**1.0728**	**2.1035**
11743487_a_at	**IK**	***IK cytokine, down-regulator of HLA II***	**1.0727**	**2.1033**
11718178_a_at	**CMTM4**	***CKLF like MARVEL transmembrane domain containing 4***	**1.0724**	**2.1030**
11750864_a_at	**CRISPLD1**	***cysteine rich secretory protein LCCL domain containing 1***	**1.0716**	**2.1017**
11720044_at	**SKAP2**	***src kinase associated phosphoprotein 2***	**1.0714**	**2.1014**
11730049_at	**CA13**	***carbonic anhydrase 13***	**1.0703**	**2.0999**
11719025_a_at	**ZNF652**	***zinc finger protein 652***	**1.0702**	**2.0997**
11735269_x_at	**SLC41A2**	***solute carrier family 41 member 2***	**1.0691**	**2.0981**
11759572_a_at	**STAU2**	***staufen double-stranded RNA binding protein 2***	**1.0682**	**2.0968**

11748433_x_at	**NDUFC2**	***NADH:ubiquinone oxidoreductase subunit C2***	**1.0680**	**2.0965**
11726561_at	**SAP18**	***Sin3A associated protein 18***	**1.0680**	**2.0965**
11729861_x_at	**H6PD**	***hexose-6-phosphate dehydrogenase/glucose 1-dehydrogenase***	**1.0670**	**2.0951**
11720740_a_at	**MCF2L**	***MCF.2 cell line derived transforming sequence like***	**1.0666**	**2.0945**
11723176_s_at	**PLEKHA6**	***pleckstrin homology domain containing A6***	**1.0662**	**2.0939**
11739402_a_at	**KMT5B**	***lysine methyltransferase 5B***	**1.0659**	**2.0935**
11731622_x_at	**ZNF91**	***zinc finger protein 91***	**1.0656**	**2.0930**
11741911_a_at	**GBP3**	***guanylate binding protein 3***	**1.0650**	**2.0921**
11744283_a_at	**COQ4**	***coenzyme Q4***	**1.0629**	**2.0891**
11728474_a_at	**CLHC1**	***clathrin heavy chain linker domain containing 1***	**1.0608**	**2.0861**
11754914_x_at	**PGAP3**	***post-GPI attachment to proteins 3***	**1.0607**	**2.0860**
11740148_x_at	**ZNF429**	***zinc finger protein 429***	**1.0596**	**2.0843**
11726337_a_at	**ALOX5**	***arachidonate 5-lipoxygenase***	**1.0586**	**2.0829**
11720760_x_at	**IVNS1ABP**	***influenza virus NS1A binding protein***	**1.0577**	**2.0816**
11757977_s_at	**SLC12A7**	***solute carrier family 12 member 7***	**1.0576**	**2.0815**
11736422_s_at	**POSTN**	***periostin***	**1.0576**	**2.0815**
11716553_a_at	**RHBDD2**	***rhomboid domain containing 2***	**1.0558**	**2.0789**

11745024_a_at	**A4GALT**	***alpha 1,4-galactosyltransferase***	**1.0552**	**2.0780**
11744453_s_at	**TMBIM4**	***transmembrane BAX inhibitor motif containing 4***	**1.0541**	**2.0764**
11726618_a_at	**C1GALT1C1**	***C1GALT1 specific chaperone 1***	**1.0537**	**2.0758**
11757197_s_at	**HNRNPU**	***Heterogeneous Nuclear Ribonucleoprotein U***	**1.0530**	**2.0749**
11720262_a_at	**MITF**	***melanogenesis associated transcription factor***	**1.0520**	**2.0734**
11722425_s_at	**NEDD4L**	***neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase***	**1.0520**	**2.0734**
11735271_a_at	**GCNT1**	***Glucosaminyl (N-Acetyl) Transferase 1, Core 2***	**1.0520**	**2.0734**
11759568_at	**SLC45A4**	***solute carrier family 45 member 4***	**1.0515**	**2.0727**
11745669_a_at	**KANSL1L**	***KAT8 regulatory NSL complex subunit 1 like***	**1.0512**	**2.0723**
11725035_s_at	**LMBRD1**	***LMBR1 domain containing 1***	**1.0511**	**2.0721**
11717600_a_at	**SECISBP2**	***SECIS binding protein 2***	**1.0495**	**2.0698**
11724862_at	**THNSL1**	***threonine synthase like 1***	**1.0495**	**2.0698**
11764240_s_at	**WDR31**	***WD repeat domain 31***	**1.0494**	**2.0697**
11748462_a_at	**NSF**	***N-ethylmaleimide sensitive factor, vesicle fusing ATPase***	**1.0477**	**2.0672**
11726437_a_at	**CMTM8**	***CKLF like MARVEL transmembrane domain containing 8***	**1.0462**	**2.0651**
11719491_a_at	**IFI35**	***interferon induced protein 35***	**1.0454**	**2.0640**
11726693_s_at	**ANGPT1**	***angiopoietin 1***	**1.0436**	**2.0614**

11718452_at	**AXIN2**	***axin 2***	**1.0428**	**2.0602**
11751286_a_at	**SLC35A5**	***solute carrier family 35 member A5***	**1.0410**	**2.0577**
11740462_a_at	**SMIM19**	***small integral membrane protein 19***	**1.0408**	**2.0574**
11732259_at	**SH2D4A**	***SH2 domain containing 4A***	**1.0402**	**2.0565**
11717127_a_at	**ANPEP**	***alanyl aminopeptidase, membrane***	**1.0402**	**2.0565**
11721196_a_at	**SLC18B1**	***solute carrier family 18 member B1***	**1.0393**	**2.0553**
11756509_a_at	**BAMBI**	***BMP and activin membrane bound inhibitor***	**1.0386**	**2.0542**
11718608_at	**MIR5193**	***microRNA 5193***	**1.0350**	**2.0491**
11735898_s_at	**TOM1**	***target of myb1 membrane trafficking protein***	**1.0347**	**2.0487**
11728212_at	**TRMT1L**	***tRNA methyltransferase 1 like***	**1.0345**	**2.0484**
11731585_a_at	**OMA1**	***OMA1 zinc metallopeptidase***	**1.0344**	**2.0483**
11737751_x_at	**TMEM254**	***transmembrane protein 254***	**1.0339**	**2.0476**
11721342_a_at	**NCOA1**	***nuclear receptor coactivator 1***	**1.0337**	**2.0473**
11762940_x_at	**HLA-C**	***major histocompatibility complex, class I, C***	**1.0332**	**2.0466**
11735948_a_at	**ANAPC7**	***anaphase promoting complex subunit 7***	**1.0327**	**2.0459**
11738835_x_at	**NDRG2**	***NDRG family member 2***	**1.0320**	**2.0449**
11732148_at	**CAT**	***catalase***	**1.0306**	**2.0429**

11724650_a_at	**MEIS2**	***Meis homeobox 2***	**1.0296**	**2.0414**
11747118_a_at	**BRINP1**	***BMP/retinoic acid inducible neural specific 1***	**1.0289**	**2.0405**
11724118_a_at	**SAMD9L**	***sterile alpha motif domain containing 9 like***	**1.0282**	**2.0395**
11731181_a_at	**EPSTI1**	***epithelial stromal interaction 1***	**1.0271**	**2.0379**
11728534_a_at	**SPSB2**	***splA/ryanodine receptor domain and SOCS box containing 2***	**1.0269**	**2.0376**
11723604_a_at	**INPP5J**	***inositol polyphosphate-5-phosphatase J***	**1.0261**	**2.0365**
11745857_a_at	**SGSM3**	***small G protein signaling modulator 3***	**1.0260**	**2.0364**
11730455_a_at	**SLC35A3**	***solute carrier family 35 member A3***	**1.0252**	**2.0352**
11742736_at	**MCEE**	***methylmalonyl-CoA epimerase***	**1.0242**	**2.0338**
11723221_a_at	**EXOC6**	***exocyst complex component 6***	**1.0227**	**2.0317**
11746027_a_at	**NMI**	***N-myc and STAT interactor***	**1.0223**	**2.0312**
11716302_s_at	**ACSL1**	***acyl-CoA synthetase long-chain family member 1***	**1.0222**	**2.0310**
11758208_s_at	**KLF2**	***Kruppel like factor 2***	**1.0220**	**2.0308**
11733253_a_at	**FBLN2**	***fibulin 2***	**1.0217**	**2.0303**
11723161_a_at	**ZNF776**	***zinc finger protein 776***	**1.0206**	**2.0287**
11724093_s_at	**SLC35E2B**	***solute carrier family 35 member E2B***	**1.0201**	**2.0280**
11755933_x_at	**HLA-B**	***major histocompatibility complex, class I, B***	**1.0198**	**2.0277**

11720377_s_at	**SAP30L**	***SAP30 like***	**1.0193**	**2.0269**
11717136_x_at	**PCSK1N**	***proprotein convertase subtilisin/kexin type 1 inhibitor***	**1.0186**	**2.0260**
11755498_s_at	**ATP6V0E2**	***ATPase H+ transporting V0 subunit e2***	**1.0183**	**2.0255**
11727377_a_at	**TBC1D15**	***TBC1 domain family member 15***	**1.0138**	**2.0192**
11731874_x_at	**MIA2**	***melanoma inhibitory activity 2***	**1.0136**	**2.0189**
11751880_x_at	**PIK3C2B**	***phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 beta***	**1.0132**	**2.0184**
11720279_a_at	**FAM174B**	***family with sequence similarity 174 member B***	**1.0125**	**2.0174**
11741124_a_at	**SAR1B**	***secretion associated Ras related GTPase 1B***	**1.0119**	**2.0166**
11725400_a_at	**TTLL1**	***tubulin tyrosine ligase like 1***	**1.0116**	**2.0162**
11718556_s_at	**CREB3L2**	***cAMP responsive element binding protein 3 like 2***	**1.0091**	**2.0127**
11754420_a_at	**PREPL**	***prolyl endopeptidase-like***	**1.0072**	**2.0100**
11758736_at	**PSMC2**	***proteasome 26S subunit, ATPase 2***	**1.0070**	**2.0097**
11720204_at	**NT5DC1**	***5'-nucleotidase domain containing 1***	**1.0062**	**2.0086**
11730509_s_at	**ABCC5**	***ATP binding cassette subfamily C member 5***	**1.0046**	**2.0064**
11754725_x_at	**SATB1**	***SATB homeobox 1***	**1.0027**	**2.0037**
11737904_a_at	**CASC4**	***cancer susceptibility candidate 4***	**1.0023**	**2.0032**
11754571_a_at	**GMDS**	***GDP-mannose 4,6-dehydratase***	**1.0017**	**2.0023**

11726152_a_at	**ZBTB21**	***zinc finger and BTB domain containing 21***	**1.0015**	**2.0021**
11718332_a_at	**TSPAN3**	***tetraspanin 3***	**1.0009**	**2.0012**
DOWNREGULATED mRNAs (761)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11724398_a_at	**RHCG**	***Rh family C glycoprotein***	**-3.8783**	**0.0680**
11733695_a_at	**UBE2C**	***ubiquitin conjugating enzyme E2 C***	**-3.8594**	**0.0689**
11732719_at	**EREG**	***epiregulin***	**-3.8448**	**0.0696**
11754360_a_at	**RRM2**	***ribonucleotide reductase regulatory subunit M2***	**-3.7779**	**0.0729**
11758261_s_at	**CEP55**	***centrosomal protein 55***	**-3.7661**	**0.0735**
11717355_a_at	**FEZ1**	***fasciculation and elongation protein zeta 1***	**-3.7544**	**0.0741**
11733115_a_at	**CA2**	***carbonic anhydrase 2***	**-3.7274**	**0.0755**
11757698_s_at	**MIG7**	***mig-7***	**-3.7084**	**0.0765**
11716358_s_at	**PRC1**	***protein regulator of cytokinesis 1***	**-3.5907**	**0.0830**
11758478_s_at	**CDCA7**	***cell division cycle associated 7***	**-3.5821**	**0.0835**
11729265_at	**SPRR2D**	***small proline rich protein 2D***	**-3.5700**	**0.0842**
11735693_x_at	**SPRR2E**	***small proline rich protein 2E***	**-3.5683**	**0.0843**
11725703_a_at	**KLK6**	***kallikrein related peptidase 6***	**-3.5047**	**0.0881**

11737798_a_at	**PROCR**	***protein C receptor***	**-3.4675**	**0.0904**
11720970_at	**TOP2A**	***Topoisomerase (DNA) II Alpha***	**-3.4173**	**0.0936**
11718058_a_at	**TYMS**	***thymidylate synthetase***	**-3.3306**	**0.0994**
11754662_s_at	**ADAMTS1**	***ADAM metallopeptidase with thrombospondin type 1 motif 1***	**-3.3277**	**0.0996**
11730821_x_at	**CDKN3**	***cyclin dependent kinase inhibitor 3***	**-3.3147**	**0.1005**
11719916_at	**IL1B**	***interleukin 1 beta***	**-3.2835**	**0.1027**
11758672_s_at	**UCHL1**	***ubiquitin C-terminal hydrolase L1***	**-3.2807**	**0.1029**
11758125_s_at	**DEPDC1B**	***DEP domain containing 1B***	**-3.2779**	**0.1031**
11720020_x_at	**RTEL1-TNFRSF6B**	***RTEL1-TNFRSF6B Readthrough (NMD Candidate)***	**-3.2640**	**0.1041**
11722572_at	**CCNA2**	***cyclin A2***	**-3.2570**	**0.1046**
11729579_at	**CDH13**	***cadherin 13***	**-3.2557**	**0.1047**
11729712_at	**SPRR2A**	***small proline rich protein 2A***	**-3.2461**	**0.1054**
11715524_a_at	**COTL1**	***coactosin like F-actin binding protein 1***	**-3.2216**	**0.1072**
11715306_s_at	**AREG**	***amphiregulin***	**-3.2203**	**0.1073**
11744425_a_at	**KIAA0101**	***KIAA0101***	**-3.2163**	**0.1076**
11717481_s_at	**FKBP10**	***FK506 binding protein 10***	**-3.2163**	**0.1076**
11753255_a_at	**KLK7**	***kallikrein related peptidase 7***	**-3.1740**	**0.1108**

11726909_at	**ZBED2**	***zinc finger BED-type containing 2***	**-3.1701**	**0.1111**
11742735_a_at	**NUSAP1**	***nucleolar and spindle associated protein 1***	**-3.1253**	**0.1146**
11755207_a_at	**NT5E**	***5'-nucleotidase ecto***	**-3.0625**	**0.1197**
11719898_s_at	**HBEGF**	***heparin binding EGF like growth factor***	**-3.0553**	**0.1203**
11729243_s_at	**FBN2**	***fibrillin 2***	**-3.0505**	**0.1207**
11722826_a_at	**NCAPG**	***non-SMC condensin I complex subunit G***	**-3.0151**	**0.1237**
11721143_a_at	**MKI67**	***marker of proliferation Ki-67***	**-2.9874**	**0.1261**
11750598_s_at	**TPX2**	***TPX2, microtubule nucleation factor***	**-2.9817**	**0.1266**
11728863_at	**GINS1**	***GINS complex subunit 1***	**-2.9613**	**0.1284**
11724032_a_at	**FST**	***follistatin***	**-2.9534**	**0.1291**
11715562_x_at	**SCD**	***stearoyl-CoA desaturase***	**-2.9291**	**0.1313**
11740656_a_at	**HMGA2**	***high mobility group AT-hook 2***	**-2.9105**	**0.1330**
11721307_at	**PHLDA1**	***pleckstrin homology like domain family A member 1***	**-2.8879**	**0.1351**
11723939_a_at	**CCNB1**	***cyclin B1***	**-2.8804**	**0.1358**
11727454_at	**SCGB1A1**	***secretoglobin family 1A member 1***	**-2.8334**	**0.1403**
11738511_at	**DEFB4B**	***defensin beta 4B***	**-2.7859**	**0.1450**
11742832_a_at	**ASPM**	***abnormal spindle microtubule assembly***	**-2.7226**	**0.1515**

11718127_at	**TK1**	***thymidine kinase 1***	**-2.7179**	**0.1520**
11758089_s_at	**HMMR**	***hyaluronan mediated motility receptor***	**-2.7160**	**0.1522**
11723950_a_at	**PBK**	***PDZ binding kinase***	**-2.7141**	**0.1524**
11733957_x_at	**SPRR2F**	***small proline rich protein 2F***	**-2.6962**	**0.1543**
11728404_at	**SHCBP1**	***SHC binding and spindle associated 1***	**-2.6484**	**0.1595**
11753008_a_at	**IL36G**	***interleukin 36, gamma***	**-2.6394**	**0.1605**
11716793_a_at	**CCNB2**	***cyclin B2***	**-2.6304**	**0.1615**
11758529_s_at	**CENPA**	***centromere protein A***	**-2.6250**	**0.1621**
11733864_a_at	**BIRC5**	***baculoviral IAP repeat containing 5***	**-2.6126**	**0.1635**
11732997_a_at	**MCM6**	***minichromosome maintenance complex component 6***	**-2.5821**	**0.1670**
11724478_s_at	**FOSL1**	***FOS like 1, AP-1 transcription factor subunit***	**-2.5692**	**0.1685**
11745948_a_at	**CHEK1**	***checkpoint kinase 1***	**-2.5658**	**0.1689**
11728376_s_at	**NMU**	***neuromedin U***	**-2.5615**	**0.1694**
11755719_a_at	**MLLT11**	***myeloid/lymphoid or mixed-lineage leukemia; translocated to, 11***	**-2.5496**	**0.1708**
11722367_a_at	**DLGAP5**	***DLG associated protein 5***	**-2.5228**	**0.1740**
11717566_at	**EMP1**	***epithelial membrane protein 1***	**-2.5023**	**0.1765**
11724464_a_at	**ANLN**	***anillin actin binding protein***	**-2.4901**	**0.1780**

11718005_a_at	**CDC25B**	***cell division cycle 25B***	**-2.4820**	**0.1790**
11745868_a_at	**KIF2C**	***kinesin family member 2C***	**-2.4675**	**0.1808**
11727504_at	**SOX7**	***SRY-box 7***	**-2.4635**	**0.1813**
11721932_a_at	**KIF23**	***kinesin family member 23***	**-2.4532**	**0.1826**
11723010_a_at	**KIF20A**	***kinesin family member 20A***	**-2.4477**	**0.1833**
11757783_s_at	**VCAN**	***versican***	**-2.4367**	**0.1847**
11724459_x_at	**MIR6756**	***microRNA 6756***	**-2.4328**	**0.1852**
11743513_a_at	**GINS2**	***GINS complex subunit 2***	**-2.4266**	**0.1860**
11728024_a_at	**KLK5**	***kallikrein related peptidase 5***	**-2.3967**	**0.1899**
11718943_a_at	**AURKA**	***aurora kinase A***	**-2.3967**	**0.1899**
11717521_x_at	**PTTG3P**	***pituitary tumor-transforming 3, pseudogene***	**-2.3959**	**0.1900**
11755219_a_at	**THBD**	***thrombomodulin***	**-2.3861**	**0.1913**
11727215_a_at	**NRG1**	***neuregulin 1***	**-2.3853**	**0.1914**
11743160_a_at	**HJURP**	***Holliday junction recognition protein***	**-2.3838**	**0.1916**
11723192_a_at	**UHRF1**	***ubiquitin like with PHD and ring finger domains 1***	**-2.3696**	**0.1935**
11725749_a_at	**GAL**	***galanin and GMAP prepropeptide***	**-2.3607**	**0.1947**
11719666_a_at	**STMN1**	***stathmin 1***	**-2.3562**	**0.1953**

11720647_a_at	**BUB1B**	***BUB1 mitotic checkpoint serine/threonine kinase B***	**-2.3562**	**0.1953**
11723151_s_at	**SUGCT**	***succinyl-CoA:glutarate-CoA transferase***	**-2.3555**	**0.1954**
11725274_s_at	**RGS20**	***regulator of G-protein signaling 20***	**-2.3533**	**0.1957**
11733884_a_at	**DEPDC1**	***DEP domain containing 1***	**-2.3474**	**0.1965**
11716587_at	**AXL**	***AXL receptor tyrosine kinase***	**-2.3445**	**0.1969**
11749367_a_at	**FXYD5**	***FXYD domain containing ion transport regulator 5***	**-2.3445**	**0.1969**
11724139_s_at	**SACS**	***sacsin molecular chaperone***	**-2.3372**	**0.1979**
11745722_x_at	**FHL1**	***four and a half LIM domains 1***	**-2.3313**	**0.1987**
11720203_a_at	**AURKB**	***aurora kinase B***	**-2.3162**	**0.2008**
11729263_x_at	**SERPINB9**	***serpin family B member 9***	**-2.3069**	**0.2021**
11757789_a_at	**EPB41L2**	***erythrocyte membrane protein band 4.1 like 2***	**-2.2990**	**0.2032**
11737324_x_at	**LAMC2**	***laminin subunit gamma 2***	**-2.2955**	**0.2037**
11743296_a_at	**CENPF**	***centromere protein F***	**-2.2891**	**0.2046**
11743721_at	**LGALS1**	***galectin 1***	**-2.2884**	**0.2047**
11758136_s_at	**SLC35G2**	***solute carrier family 35 member G2***	**-2.2877**	**0.2048**
11725198_at	**IL1A**	***interleukin 1 alpha***	**-2.2863**	**0.2050**
11727489_a_at	**KIF11**	***kinesin family member 11***	**-2.2863**	**0.2050**

11743065_at	**CDC6**	***cell division cycle 6***	**-2.2849**	**0.2052**
11715491_s_at	**FSCN1**	***fascin actin-bundling protein 1***	**-2.2800**	**0.2059**
11723487_a_at	**LAMB1**	***laminin subunit beta 1***	**-2.2800**	**0.2059**
11723435_s_at	**TTK**	***TTK protein kinase***	**-2.2793**	**0.2060**
11730264_a_at	**FAM83D**	***family with sequence similarity 83 member D***	**-2.2751**	**0.2066**
11754676_a_at	**CENPE**	***centromere protein E***	**-2.2709**	**0.2072**
11760436_a_at	**DST**	***dystonin***	**-2.2626**	**0.2084**
11728054_a_at	**DIAPH3**	***diaphanous related formin 3***	**-2.2570**	**0.2092**
11718183_at	**CDCA5**	***cell division cycle associated 5***	**-2.2557**	**0.2094**
11723829_s_at	**ANO1**	***anoctamin 1***	**-2.2502**	**0.2102**
11728716_x_at	**CXCL5**	***C-X-C motif chemokine ligand 5***	**-2.2488**	**0.2104**
11728135_at	**NIPAL4**	***NIPA like domain containing 4***	**-2.2488**	**0.2104**
11763188_a_at	**SNX5**	***sorting nexin 5***	**-2.2467**	**0.2107**
11739061_at	**SLC7A5**	***solute carrier family 7 member 5***	**-2.2433**	**0.2112**
11719699_a_at	**CDC45**	***cell division cycle 45***	**-2.2372**	**0.2121**
11722880_a_at	**PHF19**	***PHD finger protein 19***	**-2.2345**	**0.2125**
11745459_a_at	**MIR1908**	***microRNA 1908***	**-2.2331**	**0.2127**
11747361_x_at	**HMGA1**	***high mobility group AT-hook 1***	**-2.2243**	**0.2140**
11756626_s_at	**ZWINT**	***ZW10 interacting kinetochore protein***	**-2.2243**	**0.2140**
11717163_s_at	**CDC20**	***cell division cycle 20***	**-2.2230**	**0.2142**
11739328_x_at	**CENPH**	***centromere protein H***	**-2.2142**	**0.2155**
11759328_at	**KNL1**	***kinetochore scaffold 1***	**-2.1976**	**0.2180**
11720185_a_at	**MAD2L1**	***MAD2 mitotic arrest deficient-like 1 (yeast)***	**-2.1923**	**0.2188**
11723499_a_at	**PCSK9**	***proprotein convertase subtilisin/kexin type 9***	**-2.1798**	**0.2207**
11723591_at	**LRRC8C**	***leucine rich repeat containing 8 family member C***	**-2.1759**	**0.2213**
11740957_x_at	**SLC2A6**	***solute carrier family 2 member 6***	**-2.1759**	**0.2213**
11730096_a_at	**BCL2A1**	***BCL2 related protein A1***	**-2.1720**	**0.2219**
11760935_x_at	**KRT6B**	***keratin 6B***	**-2.1591**	**0.2239**
11724562_x_at	**RHOF**	***ras homolog family member F, filopodia associated***	**-2.1399**	**0.2269**

11723804_a_at	AKAP12	*A-kinase anchoring protein 12*	-2.1272	0.2289
11745021_a_at	MYC	*v-myc avian myelocytomatosis viral oncogene homolog*	-2.1247	0.2293
11723883_at	SOWAHC	*sosondowah ankyrin repeat domain family member C*	-2.1247	0.2293
11720527_at	LTBP2	*latent transforming growth factor beta binding protein 2*	-2.1228	0.2296
11743530_a_at	CENPK	*centromere protein K*	-2.1016	0.2330
11735400_a_at	BNC1	*basonuclin 1*	-2.0899	0.2349
11725155_at	FJX1	*four jointed box 1*	-2.0862	0.2355
11744263_s_at	RAC2	*Ras-Related C3 Botulinum Toxin Substrate 2 (Rho Family, Small GTP Binding Protein Rac2)*	-2.0807	0.2364
11748775_a_at	UPP1	*uridine phosphorylase 1*	-2.0752	0.2373
11756882_a_at	RTTN	*rotatin*	-2.0469	0.2420
11715716_at	MSN	*moesin*	-2.0433	0.2426
11750723_x_at	MICB	*MHC class I polypeptide-related sequence B*	-2.0416	0.2429
11741980_a_at	DUSP6	*dual specificity phosphatase 6*	-2.0362	0.2438
11717860_a_at	EGR1	*early growth response 1*	-2.0339	0.2442
11763367_at	NABP1	*nucleic acid binding protein 1*	-2.0327	0.2444
11726617_s_at	CDK1	*cyclin dependent kinase 1*	-2.0309	0.2447
11740744_x_at	TPM2	*tropomyosin 2 (beta)*	-2.0297	0.2449
11751206_s_at	RAB3GAP2	*RAB3 GTPase activating non-catalytic protein subunit 2*	-2.0203	0.2465
11754074_s_at	G0S2	*G0/G1 switch 2*	-2.0157	0.2473
11719194_a_at	DFNA5	*DFNA5, deafness associated tumor suppressor*	-2.0093	0.2484
11759428_a_at	KLF7	*Kruppel like factor 7*	-2.0081	0.2486
11719262_a_at	SMTN	*smoothelin*	-2.0012	0.2498
11744274_at	NDC80	*NDC80, kinetochore complex component*	-1.9874	0.2522
11758149_s_at	RACGAP1	*Rac GTPase activating protein 1*	-1.9856	0.2525
11724888_a_at	CARD10	*caspase recruitment domain family member 10*	-1.9856	0.2525
11727543_at	OIP5	*Opa interacting protein 5*	-1.9856	0.2525
11715803_a_at	ANXA6	*annexin A6*	-1.9817	0.2532
11723051_at	FGFBP1	*fibroblast growth factor binding protein 1*	-1.9805	0.2534
11731909_a_at	KLK8	*kallikrein related peptidase 8*	-1.9805	0.2534
11725788_a_at	CENPN	*centromere protein N*	-1.9777	0.2539
11723389_a_at	C16orf74	*chromosome 16 open reading frame 74*	-1.9697	0.2553
11723298_s_at	AKAP2	*A-kinase anchoring protein 2*	-1.9669	0.2558
11755466_a_at	CDCA2	*cell division cycle associated 2*	-1.9607	0.2569
11721068_a_at	FHOD3	*formin homology 2 domain containing 3*	-1.9557	0.2578
11718404_at	RFC3	*replication factor C subunit 3*	-1.9557	0.2578
11742409_x_at	KLK8	*kallikrein related peptidase 8*	-1.9351	0.2615
11724285_at	FRMD4A	*FERM domain containing 4A*	-1.9187	0.2645
11717055_a_at	CORO1C	*coronin 1C*	-1.9181	0.2646
11715436_at	TIMP3	*TIMP metallopeptidase inhibitor 3*	-1.9181	0.2646
11758842_at	THBS1	*thrombospondin 1*	-1.9089	0.2663
11755046_a_at	SPHK1	*sphingosine kinase 1*	-1.9018	0.2676
11732542_at	TRIM7	*tripartite motif containing 7*	-1.8831	0.2711

11754180_s_at	SPRR1A	*small proline rich protein 1A*	-1.8826	0.2712
11726757_s_at	CDC25A	*cell division cycle 25A*	-1.8815	0.2714
11720353_s_at	ETV5	*ETS variant 5*	-1.8789	0.2719
11720794_a_at	SRPX	*sushi repeat containing protein, X-linked*	-1.8741	0.2728
11755103_a_at	CDA	*cytidine deaminase*	-1.8741	0.2728
11728894_at	HES2	*hes family bHLH transcription factor 2*	-1.8678	0.2740
11724828_at	CCL20	*C-C motif chemokine ligand 20*	-1.8672	0.2741
11741819_a_at	TGM1	*transglutaminase 1*	-1.8651	0.2745
11736810_at	RPL27A	*ribosomal protein L27a*	-1.8625	0.2750
11744218_at	SNAI2	*snail family transcriptional repressor 2*	-1.8531	0.2768
11746880_x_at	FLNA	*filamin A*	-1.8515	0.2771
11729422_a_at	POPDC3	*popeye domain containing 3*	-1.8505	0.2773
11749650_x_at	A2ML1	*alpha-2-macroglobulin like 1*	-1.8411	0.2791
11722300_a_at	ETS1	*ETS proto-oncogene 1, transcription factor*	-1.8360	0.2801
11719173_s_at	PAICS	*phosphoribosylaminoimidazole carboxylase; phosphoribosylaminoimidazolesuccinocarboxamide synthase*	-1.8355	0.2802
11720047_a_at	ARMCX1	*armadillo repeat containing, X-linked 1*	-1.8314	0.2810
11727837_at	ORC6	*origin recognition complex subunit 6*	-1.8303	0.2812
11729887_at	HACD1	*3-hydroxyacyl-CoA dehydratase 1*	-1.8232	0.2826
11747230_a_at	BUB1	*BUB1 mitotic checkpoint serine/threonine kinase*	-1.8211	0.2830
11758499_s_at	DTL	*denticleless E3 ubiquitin protein ligase homolog*	-1.8196	0.2833
11755200_a_at	DCBLD2	*discoidin, CUB and LCCL domain containing 2*	-1.8165	0.2839
11743452_s_at	CDCA4	*cell division cycle associated 4*	-1.8150	0.2842
11722532_s_at	CALD1	*caldesmon 1*	-1.8115	0.2849
11731394_a_at	VIM	*vimentin*	-1.8094	0.2853
11757940_at	PGF	*placental growth factor*	-1.8089	0.2854
11750189_s_at	CD44	*CD44 Molecule (Indian Blood Group)*	-1.8089	0.2854
11719197_at	CCND2	*cyclin D2*	-1.8059	0.2860
11719826_x_at	ZAK	*sterile alpha motif and leucine zipper containing kinase AZK*	-1.8049	0.2862
11733126_a_at	PRIM1	*Primase (DNA) Subunit 1*	-1.8009	0.2870
11723747_a_at	FAM64A	*family with sequence similarity 64 member A*	-1.7989	0.2874
11722839_at	LYAR	*Ly1 antibody reactive*	-1.7939	0.2884
11743169_a_at	LPXN	*leupaxin*	-1.7914	0.2889
11754375_s_at	SNX10	*sorting nexin 10*	-1.7889	0.2894
11754313_s_at	ARL4C	*ADP ribosylation factor like GTPase 4C*	-1.7824	0.2907
11754119_a_at	PLAU	*plasminogen activator, urokinase*	-1.7804	0.2911
11745377_x_at	PTRF	*polymerase I and transcript release factor*	-1.7784	0.2915
11755252_a_at	AMIGO2	*adhesion molecule with Ig like domain 2*	-1.7774	0.2917
11741376_a_at	LRP8	*LDL receptor related protein 8*	-1.7765	0.2919
11718141_at	DKK1	*dickkopf WNT signaling pathway inhibitor 1*	-1.7715	0.2929
11755032_s_at	ASAP1	*ArfGAP with SH3 domain, ankyrin repeat and PH domain 1*	-1.7691	0.2934
11744519_a_at	POLE2	*DNA polymerase epsilon 2, accessory subunit*	-1.7691	0.2934
11722308_a_at	TP63	*tumor protein p63*	-1.7676	0.2937

11718297_a_at	TACC3	*transforming acidic coiled-coil containing protein 3*	-1.7627	0.2947
11750141_a_at	CTPS1	*CTP synthase 1*	-1.7622	0.2948
11751389_s_at	FEN1	*flap structure-specific endonuclease 1*	-1.7578	0.2957
11732756_a_at	ELAVL2	*ELAV like RNA binding protein 2*	-1.7563	0.2960
11726779_a_at	IKBIP	*IKBKB interacting protein*	-1.7486	0.2976
11736367_a_at	MCM10	*minichromosome maintenance 10 replication initiation factor*	-1.7481	0.2977
11737197_s_at	KIF4A	*kinesin family member 4A*	-1.7408	0.2992
11728731_s_at	DSCC1	*DNA replication and sister chromatid cohesion 1*	-1.7394	0.2995
11719849_s_at	UBE2S	*ubiquitin conjugating enzyme E2 S*	-1.7389	0.2996
11717909_at	IGFBP6	*insulin like growth factor binding protein 6*	-1.7370	0.3000
11720566_at	BCAT1	*branched chain amino acid transaminase 1*	-1.7370	0.3000
11746931_a_at	INHBA	*inhibin beta A subunit*	-1.7350	0.3004
11723274_a_at	SLC35F2	*solute carrier family 35 member F2*	-1.7293	0.3016
11719899_at	C11orf96	*chromosome 11 open reading frame 96*	-1.7283	0.3018
11722122_at	CYP27B1	*cytochrome P450 family 27 subfamily B member 1*	-1.7264	0.3022
11738052_at	MRGPRX3	*MAS related GPR family member X3*	-1.7221	0.3031
11727731_at	RASGEF1A	*RasGEF domain family member 1A*	-1.7188	0.3038
11724963_s_at	FBXO5	*F-box protein 5*	-1.7169	0.3042
11742890_at	MND1	*meiotic nuclear divisions 1*	-1.7155	0.3045
11743373_a_at	KNSTRN	*kinetochore localized astrin/SPAG5 binding protein*	-1.7141	0.3048
11725842_a_at	PIF1	*PIF1 5'-to-3' DNA helicase*	-1.7108	0.3055
11717863_a_at	DUSP5	*dual specificity phosphatase 5*	-1.7108	0.3055
11740375_a_at	RGS10	*regulator of G-protein signaling 10*	-1.7089	0.3059
11738997_s_at	DPYSL2	*dihydropyrimidinase like 2*	-1.7046	0.3068
11718140_a_at	EMP3	*epithelial membrane protein 3*	-1.7009	0.3076
11718788_a_at	ADA	*adenosine deaminase*	-1.7004	0.3077
11744297_a_at	RMI2	*RecQ mediated genome instability 2*	-1.6957	0.3087
11721345_at	PLEK2	*pleckstrin 2*	-1.6887	0.3102
11725910_a_at	COL4A6	*collagen type IV alpha 6 chain*	-1.6785	0.3124
11723225_a_at	CLDN11	*claudin 11*	-1.6758	0.3130
11737223_a_at	ARTN	*artemin*	-1.6739	0.3134
11720967_a_at	GPSM2	*G-protein signaling modulator 2*	-1.6739	0.3134
11756666_x_at	MCM2	*minichromosome maintenance complex component 2*	-1.6716	0.3139
11727968_at	ESCO2	*establishment of sister chromatid cohesion N-acetyltransferase 2*	-1.6661	0.3151
11721854_a_at	NCAPH	*non-SMC condensin I complex subunit H*	-1.6643	0.3155
11722818_a_at	GGH	*gamma-glutamyl hydrolase*	-1.6638	0.3156
11723998_at	SPC25	*SPC25, NDC80 kinetochore complex component*	-1.6579	0.3169
11739910_a_at	ELOVL6	*ELOVL fatty acid elongase 6*	-1.6565	0.3172
11717436_a_at	CDCA7L	*cell division cycle associated 7 like*	-1.6556	0.3174
11725825_a_at	GJB3	*gap junction protein beta 3*	-1.6543	0.3177
11717743_a_at	ACOT7	*acyl-CoA thioesterase 7*	-1.6543	0.3177
11758864_at	SRP19	*signal recognition particle 19*	-1.6497	0.3187

11736596_s_at	**GINS4**	***GINS complex subunit 4***	**-1.6488**	**0.3189**
11743922_at	**NUDT11**	***nudix hydrolase 11***	**-1.6475**	**0.3192**
11718832_a_at	**LOXL2**	***lysyl oxidase like 2***	**-1.6425**	**0.3203**
11752515_a_at	**ODC1**	***ornithine decarboxylase 1***	**-1.6394**	**0.3210**
11727459_x_at	**KRT14**	***keratin 14***	**-1.6376**	**0.3214**
11757631_s_at	**VGLL3**	***vestigial like family member 3***	**-1.6335**	**0.3223**
11741015_a_at	**CDCA8**	***cell division cycle associated 8***	**-1.6308**	**0.3229**
11753856_a_at	**CKS2**	***CDC28 protein kinase regulatory subunit 2***	**-1.6304**	**0.3230**
11735061_a_at	**LY6D**	***lymphocyte antigen 6 complex, locus D***	**-1.6224**	**0.3248**
11727364_s_at	**SHC1**	***SHC adaptor protein 1***	**-1.6197**	**0.3254**
11728303_at	**TGFA**	***transforming growth factor alpha***	**-1.6153**	**0.3264**
11737852_s_at	**PPP1R18**	***protein phosphatase 1 regulatory subunit 18***	**-1.6122**	**0.3271**
11724337_s_at	**NRCAM**	***neuronal cell adhesion molecule***	**-1.6118**	**0.3272**
11724209_a_at	**KIFC1**	***kinesin family member C1***	**-1.6113**	**0.3273**
11755448_s_at	**CAPRIN2**	***caprin family member 2***	**-1.6096**	**0.3277**
11724407_s_at	**CCNE1**	***cyclin E1***	**-1.6091**	**0.3278**
11755614_s_at	**FERMT1**	***fermitin family member 1***	**-1.6091**	**0.3278**
11734177_a_at	**SLC2A9**	***solute carrier family 2 member 9***	**-1.6082**	**0.3280**
11728410_a_at	**INO80C**	***INO80 complex subunit C***	**-1.6030**	**0.3292**
11743687_s_at	**HMGB2**	***high mobility group box 2***	**-1.6003**	**0.3298**
11739809_at	**TMEM156**	***transmembrane protein 156***	**-1.5977**	**0.3304**
11731925_at	**CRCT1**	***cysteine rich C-terminal 1***	**-1.5955**	**0.3309**
11758536_s_at	**KCTD15**	***potassium channel tetramerization domain containing 15***	**-1.5934**	**0.3314**
11749094_a_at	**DSE**	***dermatan sulfate epimerase***	**-1.5929**	**0.3315**
11745571_a_at	**CENPA**	***centromere protein A***	**-1.5886**	**0.3325**
11728300_at	**CCNE2**	***cyclin E2***	**-1.5873**	**0.3328**
11727063_a_at	**MIR3658**	***microRNA 3658***	**-1.5851**	**0.3333**
11736670_a_at	**MCM4**	***minichromosome maintenance complex component 4***	**-1.5829**	**0.3338**
11741779_s_at	**HSD11B1**	***hydroxysteroid 11-beta dehydrogenase 1***	**-1.5821**	**0.3340**
11719227_x_at	**KCNN4**	***potassium calcium-activated channel subfamily N member 4***	**-1.5821**	**0.3340**
11724152_a_at	**TNS4**	***tensin 4***	**-1.5795**	**0.3346**
11716322_s_at	**PRKCDBP**	***protein kinase C delta binding protein***	**-1.5773**	**0.3351**
11744789_a_at	**CENPU**	***centromere protein U***	**-1.5765**	**0.3353**
11721840_at	**GLIPR1**	***GLI pathogenesis related 1***	**-1.5748**	**0.3357**
11742944_a_at	**CORO1A**	***coronin 1A***	**-1.5735**	**0.3360**
11725584_at	**HAS3**	***hyaluronan synthase 3***	**-1.5718**	**0.3364**
11744127_at	**CXCL2**	***C-X-C motif chemokine ligand 2***	**-1.5713**	**0.3365**
11746650_a_at	**ACER3**	***alkaline ceramidase 3***	**-1.5658**	**0.3378**
11760209_a_at	**RPL37A**	***ribosomal protein L37a***	**-1.5653**	**0.3379**
11733465_at	**XDH**	***xanthine dehydrogenase***	**-1.5649**	**0.3380**
11727658_s_at	**KLK10**	***kallikrein related peptidase 10***	**-1.5636**	**0.3383**
11745929_a_at	**AHCY**	***adenosylhomocysteinase***	**-1.5632**	**0.3384**

11732191_s_at	RAD51AP1	*RAD51 associated protein 1*	-1.5632	0.3384
11739144_a_at	SKP2	*S-phase kinase associated protein 2*	-1.5615	0.3388
11749291_a_at	FOS	*Fos proto-oncogene, AP-1 transcription factor subunit*	-1.5606	0.3390
11736029_a_at	ITGA6	*integrin subunit alpha 6*	-1.5560	0.3401
11756121_a_at	DUSP7	*dual specificity phosphatase 7*	-1.5534	0.3407
11715913_s_at	EFNB1	*ephrin B1*	-1.5496	0.3416
11757013_x_at	CAV1	*caveolin 1*	-1.5479	0.3420
11716996_a_at	TSPAN4	*tetraspanin 4*	-1.5454	0.3426
11724147_at	RAB38	*RAB38, member RAS oncogene family*	-1.5454	0.3426
11756790_a_at	ITGA3	*integrin subunit alpha 3*	-1.5433	0.3431
11720163_at	VEGFC	*vascular endothelial growth factor C*	-1.5425	0.3433
11756784_x_at	NCAPG2	*non-SMC condensin II complex subunit G2*	-1.5399	0.3439
11721563_a_at	MELK	*maternal embryonic leucine zipper kinase*	-1.5395	0.3440
11754939_x_at	FADS2	*fatty acid desaturase 2*	-1.5387	0.3442
11755469_x_at	MCM7	*minichromosome maintenance complex component 7*	-1.5353	0.3450
11717305_a_at	ADIRF	*adipogenesis regulatory factor*	-1.5324	0.3457
11725588_a_at	CBLC	*Cbl proto-oncogene C*	-1.5316	0.3459
11729239_x_at	CSRP2	*cysteine and glycine rich protein 2*	-1.5303	0.3462
11721615_a_at	THEMIS2	*thymocyte selection associated family member 2*	-1.5299	0.3463
11726887_a_at	SOX15	*SRY-box 15*	-1.5287	0.3466
11748174_x_at	MCM3	*minichromosome maintenance complex component 3*	-1.5270	0.3470
11735324_s_at	FAM72C	*family with sequence similarity 72 member C*	-1.5257	0.3473
11754652_a_at	ECI2	*enoyl-CoA delta isomerase 2*	-1.5245	0.3476
11739606_x_at	CCDC88A	*coiled-coil domain containing 88A*	-1.5237	0.3478
11759497_at	CHST11	*carbohydrate sulfotransferase 11*	-1.5237	0.3478
11716847_a_at	SLC43A3	*solute carrier family 43 member 3*	-1.5228	0.3480
11727937_x_at	MSANTD3	*Myb/SANT DNA binding domain containing 3*	-1.5224	0.3481
11718283_a_at	EIF4EBP1	*eukaryotic translation initiation factor 4E binding protein 1*	-1.5212	0.3484
11743602_a_at	RRM1	*ribonucleotide reductase catalytic subunit M1*	-1.5208	0.3485
11719218_at	SOCS3	*suppressor of cytokine signaling 3*	-1.5195	0.3488
11728233_a_at	CLDN1	*claudin 1*	-1.5191	0.3489
11758619_s_at	LIF	*leukemia inhibitory factor*	-1.5166	0.3495
11718578_a_at	GSTM3	*glutathione S-transferase mu 3*	-1.5154	0.3498
11722069_a_at	SKA1	*spindle and kinetochore associated complex subunit 1*	-1.5150	0.3499
11749461_a_at	CDH11	*cadherin 11*	-1.5047	0.3524
11722121_a_at	PC	*pyruvate carboxylase*	-1.4953	0.3547
11746438_a_at	SHMT2	*serine hydroxymethyltransferase 2*	-1.4941	0.3550
11725441_a_at	FOXM1	*forkhead box M1*	-1.4937	0.3551
11727081_a_at	TIPIN	*TIMELESS interacting protein*	-1.4933	0.3552
11720803_at	S100A14	*S100 calcium binding protein A14*	-1.4880	0.3565
11715703_s_at	ITGA5	*integrin subunit alpha 5*	-1.4876	0.3566
11719586_a_at	TAGLN3	*transgelin 3*	-1.4828	0.3578

11715452_s_at	COL4A2	*collagen type IV alpha 2 chain*	-1.4824	0.3579
11747072_s_at	TUBB6	*tubulin beta 6 class V*	-1.4820	0.3580
11717349_a_at	RBP1	*retinol binding protein 1*	-1.4820	0.3580
11731068_s_at	FIGNL1	*fidgetin like 1*	-1.4792	0.3587
11751116_a_at	ACTN1	*actinin alpha 1*	-1.4715	0.3606
11736687_a_at	FGF5	*fibroblast growth factor 5*	-1.4675	0.3616
11747334_a_at	DDX39A	*DExD-box helicase 39A*	-1.4632	0.3627
11757117_at	SNORA64	*small nucleolar RNA, H/ACA box 64*	-1.4604	0.3634
11715948_at	KCTD12	*potassium channel tetramerization domain containing 12*	-1.4572	0.3642
11746471_s_at	MAP4K4	*mitogen-activated protein kinase 4*	-1.4560	0.3645
11754593_x_at	TUBB3	*tubulin beta 3 class III*	-1.4556	0.3646
11721705_at	COL7A1	*collagen type VII alpha 1 chain*	-1.4548	0.3648
11746242_a_at	ARNTL2	*aryl hydrocarbon receptor nuclear translocator like 2*	-1.4532	0.3652
11739763_a_at	GINS3	*GINS complex subunit 3*	-1.4513	0.3657
11754630_a_at	MLKL	*mixed lineage kinase domain like*	-1.4497	0.3661
11725705_a_at	AMOTL1	*angiomotin like 1*	-1.4489	0.3663
11743596_a_at	PTPRE	*protein tyrosine phosphatase, receptor type E*	-1.4465	0.3669
11748355_a_at	SLC16A1	*solute carrier family 16 member 1*	-1.4442	0.3675
11737413_at	MICALCL	*MICAL C-terminal like*	-1.4442	0.3675
11726441_a_at	ERCC6L	*ERCC excision repair 6 like, spindle assembly checkpoint helicase*	-1.4418	0.3681
11755006_x_at	BCAR3	*breast cancer anti-estrogen resistance 3*	-1.4410	0.3683
11758222_s_at	SLC20A1	*solute carrier family 20 member 1*	-1.4387	0.3689
11756303_a_at	SH3TC1	*SH3 domain and tetratricopeptide repeats 1*	-1.4375	0.3692
11724405_at	NDUFC2-KCTD14	*NDUFC2-KCTD14 readthrough*	-1.4360	0.3696
11733663_a_at	ARHGAP11A	*Rho GTPase activating protein 11A*	-1.4344	0.3700
11756952_a_at	TKT	*transketolase*	-1.4340	0.3701
11719488_at	EDNRA	*endothelin receptor type A*	-1.4328	0.3704
11735123_x_at	POLR1E	*RNA polymerase I subunit E*	-1.4325	0.3705
11716872_a_at	ADCY3	*adenylate cyclase 3*	-1.4305	0.3710
11722872_a_at	RFC4	*replication factor C subunit 4*	-1.4274	0.3718
11729514_a_at	CSF3	*colony stimulating factor 3*	-1.4266	0.3720
11716171_s_at	LMNB2	*lamin B2*	-1.4262	0.3721
11733240_at	IRAK2	*interleukin 1 receptor associated kinase 2*	-1.4224	0.3731
11719980_a_at	FMNL2	*formin like 2*	-1.4200	0.3737
11725469_at	LIPG	*lipase G, endothelial type*	-1.4177	0.3743
11734867_a_at	TPRG1	*tumor protein p63 regulated 1*	-1.4162	0.3747
11734557_a_at	GALNT5	*polypeptide N-acetylgalactosaminyltransferase 5*	-1.4147	0.3751
11718076_at	MAPKAPK3	*mitogen-activated protein kinase-activated protein kinase 3*	-1.4139	0.3753
11750554_a_at	NEDD4	*neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase*	-1.4127	0.3756
11728062_a_at	SH3BP1	*SH3 domain binding protein 1*	-1.4100	0.3763
11736083_x_at	GTSE1	*G2 and S-phase expressed 1*	-1.4089	0.3766
11716094_a_at	KLF6	*Kruppel like factor 6*	-1.4081	0.3768

11754524_x_at	TFPI2	*tissue factor pathway inhibitor 2*	-1.4074	0.3770
11736047_a_at	ANTXR2	*anthrax toxin receptor 2*	-1.4070	0.3771
11721421_s_at	RAP1GAP2	*RAP1 GTPase activating protein 2*	-1.4028	0.3782
11746863_x_at	ARSJ	*arylsulfatase family member J*	-1.3986	0.3793
11726717_at	C1orf74	*chromosome 1 open reading frame 74*	-1.3986	0.3793
11723104_at	GNB4	*G protein subunit beta 4*	-1.3895	0.3817
11726536_at	CYP1A1	*cytochrome P450 family 1 subfamily A member 1*	-1.3891	0.3818
11719811_a_at	TRIB3	*tribbles pseudokinase 3*	-1.3887	0.3819
11747039_x_at	EHD1	*EH domain containing 1*	-1.3884	0.3820
11717576_a_at	SFN	*stratifin*	-1.3876	0.3822
11716332_a_at	MIR6805	*microRNA 6805*	-1.3846	0.3830
11716631_s_at	SERPINB2	*serpin family B member 2*	-1.3831	0.3834
11756409_a_at	BLM	*Bloom syndrome RecQ like helicase*	-1.3827	0.3835
11729158_at	UBE2T	*ubiquitin conjugating enzyme E2 T*	-1.3816	0.3838
11732818_at	TMEM171	*transmembrane protein 171*	-1.3812	0.3839
11747427_a_at	SEC14L2	*SEC14 like lipid binding 2*	-1.3797	0.3843
11725460_x_at	S100A7	*S100 calcium binding protein A7*	-1.3778	0.3848
11745543_x_at	AJUBA	*ajuba LIM protein*	-1.3774	0.3849
11756412_a_at	NT5DC2	*5'-nucleotidase domain containing 2*	-1.3767	0.3851
11719598_s_at	CDCA3	*cell division cycle associated 3*	-1.3763	0.3852
11729227_a_at	GRK5	*G protein-coupled receptor kinase 5*	-1.3730	0.3861
11763693_a_at	GLS	*glutaminase*	-1.3730	0.3861
11752502_s_at	ALDH7A1	*aldehyde dehydrogenase 7 family member A1*	-1.3715	0.3865
11747399_x_at	PLAT	*plasminogen activator, tissue type*	-1.3715	0.3865
11733828_x_at	SNORD88C	*small nucleolar RNA, C/D box 88C*	-1.3700	0.3869
11722864_at	NETO2	*neuropilin and tolloid like 2*	-1.3700	0.3869
11722442_a_at	NUF2	*NUF2, NDC80 kinetochore complex component*	-1.3685	0.3873
11728469_a_at	BTBD11	*BTB domain containing 11*	-1.3677	0.3875
11723032_a_at	PLP2	*proteolipid protein 2*	-1.3659	0.3880
11725714_a_at	RPS14	*ribosomal protein S14*	-1.3655	0.3881
11723227_at	SGCB	*sarcoglycan beta*	-1.3633	0.3887
11731899_s_at	PPAT	*phosphoribosyl pyrophosphate amidotransferase*	-1.3622	0.3890
11727269_at	S100A3	*S100 calcium binding protein A3*	-1.3618	0.3891
11756358_a_at	PLK3	*polo like kinase 3*	-1.3596	0.3897
11740840_a_at	ABL2	*ABL proto-oncogene 2, non-receptor tyrosine kinase*	-1.3573	0.3903
11740722_a_at	IL1RN	*interleukin 1 receptor antagonist*	-1.3503	0.3922
11748808_a_at	ARID3B	*AT-rich interaction domain 3B*	-1.3500	0.3923
11763556_at	EIF4A1	*eukaryotic translation initiation factor 4A1*	-1.3485	0.3927
11725945_x_at	TINAGL1	*tubulointerstitial nephritis antigen like 1*	-1.3478	0.3929
11744887_s_at	ZWILCH	*zwilch kinetochore protein*	-1.3474	0.3930
11731526_s_at	TRIP13	*thyroid hormone receptor interactor 13*	-1.3437	0.3940
11738203_x_at	IMPDH1	*inosine monophosphate dehydrogenase 1*	-1.3423	0.3944

11739524_a_at	MPRIP	*myosin phosphatase Rho interacting protein*	-1.3415	0.3946
11730875_a_at	FANCI	*Fanconi anemia complementation group I*	-1.3397	0.3951
11758396_s_at	POLR3G	*RNA polymerase III subunit G*	-1.3397	0.3951
11757152_s_at	MIR1304	*microRNA 1304*	-1.3375	0.3957
11716413_x_at	MT1E	*metallothionein 1E*	-1.3372	0.3958
11757458_s_at	LRRC8A	*leucine rich repeat containing 8 family member A*	-1.3350	0.3964
11744868_a_at	SMC2	*structural maintenance of chromosomes 2*	-1.3324	0.3971
11740312_at	HAS2	*hyaluronan synthase 2*	-1.3302	0.3977
11728810_a_at	ECHDC3	*enoyl-CoA hydratase domain containing 3*	-1.3277	0.3984
11726116_at	MTAP	*methylthioadenosine phosphorylase*	-1.3266	0.3987
11727324_at	NAGS	*N-acetylglutamate synthase*	-1.3263	0.3988
11716126_x_at	ZYX	*zyxin*	-1.3223	0.3999
11717320_a_at	OAF	*out at first homolog*	-1.3208	0.4003
11718400_a_at	PNP	*purine nucleoside phosphorylase*	-1.3201	0.4005
11725459_s_at	S100A7A	*S100 calcium binding protein A7A*	-1.3162	0.4016
11730887_a_at	ACOT11	*acyl-CoA thioesterase 11*	-1.3155	0.4018
11722120_a_at	KNTC1	*kinetochore associated 1*	-1.3151	0.4019
11751983_a_at	EGFR	*epidermal growth factor receptor*	-1.3144	0.4021
11743063_x_at	PLAUR	*plasminogen activator, urokinase receptor*	-1.3133	0.4024
11720562_a_at	PLXNA2	*plexin A2*	-1.3083	0.4038
11715359_a_at	TIMP1	*TIMP metallopeptidase inhibitor 1*	-1.3079	0.4039
11723169_s_at	FOXN2	*forkhead box N2*	-1.3076	0.4040
11759176_at	GTSE1	*G2 and S-phase expressed 1*	-1.3076	0.4040
11739654_at	TNFRSF10A	*TNF receptor superfamily member 10a*	-1.3061	0.4044
11732999_a_at	ICAM1	*intercellular adhesion molecule 1*	-1.3061	0.4044
11720154_at	NRIP1	*nuclear receptor interacting protein 1*	-1.3047	0.4048
11754516_a_at	CD109	*CD109 molecule*	-1.3033	0.4052
11719330_s_at	FNDC4	*fibronectin type III domain containing 4*	-1.3026	0.4054
11722615_s_at	HCAR2	*hydroxycarboxylic acid receptor 2*	-1.3015	0.4057
11719032_a_at	FADS3	*fatty acid desaturase 3*	-1.3015	0.4057
11747079_x_at	ALDOC	*aldolase, fructose-bisphosphate C*	-1.2990	0.4064
11744748_x_at	FGFR1OP2	*FGFR1 oncogene partner 2*	-1.2980	0.4067
11719891_s_at	CRYZ	*crystallin zeta*	-1.2937	0.4079
11742184_a_at	LAMA3	*laminin subunit alpha 3*	-1.2930	0.4081
11718399_s_at	TGM2	*transglutaminase 2*	-1.2877	0.4096
11733876_x_at	SMC4	*structural maintenance of chromosomes 4*	-1.2849	0.4104
11745820_s_at	PLAGL1	*PLAG1 like zinc finger 1*	-1.2814	0.4114
11723188_s_at	ADAM19	*ADAM metallopeptidase domain 19*	-1.2786	0.4122
11718576_s_at	NET1	*neuroepithelial cell transforming 1*	-1.2782	0.4123
11725642_at	EFHD2	*EF-hand domain family member D2*	-1.2768	0.4127
11722691_at	AVEN	*apoptosis and caspase activation inhibitor*	-1.2751	0.4132
11728749_a_at	TCF19	*transcription factor 19*	-1.2751	0.4132

11758314_s_at	**NDUFAF2**	***NADH:ubiquinone oxidoreductase complex assembly factor 2***	**-1.2740**	**0.4135**
11755618_a_at	**ALDH4A1**	***aldehyde dehydrogenase 4 family member A1***	**-1.2733**	**0.4137**
11755024_a_at	**MYEOV**	***myeloma overexpressed***	**-1.2719**	**0.4141**
11728538_a_at	**MCC**	***mutated in colorectal cancers***	**-1.2719**	**0.4141**
11728415_s_at	**POMZP3**	***POM121 and ZP3 fusion***	**-1.2688**	**0.4150**
11727092_x_at	**IL18**	***interleukin 18***	**-1.2678**	**0.4153**
11723697_s_at	**FLI1**	***Fli-1 proto-oncogene, ETS transcription factor***	**-1.2671**	**0.4155**
11731317_a_at	**MMP28**	***matrix metallopeptidase 28***	**-1.2636**	**0.4165**
11746588_a_at	**ALDH1B1**	***aldehyde dehydrogenase 1 family member B1***	**-1.2622**	**0.4169**
11744005_at	**PHLDA2**	***pleckstrin homology like domain family A member 2***	**-1.2591**	**0.4178**
11731992_x_at	**TROAP**	***trophinin associated protein***	**-1.2570**	**0.4184**
11757860_s_at	**QKI**	***QKI, KH domain containing RNA binding***	**-1.2560**	**0.4187**
11727833_at	**WDR43**	***WD repeat domain 43***	**-1.2557**	**0.4188**
11738887_s_at	**MICA**	***MHC class I polypeptide-related sequence A***	**-1.2526**	**0.4197**
11728391_s_at	**LRP12**	***LDL receptor related protein 12***	**-1.2505**	**0.4203**
11720241_at	**KIF4A**	***kinesin family member 4A***	**-1.2481**	**0.4210**
11751993_a_at	**JAG1**	***jagged 1***	**-1.2457**	**0.4217**
11756160_x_at	**CTNNAL1**	***catenin alpha like 1***	**-1.2447**	**0.4220**
11719384_at	**PRSS3**	***protease, serine 3***	**-1.2437**	**0.4223**
11718635_at	**KIF1B**	***kinesin family member 1B***	**-1.2433**	**0.4224**
11724605_a_at	**HS6ST2**	***heparan sulfate 6-O-sulfotransferase 2***	**-1.2420**	**0.4228**
11734826_s_at	**SPRED1**	***sprouty related EVH1 domain containing 1***	**-1.2413**	**0.4230**
11720547_a_at	**PDSS1**	***Decaprenyl Diphosphate Synthase Subunit 1***	**-1.2406**	**0.4232**
11730912_at	**NPM1**	***nucleophosmin***	**-1.2402**	**0.4233**
11733915_a_at	**DSC3**	***desmocollin 3***	**-1.2402**	**0.4233**
11716630_a_at	**ANGPTL4**	***angiopoietin like 4***	**-1.2392**	**0.4236**
11722655_s_at	**STK17A**	***serine/threonine kinase 17a***	**-1.2372**	**0.4242**
11743546_a_at	**MYO1B**	***myosin IB***	**-1.2362**	**0.4245**
11759151_at	**SPC24**	***SPC24, NDC80 kinetochore complex component***	**-1.2358**	**0.4246**
11716982_at	**CMSS1**	***Cms1 Ribosomal Small Subunit Homolog (Yeast)***	**-1.2345**	**0.4250**
11744604_at	**ERVMER34-1**	***endogenous retrovirus group MER34 member 1***	**-1.2341**	**0.4251**
11759113_at	**LOC100506548**	***uncharacterized LOC100506548***	**-1.2338**	**0.4252**
11734548_a_at	**TGFBI**	***transforming growth factor beta induced***	**-1.2331**	**0.4254**
11737162_at	**FAM83B**	***family with sequence similarity 83 member B***	**-1.2311**	**0.4260**
11722759_a_at	**CAMSAP2**	***calmodulin regulated spectrin associated protein family member 2***	**-1.2304**	**0.4262**
11724252_s_at	**SLC39A8**	***solute carrier family 39 member 8***	**-1.2304**	**0.4262**
11754937_a_at	**GMNN**	***geminin, DNA replication inhibitor***	**-1.2287**	**0.4267**
11734619_x_at	**ALOX15B**	***arachidonate 15-lipoxygenase, type B***	**-1.2277**	**0.4270**
11756230_a_at	**FLNB**	***filamin B***	**-1.2277**	**0.4270**
11715757_a_at	**RGS2**	***regulator of G-protein signaling 2***	**-1.2257**	**0.4276**
11733816_a_at	**RPL22L1**	***ribosomal protein L22 like 1***	**-1.2253**	**0.4277**
11718260_at	**NOTCH1**	***notch 1***	**-1.2253**	**0.4277**

11744286_s_at	CBS	*cystathionine-beta-synthase*	-1.2236	0.4282
11731887_at	KIF14	*kinesin family member 14*	-1.2233	0.4283
11755100_a_at	COL16A1	*collagen type XVI alpha 1 chain*	-1.2223	0.4286
11747731_a_at	DBF4	*DBF4 zinc finger*	-1.2220	0.4287
11728984_a_at	LOC100996643	*monofunctional C1-tetrahydrofolate synthase, mitochondrial-like*	-1.2216	0.4288
11734142_a_at	METTL8	*methyltransferase like 8*	-1.2210	0.4290
11715698_a_at	NOLC1	*nucleolar and coiled-body phosphoprotein 1*	-1.2203	0.4292
11754319_at	SSH1	*slingshot protein phosphatase 1*	-1.2179	0.4299
11729834_at	EIF5A2	*eukaryotic translation initiation factor 5A2*	-1.2179	0.4299
11736104_a_at	ZNF750	*zinc finger protein 750*	-1.2176	0.4300
11716092_x_at	CKS1B	*CDC28 protein kinase regulatory subunit 1B*	-1.2169	0.4302
11743822_a_at	WHSC1	*Wolf-Hirschhorn syndrome candidate 1*	-1.2169	0.4302
11758106_at	NRM	*Nurim (Nuclear Envelope Membrane Protein)*	-1.2149	0.4308
11722379_at	GNG11	*G protein subunit gamma 11*	-1.2132	0.4313
11726559_s_at	LCP1	*lymphocyte cytosolic protein 1*	-1.2132	0.4313
11724735_a_at	PDPN	*podoplanin*	-1.2122	0.4316
11745731_x_at	TNIP1	*TNFAIP3 interacting protein 1*	-1.2112	0.4319
11727784_x_at	TPM4	*tropomyosin 4*	-1.2106	0.4321
11735576_a_at	LETM2	*leucine zipper and EF-hand containing transmembrane protein 2*	-1.2099	0.4323
11716919_a_at	MIR7110	*microRNA 7110*	-1.2096	0.4324
11758151_s_at	RNASEH2A	*ribonuclease H2 subunit A*	-1.2089	0.4326
11740349_at	RNASE7	*ribonuclease A family member 7*	-1.2086	0.4327
11728161_at	WNT7A	*Wnt family member 7A*	-1.2086	0.4327
11723732_at	GNPNAT1	*glucosamine-phosphate N-acetyltransferase 1*	-1.2066	0.4333
11744277_x_at	CAPG	*capping actin protein, gelsolin like*	-1.2052	0.4337
11719719_at	LAD1	*ladinin 1*	-1.2046	0.4339
11732533_a_at	LMNB1	*lamin B1*	-1.2046	0.4339
11719258_at	TICAM1	*toll like receptor adaptor molecule 1*	-1.2039	0.4341
11718119_s_at	CFL2	*cofilin 2*	-1.1999	0.4353
11720747_a_at	ADCY7	*adenylate cyclase 7*	-1.1999	0.4353
11737184_at	SAA2	*serum amyloid A2*	-1.1979	0.4359
11723803_a_at	TREM2	*triggering receptor expressed on myeloid cells 2*	-1.1979	0.4359
11757036_x_at	SAC3D1	*SAC3 domain containing 1*	-1.1966	0.4363
11716642_s_at	DTYMK	*deoxythymidylate kinase*	-1.1966	0.4363
11746283_s_at	KRTAP2-3	*keratin associated protein 2-3*	-1.1959	0.4365
11716987_a_at	HMGCS1	*3-hydroxy-3-methylglutaryl-CoA synthase 1*	-1.1940	0.4371
11743536_at	VRK1	*vaccinia related kinase 1*	-1.1913	0.4379
11763431_x_at	ARHGAP8	*Rho GTPase activating protein 8*	-1.1890	0.4386
11728843_a_at	PROSER2	*proline and serine rich 2*	-1.1880	0.4389
11741056_a_at	ADORA2B	*adenosine A2b receptor*	-1.1871	0.4392
11749410_x_at	DMKN	*dermokine*	-1.1867	0.4393
11718802_a_at	PSRC1	*proline and serine rich coiled-coil 1*	-1.1864	0.4394

11757716_x_at	MIR205	*microRNA 205*	-1.1857	0.4396
11752673_x_at	LMNA	*lamin A/C*	-1.1851	0.4398
11754344_s_at	SPRY4	*sprouty RTK signaling antagonist 4*	-1.1838	0.4402
11743653_x_at	DEK	*DEK proto-oncogene*	-1.1838	0.4402
11754573_a_at	LPIN1	*lipin 1*	-1.1838	0.4402
11724978_a_at	ITGB4	*integrin subunit beta 4*	-1.1818	0.4408
11743467_at	MIR664B	*microRNA 664b*	-1.1811	0.4410
11758583_s_at	TMEM154	*transmembrane protein 154*	-1.1782	0.4419
11720550_a_at	NCAPD3	*non-SMC condensin II complex subunit D3*	-1.1776	0.4421
11723326_at	CA9	*carbonic anhydrase 9*	-1.1766	0.4424
11717196_a_at	MEST	*mesoderm specific transcript*	-1.1763	0.4425
11737802_a_at	MAD1L1	*MAD1 mitotic arrest deficient like 1*	-1.1763	0.4425
11752409_a_at	NDC1	*NDC1 transmembrane nucleoporin*	-1.1759	0.4426
11721907_at	SGPP1	*sphingosine-1-phosphate phosphatase 1*	-1.1759	0.4426
11716638_s_at	COL4A1	*collagen type IV alpha 1 chain*	-1.1759	0.4426
11763164_at	DNAJC9	*DnaJ Heat Shock Protein Family (Hsp40) Member C9*	-1.1749	0.4429
11719732_at	TIGAR	*TP53 induced glycolysis regulatory phosphatase*	-1.1733	0.4434
11749983_a_at	SERPINB5	*serpin family B member 5*	-1.1723	0.4437
11758165_s_at	MRTO4	*MRT4 homolog, ribosome maturation factor*	-1.1717	0.4439
11722213_at	NPM3	*nucleophosmin/nucleoplasmin 3*	-1.1714	0.4440
11734841_a_at	RAD51	*RAD51 recombinase*	-1.1684	0.4449
11721633_s_at	TMEM97	*transmembrane protein 97*	-1.1662	0.4456
11744242_a_at	ANKRD29	*ankyrin repeat domain 29*	-1.1655	0.4458
11726597_a_at	DUT	*deoxyuridine triphosphatase*	-1.1652	0.4459
11758216_s_at	SOX9	*SRY-box 9*	-1.1642	0.4462
11717315_a_at	DTD1	*D-tyrosyl-tRNA deacylase 1*	-1.1617	0.4470
11732925_s_at	PEAR1	*platelet endothelial aggregation receptor 1*	-1.1600	0.4475
11746200_s_at	EHD2	*EH domain containing 2*	-1.1600	0.4475
11728101_at	ZNF367	*zinc finger protein 367*	-1.1565	0.4486
11725793_s_at	PTGER4	*prostaglandin E receptor 4*	-1.1533	0.4496
11733215_a_at	STAT4	*signal transducer and activator of transcription 4*	-1.1514	0.4502
11728203_a_at	PHGDH	*phosphoglycerate dehydrogenase*	-1.1514	0.4502
11759656_a_at	KLHL7	*kelch like family member 7*	-1.1514	0.4502
11725709_a_at	WDHD1	*WD repeat and HMG-box DNA binding protein 1*	-1.1510	0.4503
11744270_a_at	SNRPA	*small nuclear ribonucleoprotein polypeptide A*	-1.1507	0.4504
11740068_at	CCDC8	*coiled-coil domain containing 8*	-1.1504	0.4505
11721702_a_at	CMTM7	*CKLF like MARVEL transmembrane domain containing 7*	-1.1498	0.4507
11741284_a_at	RFC5	*replication factor C subunit 5*	-1.1498	0.4507
11719587_a_at	MICALL1	*MICAL like 1*	-1.1494	0.4508
11748409_a_at	PLEKHG3	*pleckstrin homology and RhoGEF domain containing G3*	-1.1494	0.4508
11721070_a_at	DEF8	*differentially expressed in FDCP 8 homolog*	-1.1491	0.4509
11729707_at	FKBP1A	*FK506 binding protein 1A*	-1.1488	0.4510

11736035_a_at	**EXOSC2**	***exosome component 2***	**-1.1482**	**0.4512**
11723256_a_at	**PKMYT1**	***protein kinase, membrane associated tyrosine/threonine 1***	**-1.1469**	**0.4516**
11757751_s_at	**NRP1**	***neuropilin 1***	**-1.1411**	**0.4534**
11740062_a_at	**SIGMAR1**	***sigma non-opioid intracellular receptor 1***	**-1.1396**	**0.4539**
11723616_a_at	**PLTP**	***phospholipid transfer protein***	**-1.1396**	**0.4539**
11725117_a_at	**NLN**	***neurolysin***	**-1.1386**	**0.4542**
11757018_a_at	**COL12A1**	***collagen type XII alpha 1 chain***	**-1.1380**	**0.4544**
11726724_a_at	**CKAP2L**	***cytoskeleton associated protein 2 like***	**-1.1370**	**0.4547**
11725167_at	**MOB3B**	***MOB kinase activator 3B***	**-1.1370**	**0.4547**
11754243_a_at	**H2AFX**	***H2A histone family member X***	**-1.1361**	**0.4550**
11739782_a_at	**SNCA**	***synuclein alpha***	**-1.1354**	**0.4552**
11726136_a_at	**TMSB15A**	***thymosin beta 15a***	**-1.1348**	**0.4554**
11763856_a_at	**HOMER3**	***homer scaffolding protein 3***	**-1.1348**	**0.4554**
11724948_at	**CITED4**	***Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 4***	**-1.1338**	**0.4557**
11734804_a_at	**KIF20B**	***kinesin family member 20B***	**-1.1335**	**0.4558**
11754959_a_at	**AK4**	***adenylate kinase 4***	**-1.1316**	**0.4564**
11725052_a_at	**TOP1MT**	***Topoisomerase (DNA) I, Mitochondrial***	**-1.1304**	**0.4568**
11739932_a_at	**FAM111B**	***family with sequence similarity 111 member B***	**-1.1282**	**0.4575**
11722134_a_at	**TNFRSF25**	***TNF receptor superfamily member 25***	**-1.1272**	**0.4578**
11729886_at	**C18orf54**	***chromosome 18 open reading frame 54***	**-1.1272**	**0.4578**
11743965_s_at	**CERCAM**	***cerebral endothelial cell adhesion molecule***	**-1.1269**	**0.4579**
11724424_at	**GPR68**	***G protein-coupled receptor 68***	**-1.1247**	**0.4586**
11726217_a_at	**PRDM1**	***PR/SET domain 1***	**-1.1244**	**0.4587**
11746116_a_at	**PINX1**	***PIN2/TERF1 interacting, telomerase inhibitor 1***	**-1.1231**	**0.4591**
11757682_a_at	**CYB5R2**	***cytochrome b5 reductase 2***	**-1.1219**	**0.4595**
11763888_at	**SNORA33**	***small nucleolar RNA, H/ACA box 33***	**-1.1197**	**0.4602**
11757776_s_at	**ARG2**	***arginase 2***	**-1.1181**	**0.4607**
11735167_x_at	**RFC2**	***replication factor C subunit 2***	**-1.1172**	**0.4610**
11756878_a_at	**FBL**	***fibrillarin***	**-1.1168**	**0.4611**
11742775_a_at	**GPR161**	***G protein-coupled receptor 161***	**-1.1168**	**0.4611**
11731880_at	**NLRP1**	***NLR family pyrin domain containing 1***	**-1.1137**	**0.4621**
11743858_at	**IL33**	***interleukin 33***	**-1.1125**	**0.4625**
11746331_a_at	**ADK**	***adenosine kinase***	**-1.1122**	**0.4626**
11715430_a_at	**AKR1B1**	***aldo-keto reductase family 1 member B***	**-1.1122**	**0.4626**
11744034_a_at	**VASP**	***vasodilator-stimulated phosphoprotein***	**-1.1119**	**0.4627**
11716459_at	**TUBA4A**	***tubulin alpha 4a***	**-1.1115**	**0.4628**

11722327_at	**PGBD5**	***piggyBac transposable element derived 5***	**-1.1097**	**0.4634**
11757033_a_at	**IL13RA2**	***interleukin 13 receptor subunit alpha 2***	**-1.1097**	**0.4634**
11727536_x_at	**CCNF**	***cyclin F***	**-1.1084**	**0.4638**
11747606_a_at	**NCAPD2**	***non-SMC condensin I complex subunit D2***	**-1.1084**	**0.4638**
11743314_a_at	**FASN**	***fatty acid synthase***	**-1.1072**	**0.4642**
11753130_at	**TM4SF1**	***transmembrane 4 L six family member 1***	**-1.1062**	**0.4645**
11726963_s_at	**SGTB**	***small glutamine rich tetratricopeptide repeat containing beta***	**-1.1056**	**0.4647**
11727458_at	**KIF18A**	***kinesin family member 18A***	**-1.1053**	**0.4648**
11733320_a_at	**HRAS**	***HRas proto-oncogene, GTPase***	**-1.1035**	**0.4654**
11724551_x_at	**TMEM55A**	***transmembrane protein 55A***	**-1.1028**	**0.4656**
11728840_at	**TMCC3**	***transmembrane and coiled-coil domain family 3***	**-1.1016**	**0.4660**
11726024_at	**EDN1**	***endothelin 1***	**-1.1013**	**0.4661**
11723677_a_at	**CKAP2**	***cytoskeleton associated protein 2***	**-1.1007**	**0.4663**
11717155_a_at	**NME1**	***NME/NM23 nucleoside diphosphate kinase 1***	**-1.0994**	**0.4667**
11721843_a_at	**ATL3**	***atlastin GTPase 3***	**-1.0985**	**0.4670**
11722305_at	**ARHGAP23**	***Rho GTPase activating protein 23***	**-1.0970**	**0.4675**
11726590_at	**ELOVL4**	***ELOVL fatty acid elongase 4***	**-1.0960**	**0.4678**

11749168_a_at	**KRT6A**	***keratin 6A***	**-1.0957**	**0.4679**
11756347_x_at	**PRR11**	***proline rich 11***	**-1.0954**	**0.4680**
11729062_a_at	**PDGFA**	***platelet derived growth factor subunit A***	**-1.0951**	**0.4681**
11722225_a_at	**ADAM8**	***ADAM metallopeptidase domain 8***	**-1.0948**	**0.4682**
11745837_x_at	**FN1**	***fibronectin 1***	**-1.0945**	**0.4683**
11726551_s_at	**RAET1L**	***retinoic acid early transcript 1L***	**-1.0920**	**0.4691**
11717444_at	**BYSL**	***bystin like***	**-1.0914**	**0.4693**
11728524_a_at	**SPOCD1**	***SPOC domain containing 1***	**-1.0908**	**0.4695**
11725987_a_at	**MMP14**	***matrix metallopeptidase 14***	**-1.0883**	**0.4703**
11752370_x_at	**IMPDH2**	***inosine monophosphate dehydrogenase 2***	**-1.0874**	**0.4706**
11731987_a_at	**DNAJC9**	***DnaJ Heat Shock Protein Family (Hsp40) Member C9***	**-1.0853**	**0.4713**
11756775_a_at	**KLHL42**	***kelch like family member 42***	**-1.0850**	**0.4714**
11749354_x_at	**WDR41**	***WD repeat domain 41***	**-1.0816**	**0.4725**
11724316_a_at	**LUZP1**	***leucine zipper protein 1***	**-1.0804**	**0.4729**
11719827_a_at	**QPCT**	***glutaminyl-peptide cyclotransferase***	**-1.0804**	**0.4729**
11758780_a_at	**NOP16**	***NOP16 nucleolar protein***	**-1.0798**	**0.4731**
11729742_x_at	**IFI27L2**	***interferon alpha inducible protein 27 like 2***	**-1.0776**	**0.4738**

11717812_a_at	**KIF3C**	***kinesin family member 3C***	**-1.0770**	**0.4740**
11717409_at	**SH2B3**	***SH2B adaptor protein 3***	**-1.0758**	**0.4744**
11731134_a_at	**LTB4R**	***leukotriene B4 receptor***	**-1.0755**	**0.4745**
11739204_a_at	**TTL**	***tubulin tyrosine ligase***	**-1.0752**	**0.4746**
11734724_a_at	**IRF6**	***interferon regulatory factor 6***	**-1.0743**	**0.4749**
11728809_a_at	**COL8A1**	***collagen type VIII alpha 1 chain***	**-1.0743**	**0.4749**
11719135_a_at	**PKP1**	***plakophilin 1***	**-1.0743**	**0.4749**
11756910_x_at	**FANCD2**	***Fanconi anemia complementation group D2***	**-1.0734**	**0.4752**
11717900_at	**ASF1B**	***anti-silencing function 1B histone chaperone***	**-1.0725**	**0.4755**
11733620_a_at	**BCL11B**	***B-cell CLL/lymphoma 11B***	**-1.0719**	**0.4757**
11732684_a_at	**ABCA12**	***ATP binding cassette subfamily A member 12***	**-1.0707**	**0.4761**
11724326_a_at	**ARHGAP25**	***Rho GTPase activating protein 25***	**-1.0707**	**0.4761**
11743448_s_at	**BICD2**	***BICD cargo adaptor 2***	**-1.0704**	**0.4762**
11718813_a_at	**NECTIN1**	***nectin cell adhesion molecule 1***	**-1.0698**	**0.4764**
11721598_a_at	**EFS**	***embryonal Fyn-associated substrate***	**-1.0695**	**0.4765**
11728808_at	**CHAC2**	***ChaC cation transport regulator homolog 2***	**-1.0685**	**0.4768**
11723138_at	**POP1**	***POP1 homolog, ribonuclease P/MRP subunit***	**-1.0658**	**0.4777**

11733975_a_at	**DDHD2**	***DDHD domain containing 2***	**-1.0646**	**0.4781**
11732425_at	**ANKRD22**	***ankyrin repeat domain 22***	**-1.0640**	**0.4783**
11730390_at	**SEMA3A**	***semaphorin 3A***	**-1.0628**	**0.4787**
11726433_a_at	**OSBPL3**	***oxysterol binding protein like 3***	**-1.0616**	**0.4791**
11741434_s_at	**SEPT10**	***septin 10***	**-1.0577**	**0.4804**
11752877_x_at	**TUBB**	***tubulin beta class I***	**-1.0574**	**0.4805**
11737795_a_at	**KIAA1524**	***KIAA1524***	**-1.0568**	**0.4807**
11716234_s_at	**CTNNBIP1**	***catenin beta interacting protein 1***	**-1.0565**	**0.4808**
11717833_a_at	**TEX10**	***testis expressed 10***	**-1.0562**	**0.4809**
11722931_a_at	**GART**	***phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase***	**-1.0553**	**0.4812**
11744146_x_at	**RBM3**	***RNA Binding Motif (RNP1, RRM) Protein 3***	**-1.0538**	**0.4817**
11754556_x_at	**EIF2AK4**	***eukaryotic translation initiation factor 2 alpha kinase 4***	**-1.0532**	**0.4819**
11729173_a_at	**SKA2**	***spindle and kinetochore associated complex subunit 2***	**-1.0526**	**0.4821**
11747989_a_at	**TEAD2**	***TEA domain transcription factor 2***	**-1.0520**	**0.4823**
11722721_a_at	**CENPV**	***centromere protein V***	**-1.0502**	**0.4829**
11726438_a_at	**MALT1**	***MALT1 paracaspase***	**-1.0493**	**0.4832**
11755059_s_at	**TCF3**	***transcription factor 3***	**-1.0490**	**0.4833**

11722236_at	**FBXO2**	***F-box protein 2***	**-1.0490**	**0.4833**
11753582_x_at	**PTTG3P**	***pituitary tumor-transforming 3, pseudogene***	**-1.0454**	**0.4845**
11735692_a_at	**RAP1GDS1**	***Rap1 GTPase-GDP dissociation stimulator 1***	**-1.0451**	**0.4846**
11746339_a_at	**MTSS1**	***MTSS1, I-BAR domain containing***	**-1.0445**	**0.4848**
11726723_a_at	**WDFY2**	***WD repeat and FYVE domain containing 2***	**-1.0442**	**0.4849**
11720403_at	**EFNB2**	***ephrin B2***	**-1.0439**	**0.4850**
11721554_a_at	**COLGALT1**	***Collagen Beta(1-O)Galactosyltransferase 1***	**-1.0436**	**0.4851**
11734701_a_at	**DKK3**	***dickkopf WNT signaling pathway inhibitor 3***	**-1.0428**	**0.4854**
11716494_a_at	**MAP4**	***microtubule associated protein 4***	**-1.0425**	**0.4855**
11728832_at	**DSG3**	***desmoglein 3***	**-1.0419**	**0.4857**
11736570_a_at	**SLC39A14**	***solute carrier family 39 member 14***	**-1.0416**	**0.4858**
11726186_x_at	**PARPBP**	***PARP1 binding protein***	**-1.0413**	**0.4859**
11757715_a_at	**MIR205**	***microRNA 205***	**-1.0410**	**0.4860**
11737748_a_at	**GMFB**	***glia maturation factor beta***	**-1.0407**	**0.4861**
11736424_a_at	**STARD4**	***StAR related lipid transfer domain containing 4***	**-1.0407**	**0.4861**
11743084_s_at	**BNIP3**	***BCL2 interacting protein 3***	**-1.0404**	**0.4862**
11717345_a_at	**FOSB**	***FosB proto-oncogene, AP-1 transcription factor subunit***	**-1.0404**	**0.4862**

11721806_a_at	**EMC1**	***ER membrane protein complex subunit 1***	**-1.0398**	**0.4864**
11751697_a_at	**NAA50**	***N(Alpha)-Acetyltransferase 50, NatE Catalytic Subunit***	**-1.0389**	**0.4867**
11754678_a_at	**SLC25A43**	***solute carrier family 25 member 43***	**-1.0386**	**0.4868**
11715919_a_at	**SH3BGRL3**	***SH3 domain binding glutamate rich protein like 3***	**-1.0380**	**0.4870**
11719411_at	**RAB32**	***RAB32, member RAS oncogene family***	**-1.0380**	**0.4870**
11757302_s_at	**GMPS**	***guanine monophosphate synthase***	**-1.0377**	**0.4871**
11757556_s_at	**BLMH**	***bleomycin hydrolase***	**-1.0368**	**0.4874**
11755027_a_at	**TGFB1I1**	***transforming growth factor beta 1 induced transcript 1***	**-1.0368**	**0.4874**
11734553_s_at	**ANXA8**	***annexin A8***	**-1.0342**	**0.4883**
11744488_a_at	**ACOT9**	***acyl-CoA thioesterase 9***	**-1.0315**	**0.4892**
11750151_a_at	**HAUS6**	***HAUS augmin like complex subunit 6***	**-1.0309**	**0.4894**
11724505_at	**MIS18A**	***MIS18 kinetochore protein A***	**-1.0289**	**0.4901**
11723414_a_at	**CNN2**	***calponin 2***	**-1.0277**	**0.4905**
11729156_a_at	**SLC25A32**	***solute carrier family 25 member 32***	**-1.0259**	**0.4911**
11744325_a_at	**STRIP2**	***striatin interacting protein 2***	**-1.0241**	**0.4917**
11720213_x_at	**PPAN**	***Peter Pan Homolog (Drosophila)***	**-1.0241**	**0.4917**
11742436_at	**SLC6A15**	***solute carrier family 6 member 15***	**-1.0224**	**0.4923**

11760362_x_at	**PGAM5**	***PGAM family member 5, mitochondrial serine/threonine protein phosphatase***	**-1.0224**	**0.4923**
11725291_at	**FUT1**	***Fucosyltransferase 1 (H Blood Group)***	**-1.0215**	**0.4926**
11720948_a_at	**CA12**	***carbonic anhydrase 12***	**-1.0215**	**0.4926**
11755028_a_at	**DENND1A**	***DENN domain containing 1A***	**-1.0209**	**0.4928**
11752051_a_at	**MYH9**	***myosin heavy chain 9***	**-1.0206**	**0.4929**
11723860_a_at	**MPP6**	***membrane palmitoylated protein 6***	**-1.0183**	**0.4937**
11724005_s_at	**FYB**	***FYN binding protein***	**-1.0180**	**0.4938**
11744135_a_at	**MIB2**	***mindbomb E3 ubiquitin protein ligase 2***	**-1.0177**	**0.4939**
11719365_x_at	**SPATS2L**	***spermatogenesis associated serine rich 2 like***	**-1.0168**	**0.4942**
11747298_a_at	**S100A16**	***S100 calcium binding protein A16***	**-1.0160**	**0.4945**
11725382_a_at	**RAPGEF3**	***Rap guanine nucleotide exchange factor 3***	**-1.0160**	**0.4945**
11719750_s_at	**POLE**	***DNA polymerase epsilon, catalytic subunit***	**-1.0154**	**0.4947**
11755137_a_at	**MCUB**	***mitochondrial calcium uniporter dominant negative beta subunit***	**-1.0145**	**0.4950**
11720382_at	**STX6**	***syntaxin 6***	**-1.0130**	**0.4955**
11726174_at	**SAMD5**	***sterile alpha motif domain containing 5***	**-1.0104**	**0.4964**
11732142_at	**TSR1**	***TSR1, ribosome maturation factor***	**-1.0087**	**0.4970**
11716148_a_at	**TRAF3IP2**	***TRAF3 interacting protein 2***	**-1.0081**	**0.4972**

11718422_s_at	**CCNB1IP1**	***cyclin B1 interacting protein 1***	**-1.0075**	**0.4974**
11717656_a_at	**SPRED2**	***sprouty related EVH1 domain containing 2***	**-1.0069**	**0.4976**
11721115_at	**SPCS3**	***signal peptidase complex subunit 3***	**-1.0058**	**0.4980**
11737787_at	**SHISA5**	***shisa family member 5***	**-1.0055**	**0.4981**
11719067_s_at	**EIF2S3**	***eukaryotic translation initiation factor 2 subunit gamma***	**-1.0049**	**0.4983**
11721278_s_at	**SUV39H1**	***suppressor of variegation 3-9 homolog 1***	**-1.0046**	**0.4984**
11759185_at	**GPR153**	***G protein-coupled receptor 153***	**-1.0046**	**0.4984**
11717161_at	**RRAS**	***Related RAS Viral (R-Ras) Oncogene Homolog***	**-1.0038**	**0.4987**
11734988_s_at	**FEM1B**	***fem-1 homolog B***	**-1.0029**	**0.4990**
11736226_a_at	**SPATS2**	***spermatogenesis associated serine rich 2***	**-1.0026**	**0.4991**
11719949_a_at	**SPDL1**	***spindle apparatus coiled-coil protein 1***	**-1.0023**	**0.4992**
11725161_a_at	**DDIAS**	***DNA damage induced apoptosis suppressor***	**-1.0017**	**0.4994**
11742698_at	**SCG5**	***secretogranin V***	**-1.0014**	**0.4995**
11745958_a_at	**CD99**	***CD99 molecule***	**-1.0014**	**0.4995**
11726245_s_at	**HIST4H4**	***histone cluster 4 H4***	**-1.0009**	**0.4997**
11758448_s_at	**TMED7-TICAM2**	***TMED7-TICAM2 readthrough***	**-1.0009**	**0.4997**
11743466_at	**MPHOSPH6**	***M-phase phosphoprotein 6***	**-1.0009**	**0.4997**

***Diferentially expressed mRNAs were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ([Log_2Ratio > 1] or [Log_2Ratio < -1] for both upregulated or downregulated mRNAs, respectively), followed by multiple correction using a False Discovery Rate (FDR) threshold of 1% (p-adjusted value or q < 0.01).**

TABLE S3. Differentially expressed mRNAs in CRSwNP air-liquid interface culture after 14 days of differentiation compared to day 0 (monolayer of hNP-BSCs).*

UPREGULATED mRNAs (684)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11721175_at	RARRES1	*retinoic acid receptor responder 1*	5.7587	54.1429
11726981_a_at	CP	*ceruloplasmin*	5.6304	49.5345
11727698_a_at	VMO1	*vitelline membrane outer layer 1 homolog*	5.4537	43.8258
11716109_a_at	PIGR	*polymeric immunoglobulin receptor*	5.0101	32.2259
11724692_a_at	CAPN13	*calpain 13*	4.9243	30.3644
11726124_at	TCN1	*transcobalamin 1*	4.7755	27.3883
11749912_x_at	IGFBP3	*insulin like growth factor binding protein 3*	4.7174	26.3076
11727440_at	LOXL4	*lysyl oxidase like 4*	4.6543	25.1809
11728771_a_at	CLCA4	*chloride channel accessory 4*	4.5972	24.2037
11719818_at	PIP	*prolactin induced protein*	4.5920	24.1177
11716490_a_at	SERPINA3	*serpin family A member 3*	4.3978	21.0795
11724085_at	DAPL1	*death associated protein like 1*	4.3859	20.9070
11723642_a_at	BPIFA1	*BPI fold containing family A member 1*	4.3402	20.2548
11758952_at	AGR2	*anterior gradient 2, protein disulphide isomerase family member*	4.2056	18.4510
11720917_a_at	BPIFB1	*BPI fold containing family B member 1*	4.2010	18.3916
11721895_x_at	GAS1	*growth arrest specific 1*	4.1815	18.1454
11744030_a_at	MMP7	*matrix metallopeptidase 7*	4.0233	16.2609
11727454_at	SCGB1A1	*secretoglobin family 1A member 1*	3.9946	15.9406
11733725_a_at	CFB	*complement factor B*	3.9297	15.2388
11732657_a_at	CYP26A1	*cytochrome P450 family 26 subfamily A member 1*	3.8956	14.8834
11719657_a_at	MMP9	*matrix metallopeptidase 9*	3.8732	14.6534
11722838_a_at	GABRP	*gamma-aminobutyric acid type A receptor pi subunit*	3.8140	14.0646
11744556_x_at	CYP2B7P	*cytochrome P450 family 2 subfamily B member 7, pseudogene*	3.7281	13.2517
11753201_a_at	SERPINB3	*serpin family B member 3*	3.5463	11.6829
11758272_at	SLC34A2	*solute carrier family 34 member 2*	3.4326	10.7976
11750860_a_at	CMAHP	*cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene*	3.3975	10.5378
11722054_a_at	CYP4X1	*cytochrome P450 family 4 subfamily X member 1*	3.3074	9.9000
11727966_a_at	MSMB	*microseminoprotein beta*	3.3004	9.8519
11729692_a_at	SERPINB3	*serpin family B member 3*	3.2852	9.7488
11739440_a_at	KRT4	*keratin 4*	3.2387	9.4394
11732460_a_at	PLEKHS1	*pleckstrin homology domain containing S1*	3.2203	9.3198
11723899_a_at	DHRS9	*dehydrogenase/reductase 9*	3.1973	9.1726
11717820_a_at	SLC4A4	*solute carrier family 4 member 4*	3.1718	9.0116
11718722_at	PSCA	*prostate stem cell antigen*	3.1652	8.9707
11754888_a_at	ADSSL1	*adenylosuccinate synthase like 1*	3.1621	8.9515
11724762_a_at	DEPTOR	*DEP domain containing MTOR-interacting protein*	3.1588	8.9306
11743003_a_at	CYP4B1	*cytochrome P450 family 4 subfamily B member 1*	3.1568	8.9186

11743044_a_at	ALDH1A1	*aldehyde dehydrogenase 1 family member A1*	3.1369	8.7962
11734503_x_at	ALOX15	*arachidonate 15-lipoxygenase*	3.1139	8.6569
11718481_s_at	CFI	*complement factor I*	3.1078	8.6206
11727281_a_at	MMP28	*matrix metallopeptidase 28*	3.1046	8.6013
11731657_s_at	VAV3	*vav guanine nucleotide exchange factor 3*	3.0897	8.5134
11731722_a_at	ALDH3B1	*aldehyde dehydrogenase 3 family member B1*	3.0578	8.3268
11758544_s_at	RDH10	*Retinol Dehydrogenase 10*	3.0381	8.2140
11730245_a_at	FMO2	*flavin containing monooxygenase 2*	3.0211	8.1178
11758013_s_at	C8orf4	*chromosome 8 open reading frame 4*	3.0188	8.1049
11716401_a_at	SELENBP1	*selenium binding protein 1*	3.0074	8.0412
11717917_a_at	WFDC2	*WAP four-disulfide core domain 2*	2.9868	7.9270
11715994_x_at	ID2	*inhibitor of DNA binding 2, HLH protein*	2.9837	7.9101
11717595_s_at	ELF3	*E74 like ETS transcription factor 3*	2.9742	7.8582
11736917_at	LYPD2	*LY6/PLAUR domain containing 2*	2.9725	7.8491
11744484_s_at	HLA-DRA	*major histocompatibility complex, class II, DR alpha*	2.9449	7.7004
11756098_a_at	SYTL5	*synaptotagmin like 5*	2.9369	7.6576
11753973_x_at	MUC1	*mucin 1, cell surface associated*	2.9070	7.5008
11755202_a_at	VTCN1	*V-set domain containing T cell activation inhibitor 1*	2.9023	7.4764
11727243_a_at	WNT4	*Wnt family member 4*	2.8831	7.3774
11758221_s_at	ARRDC3	*arrestin domain containing 3*	2.8753	7.3377
11758196_s_at	IGFBP5	*insulin like growth factor binding protein 5*	2.8716	7.3187
11733687_s_at	STRA6	*stimulated by retinoic acid 6*	2.8584	7.2519
11728753_at	ADH7	*Alcohol Dehydrogenase 7 (Class IV), Mu Or Sigma Polypeptide*	2.8045	6.9862
11756547_a_at	CLU	*clusterin*	2.8002	6.9654
11729770_at	BPIFA2	*BPI fold containing family A member 2*	2.7920	6.9261
11755588_a_at	SLC5A5	*solute carrier family 5 member 5*	2.7731	6.8356
11739761_a_at	CLDN10	*claudin 10*	2.7686	6.8146
11729297_at	MMP13	*matrix metallopeptidase 13*	2.7613	6.7801
11733474_at	SOX21	*SRY-box 21*	2.7432	6.6955
11747509_a_at	FAM107B	*family with sequence similarity 107 member B*	2.7362	6.6631
11744104_a_at	TMC5	*transmembrane channel like 5*	2.7067	6.5284
11734552_a_at	CX3CL1	*C-X3-C motif chemokine ligand 1*	2.6731	6.3780
11723441_a_at	EPHA4	*EPH receptor A4*	2.6651	6.3428
11717885_a_at	CCDC3	*coiled-coil domain containing 3*	2.6586	6.3142
11724795_at	ZG16B	*zymogen granule protein 16B*	2.6419	6.2417
11759322_at	BCL6	*B-cell CLL/lymphoma 6*	2.6289	6.1854
11763986_a_at	APOL1	*apolipoprotein L1*	2.6280	6.1815
11748046_a_at	SLC44A4	*solute carrier family 44 member 4*	2.6154	6.1278
11724720_a_at	GALNT12	*polypeptide N-acetylgalactosaminyltransferase 12*	2.6143	6.1233
11730801_at	CXCL6	*C-X-C motif chemokine ligand 6*	2.5647	5.9162
11757815_s_at	METTL7A	*methyltransferase like 7A*	2.5634	5.9111
11719394_a_at	FBXO32	*F-box protein 32*	2.5620	5.9051

11719658_a_at	TF	*transferrin*	2.5556	5.8792
11717465_s_at	LXN	*latexin*	2.5329	5.7874
11715788_a_at	SLC40A1	*solute carrier family 40 member 1*	2.5323	5.7851
11743168_at	IDO1	*indoleamine 2,3-dioxygenase 1*	2.5312	5.7806
11737791_s_at	APOL2	*apolipoprotein L2*	2.4964	5.6427
11723069_at	UBD	*ubiquitin D*	2.4902	5.6187
11722116_a_at	RARB	*retinoic acid receptor beta*	2.4879	5.6096
11755748_s_at	PLAC8	*placenta specific 8*	2.4719	5.5479
11723404_at	PPARGC1A	*PPARG coactivator 1 alpha*	2.4697	5.5394
11721456_x_at	SERPINA1	*serpin family A member 1*	2.4656	5.5236
11719307_a_at	RASSF4	*Ras association domain family member 4*	2.4144	5.3310
11756588_a_at	ST6GALNAC1	*ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1*	2.4115	5.3203
11724875_a_at	CD36	*CD36 molecule*	2.4074	5.3053
11756191_a_at	MAN1C1	*mannosidase alpha class 1C member 1*	2.3965	5.2654
11726434_at	CHL1	*cell adhesion molecule L1 like*	2.3946	5.2583
11725892_a_at	PLEKHH1	*pleckstrin homology, MyTH4 and FERM domain containing H1*	2.3869	5.2304
11719692_a_at	RARRES3	*retinoic acid receptor responder 3*	2.3682	5.1629
11723367_a_at	RAB26	*RAB26, member RAS oncogene family*	2.3676	5.1607
11724528_a_at	GCNT3	*Glucosaminyl (N-Acetyl) Transferase 3, Mucin Type*	2.3492	5.0954
11719265_a_at	MLPH	*melanophilin*	2.3422	5.0708
11725789_at	DPYD	*dihydropyrimidine dehydrogenase*	2.3376	5.0546
11730779_at	ADH1C	*Alcohol Dehydrogenase 1C (Class I), Gamma Polypeptide*	2.3322	5.0359
11754526_a_at	PTGES	*prostaglandin E synthase*	2.3214	4.9983
11722994_s_at	ADH1A	*Alcohol Dehydrogenase 1A (Class I), Alpha Polypeptide*	2.3198	4.9928
11739916_a_at	SERPINB11	*Serpin Family B Member 11 (Gene/Pseudogene)*	2.3170	4.9829
11721267_s_at	TMPRSS4	*transmembrane protease, serine 4*	2.3095	4.9571
11721531_a_at	AQP5	*aquaporin 5*	2.3088	4.9548
11717720_a_at	ST6GAL1	*ST6 beta-galactoside alpha-2,6-sialyltransferase 1*	2.3083	4.9531
11726054_a_at	MUC4	*mucin 4, cell surface associated*	2.3071	4.9488
11722758_at	NPR3	*natriuretic peptide receptor 3*	2.3060	4.9451
11744138_at	CAMK1D	*calcium/calmodulin dependent protein kinase ID*	2.2975	4.9161
11736678_s_at	PODXL	*podocalyxin like*	2.2880	4.8839
11726051_a_at	FMO3	*flavin containing monooxygenase 3*	2.2864	4.8784
11716835_a_at	DHRS3	*dehydrogenase/reductase 3*	2.2771	4.8470
11730214_at	DUOX2	*dual oxidase 2*	2.2741	4.8368
11736275_x_at	CEL	*carboxyl ester lipase*	2.2642	4.8039
11755671_a_at	SYTL2	*synaptotagmin like 2*	2.2604	4.7911
11716532_a_at	EGFL6	*EGF like domain multiple 6*	2.2601	4.7904
11725922_a_at	CLIC6	*chloride intracellular channel 6*	2.2531	4.7672
11723785_s_at	LIMCH1	*LIM and calponin homology domains 1*	2.2355	4.7093
11758134_s_at	PPM1H	*protein phosphatase, Mg2+/Mn2+ dependent 1H*	2.2312	4.6954
11758070_s_at	PBX1	*PBX homeobox 1*	2.2202	4.6595

11739045_a_at	SLC15A2	*solute carrier family 15 member 2*	2.2201	4.6594
11741874_x_at	SELENOP	*selenoprotein P*	2.2139	4.6392
11757570_s_at	PRR15	*proline rich 15*	2.2120	4.6332
11719447_s_at	GBP2	*guanylate binding protein 2*	2.2035	4.6061
11730467_at	NTN1	*netrin 1*	2.2007	4.5970
11746144_a_at	PTPRZ1	*protein tyrosine phosphatase, receptor type Z1*	2.1880	4.5567
11740326_x_at	SORBS2	*sorbin and SH3 domain containing 2*	2.1874	4.5549
11720007_a_at	STEAP4	*STEAP4 metalloreductase*	2.1801	4.5318
11725662_a_at	SLC16A14	*solute carrier family 16 member 14*	2.1774	4.5233
11725474_a_at	MAP3K5	*mitogen-activated protein kinase 5*	2.1765	4.5205
11728163_a_at	HSD17B3	*hydroxysteroid 17-beta dehydrogenase 3*	2.1727	4.5087
11743657_x_at	HPGD	*hydroxyprostaglandin dehydrogenase 15-*	2.1713	4.5042
11718213_a_at	SLC27A2	*solute carrier family 27 member 2*	2.1468	4.4285
11717582_a_at	RGCC	*regulator of cell cycle*	2.1335	4.3878
11730881_a_at	NEBL	*nebulette*	2.1330	4.3863
11730632_a_at	OCA2	*OCA2 melanosomal transmembrane protein*	2.1211	4.3504
11721572_at	C10orf99	*chromosome 10 open reading frame 99*	2.1184	4.3422
11764253_s_at	IFITM10	*interferon induced transmembrane protein 10*	2.1184	4.3421
11744063_a_at	MUC5B	*mucin 5B, oligomeric mucus/gel-forming*	2.0991	4.2844
11719538_at	BBOX1	*gamma-butyrobetaine hydroxylase 1*	2.0987	4.2833
11747755_a_at	KRT13	*keratin 13*	2.0983	4.2819
11732350_a_at	CCNA1	*cyclin A1*	2.0979	4.2808
11758031_s_at	BHLHE41	*basic helix-loop-helix family member e41*	2.0973	4.2791
11731096_at	WNT10A	*Wnt family member 10A*	2.0932	4.2668
11722860_a_at	TRIM2	*tripartite motif containing 2*	2.0905	4.2590
11715393_a_at	C3	*complement C3*	2.0858	4.2452
11726916_at	SLCO4C1	*solute carrier organic anion transporter family member 4C1*	2.0851	4.2431
11715343_at	MUC16	*mucin 16, cell surface associated*	2.0823	4.2347
11736746_a_at	ADAM28	*ADAM metallopeptidase domain 28*	2.0755	4.2149
11732521_a_at	CHST9	*carbohydrate sulfotransferase 9*	2.0732	4.2082
11748543_a_at	TXNIP	*thioredoxin interacting protein*	2.0719	4.2044
11756312_a_at	SERPINF1	*serpin family F member 1*	2.0658	4.1867
11720139_a_at	VSTM2L	*V-set and transmembrane domain containing 2 like*	2.0651	4.1846
11751791_a_at	CCDC80	*coiled-coil domain containing 80*	2.0634	4.1797
11724515_a_at	GPD1L	*glycerol-3-phosphate dehydrogenase 1-like*	2.0594	4.1681
11729025_a_at	ILDR1	*immunoglobulin like domain containing receptor 1*	2.0423	4.1190
11750205_a_at	BCAS1	*breast carcinoma amplified sequence 1*	2.0395	4.1111
11726896_a_at	IRAK3	*interleukin 1 receptor associated kinase 3*	2.0387	4.1088
11728200_a_at	LOX	*lysyl oxidase*	2.0369	4.1035
11740782_a_at	RNF128	*ring finger protein 128, E3 ubiquitin protein ligase*	2.0242	4.0676
11728239_at	RRAGD	*Ras related GTP binding D*	2.0145	4.0404
11723878_a_at	ATP7B	*ATPase copper transporting beta*	1.9973	3.9925

11744969_a_at	PAPLN	papilin, proteoglycan like sulfated glycoprotein	1.9948	3.9857
11743321_at	CTSO	cathepsin O	1.9877	3.9660
11722310_a_at	TMC4	transmembrane channel like 4	1.9750	3.9313
11755020_a_at	SLC46A3	solute carrier family 46 member 3	1.9746	3.9303
11727132_at	CPD	carboxypeptidase D	1.9668	3.9091
11732240_a_at	SLITRK6	SLIT and NTRK like family member 6	1.9611	3.8936
11743071_a_at	LPAR6	lysophosphatidic acid receptor 6	1.9600	3.8906
11729998_a_at	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	1.9598	3.8902
11723845_a_at	DEFB1	defensin beta 1	1.9524	3.8702
11758468_s_at	TSHZ2	teashirt zinc finger homeobox 2	1.9464	3.8542
11742378_a_at	AKR1B15	aldo-keto reductase family 1 member B15	1.9304	3.8117
11723063_a_at	GCHFR	GTP cyclohydrolase I feedback regulator	1.9294	3.8089
11726029_a_at	UPK1B	uroplakin 1B	1.9239	3.7944
11740995_x_at	GLUL	glutamate-ammonia ligase	1.9224	3.7904
11739375_at	SYT7	synaptotagmin 7	1.9143	3.7692
11730374_a_at	FYB	FYN binding protein	1.9104	3.7591
11724796_at	DDIT4L	DNA damage inducible transcript 4 like	1.8988	3.7289
11734614_a_at	GABRE	gamma-aminobutyric acid type A receptor epsilon subunit	1.8941	3.7169
11716554_a_at	HLA-DMA	major histocompatibility complex, class II, DM alpha	1.8919	3.7112
11760254_at	IFI44	interferon induced protein 44	1.8915	3.7101
11732060_a_at	LEMD1	LEM domain containing 1	1.8884	3.7022
11743576_at	CPE	carboxypeptidase E	1.8835	3.6898
11734619_x_at	ALOX15B	arachidonate 15-lipoxygenase, type B	1.8830	3.6883
11754640_a_at	EPHX2	epoxide hydrolase 2	1.8825	3.6872
11718302_at	HSD11B2	hydroxysteroid 11-beta dehydrogenase 2	1.8757	3.6697
11727918_s_at	MUC20	mucin 20, cell surface associated	1.8730	3.6630
11754734_a_at	ATP6V1C2	ATPase H+ transporting V1 subunit C2	1.8718	3.6598
11756766_x_at	CD74	CD74 molecule	1.8694	3.6537
11754461_s_at	UCP2	uncoupling protein 2	1.8661	3.6454
11721460_s_at	TAPBPL	TAP binding protein like	1.8659	3.6449
11744508_a_at	CCDC146	coiled-coil domain containing 146	1.8650	3.6427
11754354_s_at	PROM1	prominin 1	1.8615	3.6338
11758053_s_at	NCOA4	nuclear receptor coactivator 4	1.8565	3.6212
11724219_x_at	GSTA1	glutathione S-transferase alpha 1	1.8564	3.6211
11720387_a_at	MRC2	mannose receptor C type 2	1.8563	3.6208
11715411_a_at	EPAS1	endothelial PAS domain protein 1	1.8536	3.6141
11720713_a_at	KCNE3	potassium voltage-gated channel subfamily E regulatory subunit 3	1.8494	3.6035
11754627_s_at	RAB37	RAB37, member RAS oncogene family	1.8446	3.5916
11754650_a_at	ATP10B	ATPase Phospholipid Transporting 10B (Putative)	1.8437	3.5892
11757383_a_at	CTSH	cathepsin H	1.8410	3.5827
11721539_at	RAB15	RAB15, member RAS oncogene family	1.8350	3.5677
11753661_a_at	ID1	inhibitor of DNA binding 1, HLH protein	1.8303	3.5561

11754601_s_at	LOC100130872	*uncharacterized LOC100130872*	1.8302	3.5558
11730310_at	TFCP2L1	*transcription factor CP2 like 1*	1.8254	3.5441
11747104_s_at	CYP1B1	*cytochrome P450 family 1 subfamily B member 1*	1.8186	3.5274
11764077_s_at	EDIL3	*EGF like repeats and discoidin domains 3*	1.8173	3.5243
11722852_s_at	BIRC3	*baculoviral IAP repeat containing 3*	1.8170	3.5235
11741065_a_at	EPHX1	*epoxide hydrolase 1*	1.8155	3.5199
11716609_a_at	CRABP2	*cellular retinoic acid binding protein 2*	1.8125	3.5126
11722597_a_at	ACKR3	*atypical chemokine receptor 3*	1.8120	3.5114
11715490_s_at	AMY1A	*Amylase, Alpha 1A (Salivary)*	1.8094	3.5050
11732444_a_at	RBPMS	*RNA binding protein with multiple splicing*	1.8069	3.4989
11731200_a_at	TLR5	*toll like receptor 5*	1.7975	3.4761
11757612_a_at	ASRGL1	*asparaginase like 1*	1.7950	3.4701
11727239_a_at	C4orf19	*chromosome 4 open reading frame 19*	1.7922	3.4634
11728363_s_at	IL20RA	*interleukin 20 receptor subunit alpha*	1.7920	3.4629
11724832_at	STS	*Steroid Sulfatase (Microsomal), Isozyme S*	1.7878	3.4528
11720993_at	SOX2	*SRY-box 2*	1.7836	3.4428
11734454_a_at	WFDC3	*WAP four-disulfide core domain 3*	1.7769	3.4268
11724490_x_at	AKR1B10	*aldo-keto reductase family 1 member B10*	1.7734	3.4185
11728523_a_at	MYCL	*v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog*	1.7699	3.4102
11720146_a_at	DAPK1	*death associated protein kinase 1*	1.7654	3.3997
11757005_a_at	FUCA1	*fucosidase, alpha-L- 1, tissue*	1.7595	3.3857
11731248_a_at	TMEM116	*transmembrane protein 116*	1.7572	3.3804
11721318_at	PARM1	*prostate androgen-regulated mucin-like protein 1*	1.7545	3.3742
11754735_s_at	ABCA13	*ATP binding cassette subfamily A member 13*	1.7527	3.3700
11751415_a_at	TSC22D3	*TSC22 domain family member 3*	1.7522	3.3687
11718201_at	HEY1	*hes related family bHLH transcription factor with YRPW motif 1*	1.7500	3.3637
11749583_a_at	FUT2	*fucosyltransferase 2*	1.7497	3.3629
11734214_a_at	MPP7	*membrane palmitoylated protein 7*	1.7464	3.3551
11715752_at	TSPAN7	*tetraspanin 7*	1.7439	3.3495
11732565_at	SLC6A14	*solute carrier family 6 member 14*	1.7426	3.3464
11754316_a_at	PIK3R3	*phosphoinositide-3-kinase regulatory subunit 3*	1.7426	3.3463
11729400_at	PCP4L1	*Purkinje cell protein 4 like 1*	1.7383	3.3365
11719176_a_at	GPRC5B	*G protein-coupled receptor class C group 5 member B*	1.7281	3.3128
11757645_s_at	FIBIN	*Fin Bud Initiation Factor Homolog (Zebrafish)*	1.7272	3.3108
11758588_s_at	SORCS2	*sortilin related VPS10 domain containing receptor 2*	1.7130	3.2785
11763360_a_at	VSIG2	*V-set and immunoglobulin domain containing 2*	1.6981	3.2447
11741221_a_at	COLCA2	*colorectal cancer associated 2*	1.6969	3.2420
11721898_at	FAM3D	*family with sequence similarity 3 member D*	1.6967	3.2416
11722242_at	TSPAN12	*tetraspanin 12*	1.6943	3.2363
11745242_a_at	TNFRSF21	*TNF receptor superfamily member 21*	1.6933	3.2339
11723687_a_at	FAM46A	*family with sequence similarity 46 member A*	1.6918	3.2306
11718651_at	TMTC1	*transmembrane and tetratricopeptide repeat containing 1*	1.6893	3.2250

11735726_a_at	SERPINB13	*serpin family B member 13*	1.6844	3.2141
11742700_s_at	C1R	*complement C1r*	1.6820	3.2088
11730265_x_at	CCDC69	*coiled-coil domain containing 69*	1.6753	3.1939
11725225_at	CHP2	*calcineurin like EF-hand protein 2*	1.6696	3.1813
11720857_a_at	INSR	*insulin receptor*	1.6695	3.1810
11749550_a_at	SCPEP1	*serine carboxypeptidase 1*	1.6628	3.1662
11739882_a_at	GLIS3	*GLIS family zinc finger 3*	1.6575	3.1546
11721688_at	ID4	*inhibitor of DNA binding 4, HLH protein*	1.6558	3.1509
11723007_a_at	DYX1C1-CCPG1	*DYX1C1-CCPG1 Readthrough (NMD Candidate)*	1.6548	3.1489
11722783_at	FOXQ1	*forkhead box Q1*	1.6535	3.1460
11755255_a_at	BAG1	*BCL2 associated athanogene 1*	1.6506	3.1397
11755044_x_at	GSAP	*gamma-secretase activating protein*	1.6439	3.1252
11740755_a_at	LYNX1	*Ly6/neurotoxin 1*	1.6437	3.1246
11727500_at	ALDH3B2	*aldehyde dehydrogenase 3 family member B2*	1.6411	3.1190
11743417_a_at	P3H2	*prolyl 3-hydroxylase 2*	1.6410	3.1188
11741519_s_at	CD14	*CD14 molecule*	1.6410	3.1188
11747474_a_at	NR4A2	*nuclear receptor subfamily 4 group A member 2*	1.6400	3.1167
11728939_at	RASEF	*RAS and EF-hand domain containing*	1.6365	3.1090
11743286_at	DTX4	*deltex E3 ubiquitin ligase 4*	1.6333	3.1023
11723163_s_at	NR3C2	*nuclear receptor subfamily 3 group C member 2*	1.6257	3.0860
11743087_at	PPBP	*pro-platelet basic protein*	1.6256	3.0857
11757307_s_at	CTSD	*cathepsin D*	1.6245	3.0834
11727906_at	MMP10	*matrix metallopeptidase 10*	1.6240	3.0822
11742816_a_at	FAM13A	*family with sequence similarity 13 member A*	1.6219	3.0778
11719148_a_at	ARRDC2	*arrestin domain containing 2*	1.6216	3.0772
11722743_a_at	TLE2	*transducin like enhancer of split 2*	1.6212	3.0764
11734939_a_at	SLC16A9	*solute carrier family 16 member 9*	1.6155	3.0642
11751769_a_at	LOC100287413	*uncharacterized LOC100287413*	1.6150	3.0631
11721957_at	YPEL2	*yippee like 2*	1.6129	3.0587
11727146_at	GPR160	*G protein-coupled receptor 160*	1.6073	3.0468
11725022_a_at	VILL	*villin like*	1.6072	3.0467
11742813_at	SEMA6A	*semaphorin 6A*	1.6071	3.0463
11719761_at	ARRDC4	*arrestin domain containing 4*	1.6050	3.0420
11720134_s_at	PROS1	*Protein S (Alpha)*	1.5996	3.0305
11743731_a_at	TNFSF10	*tumor necrosis factor superfamily member 10*	1.5993	3.0300
11737992_s_at	GPR37	*G protein-coupled receptor 37*	1.5975	3.0261
11717742_a_at	GPRC5C	*G protein-coupled receptor class C group 5 member C*	1.5935	3.0179
11719499_at	MAOB	*monoamine oxidase B*	1.5930	3.0167
11733530_at	C1RL	*complement C1r subcomponent like*	1.5918	3.0142
11731126_at	GXYLT2	*glucoside xylosyltransferase 2*	1.5887	3.0078
11724909_a_at	TMPRSS2	*transmembrane protease, serine 2*	1.5887	3.0077
11740565_at	PNLIPRP3	*pancreatic lipase related protein 3*	1.5884	3.0071

11727296_s_at	TGFB3	*transforming growth factor beta 3*	1.5844	2.9988
11729976_a_at	PTPRN2	*protein tyrosine phosphatase, receptor type N2*	1.5763	2.9820
11720105_a_at	SLC26A2	*solute carrier family 26 member 2*	1.5758	2.9810
11727186_a_at	WNT5A	*Wnt family member 5A*	1.5689	2.9667
11724476_a_at	MTUS1	*microtubule associated tumor suppressor 1*	1.5670	2.9629
11746991_a_at	ATP1B1	*ATPase Na+/K+ transporting subunit beta 1*	1.5588	2.9461
11748751_a_at	GPNMB	*glycoprotein nmb*	1.5540	2.9362
11737749_a_at	SGK1	*serum/glucocorticoid regulated kinase 1*	1.5533	2.9349
11751459_x_at	LRG1	*leucine rich alpha-2-glycoprotein 1*	1.5502	2.9285
11746779_a_at	NCOA7	*nuclear receptor coactivator 7*	1.5502	2.9285
11716974_a_at	PDK4	*pyruvate dehydrogenase kinase 4*	1.5485	2.9251
11722969_s_at	TRPV4	*transient receptor potential cation channel subfamily V member 4*	1.5444	2.9168
11744086_a_at	PRR15L	*proline rich 15 like*	1.5421	2.9122
11718025_at	IL1R1	*interleukin 1 receptor type 1*	1.5396	2.9072
11726360_a_at	ALDH3A1	*aldehyde dehydrogenase 3 family member A1*	1.5388	2.9055
11750700_a_at	ACSL1	*acyl-CoA synthetase long-chain family member 1*	1.5370	2.9019
11758225_s_at	IQGAP2	*IQ motif containing GTPase activating protein 2*	1.5339	2.8956
11721368_at	CRLF1	*cytokine receptor like factor 1*	1.5268	2.8814
11750170_a_at	TRIM22	*tripartite motif containing 22*	1.5265	2.8809
11736144_at	ENPP4	*Ectonucleotide Pyrophosphatase/Phosphodiesterase 4 (Putative)*	1.5245	2.8768
11721630_at	MAFB	*MAF bZIP transcription factor B*	1.5245	2.8768
11716144_a_at	PDCD6IP	*programmed cell death 6 interacting protein*	1.5224	2.8726
11736285_a_at	CHKA	*choline kinase alpha*	1.5204	2.8687
11731606_at	SCIN	*scinderin*	1.5158	2.8595
11748761_a_at	KLF5	*Kruppel like factor 5*	1.5155	2.8590
11720002_at	NRARP	*NOTCH-regulated ankyrin repeat protein*	1.5135	2.8550
11715682_a_at	CREG1	*cellular repressor of E1A stimulated genes 1*	1.5133	2.8546
11717823_s_at	TNFAIP2	*TNF alpha induced protein 2*	1.5115	2.8511
11723194_x_at	HLA-DQB1	*major histocompatibility complex, class II, DQ beta 1*	1.5115	2.8510
11723329_a_at	GSN	*gelsolin*	1.5091	2.8464
11720243_x_at	TCN2	*transcobalamin 2*	1.5081	2.8444
11731874_x_at	MIA2	*melanoma inhibitory activity 2*	1.5074	2.8430
11732526_s_at	CSGALNACT1	*chondroitin sulfate N-acetylgalactosaminyltransferase 1*	1.5060	2.8403
11758474_s_at	COLCA1	*colorectal cancer associated 1*	1.5059	2.8400
11745075_x_at	GSTA4	*glutathione S-transferase alpha 4*	1.5046	2.8375
11723946_a_at	ACSL5	*acyl-CoA synthetase long-chain family member 5*	1.5020	2.8324
11719554_at	CTSS	*cathepsin S*	1.4986	2.8256
11727590_a_at	IL20RB	*interleukin 20 receptor subunit beta*	1.4983	2.8250
11731177_at	BCL2L15	*BCL2 like 15*	1.4964	2.8214
11756236_a_at	FBLN1	*fibulin 1*	1.4962	2.8210
11725223_at	SNTB1	*syntrophin beta 1*	1.4941	2.8168
11719432_at	KIAA0513	*KIAA0513*	1.4917	2.8122

11743917_a_at	FKBP5	*FK506 binding protein 5*	1.4894	2.8078
11757496_s_at	RAPGEFL1	*Rap guanine nucleotide exchange factor like 1*	1.4855	2.8001
11731756_at	KLHDC7B	*kelch domain containing 7B*	1.4853	2.7998
11744516_a_at	SLC2A10	*solute carrier family 2 member 10*	1.4851	2.7994
11722658_at	CXCL17	*C-X-C motif chemokine ligand 17*	1.4849	2.7989
11721759_a_at	ASAP3	*ArfGAP with SH3 domain, ankyrin repeat and PH domain 3*	1.4833	2.7959
11717614_at	KIF13B	*kinesin family member 13B*	1.4801	2.7897
11758100_s_at	C1S	*complement C1s*	1.4770	2.7836
11718608_at	MIR5193	*microRNA 5193*	1.4754	2.7807
11729575_a_at	XBP1	*X-box binding protein 1*	1.4724	2.7748
11758315_s_at	PER2	*period circadian clock 2*	1.4681	2.7665
11731538_a_at	ADGRF1	*adhesion G protein-coupled receptor F1*	1.4672	2.7648
11735786_at	BARX2	*BARX homeobox 2*	1.4632	2.7572
11731015_at	C2CD4A	*C2 calcium dependent domain containing 4A*	1.4623	2.7555
11724703_a_at	ELF5	*E74 like ETS transcription factor 5*	1.4615	2.7540
11727007_at	SORT1	*sortilin 1*	1.4594	2.7500
11729679_a_at	PCDHB14	*protocadherin beta 14*	1.4575	2.7463
11750242_a_at	KLK13	*kallikrein related peptidase 13*	1.4571	2.7455
11728981_at	ERICH5	*glutamate rich 5*	1.4553	2.7421
11724961_a_at	SRGAP3	*SLIT-ROBO Rho GTPase activating protein 3*	1.4541	2.7399
11758955_at	LGALS8	*galectin 8*	1.4529	2.7376
11759191_at	NIPAL2	*NIPA like domain containing 2*	1.4510	2.7339
11759310_at	FAM171B	*family with sequence similarity 171 member B*	1.4408	2.7147
11730699_at	LOC100652777	*group 10 secretory phospholipase A2-like*	1.4388	2.7109
11718066_a_at	TCTN1	*tectonic family member 1*	1.4383	2.7100
11748152_a_at	IFNGR1	*interferon gamma receptor 1*	1.4371	2.7077
11750031_a_at	CRYL1	*crystallin lambda 1*	1.4354	2.7045
11721025_a_at	TRAPPC6A	*trafficking protein particle complex 6A*	1.4284	2.6914
11757278_x_at	ASS1	*argininosuccinate synthase 1*	1.4282	2.6911
11757793_s_at	TFPI	*tissue factor pathway inhibitor*	1.4258	2.6866
11718130_s_at	OLFM4	*olfactomedin 4*	1.4249	2.6849
11724589_s_at	MMP12	*matrix metallopeptidase 12*	1.4234	2.6822
11727995_a_at	SPINK5	*serine peptidase inhibitor, Kazal type 5*	1.4181	2.6724
11721606_a_at	ADD3	*adducin 3*	1.4180	2.6722
11725692_a_at	VWA5A	*von Willebrand factor A domain containing 5A*	1.4178	2.6717
11730195_at	SEC14L2	*SEC14 like lipid binding 2*	1.4150	2.6666
11715708_s_at	MB	*myoglobin*	1.4115	2.6602
11738201_a_at	EYA2	*EYA transcriptional coactivator and phosphatase 2*	1.4095	2.6564
11731543_at	SESTD1	*SEC14 and spectrin domain containing 1*	1.4085	2.6547
11739292_at	EHF	*ETS homologous factor*	1.4063	2.6506
11726412_s_at	ZBTB7C	*zinc finger and BTB domain containing 7C*	1.4007	2.6403
11749140_a_at	RCBTB2	*RCC1 and BTB domain containing protein 2*	1.3996	2.6382

11719843_a_at	ABI3BP	*ABI family member 3 binding protein*	1.3984	2.6360
11746952_x_at	MDK	*Midkine (Neurite Growth-Promoting Factor 2)*	1.3954	2.6307
11725625_s_at	ACE2	*angiotensin I converting enzyme 2*	1.3919	2.6242
11729101_a_at	AKR1C2	*aldo-keto reductase family 1 member C2*	1.3915	2.6236
11756274_a_at	ALDH1L1	*aldehyde dehydrogenase 1 family member L1*	1.3915	2.6236
11735271_a_at	GCNT1	*Glucosaminyl (N-Acetyl) Transferase 1, Core 2*	1.3899	2.6206
11724258_a_at	MUC15	*mucin 15, cell surface associated*	1.3851	2.6119
11742423_a_at	STEAP2	*STEAP2 metalloreductase*	1.3848	2.6114
11733027_at	CLCA2	*chloride channel accessory 2*	1.3818	2.6060
11716878_s_at	B4GALT5	*beta-1,4-galactosyltransferase 5*	1.3812	2.6048
11744596_a_at	LYPD6B	*LY6/PLAUR domain containing 6B*	1.3790	2.6009
11730549_a_at	IKZF2	*IKAROS family zinc finger 2*	1.3788	2.6005
11761114_x_at	AKR1C2	*aldo-keto reductase family 1 member C2*	1.3753	2.5943
11734506_a_at	MECOM	*MDS1 and EVI1 complex locus*	1.3738	2.5915
11726548_at	PITPNM3	*PITPNM family member 3*	1.3707	2.5860
11734359_a_at	RNASEL	*ribonuclease L*	1.3654	2.5765
11726303_a_at	MFSD4A	*major facilitator superfamily domain containing 4A*	1.3645	2.5749
11723282_a_at	CEACAM1	*carcinoembryonic antigen related cell adhesion molecule 1*	1.3629	2.5721
11733091_a_at	TSPAN8	*tetraspanin 8*	1.3612	2.5690
11730338_a_at	SMAD6	*SMAD family member 6*	1.3585	2.5642
11741317_a_at	NHLH2	*nescient helix-loop-helix 2*	1.3569	2.5613
11742379_x_at	AKR1B15	*aldo-keto reductase family 1 member B15*	1.3563	2.5603
11752737_a_at	CLEC7A	*C-type lectin domain family 7 member A*	1.3556	2.5591
11719408_a_at	HIPK2	*homeodomain interacting protein kinase 2*	1.3537	2.5557
11725000_at	DUOXA2	*dual oxidase maturation factor 2*	1.3512	2.5512
11742709_s_at	P4HTM	*prolyl 4-hydroxylase, transmembrane*	1.3496	2.5484
11730250_a_at	LNX1	*ligand of numb-protein X 1*	1.3481	2.5457
11759642_x_at	HLA-DRB1	*major histocompatibility complex, class II, DR beta 1*	1.3436	2.5378
11721445_x_at	ERBB3	*erb-b2 receptor tyrosine kinase 3*	1.3428	2.5365
11729571_a_at	FAM83A	*family with sequence similarity 83 member A*	1.3428	2.5365
11763594_a_at	HS3ST3B1	*heparan sulfate-glucosamine 3-sulfotransferase 3B1*	1.3425	2.5359
11755010_s_at	POC1B-GALNT4	*POC1B-GALNT4 readthrough*	1.3394	2.5305
11730509_s_at	ABCC5	*ATP binding cassette subfamily C member 5*	1.3383	2.5285
11755282_a_at	SCNN1A	*sodium channel epithelial 1 alpha subunit*	1.3380	2.5280
11719171_a_at	AKR1C1	*aldo-keto reductase family 1 member C1*	1.3377	2.5274
11718491_x_at	FABP5	*fatty acid binding protein 5*	1.3327	2.5188
11730465_at	KCNJ2	*potassium voltage-gated channel subfamily J member 2*	1.3316	2.5169
11718754_at	CAPN5	*calpain 5*	1.3312	2.5161
11764261_s_at	TMPRSS11A	*transmembrane protease, serine 11A*	1.3311	2.5160
11751426_a_at	IL33	*interleukin 33*	1.3288	2.5120
11720281_a_at	EVA1C	*eva-1 homolog C*	1.3288	2.5119
11717707_s_at	VPS13D	*vacuolar protein sorting 13 homolog D*	1.3279	2.5104

11717295_s_at	APOD	*apolipoprotein D*	1.3265	2.5079
11754833_a_at	TLR2	*toll like receptor 2*	1.3260	2.5070
11758954_at	ENPP5	*Ectonucleotide Pyrophosphatase/Phosphodiesterase 5 (Putative)*	1.3252	2.5057
11746995_a_at	NPL	*N-acetylneuraminate pyruvate lyase*	1.3222	2.5005
11759546_a_at	CXXC5	*CXXC finger protein 5*	1.3215	2.4993
11716569_at	NOTCH3	*notch 3*	1.3184	2.4939
11740361_s_at	FOXN3	*forkhead box N3*	1.3182	2.4935
11734578_a_at	CFH	*complement factor H*	1.3172	2.4919
11734893_s_at	SOBP	*sine oculis binding protein homolog*	1.3166	2.4908
11722524_s_at	TMCO4	*transmembrane and coiled-coil domains 4*	1.3149	2.4879
11757390_s_at	KLHL24	*kelch like family member 24*	1.3140	2.4863
11721141_x_at	TCEA3	*transcription elongation factor A3*	1.3140	2.4863
11718490_s_at	FABP5	*fatty acid binding protein 5*	1.3117	2.4824
11716390_a_at	BACE1	*beta-secretase 1*	1.3092	2.4780
11718448_at	SH3BGRL2	*SH3 domain binding glutamate rich protein like 2*	1.3092	2.4780
11755226_s_at	KLHDC7A	*kelch domain containing 7A*	1.3050	2.4708
11744282_at	PLBD1	*phospholipase B domain containing 1*	1.3032	2.4678
11718293_a_at	CDKN2A	*cyclin dependent kinase inhibitor 2A*	1.2986	2.4599
11721660_s_at	LMO4	*LIM domain only 4*	1.2985	2.4597
11727198_a_at	PCDHAC2	*protocadherin alpha subfamily C, 2*	1.2962	2.4558
11715537_x_at	IDH2	*Isocitrate Dehydrogenase (NADP(+)) 2, Mitochondrial*	1.2934	2.4510
11716399_at	TP53INP2	*tumor protein p53 inducible nuclear protein 2*	1.2915	2.4478
11724372_at	ANXA10	*annexin A10*	1.2914	2.4477
11719676_s_at	MAOA	*monoamine oxidase A*	1.2888	2.4433
11753004_a_at	CKB	*creatine kinase B*	1.2887	2.4430
11743547_a_at	ASAH1	*N-acylsphingosine amidohydrolase 1*	1.2886	2.4429
11723525_at	TBC1D8	*TBC1 domain family member 8*	1.2854	2.4375
11731617_x_at	SIDT1	*SID1 transmembrane family member 1*	1.2854	2.4375
11735610_a_at	RPS6KA5	*ribosomal protein S6 kinase A5*	1.2852	2.4371
11720594_a_at	DLG3	*discs large MAGUK scaffold protein 3*	1.2831	2.4336
11739725_a_at	TC2N	*tandem C2 domains, nuclear*	1.2823	2.4322
11727113_at	EGF	*epidermal growth factor*	1.2819	2.4316
11716509_a_at	AKR1A1	*aldo-keto reductase family 1 member A1*	1.2801	2.4286
11755450_a_at	ZNF608	*zinc finger protein 608*	1.2752	2.4203
11744307_a_at	TTC39A	*tetratricopeptide repeat domain 39A*	1.2751	2.4202
11721661_a_at	TBXAS1	*thromboxane A synthase 1*	1.2744	2.4190
11739564_s_at	ITPR1	*inositol 1,4,5-trisphosphate receptor type 1*	1.2741	2.4185
11727514_at	TTC9	*tetratricopeptide repeat domain 9*	1.2731	2.4168
11742683_x_at	HIST1H1C	*histone cluster 1 H1 family member c*	1.2731	2.4168
11729832_s_at	CLDN8	*claudin 8*	1.2726	2.4160
11727336_at	SAMD12	*sterile alpha motif domain containing 12*	1.2713	2.4138
11756677_a_at	CYB5D2	*cytochrome b5 domain containing 2*	1.2669	2.4064

11763271_at	PEX11A	*peroxisomal biogenesis factor 11 alpha*	1.2667	2.4061
11758385_s_at	HEY2	*hes related family bHLH transcription factor with YRPW motif 2*	1.2662	2.4052
11755276_a_at	GPX2	*glutathione peroxidase 2*	1.2657	2.4044
11724420_at	ZC3H6	*zinc finger CCCH-type containing 6*	1.2644	2.4022
11721223_at	ACOX2	*acyl-CoA oxidase 2*	1.2644	2.4022
11724983_at	PCDH7	*protocadherin 7*	1.2639	2.4015
11724321_s_at	C11orf54	*chromosome 11 open reading frame 54*	1.2610	2.3967
11715419_at	LY6E	*lymphocyte antigen 6 complex, locus E*	1.2607	2.3962
11739349_a_at	AMOT	*angiomotin*	1.2607	2.3961
11726682_a_at	MEIS1	*Meis homeobox 1*	1.2601	2.3952
11730073_at	CNTN3	*contactin 3*	1.2588	2.3930
11721993_at	SLC6A6	*solute carrier family 6 member 6*	1.2583	2.3922
11750813_a_at	RIPK4	*receptor interacting serine/threonine kinase 4*	1.2568	2.3897
11724588_a_at	ANKRD35	*ankyrin repeat domain 35*	1.2568	2.3896
11729992_at	DQX1	*DEAQ-box RNA dependent ATPase 1*	1.2547	2.3861
11747118_a_at	BRINP1	*BMP/retinoic acid inducible neural specific 1*	1.2486	2.3761
11727286_a_at	ZSCAN31	*zinc finger and SCAN domain containing 31*	1.2459	2.3717
11748971_a_at	FOXA1	*forkhead box A1*	1.2452	2.3705
11724063_s_at	FA2H	*fatty acid 2-hydroxylase*	1.2441	2.3687
11753739_a_at	CYB5A	*cytochrome b5 type A*	1.2411	2.3638
11716871_at	GAA	*glucosidase alpha, acid*	1.2411	2.3638
11718824_at	IGIP	*IgA inducing protein*	1.2383	2.3592
11730066_s_at	MAPK10	*mitogen-activated protein kinase 10*	1.2366	2.3564
11757404_x_at	ID3	*inhibitor of DNA binding 3, HLH protein*	1.2354	2.3544
11725240_at	RTP4	*receptor transporter protein 4*	1.2352	2.3541
11721167_a_at	EPB41L1	*erythrocyte membrane protein band 4.1 like 1*	1.2335	2.3514
11734201_s_at	GK	*glycerol kinase*	1.2326	2.3499
11716640_a_at	PSMB10	*proteasome subunit beta 10*	1.2304	2.3463
11728342_at	DCLK1	*doublecortin like kinase 1*	1.2290	2.3440
11720277_a_at	OLFML2A	*olfactomedin like 2A*	1.2265	2.3400
11743405_a_at	SMIM14	*small integral membrane protein 14*	1.2261	2.3394
11718781_s_at	SSBP2	*single stranded DNA binding protein 2*	1.2240	2.3360
11723326_at	CA9	*carbonic anhydrase 9*	1.2229	2.3341
11739557_a_at	VAMP5	*vesicle associated membrane protein 5*	1.2219	2.3325
11733139_a_at	ARL4A	*ADP ribosylation factor like GTPase 4A*	1.2211	2.3313
11721897_a_at	DHX58	*DExH-box helicase 58*	1.2200	2.3294
11726693_s_at	ANGPT1	*angiopoietin 1*	1.2183	2.3267
11741044_a_at	PLS1	*plastin 1*	1.2165	2.3239
11718786_a_at	PAN2	*PAN2 Poly(A) Specific Ribonuclease Subunit*	1.2148	2.3211
11756443_x_at	PROM2	*prominin 2*	1.2144	2.3204
11720124_at	SRD5A3	*steroid 5 alpha-reductase 3*	1.2128	2.3178
11755084_x_at	CD55	*CD55 Molecule (Cromer Blood Group)*	1.2105	2.3142

11732569_at	SLCO1B3	*solute carrier organic anion transporter family member 1B3*	1.2088	2.3115
11732436_at	RHOV	*ras homolog family member V*	1.2081	2.3104
11747975_x_at	RNF145	*ring finger protein 145*	1.2071	2.3087
11757453_s_at	CEP68	*centrosomal protein 68*	1.2067	2.3081
11716114_x_at	POR	*cytochrome p450 oxidoreductase*	1.2053	2.3059
11732580_a_at	ME3	*malic enzyme 3*	1.2050	2.3053
11716455_at	RHOBTB3	*Rho related BTB domain containing 3*	1.2042	2.3041
11736369_at	MBOAT1	*membrane bound O-acyltransferase domain containing 1*	1.2034	2.3028
11729365_at	PRKAA2	*protein kinase AMP-activated catalytic subunit alpha 2*	1.2031	2.3023
11717370_at	ARSD	*arylsulfatase D*	1.2018	2.3003
11718001_a_at	C10orf54	*chromosome 10 open reading frame 54*	1.2014	2.2996
11745830_a_at	ALAD	*aminolevulinate dehydratase*	1.2003	2.2978
11758092_s_at	EFNA5	*ephrin A5*	1.1972	2.2930
11717123_a_at	PPP1R12B	*protein phosphatase 1 regulatory subunit 12B*	1.1969	2.2924
11717909_at	IGFBP6	*insulin like growth factor binding protein 6*	1.1959	2.2909
11718919_a_at	ATP6V1B1	*ATPase H+ transporting V1 subunit B1*	1.1959	2.2908
11754930_x_at	ATP1A1	*ATPase Na+/K+ transporting subunit alpha 1*	1.1954	2.2901
11751973_x_at	LZTS3	*leucine zipper tumor suppressor family member 3*	1.1946	2.2888
11748913_a_at	B4GALT4	*beta-1,4-galactosyltransferase 4*	1.1941	2.2880
11718347_a_at	S100P	*S100 calcium binding protein P*	1.1929	2.2861
11720452_at	PLEKHH2	*pleckstrin homology, MyTH4 and FERM domain containing H2*	1.1911	2.2832
11725180_a_at	RUNX2	*runt related transcription factor 2*	1.1907	2.2826
11755212_a_at	SVOPL	*SVOP like*	1.1906	2.2825
11739787_a_at	IGF2	*insulin like growth factor 2*	1.1875	2.2776
11718435_a_at	NPNT	*nephronectin*	1.1865	2.2760
11754801_x_at	PLPP1	*phospholipid phosphatase 1*	1.1860	2.2752
11744503_x_at	RSRP1	*arginine and serine rich protein 1*	1.1859	2.2751
11721783_a_at	SLC9A8	*solute carrier family 9 member A8*	1.1848	2.2733
11758988_at	SYT17	*synaptotagmin 17*	1.1838	2.2718
11742868_at	CDH6	*cadherin 6*	1.1817	2.2685
11744374_x_at	HLA-DRB1	*major histocompatibility complex, class II, DR beta 1*	1.1807	2.2669
11743534_a_at	PPP2R5C	*protein phosphatase 2 regulatory subunit B'gamma*	1.1774	2.2617
11717417_s_at	RHOU	*ras homolog family member U*	1.1770	2.2611
11733923_a_at	CROT	*carnitine O-octanoyltransferase*	1.1747	2.2574
11717687_a_at	JAK1	*Janus kinase 1*	1.1730	2.2548
11750611_a_at	ERBB2	*erb-b2 receptor tyrosine kinase 2*	1.1718	2.2530
11717575_at	PPP1R3C	*protein phosphatase 1 regulatory subunit 3C*	1.1672	2.2458
11715583_s_at	HLA-DPA1	*major histocompatibility complex, class II, DP alpha 1*	1.1664	2.2445
11728349_a_at	STIM2	*stromal interaction molecule 2*	1.1634	2.2398
11753966_a_at	ZNF204P	*zinc finger protein 204, pseudogene*	1.1620	2.2376
11755091_a_at	ABCA7	*ATP binding cassette subfamily A member 7*	1.1610	2.2362
11755620_a_at	HYAL1	*hyaluronoglucosaminidase 1*	1.1605	2.2354

11721417_at	SCNN1B	*sodium channel epithelial 1 beta subunit*	1.1604	2.2352
11718627_at	TRAK1	*trafficking kinesin protein 1*	1.1598	2.2342
11758048_s_at	THRB	*thyroid hormone receptor beta*	1.1597	2.2341
11741731_a_at	FBXO34	*F-box protein 34*	1.1595	2.2338
11751783_a_at	MFSD1	*major facilitator superfamily domain containing 1*	1.1594	2.2336
11758460_s_at	FAAH2	*fatty acid amide hydrolase 2*	1.1589	2.2329
11753509_a_at	FOXC1	*forkhead box C1*	1.1587	2.2326
11759889_a_at	BCL2L11	*BCL2 like 11*	1.1579	2.2313
11716183_a_at	ALCAM	*activated leukocyte cell adhesion molecule*	1.1574	2.2305
11728954_a_at	KITLG	*KIT ligand*	1.1559	2.2283
11736257_at	PRKCE	*protein kinase C epsilon*	1.1556	2.2278
11757882_x_at	GSTA1	*glutathione S-transferase alpha 1*	1.1520	2.2222
11754091_s_at	SMAD3	*SMAD family member 3*	1.1497	2.2187
11732468_at	ATP12A	*ATPase H+/K+ transporting non-gastric alpha2 subunit*	1.1487	2.2172
11743846_s_at	CFH	*complement factor H*	1.1479	2.2159
11720503_a_at	ALDH3A2	*aldehyde dehydrogenase 3 family member A2*	1.1477	2.2156
11751564_a_at	TSPAN6	*tetraspanin 6*	1.1437	2.2094
11724196_s_at	STC1	*stanniocalcin 1*	1.1425	2.2077
11726581_a_at	GUCY1B3	*guanylate cyclase 1 soluble subunit beta*	1.1425	2.2076
11716663_a_at	GDF15	*growth differentiation factor 15*	1.1406	2.2047
11723996_a_at	GLCCI1	*glucocorticoid induced 1*	1.1399	2.2036
11723955_a_at	CLINT1	*clathrin interactor 1*	1.1389	2.2021
11723703_s_at	ABHD5	*abhydrolase domain containing 5*	1.1365	2.1985
11723325_a_at	KCNQ1	*potassium voltage-gated channel subfamily Q member 1*	1.1344	2.1953
11737322_a_at	PLD1	*phospholipase D1*	1.1342	2.1949
11734849_a_at	CELSR2	*cadherin EGF LAG seven-pass G-type receptor 2*	1.1321	2.1917
11725450_a_at	TMEM45B	*transmembrane protein 45B*	1.1309	2.1899
11720901_a_at	GRAMD1C	*GRAM domain containing 1C*	1.1299	2.1885
11743686_a_at	ZNF436	*zinc finger protein 436*	1.1293	2.1875
11739437_at	PPTC7	*PTC7 protein phosphatase homolog*	1.1288	2.1868
11756604_a_at	PCDHB2	*protocadherin beta 2*	1.1275	2.1848
11742865_a_at	TJP3	*tight junction protein 3*	1.1275	2.1848
11732624_at	WFDC5	*WAP four-disulfide core domain 5*	1.1270	2.1840
11726294_s_at	CEBPA	*CCAAT/enhancer binding protein alpha*	1.1257	2.1820
11718287_at	UBL3	*ubiquitin like 3*	1.1253	2.1815
11718433_a_at	SASH1	*SAM and SH3 domain containing 1*	1.1234	2.1786
11727702_at	C9orf152	*chromosome 9 open reading frame 152*	1.1225	2.1772
11748009_a_at	RHBDL2	*rhomboid like 2*	1.1214	2.1756
11727016_s_at	PAPPA	*pappalysin 1*	1.1210	2.1750
11757868_a_at	PIK3IP1	*phosphoinositide-3-kinase interacting protein 1*	1.1195	2.1727
11758377_s_at	TLR1	*toll like receptor 1*	1.1184	2.1711
11748463_a_at	LOC100505984	*uncharacterized LOC100505984*	1.1163	2.1679

11724282_a_at	UGT1A10	*UDP glucuronosyltransferase family 1 member A10*	1.1162	2.1677
11734956_a_at	CNTNAP2	*contactin associated protein-like 2*	1.1155	2.1667
11723524_at	AGR3	*anterior gradient 3, protein disulphide isomerase family member*	1.1144	2.1651
11722757_at	CFTR	*cystic fibrosis transmembrane conductance regulator*	1.1140	2.1644
11759611_at	SMIM11A	*small integral membrane protein 11A*	1.1132	2.1632
11763193_at	GDPD1	*glycerophosphodiester phosphodiesterase domain containing 1*	1.1112	2.1602
11754189_s_at	AKR1C1	*aldo-keto reductase family 1 member C1*	1.1106	2.1594
11744255_a_at	ACADVL	*acyl-CoA dehydrogenase, very long chain*	1.1099	2.1583
11721030_a_at	PIP5K1B	*phosphatidylinositol-4-phosphate 5-kinase type 1 beta*	1.1098	2.1581
11755001_a_at	ARHGAP32	*Rho GTPase activating protein 32*	1.1098	2.1581
11726892_a_at	SLC51A	*solute carrier family 51 alpha subunit*	1.1078	2.1552
11729333_at	PADI1	*peptidyl arginine deiminase 1*	1.1068	2.1536
11760107_a_at	PHF10	*PHD finger protein 10*	1.1044	2.1501
11717090_a_at	HIST2H2BE	*histone cluster 2 H2B family member e*	1.1040	2.1495
11736801_a_at	PLAG1	*PLAG1 zinc finger*	1.1014	2.1457
11733742_a_at	DCXR	*dicarbonyl and L-xylulose reductase*	1.1004	2.1441
11759103_at	CYP4F3	*cytochrome P450 family 4 subfamily F member 3*	1.1004	2.1441
11720287_a_at	CDC42BPA	*CDC42 binding protein kinase alpha*	1.1002	2.1439
11729453_s_at	CYP2B6	*cytochrome P450 family 2 subfamily B member 6*	1.0996	2.1430
11726628_a_at	SEMA4A	*semaphorin 4A*	1.0994	2.1426
11741113_a_at	MIR4680	*microRNA 4680*	1.0959	2.1375
11727302_a_at	TMEM71	*transmembrane protein 71*	1.0950	2.1362
11718565_at	KIAA1147	*KIAA1147*	1.0937	2.1342
11751266_a_at	SLC44A3	*solute carrier family 44 member 3*	1.0930	2.1332
11732773_at	CCDC57	*coiled-coil domain containing 57*	1.0928	2.1329
11736232_at	ZNF362	*zinc finger protein 362*	1.0909	2.1300
11725941_at	WNT7B	*Wnt family member 7B*	1.0891	2.1274
11723613_s_at	SERHL2	*serine hydrolase-like 2*	1.0877	2.1254
11737805_a_at	TMPRSS11D	*transmembrane protease, serine 11D*	1.0871	2.1244
11752318_a_at	BTN3A3	*butyrophilin subfamily 3 member A3*	1.0866	2.1237
11719012_at	FZD4	*frizzled class receptor 4*	1.0839	2.1197
11726927_a_at	EPHX3	*epoxide hydrolase 3*	1.0827	2.1180
11762940_x_at	HLA-C	*major histocompatibility complex, class I, C*	1.0814	2.1161
11732148_at	CAT	*catalase*	1.0805	2.1148
11755640_s_at	RALGPS1	*Ral GEF with PH domain and SH3 binding motif 1*	1.0797	2.1136
11739975_at	ZNF117	*zinc finger protein 117*	1.0768	2.1093
11715722_a_at	GOLM1	*golgi membrane protein 1*	1.0760	2.1082
11719059_a_at	ATRN	*attractin*	1.0756	2.1076
11728085_s_at	BMPR1B	*bone morphogenetic protein receptor type 1B*	1.0744	2.1059
11754637_a_at	SYTL1	*synaptotagmin like 1*	1.0744	2.1058
11724093_s_at	SLC35E2B	*solute carrier family 35 member E2B*	1.0702	2.0997
11721974_a_at	SUOX	*sulfite oxidase*	1.0696	2.0988

11756059_a_at	CXCL14	*C-X-C motif chemokine ligand 14*	1.0678	2.0962
11748362_s_at	ABCC3	*ATP binding cassette subfamily C member 3*	1.0670	2.0951
11736745_a_at	ZBTB20	*zinc finger and BTB domain containing 20*	1.0669	2.0949
11736238_a_at	ABCA5	*ATP binding cassette subfamily A member 5*	1.0659	2.0935
11755310_s_at	ACOT2	*acyl-CoA thioesterase 2*	1.0652	2.0924
11717339_s_at	SORD	*sorbitol dehydrogenase*	1.0648	2.0919
11736909_at	C1orf210	*chromosome 1 open reading frame 210*	1.0637	2.0903
11735478_a_at	CHST6	*carbohydrate sulfotransferase 6*	1.0608	2.0861
11721788_at	C1orf226	*chromosome 1 open reading frame 226*	1.0595	2.0842
11755966_x_at	HLA-B	*major histocompatibility complex, class I, B*	1.0585	2.0827
11752897_a_at	HBP1	*HMG-box transcription factor 1*	1.0582	2.0823
11724394_at	KIAA1211L	*KIAA1211 like*	1.0567	2.0802
11749150_a_at	ABCD3	*ATP binding cassette subfamily D member 3*	1.0549	2.0776
11720678_a_at	CREB3L1	*cAMP responsive element binding protein 3 like 1*	1.0518	2.0731
11719521_at	SEMA5A	*semaphorin 5A*	1.0502	2.0708
11725249_at	LY75	*lymphocyte antigen 75*	1.0470	2.0663
11728477_at	CXCL3	*C-X-C motif chemokine ligand 3*	1.0454	2.0640
11720283_at	JMY	*junction mediating and regulatory protein, p53 cofactor*	1.0442	2.0622
11743598_a_at	RNF207	*ring finger protein 207*	1.0429	2.0603
11721700_a_at	RERG	*RAS like estrogen regulated growth inhibitor*	1.0399	2.0561
11745580_x_at	GOLGA6L9	*golgin A6 family-like 9*	1.0394	2.0554
11744171_a_at	DNAJC4	*DnaJ Heat Shock Protein Family (Hsp40) Member C4*	1.0389	2.0547
11755903_x_at	N4BP2L1	*NEDD4 binding protein 2 like 1*	1.0386	2.0542
11756342_s_at	GDA	*guanine deaminase*	1.0385	2.0541
11743856_a_at	CTHRC1	*collagen triple helix repeat containing 1*	1.0383	2.0538
11716941_at	TRIB2	*tribbles pseudokinase 2*	1.0370	2.0519
11722348_a_at	REPS2	*RALBP1 associated Eps domain containing 2*	1.0367	2.0516
11742745_a_at	PLIN2	*perilipin 2*	1.0367	2.0516
11718738_a_at	ST3GAL1	*ST3 beta-galactoside alpha-2,3-sialyltransferase 1*	1.0361	2.0507
11757444_a_at	EGLN3	*egl-9 family hypoxia inducible factor 3*	1.0339	2.0475
11721978_a_at	PLCE1	*phospholipase C epsilon 1*	1.0329	2.0461
11716167_a_at	MX1	*MX dynamin like GTPase 1*	1.0315	2.0442
11757030_at	ECH1	*enoyl-CoA hydratase 1*	1.0312	2.0437
11755152_a_at	DUOX1	*dual oxidase 1*	1.0301	2.0421
11737045_a_at	PLA2R1	*phospholipase A2 receptor 1*	1.0300	2.0420
11732500_a_at	FAM3B	*family with sequence similarity 3 member B*	1.0297	2.0416
11723096_a_at	CYLD	*CYLD lysine 63 deubiquitinase*	1.0284	2.0398
11723008_s_at	CCPG1	*cell cycle progression 1*	1.0277	2.0388
11759568_at	SLC45A4	*solute carrier family 45 member 4*	1.0274	2.0383
11747888_a_at	SH3YL1	*SH3 and SYLF domain containing 1*	1.0228	2.0319
11746023_a_at	PGD	*phosphogluconate dehydrogenase*	1.0225	2.0314
11757929_s_at	RALGAPA2	*Ral GTPase activating protein catalytic alpha subunit 2*	1.0224	2.0313

11724094_a_at	COL4A5	*collagen type IV alpha 5 chain*	1.0218	2.0305
11734658_s_at	FOS	*Fos proto-oncogene, AP-1 transcription factor subunit*	1.0205	2.0286
11716210_at	CITED2	*Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2*	1.0201	2.0280
11724667_s_at	ENPP3	*ectonucleotide pyrophosphatase/phosphodiesterase 3*	1.0194	2.0271
11744236_a_at	DDX60	*DExD/H-box helicase 60*	1.0173	2.0241
11742763_a_at	FAM214A	*family with sequence similarity 214 member A*	1.0148	2.0206
11737811_a_at	NNT	*nicotinamide nucleotide transhydrogenase*	1.0145	2.0202
11720294_a_at	PLPP2	*phospholipid phosphatase 2*	1.0121	2.0169
11754973_x_at	MANSC1	*MANSC domain containing 1*	1.0105	2.0146
11717496_a_at	IMPA2	*inositol monophosphatase 2*	1.0101	2.0140
11722756_at	TMEM37	*transmembrane protein 37*	1.0078	2.0108
11746681_a_at	VNN3	*vanin 3*	1.0051	2.0071
11737329_at	SLC26A4	*solute carrier family 26 member 4*	1.0043	2.0060
11721837_a_at	MYLK	*myosin light chain kinase*	1.0042	2.0058
11744858_a_at	LHPP	*phospholysine phosphohistidine inorganic pyrophosphate phosphatase*	1.0019	2.0026
11720518_a_at	TACC2	*transforming acidic coiled-coil containing protein 2*	1.0012	2.0016
11717936_a_at	ERMP1	*endoplasmic reticulum metallopeptidase 1*	1.0011	2.0015

DOWNREGULATED mRNAs (651)

Probe Set IDs	GENE SYMBOL	GENE NAME	Log_2 Ratio	Fold Change
11732713_at	FST	*follistatin*	-4.0422	0.0607
11735693_x_at	SPRR2E	*small proline rich protein 2E*	-3.7544	0.0741
11736422_s_at	POSTN	*periostin*	-3.7331	0.0752
11717386_s_at	MT1G	*metallothionein 1G*	-3.6675	0.0787
11757698_s_at	MIG7	*mig-7*	-3.5890	0.0831
11746283_s_at	KRTAP2-3	*keratin associated protein 2-3*	-3.5278	0.0867
11758672_s_at	UCHL1	*ubiquitin C-terminal hydrolase L1*	-3.4469	0.0917
11757033_a_at	IL13RA2	*interleukin 13 receptor subunit alpha 2*	-3.2096	0.1081
11720353_s_at	ETV5	*ETS variant 5*	-3.0233	0.1230
11723151_s_at	SUGCT	*succinyl-CoA:glutarate-CoA transferase*	-3.0104	0.1241
11754662_s_at	ADAMTS1	*ADAM metallopeptidase with thrombospondin type 1 motif 1*	-2.9737	0.1273
11749461_a_at	CDH11	*cadherin 11*	-2.9390	0.1304
11755207_a_at	NT5E	*5'-nucleotidase ecto*	-2.8678	0.1370
11731857_x_at	MT1H	*metallothionein 1H*	-2.8635	0.1374
11729265_at	SPRR2D	*small proline rich protein 2D*	-2.8334	0.1403
11728397_at	MT1M	*metallothionein 1M*	-2.8069	0.1429
11729712_at	SPRR2A	*small proline rich protein 2A*	-2.7122	0.1526
11737324_x_at	LAMC2	*laminin subunit gamma 2*	-2.7056	0.1533
11725749_a_at	GAL	*galanin and GMAP prepropeptide*	-2.7037	0.1535
11726909_at	ZBED2	*zinc finger BED-type containing 2*	-2.6841	0.1556
11745722_x_at	FHL1	*four and a half LIM domains 1*	-2.6822	0.1558
11731925_at	CRCT1	*cysteine rich C-terminal 1*	-2.6767	0.1564

11731168_at	IGFL1	*IGF like family member 1*	-2.6466	0.1597
11758842_at	THBS1	*thrombospondin 1*	-2.6439	0.1600
11723298_s_at	AKAP2	*A-kinase anchoring protein 2*	-2.6367	0.1608
11741779_s_at	HSD11B1	*hydroxysteroid 11-beta dehydrogenase 1*	-2.5986	0.1651
11737798_a_at	PROCR	*protein C receptor*	-2.5916	0.1659
11717355_a_at	FEZ1	*fasciculation and elongation protein zeta 1*	-2.5812	0.1671
11753736_s_at	MT1P3	*metallothionein 1 pseudogene 3*	-2.5718	0.1682
11754360_a_at	RRM2	*ribonucleotide reductase regulatory subunit M2*	-2.5195	0.1744
11740349_at	RNASE7	*ribonuclease A family member 7*	-2.4949	0.1774
11719032_a_at	FADS3	*fatty acid desaturase 3*	-2.4572	0.1821
11726206_a_at	SH2D5	*SH2 domain containing 5*	-2.4150	0.1875
11725459_s_at	S100A7A	*S100 calcium binding protein A7A*	-2.3423	0.1972
11724478_s_at	FOSL1	*FOS like 1, AP-1 transcription factor subunit*	-2.3234	0.1998
11728404_at	SHCBP1	*SHC binding and spindle associated 1*	-2.3190	0.2004
11736687_a_at	FGF5	*fibroblast growth factor 5*	-2.2955	0.2037
11721842_a_at	GLIPR1	*GLI pathogenesis related 1*	-2.2912	0.2043
11746463_a_at	IL6	*interleukin 6*	-2.2577	0.2091
11721307_at	PHLDA1	*pleckstrin homology like domain family A member 1*	-2.2577	0.2091
11727215_a_at	NRG1	*neuregulin 1*	-2.2338	0.2126
11752515_a_at	ODC1	*ornithine decarboxylase 1*	-2.2223	0.2143
11734701_a_at	DKK3	*dickkopf WNT signaling pathway inhibitor 3*	-2.2203	0.2146
11731526_s_at	TRIP13	*thyroid hormone receptor interactor 13*	-2.2069	0.2166
11724139_s_at	SACS	*sacsin molecular chaperone*	-2.2042	0.2170
11718141_at	DKK1	*dickkopf WNT signaling pathway inhibitor 1*	-2.1950	0.2184
11744286_s_at	CBS	*cystathionine-beta-synthase*	-2.1890	0.2193
11737223_a_at	ARTN	*artemin*	-2.1884	0.2194
11744584_a_at	HYI	*Hydroxypyruvate Isomerase (Putative)*	-2.1844	0.2200
11725703_a_at	KLK6	*kallikrein related peptidase 6*	-2.1818	0.2204
11722122_at	CYP27B1	*cytochrome P450 family 27 subfamily B member 1*	-2.1740	0.2216
11744141_x_at	FOLR3	*folate receptor 3*	-2.1714	0.2220
11744047_a_at	MAP1B	*microtubule associated protein 1B*	-2.1668	0.2227
11739061_at	SLC7A5	*solute carrier family 7 member 5*	-2.1617	0.2235
11733957_x_at	SPRR2F	*small proline rich protein 2F*	-2.1571	0.2242
11715524_a_at	COTL1	*coactosin like F-actin binding protein 1*	-2.1559	0.2244
11724459_x_at	MIR6756	*microRNA 6756*	-2.1475	0.2257
11728054_a_at	DIAPH3	*diaphanous related formin 3*	-2.1475	0.2257
11719262_a_at	SMTN	*smoothelin*	-2.1361	0.2275
11753008_a_at	IL36G	*interleukin 36, gamma*	-2.1260	0.2291
11730029_a_at	E2F7	*E2F transcription factor 7*	-2.1215	0.2298
11729663_a_at	CHEK1	*checkpoint kinase 1*	-2.0979	0.2336
11733695_a_at	UBE2C	*ubiquitin conjugating enzyme E2 C*	-2.0874	0.2353
11748382_a_at	SMURF2	*SMAD specific E3 ubiquitin protein ligase 2*	-2.0850	0.2357

11743065_at	**CDC6**	***cell division cycle 6***	**-2.0801**	**0.2365**
11718183_at	**CDCA5**	***cell division cycle associated 5***	**-2.0746**	**0.2374**
11748328_s_at	**KRT16**	***keratin 16***	**-2.0655**	**0.2389**
11719811_a_at	**TRIB3**	***tribbles pseudokinase 3***	**-2.0613**	**0.2396**
11724464_a_at	**ANLN**	***anillin actin binding protein***	**-2.0559**	**0.2405**
11745469_a_at	**INPP4B**	***inositol polyphosphate-4-phosphatase type II B***	**-2.0547**	**0.2407**
11722572_at	**CCNA2**	***cyclin A2***	**-2.0499**	**0.2415**
11717163_s_at	**CDC20**	***cell division cycle 20***	**-2.0356**	**0.2439**
11733884_a_at	**DEPDC1**	***DEP domain containing 1***	**-2.0315**	**0.2446**
11725517_x_at	**ABCG1**	***ATP binding cassette subfamily G member 1***	**-2.0239**	**0.2459**
11763834_a_at	**PPP1R1C**	***protein phosphatase 1 regulatory inhibitor subunit 1C***	**-2.0203**	**0.2465**
11746427_a_at	**WDR66**	***WD repeat domain 66***	**-2.0128**	**0.2478**
11724888_a_at	**CARD10**	***caspase recruitment domain family member 10***	**-2.0122**	**0.2479**
11736440_at	**INF2**	***inverted formin, FH2 and WH2 domain containing***	**-2.0087**	**0.2485**
11758125_s_at	**DEPDC1B**	***DEP domain containing 1B***	**-2.0000**	**0.2500**
11725460_x_at	**S100A7**	***S100 calcium binding protein A7***	**-1.9948**	**0.2509**
11755046_a_at	**SPHK1**	***sphingosine kinase 1***	**-1.9931**	**0.2512**
11721932_a_at	**KIF23**	***kinesin family member 23***	**-1.9748**	**0.2544**
11736813_at	**PDCD1LG2**	***programmed cell death 1 ligand 2***	**-1.9635**	**0.2564**
11754074_s_at	**G0S2**	***G0/G1 switch 2***	**-1.9613**	**0.2568**
11716587_at	**AXL**	***AXL receptor tyrosine kinase***	**-1.9607**	**0.2569**
11763188_a_at	**SNX5**	***sorting nexin 5***	**-1.9495**	**0.2589**
11743530_a_at	**CENPK**	***centromere protein K***	**-1.9401**	**0.2606**
11721143_a_at	**MKI67**	***marker of proliferation Ki-67***	**-1.9390**	**0.2608**
11726559_s_at	**LCP1**	***lymphocyte cytosolic protein 1***	**-1.9384**	**0.2609**
11751116_a_at	**ACTN1**	***actinin alpha 1***	**-1.9324**	**0.2620**
11724038_a_at	**PTGS2**	***prostaglandin-endoperoxide synthase 2***	**-1.9263**	**0.2631**
11736246_a_at	**AMIGO2**	***adhesion molecule with Ig like domain 2***	**-1.9138**	**0.2654**
11740656_a_at	**HMGA2**	***high mobility group AT-hook 2***	**-1.9100**	**0.2661**
11722826_a_at	**NCAPG**	***non-SMC condensin I complex subunit G***	**-1.9089**	**0.2663**
11758529_s_at	**CENPA**	***centromere protein A***	**-1.9056**	**0.2669**
11763100_x_at	**MT1JP**	***metallothionein 1J, pseudogene***	**-1.8943**	**0.2690**
11728863_at	**GINS1**	***GINS complex subunit 1***	**-1.8938**	**0.2691**
11715563_s_at	**SCD**	***stearoyl-CoA desaturase***	**-1.8868**	**0.2704**
11724407_s_at	**CCNE1**	***cyclin E1***	**-1.8799**	**0.2717**
11725198_at	**IL1A**	***interleukin 1 alpha***	**-1.8794**	**0.2718**
11726536_at	**CYP1A1**	***cytochrome P450 family 1 subfamily A member 1***	**-1.8725**	**0.2731**
11722880_a_at	**PHF19**	***PHD finger protein 19***	**-1.8704**	**0.2735**
11719197_at	**CCND2**	***cyclin D2***	**-1.8693**	**0.2737**
11723435_s_at	**TTK**	***TTK protein kinase***	**-1.8672**	**0.2741**
11735576_a_at	**LETM2**	***leucine zipper and EF-hand containing transmembrane protein 2***	**-1.8635**	**0.2748**
11744425_a_at	**KIAA0101**	***KIAA0101***	**-1.8583**	**0.2758**

11747230_a_at	BUB1	*BUB1 mitotic checkpoint serine/threonine kinase*	-1.8562	0.2762
11728024_a_at	KLK5	*kallikrein related peptidase 5*	-1.8526	0.2769
11715803_a_at	ANXA6	*annexin A6*	-1.8510	0.2772
11758261_s_at	CEP55	*centrosomal protein 55*	-1.8427	0.2788
11719916_at	IL1B	*interleukin 1 beta*	-1.8365	0.2800
11723804_a_at	AKAP12	*A-kinase anchoring protein 12*	-1.8360	0.2801
11722367_a_at	DLGAP5	*DLG associated protein 5*	-1.8232	0.2826
11722193_a_at	C12orf75	*chromosome 12 open reading frame 75*	-1.8221	0.2828
11740133_a_at	CALD1	*caldesmon 1*	-1.8181	0.2836
11728876_at	CSF2	*colony stimulating factor 2*	-1.8176	0.2837
11725155_at	FJX1	*four jointed box 1*	-1.8176	0.2837
11718127_at	TK1	*thymidine kinase 1*	-1.8110	0.2850
11728303_at	TGFA	*transforming growth factor alpha*	-1.8105	0.2851
11733864_a_at	BIRC5	*baculoviral IAP repeat containing 5*	-1.8079	0.2856
11757884_s_at	MSRB3	*methionine sulfoxide reductase B3*	-1.7964	0.2879
11729243_s_at	FBN2	*fibrillin 2*	-1.7884	0.2895
11754824_a_at	LGALSL	*galectin like*	-1.7879	0.2896
11728161_at	WNT7A	*Wnt family member 7A*	-1.7745	0.2923
11743675_x_at	ABL2	*ABL proto-oncogene 2, non-receptor tyrosine kinase*	-1.7681	0.2936
11745249_x_at	TMEM40	*transmembrane protein 40*	-1.7632	0.2946
11731603_at	TMEM154	*transmembrane protein 154*	-1.7622	0.2948
11750598_s_at	TPX2	*TPX2, microtubule nucleation factor*	-1.7573	0.2958
11750723_x_at	MICB	*MHC class I polypeptide-related sequence B*	-1.7563	0.2960
11745377_x_at	PTRF	*polymerase I and transcript release factor*	-1.7486	0.2976
11727837_at	ORC6	*origin recognition complex subunit 6*	-1.7413	0.2991
11719849_s_at	UBE2S	*ubiquitin conjugating enzyme E2 S*	-1.7360	0.3002
11752384_s_at	COL6A1	*collagen type VI alpha 1 chain*	-1.7326	0.3009
11730821_x_at	CDKN3	*cyclin dependent kinase inhibitor 3*	-1.7326	0.3009
11720527_at	LTBP2	*latent transforming growth factor beta binding protein 2*	-1.7207	0.3034
11757940_at	PGF	*placental growth factor*	-1.7174	0.3041
11726617_s_at	CDK1	*cyclin dependent kinase 1*	-1.7169	0.3042
11720185_a_at	MAD2L1	*MAD2 mitotic arrest deficient-like 1 (yeast)*	-1.7164	0.3043
11754676_a_at	CENPE	*centromere protein E*	-1.7141	0.3048
11757747_s_at	LPIN1	*lipin 1*	-1.7075	0.3062
11723192_a_at	UHRF1	*ubiquitin like with PHD and ring finger domains 1*	-1.7032	0.3071
11727081_a_at	TIPIN	*TIMELESS interacting protein*	-1.6953	0.3088
11725161_a_at	DDIAS	*DNA damage induced apoptosis suppressor*	-1.6934	0.3092
11726757_s_at	CDC25A	*cell division cycle 25A*	-1.6887	0.3102
11757913_x_at	TUBA1A	*tubulin alpha 1a*	-1.6878	0.3104
11723939_a_at	CCNB1	*cyclin B1*	-1.6869	0.3106
11720647_a_at	BUB1B	*BUB1 mitotic checkpoint serine/threonine kinase B*	-1.6855	0.3109
11759423_at	EPPK1	*epiplakin 1*	-1.6827	0.3115

11739328_x_at	CENPH	*centromere protein H*	-1.6795	0.3122
11716358_s_at	PRC1	*protein regulator of cytokinesis 1*	-1.6758	0.3130
11757789_a_at	EPB41L2	*erythrocyte membrane protein band 4.1 like 2*	-1.6739	0.3134
11740957_x_at	SLC2A6	*solute carrier family 2 member 6*	-1.6652	0.3153
11718704_at	IGF1R	*insulin like growth factor 1 receptor*	-1.6638	0.3156
11716793_a_at	CCNB2	*cyclin B2*	-1.6634	0.3157
11728873_s_at	RBM24	*RNA binding motif protein 24*	-1.6611	0.3162
11754593_x_at	TUBB3	*tubulin beta 3 class III*	-1.6588	0.3167
11718943_a_at	AURKA	*aurora kinase A*	-1.6574	0.3170
11751206_s_at	RAB3GAP2	*RAB3 GTPase activating non-catalytic protein subunit 2*	-1.6443	0.3199
11758089_s_at	HMMR	*hyaluronan mediated motility receptor*	-1.6439	0.3200
11754344_s_at	SPRY4	*sprouty RTK signaling antagonist 4*	-1.6434	0.3201
11755466_a_at	CDCA2	*cell division cycle associated 2*	-1.6421	0.3204
11745868_a_at	KIF2C	*kinesin family member 2C*	-1.6344	0.3221
11718571_at	NT5DC3	*5'-nucleotidase domain containing 3*	-1.6246	0.3243
11736810_at	RPL27A	*ribosomal protein L27a*	-1.6210	0.3251
11726678_a_at	AFAP1L2	*actin filament associated protein 1 like 2*	-1.6197	0.3254
11723104_at	GNB4	*G protein subunit beta 4*	-1.6144	0.3266
11719586_a_at	TAGLN3	*transgelin 3*	-1.6126	0.3270
11718404_at	RFC3	*replication factor C subunit 3*	-1.6118	0.3272
11721071_s_at	DEF8	*differentially expressed in FDCP 8 homolog*	-1.6091	0.3278
11717481_s_at	FKBP10	*FK506 binding protein 10*	-1.6087	0.3279
11754375_s_at	SNX10	*sorting nexin 10*	-1.6074	0.3282
11744274_at	NDC80	*NDC80, kinetochore complex component*	-1.6060	0.3285
11756121_a_at	DUSP7	*dual specificity phosphatase 7*	-1.6056	0.3286
11747047_a_at	MAP3K7CL	*MAP3K7 C-terminal like*	-1.5995	0.3300
11747039_x_at	EHD1	*EH domain containing 1*	-1.5960	0.3308
11758294_s_at	ARMCX1	*armadillo repeat containing, X-linked 1*	-1.5920	0.3317
11720970_at	TOP2A	*Topoisomerase (DNA) II Alpha*	-1.5912	0.3319
11725469_at	LIPG	*lipase G, endothelial type*	-1.5890	0.3324
11751805_a_at	TYMS	*thymidylate synthetase*	-1.5851	0.3333
11739945_a_at	PKP1	*plakophilin 1*	-1.5825	0.3339
11756626_s_at	ZWINT	*ZW10 interacting kinetochore protein*	-1.5825	0.3339
11758598_s_at	SERPINE2	*serpin family E member 2*	-1.5804	0.3344
11719699_a_at	CDC45	*cell division cycle 45*	-1.5795	0.3346
11729579_at	CDH13	*cadherin 13*	-1.5670	0.3375
11742832_a_at	ASPM	*abnormal spindle microtubule assembly*	-1.5662	0.3377
11724405_at	NDUFC2-KCTD14	*NDUFC2-KCTD14 readthrough*	-1.5594	0.3393
11716094_a_at	KLF6	*Kruppel like factor 6*	-1.5572	0.3398
11724326_a_at	ARHGAP25	*Rho GTPase activating protein 25*	-1.5568	0.3399
11755009_s_at	VCAN	*versican*	-1.5538	0.3406
11756882_a_at	RTTN	*rotatin*	-1.5530	0.3408

11723147_a_at	NAV3	*neuron navigator 3*	-1.5522	0.3410
11759656_a_at	KLHL7	*kelch like family member 7*	-1.5509	0.3413
11759698_at	STEAP1B	*STEAP family member 1B*	-1.5505	0.3414
11758499_s_at	DTL	*denticleless E3 ubiquitin protein ligase homolog*	-1.5488	0.3418
11752387_a_at	ETS1	*ETS proto-oncogene 1, transcription factor*	-1.5471	0.3422
11725169_at	MOB3B	*MOB kinase activator 3B*	-1.5395	0.3440
11741015_a_at	CDCA8	*cell division cycle associated 8*	-1.5391	0.3441
11727543_at	OIP5	*Opa interacting protein 5*	-1.5345	0.3452
11719041_at	CYGB	*cytoglobin*	-1.5332	0.3455
11717436_a_at	CDCA7L	*cell division cycle associated 7 like*	-1.5312	0.3460
11728076_at	HDAC9	*histone deacetylase 9*	-1.5307	0.3461
11718980_a_at	YKT6	*YKT6 V-SNARE Homolog (S. Cerevisiae)*	-1.5295	0.3464
11721563_a_at	MELK	*maternal embryonic leucine zipper kinase*	-1.5245	0.3476
11717758_x_at	RALA	*RAS like proto-oncogene A*	-1.5191	0.3489
11743160_a_at	HJURP	*Holliday junction recognition protein*	-1.5179	0.3492
11759328_at	KNL1	*kinetochore scaffold 1*	-1.5137	0.3502
11723950_a_at	PBK	*PDZ binding kinase*	-1.5137	0.3502
11727324_at	NAGS	*N-acetylglutamate synthase*	-1.5125	0.3505
11742735_a_at	NUSAP1	*nucleolar and spindle associated protein 1*	-1.5092	0.3513
11729227_a_at	GRK5	*G protein-coupled receptor kinase 5*	-1.5055	0.3522
11741400_a_at	STMN1	*stathmin 1*	-1.5006	0.3534
11722839_at	LYAR	*Ly1 antibody reactive*	-1.4994	0.3537
11727937_x_at	MSANTD3	*Myb/SANT DNA binding domain containing 3*	-1.4990	0.3538
11747820_x_at	UPP1	*uridine phosphorylase 1*	-1.4974	0.3542
11736570_a_at	SLC39A14	*solute carrier family 39 member 14*	-1.4970	0.3543
11743373_a_at	KNSTRN	*kinetochore localized astrin/SPAG5 binding protein*	-1.4941	0.3550
11719179_a_at	PVR	*poliovirus receptor*	-1.4925	0.3554
11754180_s_at	SPRR1A	*small proline rich protein 1A*	-1.4872	0.3567
11758396_s_at	POLR3G	*RNA polymerase III subunit G*	-1.4836	0.3576
11716847_a_at	SLC43A3	*solute carrier family 43 member 3*	-1.4824	0.3579
11758478_s_at	CDCA7	*cell division cycle associated 7*	-1.4812	0.3582
11731653_a_at	IVL	*involucrin*	-1.4812	0.3582
11718297_a_at	TACC3	*transforming acidic coiled-coil containing protein 3*	-1.4800	0.3585
11737197_s_at	KIF4A	*kinesin family member 4A*	-1.4779	0.3590
11715947_a_at	KCTD12	*potassium channel tetramerization domain containing 12*	-1.4775	0.3591
11728612_at	ADAMTS6	*ADAM metallopeptidase with thrombospondin type 1 motif 6*	-1.4731	0.3602
11744630_a_at	NXPE3	*neurexophilin and PC-esterase domain family member 3*	-1.4711	0.3607
11743151_a_at	GLS	*glutaminase*	-1.4683	0.3614
11756230_a_at	FLNB	*filamin B*	-1.4655	0.3621
11722442_a_at	NUF2	*NUF2, NDC80 kinetochore complex component*	-1.4608	0.3633
11724122_a_at	SLC35G2	*solute carrier family 35 member G2*	-1.4604	0.3634
11720203_a_at	AURKB	*aurora kinase B*	-1.4568	0.3643

11754440_s_at	GAS6	*growth arrest specific 6*	-1.4556	0.3646
11723747_a_at	FAM64A	*family with sequence similarity 64 member A*	-1.4540	0.3650
11738222_x_at	RAET1L	*retinoic acid early transcript 1L*	-1.4528	0.3653
11717055_a_at	CORO1C	*coronin 1C*	-1.4525	0.3654
11743513_a_at	GINS2	*GINS complex subunit 2*	-1.4521	0.3655
11718140_a_at	EMP3	*epithelial membrane protein 3*	-1.4501	0.3660
11727459_x_at	KRT14	*keratin 14*	-1.4446	0.3674
11728558_a_at	HSF2BP	*heat shock transcription factor 2 binding protein*	-1.4430	0.3678
11719258_at	TICAM1	*toll like receptor adaptor molecule 1*	-1.4367	0.3694
11727489_a_at	KIF11	*kinesin family member 11*	-1.4360	0.3696
11758164_s_at	FEN1	*flap structure-specific endonuclease 1*	-1.4344	0.3700
11736596_s_at	GINS4	*GINS complex subunit 4*	-1.4328	0.3704
11744435_a_at	DUSP6	*dual specificity phosphatase 6*	-1.4317	0.3707
11719173_s_at	PAICS	*phosphoribosylaminoimidazole carboxylase; phosphoribosylaminoimidazolesuccinocarboxamide synthase*	-1.4301	0.3711
11719882_s_at	OSTM1	*osteopetrosis associated transmembrane protein 1*	-1.4293	0.3713
11720842_at	RHOD	*ras homolog family member D*	-1.4274	0.3718
11726724_a_at	CKAP2L	*cytoskeleton associated protein 2 like*	-1.4270	0.3719
11754559_a_at	SBSN	*suprabasin*	-1.4259	0.3722
11739144_a_at	SKP2	*S-phase kinase associated protein 2*	-1.4251	0.3724
11723983_at	KRT6B	*keratin 6B*	-1.4251	0.3724
11738062_x_at	S100A7A	*S100 calcium binding protein A7A*	-1.4251	0.3724
11721345_at	PLEK2	*pleckstrin 2*	-1.4239	0.3727
11748338_a_at	SLC31A2	*solute carrier family 31 member 2*	-1.4235	0.3728
11733126_a_at	PRIM1	*Primase (DNA) Subunit 1*	-1.4212	0.3734
11730264_a_at	FAM83D	*family with sequence similarity 83 member D*	-1.4208	0.3735
11747334_a_at	DDX39A	*DExD-box helicase 39A*	-1.4189	0.3740
11732191_s_at	RAD51AP1	*RAD51 associated protein 1*	-1.4177	0.3743
11726963_s_at	SGTB	*small glutamine rich tetratricopeptide repeat containing beta*	-1.4150	0.3750
11718578_a_at	GSTM3	*glutathione S-transferase mu 3*	-1.4131	0.3755
11726441_a_at	ERCC6L	*ERCC excision repair 6 like, spindle assembly checkpoint helicase*	-1.4112	0.3760
11744880_a_at	ZNF165	*zinc finger protein 165*	-1.4085	0.3767
11745459_a_at	MIR1908	*microRNA 1908*	-1.4066	0.3772
11716131_s_at	FSTL3	*follistatin like 3*	-1.4051	0.3776
11728565_x_at	FAM210A	*family with sequence similarity 210 member A*	-1.4039	0.3779
11742819_at	PLAUR	*plasminogen activator, urokinase receptor*	-1.4028	0.3782
11749980_x_at	HOPX	*HOP homeobox*	-1.3990	0.3792
11720794_a_at	SRPX	*sushi repeat containing protein, X-linked*	-1.3955	0.3801
11735123_x_at	POLR1E	*RNA polymerase I subunit E*	-1.3906	0.3814
11720401_at	NCS1	*neuronal calcium sensor 1*	-1.3902	0.3815
11748436_x_at	yeast	*CAP, adenylate cyclase-associated protein, 2*	-1.3902	0.3815
11754574_a_at	C6orf52	*chromosome 6 open reading frame 52*	-1.3891	0.3818
11725441_a_at	FOXM1	*forkhead box M1*	-1.3842	0.3831

11716638_s_at	COL4A1	*collagen type IV alpha 1 chain*	-1.3808	0.3840
11732925_s_at	PEAR1	*platelet endothelial aggregation receptor 1*	-1.3801	0.3842
11725788_a_at	CENPN	*centromere protein N*	-1.3801	0.3842
11727833_at	WDR43	*WD repeat domain 43*	-1.3797	0.3843
11756182_s_at	PSAT1	*phosphoserine aminotransferase 1*	-1.3730	0.3861
11734865_a_at	PSMC3IP	*PSMC3 interacting protein*	-1.3722	0.3863
11746931_a_at	INHBA	*inhibin beta A subunit*	-1.3711	0.3866
11748602_a_at	BAG2	*BCL2 associated athanogene 2*	-1.3711	0.3866
11729458_a_at	FANCI	*Fanconi anemia complementation group I*	-1.3685	0.3873
11724963_s_at	FBXO5	*F-box protein 5*	-1.3666	0.3878
11716459_at	TUBA4A	*tubulin alpha 4a*	-1.3603	0.3895
11728233_a_at	CLDN1	*claudin 1*	-1.3599	0.3896
11744005_at	PHLDA2	*pleckstrin homology like domain family A member 2*	-1.3573	0.3903
11746880_x_at	FLNA	*filamin A*	-1.3562	0.3906
11727968_at	ESCO2	*establishment of sister chromatid cohesion N-acetyltransferase 2*	-1.3537	0.3913
11717565_s_at	EMP1	*epithelial membrane protein 1*	-1.3518	0.3918
11743721_at	LGALS1	*galectin 1*	-1.3492	0.3925
11725152_at	L3HYPDH	*trans-L-3-hydroxyproline dehydratase*	-1.3467	0.3932
11718305_a_at	PDLIM2	*PDZ and LIM domain 2*	-1.3463	0.3933
11750141_a_at	CTPS1	*CTP synthase 1*	-1.3456	0.3935
11723591_at	LRRC8C	*leucine rich repeat containing 8 family member C*	-1.3441	0.3939
11730740_a_at	PDLIM4	*PDZ and LIM domain 4*	-1.3430	0.3942
11744887_s_at	ZWILCH	*zwilch kinetochore protein*	-1.3419	0.3945
11725825_a_at	GJB3	*gap junction protein beta 3*	-1.3404	0.3949
11727773_at	LARP6	*La ribonucleoprotein domain family member 6*	-1.3379	0.3956
11728300_at	CCNE2	*cyclin E2*	-1.3379	0.3956
11746116_a_at	PINX1	*PIN2/TERF1 interacting, telomerase inhibitor 1*	-1.3350	0.3964
11723883_at	SOWAHC	*sosondowah ankyrin repeat domain family member C*	-1.3342	0.3966
11718591_at	SDF2L1	*stromal cell derived factor 2 like 1*	-1.3328	0.3970
11723010_a_at	KIF20A	*kinesin family member 20A*	-1.3328	0.3970
11753255_a_at	KLK7	*kallikrein related peptidase 7*	-1.3270	0.3986
11718290_a_at	FXYD5	*FXYD domain containing ion transport regulator 5*	-1.3263	0.3988
11743434_a_at	CHST11	*carbohydrate sulfotransferase 11*	-1.3259	0.3989
11734070_x_at	SSR3	*signal sequence receptor subunit 3*	-1.3248	0.3992
11744764_s_at	WHSC1	*Wolf-Hirschhorn syndrome candidate 1*	-1.3230	0.3997
11720770_a_at	PPIF	*peptidylprolyl isomerase F*	-1.3226	0.3998
11726013_a_at	AJUBA	*ajuba LIM protein*	-1.3205	0.4004
11731887_at	KIF14	*kinesin family member 14*	-1.3165	0.4015
11719411_at	RAB32	*RAB32, member RAS oncogene family*	-1.3165	0.4015
11758266_s_at	PSMD2	*proteasome 26S subunit, non-ATPase 2*	-1.3162	0.4016
11719154_a_at	DRAM1	*DNA damage regulated autophagy modulator 1*	-1.3158	0.4017
11757117_at	SNORA64	*small nucleolar RNA, H/ACA box 64*	-1.3158	0.4017

11744747_a_at	FGFR1OP2	*FGFR1 oncogene partner 2*	-1.3126	0.4026
11755028_a_at	DENND1A	*DENN domain containing 1A*	-1.3108	0.4031
11733833_a_at	MAP2	*microtubule associated protein 2*	-1.3101	0.4033
11760362_x_at	PGAM5	*PGAM family member 5, mitochondrial serine/threonine protein phosphatase*	-1.3072	0.4041
11734846_x_at	TAF1B	*TATA-box binding protein associated factor, RNA polymerase I subunit B*	-1.3069	0.4042
11737413_at	MICALCL	*MICAL C-terminal like*	-1.3047	0.4048
11722379_at	GNG11	*G protein subunit gamma 11*	-1.3033	0.4052
11743296_a_at	CENPF	*centromere protein F*	-1.3001	0.4061
11722069_a_at	SKA1	*spindle and kinetochore associated complex subunit 1*	-1.2994	0.4063
11729140_x_at	SLAMF7	*SLAM family member 7*	-1.2980	0.4067
11726193_at	MARCH4	*membrane associated ring-CH-type finger 4*	-1.2969	0.4070
11759444_x_at	BAX	*BCL2 associated X, apoptosis regulator*	-1.2944	0.4077
11732542_at	TRIM7	*tripartite motif containing 7*	-1.2937	0.4079
11728135_at	NIPAL4	*NIPA like domain containing 4*	-1.2934	0.4080
11729834_at	EIF5A2	*eukaryotic translation initiation factor 5A2*	-1.2909	0.4087
11718262_a_at	ERF	*ETS2 repressor factor*	-1.2888	0.4093
11733037_a_at	DPH3	*diphthamide biosynthesis 3*	-1.2863	0.4100
11722235_a_at	FBXO2	*F-box protein 2*	-1.2863	0.4100
11749656_a_at	ARHGAP11A	*Rho GTPase activating protein 11A*	-1.2860	0.4101
11741126_s_at	SLFN11	*schlafen family member 11*	-1.2860	0.4101
11725274_s_at	RGS20	*regulator of G-protein signaling 20*	-1.2860	0.4101
11724579_a_at	L1CAM	*L1 cell adhesion molecule*	-1.2856	0.4102
11724993_at	RFLNB	*refilin B*	-1.2852	0.4103
11718315_at	SLC16A2	*solute carrier family 16 member 2*	-1.2842	0.4106
11720163_at	VEGFC	*vascular endothelial growth factor C*	-1.2835	0.4108
11741152_x_at	PLAGL1	*PLAG1 like zinc finger 1*	-1.2828	0.4110
11747193_a_at	ZNF185	*Zinc Finger Protein 185 (LIM Domain)*	-1.2782	0.4123
11729131_a_at	PSME3	*proteasome activator subunit 3*	-1.2772	0.4126
11748733_a_at	KCTD7	*potassium channel tetramerization domain containing 7*	-1.2772	0.4126
11737852_s_at	PPP1R18	*protein phosphatase 1 regulatory subunit 18*	-1.2772	0.4126
11741710_a_at	COL6A3	*collagen type VI alpha 3 chain*	-1.2730	0.4138
11725117_a_at	NLN	*neurolysin*	-1.2702	0.4146
11739763_a_at	GINS3	*GINS complex subunit 3*	-1.2674	0.4154
11719898_s_at	HBEGF	*heparin binding EGF like growth factor*	-1.2674	0.4154
11726572_a_at	SEMA7A	*Semaphorin 7A (John Milton Hagen Blood Group)*	-1.2660	0.4158
11721632_a_at	TMEM97	*transmembrane protein 97*	-1.2657	0.4159
11757017_x_at	RNASEH2A	*ribonuclease H2 subunit A*	-1.2653	0.4160
11728808_at	CHAC2	*ChaC cation transport regulator homolog 2*	-1.2647	0.4162
11743633_a_at	STX2	*syntaxin 2*	-1.2636	0.4165
11753830_a_at	MLLT11	*myeloid/lymphoid or mixed-lineage leukemia; translocated to, 11*	-1.2595	0.4177
11739654_at	TNFRSF10A	*TNF receptor superfamily member 10a*	-1.2584	0.4180
11755624_a_at	MTFR2	*mitochondrial fission regulator 2*	-1.2570	0.4184

11757860_s_at	QKI	*QKI, KH domain containing RNA binding*	-1.2560	0.4187
11723707_a_at	AIFM2	*apoptosis inducing factor, mitochondria associated 2*	-1.2553	0.4189
11758165_s_at	MRTO4	*MRT4 homolog, ribosome maturation factor*	-1.2550	0.4190
11719830_a_at	ERCC1	*ERCC excision repair 1, endonuclease non-catalytic subunit*	-1.2539	0.4193
11722252_x_at	NEK2	*NIMA related kinase 2*	-1.2536	0.4194
11753856_a_at	CKS2	*CDC28 protein kinase regulatory subunit 2*	-1.2529	0.4196
11737671_at	GLB1L3	*galactosidase beta 1 like 3*	-1.2519	0.4199
11726006_at	SLC30A1	*solute carrier family 30 member 1*	-1.2512	0.4201
11731068_s_at	FIGNL1	*fidgetin like 1*	-1.2474	0.4212
11746206_a_at	RHOF	*ras homolog family member F, filopodia associated*	-1.2467	0.4214
11720967_a_at	GPSM2	*G-protein signaling modulator 2*	-1.2467	0.4214
11749905_a_at	CYR61	*cysteine rich angiogenic inducer 61*	-1.2461	0.4216
11716537_s_at	SZRD1	*SUZ RNA binding domain containing 1*	-1.2443	0.4221
11736366_x_at	MCM10	*minichromosome maintenance 10 replication initiation factor*	-1.2437	0.4223
11732756_a_at	ELAVL2	*ELAV like RNA binding protein 2*	-1.2416	0.4229
11760436_a_at	DST	*dystonin*	-1.2406	0.4232
11728896_a_at	LRP8	*LDL receptor related protein 8*	-1.2406	0.4232
11745845_a_at	NME7	*NME/NM23 family member 7*	-1.2392	0.4236
11715306_s_at	AREG	*amphiregulin*	-1.2382	0.4239
11722971_a_at	LOC401317	*uncharacterized LOC401317*	-1.2379	0.4240
11726779_a_at	IKBIP	*IKBKB interacting protein*	-1.2365	0.4244
11726023_a_at	EDN1	*endothelin 1*	-1.2362	0.4245
11726136_a_at	TMSB15A	*thymosin beta 15a*	-1.2345	0.4250
11722225_a_at	ADAM8	*ADAM metallopeptidase domain 8*	-1.2321	0.4257
11753254_a_at	SGO2	*shugoshin 2*	-1.2287	0.4267
11759011_at	PRPF4	*pre-mRNA processing factor 4*	-1.2284	0.4268
11742945_a_at	MIR6733	*microRNA 6733*	-1.2247	0.4279
11728257_at	RAD18	*RAD18, E3 ubiquitin protein ligase*	-1.2230	0.4284
11726407_at	SRRD	*SRR1 domain containing*	-1.2223	0.4286
11754438_x_at	GJC1	*gap junction protein gamma 1*	-1.2206	0.4291
11718119_s_at	CFL2	*cofilin 2*	-1.2203	0.4292
11744488_a_at	ACOT9	*acyl-CoA thioesterase 9*	-1.2199	0.4293
11751697_a_at	NAA50	*N(Alpha)-Acetyltransferase 50, NatE Catalytic Subunit*	-1.2163	0.4304
11732661_x_at	STIL	*SCL/TAL1 interrupting locus*	-1.2163	0.4304
11721208_at	IFFO2	*intermediate filament family orphan 2*	-1.2126	0.4315
11723682_at	ALYREF	*Aly/REF export factor*	-1.2116	0.4318
11736461_at	RAB3B	*RAB3B, member RAS oncogene family*	-1.2116	0.4318
11758572_s_at	HELLS	*helicase, lymphoid-specific*	-1.2106	0.4321
11717444_at	BYSL	*bystin like*	-1.2102	0.4322
11718076_at	MAPKAPK3	*mitogen-activated protein kinase-activated protein kinase 3*	-1.2099	0.4323
11743452_s_at	CDCA4	*cell division cycle associated 4*	-1.2092	0.4325
11743169_a_at	LPXN	*leupaxin*	-1.2039	0.4341

11725842_a_at	PIF1	*PIF1 5'-to-3' DNA helicase*	-1.2029	0.4344
11731834_a_at	IL24	*interleukin 24*	-1.2022	0.4346
11716631_s_at	SERPINB2	*serpin family B member 2*	-1.2002	0.4352
11759176_at	GTSE1	*G2 and S-phase expressed 1*	-1.1976	0.4360
11738997_s_at	DPYSL2	*dihydropyrimidinase like 2*	-1.1943	0.4370
11752792_a_at	TACC1	*transforming acidic coiled-coil containing protein 1*	-1.1917	0.4378
11746588_a_at	ALDH1B1	*aldehyde dehydrogenase 1 family member B1*	-1.1894	0.4385
11756160_x_at	CTNNAL1	*catenin alpha like 1*	-1.1884	0.4388
11729310_a_at	SKA3	*spindle and kinetochore associated complex subunit 3*	-1.1880	0.4389
11761579_at	DMKN	*dermokine*	-1.1867	0.4393
11727063_a_at	MIR3658	*microRNA 3658*	-1.1844	0.4400
11717863_a_at	DUSP5	*dual specificity phosphatase 5*	-1.1838	0.4402
11725046_a_at	ANP32E	*acidic nuclear phosphoprotein 32 family member E*	-1.1815	0.4409
11753435_x_at	SLC3A2	*solute carrier family 3 member 2*	-1.1805	0.4412
11717833_a_at	TEX10	*testis expressed 10*	-1.1802	0.4413
11754193_a_at	PCYT1A	*phosphate cytidylyltransferase 1, choline, alpha*	-1.1792	0.4416
11752905_a_at	MCM7	*minichromosome maintenance complex component 7*	-1.1785	0.4418
11715442_s_at	CTGF	*connective tissue growth factor*	-1.1779	0.4420
11743841_at	PLCXD2	*phosphatidylinositol specific phospholipase C X domain containing 2*	-1.1763	0.4425
11754313_s_at	ARL4C	*ADP ribosylation factor like GTPase 4C*	-1.1756	0.4427
11730470_at	CALML5	*calmodulin like 5*	-1.1749	0.4429
11725232_at	ATP8B2	*ATPase phospholipid transporting 8B2*	-1.1740	0.4432
11735324_s_at	FAM72C	*family with sequence similarity 72 member C*	-1.1740	0.4432
11738840_a_at	NUDT10	*nudix hydrolase 10*	-1.1717	0.4439
11730525_a_at	SSC4D	*scavenger receptor cysteine rich family member with 4 domains*	-1.1710	0.4441
11725687_s_at	PRIM2	*Primase (DNA) Subunit 2*	-1.1684	0.4449
11725064_x_at	TCOF1	*treacle ribosome biogenesis factor 1*	-1.1681	0.4450
11724551_x_at	TMEM55A	*transmembrane protein 55A*	-1.1675	0.4452
11755424_a_at	HMOX2	*heme oxygenase 2*	-1.1665	0.4455
11749874_a_at	OXCT1	*3-oxoacid CoA-transferase 1*	-1.1662	0.4456
11745020_a_at	TNFRSF12A	*TNF receptor superfamily member 12A*	-1.1659	0.4457
11726551_s_at	RAET1L	*retinoic acid early transcript 1L*	-1.1655	0.4458
11717409_at	SH2B3	*SH2B adaptor protein 3*	-1.1652	0.4459
11718400_a_at	PNP	*purine nucleoside phosphorylase*	-1.1649	0.4460
11743922_at	NUDT11	*nudix hydrolase 11*	-1.1646	0.4461
11728825_at	TRNP1	*TMF1-regulated nuclear protein 1*	-1.1642	0.4462
11722248_a_at	RASSF1	*Ras association domain family member 1*	-1.1629	0.4466
11721435_at	STC2	*stanniocalcin 2*	-1.1626	0.4467
11716982_at	CMSS1	*Cms1 Ribosomal Small Subunit Homolog (Yeast)*	-1.1617	0.4470
11725714_a_at	RPS14	*ribosomal protein S14*	-1.1584	0.4480
11726807_a_at	ZAK	*sterile alpha motif and leucine zipper containing kinase AZK*	-1.1568	0.4485
11746242_a_at	ARNTL2	*aryl hydrocarbon receptor nuclear translocator like 2*	-1.1562	0.4487

11727247_x_at	CHRNB1	*cholinergic receptor nicotinic beta 1 subunit*	-1.1555	0.4489
11730614_a_at	SLC1A4	*solute carrier family 1 member 4*	-1.1549	0.4491
11747996_a_at	ETV4	*ETS variant 4*	-1.1546	0.4492
11716872_a_at	ADCY3	*adenylate cyclase 3*	-1.1542	0.4493
11749139_a_at	SEMA3C	*semaphorin 3C*	-1.1542	0.4493
11751165_a_at	RBMS2	*RNA binding motif single stranded interacting protein 2*	-1.1517	0.4501
11715452_s_at	COL4A2	*collagen type IV alpha 2 chain*	-1.1507	0.4504
11756742_a_at	AGPAT5	*1-acylglycerol-3-phosphate O-acyltransferase 5*	-1.1494	0.4508
11757547_a_at	SUN1	*Sad1 and UNC84 domain containing 1*	-1.1466	0.4517
11734825_at	SPRED1	*sprouty related EVH1 domain containing 1*	-1.1466	0.4517
11734557_a_at	GALNT5	*polypeptide N-acetylgalactosaminyltransferase 5*	-1.1462	0.4518
11763164_at	DNAJC9	*DnaJ Heat Shock Protein Family (Hsp40) Member C9*	-1.1453	0.4521
11723256_a_at	PKMYT1	*protein kinase, membrane associated tyrosine/threonine 1*	-1.1453	0.4521
11738259_s_at	CXorf49	*chromosome X open reading frame 49*	-1.1446	0.4523
11740490_at	KRT75	*keratin 75*	-1.1446	0.4523
11743191_a_at	NTM	*neurotrimin*	-1.1424	0.4530
11757791_s_at	DUSP3	*dual specificity phosphatase 3*	-1.1418	0.4532
11717521_x_at	PTTG3P	*pituitary tumor-transforming 3, pseudogene*	-1.1418	0.4532
11755278_a_at	CYP2S1	*cytochrome P450 family 2 subfamily S member 1*	-1.1408	0.4535
11733876_x_at	SMC4	*structural maintenance of chromosomes 4*	-1.1405	0.4536
11743536_at	VRK1	*vaccinia related kinase 1*	-1.1376	0.4545
11731880_at	NLRP1	*NLR family pyrin domain containing 1*	-1.1370	0.4547
11734867_a_at	TPRG1	*tumor protein p63 regulated 1*	-1.1361	0.4550
11721666_at	CDT1	*chromatin licensing and DNA replication factor 1*	-1.1354	0.4552
11747245_a_at	UTP15	*UTP15, small subunit processome component*	-1.1351	0.4553
11716092_x_at	CKS1B	*CDC28 protein kinase regulatory subunit 1B*	-1.1348	0.4554
11757447_s_at	CYTH3	*cytohesin 3*	-1.1338	0.4557
11744734_a_at	SIN3B	*SIN3 transcription regulator family member B*	-1.1335	0.4558
11745571_a_at	CENPA	*centromere protein A*	-1.1335	0.4558
11719598_s_at	CDCA3	*cell division cycle associated 3*	-1.1307	0.4567
11728731_s_at	DSCC1	*DNA replication and sister chromatid cohesion 1*	-1.1300	0.4569
11719681_a_at	TNFRSF10B	*TNF receptor superfamily member 10b*	-1.1297	0.4570
11754068_a_at	CSRP1	*cysteine and glycine rich protein 1*	-1.1282	0.4575
11729096_a_at	POLQ	*DNA polymerase theta*	-1.1275	0.4577
11744289_a_at	JMJD6	*arginine demethylase and lysine hydroxylase*	-1.1263	0.4581
11725704_a_at	AMOTL1	*angiomotin like 1*	-1.1260	0.4582
11719634_a_at	KLF4	*Kruppel like factor 4*	-1.1253	0.4584
11756393_x_at	CORO1A	*coronin 1A*	-1.1250	0.4585
11733539_a_at	MROH1	*maestro heat like repeat family member 1*	-1.1244	0.4587
11744604_at	ERVMER34-1	*endogenous retrovirus group MER34 member 1*	-1.1237	0.4589
11759661_at	MYO10	*myosin X*	-1.1215	0.4596
11723985_a_at	PDCD11	*programmed cell death 11*	-1.1209	0.4598

11724402_s_at	HS3ST2	*heparan sulfate-glucosamine 3-sulfotransferase 2*	-1.1194	0.4603
11720213_x_at	PPAN	*Peter Pan Homolog (Drosophila)*	-1.1162	0.4613
11756409_a_at	BLM	*Bloom syndrome RecQ like helicase*	-1.1162	0.4613
11740885_a_at	OSBPL3	*oxysterol binding protein like 3*	-1.1156	0.4615
11719732_at	TIGAR	*TP53 induced glycolysis regulatory phosphatase*	-1.1143	0.4619
11721530_at	ZDHHC2	*zinc finger DHHC-type containing 2*	-1.1140	0.4620
11745424_a_at	SMC2	*structural maintenance of chromosomes 2*	-1.1134	0.4622
11723803_a_at	TREM2	*triggering receptor expressed on myeloid cells 2*	-1.1131	0.4623
11756872_a_at	SAMD4A	*sterile alpha motif domain containing 4A*	-1.1125	0.4625
11715926_s_at	PLEC	*plectin*	-1.1125	0.4625
11736405_a_at	DNMT1	*DNA methyltransferase 1*	-1.1119	0.4627
11745010_a_at	DCBLD2	*discoidin, CUB and LCCL domain containing 2*	-1.1112	0.4629
11716011_a_at	TNFAIP1	*TNF alpha induced protein 1*	-1.1100	0.4633
11716642_s_at	DTYMK	*deoxythymidylate kinase*	-1.1084	0.4638
11736240_a_at	AAED1	*AhpC/TSA antioxidant enzyme domain containing 1*	-1.1084	0.4638
11754098_a_at	AGO2	*argonaute 2, RISC catalytic component*	-1.1066	0.4644
11754314_a_at	TTC7B	*tetratricopeptide repeat domain 7B*	-1.1066	0.4644
11721854_a_at	NCAPH	*non-SMC condensin I complex subunit H*	-1.1044	0.4651
11735167_x_at	RFC2	*replication factor C subunit 2*	-1.1035	0.4654
11754071_x_at	TAGLN2	*transgelin 2*	-1.1031	0.4655
11717154_a_at	PLAU	*plasminogen activator, urokinase*	-1.0994	0.4667
11752409_a_at	NDC1	*NDC1 transmembrane nucleoporin*	-1.0994	0.4667
11732078_a_at	EVA1A	*eva-1 homolog A, regulator of programmed cell death*	-1.0985	0.4670
11736083_x_at	GTSE1	*G2 and S-phase expressed 1*	-1.0973	0.4674
11726717_at	C1orf74	*chromosome 1 open reading frame 74*	-1.0970	0.4675
11723829_s_at	ANO1	*anoctamin 1*	-1.0967	0.4676
11727236_a_at	C18orf25	*chromosome 18 open reading frame 25*	-1.0963	0.4677
11717754_a_at	SEC14L1	*SEC14 like lipid binding 1*	-1.0957	0.4679
11729341_at	POU2F2	*POU class 2 homeobox 2*	-1.0957	0.4679
11724064_a_at	SLC25A19	*solute carrier family 25 member 19*	-1.0951	0.4681
11727458_at	KIF18A	*kinesin family member 18A*	-1.0951	0.4681
11726116_at	MTAP	*methylthioadenosine phosphorylase*	-1.0948	0.4682
11748400_s_at	TPM4	*tropomyosin 4*	-1.0945	0.4683
11721767_s_at	ATAD3A	*ATPase family, AAA domain containing 3A*	-1.0939	0.4685
11716987_a_at	HMGCS1	*3-hydroxy-3-methylglutaryl-CoA synthase 1*	-1.0939	0.4685
11723998_at	SPC25	*SPC25, NDC80 kinetochore complex component*	-1.0936	0.4686
11727141_s_at	EPB41L3	*erythrocyte membrane protein band 4.1 like 3*	-1.0920	0.4691
11749650_x_at	A2ML1	*alpha-2-macroglobulin like 1*	-1.0917	0.4692
11715717_s_at	MSN	*moesin*	-1.0911	0.4694
11758149_s_at	RACGAP1	*Rac GTPase activating protein 1*	-1.0911	0.4694
11745130_x_at	HMGB3	*high mobility group box 3*	-1.0908	0.4695
11718376_s_at	WDR5	*WD repeat domain 5*	-1.0899	0.4698

11751918_a_at	BNC1	*basonuclin 1*	-1.0899	0.4698
11741967_a_at	CDYL	*chromodomain Y-like*	-1.0896	0.4699
11721209_a_at	EXO1	*exonuclease 1*	-1.0871	0.4707
11723499_a_at	PCSK9	*proprotein convertase subtilisin/kexin type 9*	-1.0856	0.4712
11717282_at	ASAP1	*ArfGAP with SH3 domain, ankyrin repeat and PH domain 1*	-1.0856	0.4712
11718802_a_at	PSRC1	*proline and serine rich coiled-coil 1*	-1.0850	0.4714
11717257_s_at	PIM1	*Pim-1 proto-oncogene, serine/threonine kinase*	-1.0847	0.4715
11740032_s_at	DUSP14	*dual specificity phosphatase 14*	-1.0847	0.4715
11729185_at	PNO1	*partner of NOB1 homolog*	-1.0844	0.4716
11758629_s_at	SPTBN1	*spectrin beta, non-erythrocytic 1*	-1.0838	0.4718
11721843_a_at	ATL3	*atlastin GTPase 3*	-1.0831	0.4720
11715593_s_at	YWHAH	*tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta*	-1.0825	0.4722
11736978_at	PADI3	*peptidyl arginine deiminase 3*	-1.0825	0.4722
11757853_s_at	TWIST2	*twist family bHLH transcription factor 2*	-1.0816	0.4725
11758997_at	SYNPO	*synaptopodin*	-1.0804	0.4729
11731896_a_at	TNFSF4	*tumor necrosis factor superfamily member 4*	-1.0801	0.4730
11746700_s_at	ITM2A	*integral membrane protein 2A*	-1.0786	0.4735
11759746_a_at	ARHGEF28	*Rho guanine nucleotide exchange factor 28*	-1.0770	0.4740
11735012_a_at	DYNLL2	*dynein light chain LC8-type 2*	-1.0740	0.4750
11724283_a_at	ANXA3	*annexin A3*	-1.0728	0.4754
11738279_a_at	KLK12	*kallikrein related peptidase 12*	-1.0722	0.4756
11719686_a_at	MICAL1	*microtubule associated monooxygenase, calponin and LIM domain containing 1*	-1.0719	0.4757
11746197_a_at	HUS1	*HUS1 checkpoint clamp component*	-1.0716	0.4758
11742890_at	MND1	*meiotic nuclear divisions 1*	-1.0710	0.4760
11716364_s_at	ASNS	*Asparagine Synthetase (Glutamine-Hydrolyzing)*	-1.0710	0.4760
11719188_at	NRAS	*neuroblastoma RAS viral oncogene homolog*	-1.0704	0.4762
11757843_s_at	PEA15	*phosphoprotein enriched in astrocytes 15*	-1.0691	0.4766
11763556_at	EIF4A1	*eukaryotic translation initiation factor 4A1*	-1.0658	0.4777
11754318_at	SSH1	*slingshot protein phosphatase 1*	-1.0655	0.4778
11715431_a_at	MIR6513	*microRNA 6513*	-1.0652	0.4779
11734841_a_at	RAD51	*RAD51 recombinase*	-1.0649	0.4780
11732902_x_at	APOBEC3B	*apolipoprotein B mRNA editing enzyme catalytic subunit 3B*	-1.0649	0.4780
11727536_x_at	CCNF	*cyclin F*	-1.0646	0.4781
11720042_a_at	RRP7A	*ribosomal RNA processing 7 homolog A*	-1.0631	0.4786
11717364_a_at	BCL2L12	*BCL2 like 12*	-1.0631	0.4786
11731516_at	XPO4	*exportin 4*	-1.0625	0.4788
11748065_a_at	LRRC49	*leucine rich repeat containing 49*	-1.0616	0.4791
11727850_x_at	NIP7	*NIP7, nucleolar pre-rRNA processing protein*	-1.0604	0.4795
11741153_a_at	NCF2	*neutrophil cytosolic factor 2*	-1.0598	0.4797
11754675_a_at	CLIP4	*CAP-Gly domain containing linker protein family member 4*	-1.0598	0.4797
11758222_s_at	SLC20A1	*solute carrier family 20 member 1*	-1.0595	0.4798
11732996_at	HSP90AA1	*heat shock protein 90 alpha family class A member 1*	-1.0592	0.4799

11720062_s_at	IER3	*immediate early response 3*	-1.0586	0.4801
11757156_s_at	SNORA44	*small nucleolar RNA, H/ACA box 44*	-1.0577	0.4804
11748317_s_at	MCFD2	*multiple coagulation factor deficiency 2*	-1.0571	0.4806
11756303_a_at	SH3TC1	*SH3 domain and tetratricopeptide repeats 1*	-1.0565	0.4808
11715757_a_at	RGS2	*regulator of G-protein signaling 2*	-1.0565	0.4808
11730376_at	SURF2	*surfeit 2*	-1.0556	0.4811
11723860_a_at	MPP6	*membrane palmitoylated protein 6*	-1.0556	0.4811
11718397_s_at	JUN	*Jun proto-oncogene, AP-1 transcription factor subunit*	-1.0529	0.4820
11734142_a_at	METTL8	*methyltransferase like 8*	-1.0526	0.4821
11728013_s_at	RIMKLB	*ribosomal modification protein rimK like family member B*	-1.0520	0.4823
11745181_a_at	NAA15	*N(Alpha)-Acetyltransferase 15, NatA Auxiliary Subunit*	-1.0520	0.4823
11756358_a_at	PLK3	*polo like kinase 3*	-1.0520	0.4823
11732520_a_at	RAD51C	*RAD51 paralog C*	-1.0517	0.4824
11731992_x_at	TROAP	*trophinin associated protein*	-1.0511	0.4826
11729665_a_at	STK38L	*serine/threonine kinase 38 like*	-1.0499	0.4830
11744345_x_at	TUBA1B	*tubulin alpha 1b*	-1.0496	0.4831
11727092_x_at	IL18	*interleukin 18*	-1.0484	0.4835
11719260_x_at	LMNA	*lamin A/C*	-1.0475	0.4838
11742128_x_at	DEGS1	*delta 4-desaturase, sphingolipid 1*	-1.0472	0.4839
11749031_a_at	PTBP3	*polypyrimidine tract binding protein 3*	-1.0466	0.4841
11734713_s_at	DBF4	*DBF4 zinc finger*	-1.0451	0.4846
11750554_a_at	NEDD4	*neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase*	-1.0442	0.4849
11745609_x_at	WDR1	*WD repeat domain 1*	-1.0422	0.4856
11728296_a_at	RNMT	*RNA guanine-7 methyltransferase*	-1.0404	0.4862
11729374_at	LOC100653049	*keratin, type I cuticular Ha4*	-1.0404	0.4862
11728985_s_at	LOC100996643	*monofunctional C1-tetrahydrofolate synthase, mitochondrial-like*	-1.0401	0.4863
11722872_a_at	RFC4	*replication factor C subunit 4*	-1.0392	0.4866
11756968_a_at	RBM28	*RNA binding motif protein 28*	-1.0371	0.4873
11746863_x_at	ARSJ	*arylsulfatase family member J*	-1.0356	0.4878
11729158_at	UBE2T	*ubiquitin conjugating enzyme E2 T*	-1.0356	0.4878
11722805_at	RAB35	*RAB35, member RAS oncogene family*	-1.0350	0.4880
11764033_s_at	RFC5	*replication factor C subunit 5*	-1.0342	0.4883
11733320_a_at	HRAS	*HRas proto-oncogene, GTPase*	-1.0327	0.4888
11736411_s_at	NUP62	*nucleoporin 62*	-1.0324	0.4889
11745833_s_at	ECT2	*epithelial cell transforming 2*	-1.0318	0.4891
11739364_s_at	FAM92A	*family with sequence similarity 92 member A*	-1.0318	0.4891
11757658_a_at	LZIC	*leucine zipper and CTNNBIP1 domain containing*	-1.0318	0.4891
11727901_a_at	HPS1	*HPS1, biogenesis of lysosomal organelles complex 3 subunit 1*	-1.0315	0.4892
11733816_a_at	RPL22L1	*ribosomal protein L22 like 1*	-1.0294	0.4899
11757642_a_at	FHOD1	*formin homology 2 domain containing 1*	-1.0291	0.4900
11744519_a_at	POLE2	*DNA polymerase epsilon 2, accessory subunit*	-1.0268	0.4908
11758679_s_at	MIR1292	*microRNA 1292*	-1.0259	0.4911

11716288_s_at	ESYT1	*extended synaptotagmin 1*	-1.0259	0.4911
11728820_a_at	HAUS2	*HAUS augmin like complex subunit 2*	-1.0256	0.4912
11729707_at	FKBP1A	*FK506 binding protein 1A*	-1.0256	0.4912
11746438_a_at	SHMT2	*serine hydroxymethyltransferase 2*	-1.0253	0.4913
11731838_at	SPTLC1	*serine palmitoyltransferase long chain base subunit 1*	-1.0250	0.4914
11716322_s_at	PRKCDBP	*protein kinase C delta binding protein*	-1.0250	0.4914
11757162_s_at	MIR1304	*microRNA 1304*	-1.0239	0.4918
11733352_a_at	NF2	*neurofibromin 2*	-1.0236	0.4919
11755691_a_at	DLC1	*DLC1 Rho GTPase activating protein*	-1.0218	0.4925
11734495_a_at	GRB10	*growth factor receptor bound protein 10*	-1.0218	0.4925
11764157_s_at	TDRP	*testis development related protein*	-1.0209	0.4928
11737748_a_at	GMFB	*glia maturation factor beta*	-1.0209	0.4928
11724322_a_at	CST6	*cystatin E/M*	-1.0198	0.4932
11722231_at	PDP1	*pyruvate dehyrogenase phosphatase catalytic subunit 1*	-1.0192	0.4934
11715834_x_at	RUVBL1	*RuvB like AAA ATPase 1*	-1.0183	0.4937
11716546_s_at	DRAP1	*DR1 associated protein 1*	-1.0174	0.4940
11721621_a_at	KATNAL1	*katanin catalytic subunit A1 like 1*	-1.0171	0.4941
11724357_a_at	MYO5A	*myosin VA*	-1.0168	0.4942
11759540_a_at	RPL35A	*ribosomal protein L35a*	-1.0165	0.4943
11728749_a_at	TCF19	*transcription factor 19*	-1.0136	0.4953
11727785_s_at	CACYBP	*calcyclin binding protein*	-1.0130	0.4955
11745234_a_at	HACD4	*3-hydroxyacyl-CoA dehydratase 4*	-1.0119	0.4959
11743580_s_at	ACTR2	*ARP2 actin related protein 2 homolog*	-1.0116	0.4960
11717341_at	PTGFRN	*prostaglandin F2 receptor inhibitor*	-1.0104	0.4964
11736054_a_at	CELF1	*CUGBP, Elav-like family member 1*	-1.0096	0.4967
11761505_a_at	USB1	*U6 snRNA biogenesis phosphodiesterase 1*	-1.0093	0.4968
11751434_a_at	ACER3	*alkaline ceramidase 3*	-1.0072	0.4975
11723328_a_at	PTRH1	*peptidyl-tRNA hydrolase 1 homolog*	-1.0072	0.4975
11754677_a_at	FAM169A	*family with sequence similarity 169 member A*	-1.0069	0.4976
11737802_a_at	MAD1L1	*MAD1 mitotic arrest deficient like 1*	-1.0067	0.4977
11748808_a_at	ARID3B	*AT-rich interaction domain 3B*	-1.0055	0.4981
11760316_x_at	PXN	*paxillin*	-1.0052	0.4982
11736021_a_at	FKBP4	*FK506 binding protein 4*	-1.0046	0.4984
11720241_at	KIF4A	*kinesin family member 4A*	-1.0046	0.4984
11720421_at	AFF4	*AF4/FMR2 family member 4*	-1.0032	0.4989
11732329_a_at	MAP7D1	*MAP7 domain containing 1*	-1.0023	0.4992
11732901_a_at	APOBEC3A_B	*APOBEC3A and APOBEC3B deletion hybrid*	-1.0023	0.4992
11727879_s_at	CHAF1A	*chromatin assembly factor 1 subunit A*	-1.0012	0.4996
11720566_at	BCAT1	*branched chain amino acid transaminase 1*	-1.0009	0.4997
11730795_at	MRPL4	*mitochondrial ribosomal protein L4*	-1.0009	0.4997
11729886_at	C18orf54	*chromosome 18 open reading frame 54*	-1.0009	0.4997
11715167_at	ARHGAP22	*Rho GTPase activating protein 22*	-1.0009	0.4997

***Diferentially expressed mRNAs were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ([Log_2Ratio > 1] or [Log_2Ratio < -1] for both upregulated or downregulated mRNAs, respectively), followed by multiple correction using a False Discovery Rate (FDR) threshold of 1% (p-adjusted value or q < 0.01).**

TABLE S4. Differentially expressed mRNAs in CRSwNP air-liquid interface culture after 28 days of differentiation compared to day 0 (monolayer of hNP-BSCs).*

UPREGULATED mRNAs (1129)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11719818_at	PIP	*prolactin induced protein*	6.6893	103.2021
11720917_a_at	BPIFB1	*BPI fold containing family B member 1*	6.6443	100.0335
11726981_a_at	CP	*ceruloplasmin*	6.2880	78.1424
11735643_a_at	RARRES1	*retinoic acid receptor responder 1*	6.2632	76.8095
11724692_a_at	CAPN13	*calpain 13*	6.1143	69.2786
11716109_a_at	PIGR	*polymeric immunoglobulin receptor*	5.9978	63.9040
11727698_a_at	VMO1	*vitelline membrane outer layer 1 homolog*	5.7412	53.4894
11758272_at	SLC34A2	*solute carrier family 34 member 2*	5.5933	48.2789
11723642_a_at	BPIFA1	*BPI fold containing family A member 1*	5.1977	36.6996
11726124_at	TCN1	*transcobalamin 1*	5.1322	35.0714
11744556_x_at	CYP2B7P	*cytochrome P450 family 2 subfamily B member 7, pseudogene*	5.0543	33.2271
11724085_at	DAPL1	*death associated protein like 1*	5.0078	32.1726
11743003_a_at	CYP4B1	*cytochrome P450 family 4 subfamily B member 1*	4.9671	31.2783
11730779_at	ADH1C	*Alcohol Dehydrogenase 1C (Class I), Gamma Polypeptide*	4.8816	29.4785
11722994_s_at	ADH1A	*Alcohol Dehydrogenase 1A (Class I), Alpha Polypeptide*	4.8439	28.7183
11749912_x_at	IGFBP3	*insulin like growth factor binding protein 3*	4.7741	27.3629
11758952_at	AGR2	*anterior gradient 2, protein disulphide isomerase family member*	4.7276	26.4949
11721895_x_at	GAS1	*growth arrest specific 1*	4.6334	24.8190
11758196_s_at	IGFBP5	*insulin like growth factor binding protein 5*	4.5095	22.7767
11744484_s_at	HLA-DRA	*major histocompatibility complex, class II, DR alpha*	4.4048	21.1830
11744104_a_at	TMC5	*transmembrane channel like 5*	4.3979	21.0816
11716490_a_at	SERPINA3	*serpin family A member 3*	4.3902	20.9687
11732460_a_at	PLEKHS1	*pleckstrin homology domain containing S1*	4.3781	20.7936
11718722_at	PSCA	*prostate stem cell antigen*	4.3318	20.1368
11755588_a_at	SLC5A5	*solute carrier family 5 member 5*	4.3141	19.8916
11743044_a_at	ALDH1A1	*aldehyde dehydrogenase 1 family member A1*	4.2520	19.0542
11750860_a_at	CMAHP	*cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene*	4.1680	17.9759
11744030_a_at	MMP7	*matrix metallopeptidase 7*	4.0838	16.9573
11733725_a_at	CFB	*complement factor B*	4.0578	16.6539
11754354_s_at	PROM1	*prominin 1*	4.0342	16.3835
11724762_a_at	DEPTOR	*DEP domain containing MTOR-interacting protein*	3.9598	15.5602
11729770_at	BPIFA2	*BPI fold containing family A member 2*	3.9086	15.0179
11725562_at	C20orf85	*chromosome 20 open reading frame 85*	3.9025	14.9542
11720349_at	ROPN1L	*rhophilin associated tail protein 1 like*	3.8842	14.7657
11728771_a_at	CLCA4	*chloride channel accessory 4*	3.8771	14.6939
11723524_at	AGR3	*anterior gradient 3, protein disulphide isomerase family member*	3.8655	14.5758
11727966_a_at	MSMB	*microseminoprotein beta*	3.8405	14.3253

11755748_s_at	PLAC8	*placenta specific 8*	3.8395	14.3153
11751769_a_at	LOC100287413	*uncharacterized LOC100287413*	3.8084	14.0103
11716401_a_at	SELENBP1	*selenium binding protein 1*	3.8072	13.9981
11756098_a_at	SYTL5	*synaptotagmin like 5*	3.8013	13.9415
11757815_s_at	METTL7A	*methyltransferase like 7A*	3.7850	13.7851
11753973_x_at	MUC1	*mucin 1, cell surface associated*	3.7762	13.7013
11731722_a_at	ALDH3B1	*aldehyde dehydrogenase 3 family member B1*	3.7750	13.6891
11717595_s_at	ELF3	*E74 like ETS transcription factor 3*	3.7727	13.6673
11759322_at	BCL6	*B-cell CLL/lymphoma 6*	3.7608	13.5555
11722054_a_at	CYP4X1	*cytochrome P450 family 4 subfamily X member 1*	3.7254	13.2268
11724795_at	ZG16B	*zymogen granule protein 16B*	3.7135	13.1184
11722838_a_at	GABRP	*gamma-aminobutyric acid type A receptor pi subunit*	3.6909	12.9146
11758544_s_at	RDH10	*Retinol Dehydrogenase 10*	3.6864	12.8742
11715994_x_at	ID2	*inhibitor of DNA binding 2, HLH protein*	3.6812	12.8280
11727440_at	LOXL4	*lysyl oxidase like 4*	3.6511	12.5632
11748046_a_at	SLC44A4	*solute carrier family 44 member 4*	3.6491	12.5452
11726303_a_at	MFSD4A	*major facilitator superfamily domain containing 4A*	3.6028	12.1490
11729439_a_at	CAPSL	*calcyphosine like*	3.5874	12.0204
11726434_at	CHL1	*cell adhesion molecule L1 like*	3.5616	11.8069
11729693_at	SERPINB3	*serpin family B member 3*	3.5534	11.7405
11730044_a_at	C9orf24	*chromosome 9 open reading frame 24*	3.5388	11.6222
11715343_at	MUC16	*mucin 16, cell surface associated*	3.5017	11.3271
11729692_a_at	SERPINB3	*serpin family B member 3*	3.4769	11.1342
11720139_a_at	VSTM2L	*V-set and transmembrane domain containing 2 like*	3.4336	10.8046
11736917_at	LYPD2	*LY6/PLAUR domain containing 2*	3.4280	10.7633
11717917_a_at	WFDC2	*WAP four-disulfide core domain 2*	3.4279	10.7622
11717820_a_at	SLC4A4	*solute carrier family 4 member 4*	3.4171	10.6820
11729297_at	MMP13	*matrix metallopeptidase 13*	3.4125	10.6479
11757570_s_at	PRR15	*proline rich 15*	3.4118	10.6429
11736855_a_at	ATP6V1C2	*ATPase H+ transporting V1 subunit C2*	3.4088	10.6206
11758013_s_at	C8orf4	*chromosome 8 open reading frame 4*	3.3938	10.5107
11744240_at	SNTN	*sentan, cilia apical structure protein*	3.3896	10.4800
11734525_a_at	C11orf88	*chromosome 11 open reading frame 88*	3.3770	10.3893
11732657_a_at	CYP26A1	*cytochrome P450 family 26 subfamily A member 1*	3.3672	10.3190
11733934_a_at	PIFO	*primary cilia formation*	3.3600	10.2671
11739916_a_at	SERPINB11	*Serpin Family B Member 11 (Gene/Pseudogene)*	3.3424	10.1427
11763989_at	LOC101927057	*uncharacterized LOC101927057*	3.3232	10.0091
11739761_a_at	CLDN10	*claudin 10*	3.2856	9.7510
11733474_at	SOX21	*SRY-box 21*	3.2758	9.6855
11755202_a_at	VTCN1	*V-set domain containing T cell activation inhibitor 1*	3.2671	9.6270
11758221_s_at	ARRDC3	*arrestin domain containing 3*	3.2590	9.5732
11724875_a_at	CD36	*CD36 molecule*	3.2512	9.5217

11723404_at	PPARGC1A	*PPARG coactivator 1 alpha*	3.2503	9.5159
11723899_a_at	DHRS9	*dehydrogenase/reductase 9*	3.2485	9.5039
11754650_a_at	ATP10B	*ATPase Phospholipid Transporting 10B (Putative)*	3.2415	9.4577
11729976_a_at	PTPRN2	*protein tyrosine phosphatase, receptor type N2*	3.1614	8.9467
11723063_a_at	GCHFR	*GTP cyclohydrolase I feedback regulator*	3.1556	8.9111
11725662_a_at	SLC16A14	*solute carrier family 16 member 14*	3.1445	8.8427
11744063_a_at	MUC5B	*mucin 5B, oligomeric mucus/gel-forming*	3.1403	8.8173
11717720_a_at	ST6GAL1	*ST6 beta-galactoside alpha-2,6-sialyltransferase 1*	3.1381	8.8038
11715788_a_at	SLC40A1	*solute carrier family 40 member 1*	3.1326	8.7701
11755226_s_at	KLHDC7A	*kelch domain containing 7A*	3.1303	8.7564
11719265_a_at	MLPH	*melanophilin*	3.1279	8.7417
11754888_a_at	ADSSL1	*adenylosuccinate synthase like 1*	3.1076	8.6192
11758225_s_at	IQGAP2	*IQ motif containing GTPase activating protein 2*	3.0635	8.3598
11746414_a_at	FAM107B	*family with sequence similarity 107 member B*	3.0608	8.3445
11732910_x_at	FAM183A	*family with sequence similarity 183 member A*	3.0509	8.2875
11721898_at	FAM3D	*family with sequence similarity 3 member D*	3.0311	8.1741
11763594_a_at	HS3ST3B1	*heparan sulfate-glucosamine 3-sulfotransferase 3B1*	3.0264	8.1476
11730245_a_at	FMO2	*flavin containing monooxygenase 2*	3.0211	8.1181
11756588_a_at	ST6GALNAC1	*ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1*	3.0117	8.0649
11727734_at	CFAP126	*cilia and flagella associated protein 126*	3.0103	8.0572
11731657_s_at	VAV3	*vav guanine nucleotide exchange factor 3*	3.0036	8.0201
11717465_s_at	LXN	*latexin*	3.0010	8.0056
11723441_a_at	EPHA4	*EPH receptor A4*	2.9997	7.9985
11734552_a_at	CX3CL1	*C-X3-C motif chemokine ligand 1*	2.9966	7.9809
11756191_a_at	MAN1C1	*mannosidase alpha class 1C member 1*	2.9837	7.9101
11757612_a_at	ASRGL1	*asparaginase like 1*	2.9811	7.8958
11739045_a_at	SLC15A2	*solute carrier family 15 member 2*	2.9807	7.8938
11716489_a_at	STATH	*statherin*	2.9795	7.8871
11724796_at	DDIT4L	*DNA damage inducible transcript 4 like*	2.9595	7.7784
11728239_at	RRAGD	*Ras related GTP binding D*	2.9569	7.7645
11721531_a_at	AQP5	*aquaporin 5*	2.9544	7.7510
11724528_a_at	GCNT3	*Glucosaminyl (N-Acetyl) Transferase 3, Mucin Type*	2.9519	7.7375
11756766_x_at	CD74	*CD74 molecule*	2.9378	7.6626
11753068_a_at	CFI	*complement factor I*	2.9357	7.6511
11739440_a_at	KRT4	*keratin 4*	2.9163	7.5490
11721539_at	RAB15	*RAB15, member RAS oncogene family*	2.9152	7.5431
11730801_at	CXCL6	*C-X-C motif chemokine ligand 6*	2.9120	7.5267
11734503_x_at	ALOX15	*arachidonate 15-lipoxygenase*	2.9106	7.5195
11744508_a_at	CCDC146	*coiled-coil domain containing 146*	2.9087	7.5092
11755403_a_at	CHST9	*carbohydrate sulfotransferase 9*	2.9082	7.5068
11718213_a_at	SLC27A2	*solute carrier family 27 member 2*	2.9015	7.4721
11727243_a_at	WNT4	*Wnt family member 4*	2.8877	7.4007

11720993_at	SOX2	*SRY-box 2*	2.8827	7.3751
11735523_a_at	FAM47E	*family with sequence similarity 47 member E*	2.8743	7.3326
11731433_a_at	SELENOP	*selenoprotein P*	2.8558	7.2391
11718302_at	HSD11B2	*hydroxysteroid 11-beta dehydrogenase 2*	2.8453	7.1866
11725892_a_at	PLEKHH1	*pleckstrin homology, MyTH4 and FERM domain containing H1*	2.8440	7.1799
11719692_a_at	RARRES3	*retinoic acid receptor responder 3*	2.8348	7.1344
11743595_at	C5orf49	*chromosome 5 open reading frame 49*	2.8309	7.1153
11732833_a_at	C9orf135	*chromosome 9 open reading frame 135*	2.8270	7.0959
11730214_at	DUOX2	*dual oxidase 2*	2.8258	7.0899
11740326_x_at	SORBS2	*sorbin and SH3 domain containing 2*	2.8199	7.0609
11758468_s_at	TSHZ2	*teashirt zinc finger homeobox 2*	2.8079	7.0028
11758134_s_at	PPM1H	*protein phosphatase, Mg2+/Mn2+ dependent 1H*	2.7942	6.9364
11746749_a_at	ZBBX	*zinc finger B-box domain containing*	2.7930	6.9307
11720713_a_at	KCNE3	*potassium voltage-gated channel subfamily E regulatory subunit 3*	2.7747	6.8435
11715490_s_at	AMY1A	*Amylase, Alpha 1A (Salivary)*	2.7719	6.8301
11756495_a_at	SPAG6	*sperm associated antigen 6*	2.7697	6.8198
11728753_at	ADH7	*Alcohol Dehydrogenase 7 (Class IV), Mu Or Sigma Polypeptide*	2.7564	6.7573
11730265_x_at	CCDC69	*coiled-coil domain containing 69*	2.7497	6.7258
11725789_at	DPYD	*dihydropyrimidine dehydrogenase*	2.7487	6.7211
11755020_a_at	SLC46A3	*solute carrier family 46 member 3*	2.7462	6.7096
11736678_s_at	PODXL	*podocalyxin like*	2.7331	6.6486
11719657_a_at	MMP9	*matrix metallopeptidase 9*	2.7314	6.6409
11741519_s_at	CD14	*CD14 molecule*	2.7157	6.5689
11723194_x_at	HLA-DQB1	*major histocompatibility complex, class II, DQ beta 1*	2.7089	6.5383
11733687_s_at	STRA6	*stimulated by retinoic acid 6*	2.7079	6.5339
11740565_at	PNLIPRP3	*pancreatic lipase related protein 3*	2.7066	6.5280
11744138_at	CAMK1D	*calcium/calmodulin dependent protein kinase ID*	2.7000	6.4981
11725922_a_at	CLIC6	*chloride intracellular channel 6*	2.6996	6.4962
11722783_at	FOXQ1	*forkhead box Q1*	2.6965	6.4824
11732500_a_at	FAM3B	*family with sequence similarity 3 member B*	2.6939	6.4704
11756547_a_at	CLU	*clusterin*	2.6900	6.4533
11719307_a_at	RASSF4	*Ras association domain family member 4*	2.6818	6.4167
11737141_a_at	RSPH1	*radial spoke head 1 homolog*	2.6731	6.3779
11734614_a_at	GABRE	*gamma-aminobutyric acid type A receptor epsilon subunit*	2.6556	6.3011
11716554_a_at	HLA-DMA	*major histocompatibility complex, class II, DM alpha*	2.6361	6.2167
11743657_x_at	HPGD	*hydroxyprostaglandin dehydrogenase 15-*	2.6259	6.1728
11717417_s_at	RHOU	*ras homolog family member U*	2.6241	6.1650
11746662_a_at	ARMC3	*armadillo repeat containing 3*	2.6162	6.1313
11739882_a_at	GLIS3	*GLIS family zinc finger 3*	2.6036	6.0781
11754421_a_at	VSIG2	*V-set and immunoglobulin domain containing 2*	2.6028	6.0745
11719321_a_at	DNALI1	*dynein axonemal light intermediate chain 1*	2.6017	6.0699
11723878_a_at	ATP7B	*ATPase copper transporting beta*	2.5955	6.0439

11756684_a_at	DYNLRB2	*dynein light chain roadblock-type 2*	2.5807	5.9825
11727281_a_at	MMP28	*matrix metallopeptidase 28*	2.5792	5.9761
11759642_x_at	HLA-DRB1	*major histocompatibility complex, class II, DR beta 1*	2.5790	5.9753
11718169_a_at	AZGP1	*alpha-2-glycoprotein 1, zinc-binding*	2.5735	5.9525
11750205_a_at	BCAS1	*breast carcinoma amplified sequence 1*	2.5685	5.9319
11724109_a_at	C9orf116	*chromosome 9 open reading frame 116*	2.5565	5.8828
11723367_a_at	RAB26	*RAB26, member RAS oncogene family*	2.5549	5.8761
11717582_a_at	RGCC	*regulator of cell cycle*	2.5498	5.8555
11720007_a_at	STEAP4	*STEAP4 metalloreductase*	2.5415	5.8221
11722310_a_at	TMC4	*transmembrane channel like 4*	2.5389	5.8113
11758031_s_at	BHLHE41	*basic helix-loop-helix family member e41*	2.5210	5.7396
11716934_a_at	CCDC80	*coiled-coil domain containing 80*	2.5207	5.7386
11718651_at	TMTC1	*transmembrane and tetratricopeptide repeat containing 1*	2.5206	5.7381
11729025_a_at	ILDR1	*immunoglobulin like domain containing receptor 1*	2.5201	5.7363
11722863_at	SCGB2A1	*secretoglobin family 2A member 1*	2.5165	5.7219
11716974_a_at	PDK4	*pyruvate dehydrogenase kinase 4*	2.5136	5.7105
11718919_a_at	ATP6V1B1	*ATPase H+ transporting V1 subunit B1*	2.5045	5.6747
11721704_a_at	CRIP1	*cysteine rich protein 1*	2.4947	5.6361
11764077_s_at	EDIL3	*EGF like repeats and discoidin domains 3*	2.4937	5.6324
11730881_a_at	NEBL	*nebulette*	2.4867	5.6051
11719538_at	BBOX1	*gamma-butyrobetaine hydroxylase 1*	2.4853	5.5996
11754627_s_at	RAB37	*RAB37, member RAS oncogene family*	2.4835	5.5927
11728200_a_at	LOX	*lysyl oxidase*	2.4805	5.5811
11717829_s_at	TSC22D3	*TSC22 domain family member 3*	2.4797	5.5780
11743071_a_at	LPAR6	*lysophosphatidic acid receptor 6*	2.4789	5.5747
11718754_at	CAPN5	*calpain 5*	2.4773	5.5685
11744086_a_at	PRR15L	*proline rich 15 like*	2.4707	5.5430
11737857_a_at	DNAAF1	*dynein axonemal assembly factor 1*	2.4640	5.5173
11721456_x_at	SERPINA1	*serpin family A member 1*	2.4621	5.5101
11724515_a_at	GPD1L	*glycerol-3-phosphate dehydrogenase 1-like*	2.4620	5.5098
11731248_a_at	TMEM116	*transmembrane protein 116*	2.4520	5.4717
11749583_a_at	FUT2	*fucosyltransferase 2*	2.4490	5.4604
11742730_a_at	CAPS	*calcyphosine*	2.4457	5.4479
11727918_s_at	MUC20	*mucin 20, cell surface associated*	2.4454	5.4469
11735674_a_at	AKAP14	*A-kinase anchoring protein 14*	2.4443	5.4427
11754461_s_at	UCP2	*uncoupling protein 2*	2.4404	5.4280
11743576_at	CPE	*carboxypeptidase E*	2.4381	5.4192
11737749_a_at	SGK1	*serum/glucocorticoid regulated kinase 1*	2.4332	5.4010
11725474_a_at	MAP3K5	*mitogen-activated protein kinase kinase kinase 5*	2.4211	5.3559
11716835_a_at	DHRS3	*dehydrogenase/reductase 3*	2.4160	5.3370
11730467_at	NTN1	*netrin 1*	2.4140	5.3295
11721318_at	PARM1	*prostate androgen-regulated mucin-like protein 1*	2.4088	5.3102

11722743_a_at	TLE2	*transducin like enhancer of split 2*	2.4080	5.3074
11723163_s_at	NR3C2	*nuclear receptor subfamily 3 group C member 2*	2.3962	5.2641
11722860_a_at	TRIM2	*tripartite motif containing 2*	2.3957	5.2623
11724219_x_at	GSTA1	*glutathione S-transferase alpha 1*	2.3949	5.2593
11756097_s_at	ZMYND10	*zinc finger MYND-type containing 10*	2.3883	5.2354
11724258_a_at	MUC15	*mucin 15, cell surface associated*	2.3844	5.2212
11755671_a_at	SYTL2	*synaptotagmin like 2*	2.3831	5.2164
11729920_at	BBOF1	*basal body orientation factor 1*	2.3793	5.2030
11754526_a_at	PTGES	*prostaglandin E synthase*	2.3789	5.2013
11732526_s_at	CSGALNACT1	*chondroitin sulfate N-acetylgalactosaminyltransferase 1*	2.3759	5.1907
11727921_a_at	TEKT1	*tektin 1*	2.3641	5.1482
11719767_a_at	TPPP3	*tubulin polymerization promoting protein family member 3*	2.3636	5.1466
11729998_a_at	B3GNT7	*UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7*	2.3475	5.0894
11743321_at	CTSO	*cathepsin O*	2.3400	5.0632
11726412_s_at	ZBTB7C	*zinc finger and BTB domain containing 7C*	2.3379	5.0556
11757871_s_at	PBX1	*PBX homeobox 1*	2.3317	5.0340
11747104_s_at	CYP1B1	*cytochrome P450 family 1 subfamily B member 1*	2.3314	5.0328
11723007_a_at	DYX1C1-CCPG1	*DYX1C1-CCPG1 Readthrough (NMD Candidate)*	2.3235	5.0053
11732240_a_at	SLITRK6	*SLIT and NTRK like family member 6*	2.3155	4.9776
11726054_a_at	MUC4	*mucin 4, cell surface associated*	2.3120	4.9657
11721267_s_at	TMPRSS4	*transmembrane protease, serine 4*	2.3112	4.9630
11715709_x_at	MB	*myoglobin*	2.3101	4.9593
11722070_a_at	CHPT1	*choline phosphotransferase 1*	2.3094	4.9568
11719447_s_at	GBP2	*guanylate binding protein 2*	2.3082	4.9528
11740868_a_at	LDLRAD1	*low density lipoprotein receptor class A domain containing 1*	2.3019	4.9310
11726535_a_at	MORN5	*MORN repeat containing 5*	2.2960	4.9108
11756888_a_at	TFCP2L1	*transcription factor CP2 like 1*	2.2954	4.9088
11720146_a_at	DAPK1	*death associated protein kinase 1*	2.2915	4.8957
11728523_a_at	MYCL	*v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog*	2.2855	4.8752
11754601_s_at	LOC100130872	*uncharacterized LOC100130872*	2.2847	4.8725
11734176_a_at	CFAP52	*cilia and flagella associated protein 52*	2.2835	4.8686
11719394_a_at	FBXO32	*F-box protein 32*	2.2800	4.8567
11727239_a_at	C4orf19	*chromosome 4 open reading frame 19*	2.2784	4.8514
11736285_a_at	CHKA	*choline kinase alpha*	2.2771	4.8469
11719658_a_at	TF	*transferrin*	2.2725	4.8316
11732444_a_at	RBPMS	*RNA binding protein with multiple splicing*	2.2723	4.8310
11721630_at	MAFB	*MAF bZIP transcription factor B*	2.2704	4.8246
11740995_x_at	GLUL	*glutamate-ammonia ligase*	2.2680	4.8164
11739375_at	SYT7	*synaptotagmin 7*	2.2652	4.8072
11742709_s_at	P4HTM	*prolyl 4-hydroxylase, transmembrane*	2.2622	4.7971
11730632_a_at	OCA2	*OCA2 melanosomal transmembrane protein*	2.2509	4.7598
11754316_a_at	PIK3R3	*phosphoinositide-3-kinase regulatory subunit 3*	2.2443	4.7381

11726916_at	SLCO4C1	*solute carrier organic anion transporter family member 4C1*	2.2381	4.7178
11719148_a_at	ARRDC2	*arrestin domain containing 2*	2.2325	4.6996
11739351_a_at	AMOT	*angiomotin*	2.2287	4.6870
11757005_a_at	FUCA1	*fucosidase, alpha-L- 1, tissue*	2.2284	4.6862
11718130_s_at	OLFM4	*olfactomedin 4*	2.2276	4.6834
11717339_s_at	SORD	*sorbitol dehydrogenase*	2.2138	4.6391
11752737_a_at	CLEC7A	*C-type lectin domain family 7 member A*	2.2117	4.6323
11727146_at	GPR160	*G protein-coupled receptor 160*	2.2077	4.6195
11748543_a_at	TXNIP	*thioredoxin interacting protein*	2.1969	4.5850
11760254_at	IFI44	*interferon induced protein 44*	2.1961	4.5825
11741065_a_at	EPHX1	*epoxide hydrolase 1*	2.1883	4.5577
11756356_a_at	FAM81B	*family with sequence similarity 81 member B*	2.1748	4.5153
11722851_at	BIRC3	*baculoviral IAP repeat containing 3*	2.1734	4.5108
11764253_s_at	IFITM10	*interferon induced transmembrane protein 10*	2.1726	4.5084
11718066_a_at	TCTN1	*tectonic family member 1*	2.1707	4.5023
11733432_at	AK7	*adenylate kinase 7*	2.1582	4.4637
11731538_a_at	ADGRF1	*adhesion G protein-coupled receptor F1*	2.1581	4.4634
11735488_a_at	CASC1	*cancer susceptibility candidate 1*	2.1557	4.4559
11717885_a_at	CCDC3	*coiled-coil domain containing 3*	2.1513	4.4423
11724720_a_at	GALNT12	*polypeptide N-acetylgalactosaminyltransferase 12*	2.1425	4.4153
11749589_x_at	CTSS	*cathepsin S*	2.1378	4.4010
11743168_at	IDO1	*indoleamine 2,3-dioxygenase 1*	2.1325	4.3847
11754735_s_at	ABCA13	*ATP binding cassette subfamily A member 13*	2.1310	4.3802
11743943_a_at	RSPH4A	*radial spoke head 4 homolog A*	2.1296	4.3760
11726896_a_at	IRAK3	*interleukin 1 receptor associated kinase 3*	2.1275	4.3696
11750687_a_at	ADAM28	*ADAM metallopeptidase domain 28*	2.1260	4.3652
11737634_a_at	UGT2A1	*UDP glucuronosyltransferase family 2 member A1 complex locus*	2.1216	4.3518
11724620_a_at	WDR78	*WD repeat domain 78*	2.1209	4.3496
11725692_a_at	VWA5A	*von Willebrand factor A domain containing 5A*	2.1184	4.3421
11730944_a_at	CCDC65	*coiled-coil domain containing 65*	2.1118	4.3224
11725450_a_at	TMEM45B	*transmembrane protein 45B*	2.1076	4.3097
11736144_at	ENPP4	*Ectonucleotide Pyrophosphatase/Phosphodiesterase 4 (Putative)*	2.1073	4.3088
11744588_a_at	CCDC17	*coiled-coil domain containing 17*	2.1036	4.2979
11727132_at	CPD	*carboxypeptidase D*	2.1030	4.2960
11750700_a_at	ACSL1	*acyl-CoA synthetase long-chain family member 1*	2.0951	4.2725
11744374_x_at	HLA-DRB1	*major histocompatibility complex, class II, DR beta 1*	2.0918	4.2629
11720243_x_at	TCN2	*transcobalamin 2*	2.0880	4.2516
11722758_at	NPR3	*natriuretic peptide receptor 3*	2.0879	4.2514
11763986_a_at	APOL1	*apolipoprotein L1*	2.0857	4.2448
11732678_a_at	DNAH12	*dynein axonemal heavy chain 12*	2.0849	4.2426
11740438_a_at	FUT6	*fucosyltransferase 6*	2.0824	4.2352
11717742_a_at	GPRC5C	*G protein-coupled receptor class C group 5 member C*	2.0823	4.2348

11747755_a_at	KRT13	*keratin 13*	2.0792	4.2256
11747474_a_at	NR4A2	*nuclear receptor subfamily 4 group A member 2*	2.0791	4.2255
11757307_s_at	CTSD	*cathepsin D*	2.0758	4.2157
11754238_a_at	DYDC2	*DPY30 domain containing 2*	2.0744	4.2118
11726159_a_at	IQCG	*IQ motif containing G*	2.0696	4.1978
11728727_at	CEACAM7	*carcinoembryonic antigen related cell adhesion molecule 7*	2.0691	4.1963
11715290_s_at	CLDN3	*claudin 3*	2.0682	4.1936
11721700_a_at	RERG	*RAS like estrogen regulated growth inhibitor*	2.0654	4.1856
11751459_x_at	LRG1	*leucine rich alpha-2-glycoprotein 1*	2.0653	4.1851
11733359_a_at	CFAP45	*cilia and flagella associated protein 45*	2.0647	4.1835
11739725_a_at	TC2N	*tandem C2 domains, nuclear*	2.0646	4.1831
11720134_s_at	PROS1	*Protein S (Alpha)*	2.0611	4.1730
11725223_at	SNTB1	*syntrophin beta 1*	2.0583	4.1650
11721688_at	ID4	*inhibitor of DNA binding 4, HLH protein*	2.0582	4.1647
11753334_x_at	BAG1	*BCL2 associated athanogene 1*	2.0525	4.1483
11729575_a_at	XBP1	*X-box binding protein 1*	2.0520	4.1468
11752898_a_at	PPIL6	*peptidylprolyl isomerase like 6*	2.0491	4.1386
11743286_at	DTX4	*deltex E3 ubiquitin ligase 4*	2.0484	4.1364
11758315_s_at	PER2	*period circadian clock 2*	2.0429	4.1207
11744596_a_at	LYPD6B	*LY6/PLAUR domain containing 6B*	2.0426	4.1199
11757645_s_at	FIBIN	*Fin Bud Initiation Factor Homolog (Zebrafish)*	2.0409	4.1149
11723785_s_at	LIMCH1	*LIM and calponin homology domains 1*	2.0367	4.1032
11734939_a_at	SLC16A9	*solute carrier family 16 member 9*	2.0352	4.0989
11758474_s_at	COLCA1	*colorectal cancer associated 1*	2.0342	4.0959
11758595_at	NBEA	*neurobeachin*	2.0322	4.0903
11724394_at	KIAA1211L	*KIAA1211 like*	2.0284	4.0795
11715393_a_at	C3	*complement C3*	2.0270	4.0755
11742816_a_at	FAM13A	*family with sequence similarity 13 member A*	2.0264	4.0740
11745242_a_at	TNFRSF21	*TNF receptor superfamily member 21*	2.0249	4.0695
11728939_at	RASEF	*RAS and EF-hand domain containing*	2.0230	4.0642
11727995_a_at	SPINK5	*serine peptidase inhibitor, Kazal type 5*	2.0219	4.0611
11722116_a_at	RARB	*retinoic acid receptor beta*	2.0206	4.0576
11755010_s_at	POC1B-GALNT4	*POC1B-GALNT4 readthrough*	2.0191	4.0534
11718448_at	SH3BGRL2	*SH3 domain binding glutamate rich protein like 2*	2.0182	4.0507
11736369_at	MBOAT1	*membrane bound O-acyltransferase domain containing 1*	2.0140	4.0391
11721572_at	C10orf99	*chromosome 10 open reading frame 99*	2.0065	4.0181
11727007_at	SORT1	*sortilin 1*	2.0001	4.0004
11746991_a_at	ATP1B1	*ATPase Na+/K+ transporting subunit beta 1*	1.9941	3.9838
11721460_s_at	TAPBPL	*TAP binding protein like*	1.9941	3.9836
11745292_a_at	C22orf15	*chromosome 22 open reading frame 15*	1.9915	3.9765
11744282_at	PLBD1	*phospholipase B domain containing 1*	1.9909	3.9749
11722242_at	TSPAN12	*tetraspanin 12*	1.9854	3.9597

11729061_a_at	DNAH5	*dynein axonemal heavy chain 5*	1.9830	3.9532
11731200_a_at	TLR5	*toll like receptor 5*	1.9809	3.9473
11747167_x_at	ADH1B	*Alcohol Dehydrogenase 1B (Class I), Beta Polypeptide*	1.9763	3.9348
11723703_s_at	ABHD5	*abhydrolase domain containing 5*	1.9752	3.9319
11758053_s_at	NCOA4	*nuclear receptor coactivator 4*	1.9704	3.9188
11735637_a_at	LRRC23	*leucine rich repeat containing 23*	1.9693	3.9159
11734215_x_at	MPP7	*membrane palmitoylated protein 7*	1.9663	3.9077
11720901_a_at	GRAMD1C	*GRAM domain containing 1C*	1.9642	3.9020
11724476_a_at	MTUS1	*microtubule associated tumor suppressor 1*	1.9579	3.8850
11721417_at	SCNN1B	*sodium channel epithelial 1 beta subunit*	1.9578	3.8848
11749140_a_at	RCBTB2	*RCC1 and BTB domain containing protein 2*	1.9541	3.8748
11720105_a_at	SLC26A2	*solute carrier family 26 member 2*	1.9518	3.8687
11758504_s_at	FAM216B	*family with sequence similarity 216 member B*	1.9495	3.8625
11757882_x_at	GSTA1	*glutathione S-transferase alpha 1*	1.9450	3.8505
11721957_at	YPEL2	*yippee like 2*	1.9419	3.8422
11730037_at	DEGS2	*delta 4-desaturase, sphingolipid 2*	1.9385	3.8332
11732552_a_at	ENKUR	*enkurin, TRPC channel interacting protein*	1.9336	3.8201
11756274_a_at	ALDH1L1	*aldehyde dehydrogenase 1 family member L1*	1.9312	3.8137
11758955_at	LGALS8	*galectin 8*	1.9277	3.8046
11726360_a_at	ALDH3A1	*aldehyde dehydrogenase 3 family member A1*	1.9267	3.8019
11721445_x_at	ERBB3	*erb-b2 receptor tyrosine kinase 3*	1.9241	3.7950
11725625_s_at	ACE2	*angiotensin I converting enzyme 2*	1.9230	3.7920
11729100_a_at	CFAP70	*cilia and flagella associated protein 70*	1.9209	3.7867
11727198_a_at	PCDHAC2	*protocadherin alpha subfamily C, 2*	1.9199	3.7840
11755084_x_at	CD55	*CD55 Molecule (Cromer Blood Group)*	1.9179	3.7787
11737791_s_at	APOL2	*apolipoprotein L2*	1.9169	3.7762
11727296_s_at	TGFB3	*transforming growth factor beta 3*	1.9168	3.7759
11733530_at	C1RL	*complement C1r subcomponent like*	1.9125	3.7645
11731606_at	SCIN	*scinderin*	1.9112	3.7611
11759546_a_at	CXXC5	*CXXC finger protein 5*	1.9088	3.7550
11758460_s_at	FAAH2	*fatty acid amide hydrolase 2*	1.9079	3.7525
11729031_a_at	C1orf194	*chromosome 1 open reading frame 194*	1.9068	3.7498
11744920_a_at	ODF3B	*outer dense fiber of sperm tails 3B*	1.9064	3.7487
11744866_x_at	CEL	*carboxyl ester lipase*	1.9060	3.7477
11727416_a_at	CRYL1	*crystallin lambda 1*	1.9060	3.7476
11721759_a_at	ASAP3	*ArfGAP with SH3 domain, ankyrin repeat and PH domain 3*	1.9057	3.7469
11717614_at	KIF13B	*kinesin family member 13B*	1.9049	3.7447
11732580_a_at	ME3	*malic enzyme 3*	1.9042	3.7430
11754640_a_at	EPHX2	*epoxide hydrolase 2*	1.9035	3.7411
11729365_at	PRKAA2	*protein kinase AMP-activated catalytic subunit alpha 2*	1.9011	3.7349
11734454_a_at	WFDC3	*WAP four-disulfide core domain 3*	1.8999	3.7319
11724909_a_at	TMPRSS2	*transmembrane protease, serine 2*	1.8998	3.7315

11726051_a_at	FMO3	*flavin containing monooxygenase 3*	1.8987	3.7288
11730699_at	LOC100652777	*group 10 secretory phospholipase A2-like*	1.8984	3.7280
11755640_s_at	RALGPS1	*Ral GEF with PH domain and SH3 binding motif 1*	1.8979	3.7266
11744875_a_at	C11orf70	*chromosome 11 open reading frame 70*	1.8977	3.7261
11727702_at	C9orf152	*chromosome 9 open reading frame 152*	1.8904	3.7074
11742683_x_at	HIST1H1C	*histone cluster 1 H1 family member c*	1.8763	3.6713
11732060_a_at	LEMD1	*LEM domain containing 1*	1.8761	3.6707
11722348_a_at	REPS2	*RALBP1 associated Eps domain containing 2*	1.8647	3.6419
11755544_a_at	EFHB	*EF-hand domain family member B*	1.8585	3.6263
11730250_a_at	LNX1	*ligand of numb-protein X 1*	1.8584	3.6260
11729453_s_at	CYP2B6	*cytochrome P450 family 2 subfamily B member 6*	1.8539	3.6148
11757390_s_at	KLHL24	*kelch like family member 24*	1.8532	3.6129
11756312_a_at	SERPINF1	*serpin family F member 1*	1.8518	3.6095
11755282_a_at	SCNN1A	*sodium channel epithelial 1 alpha subunit*	1.8475	3.5987
11715752_at	TSPAN7	*tetraspanin 7*	1.8471	3.5977
11723846_at	DEFB1	*defensin beta 1*	1.8467	3.5968
11731126_at	GXYLT2	*glucoside xylosyltransferase 2*	1.8417	3.5842
11721993_at	SLC6A6	*solute carrier family 6 member 6*	1.8301	3.5557
11750836_a_at	EFHC1	*EF-hand domain containing 1*	1.8295	3.5541
11727983_a_at	LRRC46	*leucine rich repeat containing 46*	1.8294	3.5538
11728363_s_at	IL20RA	*interleukin 20 receptor subunit alpha*	1.8283	3.5512
11725522_at	MESP1	*mesoderm posterior bHLH transcription factor 1*	1.8271	3.5483
11721660_s_at	LMO4	*LIM domain only 4*	1.8214	3.5343
11725494_at	RSPH9	*radial spoke head 9 homolog*	1.8205	3.5320
11753661_a_at	ID1	*inhibitor of DNA binding 1, HLH protein*	1.8198	3.5303
11718433_a_at	SASH1	*SAM and SH3 domain containing 1*	1.8175	3.5247
11734201_s_at	GK	*glycerol kinase*	1.8160	3.5211
11718025_at	IL1R1	*interleukin 1 receptor type 1*	1.8091	3.5042
11722523_a_at	TMCO4	*transmembrane and coiled-coil domains 4*	1.8074	3.5001
11736050_s_at	FAM229B	*family with sequence similarity 229 member B*	1.8049	3.4941
11717823_s_at	TNFAIP2	*TNF alpha induced protein 2*	1.8042	3.4924
11729679_a_at	PCDHB14	*protocadherin beta 14*	1.8032	3.4899
11716399_at	TP53INP2	*tumor protein p53 inducible nuclear protein 2*	1.8001	3.4824
11718790_at	HES6	*hes family bHLH transcription factor 6*	1.7980	3.4774
11724940_x_at	CDHR3	*cadherin related family member 3*	1.7907	3.4599
11732565_at	SLC6A14	*solute carrier family 6 member 14*	1.7892	3.4563
11721025_a_at	TRAPPC6A	*trafficking protein particle complex 6A*	1.7879	3.4532
11755450_a_at	ZNF608	*zinc finger protein 608*	1.7857	3.4479
11744307_a_at	TTC39A	*tetratricopeptide repeat domain 39A*	1.7783	3.4303
11734359_a_at	RNASEL	*ribonuclease L*	1.7760	3.4248
11756809_a_at	EFHC2	*EF-hand domain containing 2*	1.7756	3.4238
11733622_x_at	NCMAP	*non-compact myelin associated protein*	1.7718	3.4148

11732350_a_at	CCNA1	*cyclin A1*	1.7677	3.4051
11722658_at	CXCL17	*C-X-C motif chemokine ligand 17*	1.7654	3.3998
11738201_a_at	EYA2	*EYA transcriptional coactivator and phosphatase 2*	1.7644	3.3974
11726063_a_at	C2orf40	*chromosome 2 open reading frame 40*	1.7594	3.3856
11724832_at	STS	*Steroid Sulfatase (Microsomal), Isozyme S*	1.7586	3.3836
11726233_a_at	DRC3	*dynein regulatory complex subunit 3*	1.7580	3.3824
11721030_a_at	PIP5K1B	*phosphatidylinositol-4-phosphate 5-kinase type 1 beta*	1.7577	3.3815
11743952_a_at	CFAP206	*cilia and flagella associated protein 206*	1.7572	3.3803
11742423_a_at	STEAP2	*STEAP2 metalloreductase*	1.7571	3.3801
11721619_at	FOXJ1	*forkhead box J1*	1.7556	3.3766
11740782_a_at	RNF128	*ring finger protein 128, E3 ubiquitin protein ligase*	1.7529	3.3704
11719843_a_at	ABI3BP	*ABI family member 3 binding protein*	1.7527	3.3699
11744615_s_at	KLHDC9	*kelch domain containing 9*	1.7512	3.3664
11741221_a_at	COLCA2	*colorectal cancer associated 2*	1.7506	3.3651
11731855_at	C10orf107	*chromosome 10 open reading frame 107*	1.7480	3.3589
11731177_at	BCL2L15	*BCL2 like 15*	1.7429	3.3471
11757383_a_at	CTSH	*cathepsin H*	1.7422	3.3455
11740239_a_at	CFAP161	*cilia and flagella associated protein 161*	1.7386	3.3372
11731273_a_at	KCNE1	*potassium voltage-gated channel subfamily E regulatory subunit 1*	1.7332	3.3247
11743917_a_at	FKBP5	*FK506 binding protein 5*	1.7330	3.3242
11715419_at	LY6E	*lymphocyte antigen 6 complex, locus E*	1.7291	3.3152
11749550_a_at	SCPEP1	*serine carboxypeptidase 1*	1.7269	3.3101
11755814_a_at	CFAP43	*cilia and flagella associated protein 43*	1.7221	3.2992
11724667_s_at	ENPP3	*ectonucleotide pyrophosphatase/phosphodiesterase 3*	1.7198	3.2938
11716486_at	FCGBP	*Fc fragment of IgG binding protein*	1.7181	3.2900
11741044_a_at	PLS1	*plastin 1*	1.7174	3.2885
11733545_x_at	NWD1	*NACHT and WD repeat domain containing 1*	1.7143	3.2814
11756702_a_at	CYP39A1	*cytochrome P450 family 39 subfamily A member 1*	1.7116	3.2752
11715583_s_at	HLA-DPA1	*major histocompatibility complex, class II, DP alpha 1*	1.7115	3.2749
11754930_x_at	ATP1A1	*ATPase Na+/K+ transporting subunit alpha 1*	1.7100	3.2715
11754681_s_at	HLA-DMB	*major histocompatibility complex, class II, DM beta*	1.7096	3.2707
11728953_a_at	ADGRV1	*adhesion G protein-coupled receptor V1*	1.7087	3.2687
11721141_x_at	TCEA3	*transcription elongation factor A3*	1.7065	3.2637
11724017_a_at	OSCP1	*organic solute carrier partner 1*	1.7058	3.2620
11757824_s_at	RGL1	*ral guanine nucleotide dissociation stimulator like 1*	1.7039	3.2578
11763714_a_at	SSBP2	*single stranded DNA binding protein 2*	1.6944	3.2365
11757278_x_at	ASS1	*argininosuccinate synthase 1*	1.6935	3.2344
11746779_a_at	NCOA7	*nuclear receptor coactivator 7*	1.6880	3.2220
11723876_at	KCNK5	*potassium two pore domain channel subfamily K member 5*	1.6878	3.2216
11727185_at	DRC1	*dynein regulatory complex subunit 1*	1.6859	3.2174
11743731_a_at	TNFSF10	*tumor necrosis factor superfamily member 10*	1.6848	3.2149
11742865_a_at	TJP3	*tight junction protein 3*	1.6826	3.2101

11746144_a_at	PTPRZ1	*protein tyrosine phosphatase, receptor type Z1*	1.6797	3.2036
11725249_at	LY75	*lymphocyte antigen 75*	1.6774	3.1986
11737992_s_at	GPR37	*G protein-coupled receptor 37*	1.6702	3.1826
11751973_x_at	LZTS3	*leucine zipper tumor suppressor family member 3*	1.6677	3.1771
11726693_s_at	ANGPT1	*angiopoietin 1*	1.6648	3.1707
11759103_at	CYP4F3	*cytochrome P450 family 4 subfamily F member 3*	1.6640	3.1689
11719408_a_at	HIPK2	*homeodomain interacting protein kinase 2*	1.6628	3.1662
11718287_at	UBL3	*ubiquitin like 3*	1.6628	3.1662
11729503_at	CFAP53	*cilia and flagella associated protein 53*	1.6594	3.1588
11727957_a_at	DNAI1	*dynein axonemal intermediate chain 1*	1.6586	3.1570
11731874_x_at	MIA2	*melanoma inhibitory activity 2*	1.6574	3.1544
11722969_s_at	TRPV4	*transient receptor potential cation channel subfamily V member 4*	1.6535	3.1459
11750170_a_at	TRIM22	*tripartite motif containing 22*	1.6511	3.1407
11736948_at	TEX26	*testis expressed 26*	1.6477	3.1333
11717661_a_at	PPP1R16B	*protein phosphatase 1 regulatory subunit 16B*	1.6475	3.1329
11740409_a_at	FGFR2	*fibroblast growth factor receptor 2*	1.6450	3.1274
11743405_a_at	SMIM14	*small integral membrane protein 14*	1.6438	3.1248
11721032_s_at	FAM107A	*family with sequence similarity 107 member A*	1.6384	3.1132
11729832_s_at	CLDN8	*claudin 8*	1.6377	3.1116
11756677_a_at	CYB5D2	*cytochrome b5 domain containing 2*	1.6376	3.1114
11747526_a_at	TSPAN6	*tetraspanin 6*	1.6320	3.0994
11725518_at	FRAT2	*frequently rearranged in advanced T-cell lymphomas 2*	1.6299	3.0950
11721665_a_at	PLA2G16	*phospholipase A2 group XVI*	1.6298	3.0947
11715112_at	ERICH3	*glutamate rich 3*	1.6293	3.0936
11724321_s_at	C11orf54	*chromosome 11 open reading frame 54*	1.6282	3.0912
11744051_at	TSPAN1	*tetraspanin 1*	1.6219	3.0779
11727500_at	ALDH3B2	*aldehyde dehydrogenase 3 family member B2*	1.6203	3.0744
11731756_at	KLHDC7B	*kelch domain containing 7B*	1.6200	3.0737
11725941_at	WNT7B	*Wnt family member 7B*	1.6191	3.0718
11743547_a_at	ASAH1	*N-acylsphingosine amidohydrolase 1*	1.6185	3.0705
11745830_a_at	ALAD	*aminolevulinate dehydratase*	1.6162	3.0656
11717929_s_at	FOLR1	*folate receptor 1*	1.6151	3.0633
11723325_a_at	KCNQ1	*potassium voltage-gated channel subfamily Q member 1*	1.6150	3.0631
11746995_a_at	NPL	*N-acetylneuraminate pyruvate lyase*	1.6126	3.0580
11746264_a_at	PLPP1	*phospholipid phosphatase 1*	1.6118	3.0563
11717127_a_at	ANPEP	*alanyl aminopeptidase, membrane*	1.6115	3.0557
11718293_a_at	CDKN2A	*cyclin dependent kinase inhibitor 2A*	1.6109	3.0545
11736745_a_at	ZBTB20	*zinc finger and BTB domain containing 20*	1.6099	3.0523
11720857_a_at	INSR	*insulin receptor*	1.6090	3.0504
11730066_s_at	MAPK10	*mitogen-activated protein kinase 10*	1.6088	3.0499
11719171_a_at	AKR1C1	*aldo-keto reductase family 1 member C1*	1.6080	3.0483
11742251_s_at	CYP2A6	*cytochrome P450 family 2 subfamily A member 6*	1.6078	3.0478

11736909_at	C1orf210	*chromosome 1 open reading frame 210*	1.6063	3.0448
11729400_at	PCP4L1	*Purkinje cell protein 4 like 1*	1.6055	3.0430
11755362_a_at	IFT172	*intraflagellar transport 172*	1.6054	3.0428
11725000_at	DUOXA2	*dual oxidase maturation factor 2*	1.6034	3.0385
11755044_x_at	GSAP	*gamma-secretase activating protein*	1.6021	3.0359
11716144_a_at	PDCD6IP	*programmed cell death 6 interacting protein*	1.6020	3.0357
11727336_at	SAMD12	*sterile alpha motif domain containing 12*	1.5992	3.0298
11730549_a_at	IKZF2	*IKAROS family zinc finger 2*	1.5984	3.0281
11759674_a_at	CAPS2	*calcyphosine 2*	1.5963	3.0237
11726682_a_at	MEIS1	*Meis homeobox 1*	1.5956	3.0221
11720283_at	JMY	*junction mediating and regulatory protein, p53 cofactor*	1.5952	3.0214
11733164_a_at	TTC29	*tetratricopeptide repeat domain 29*	1.5942	3.0193
11727113_at	EGF	*epidermal growth factor*	1.5938	3.0184
11764261_s_at	TMPRSS11A	*transmembrane protease, serine 11A*	1.5923	3.0152
11724589_s_at	MMP12	*matrix metallopeptidase 12*	1.5921	3.0149
11753966_a_at	ZNF204P	*zinc finger protein 204, pseudogene*	1.5912	3.0131
11724703_a_at	ELF5	*E74 like ETS transcription factor 5*	1.5902	3.0109
11741477_a_at	NPHP1	*nephrocystin 1*	1.5892	3.0088
11723687_a_at	FAM46A	*family with sequence similarity 46 member A*	1.5890	3.0084
11763271_at	PEX11A	*peroxisomal biogenesis factor 11 alpha*	1.5889	3.0083
11758954_at	ENPP5	*Ectonucleotide Pyrophosphatase/Phosphodiesterase 5 (Putative)*	1.5873	3.0048
11752531_a_at	MDH1B	*malate dehydrogenase 1B*	1.5872	3.0047
11723008_s_at	CCPG1	*cell cycle progression 1*	1.5840	2.9979
11720678_a_at	CREB3L1	*cAMP responsive element binding protein 3 like 1*	1.5792	2.9881
11724063_s_at	FA2H	*fatty acid 2-hydroxylase*	1.5779	2.9853
11748761_a_at	KLF5	*Kruppel like factor 5*	1.5778	2.9851
11724588_a_at	ANKRD35	*ankyrin repeat domain 35*	1.5774	2.9844
11720124_at	SRD5A3	*steroid 5 alpha-reductase 3*	1.5751	2.9796
11755310_s_at	ACOT2	*acyl-CoA thioesterase 2*	1.5745	2.9783
11748848_a_at	DAW1	*dynein assembly factor with WD repeats 1*	1.5727	2.9747
11735478_a_at	CHST6	*carbohydrate sulfotransferase 6*	1.5725	2.9741
11715682_a_at	CREG1	*cellular repressor of E1A stimulated genes 1*	1.5718	2.9728
11720518_a_at	TACC2	*transforming acidic coiled-coil containing protein 2*	1.5709	2.9710
11750527_s_at	HLA-DQA1	*major histocompatibility complex, class II, DQ alpha 1*	1.5697	2.9685
11738149_a_at	TOX3	*TOX high mobility group box family member 3*	1.5689	2.9667
11752557_a_at	CREBRF	*CREB3 regulatory factor*	1.5687	2.9663
11721430_a_at	SYBU	*syntabulin*	1.5674	2.9637
11741731_a_at	FBXO34	*F-box protein 34*	1.5655	2.9598
11735169_at	C6orf118	*chromosome 6 open reading frame 118*	1.5632	2.9551
11717774_a_at	PLEKHB1	*pleckstrin homology domain containing B1*	1.5622	2.9530
11760972_x_at	SPACA9	*sperm acrosome associated 9*	1.5620	2.9526
11723329_a_at	GSN	*gelsolin*	1.5611	2.9507

11731352_a_at	IL19	*interleukin 19*	1.5582	2.9448
11728085_s_at	BMPR1B	*bone morphogenetic protein receptor type 1B*	1.5575	2.9435
11754833_a_at	TLR2	*toll like receptor 2*	1.5560	2.9404
11732082_s_at	STOML3	*stomatin like 3*	1.5557	2.9398
11758586_s_at	GGT6	*gamma-glutamyltransferase 6*	1.5544	2.9372
11744969_a_at	PAPLN	*papilin, proteoglycan like sulfated glycoprotein*	1.5537	2.9357
11748810_a_at	EVA1C	*eva-1 homolog C*	1.5510	2.9302
11753739_a_at	CYB5A	*cytochrome b5 type A*	1.5509	2.9300
11758988_at	SYT17	*synaptotagmin 17*	1.5498	2.9278
11719176_a_at	GPRC5B	*G protein-coupled receptor class C group 5 member B*	1.5457	2.9195
11717440_a_at	EPS8	*epidermal growth factor receptor pathway substrate 8*	1.5431	2.9143
11743921_at	TMEM125	*transmembrane protein 125*	1.5385	2.9050
11727667_at	DNAH7	*dynein axonemal heavy chain 7*	1.5374	2.9027
11716114_x_at	POR	*cytochrome p450 oxidoreductase*	1.5371	2.9021
11717348_a_at	ADD3	*adducin 3*	1.5355	2.8988
11734506_a_at	MECOM	*MDS1 and EVI1 complex locus*	1.5342	2.8963
11731924_a_at	KCNRG	*potassium channel regulator*	1.5341	2.8960
11744099_a_at	HSD17B2	*hydroxysteroid 17-beta dehydrogenase 2*	1.5336	2.8951
11731617_x_at	SIDT1	*SID1 transmembrane family member 1*	1.5308	2.8895
11740755_a_at	LYNX1	*Ly6/neurotoxin 1*	1.5307	2.8892
11737546_at	ZNF648	*zinc finger protein 648*	1.5289	2.8856
11719761_at	ARRDC4	*arrestin domain containing 4*	1.5287	2.8852
11718824_at	IGIP	*IgA inducing protein*	1.5267	2.8813
11721412_a_at	BSPRY	*B-box and SPRY domain containing*	1.5243	2.8764
11723946_a_at	ACSL5	*acyl-CoA synthetase long-chain family member 5*	1.5233	2.8744
11740841_a_at	NFIA	*nuclear factor I A*	1.5228	2.8735
11743794_a_at	CFAP69	*cilia and flagella associated protein 69*	1.5197	2.8673
11716184_s_at	ALCAM	*activated leukocyte cell adhesion molecule*	1.5187	2.8653
11720651_x_at	DUSP23	*dual specificity phosphatase 23*	1.5177	2.8634
11726442_a_at	YBX2	*Y-box binding protein 2*	1.5170	2.8620
11755220_a_at	C17orf97	*chromosome 17 open reading frame 97*	1.5167	2.8614
11742378_a_at	AKR1B15	*aldo-keto reductase family 1 member B15*	1.5164	2.8608
11730073_at	CNTN3	*contactin 3*	1.5164	2.8607
11756342_s_at	GDA	*guanine deaminase*	1.5139	2.8559
11747377_a_at	SPATA18	*spermatogenesis associated 18*	1.5074	2.8429
11730972_x_at	CYP4F12	*cytochrome P450 family 4 subfamily F member 12*	1.5072	2.8426
11729101_a_at	AKR1C2	*aldo-keto reductase family 1 member C2*	1.5041	2.8365
11737644_a_at	RNF183	*ring finger protein 183*	1.5030	2.8343
11732468_at	ATP12A	*ATPase H+/K+ transporting non-gastric alpha2 subunit*	1.5017	2.8318
11739097_x_at	ALDH3A2	*aldehyde dehydrogenase 3 family member A2*	1.5014	2.8311
11735610_a_at	RPS6KA5	*ribosomal protein S6 kinase A5*	1.4978	2.8242
11717370_at	ARSD	*arylsulfatase D*	1.4973	2.8232

11731096_at	WNT10A	*Wnt family member 10A*	1.4928	2.8143
11759102_at	UBXN10	*UBX domain protein 10*	1.4927	2.8142
11719432_at	KIAA0513	*KIAA0513*	1.4902	2.8092
11728981_at	ERICH5	*glutamate rich 5*	1.4887	2.8064
11718001_a_at	C10orf54	*chromosome 10 open reading frame 54*	1.4881	2.8051
11731050_at	CEP126	*centrosomal protein 126*	1.4857	2.8005
11758637_x_at	AMY1A	*Amylase, Alpha 1A (Salivary)*	1.4852	2.7995
11739564_s_at	ITPR1	*inositol 1,4,5-trisphosphate receptor type 1*	1.4848	2.7987
11718608_at	MIR5193	*microRNA 5193*	1.4820	2.7933
11717955_a_at	STK39	*serine/threonine kinase 39*	1.4814	2.7921
11727186_a_at	WNT5A	*Wnt family member 5A*	1.4807	2.7909
11739292_at	EHF	*ETS homologous factor*	1.4803	2.7900
11724490_x_at	AKR1B10	*aldo-keto reductase family 1 member B10*	1.4774	2.7845
11719453_a_at	BBS1	*Bardet-Biedl syndrome 1*	1.4739	2.7778
11740586_a_at	PTGFR	*prostaglandin F receptor*	1.4707	2.7715
11748971_a_at	FOXA1	*forkhead box A1*	1.4704	2.7709
11735786_at	BARX2	*BARX homeobox 2*	1.4703	2.7708
11733330_at	CCDC170	*coiled-coil domain containing 170*	1.4698	2.7699
11726548_at	PITPNM3	*PITPNM family member 3*	1.4683	2.7669
11759191_at	NIPAL2	*NIPA like domain containing 2*	1.4653	2.7613
11731543_at	SESTD1	*SEC14 and spectrin domain containing 1*	1.4637	2.7581
11759343_x_at	FMN1	*formin 1*	1.4605	2.7521
11731341_a_at	AGBL2	*ATP/GTP binding protein like 2*	1.4582	2.7476
11722283_at	CA11	*carbonic anhydrase 11*	1.4566	2.7447
11725180_a_at	RUNX2	*runt related transcription factor 2*	1.4561	2.7437
11754171_a_at	TMEM37	*transmembrane protein 37*	1.4534	2.7386
11749150_a_at	ABCD3	*ATP binding cassette subfamily D member 3*	1.4531	2.7380
11727664_x_at	STOX1	*storkhead box 1*	1.4529	2.7375
11726892_a_at	SLC51A	*solute carrier family 51 alpha subunit*	1.4505	2.7330
11763193_at	GDPD1	*glycerophosphodiester phosphodiesterase domain containing 1*	1.4492	2.7306
11724961_a_at	SRGAP3	*SLIT-ROBO Rho GTPase activating protein 3*	1.4475	2.7274
11716455_at	RHOBTB3	*Rho related BTB domain containing 3*	1.4456	2.7238
11716878_s_at	B4GALT5	*beta-1,4-galactosyltransferase 5*	1.4451	2.7229
11726337_a_at	ALOX5	*arachidonate 5-lipoxygenase*	1.4448	2.7223
11750611_a_at	ERBB2	*erb-b2 receptor tyrosine kinase 2*	1.4444	2.7215
11716641_x_at	PSMB10	*proteasome subunit beta 10*	1.4433	2.7195
11732287_at	DZIP3	*DAZ interacting zinc finger protein 3*	1.4410	2.7150
11733091_a_at	TSPAN8	*tetraspanin 8*	1.4408	2.7147
11727590_a_at	IL20RB	*interleukin 20 receptor subunit beta*	1.4405	2.7141
11744505_x_at	TP53I11	*tumor protein p53 inducible protein 11*	1.4387	2.7107
11756011_a_at	PTPRJ	*protein tyrosine phosphatase, receptor type J*	1.4359	2.7055
11726029_a_at	UPK1B	*uroplakin 1B*	1.4359	2.7055

11716532_a_at	EGFL6	*EGF like domain multiple 6*	1.4358	2.7053
11722820_at	GGT7	*gamma-glutamyltransferase 7*	1.4349	2.7037
11752544_a_at	GPNMB	*glycoprotein nmb*	1.4339	2.7017
11726581_a_at	GUCY1B3	*guanylate cyclase 1 soluble subunit beta*	1.4317	2.6977
11748622_s_at	CTSA	*cathepsin A*	1.4300	2.6944
11731817_s_at	RAB17	*RAB17, member RAS oncogene family*	1.4279	2.6906
11729682_a_at	TMEM231	*transmembrane protein 231*	1.4260	2.6870
11723912_at	MS4A8	*membrane spanning 4-domains A8*	1.4257	2.6864
11730661_a_at	CCDC78	*coiled-coil domain containing 78*	1.4241	2.6834
11728954_a_at	KITLG	*KIT ligand*	1.4239	2.6831
11715536_a_at	IDH2	*Isocitrate Dehydrogenase (NADP(+)) 2, Mitochondrial*	1.4233	2.6820
11720594_a_at	DLG3	*discs large MAGUK scaffold protein 3*	1.4227	2.6808
11721788_at	C1orf226	*chromosome 1 open reading frame 226*	1.4217	2.6790
11724866_a_at	SCGB3A1	*secretoglobin family 3A member 1*	1.4207	2.6772
11735271_a_at	GCNT1	*Glucosaminyl (N-Acetyl) Transferase 1, Core 2*	1.4206	2.6769
11727454_at	SCGB1A1	*secretoglobin family 1A member 1*	1.4191	2.6742
11722157_a_at	CCNO	*cyclin O*	1.4189	2.6739
11742224_a_at	CDC20B	*cell division cycle 20B*	1.4189	2.6738
11756443_x_at	PROM2	*prominin 2*	1.4171	2.6705
11716663_a_at	GDF15	*growth differentiation factor 15*	1.4167	2.6698
11732856_at	CDHR4	*cadherin related family member 4*	1.4163	2.6690
11740361_s_at	FOXN3	*forkhead box N3*	1.4155	2.6675
11744517_a_at	SLC2A10	*solute carrier family 2 member 10*	1.4145	2.6657
11727315_at	EFCAB1	*EF-hand calcium binding domain 1*	1.4138	2.6644
11716316_x_at	CYTH2	*cytohesin 2*	1.4137	2.6642
11723955_a_at	CLINT1	*clathrin interactor 1*	1.4135	2.6638
11739527_a_at	SECTM1	*secreted and transmembrane 1*	1.4128	2.6626
11721890_s_at	ADGRL1	*adhesion G protein-coupled receptor L1*	1.4109	2.6590
11724691_at	RIBC2	*RIB43A domain with coiled-coils 2*	1.4107	2.6586
11733607_a_at	LRRC34	*leucine rich repeat containing 34*	1.4101	2.6575
11745580_x_at	GOLGA6L9	*golgin A6 family-like 9*	1.4087	2.6550
11732589_a_at	ZNF467	*zinc finger protein 467*	1.4059	2.6498
11743226_at	CCDC160	*coiled-coil domain containing 160*	1.4049	2.6480
11752942_s_at	DBP	*D-box binding PAR bZIP transcription factor*	1.4041	2.6465
11742763_a_at	FAM214A	*family with sequence similarity 214 member A*	1.3977	2.6348
11737637_a_at	CFAP77	*cilia and flagella associated protein 77*	1.3976	2.6346
11745295_a_at	ANKRD66	*ankyrin repeat domain 66*	1.3951	2.6300
11715558_a_at	TMEM59	*transmembrane protein 59*	1.3948	2.6295
11726055_at	B3GALT4	*beta-1,3-galactosyltransferase 4*	1.3946	2.6292
11757928_s_at	TMEM178A	*transmembrane protein 178A*	1.3928	2.6258
11759572_a_at	STAU2	*staufen double-stranded RNA binding protein 2*	1.3920	2.6244
11730338_a_at	SMAD6	*SMAD family member 6*	1.3896	2.6200

11748462_a_at	NSF	*N-ethylmaleimide sensitive factor, vesicle fusing ATPase*	1.3894	2.6197
11757929_s_at	RALGAPA2	*Ral GTPase activating protein catalytic alpha subunit 2*	1.3869	2.6151
11757496_s_at	RAPGEFL1	*Rap guanine nucleotide exchange factor like 1*	1.3843	2.6105
11741317_a_at	NHLH2	*nescient helix-loop-helix 2*	1.3817	2.6058
11760107_a_at	PHF10	*PHD finger protein 10*	1.3778	2.5988
11751783_a_at	MFSD1	*major facilitator superfamily domain containing 1*	1.3749	2.5935
11738656_a_at	PACRG	*PARK2 coregulated*	1.3748	2.5934
11729258_at	MNS1	*meiosis specific nuclear structural 1*	1.3747	2.5931
11723282_a_at	CEACAM1	*carcinoembryonic antigen related cell adhesion molecule 1*	1.3697	2.5842
11746952_x_at	MDK	*Midkine (Neurite Growth-Promoting Factor 2)*	1.3687	2.5824
11718078_a_at	BCL2L11	*BCL2 like 11*	1.3686	2.5822
11721974_a_at	SUOX	*sulfite oxidase*	1.3681	2.5813
11717295_s_at	APOD	*apolipoprotein D*	1.3673	2.5798
11723996_a_at	GLCCI1	*glucocorticoid induced 1*	1.3671	2.5796
11758588_s_at	SORCS2	*sortilin related VPS10 domain containing receptor 2*	1.3663	2.5780
11755110_a_at	LRIG1	*leucine rich repeats and immunoglobulin like domains 1*	1.3661	2.5777
11729371_a_at	ZBTB16	*zinc finger and BTB domain containing 16*	1.3657	2.5770
11730976_a_at	NSUN7	*NOP2/Sun RNA methyltransferase family member 7*	1.3653	2.5763
11715411_a_at	EPAS1	*endothelial PAS domain protein 1*	1.3646	2.5750
11724842_a_at	ARMC4	*armadillo repeat containing 4*	1.3631	2.5723
11721887_a_at	CRYM	*crystallin mu*	1.3618	2.5700
11736239_a_at	ABCA5	*ATP binding cassette subfamily A member 5*	1.3615	2.5695
11758110_s_at	SIX1	*SIX homeobox 1*	1.3613	2.5692
11723823_a_at	MYO5C	*myosin VC*	1.3612	2.5689
11745361_a_at	CRNDE	*Colorectal Neoplasia Differentially Expressed (Non-Protein Coding)*	1.3578	2.5629
11734231_x_at	CSAD	*cysteine sulfinic acid decarboxylase*	1.3559	2.5596
11748127_s_at	MFSD6	*major facilitator superfamily domain containing 6*	1.3547	2.5574
11733636_at	FAM92B	*family with sequence similarity 92 member B*	1.3543	2.5567
11729418_a_at	TEKT2	*tektin 2*	1.3533	2.5549
11715722_a_at	GOLM1	*golgi membrane protein 1*	1.3516	2.5519
11718627_at	TRAK1	*trafficking kinesin protein 1*	1.3505	2.5500
11758092_s_at	EFNA5	*ephrin A5*	1.3504	2.5498
11730465_at	KCNJ2	*potassium voltage-gated channel subfamily J member 2*	1.3503	2.5496
11755087_a_at	C4orf47	*chromosome 4 open reading frame 47*	1.3501	2.5493
11719499_at	MAOB	*monoamine oxidase B*	1.3491	2.5476
11715222_at	MAGI3	*membrane associated guanylate kinase, WW and PDZ domain containing 3*	1.3474	2.5445
11727238_at	UST	*uronyl 2-sulfotransferase*	1.3473	2.5443
11723069_at	UBD	*ubiquitin D*	1.3457	2.5416
11741768_a_at	VNN2	*vanin 2*	1.3449	2.5401
11742736_at	MCEE	*methylmalonyl-CoA epimerase*	1.3435	2.5377
11729130_at	ANAPC16	*anaphase promoting complex subunit 16*	1.3427	2.5363
11747866_a_at	RBL2	*RB transcriptional corepressor like 2*	1.3422	2.5353

11723585_a_at	SMPDL3A	*sphingomyelin phosphodiesterase acid like 3A*	1.3389	2.5296
11731660_a_at	VWA3B	*von Willebrand factor A domain containing 3B*	1.3368	2.5259
11759602_a_at	RSRP1	*arginine and serine rich protein 1*	1.3357	2.5240
11716485_at	STK38	*serine/threonine kinase 38*	1.3355	2.5237
11721897_a_at	DHX58	*DExH-box helicase 58*	1.3355	2.5236
11722597_a_at	ACKR3	*atypical chemokine receptor 3*	1.3337	2.5205
11763717_a_at	CDKN1C	*cyclin dependent kinase inhibitor 1C*	1.3336	2.5203
11718307_a_at	GSE1	*Gse1 coiled-coil protein*	1.3330	2.5192
11755091_a_at	ABCA7	*ATP binding cassette subfamily A member 7*	1.3327	2.5188
11717496_a_at	IMPA2	*inositol monophosphatase 2*	1.3327	2.5188
11743089_a_at	LRRC6	*leucine rich repeat containing 6*	1.3324	2.5182
11725022_a_at	VILL	*villin like*	1.3317	2.5170
11740000_a_at	CPEB3	*cytoplasmic polyadenylation element binding protein 3*	1.3307	2.5153
11732851_at	CCDC60	*coiled-coil domain containing 60*	1.3306	2.5150
11756271_a_at	FANK1	*fibronectin type III and ankyrin repeat domains 1*	1.3305	2.5149
11762466_x_at	GOLGA2P10	*golgin A2 pseudogene 10*	1.3292	2.5126
11720865_a_at	IFT27	*intraflagellar transport 27*	1.3277	2.5100
11759568_at	SLC45A4	*solute carrier family 45 member 4*	1.3274	2.5095
11725841_at	ZSCAN16	*zinc finger and SCAN domain containing 16*	1.3265	2.5080
11742912_a_at	GAREM1	*GRB2 associated regulator of MAPK1 subtype 1*	1.3261	2.5072
11718786_a_at	PAN2	*PAN2 Poly(A) Specific Ribonuclease Subunit*	1.3254	2.5060
11724983_at	PCDH7	*protocadherin 7*	1.3252	2.5056
11748152_a_at	IFNGR1	*interferon gamma receptor 1*	1.3236	2.5029
11721147_at	SYNGR1	*synaptogyrin 1*	1.3219	2.4999
11750107_a_at	SEL1L3	*SEL1L family member 3*	1.3210	2.4984
11716553_a_at	RHBDD2	*rhomboid domain containing 2*	1.3207	2.4978
11724195_at	MIR1282	*microRNA 1282*	1.3171	2.4917
11724093_s_at	SLC35E2B	*solute carrier family 35 member E2B*	1.3165	2.4906
11731325_a_at	CAPN8	*calpain 8*	1.3156	2.4891
11754973_x_at	MANSC1	*MANSC domain containing 1*	1.3148	2.4877
11736232_at	ZNF362	*zinc finger protein 362*	1.3145	2.4871
11744171_a_at	DNAJC4	*DnaJ Heat Shock Protein Family (Hsp40) Member C4*	1.3143	2.4868
11726430_at	HSPB2-C11orf52	*HSPB2-C11orf52 Readthrough (NMD Candidate)*	1.3133	2.4851
11764283_s_at	PNISR	*PNN interacting serine and arginine rich protein*	1.3091	2.4778
11727514_at	TTC9	*tetratricopeptide repeat domain 9*	1.3090	2.4777
11751921_s_at	AHR	*aryl hydrocarbon receptor*	1.3089	2.4776
11733761_at	TMEM190	*transmembrane protein 190*	1.3088	2.4774
11725912_a_at	ERBB4	*erb-b2 receptor tyrosine kinase 4*	1.3087	2.4771
11742669_s_at	HIST4H4	*histone cluster 4 H4*	1.3084	2.4766
11724420_at	ZC3H6	*zinc finger CCCH-type containing 6*	1.3075	2.4751
11718565_at	KIAA1147	*KIAA1147*	1.3071	2.4745
11721352_at	SLC1A1	*solute carrier family 1 member 1*	1.3052	2.4712

11734013_a_at	BMP4	*bone morphogenetic protein 4*	1.3043	2.4697
11753938_a_at	FAM166B	*family with sequence similarity 166 member B*	1.3015	2.4649
11721988_at	CCDC191	*coiled-coil domain containing 191*	1.3002	2.4627
11726652_a_at	ARHGAP32	*Rho GTPase activating protein 32*	1.2994	2.4613
11737811_a_at	NNT	*nicotinamide nucleotide transhydrogenase*	1.2978	2.4586
11717773_a_at	THRA	*thyroid hormone receptor, alpha*	1.2978	2.4585
11740224_a_at	CHST4	*carbohydrate sulfotransferase 4*	1.2973	2.4577
11717212_a_at	NEO1	*neogenin 1*	1.2955	2.4547
11716210_at	CITED2	*Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2*	1.2940	2.4521
11754518_a_at	MIR631	*microRNA 631*	1.2940	2.4520
11756059_a_at	CXCL14	*C-X-C motif chemokine ligand 14*	1.2924	2.4494
11725240_at	RTP4	*receptor transporter protein 4*	1.2891	2.4438
11732634_a_at	TSGA10	*testis specific 10*	1.2862	2.4389
11752897_a_at	HBP1	*HMG-box transcription factor 1*	1.2858	2.4381
11741540_a_at	CDC42BPA	*CDC42 binding protein kinase alpha*	1.2852	2.4372
11719012_at	FZD4	*frizzled class receptor 4*	1.2840	2.4351
11729137_at	UGT2B7	*UDP glucuronosyltransferase family 2 member B7*	1.2834	2.4341
11734578_a_at	CFH	*complement factor H*	1.2833	2.4340
11733298_a_at	VIPR1	*vasoactive intestinal peptide receptor 1*	1.2826	2.4327
11742497_x_at	SSX6	*SSX family member 6, pseudogene*	1.2811	2.4302
11722757_at	CFTR	*cystic fibrosis transmembrane conductance regulator*	1.2789	2.4265
11724988_a_at	CCDC113	*coiled-coil domain containing 113*	1.2781	2.4252
11734956_a_at	CNTNAP2	*contactin associated protein-like 2*	1.2779	2.4249
11729455_x_at	CYP2B6	*cytochrome P450 family 2 subfamily B member 6*	1.2777	2.4246
11730261_a_at	PRKAR2B	*protein kinase cAMP-dependent type II regulatory subunit beta*	1.2772	2.4237
11721783_a_at	SLC9A8	*solute carrier family 9 member A8*	1.2768	2.4230
11754491_a_at	C16orf46	*chromosome 16 open reading frame 46*	1.2746	2.4193
11722507_a_at	CLIC5	*chloride intracellular channel 5*	1.2740	2.4183
11752060_x_at	ERN2	*endoplasmic reticulum to nucleus signaling 2*	1.2738	2.4179
11721026_a_at	OCEL1	*occludin/ELL domain containing 1*	1.2721	2.4152
11756604_a_at	PCDHB2	*protocadherin beta 2*	1.2688	2.4096
11756236_a_at	FBLN1	*fibulin 1*	1.2667	2.4061
11731762_s_at	RPS6KA2	*ribosomal protein S6 kinase A2*	1.2665	2.4057
11754189_s_at	AKR1C1	*aldo-keto reductase family 1 member C1*	1.2653	2.4037
11724277_a_at	SLC35C1	*solute carrier family 35 member C1*	1.2650	2.4032
11731681_a_at	KATNAL2	*katanin catalytic subunit A1 like 2*	1.2649	2.4031
11761114_x_at	AKR1C2	*aldo-keto reductase family 1 member C2*	1.2633	2.4004
11731271_a_at	MGAM	*maltase-glucoamylase*	1.2630	2.3999
11754776_x_at	CCDC74A	*coiled-coil domain containing 74A*	1.2618	2.3980
11734720_a_at	PLPP2	*phospholipid phosphatase 2*	1.2612	2.3969
11743417_a_at	P3H2	*prolyl 3-hydroxylase 2*	1.2610	2.3967
11718007_a_at	MYLIP	*myosin regulatory light chain interacting protein*	1.2603	2.3955

11748009_a_at	RHBDL2	*rhomboid like 2*	1.2587	2.3928
11715617_a_at	RNF130	*ring finger protein 130*	1.2582	2.3919
11724454_at	SLC22A4	*solute carrier family 22 member 4*	1.2577	2.3911
11744265_a_at	LAMB2	*laminin subunit beta 2*	1.2570	2.3900
11717036_a_at	HDAC5	*histone deacetylase 5*	1.2564	2.3890
11727166_a_at	FBXO15	*F-box protein 15*	1.2563	2.3889
11722052_at	PLLP	*plasmolipin*	1.2557	2.3879
11732773_at	CCDC57	*coiled-coil domain containing 57*	1.2552	2.3870
11730456_at	CCDC96	*coiled-coil domain containing 96*	1.2533	2.3838
11755966_x_at	HLA-B	*major histocompatibility complex, class I, B*	1.2530	2.3834
11728757_a_at	NHLRC3	*NHL repeat containing 3*	1.2493	2.3772
11725035_s_at	LMBRD1	*LMBR1 domain containing 1*	1.2490	2.3768
11747118_a_at	BRINP1	*BMP/retinoic acid inducible neural specific 1*	1.2473	2.3740
11748631_a_at	REEP5	*receptor accessory protein 5*	1.2471	2.3737
11754404_a_at	PARP14	*Poly(ADP-Ribose) Polymerase Family Member 14*	1.2468	2.3731
11725697_at	TRIM56	*tripartite motif containing 56*	1.2467	2.3730
11728349_a_at	STIM2	*stromal interaction molecule 2*	1.2467	2.3729
11716169_at	CCDC28A	*coiled-coil domain containing 28A*	1.2459	2.3717
11741447_s_at	RNASE4	*ribonuclease A family member 4*	1.2455	2.3710
11746681_a_at	VNN3	*vanin 3*	1.2449	2.3700
11724051_at	TRIM68	*tripartite motif containing 68*	1.2446	2.3695
11719521_at	SEMA5A	*semaphorin 5A*	1.2443	2.3691
11718617_a_at	DNAJA4	*DnaJ Heat Shock Protein Family (Hsp40) Member A4*	1.2442	2.3688
11762748_s_at	TRA2A	*transformer 2 alpha homolog*	1.2440	2.3686
11720520_s_at	LOC100996724	*phosphodiesterase 4D interacting protein-like*	1.2438	2.3682
11716871_at	GAA	*glucosidase alpha, acid*	1.2428	2.3665
11737564_a_at	CCDC74A	*coiled-coil domain containing 74A*	1.2428	2.3665
11736801_a_at	PLAG1	*PLAG1 zinc finger*	1.2413	2.3641
11719202_a_at	MORN2	*MORN repeat containing 2*	1.2395	2.3611
11755609_a_at	HYDIN2	*HYDIN2, Axonemal Central Pair Apparatus Protein (Pseudogene)*	1.2376	2.3580
11733742_a_at	DCXR	*dicarbonyl and L-xylulose reductase*	1.2338	2.3518
11739493_at	MGAT4A	*Mannosyl (Alpha-1,3-)-Glycoprotein Beta-1,4-N-Acetylglucosaminyltransferase, Isozyme A*	1.2335	2.3514
11719763_a_at	VPS13C	*vacuolar protein sorting 13 homolog C*	1.2322	2.3493
11738255_x_at	C7orf57	*chromosome 7 open reading frame 57*	1.2319	2.3487
11731862_at	CDH19	*cadherin 19*	1.2308	2.3470
11750191_x_at	PIGT	*phosphatidylinositol glycan anchor biosynthesis class T*	1.2284	2.3431
11732932_at	SAXO2	*stabilizer of axonemal microtubules 2*	1.2280	2.3425
11753199_x_at	SMARCA2	*SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2*	1.2279	2.3423
11746462_a_at	LMO7	*LIM domain 7*	1.2260	2.3391
11728008_x_at	FUT3	*Fucosyltransferase 3 (Lewis Blood Group)*	1.2258	2.3389
11724068_at	PELI2	*pellino E3 ubiquitin protein ligase family member 2*	1.2256	2.3386
11755367_s_at	DNAAF3	*dynein axonemal assembly factor 3*	1.2250	2.3375

11730509_s_at	ABCC5	*ATP binding cassette subfamily C member 5*	1.2235	2.3352
11723604_a_at	INPP5J	*inositol polyphosphate-5-phosphatase J*	1.2231	2.3345
11731030_at	BICDL2	*BICD family like cargo adaptor 2*	1.2226	2.3337
11751266_a_at	SLC44A3	*solute carrier family 44 member 3*	1.2224	2.3334
11716071_s_at	PIM3	*Pim-3 proto-oncogene, serine/threonine kinase*	1.2219	2.3325
11718201_at	HEY1	*hes related family bHLH transcription factor with YRPW motif 1*	1.2193	2.3283
11727385_a_at	PCCA	*propionyl-CoA carboxylase alpha subunit*	1.2180	2.3263
11758023_x_at	GABARAPL1	*GABA type A receptor associated protein like 1*	1.2177	2.3257
11719544_a_at	MSLN	*mesothelin*	1.2167	2.3242
11749250_a_at	ZMYND12	*zinc finger MYND-type containing 12*	1.2149	2.3212
11731945_a_at	WDR38	*WD repeat domain 38*	1.2147	2.3209
11723361_a_at	MED12	*mediator complex subunit 12*	1.2141	2.3199
11717677_a_at	CYFIP2	*cytoplasmic FMR1 interacting protein 2*	1.2138	2.3194
11755903_x_at	N4BP2L1	*NEDD4 binding protein 2 like 1*	1.2135	2.3190
11726479_a_at	MX2	*MX dynamin like GTPase 2*	1.2133	2.3187
11718920_a_at	IQSEC1	*IQ motif and Sec7 domain 1*	1.2129	2.3180
11739437_at	PPTC7	*PTC7 protein phosphatase homolog*	1.2121	2.3168
11727309_a_at	GRAMD2	*GRAM domain containing 2*	1.2106	2.3143
11729377_a_at	TMEM205	*transmembrane protein 205*	1.2097	2.3129
11740596_a_at	TGFB2	*transforming growth factor beta 2*	1.2086	2.3112
11755152_a_at	DUOX1	*dual oxidase 1*	1.2084	2.3108
11717090_a_at	HIST2H2BE	*histone cluster 2 H2B family member e*	1.2070	2.3086
11723474_a_at	LYPLAL1	*lysophospholipase like 1*	1.2062	2.3073
11720280_at	KCNMA1	*potassium calcium-activated channel subfamily M alpha 1*	1.2051	2.3056
11752329_a_at	DNAI2	*dynein axonemal intermediate chain 2*	1.2041	2.3039
11730651_a_at	SYTL4	*synaptotagmin like 4*	1.2018	2.3003
11716033_at	SLPI	*secretory leukocyte peptidase inhibitor*	1.2011	2.2991
11736244_s_at	HIST1H2AC	*histone cluster 1 H2A family member c*	1.2004	2.2980
11724374_at	BATF	*basic leucine zipper ATF-like transcription factor*	1.1981	2.2943
11730035_at	FMO4	*flavin containing monooxygenase 4*	1.1976	2.2936
11719676_s_at	MAOA	*monoamine oxidase A*	1.1974	2.2933
11716509_a_at	AKR1A1	*aldo-keto reductase family 1 member A1*	1.1965	2.2919
11757030_at	ECH1	*enoyl-CoA hydratase 1*	1.1952	2.2897
11720190_s_at	C15orf38-AP3S2	*C15orf38-AP3S2 readthrough*	1.1951	2.2896
11728184_a_at	PLEKHA7	*pleckstrin homology domain containing A7*	1.1948	2.2891
11741192_a_at	RBKS	*ribokinase*	1.1943	2.2884
11722423_a_at	NEDD4L	*neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase*	1.1937	2.2874
11717993_at	CBX7	*chromobox 7*	1.1919	2.2845
11718563_a_at	ANKRD10	*ankyrin repeat domain 10*	1.1918	2.2844
11753509_a_at	FOXC1	*forkhead box C1*	1.1897	2.2810
11753718_a_at	LRTOMT	*leucine rich transmembrane and O-methyltransferase domain containing*	1.1897	2.2810
11762940_x_at	HLA-C	*major histocompatibility complex, class I, C*	1.1895	2.2807

11732148_at	CAT	*catalase*	1.1892	2.2802
11758348_s_at	PTTG1IP	*pituitary tumor-transforming 1 interacting protein*	1.1873	2.2773
11759611_at	SMIM11A	*small integral membrane protein 11A*	1.1862	2.2755
11755223_a_at	KDM7A	*lysine demethylase 7A*	1.1843	2.2725
11724157_x_at	SULT1E1	*sulfotransferase family 1E member 1*	1.1820	2.2689
11719556_a_at	PDK2	*pyruvate dehydrogenase kinase 2*	1.1819	2.2688
11727302_a_at	TMEM71	*transmembrane protein 71*	1.1819	2.2688
11721356_s_at	YPEL3	*yippee like 3*	1.1815	2.2682
11737207_at	C1orf189	*chromosome 1 open reading frame 189*	1.1789	2.2641
11728342_at	DCLK1	*doublecortin like kinase 1*	1.1787	2.2638
11755276_a_at	GPX2	*glutathione peroxidase 2*	1.1781	2.2628
11718766_at	PRSS23	*protease, serine 23*	1.1778	2.2623
11737045_a_at	PLA2R1	*phospholipase A2 receptor 1*	1.1776	2.2620
11716167_a_at	MX1	*MX dynamin like GTPase 1*	1.1772	2.2613
11729073_a_at	TSPAN19	*tetraspanin 19*	1.1769	2.2609
11729555_a_at	SUSD4	*sushi domain containing 4*	1.1761	2.2596
11723176_s_at	PLEKHA6	*pleckstrin homology domain containing A6*	1.1752	2.2583
11756829_x_at	HEXA	*hexosaminidase subunit alpha*	1.1747	2.2574
11752283_a_at	ALOX15B	*arachidonate 15-lipoxygenase, type B*	1.1746	2.2573
11720377_s_at	SAP30L	*SAP30 like*	1.1741	2.2565
11747888_a_at	SH3YL1	*SH3 and SYLF domain containing 1*	1.1732	2.2551
11732569_at	SLCO1B3	*solute carrier organic anion transporter family member 1B3*	1.1731	2.2549
11744236_a_at	DDX60	*DExD/H-box helicase 60*	1.1715	2.2524
11754725_x_at	SATB1	*SATB homeobox 1*	1.1690	2.2486
11719844_at	SMAP2	*small ArfGAP2*	1.1688	2.2483
11717687_a_at	JAK1	*Janus kinase 1*	1.1688	2.2483
11723525_at	TBC1D8	*TBC1 domain family member 8*	1.1660	2.2439
11759623_at	C11orf71	*chromosome 11 open reading frame 71*	1.1656	2.2433
11746280_a_at	SYTL3	*synaptotagmin like 3*	1.1652	2.2427
11728956_at	ZSWIM4	*zinc finger SWIM-type containing 4*	1.1629	2.2391
11716941_at	TRIB2	*tribbles pseudokinase 2*	1.1608	2.2358
11758377_s_at	TLR1	*toll like receptor 1*	1.1600	2.2345
11736744_x_at	C1orf168	*chromosome 1 open reading frame 168*	1.1588	2.2327
11747975_x_at	RNF145	*ring finger protein 145*	1.1587	2.2326
11717679_a_at	UNC13B	*unc-13 homolog B*	1.1582	2.2318
11718735_at	PCMTD1	*Protein-L-Isoaspartate (D-Aspartate) O-Methyltransferase Domain Containing 1*	1.1581	2.2317
11725890_s_at	ABCC6	*ATP binding cassette subfamily C member 6*	1.1576	2.2308
11727030_s_at	MAP1A	*microtubule associated protein 1A*	1.1573	2.2304
11730469_s_at	LMO2	*LIM domain only 2*	1.1561	2.2286
11730623_at	DSEL	*dermatan sulfate epimerase-like*	1.1555	2.2276
11736257_at	PRKCE	*protein kinase C epsilon*	1.1552	2.2272
11734144_s_at	LRRC37A2	*leucine rich repeat containing 37 member A2*	1.1546	2.2262

11723885_at	NATD1	*N-acetyltransferase domain containing 1*	1.1543	2.2257
11752993_a_at	DUSP1	*dual specificity phosphatase 1*	1.1539	2.2252
11743949_s_at	FRAT1	*frequently rearranged in advanced T-cell lymphomas 1*	1.1537	2.2249
11716985_x_at	PNKD	*paroxysmal nonkinesigenic dyskinesia*	1.1526	2.2231
11718384_at	C2orf68	*chromosome 2 open reading frame 68*	1.1524	2.2229
11752552_a_at	MCCC1	*methylcrotonoyl-CoA carboxylase 1*	1.1514	2.2213
11732244_at	APOL6	*apolipoprotein L6*	1.1513	2.2211
11721204_a_at	ANK3	*ankyrin 3*	1.1513	2.2211
11721167_a_at	EPB41L1	*erythrocyte membrane protein band 4.1 like 1*	1.1495	2.2183
11723205_a_at	PGD	*phosphogluconate dehydrogenase*	1.1491	2.2178
11717936_a_at	ERMP1	*endoplasmic reticulum metallopeptidase 1*	1.1483	2.2165
11723221_a_at	EXOC6	*exocyst complex component 6*	1.1472	2.2149
11721661_a_at	TBXAS1	*thromboxane A synthase 1*	1.1448	2.2112
11741772_a_at	TCEA2	*transcription elongation factor A2*	1.1426	2.2078
11724452_a_at	PATZ1	*POZ/BTB and AT hook containing zinc finger 1*	1.1421	2.2070
11739975_at	ZNF117	*zinc finger protein 117*	1.1420	2.2068
11727906_at	MMP10	*matrix metallopeptidase 10*	1.1414	2.2059
11743800_a_at	DNAH2	*dynein axonemal heavy chain 2*	1.1410	2.2054
11718237_a_at	C1orf115	*chromosome 1 open reading frame 115*	1.1389	2.2022
11721118_a_at	ANKHD1-EIF4EBP3	*ANKHD1-EIF4EBP3 readthrough*	1.1388	2.2020
11744860_at	LOC100287290	*cytokine receptor CRL2*	1.1384	2.2013
11749388_x_at	IQCK	*IQ motif containing K*	1.1365	2.1985
11716464_at	SIAE	*sialic acid acetylesterase*	1.1364	2.1983
11732966_a_at	MIA	*melanoma inhibitory activity*	1.1362	2.1980
11750813_a_at	RIPK4	*receptor interacting serine/threonine kinase 4*	1.1360	2.1977
11723096_a_at	CYLD	*CYLD lysine 63 deubiquitinase*	1.1355	2.1969
11726294_s_at	CEBPA	*CCAAT/enhancer binding protein alpha*	1.1340	2.1946
11757453_s_at	CEP68	*centrosomal protein 68*	1.1314	2.1907
11734103_a_at	FGGY	*FGGY carbohydrate kinase domain containing*	1.1265	2.1833
11722918_a_at	KCNS3	*potassium voltage-gated channel modifier subfamily S member 3*	1.1235	2.1788
11731478_x_at	CHMP1B	*charged multivesicular body protein 1B*	1.1228	2.1777
11740038_s_at	ANKRD36	*ankyrin repeat domain 36*	1.1227	2.1776
11747233_a_at	KBTBD7	*kelch repeat and BTB domain containing 7*	1.1204	2.1741
11744052_a_at	SLC11A2	*solute carrier family 11 member 2*	1.1203	2.1739
11726413_a_at	USP54	*ubiquitin specific peptidase 54*	1.1200	2.1735
11723550_a_at	ABHD6	*abhydrolase domain containing 6*	1.1178	2.1702
11719584_s_at	CNNM3	*cyclin and CBS domain divalent metal cation transport mediator 3*	1.1174	2.1696
11721491_a_at	FBP1	*fructose-bisphosphatase 1*	1.1174	2.1695
11754521_a_at	MBNL2	*muscleblind like splicing regulator 2*	1.1156	2.1669
11725109_a_at	FAM98C	*family with sequence similarity 98 member C*	1.1153	2.1664
11716211_a_at	HIBADH	*3-hydroxyisobutyrate dehydrogenase*	1.1151	2.1661
11718523_s_at	ANTXR1	*anthrax toxin receptor 1*	1.1143	2.1649

11722568_at	NT5C2	*5'-nucleotidase, cytosolic II*	1.1127	2.1625
11716217_a_at	PRKAB1	*protein kinase AMP-activated non-catalytic subunit beta 1*	1.1126	2.1623
11745737_x_at	ACADVL	*acyl-CoA dehydrogenase, very long chain*	1.1112	2.1603
11729079_s_at	ESRRG	*estrogen related receptor gamma*	1.1110	2.1599
11743534_a_at	PPP2R5C	*protein phosphatase 2 regulatory subunit B'gamma*	1.1105	2.1592
11733923_a_at	CROT	*carnitine O-octanoyltransferase*	1.1093	2.1574
11732414_a_at	LRRC8B	*leucine rich repeat containing 8 family member B*	1.1090	2.1569
11744131_a_at	SECISBP2L	*SECIS binding protein 2 like*	1.1089	2.1568
11757868_a_at	PIK3IP1	*phosphoinositide-3-kinase interacting protein 1*	1.1082	2.1558
11738073_s_at	SPRY1	*sprouty RTK signaling antagonist 1*	1.1065	2.1533
11753111_x_at	IL10RB	*interleukin 10 receptor subunit beta*	1.1065	2.1532
11730820_at	PCDHB10	*protocadherin beta 10*	1.1045	2.1502
11718544_s_at	ZBTB44	*zinc finger and BTB domain containing 44*	1.1040	2.1495
11756645_x_at	CXCL16	*C-X-C motif chemokine ligand 16*	1.1031	2.1482
11727563_at	PCDHB5	*protocadherin beta 5*	1.1029	2.1479
11756624_x_at	RABL2A	*RAB, member of RAS oncogene family-like 2A*	1.1026	2.1474
11721770_x_at	BICDL1	*BICD family like cargo adaptor 1*	1.1023	2.1469
11745075_x_at	GSTA4	*glutathione S-transferase alpha 4*	1.1012	2.1453
11719255_s_at	CDK19	*cyclin dependent kinase 19*	1.0998	2.1432
11718190_s_at	C14orf159	*chromosome 14 open reading frame 159*	1.0977	2.1402
11734149_x_at	PRRT3	*proline rich transmembrane protein 3*	1.0972	2.1394
11717123_a_at	PPP1R12B	*protein phosphatase 1 regulatory subunit 12B*	1.0959	2.1375
11716823_s_at	BDH2	*3-hydroxybutyrate dehydrogenase, type 2*	1.0953	2.1366
11734336_x_at	SIGIRR	*single Ig and TIR domain containing*	1.0950	2.1361
11716406_x_at	LGALS9	*galectin 9*	1.0949	2.1360
11726437_a_at	CMTM8	*CKLF like MARVEL transmembrane domain containing 8*	1.0948	2.1358
11753004_a_at	CKB	*creatine kinase B*	1.0936	2.1341
11716390_a_at	BACE1	*beta-secretase 1*	1.0934	2.1337
11738850_a_at	BCL2L14	*BCL2 like 14*	1.0926	2.1326
11739839_a_at	GNAL	*G protein subunit alpha L*	1.0926	2.1326
11757316_a_at	FLOT1	*flotillin 1*	1.0924	2.1323
11726883_s_at	ATAD2B	*ATPase family, AAA domain containing 2B*	1.0921	2.1319
11718989_s_at	OS9	*OS9, endoplasmic reticulum lectin*	1.0919	2.1315
11745450_a_at	AUH	*AU RNA binding methylglutaconyl-CoA hydratase*	1.0911	2.1304
11724985_a_at	EXPH5	*exophilin 5*	1.0907	2.1297
11740832_at	PLEKHG7	*pleckstrin homology and RhoGEF domain containing G7*	1.0899	2.1286
11734530_x_at	HLA-F	*major histocompatibility complex, class I, F*	1.0890	2.1272
11733088_at	MAF	*MAF bZIP transcription factor*	1.0871	2.1244
11721368_at	CRLF1	*cytokine receptor like factor 1*	1.0871	2.1244
11750334_a_at	REL	*REL proto-oncogene, NF-kB subunit*	1.0862	2.1232
11754931_a_at	GCLC	*glutamate-cysteine ligase catalytic subunit*	1.0858	2.1225
11745723_a_at	MALAT1	*Metastasis Associated Lung Adenocarcinoma Transcript 1 (Non-Protein Coding)*	1.0846	2.1208

11738092_a_at	PDE9A	*phosphodiesterase 9A*	1.0835	2.1192
11717111_a_at	REPIN1	*replication initiator 1*	1.0832	2.1187
11721433_a_at	CRBN	*cereblon*	1.0829	2.1183
11739539_a_at	PIK3R1	*phosphoinositide-3-kinase regulatory subunit 1*	1.0828	2.1181
11717215_a_at	ATP9A	*ATPase Phospholipid Transporting 9A (Putative)*	1.0820	2.1170
11718452_at	AXIN2	*axin 2*	1.0813	2.1160
11737904_a_at	CASC4	*cancer susceptibility candidate 4*	1.0799	2.1139
11718178_a_at	CMTM4	*CKLF like MARVEL transmembrane domain containing 4*	1.0796	2.1134
11729967_a_at	CLYBL	*citrate lyase beta like*	1.0793	2.1130
11729972_at	CYP4Z1	*cytochrome P450 family 4 subfamily Z member 1*	1.0792	2.1129
11756592_a_at	CCDC115	*coiled-coil domain containing 115*	1.0773	2.1101
11743025_at	ATP7A	*ATPase copper transporting alpha*	1.0766	2.1091
11723822_a_at	ZNF862	*zinc finger protein 862*	1.0753	2.1072
11725726_a_at	C1orf56	*chromosome 1 open reading frame 56*	1.0751	2.1068
11721020_a_at	MTMR3	*myotubularin related protein 3*	1.0750	2.1067
11717691_a_at	ANKRD13A	*ankyrin repeat domain 13A*	1.0739	2.1051
11756881_a_at	LOC101926951	*uncharacterized LOC101926951*	1.0735	2.1046
11718738_a_at	ST3GAL1	*ST3 beta-galactoside alpha-2,3-sialyltransferase 1*	1.0730	2.1038
11747268_s_at	NBR1	*NBR1, autophagy cargo receptor*	1.0729	2.1036
11733253_a_at	FBLN2	*fibulin 2*	1.0724	2.1029
11758993_at	TRIM52	*tripartite motif containing 52*	1.0720	2.1023
11743747_a_at	PHKA1	*phosphorylase kinase regulatory subunit alpha 1*	1.0710	2.1009
11758190_s_at	SDHD	*succinate dehydrogenase complex subunit D*	1.0698	2.0992
11747075_a_at	TMEM165	*transmembrane protein 165*	1.0685	2.0972
11729890_at	ZFP3	*ZFP3 zinc finger protein*	1.0675	2.0958
11727638_a_at	AHI1	*Abelson helper integration site 1*	1.0654	2.0928
11759063_x_at	SIK2	*salt inducible kinase 2*	1.0635	2.0900
11741275_a_at	TMEM144	*transmembrane protein 144*	1.0635	2.0900
11721780_a_at	LLGL2	*LLGL2, scribble cell polarity complex component*	1.0632	2.0896
11759039_at	SVIP	*small VCP interacting protein*	1.0622	2.0881
11736159_a_at	MPPE1	*metallophosphoesterase 1*	1.0617	2.0874
11760540_at	PTCHD4	*patched domain containing 4*	1.0616	2.0873
11721217_s_at	TMEM106B	*transmembrane protein 106B*	1.0615	2.0871
11726508_a_at	CDKN2B	*cyclin dependent kinase inhibitor 2B*	1.0614	2.0869
11758934_x_at	RAB27A	*RAB27A, member RAS oncogene family*	1.0612	2.0867
11746092_a_at	ROGDI	*rogdi homolog*	1.0611	2.0865
11742024_a_at	TBL1X	*transducin beta like 1X-linked*	1.0604	2.0855
11716304_a_at	ABHD14B	*abhydrolase domain containing 14B*	1.0594	2.0841
11752697_a_at	PCED1A	*PC-esterase domain containing 1A*	1.0592	2.0838
11755839_x_at	ARFGEF3	*ARFGEF family member 3*	1.0589	2.0834
11722307_at	GLCE	*glucuronic acid epimerase*	1.0588	2.0832
11757793_s_at	TFPI	*tissue factor pathway inhibitor*	1.0587	2.0831

11728449_at	SPTSSB	*serine palmitoyltransferase small subunit B*	1.0578	2.0817
11716213_a_at	PLXNB2	*plexin B2*	1.0574	2.0812
11735210_a_at	SGPP2	*sphingosine-1-phosphate phosphatase 2*	1.0565	2.0799
11721568_a_at	C9orf3	*chromosome 9 open reading frame 3*	1.0559	2.0790
11718602_a_at	MTURN	*maturin, neural progenitor differentiation regulator homolog*	1.0552	2.0780
11718362_at	HS6ST1	*heparan sulfate 6-O-sulfotransferase 1*	1.0542	2.0765
11730526_x_at	DAPK2	*death associated protein kinase 2*	1.0542	2.0765
11726904_a_at	COBL	*cordon-bleu WH2 repeat protein*	1.0541	2.0764
11728829_at	INHBB	*inhibin beta B subunit*	1.0539	2.0761
11725252_at	FAM120C	*family with sequence similarity 120C*	1.0535	2.0755
11730439_a_at	AKAP9	*A-kinase anchoring protein 9*	1.0532	2.0751
11750383_a_at	ZMYND8	*zinc finger MYND-type containing 8*	1.0530	2.0748
11755174_a_at	CGN	*cingulin*	1.0525	2.0741
11741546_a_at	ECHDC1	*ethylmalonyl-CoA decarboxylase 1*	1.0519	2.0733
11717707_s_at	VPS13D	*vacuolar protein sorting 13 homolog D*	1.0507	2.0715
11715640_a_at	TTC3P1	*tetratricopeptide repeat domain 3 pseudogene 1*	1.0504	2.0711
11758582_s_at	SIX4	*SIX homeobox 4*	1.0501	2.0707
11722185_at	SPTSSA	*serine palmitoyltransferase small subunit A*	1.0499	2.0704
11755037_s_at	KIAA0319L	*KIAA0319 like*	1.0483	2.0681
11720044_at	SKAP2	*src kinase associated phosphoprotein 2*	1.0480	2.0677
11757724_x_at	HNRNPUL2-BSCL2	*HNRNPUL2-BSCL2 Readthrough (NMD Candidate)*	1.0478	2.0674
11729395_s_at	HECTD2	*HECT domain E3 ubiquitin protein ligase 2*	1.0465	2.0655
11756524_a_at	RBBP9	*RB binding protein 9, serine hydrolase*	1.0457	2.0643
11721561_a_at	AHCYL2	*adenosylhomocysteinase like 2*	1.0455	2.0641
11720936_a_at	CACFD1	*calcium channel flower domain containing 1*	1.0454	2.0639
11725688_x_at	RHPN2	*rhophilin Rho GTPase binding protein 2*	1.0451	2.0635
11720262_a_at	MITF	*melanogenesis associated transcription factor*	1.0441	2.0621
11744062_x_at	ACTR1B	*ARP1 actin-related protein 1 homolog B, centractin beta*	1.0400	2.0562
11757953_x_at	TTC39C	*tetratricopeptide repeat domain 39C*	1.0396	2.0557
11727510_at	UBN2	*ubinuclein 2*	1.0393	2.0552
11724674_a_at	FAM149B1	*family with sequence similarity 149 member B1*	1.0382	2.0537
11718090_a_at	TPCN1	*two pore segment channel 1*	1.0375	2.0527
11718312_at	ACADSB	*acyl-CoA dehydrogenase, short/branched chain*	1.0363	2.0510
11724673_a_at	BCKDHB	*branched chain keto acid dehydrogenase E1 subunit beta*	1.0356	2.0500
11726309_a_at	GLRB	*glycine receptor beta*	1.0328	2.0460
11757333_s_at	NUDT4	*nudix hydrolase 4*	1.0325	2.0455
11758907_at	ZNF827	*zinc finger protein 827*	1.0320	2.0448
11743846_s_at	CFH	*complement factor H*	1.0297	2.0416
11732453_s_at	HGD	*homogentisate 1,2-dioxygenase*	1.0289	2.0404
11762282_x_at	HLA-A	*major histocompatibility complex, class I, A*	1.0286	2.0401
11742191_a_at	LOC100506403	*uncharacterized LOC100506403*	1.0270	2.0378
11730090_a_at	TNFSF12-TNFSF13	*TNFSF12-TNFSF13 readthrough*	1.0264	2.0369

11749738_a_at	PIGS	*phosphatidylinositol glycan anchor biosynthesis class S*	1.0255	2.0356
11728483_at	ZNF181	*zinc finger protein 181*	1.0248	2.0347
11739214_at	SLC25A23	*solute carrier family 25 member 23*	1.0248	2.0347
11732896_a_at	HSD11B1L	*hydroxysteroid 11-beta dehydrogenase 1 like*	1.0243	2.0340
11724080_x_at	COL21A1	*collagen type XXI alpha 1 chain*	1.0242	2.0338
11720740_a_at	MCF2L	*MCF.2 cell line derived transforming sequence like*	1.0237	2.0331
11755498_s_at	ATP6V0E2	*ATPase H+ transporting V0 subunit e2*	1.0229	2.0320
11743548_a_at	SLC22A23	*solute carrier family 22 member 23*	1.0217	2.0303
11715739_s_at	PLPP3	*phospholipid phosphatase 3*	1.0199	2.0278
11741068_s_at	GTF2IRD2B	*GTF2I repeat domain containing 2B*	1.0197	2.0275
11756250_s_at	HMGCL	*3-hydroxymethyl-3-methylglutaryl-CoA lyase*	1.0192	2.0268
11746333_a_at	DENND4C	*DENN domain containing 4C*	1.0190	2.0265
11725367_at	IER5L	*immediate early response 5 like*	1.0189	2.0264
11718101_at	CD59	*CD59 molecule*	1.0167	2.0233
11722325_a_at	ZNF84	*zinc finger protein 84*	1.0161	2.0224
11719025_a_at	ZNF652	*zinc finger protein 652*	1.0158	2.0220
11738447_a_at	NFAT5	*nuclear factor of activated T-cells 5*	1.0156	2.0218
11722094_s_at	PPIC	*peptidylprolyl isomerase C*	1.0146	2.0204
11718750_a_at	SPG11	*Spastic Paraplegia 11 (Autosomal Recessive)*	1.0144	2.0201
11726628_a_at	SEMA4A	*semaphorin 4A*	1.0140	2.0195
11759346_a_at	MAML2	*mastermind like transcriptional coactivator 2*	1.0136	2.0190
11718122_a_at	ATP6V1A	*ATPase H+ transporting V1 subunit A*	1.0130	2.0181
11733792_a_at	SLC25A12	*solute carrier family 25 member 12*	1.0127	2.0177
11757404_x_at	ID3	*inhibitor of DNA binding 3, HLH protein*	1.0126	2.0175
11752318_a_at	BTN3A3	*butyrophilin subfamily 3 member A3*	1.0123	2.0171
11754571_a_at	GMDS	*GDP-mannose 4,6-dehydratase*	1.0122	2.0170
11726588_a_at	NPTN	*neuroplastin*	1.0121	2.0169
11754091_s_at	SMAD3	*SMAD family member 3*	1.0109	2.0152
11753024_a_at	NFIB	*nuclear factor I B*	1.0098	2.0136
11756891_a_at	ZNF12	*zinc finger protein 12*	1.0095	2.0132
11732343_at	ZNF33A	*zinc finger protein 33A*	1.0083	2.0116
11754374_a_at	HKR1	*HKR1, GLI-Kruppel zinc finger family member*	1.0078	2.0109
11736970_at	TMEM213	*transmembrane protein 213*	1.0075	2.0104
11737557_at	AMTN	*amelotin*	1.0075	2.0104
11726557_a_at	GSDMB	*gasdermin B*	1.0073	2.0101
11717338_a_at	CUX1	*cut like homeobox 1*	1.0067	2.0093
11725120_a_at	GATAD1	*GATA zinc finger domain containing 1*	1.0067	2.0093
11732436_at	RHOV	*ras homolog family member V*	1.0058	2.0080
11742046_a_at	PCMTD2	*Protein-L-Isoaspartate (D-Aspartate) O-Methyltransferase Domain Containing 2*	1.0041	2.0057
11720452_at	PLEKHH2	*pleckstrin homology, MyTH4 and FERM domain containing H2*	1.0022	2.0030
11733804_at	AMN	*amnion associated transmembrane protein*	1.0016	2.0022
11717327_at	KLF9	*Kruppel like factor 9*	1.0006	2.0009

11721601_s_at	**ZBTB18**	***zinc finger and BTB domain containing 18***	**1.0006**	**2.0008**
DOWNREGULATED mRNAs (1190)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11735693_x_at	**SPRR2E**	***small proline rich protein 2E***	**-5.1278**	**0.0286**
11729265_at	**SPRR2D**	***small proline rich protein 2D***	**-4.8039**	**0.0358**
11754360_a_at	**RRM2**	***ribonucleotide reductase regulatory subunit M2***	**-4.4454**	**0.0459**
11757698_s_at	**MIG7**	***mig-7***	**-4.4454**	**0.0459**
11733695_a_at	**UBE2C**	***ubiquitin conjugating enzyme E2 C***	**-4.3511**	**0.0490**
11731925_at	**CRCT1**	***cysteine rich C-terminal 1***	**-4.2461**	**0.0527**
11758672_s_at	**UCHL1**	***ubiquitin C-terminal hydrolase L1***	**-4.2056**	**0.0542**
11729712_at	**SPRR2A**	***small proline rich protein 2A***	**-4.1610**	**0.0559**
11732713_at	**FST**	***follistatin***	**-4.0350**	**0.0610**
11717355_a_at	**FEZ1**	***fasciculation and elongation protein zeta 1***	**-3.9390**	**0.0652**
11758261_s_at	**CEP55**	***centrosomal protein 55***	**-3.8868**	**0.0676**
11720970_at	**TOP2A**	***Topoisomerase (DNA) II Alpha***	**-3.8635**	**0.0687**
11755207_a_at	**NT5E**	***5'-nucleotidase ecto***	**-3.8594**	**0.0689**
11723151_s_at	**SUGCT**	***succinyl-CoA:glutarate-CoA transferase***	**-3.8181**	**0.0709**
11746283_s_at	**KRTAP2-3**	***keratin associated protein 2-3***	**-3.8100**	**0.0713**
11754662_s_at	**ADAMTS1**	***ADAM metallopeptidase with thrombospondin type 1 motif 1***	**-3.7350**	**0.0751**
11722572_at	**CCNA2**	***cyclin A2***	**-3.6565**	**0.0793**
11723939_a_at	**CCNB1**	***cyclin B1***	**-3.6349**	**0.0805**
11726909_at	**ZBED2**	***zinc finger BED-type containing 2***	**-3.6295**	**0.0808**
11725703_a_at	**KLK6**	***kallikrein related peptidase 6***	**-3.6082**	**0.0820**
11736422_s_at	**POSTN**	***periostin***	**-3.5995**	**0.0825**
11717385_a_at	**MT1G**	***metallothionein 1G***	**-3.5977**	**0.0826**
11749461_a_at	**CDH11**	***cadherin 11***	**-3.5649**	**0.0845**
11731168_at	**IGFL1**	***IGF like family member 1***	**-3.5462**	**0.0856**
11725749_a_at	**GAL**	***galanin and GMAP prepropeptide***	**-3.5362**	**0.0862**
11722826_a_at	**NCAPG**	***non-SMC condensin I complex subunit G***	**-3.5328**	**0.0864**
11730821_x_at	**CDKN3**	***cyclin dependent kinase inhibitor 3***	**-3.5312**	**0.0865**
11744425_a_at	**KIAA0101**	***KIAA0101***	**-3.5096**	**0.0878**
11758125_s_at	**DEPDC1B**	***DEP domain containing 1B***	**-3.5014**	**0.0883**
11724464_a_at	**ANLN**	***anillin actin binding protein***	**-3.4868**	**0.0892**
11753008_a_at	**IL36G**	***interleukin 36, gamma***	**-3.4787**	**0.0897**
11733957_x_at	**SPRR2F**	***small proline rich protein 2F***	**-3.4580**	**0.0910**
11737798_a_at	**PROCR**	***protein C receptor***	**-3.4548**	**0.0912**
11716358_s_at	**PRC1**	***protein regulator of cytokinesis 1***	**-3.4517**	**0.0914**
11758089_s_at	**HMMR**	***hyaluronan mediated motility receptor***	**-3.4501**	**0.0915**
11718058_a_at	**TYMS**	***thymidylate synthetase***	**-3.4251**	**0.0931**
11728863_at	**GINS1**	***GINS complex subunit 1***	**-3.4189**	**0.0935**
11742735_a_at	**NUSAP1**	***nucleolar and spindle associated protein 1***	**-3.3853**	**0.0957**

11757033_a_at	**IL13RA2**	***interleukin 13 receptor subunit alpha 2***	**-3.3263**	**0.0997**
11728404_at	**SHCBP1**	***SHC binding and spindle associated 1***	**-3.3219**	**0.1000**
11717163_s_at	**CDC20**	***cell division cycle 20***	**-3.3147**	**0.1005**
11745722_x_at	**FHL1**	***four and a half LIM domains 1***	**-3.3147**	**0.1005**
11720353_s_at	**ETV5**	***ETS variant 5***	**-3.2821**	**0.1028**
11716793_a_at	**CCNB2**	***cyclin B2***	**-3.2737**	**0.1034**
11737323_at	**LAMC2**	***laminin subunit gamma 2***	**-3.2681**	**0.1038**
11715524_a_at	**COTL1**	***coactosin like F-actin binding protein 1***	**-3.2502**	**0.1051**
11729579_at	**CDH13**	***cadherin 13***	**-3.2379**	**0.1060**
11750598_s_at	**TPX2**	***TPX2, microtubule nucleation factor***	**-3.1976**	**0.1090**
11721932_a_at	**KIF23**	***kinesin family member 23***	**-3.1766**	**0.1106**
11726617_s_at	**CDK1**	***cyclin dependent kinase 1***	**-3.1701**	**0.1111**
11717481_s_at	**FKBP10**	***FK506 binding protein 10***	**-3.1688**	**0.1112**
11758529_s_at	**CENPA**	***centromere protein A***	**-3.1675**	**0.1113**
11733864_a_at	**BIRC5**	***baculoviral IAP repeat containing 5***	**-3.1623**	**0.1117**
11720185_a_at	**MAD2L1**	***MAD2 mitotic arrest deficient-like 1 (yeast)***	**-3.1443**	**0.1131**
11723435_s_at	**TTK**	***TTK protein kinase***	**-3.1342**	**0.1139**
11718183_at	**CDCA5**	***cell division cycle associated 5***	**-3.0979**	**0.1168**
11747230_a_at	**BUB1**	***BUB1 mitotic checkpoint serine/threonine kinase***	**-3.0469**	**0.1210**
11758478_s_at	**CDCA7**	***cell division cycle associated 7***	**-3.0422**	**0.1214**
11756626_s_at	**ZWINT**	***ZW10 interacting kinetochore protein***	**-3.0339**	**0.1221**
11728054_a_at	**DIAPH3**	***diaphanous related formin 3***	**-3.0151**	**0.1237**
11743065_at	**CDC6**	***cell division cycle 6***	**-2.9988**	**0.1251**
11722367_a_at	**DLGAP5**	***DLG associated protein 5***	**-2.9908**	**0.1258**
11745948_a_at	**CHEK1**	***checkpoint kinase 1***	**-2.9874**	**0.1261**
11742832_a_at	**ASPM**	***abnormal spindle microtubule assembly***	**-2.9839**	**0.1264**
11724478_s_at	**FOSL1**	***FOS like 1, AP-1 transcription factor subunit***	**-2.9379**	**0.1305**
11722880_a_at	**PHF19**	***PHD finger protein 19***	**-2.9346**	**0.1308**
11727215_a_at	**NRG1**	***neuregulin 1***	**-2.9258**	**0.1316**
11739061_at	**SLC7A5**	***solute carrier family 7 member 5***	**-2.9181**	**0.1323**
11731526_s_at	**TRIP13**	***thyroid hormone receptor interactor 13***	**-2.9148**	**0.1326**
11723010_a_at	**KIF20A**	***kinesin family member 20A***	**-2.9040**	**0.1336**
11740656_a_at	**HMGA2**	***high mobility group AT-hook 2***	**-2.8847**	**0.1354**
11724139_s_at	**SACS**	***sacsin molecular chaperone***	**-2.8794**	**0.1359**
11718943_a_at	**AURKA**	***aurora kinase A***	**-2.8730**	**0.1365**
11729243_s_at	**FBN2**	***fibrillin 2***	**-2.8709**	**0.1367**
11724459_x_at	**MIR6756**	***microRNA 6756***	**-2.8635**	**0.1374**
11754676_a_at	**CENPE**	***centromere protein E***	**-2.8625**	**0.1375**
11745868_a_at	**KIF2C**	***kinesin family member 2C***	**-2.8344**	**0.1402**
11718127_at	**TK1**	***thymidine kinase 1***	**-2.8334**	**0.1403**
11723297_a_at	**AKAP2**	***A-kinase anchoring protein 2***	**-2.8303**	**0.1406**
11733884_a_at	**DEPDC1**	***DEP domain containing 1***	**-2.8262**	**0.1410**

11719916_at	**IL1B**	***interleukin 1 beta***	**-2.8079**	**0.1428**
11721143_a_at	**MKI67**	***marker of proliferation Ki-67***	**-2.8049**	**0.1431**
11746463_a_at	**IL6**	***interleukin 6***	**-2.8029**	**0.1433**
11715563_s_at	**SCD**	***stearoyl-CoA desaturase***	**-2.7949**	**0.1441**
11730264_a_at	**FAM83D**	***family with sequence similarity 83 member D***	**-2.7819**	**0.1454**
11723192_a_at	**UHRF1**	***ubiquitin like with PHD and ring finger domains 1***	**-2.7809**	**0.1455**
11759328_at	**KNL1**	***kinetochore scaffold 1***	**-2.7730**	**0.1463**
11758842_at	**THBS1**	***thrombospondin 1***	**-2.7720**	**0.1464**
11728397_at	**MT1M**	***metallothionein 1M***	**-2.7691**	**0.1467**
11731857_x_at	**MT1H**	***metallothionein 1H***	**-2.7642**	**0.1472**
11721840_at	**GLIPR1**	***GLI pathogenesis related 1***	**-2.7583**	**0.1478**
11743530_a_at	**CENPK**	***centromere protein K***	**-2.7554**	**0.1481**
11723804_a_at	**AKAP12**	***A-kinase anchoring protein 12***	**-2.7486**	**0.1488**
11721307_at	**PHLDA1**	***pleckstrin homology like domain family A member 1***	**-2.7456**	**0.1491**
11752515_a_at	**ODC1**	***ornithine decarboxylase 1***	**-2.7389**	**0.1498**
11750723_x_at	**MICB**	***MHC class I polypeptide-related sequence B***	**-2.7331**	**0.1504**
11723950_a_at	**PBK**	***PDZ binding kinase***	**-2.7264**	**0.1511**
11723104_at	**GNB4**	***G protein subunit beta 4***	**-2.7245**	**0.1513**
11719032_a_at	**FADS3**	***fatty acid desaturase 3***	**-2.7207**	**0.1517**
11716587_at	**AXL**	***AXL receptor tyrosine kinase***	**-2.7169**	**0.1521**
11740349_at	**RNASE7**	***ribonuclease A family member 7***	**-2.7160**	**0.1522**
11727489_a_at	**KIF11**	***kinesin family member 11***	**-2.6841**	**0.1556**
11757789_a_at	**EPB41L2**	***erythrocyte membrane protein band 4.1 like 2***	**-2.6602**	**0.1582**
11743296_a_at	**CENPF**	***centromere protein F***	**-2.6313**	**0.1614**
11719197_at	**CCND2**	***cyclin D2***	**-2.6277**	**0.1618**
11751206_s_at	**RAB3GAP2**	***RAB3 GTPase activating non-catalytic protein subunit 2***	**-2.6242**	**0.1622**
11720647_a_at	**BUB1B**	***BUB1 mitotic checkpoint serine/threonine kinase B***	**-2.6153**	**0.1632**
11744047_a_at	**MAP1B**	***microtubule associated protein 1B***	**-2.6118**	**0.1636**
11745459_a_at	**MIR1908**	***microRNA 1908***	**-2.6082**	**0.1640**
11717565_s_at	**EMP1**	***epithelial membrane protein 1***	**-2.6065**	**0.1642**
11755009_s_at	**VCAN**	***versican***	**-2.6047**	**0.1644**
11726206_a_at	**SH2D5**	***SH2 domain containing 5***	**-2.5951**	**0.1655**
11728303_at	**TGFA**	***transforming growth factor alpha***	**-2.5934**	**0.1657**
11740957_x_at	**SLC2A6**	***solute carrier family 2 member 6***	**-2.5847**	**0.1667**
11725155_at	**FJX1**	***four jointed box 1***	**-2.5786**	**0.1674**
11719666_a_at	**STMN1**	***stathmin 1***	**-2.5760**	**0.1677**
11725469_at	**LIPG**	***lipase G, endothelial type***	**-2.5718**	**0.1682**
11757940_at	**PGF**	***placental growth factor***	**-2.5675**	**0.1687**
11724888_a_at	**CARD10**	***caspase recruitment domain family member 10***	**-2.5522**	**0.1705**
11719262_a_at	**SMTN**	***smoothelin***	**-2.5446**	**0.1714**
11754180_s_at	**SPRR1A**	***small proline rich protein 1A***	**-2.5420**	**0.1717**
11744274_at	**NDC80**	***NDC80, kinetochore complex component***	**-2.5387**	**0.1721**

11724407_s_at	**CCNE1**	***cyclin E1***	**-2.5270**	**0.1735**
11728024_a_at	**KLK5**	***kallikrein related peptidase 5***	**-2.5270**	**0.1735**
11737223_a_at	**ARTN**	***artemin***	**-2.5204**	**0.1743**
11763188_a_at	**SNX5**	***sorting nexin 5***	**-2.5162**	**0.1748**
11736687_a_at	**FGF5**	***fibroblast growth factor 5***	**-2.5146**	**0.1750**
11718578_a_at	**GSTM3**	***glutathione S-transferase mu 3***	**-2.5137**	**0.1751**
11753736_s_at	**MT1P3**	***metallothionein 1 pseudogene 3***	**-2.4998**	**0.1768**
11745377_x_at	**PTRF**	***polymerase I and transcript release factor***	**-2.4990**	**0.1769**
11727543_at	**OIP5**	***Opa interacting protein 5***	**-2.4965**	**0.1772**
11733115_a_at	**CA2**	***carbonic anhydrase 2***	**-2.4925**	**0.1777**
11743513_a_at	**GINS2**	***GINS complex subunit 2***	**-2.4892**	**0.1781**
11743160_a_at	**HJURP**	***Holliday junction recognition protein***	**-2.4876**	**0.1783**
11727837_at	**ORC6**	***origin recognition complex subunit 6***	**-2.4707**	**0.1804**
11755046_a_at	**SPHK1**	***sphingosine kinase 1***	**-2.4683**	**0.1807**
11718404_at	**RFC3**	***replication factor C subunit 3***	**-2.4635**	**0.1813**
11755466_a_at	**CDCA2**	***cell division cycle associated 2***	**-2.4564**	**0.1822**
11740133_a_at	**CALD1**	***caldesmon 1***	**-2.4548**	**0.1824**
11736246_a_at	**AMIGO2**	***adhesion molecule with Ig like domain 2***	**-2.4446**	**0.1837**
11727081_a_at	**TIPIN**	***TIMELESS interacting protein***	**-2.4438**	**0.1838**
11720528_at	**LTBP2**	***latent transforming growth factor beta binding protein 2***	**-2.4399**	**0.1843**
11758136_s_at	**SLC35G2**	***solute carrier family 35 member G2***	**-2.4266**	**0.1860**
11730029_a_at	**E2F7**	***E2F transcription factor 7***	**-2.4266**	**0.1860**
11735576_a_at	**LETM2**	***leucine zipper and EF-hand containing transmembrane protein 2***	**-2.4135**	**0.1877**
11717521_x_at	**PTTG3P**	***pituitary tumor-transforming 3, pseudogene***	**-2.4104**	**0.1881**
11741779_s_at	**HSD11B1**	***hydroxysteroid 11-beta dehydrogenase 1***	**-2.4104**	**0.1881**
11754593_x_at	**TUBB3**	***tubulin beta 3 class III***	**-2.4081**	**0.1884**
11734701_a_at	**DKK3**	***dickkopf WNT signaling pathway inhibitor 3***	**-2.4005**	**0.1894**
11726779_a_at	**IKBIP**	***IKBKB interacting protein***	**-2.3982**	**0.1897**
11725198_at	**IL1A**	***interleukin 1 alpha***	**-2.3861**	**0.1913**
11757884_s_at	**MSRB3**	***methionine sulfoxide reductase B3***	**-2.3816**	**0.1919**
11725788_a_at	**CENPN**	***centromere protein N***	**-2.3778**	**0.1924**
11719699_a_at	**CDC45**	***cell division cycle 45***	**-2.3703**	**0.1934**
11719849_s_at	**UBE2S**	***ubiquitin conjugating enzyme E2 S***	**-2.3644**	**0.1942**
11743721_at	**LGALS1**	***galectin 1***	**-2.3599**	**0.1948**
11719898_s_at	**HBEGF**	***heparin binding EGF like growth factor***	**-2.3570**	**0.1952**
11719173_s_at	**PAICS**	***phosphoribosylaminoimidazole carboxylase; phosphoribosylaminoimidazolesuccinocarboxamide synthase***	**-2.3562**	**0.1953**
11720203_a_at	**AURKB**	***aurora kinase B***	**-2.3496**	**0.1962**
11751116_a_at	**ACTN1**	***actinin alpha 1***	**-2.3489**	**0.1963**
11736596_s_at	**GINS4**	***GINS complex subunit 4***	**-2.3481**	**0.1964**
11728876_at	**CSF2**	***colony stimulating factor 2***	**-2.3437**	**0.1970**
11725459_s_at	**S100A7A**	***S100 calcium binding protein A7A***	**-2.3335**	**0.1984**
11753856_a_at	**CKS2**	***CDC28 protein kinase regulatory subunit 2***	**-2.3292**	**0.1990**

11739328_x_at	CENPH	*centromere protein H*	-2.3083	0.2019
11715306_s_at	AREG	*amphiregulin*	-2.2983	0.2033
11722122_at	CYP27B1	*cytochrome P450 family 27 subfamily B member 1*	-2.2941	0.2039
11754375_s_at	SNX10	*sorting nexin 10*	-2.2927	0.2041
11723747_a_at	FAM64A	*family with sequence similarity 64 member A*	-2.2891	0.2046
11756882_a_at	RTTN	*rotatin*	-2.2835	0.2054
11758499_s_at	DTL	*denticleless E3 ubiquitin protein ligase homolog*	-2.2786	0.2061
11722193_a_at	C12orf75	*chromosome 12 open reading frame 75*	-2.2786	0.2061
11724963_s_at	FBXO5	*F-box protein 5*	-2.2786	0.2061
11736440_at	INF2	*inverted formin, FH2 and WH2 domain containing*	-2.2730	0.2069
11732997_a_at	MCM6	*minichromosome maintenance complex component 6*	-2.2723	0.2070
11726757_s_at	CDC25A	*cell division cycle 25A*	-2.2716	0.2071
11743373_a_at	KNSTRN	*kinetochore localized astrin/SPAG5 binding protein*	-2.2674	0.2077
11741015_a_at	CDCA8	*cell division cycle associated 8*	-2.2633	0.2083
11725460_x_at	S100A7	*S100 calcium binding protein A7*	-2.2550	0.2095
11718140_a_at	EMP3	*epithelial membrane protein 3*	-2.2550	0.2095
11731653_a_at	IVL	*involucrin*	-2.2529	0.2098
11718297_a_at	TACC3	*transforming acidic coiled-coil containing protein 3*	-2.2481	0.2105
11744141_x_at	FOLR3	*folate receptor 3*	-2.2365	0.2122
11748382_a_at	SMURF2	*SMAD specific E3 ubiquitin protein ligase 2*	-2.2297	0.2132
11715803_a_at	ANXA6	*annexin A6*	-2.2223	0.2143
11738997_s_at	DPYSL2	*dihydropyrimidinase like 2*	-2.2216	0.2144
11724038_a_at	PTGS2	*prostaglandin-endoperoxide synthase 2*	-2.2203	0.2146
11725161_a_at	DDIAS	*DNA damage induced apoptosis suppressor*	-2.2189	0.2148
11737197_s_at	KIF4A	*kinesin family member 4A*	-2.2116	0.2159
11736813_at	PDCD1LG2	*programmed cell death 1 ligand 2*	-2.1871	0.2196
11717436_a_at	CDCA7L	*cell division cycle associated 7 like*	-2.1851	0.2199
11723591_at	LRRC8C	*leucine rich repeat containing 8 family member C*	-2.1851	0.2199
11751389_s_at	FEN1	*flap structure-specific endonuclease 1*	-2.1733	0.2217
11720794_a_at	SRPX	*sushi repeat containing protein, X-linked*	-2.1707	0.2221
11752384_s_at	COL6A1	*collagen type VI alpha 1 chain*	-2.1681	0.2225
11721563_a_at	MELK	*maternal embryonic leucine zipper kinase*	-2.1559	0.2244
11722839_at	LYAR	*Ly1 antibody reactive*	-2.1501	0.2253
11716631_s_at	SERPINB2	*serpin family B member 2*	-2.1494	0.2254
11751918_a_at	BNC1	*basonuclin 1*	-2.1431	0.2264
11744584_a_at	HYI	*Hydroxypyruvate Isomerase (Putative)*	-2.1405	0.2268
11753830_a_at	MLLT11	*myeloid/lymphoid or mixed-lineage leukemia; translocated to, 11*	-2.1329	0.2280
11727968_at	ESCO2	*establishment of sister chromatid cohesion N-acetyltransferase 2*	-2.1316	0.2282
11731603_at	TMEM154	*transmembrane protein 154*	-2.1304	0.2284
11753255_a_at	KLK7	*kallikrein related peptidase 7*	-2.1260	0.2291
11754074_s_at	G0S2	*G0/G1 switch 2*	-2.1247	0.2293
11736810_at	RPL27A	*ribosomal protein L27a*	-2.1228	0.2296

11717055_a_at	CORO1C	*coronin 1C*	-2.1178	0.2304
11726559_s_at	LCP1	*lymphocyte cytosolic protein 1*	-2.1178	0.2304
11722069_a_at	SKA1	*spindle and kinetochore associated complex subunit 1*	-2.1147	0.2309
11758149_s_at	RACGAP1	*Rac GTPase activating protein 1*	-2.1128	0.2312
11732191_s_at	RAD51AP1	*RAD51 associated protein 1*	-2.1010	0.2331
11760935_x_at	KRT6B	*keratin 6B*	-2.0991	0.2334
11745249_x_at	TMEM40	*transmembrane protein 40*	-2.0985	0.2335
11746880_x_at	FLNA	*filamin A*	-2.0985	0.2335
11728300_at	CCNE2	*cyclin E2*	-2.0948	0.2341
11732542_at	TRIM7	*tripartite motif containing 7*	-2.0868	0.2354
11721345_at	PLEK2	*pleckstrin 2*	-2.0764	0.2371
11723883_at	SOWAHC	*sosondowah ankyrin repeat domain family member C*	-2.0740	0.2375
11721854_a_at	NCAPH	*non-SMC condensin I complex subunit H*	-2.0637	0.2392
11749517_x_at	EHD1	*EH domain containing 1*	-2.0571	0.2403
11741152_x_at	PLAGL1	*PLAG1 like zinc finger 1*	-2.0529	0.2410
11758396_s_at	POLR3G	*RNA polymerase III subunit G*	-2.0499	0.2415
11723998_at	SPC25	*SPC25, NDC80 kinetochore complex component*	-2.0439	0.2425
11722442_a_at	NUF2	*NUF2, NDC80 kinetochore complex component*	-2.0410	0.2430
11715757_a_at	RGS2	*regulator of G-protein signaling 2*	-2.0410	0.2430
11758294_s_at	ARMCX1	*armadillo repeat containing, X-linked 1*	-2.0398	0.2432
11759656_a_at	KLHL7	*kelch like family member 7*	-2.0368	0.2437
11736367_a_at	MCM10	*minichromosome maintenance 10 replication initiation factor*	-2.0356	0.2439
11721828_x_at	ZWILCH	*zwilch kinetochore protein*	-2.0327	0.2444
11730875_a_at	FANCI	*Fanconi anemia complementation group I*	-2.0315	0.2446
11726536_at	CYP1A1	*cytochrome P450 family 1 subfamily A member 1*	-2.0297	0.2449
11763834_a_at	PPP1R1C	*protein phosphatase 1 regulatory inhibitor subunit 1C*	-2.0291	0.2450
11720967_a_at	GPSM2	*G-protein signaling modulator 2*	-2.0286	0.2451
11719586_a_at	TAGLN3	*transgelin 3*	-2.0203	0.2465
11745469_a_at	INPP4B	*inositol polyphosphate-4-phosphatase type II B*	-2.0192	0.2467
11754344_s_at	SPRY4	*sprouty RTK signaling antagonist 4*	-2.0145	0.2475
11756121_a_at	DUSP7	*dual specificity phosphatase 7*	-2.0116	0.2480
11718141_at	DKK1	*dickkopf WNT signaling pathway inhibitor 1*	-2.0052	0.2491
11726136_a_at	TMSB15A	*thymosin beta 15a*	-2.0000	0.2500
11758598_s_at	SERPINE2	*serpin family E member 2*	-2.0000	0.2500
11754824_a_at	LGALSL	*galectin like*	-1.9965	0.2506
11724562_x_at	RHOF	*ras homolog family member F, filopodia associated*	-1.9960	0.2507
11742890_at	MND1	*meiotic nuclear divisions 1*	-1.9948	0.2509
11725274_s_at	RGS20	*regulator of G-protein signaling 20*	-1.9942	0.2510
11726441_a_at	ERCC6L	*ERCC excision repair 6 like, spindle assembly checkpoint helicase*	-1.9834	0.2529
11755200_a_at	DCBLD2	*discoidin, CUB and LCCL domain containing 2*	-1.9765	0.2541
11745198_s_at	CDCA4	*cell division cycle associated 4*	-1.9720	0.2549
11718290_a_at	FXYD5	*FXYD domain containing ion transport regulator 5*	-1.9720	0.2549

11724405_at	NDUFC2-KCTD14	*NDUFC2-KCTD14 readthrough*	-1.9658	0.2560
11759423_at	EPPK1	*epiplakin 1*	-1.9607	0.2569
11724735_a_at	PDPN	*podoplanin*	-1.9579	0.2574
11754573_a_at	LPIN1	*lipin 1*	-1.9551	0.2579
11725169_at	MOB3B	*MOB kinase activator 3B*	-1.9546	0.2580
11731068_s_at	FIGNL1	*fidgetin like 1*	-1.9534	0.2582
11723829_s_at	ANO1	*anoctamin 1*	-1.9501	0.2588
11715716_at	MSN	*moesin*	-1.9484	0.2591
11718704_at	IGF1R	*insulin like growth factor 1 receptor*	-1.9456	0.2596
11715948_at	KCTD12	*potassium channel tetramerization domain containing 12*	-1.9456	0.2596
11718980_a_at	YKT6	*YKT6 V-SNARE Homolog (S. Cerevisiae)*	-1.9445	0.2598
11747820_x_at	UPP1	*uridine phosphorylase 1*	-1.9445	0.2598
11726678_a_at	AFAP1L2	*actin filament associated protein 1 like 2*	-1.9418	0.2603
11725842_a_at	PIF1	*PIF1 5'-to-3' DNA helicase*	-1.9384	0.2609
11727459_x_at	KRT14	*keratin 14*	-1.9329	0.2619
11716638_s_at	COL4A1	*collagen type IV alpha 1 chain*	-1.9329	0.2619
11729158_at	UBE2T	*ubiquitin conjugating enzyme E2 T*	-1.9318	0.2621
11721071_s_at	DEF8	*differentially expressed in FDCP 8 homolog*	-1.9296	0.2625
11759698_at	STEAP1B	*STEAP family member 1B*	-1.9280	0.2628
11727937_x_at	MSANTD3	*Myb/SANT DNA binding domain containing 3*	-1.9230	0.2637
11729227_a_at	GRK5	*G protein-coupled receptor kinase 5*	-1.9165	0.2649
11739763_a_at	GINS3	*GINS complex subunit 3*	-1.9094	0.2662
11744005_at	PHLDA2	*pleckstrin homology like domain family A member 2*	-1.9073	0.2666
11755928_s_at	MMP1	*matrix metallopeptidase 1*	-1.9056	0.2669
11729239_x_at	CSRP2	*cysteine and glycine rich protein 2*	-1.8986	0.2682
11733876_x_at	SMC4	*structural maintenance of chromosomes 4*	-1.8986	0.2682
11763100_x_at	MT1JP	*metallothionein 1J, pseudogene*	-1.8975	0.2684
11744519_a_at	POLE2	*DNA polymerase epsilon 2, accessory subunit*	-1.8922	0.2694
11756230_a_at	FLNB	*filamin B*	-1.8895	0.2699
11723389_a_at	C16orf74	*chromosome 16 open reading frame 74*	-1.8863	0.2705
11717154_a_at	PLAU	*plasminogen activator, urokinase*	-1.8847	0.2708
11716131_s_at	FSTL3	*follistatin like 3*	-1.8826	0.2712
11734070_x_at	SSR3	*signal sequence receptor subunit 3*	-1.8799	0.2717
11749650_x_at	A2ML1	*alpha-2-macroglobulin like 1*	-1.8720	0.2732
11725714_a_at	RPS14	*ribosomal protein S14*	-1.8688	0.2738
11716322_s_at	PRKCDBP	*protein kinase C delta binding protein*	-1.8667	0.2742
11726724_a_at	CKAP2L	*cytoskeleton associated protein 2 like*	-1.8625	0.2750
11747334_a_at	DDX39A	*DExD-box helicase 39A*	-1.8583	0.2758
11754545_x_at	PLAT	*plasminogen activator, tissue type*	-1.8578	0.2759
11728161_at	WNT7A	*Wnt family member 7A*	-1.8578	0.2759
11735324_s_at	FAM72C	*family with sequence similarity 72 member C*	-1.8546	0.2765
11735123_x_at	POLR1E	*RNA polymerase I subunit E*	-1.8541	0.2766

11718571_at	NT5DC3	*5'-nucleotidase domain containing 3*	-1.8526	0.2769
11715452_s_at	COL4A2	*collagen type IV alpha 2 chain*	-1.8484	0.2777
11753254_a_at	SGO2	*shugoshin 2*	-1.8468	0.2780
11728612_at	ADAMTS6	*ADAM metallopeptidase with thrombospondin type 1 motif 6*	-1.8401	0.2793
11728376_s_at	NMU	*neuromedin U*	-1.8391	0.2795
11724326_a_at	ARHGAP25	*Rho GTPase activating protein 25*	-1.8375	0.2798
11719041_at	CYGB	*cytoglobin*	-1.8375	0.2798
11740840_a_at	ABL2	*ABL proto-oncogene 2, non-receptor tyrosine kinase*	-1.8350	0.2803
11728135_at	NIPAL4	*NIPA like domain containing 4*	-1.8339	0.2805
11722300_a_at	ETS1	*ETS proto-oncogene 1, transcription factor*	-1.8308	0.2811
11760436_a_at	DST	*dystonin*	-1.8283	0.2816
11744286_s_at	CBS	*cystathionine-beta-synthase*	-1.8232	0.2826
11727324_at	NAGS	*N-acetylglutamate synthase*	-1.8216	0.2829
11739144_a_at	SKP2	*S-phase kinase associated protein 2*	-1.8216	0.2829
11733126_a_at	PRIM1	*Primase (DNA) Subunit 1*	-1.8211	0.2830
11744435_a_at	DUSP6	*dual specificity phosphatase 6*	-1.8211	0.2830
11721632_a_at	TMEM97	*transmembrane protein 97*	-1.8206	0.2831
11717758_x_at	RALA	*RAS like proto-oncogene A*	-1.8150	0.2842
11719598_s_at	CDCA3	*cell division cycle associated 3*	-1.8125	0.2847
11755624_a_at	MTFR2	*mitochondrial fission regulator 2*	-1.8115	0.2849
11741819_a_at	TGM1	*transglutaminase 1*	-1.8115	0.2849
11726807_a_at	ZAK	*sterile alpha motif and leucine zipper containing kinase AZK*	-1.8105	0.2851
11728076_at	HDAC9	*histone deacetylase 9*	-1.8084	0.2855
11731887_at	KIF14	*kinesin family member 14*	-1.8079	0.2856
11723487_a_at	LAMB1	*laminin subunit beta 1*	-1.8069	0.2858
11727504_at	SOX7	*SRY-box 7*	-1.8039	0.2864
11732901_a_at	APOBEC3A_B	*APOBEC3A and APOBEC3B deletion hybrid*	-1.8024	0.2867
11743922_at	NUDT11	*nudix hydrolase 11*	-1.8014	0.2869
11755943_x_at	VIM	*vimentin*	-1.8014	0.2869
11757017_x_at	RNASEH2A	*ribonuclease H2 subunit A*	-1.7979	0.2876
11746009_a_at	ACAT2	*acetyl-CoA acetyltransferase 2*	-1.7959	0.2880
11732902_x_at	APOBEC3B	*apolipoprotein B mRNA editing enzyme catalytic subunit 3B*	-1.7959	0.2880
11719258_at	TICAM1	*toll like receptor adaptor molecule 1*	-1.7944	0.2883
11744068_x_at	APOE	*apolipoprotein E*	-1.7939	0.2884
11727833_at	WDR43	*WD repeat domain 43*	-1.7894	0.2893
11726963_s_at	SGTB	*small glutamine rich tetratricopeptide repeat containing beta*	-1.7894	0.2893
11744218_at	SNAI2	*snail family transcriptional repressor 2*	-1.7869	0.2898
11726717_at	C1orf74	*chromosome 1 open reading frame 74*	-1.7839	0.2904
11718005_a_at	CDC25B	*cell division cycle 25B*	-1.7839	0.2904
11745571_a_at	CENPA	*centromere protein A*	-1.7789	0.2914
11728808_at	CHAC2	*ChaC cation transport regulator homolog 2*	-1.7765	0.2919
11739945_a_at	PKP1	*plakophilin 1*	-1.7745	0.2923

11728731_s_at	DSCC1	*DNA replication and sister chromatid cohesion 1*	-1.7730	0.2926
11738222_x_at	RAET1L	*retinoic acid early transcript 1L*	-1.7710	0.2930
11719194_a_at	DFNA5	*DFNA5, deafness associated tumor suppressor*	-1.7705	0.2931
11725825_a_at	GJB3	*gap junction protein beta 3*	-1.7691	0.2934
11750141_a_at	CTPS1	*CTP synthase 1*	-1.7671	0.2938
11758572_s_at	HELLS	*helicase, lymphoid-specific*	-1.7666	0.2939
11749656_a_at	ARHGAP11A	*Rho GTPase activating protein 11A*	-1.7637	0.2945
11720566_at	BCAT1	*branched chain amino acid transaminase 1*	-1.7637	0.2945
11733832_a_at	MAP2	*microtubule associated protein 2*	-1.7602	0.2952
11747047_a_at	MAP3K7CL	*MAP3K7 C-terminal like*	-1.7597	0.2953
11716987_a_at	HMGCS1	*3-hydroxy-3-methylglutaryl-CoA synthase 1*	-1.7593	0.2954
11736978_at	PADI3	*peptidyl arginine deiminase 3*	-1.7588	0.2955
11718119_s_at	CFL2	*cofilin 2*	-1.7558	0.2961
11720494_a_at	CTNNAL1	*catenin alpha like 1*	-1.7515	0.2970
11754939_x_at	FADS2	*fatty acid desaturase 2*	-1.7481	0.2977
11719811_a_at	TRIB3	*tribbles pseudokinase 3*	-1.7476	0.2978
11732756_a_at	ELAVL2	*ELAV like RNA binding protein 2*	-1.7471	0.2979
11723051_at	FGFBP1	*fibroblast growth factor binding protein 1*	-1.7456	0.2982
11739782_a_at	SNCA	*synuclein alpha*	-1.7452	0.2983
11736083_x_at	GTSE1	*G2 and S-phase expressed 1*	-1.7447	0.2984
11725152_at	L3HYPDH	*trans-L-3-hydroxyproline dehydratase*	-1.7432	0.2987
11723147_a_at	NAV3	*neuron navigator 3*	-1.7403	0.2993
11733816_a_at	RPL22L1	*ribosomal protein L22 like 1*	-1.7379	0.2998
11719179_a_at	PVR	*poliovirus receptor*	-1.7370	0.3000
11715436_at	TIMP3	*TIMP metallopeptidase inhibitor 3*	-1.7350	0.3004
11720163_at	VEGFC	*vascular endothelial growth factor C*	-1.7350	0.3004
11723499_a_at	PCSK9	*proprotein convertase subtilisin/kexin type 9*	-1.7341	0.3006
11720241_at	KIF4A	*kinesin family member 4A*	-1.7255	0.3024
11722818_a_at	GGH	*gamma-glutamyl hydrolase*	-1.7221	0.3031
11716982_at	CMSS1	*Cms1 Ribosomal Small Subunit Homolog (Yeast)*	-1.7207	0.3034
11716092_x_at	CKS1B	*CDC28 protein kinase regulatory subunit 1B*	-1.7188	0.3038
11717863_a_at	DUSP5	*dual specificity phosphatase 5*	-1.7183	0.3039
11716459_at	TUBA4A	*tubulin alpha 4a*	-1.7084	0.3060
11728565_x_at	FAM210A	*family with sequence similarity 210 member A*	-1.7079	0.3061
11758165_s_at	MRTO4	*MRT4 homolog, ribosome maturation factor*	-1.7070	0.3063
11734713_s_at	DBF4	*DBF4 zinc finger*	-1.7027	0.3072
11720020_x_at	RTEL1-TNFRSF6B	*RTEL1-TNFRSF6B Readthrough (NMD Candidate)*	-1.7027	0.3072
11755613_a_at	FERMT1	*fermitin family member 1*	-1.6999	0.3078
11742819_at	PLAUR	*plasminogen activator, urokinase receptor*	-1.6995	0.3079
11725441_a_at	FOXM1	*forkhead box M1*	-1.6990	0.3080
11754438_x_at	GJC1	*gap junction protein gamma 1*	-1.6981	0.3082
11741126_s_at	SLFN11	*schlafen family member 11*	-1.6971	0.3084

11726013_a_at	AJUBA	*ajuba LIM protein*	-1.6967	0.3085
11724579_a_at	L1CAM	*L1 cell adhesion molecule*	-1.6934	0.3092
11716847_a_at	SLC43A3	*solute carrier family 43 member 3*	-1.6925	0.3094
11750189_s_at	CD44	*CD44 Molecule (Indian Blood Group)*	-1.6901	0.3099
11743536_at	VRK1	*vaccinia related kinase 1*	-1.6897	0.3100
11728558_a_at	HSF2BP	*heat shock transcription factor 2 binding protein*	-1.6892	0.3101
11727063_a_at	MIR3658	*microRNA 3658*	-1.6887	0.3102
11715491_s_at	FSCN1	*fascin actin-bundling protein 1*	-1.6841	0.3112
11715932_s_at	TUBB6	*tubulin beta 6 class V*	-1.6832	0.3114
11734557_a_at	GALNT5	*polypeptide N-acetylgalactosaminyltransferase 5*	-1.6795	0.3122
11729834_at	EIF5A2	*eukaryotic translation initiation factor 5A2*	-1.6795	0.3122
11757860_s_at	QKI	*QKI, KH domain containing RNA binding*	-1.6785	0.3124
11725232_at	ATP8B2	*ATPase phospholipid transporting 8B2*	-1.6767	0.3128
11744747_a_at	FGFR1OP2	*FGFR1 oncogene partner 2*	-1.6748	0.3132
11715913_s_at	EFNB1	*ephrin B1*	-1.6739	0.3134
11719154_a_at	DRAM1	*DNA damage regulated autophagy modulator 1*	-1.6735	0.3135
11728894_at	HES2	*hes family bHLH transcription factor 2*	-1.6730	0.3136
11717282_at	ASAP1	*ArfGAP with SH3 domain, ankyrin repeat and PH domain 1*	-1.6684	0.3146
11748602_a_at	BAG2	*BCL2 associated athanogene 2*	-1.6670	0.3149
11716094_a_at	KLF6	*Kruppel like factor 6*	-1.6657	0.3152
11746427_a_at	WDR66	*WD repeat domain 66*	-1.6647	0.3154
11744789_a_at	CENPU	*centromere protein U*	-1.6638	0.3156
11741376_a_at	LRP8	*LDL receptor related protein 8*	-1.6634	0.3157
11727458_at	KIF18A	*kinesin family member 18A*	-1.6524	0.3181
11725117_a_at	NLN	*neurolysin*	-1.6497	0.3187
11751697_a_at	NAA50	*N(Alpha)-Acetyltransferase 50, NatE Catalytic Subunit*	-1.6425	0.3203
11737852_s_at	PPP1R18	*protein phosphatase 1 regulatory subunit 18*	-1.6371	0.3215
11742992_s_at	PSAT1	*phosphoserine aminotransferase 1*	-1.6371	0.3215
11746588_a_at	ALDH1B1	*aldehyde dehydrogenase 1 family member B1*	-1.6344	0.3221
11721843_a_at	ATL3	*atlastin GTPase 3*	-1.6304	0.3230
11734867_a_at	TPRG1	*tumor protein p63 regulated 1*	-1.6295	0.3232
11718802_a_at	PSRC1	*proline and serine rich coiled-coil 1*	-1.6277	0.3236
11716630_a_at	ANGPTL4	*angiopoietin like 4*	-1.6250	0.3242
11759011_at	PRPF4	*pre-mRNA processing factor 4*	-1.6246	0.3243
11734846_x_at	TAF1B	*TATA-box binding protein associated factor, RNA polymerase I subunit B*	-1.6233	0.3246
11731880_at	NLRP1	*NLR family pyrin domain containing 1*	-1.6233	0.3246
11724285_at	FRMD4A	*FERM domain containing 4A*	-1.6228	0.3247
11736570_a_at	SLC39A14	*solute carrier family 39 member 14*	-1.6228	0.3247
11746863_x_at	ARSJ	*arylsulfatase family member J*	-1.6162	0.3262
11744764_s_at	WHSC1	*Wolf-Hirschhorn syndrome candidate 1*	-1.6126	0.3270
11757152_s_at	MIR1304	*microRNA 1304*	-1.6122	0.3271
11718076_at	MAPKAPK3	*mitogen-activated protein kinase-activated protein kinase 3*	-1.6087	0.3279

11760362_x_at	PGAM5	*PGAM family member 5, mitochondrial serine/threonine protein phosphatase*	-1.6087	0.3279
11718262_a_at	ERF	*ETS2 repressor factor*	-1.6082	0.3280
11720401_at	NCS1	*neuronal calcium sensor 1*	-1.6078	0.3281
11725064_x_at	TCOF1	*treacle ribosome biogenesis factor 1*	-1.6043	0.3289
11760209_a_at	RPL37A	*ribosomal protein L37a*	-1.6034	0.3291
11730740_a_at	PDLIM4	*PDZ and LIM domain 4*	-1.6034	0.3291
11746931_a_at	INHBA	*inhibin beta A subunit*	-1.6034	0.3291
11744630_a_at	NXPE3	*neurexophilin and PC-esterase domain family member 3*	-1.6016	0.3295
11734865_a_at	PSMC3IP	*PSMC3 interacting protein*	-1.6003	0.3298
11738062_x_at	S100A7A	*S100 calcium binding protein A7A*	-1.5995	0.3300
11758222_s_at	SLC20A1	*solute carrier family 20 member 1*	-1.5990	0.3301
11752409_a_at	NDC1	*NDC1 transmembrane nucleoporin*	-1.5960	0.3308
11743169_a_at	LPXN	*leupaxin*	-1.5942	0.3312
11743687_s_at	HMGB2	*high mobility group box 2*	-1.5942	0.3312
11744345_x_at	TUBA1B	*tubulin alpha 1b*	-1.5920	0.3317
11720842_at	RHOD	*ras homolog family member D*	-1.5920	0.3317
11749410_x_at	DMKN	*dermokine*	-1.5907	0.3320
11727773_at	LARP6	*La ribonucleoprotein domain family member 6*	-1.5903	0.3321
11717833_a_at	TEX10	*testis expressed 10*	-1.5860	0.3331
11764033_s_at	RFC5	*replication factor C subunit 5*	-1.5851	0.3333
11754243_a_at	H2AFX	*H2A histone family member X*	-1.5847	0.3334
11732925_s_at	PEAR1	*platelet endothelial aggregation receptor 1*	-1.5842	0.3335
11758536_s_at	KCTD15	*potassium channel tetramerization domain containing 15*	-1.5825	0.3339
11756409_a_at	BLM	*Bloom syndrome RecQ like helicase*	-1.5804	0.3344
11717444_at	BYSL	*bystin like*	-1.5804	0.3344
11740118_a_at	SMC2	*structural maintenance of chromosomes 2*	-1.5765	0.3353
11743434_a_at	CHST11	*carbohydrate sulfotransferase 11*	-1.5752	0.3356
11754765_s_at	MIR6080	*microRNA 6080*	-1.5739	0.3359
11742945_a_at	MIR6733	*microRNA 6733*	-1.5735	0.3360
11725910_a_at	COL4A6	*collagen type IV alpha 6 chain*	-1.5735	0.3360
11721208_at	IFFO2	*intermediate filament family orphan 2*	-1.5726	0.3362
11717409_at	SH2B3	*SH2B adaptor protein 3*	-1.5696	0.3369
11746116_a_at	PINX1	*PIN2/TERF1 interacting, telomerase inhibitor 1*	-1.5692	0.3370
11743151_a_at	GLS	*glutaminase*	-1.5679	0.3373
11718400_a_at	PNP	*purine nucleoside phosphorylase*	-1.5675	0.3374
11723682_at	ALYREF	*Aly/REF export factor*	-1.5658	0.3378
11721068_a_at	FHOD3	*formin homology 2 domain containing 3*	-1.5645	0.3381
11728410_a_at	INO80C	*INO80 complex subunit C*	-1.5632	0.3384
11730912_at	NPM1	*nucleophosmin*	-1.5606	0.3390
11756742_a_at	AGPAT5	*1-acylglycerol-3-phosphate O-acyltransferase 5*	-1.5598	0.3392
11744146_x_at	RBM3	*RNA Binding Motif (RNP1, RRM) Protein 3*	-1.5598	0.3392
11745833_s_at	ECT2	*epithelial cell transforming 2*	-1.5547	0.3404

11755028_a_at	DENND1A	*DENN domain containing 1A*	-1.5538	0.3406
11728873_s_at	RBM24	*RNA binding motif protein 24*	-1.5500	0.3415
11757631_s_at	VGLL3	*vestigial like family member 3*	-1.5475	0.3421
11756784_x_at	NCAPG2	*non-SMC condensin II complex subunit G2*	-1.5450	0.3427
11755137_a_at	MCUB	*mitochondrial calcium uniporter dominant negative beta subunit*	-1.5429	0.3432
11763164_at	DNAJC9	*DnaJ Heat Shock Protein Family (Hsp40) Member C9*	-1.5412	0.3436
11718283_a_at	EIF4EBP1	*eukaryotic translation initiation factor 4E binding protein 1*	-1.5412	0.3436
11716171_s_at	LMNB2	*lamin B2*	-1.5408	0.3437
11719882_s_at	OSTM1	*osteopetrosis associated transmembrane protein 1*	-1.5404	0.3438
11716338_a_at	INSIG1	*insulin induced gene 1*	-1.5391	0.3441
11732661_x_at	STIL	*SCL/TAL1 interrupting locus*	-1.5387	0.3442
11757117_at	SNORA64	*small nucleolar RNA, H/ACA box 64*	-1.5383	0.3443
11729603_a_at	MCM7	*minichromosome maintenance complex component 7*	-1.5345	0.3452
11728391_s_at	LRP12	*LDL receptor related protein 12*	-1.5337	0.3454
11728233_a_at	CLDN1	*claudin 1*	-1.5332	0.3455
11722872_a_at	RFC4	*replication factor C subunit 4*	-1.5324	0.3457
11754559_a_at	SBSN	*suprabasin*	-1.5303	0.3462
11731770_a_at	DSE	*dermatan sulfate epimerase*	-1.5299	0.3463
11750554_a_at	NEDD4	*neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase*	-1.5253	0.3474
11733539_a_at	MROH1	*maestro heat like repeat family member 1*	-1.5237	0.3478
11757458_s_at	LRRC8A	*leucine rich repeat containing 8 family member A*	-1.5237	0.3478
11734495_a_at	GRB10	*growth factor receptor bound protein 10*	-1.5195	0.3488
11747783_x_at	AHCY	*adenosylhomocysteinase*	-1.5195	0.3488
11754630_a_at	MLKL	*mixed lineage kinase domain like*	-1.5195	0.3488
11738052_at	MRGPRX3	*MAS related GPR family member X3*	-1.5170	0.3494
11732142_at	TSR1	*TSR1, ribosome maturation factor*	-1.5166	0.3495
11744263_s_at	RAC2	*Ras-Related C3 Botulinum Toxin Substrate 2 (Rho Family, Small GTP Binding Protein Rac2)*	-1.5125	0.3505
11754313_s_at	ARL4C	*ADP ribosylation factor like GTPase 4C*	-1.5117	0.3507
11734825_at	SPRED1	*sprouty related EVH1 domain containing 1*	-1.5084	0.3515
11723256_a_at	PKMYT1	*protein kinase, membrane associated tyrosine/threonine 1*	-1.5076	0.3517
11729096_a_at	POLQ	*DNA polymerase theta*	-1.5059	0.3521
11732078_a_at	EVA1A	*eva-1 homolog A, regulator of programmed cell death*	-1.5047	0.3524
11741710_a_at	COL6A3	*collagen type VI alpha 3 chain*	-1.5047	0.3524
11748808_a_at	ARID3B	*AT-rich interaction domain 3B*	-1.5039	0.3526
11759509_s_at	MCM4	*minichromosome maintenance complex component 4*	-1.5027	0.3529
11716872_a_at	ADCY3	*adenylate cyclase 3*	-1.5019	0.3531
11717900_at	ASF1B	*anti-silencing function 1B histone chaperone*	-1.5014	0.3532
11725047_x_at	ANP32E	*acidic nuclear phosphoprotein 32 family member E*	-1.4994	0.3537
11722379_at	GNG11	*G protein subunit gamma 11*	-1.4994	0.3537
11727092_x_at	IL18	*interleukin 18*	-1.4994	0.3537
11718198_at	LHFP	*lipoma HMGIC fusion partner*	-1.4970	0.3543
11720213_x_at	PPAN	*Peter Pan Homolog (Drosophila)*	-1.4961	0.3545

11729310_a_at	**SKA3**	***spindle and kinetochore associated complex subunit 3***	**-1.4945**	**0.3549**
11726887_a_at	**SOX15**	***SRY-box 15***	**-1.4945**	**0.3549**
11755278_a_at	**CYP2S1**	***cytochrome P450 family 2 subfamily S member 1***	**-1.4933**	**0.3552**
11737787_at	**SHISA5**	***shisa family member 5***	**-1.4909**	**0.3558**
11719732_at	**TIGAR**	***TP53 induced glycolysis regulatory phosphatase***	**-1.4905**	**0.3559**
11745021_a_at	**MYC**	***v-myc avian myelocytomatosis viral oncogene homolog***	**-1.4884**	**0.3564**
11735167_x_at	**RFC2**	***replication factor C subunit 2***	**-1.4868**	**0.3568**
11726572_a_at	**SEMA7A**	***Semaphorin 7A (John Milton Hagen Blood Group)***	**-1.4868**	**0.3568**
11721209_a_at	**EXO1**	***exonuclease 1***	**-1.4856**	**0.3571**
11759176_at	**GTSE1**	***G2 and S-phase expressed 1***	**-1.4820**	**0.3580**
11758629_s_at	**SPTBN1**	***spectrin beta, non-erythrocytic 1***	**-1.4812**	**0.3582**
11740068_at	**CCDC8**	***coiled-coil domain containing 8***	**-1.4808**	**0.3583**
11736048_at	**ANTXR2**	***anthrax toxin receptor 2***	**-1.4808**	**0.3583**
11747193_a_at	**ZNF185**	***Zinc Finger Protein 185 (LIM Domain)***	**-1.4787**	**0.3588**
11722308_a_at	**TP63**	***tumor protein p63***	**-1.4771**	**0.3592**
11720547_a_at	**PDSS1**	***Decaprenyl Diphosphate Synthase Subunit 1***	**-1.4763**	**0.3594**
11736405_a_at	**DNMT1**	***DNA methyltransferase 1***	**-1.4735**	**0.3601**
11755874_a_at	**BORA**	***bora, aurora kinase A activator***	**-1.4719**	**0.3605**
11724026_a_at	**TCF19**	***transcription factor 19***	**-1.4715**	**0.3606**
11717731_at	**SQLE**	***squalene epoxidase***	**-1.4711**	**0.3607**
11738887_s_at	**MICA**	***MHC class I polypeptide-related sequence A***	**-1.4711**	**0.3607**
11725704_a_at	**AMOTL1**	***angiomotin like 1***	**-1.4707**	**0.3608**
11743580_s_at	**ACTR2**	***ARP2 actin related protein 2 homolog***	**-1.4703**	**0.3609**
11743191_a_at	**NTM**	***neurotrimin***	**-1.4703**	**0.3609**
11745181_a_at	**NAA15**	***N(Alpha)-Acetyltransferase 15, NatA Auxiliary Subunit***	**-1.4699**	**0.3610**
11724151_a_at	**TNS4**	***tensin 4***	**-1.4695**	**0.3611**
11717341_at	**PTGFRN**	***prostaglandin F2 receptor inhibitor***	**-1.4687**	**0.3613**
11723274_a_at	**SLC35F2**	***solute carrier family 35 member F2***	**-1.4679**	**0.3615**
11735039_s_at	**SHTN1**	***shootin 1***	**-1.4679**	**0.3615**
11754677_a_at	**FAM169A**	***family with sequence similarity 169 member A***	**-1.4667**	**0.3618**
11719488_at	**EDNRA**	***endothelin receptor type A***	**-1.4632**	**0.3627**
11718315_at	**SLC16A2**	***solute carrier family 16 member 2***	**-1.4604**	**0.3634**
11755103_a_at	**CDA**	***cytidine deaminase***	**-1.4596**	**0.3636**
11743450_a_at	**ELOVL6**	***ELOVL fatty acid elongase 6***	**-1.4576**	**0.3641**
11749031_a_at	**PTBP3**	***polypyrimidine tract binding protein 3***	**-1.4560**	**0.3645**
11763367_at	**NABP1**	***nucleic acid binding protein 1***	**-1.4560**	**0.3645**
11744699_a_at	**TDP1**	***tyrosyl-DNA phosphodiesterase 1***	**-1.4552**	**0.3647**
11722236_at	**FBXO2**	***F-box protein 2***	**-1.4548**	**0.3648**
11724551_x_at	**TMEM55A**	***transmembrane protein 55A***	**-1.4544**	**0.3649**
11753720_x_at	**GMFB**	***glia maturation factor beta***	**-1.4536**	**0.3651**
11724206_a_at	**MAD1L1**	***MAD1 mitotic arrest deficient like 1***	**-1.4525**	**0.3654**
11724357_a_at	**MYO5A**	***myosin VA***	**-1.4525**	**0.3654**

11742997_x_at	MCM3	*minichromosome maintenance complex component 3*	-1.4521	0.3655
11739654_at	TNFRSF10A	*TNF receptor superfamily member 10a*	-1.4517	0.3656
11748951_a_at	CTNNB1	*catenin beta 1*	-1.4513	0.3657
11727731_at	RASGEF1A	*RasGEF domain family member 1A*	-1.4497	0.3661
11733320_a_at	HRAS	*HRas proto-oncogene, GTPase*	-1.4493	0.3662
11723227_at	SGCB	*sarcoglycan beta*	-1.4493	0.3662
11726116_at	MTAP	*methylthioadenosine phosphorylase*	-1.4489	0.3663
11756358_a_at	PLK3	*polo like kinase 3*	-1.4477	0.3666
11759444_x_at	BAX	*BCL2 associated X, apoptosis regulator*	-1.4454	0.3672
11729422_a_at	POPDC3	*popeye domain containing 3*	-1.4446	0.3674
11732058_a_at	CDC7	*cell division cycle 7*	-1.4438	0.3676
11726551_s_at	RAET1L	*retinoic acid early transcript 1L*	-1.4438	0.3676
11716011_a_at	TNFAIP1	*TNF alpha induced protein 1*	-1.4438	0.3676
11718305_a_at	PDLIM2	*PDZ and LIM domain 2*	-1.4430	0.3678
11720380_a_at	IMPDH1	*inosine monophosphate dehydrogenase 1*	-1.4426	0.3679
11731992_x_at	TROAP	*trophinin associated protein*	-1.4403	0.3685
11749874_a_at	OXCT1	*3-oxoacid CoA-transferase 1*	-1.4395	0.3687
11745612_a_at	TREM2	*triggering receptor expressed on myeloid cells 2*	-1.4391	0.3688
11739458_at	SYNC	*syncoilin, intermediate filament protein*	-1.4387	0.3689
11725709_a_at	WDHD1	*WD repeat and HMG-box DNA binding protein 1*	-1.4348	0.3699
11758266_s_at	PSMD2	*proteasome 26S subunit, non-ATPase 2*	-1.4348	0.3699
11722225_a_at	ADAM8	*ADAM metallopeptidase domain 8*	-1.4340	0.3701
11748521_a_at	SURF4	*surfeit 4*	-1.4340	0.3701
11732494_at	AUNIP	*aurora kinase A and ninein interacting protein*	-1.4317	0.3707
11759540_a_at	RPL35A	*ribosomal protein L35a*	-1.4317	0.3707
11724209_a_at	KIFC1	*kinesin family member C1*	-1.4293	0.3713
11716062_a_at	TNC	*tenascin C*	-1.4274	0.3718
11716642_s_at	DTYMK	*deoxythymidylate kinase*	-1.4262	0.3721
11751527_s_at	WDR1	*WD repeat domain 1*	-1.4262	0.3721
11739860_a_at	ITGA6	*integrin subunit alpha 6*	-1.4251	0.3724
11756919_a_at	CAP2	*CAP, adenylate cyclase-associated protein, 2 (yeast)*	-1.4243	0.3726
11730525_a_at	SSC4D	*scavenger receptor cysteine rich family member with 4 domains*	-1.4235	0.3728
11721435_at	STC2	*stanniocalcin 2*	-1.4235	0.3728
11733037_a_at	DPH3	*diphthamide biosynthesis 3*	-1.4231	0.3729
11748401_x_at	TPM4	*tropomyosin 4*	-1.4216	0.3733
11744488_a_at	ACOT9	*acyl-CoA thioesterase 9*	-1.4216	0.3733
11725209_at	LETM1	*leucine zipper and EF-hand containing transmembrane protein 1*	-1.4208	0.3735
11716288_s_at	ESYT1	*extended synaptotagmin 1*	-1.4197	0.3738
11723860_a_at	MPP6	*membrane palmitoylated protein 6*	-1.4193	0.3739
11729140_x_at	SLAMF7	*SLAM family member 7*	-1.4193	0.3739
11718998_x_at	DHFR	*dihydrofolate reductase*	-1.4189	0.3740
11717155_a_at	NME1	*NME/NM23 nucleoside diphosphate kinase 1*	-1.4181	0.3742

11715926_s_at	PLEC	*plectin*	-1.4170	0.3745
11740743_a_at	TPM2	*tropomyosin 2 (beta)*	-1.4170	0.3745
11763395_a_at	ZC3HAV1L	*zinc finger CCCH-type containing, antiviral 1 like*	-1.4166	0.3746
11728838_a_at	TMCC3	*transmembrane and coiled-coil domain family 3*	-1.4162	0.3747
11727554_s_at	PKIB	*CAMP-Dependent Protein Kinase Inhibitor Beta*	-1.4158	0.3748
11738259_s_at	CXorf49	*chromosome X open reading frame 49*	-1.4139	0.3753
11729707_at	FKBP1A	*FK506 binding protein 1A*	-1.4116	0.3759
11727269_at	S100A3	*S100 calcium binding protein A3*	-1.4108	0.3761
11754652_a_at	ECI2	*enoyl-CoA delta isomerase 2*	-1.4089	0.3766
11725687_s_at	PRIM2	*Primase (DNA) Subunit 2*	-1.4081	0.3768
11727536_x_at	CCNF	*cyclin F*	-1.4077	0.3769
11734841_a_at	RAD51	*RAD51 recombinase*	-1.4077	0.3769
11734548_a_at	TGFBI	*transforming growth factor beta induced*	-1.4070	0.3771
11740375_a_at	RGS10	*regulator of G-protein signaling 10*	-1.4066	0.3772
11730390_at	SEMA3A	*semaphorin 3A*	-1.4066	0.3772
11720319_at	SPAG5	*sperm associated antigen 5*	-1.4062	0.3773
11726597_a_at	DUT	*deoxyuridine triphosphatase*	-1.4062	0.3773
11756395_s_at	AP1S2	*adaptor related protein complex 1 sigma 2 subunit*	-1.4043	0.3778
11724993_at	RFLNB	*refilin B*	-1.4032	0.3781
11726024_at	EDN1	*endothelin 1*	-1.4028	0.3782
11719686_a_at	MICAL1	*microtubule associated monooxygenase, calponin and LIM domain containing 1*	-1.4009	0.3787
11715431_a_at	MIR6513	*microRNA 6513*	-1.4009	0.3787
11718591_at	SDF2L1	*stromal cell derived factor 2 like 1*	-1.4001	0.3789
11720042_a_at	RRP7A	*ribosomal RNA processing 7 homolog A*	-1.3990	0.3792
11722759_a_at	CAMSAP2	*calmodulin regulated spectrin associated protein family member 2*	-1.3978	0.3795
11715602_s_at	SPARC	*secreted protein acidic and cysteine rich*	-1.3974	0.3796
11727659_a_at	KLK10	*kallikrein related peptidase 10*	-1.3963	0.3799
11763856_a_at	HOMER3	*homer scaffolding protein 3*	-1.3963	0.3799
11723732_at	GNPNAT1	*glucosamine-phosphate N-acetyltransferase 1*	-1.3937	0.3806
11729131_a_at	PSME3	*proteasome activator subunit 3*	-1.3937	0.3806
11736240_a_at	AAED1	*AhpC/TSA antioxidant enzyme domain containing 1*	-1.3925	0.3809
11748328_s_at	KRT16	*keratin 16*	-1.3906	0.3814
11716997_x_at	TSPAN4	*tetraspanin 4*	-1.3902	0.3815
11752792_a_at	TACC1	*transforming acidic coiled-coil containing protein 1*	-1.3899	0.3816
11737413_at	MICALCL	*MICAL C-terminal like*	-1.3884	0.3820
11717743_a_at	ACOT7	*acyl-CoA thioesterase 7*	-1.3876	0.3822
11727816_at	UBASH3B	*ubiquitin associated and SH3 domain containing B*	-1.3868	0.3824
11754193_a_at	PCYT1A	*phosphate cytidylyltransferase 1, choline, alpha*	-1.3865	0.3825
11738840_a_at	NUDT10	*nudix hydrolase 10*	-1.3842	0.3831
11734142_a_at	METTL8	*methyltransferase like 8*	-1.3816	0.3838
11722970_a_at	LOC401317	*uncharacterized LOC401317*	-1.3797	0.3843
11726438_a_at	MALT1	*MALT1 paracaspase*	-1.3774	0.3849

11757441_s_at	SRRD	*SRR1 domain containing*	-1.3767	0.3851
11717364_a_at	BCL2L12	*BCL2 like 12*	-1.3741	0.3858
11746242_a_at	ARNTL2	*aryl hydrocarbon receptor nuclear translocator like 2*	-1.3741	0.3858
11754450_s_at	MTCL1	*microtubule crosslinking factor 1*	-1.3737	0.3859
11754068_a_at	CSRP1	*cysteine and glycine rich protein 1*	-1.3715	0.3865
11728984_a_at	LOC100996643	*monofunctional C1-tetrahydrofolate synthase, mitochondrial-like*	-1.3688	0.3872
11722864_at	NETO2	*neuropilin and tolloid like 2*	-1.3681	0.3874
11720770_a_at	PPIF	*peptidylprolyl isomerase F*	-1.3674	0.3876
11743084_s_at	BNIP3	*BCL2 interacting protein 3*	-1.3659	0.3880
11729374_at	LOC100653049	*keratin, type I cuticular Ha4*	-1.3659	0.3880
11744734_a_at	SIN3B	*SIN3 transcription regulator family member B*	-1.3655	0.3881
11729443_a_at	PML	*promyelocytic leukemia*	-1.3655	0.3881
11756145_s_at	SLC25A15	*solute carrier family 25 member 15*	-1.3648	0.3883
11755424_a_at	HMOX2	*heme oxygenase 2*	-1.3644	0.3884
11723138_at	POP1	*POP1 homolog, ribonuclease P/MRP subunit*	-1.3640	0.3885
11758577_s_at	ELOVL7	*ELOVL fatty acid elongase 7*	-1.3618	0.3891
11755929_a_at	THOP1	*thimet oligopeptidase 1*	-1.3614	0.3892
11727575_a_at	TMEM237	*transmembrane protein 237*	-1.3614	0.3892
11722691_at	AVEN	*apoptosis and caspase activation inhibitor*	-1.3610	0.3893
11737795_a_at	KIAA1524	*KIAA1524*	-1.3607	0.3894
11717507_at	TRAM2	*translocation associated membrane protein 2*	-1.3607	0.3894
11739364_s_at	FAM92A	*family with sequence similarity 92 member A*	-1.3599	0.3896
11732329_a_at	MAP7D1	*MAP7 domain containing 1*	-1.3588	0.3899
11743423_a_at	NSG1	*neuron specific gene family member 1*	-1.3585	0.3900
11716450_s_at	RFTN1	*raftlin, lipid raft linker 1*	-1.3577	0.3902
11755168_x_at	CENPL	*centromere protein L*	-1.3548	0.3910
11733828_x_at	SNORD88C	*small nucleolar RNA, C/D box 88C*	-1.3544	0.3911
11756393_x_at	CORO1A	*coronin 1A*	-1.3518	0.3918
11729886_at	C18orf54	*chromosome 18 open reading frame 54*	-1.3489	0.3926
11758314_s_at	NDUFAF2	*NADH:ubiquinone oxidoreductase complex assembly factor 2*	-1.3489	0.3926
11733975_a_at	DDHD2	*DDHD domain containing 2*	-1.3470	0.3931
11719411_at	RAB32	*RAB32, member RAS oncogene family*	-1.3470	0.3931
11746197_a_at	HUS1	*HUS1 checkpoint clamp component*	-1.3463	0.3933
11745234_a_at	HACD4	*3-hydroxyacyl-CoA dehydratase 4*	-1.3463	0.3933
11719260_x_at	LMNA	*lamin A/C*	-1.3441	0.3939
11726006_at	SLC30A1	*solute carrier family 30 member 1*	-1.3430	0.3942
11759430_at	KLF7	*Kruppel like factor 7*	-1.3397	0.3951
11756666_x_at	MCM2	*minichromosome maintenance complex component 2*	-1.3393	0.3952
11756612_a_at	BARD1	*BRCA1 associated RING domain 1*	-1.3393	0.3952
11748733_a_at	KCTD7	*potassium channel tetramerization domain containing 7*	-1.3386	0.3954
11736035_a_at	EXOSC2	*exosome component 2*	-1.3375	0.3957
11730080_x_at	IFNLR1	*interferon lambda receptor 1*	-1.3368	0.3959

11724506_s_at	MIS18A	*MIS18 kinetochore protein A*	-1.3364	0.3960
11730096_a_at	BCL2A1	*BCL2 related protein A1*	-1.3361	0.3961
11737162_at	FAM83B	*family with sequence similarity 83 member B*	-1.3357	0.3962
11755689_x_at	NCLN	*nicalin*	-1.3353	0.3963
11728311_x_at	ERCC1	*ERCC excision repair 1, endonuclease non-catalytic subunit*	-1.3346	0.3965
11744270_a_at	SNRPA	*small nuclear ribonucleoprotein polypeptide A*	-1.3342	0.3966
11719681_a_at	TNFRSF10B	*TNF receptor superfamily member 10b*	-1.3332	0.3969
11745130_x_at	HMGB3	*high mobility group box 3*	-1.3332	0.3969
11755311_a_at	ITGB1BP1	*integrin subunit beta 1 binding protein 1*	-1.3313	0.3974
11756334_x_at	ANXA3	*annexin A3*	-1.3295	0.3979
11716546_s_at	DRAP1	*DR1 associated protein 1*	-1.3277	0.3984
11745007_s_at	SDC2	*syndecan 2*	-1.3277	0.3984
11719719_at	LAD1	*ladinin 1*	-1.3266	0.3987
11729185_at	PNO1	*partner of NOB1 homolog*	-1.3266	0.3987
11723414_a_at	CNN2	*calponin 2*	-1.3266	0.3987
11757156_s_at	SNORA44	*small nucleolar RNA, H/ACA box 44*	-1.3245	0.3993
11731899_s_at	PPAT	*phosphoribosyl pyrophosphate amidotransferase*	-1.3245	0.3993
11733891_at	FKBP14	*FK506 binding protein 14*	-1.3234	0.3996
11717576_a_at	SFN	*stratifin*	-1.3219	0.4000
11756303_a_at	SH3TC1	*SH3 domain and tetratricopeptide repeats 1*	-1.3212	0.4002
11754440_s_at	GAS6	*growth arrest specific 6*	-1.3212	0.4002
11757036_x_at	SAC3D1	*SAC3 domain containing 1*	-1.3205	0.4004
11729887_at	HACD1	*3-hydroxyacyl-CoA dehydratase 1*	-1.3194	0.4007
11728257_at	RAD18	*RAD18, E3 ubiquitin protein ligase*	-1.3180	0.4011
11756747_a_at	RBMS2	*RNA binding motif single stranded interacting protein 2*	-1.3180	0.4011
11722248_a_at	RASSF1	*Ras association domain family member 1*	-1.3176	0.4012
11727236_a_at	C18orf25	*chromosome 18 open reading frame 25*	-1.3169	0.4014
11726590_at	ELOVL4	*ELOVL fatty acid elongase 4*	-1.3169	0.4014
11724828_at	CCL20	*C-C motif chemokine ligand 20*	-1.3165	0.4015
11718376_s_at	WDR5	*WD repeat domain 5*	-1.3162	0.4016
11756412_a_at	NT5DC2	*5'-nucleotidase domain containing 2*	-1.3151	0.4019
11740312_at	HAS2	*hyaluronan synthase 2*	-1.3151	0.4019
11737781_a_at	ARMCX2	*armadillo repeat containing, X-linked 2*	-1.3147	0.4020
11744604_at	ERVMER34-1	*endogenous retrovirus group MER34 member 1*	-1.3115	0.4029
11728825_at	TRNP1	*TMF1-regulated nuclear protein 1*	-1.3111	0.4030
11759661_at	MYO10	*myosin X*	-1.3111	0.4030
11721271_a_at	LRRC59	*leucine rich repeat containing 59*	-1.3108	0.4031
11754318_at	SSH1	*slingshot protein phosphatase 1*	-1.3104	0.4032
11727850_x_at	NIP7	*NIP7, nucleolar pre-rRNA processing protein*	-1.3097	0.4034
11722934_s_at	CHML	*CHM like, Rab escort protein 2*	-1.3086	0.4037
11721666_at	CDT1	*chromatin licensing and DNA replication factor 1*	-1.3076	0.4040
11754556_x_at	EIF2AK4	*eukaryotic translation initiation factor 2 alpha kinase 4*	-1.3072	0.4041

11736469_a_at	SLC35D1	*solute carrier family 35 member D1*	-1.3065	0.4043
11720928_at	SRM	*spermidine synthase*	-1.3058	0.4045
11739062_s_at	GTPBP4	*GTP binding protein 4*	-1.3047	0.4048
11724064_a_at	SLC25A19	*solute carrier family 25 member 19*	-1.3037	0.4051
11720781_a_at	CDK2	*cyclin dependent kinase 2*	-1.3012	0.4058
11737671_at	GLB1L3	*galactosidase beta 1 like 3*	-1.2994	0.4063
11725011_a_at	CEP78	*centrosomal protein 78*	-1.2983	0.4066
11732818_at	TMEM171	*transmembrane protein 171*	-1.2983	0.4066
11736289_a_at	PTPRG	*protein tyrosine phosphatase, receptor type G*	-1.2983	0.4066
11742697_a_at	ITM2A	*integral membrane protein 2A*	-1.2983	0.4066
11727033_at	PAPSS2	*3'-phosphoadenosine 5'-phosphosulfate synthase 2*	-1.2969	0.4070
11715781_a_at	EEF2	*eukaryotic translation elongation factor 2*	-1.2962	0.4072
11755540_a_at	PUS7	*Pseudouridylate Synthase 7 (Putative)*	-1.2944	0.4077
11728101_at	ZNF367	*zinc finger protein 367*	-1.2944	0.4077
11721615_a_at	THEMIS2	*thymocyte selection associated family member 2*	-1.2941	0.4078
11723985_a_at	PDCD11	*programmed cell death 11*	-1.2937	0.4079
11735061_a_at	LY6D	*lymphocyte antigen 6 complex, locus D*	-1.2934	0.4080
11730254_at	ELK3	*ELK3, ETS transcription factor*	-1.2934	0.4080
11717546_s_at	MPRIP	*myosin phosphatase Rho interacting protein*	-1.2927	0.4082
11727879_s_at	CHAF1A	*chromatin assembly factor 1 subunit A*	-1.2905	0.4088
11757853_s_at	TWIST2	*twist family bHLH transcription factor 2*	-1.2884	0.4094
11721115_at	SPCS3	*signal peptidase complex subunit 3*	-1.2874	0.4097
11725333_at	MZT1	*mitotic spindle organizing protein 1*	-1.2870	0.4098
11746471_s_at	MAP4K4	*mitogen-activated protein kinase kinase kinase kinase 4*	-1.2870	0.4098
11751020_a_at	RHCG	*Rh family C glycoprotein*	-1.2870	0.4098
11763528_s_at	SLC12A4	*solute carrier family 12 member 4*	-1.2867	0.4099
11751723_a_at	KRT5	*keratin 5*	-1.2863	0.4100
11728843_a_at	PROSER2	*proline and serine rich 2*	-1.2852	0.4103
11745020_a_at	TNFRSF12A	*TNF receptor superfamily member 12A*	-1.2849	0.4104
11716413_x_at	MT1E	*metallothionein 1E*	-1.2831	0.4109
11735140_at	TNFSF9	*tumor necrosis factor superfamily member 9*	-1.2828	0.4110
11726193_at	MARCH4	*membrane associated ring-CH-type finger 4*	-1.2828	0.4110
11721278_s_at	SUV39H1	*suppressor of variegation 3-9 homolog 1*	-1.2810	0.4115
11748128_a_at	SLC25A32	*solute carrier family 25 member 32*	-1.2807	0.4116
11738219_s_at	GJB4	*gap junction protein beta 4*	-1.2768	0.4127
11746438_a_at	SHMT2	*serine hydroxymethyltransferase 2*	-1.2761	0.4129
11725103_s_at	EGFR	*epidermal growth factor receptor*	-1.2744	0.4134
11757556_s_at	BLMH	*bleomycin hydrolase*	-1.2744	0.4134
11726433_a_at	OSBPL3	*oxysterol binding protein like 3*	-1.2719	0.4141
11715703_s_at	ITGA5	*integrin subunit alpha 5*	-1.2719	0.4141
11748045_x_at	LDLR	*low density lipoprotein receptor*	-1.2702	0.4146
11756790_a_at	ITGA3	*integrin subunit alpha 3*	-1.2688	0.4150

11728745_at	C4orf46	*chromosome 4 open reading frame 46*	-1.2685	0.4151
11740722_a_at	IL1RN	*interleukin 1 receptor antagonist*	-1.2640	0.4164
11740388_a_at	TFAP2A	*transcription factor AP-2 alpha*	-1.2636	0.4165
11726174_at	SAMD5	*sterile alpha motif domain containing 5*	-1.2612	0.4172
11722252_x_at	NEK2	*NIMA related kinase 2*	-1.2612	0.4172
11758780_a_at	NOP16	*NOP16 nucleolar protein*	-1.2608	0.4173
11751434_a_at	ACER3	*alkaline ceramidase 3*	-1.2598	0.4176
11727785_s_at	CACYBP	*calcyclin binding protein*	-1.2595	0.4177
11740245_a_at	PTHLH	*parathyroid hormone like hormone*	-1.2595	0.4177
11716537_s_at	SZRD1	*SUZ RNA binding domain containing 1*	-1.2577	0.4182
11734804_a_at	KIF20B	*kinesin family member 20B*	-1.2570	0.4184
11738892_a_at	TPM1	*tropomyosin 1 (alpha)*	-1.2567	0.4185
11758147_s_at	MAPK13	*mitogen-activated protein kinase 13*	-1.2543	0.4192
11728013_s_at	RIMKLB	*ribosomal modification protein rimK like family member B*	-1.2543	0.4192
11743604_s_at	RRM1	*ribonucleotide reductase catalytic subunit M1*	-1.2539	0.4193
11724901_s_at	IQCJ-SCHIP1	*IQCJ-SCHIP1 readthrough*	-1.2522	0.4198
11724402_s_at	HS3ST2	*heparan sulfate-glucosamine 3-sulfotransferase 2*	-1.2519	0.4199
11754937_a_at	GMNN	*geminin, DNA replication inhibitor*	-1.2515	0.4200
11733446_at	MMS22L	*MMS22 like, DNA repair protein*	-1.2502	0.4204
11725793_s_at	PTGER4	*prostaglandin E receptor 4*	-1.2502	0.4204
11743067_at	SIAH2	*siah E3 ubiquitin protein ligase 2*	-1.2485	0.4209
11723677_a_at	CKAP2	*cytoskeleton associated protein 2*	-1.2481	0.4210
11755006_x_at	BCAR3	*breast cancer anti-estrogen resistance 3*	-1.2474	0.4212
11753011_a_at	EXOSC9	*exosome component 9*	-1.2471	0.4213
11737041_a_at	PHLDB2	*pleckstrin homology like domain family B member 2*	-1.2467	0.4214
11743841_at	PLCXD2	*phosphatidylinositol specific phospholipase C X domain containing 2*	-1.2461	0.4216
11722587_at	EXOSC3	*exosome component 3*	-1.2440	0.4222
11726723_a_at	WDFY2	*WD repeat and FYVE domain containing 2*	-1.2430	0.4225
11757680_a_at	SLC1A4	*solute carrier family 1 member 4*	-1.2430	0.4225
11721899_x_at	FAM216A	*family with sequence similarity 216 member A*	-1.2426	0.4226
11742128_x_at	DEGS1	*delta 4-desaturase, sphingolipid 1*	-1.2399	0.4234
11718106_s_at	IPO5	*importin 5*	-1.2396	0.4235
11726261_at	DFFA	*DNA fragmentation factor subunit alpha*	-1.2365	0.4244
11726670_a_at	DCLRE1B	*DNA cross-link repair 1B*	-1.2358	0.4246
11741153_a_at	NCF2	*neutrophil cytosolic factor 2*	-1.2355	0.4247
11739065_a_at	GNG12	*G protein subunit gamma 12*	-1.2341	0.4251
11750293_a_at	RAD51C	*RAD51 paralog C*	-1.2331	0.4254
11733905_x_at	RRP15	*ribosomal RNA processing 15 homolog*	-1.2328	0.4255
11741492_x_at	FAM111B	*family with sequence similarity 111 member B*	-1.2321	0.4257
11754924_s_at	ADTRP	*androgen dependent TFPI regulating protein*	-1.2321	0.4257
11743770_at	MIR548F5	*microRNA 548f-5*	-1.2314	0.4259
11756347_x_at	PRR11	*proline rich 11*	-1.2304	0.4262

11726186_x_at	PARPBP	*PARP1 binding protein*	-1.2304	0.4262
11723032_a_at	PLP2	*proteolipid protein 2*	-1.2304	0.4262
11729742_x_at	IFI27L2	*interferon alpha inducible protein 27 like 2*	-1.2304	0.4262
11736095_a_at	GATC	*glutamyl-tRNA amidotransferase subunit C*	-1.2290	0.4266
11744467_s_at	SYNCRIP	*synaptotagmin binding cytoplasmic RNA interacting protein*	-1.2287	0.4267
11757547_a_at	SUN1	*Sad1 and UNC84 domain containing 1*	-1.2284	0.4268
11744325_a_at	STRIP2	*striatin interacting protein 2*	-1.2284	0.4268
11730350_a_at	TLDC1	*TBC/LysM-associated domain containing 1*	-1.2280	0.4269
11743650_s_at	DEK	*DEK proto-oncogene*	-1.2263	0.4274
11719188_at	NRAS	*neuroblastoma RAS viral oncogene homolog*	-1.2263	0.4274
11744289_a_at	JMJD6	*arginine demethylase and lysine hydroxylase*	-1.2253	0.4277
11718908_s_at	CHST2	*carbohydrate sulfotransferase 2*	-1.2253	0.4277
11716262_a_at	AP2B1	*adaptor related protein complex 2 beta 1 subunit*	-1.2253	0.4277
11747245_a_at	UTP15	*UTP15, small subunit processome component*	-1.2250	0.4278
11735833_a_at	CEMIP	*cell migration inducing hyaluronan binding protein*	-1.2247	0.4279
11748317_s_at	MCFD2	*multiple coagulation factor deficiency 2*	-1.2236	0.4282
11746103_a_at	DTD1	*D-tyrosyl-tRNA deacylase 1*	-1.2210	0.4290
11723814_s_at	ARHGAP29	*Rho GTPase activating protein 29*	-1.2206	0.4291
11716331_a_at	DNAJB6	*DnaJ Heat Shock Protein Family (Hsp40) Member B6*	-1.2199	0.4293
11719949_a_at	SPDL1	*spindle apparatus coiled-coil protein 1*	-1.2196	0.4294
11752824_a_at	TMEM256-PLSCR3	*TMEM256-PLSCR3 Readthrough (NMD Candidate)*	-1.2186	0.4297
11749440_a_at	WDR41	*WD repeat domain 41*	-1.2183	0.4298
11727495_at	TCEB3	*transcription elongation factor B subunit 3*	-1.2183	0.4298
11719980_a_at	FMNL2	*formin like 2*	-1.2156	0.4306
11722788_a_at	ENG	*endoglin*	-1.2146	0.4309
11736021_a_at	FKBP4	*FK506 binding protein 4*	-1.2146	0.4309
11733098_a_at	ITGB4	*integrin subunit beta 4*	-1.2146	0.4309
11723771_a_at	MASTL	*microtubule associated serine/threonine kinase like*	-1.2142	0.4310
11716766_a_at	IQGAP1	*IQ motif containing GTPase activating protein 1*	-1.2136	0.4312
11723464_s_at	CELF2	*CUGBP, Elav-like family member 2*	-1.2136	0.4312
11747561_s_at	RPS6KB2	*ribosomal protein S6 kinase B2*	-1.2126	0.4315
11725926_s_at	CLIC4	*chloride intracellular channel 4*	-1.2122	0.4316
11736226_a_at	SPATS2	*spermatogenesis associated serine rich 2*	-1.2109	0.4320
11727141_s_at	EPB41L3	*erythrocyte membrane protein band 4.1 like 3*	-1.2106	0.4321
11733981_a_at	PDK1	*pyruvate dehydrogenase kinase 1*	-1.2102	0.4322
11733120_a_at	SLC35B4	*solute carrier family 35 member B4*	-1.2099	0.4323
11738551_a_at	ANXA2	*annexin A2*	-1.2096	0.4324
11717726_s_at	HN1	*hematological and neurological expressed 1*	-1.2096	0.4324
11728062_a_at	SH3BP1	*SH3 domain binding protein 1*	-1.2096	0.4324
11763556_at	EIF4A1	*eukaryotic translation initiation factor 4A1*	-1.2082	0.4328
11737301_a_at	NUP155	*nucleoporin 155*	-1.2072	0.4331
11750029_a_at	EIF4H	*eukaryotic translation initiation factor 4H*	-1.2069	0.4332

11756952_a_at	TKT	*transketolase*	-1.2062	0.4334
11751727_s_at	TYW3	*tRNA-yW synthesizing protein 3 homolog*	-1.2052	0.4337
11722564_at	CYP51A1	*cytochrome P450 family 51 subfamily A member 1*	-1.2049	0.4338
11721648_at	GPATCH4	*G-patch domain containing 4*	-1.2046	0.4339
11722169_x_at	CSE1L	*chromosome segregation 1 like*	-1.2042	0.4340
11726711_x_at	PFAS	*phosphoribosylformylglycinamidine synthase*	-1.2029	0.4344
11727364_s_at	SHC1	*SHC adaptor protein 1*	-1.2012	0.4349
11746135_x_at	MIR1292	*microRNA 1292*	-1.2002	0.4352
11752051_a_at	MYH9	*myosin heavy chain 9*	-1.2002	0.4352
11729062_a_at	PDGFA	*platelet derived growth factor subunit A*	-1.1996	0.4354
11756968_a_at	RBM28	*RNA binding motif protein 28*	-1.1989	0.4356
11743965_s_at	CERCAM	*cerebral endothelial cell adhesion molecule*	-1.1983	0.4358
11720562_a_at	PLXNA2	*plexin A2*	-1.1976	0.4360
11755059_s_at	TCF3	*transcription factor 3*	-1.1969	0.4362
11731101_at	MELTF	*melanotransferrin*	-1.1969	0.4362
11754675_a_at	CLIP4	*CAP-Gly domain containing linker protein family member 4*	-1.1966	0.4363
11740425_at	PPP4R4	*protein phosphatase 4 regulatory subunit 4*	-1.1966	0.4363
11723460_a_at	NLE1	*notchless homolog 1*	-1.1963	0.4364
11718464_s_at	NEURL1B	*neuralized E3 ubiquitin protein ligase 1B*	-1.1963	0.4364
11736411_s_at	NUP62	*nucleoporin 62*	-1.1943	0.4370
11746633_a_at	POLA2	*DNA polymerase alpha 2, accessory subunit*	-1.1943	0.4370
11731987_a_at	DNAJC9	*DnaJ Heat Shock Protein Family (Hsp40) Member C9*	-1.1943	0.4370
11744317_x_at	BRCA1	*BRCA1, DNA repair associated*	-1.1940	0.4371
11747361_x_at	HMGA1	*high mobility group AT-hook 1*	-1.1940	0.4371
11720550_a_at	NCAPD3	*non-SMC condensin II complex subunit D3*	-1.1940	0.4371
11757956_s_at	PRTFDC1	*phosphoribosyl transferase domain containing 1*	-1.1940	0.4371
11724948_at	CITED4	*Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 4*	-1.1910	0.4380
11725074_a_at	FAM126A	*family with sequence similarity 126 member A*	-1.1910	0.4380
11727487_at	HAUS6	*HAUS augmin like complex subunit 6*	-1.1903	0.4382
11744880_a_at	ZNF165	*zinc finger protein 165*	-1.1903	0.4382
11743564_x_at	MAP7D3	*MAP7 domain containing 3*	-1.1894	0.4385
11728563_at	FOXD1	*forkhead box D1*	-1.1884	0.4388
11756872_a_at	SAMD4A	*sterile alpha motif domain containing 4A*	-1.1874	0.4391
11740092_x_at	MSMO1	*methylsterol monooxygenase 1*	-1.1874	0.4391
11728820_a_at	HAUS2	*HAUS augmin like complex subunit 2*	-1.1861	0.4395
11754391_a_at	CCDC51	*coiled-coil domain containing 51*	-1.1854	0.4397
11755417_a_at	KIAA0922	*KIAA0922*	-1.1854	0.4397
11717656_a_at	SPRED2	*sprouty related EVH1 domain containing 2*	-1.1834	0.4403
11731834_a_at	IL24	*interleukin 24*	-1.1825	0.4406
11717694_a_at	CEBPG	*CCAAT/enhancer binding protein gamma*	-1.1821	0.4407
11746875_x_at	GNAI2	*G protein subunit alpha i2*	-1.1821	0.4407
11744612_a_at	NUDCD1	*NudC domain containing 1*	-1.1808	0.4411

11754314_a_at	TTC7B	*tetratricopeptide repeat domain 7B*	-1.1805	0.4412
11719434_a_at	ETV4	*ETS variant 4*	-1.1802	0.4413
11721476_a_at	AP1S1	*adaptor related protein complex 1 sigma 1 subunit*	-1.1802	0.4413
11758864_at	SRP19	*signal recognition particle 19*	-1.1789	0.4417
11758648_s_at	KCTD10	*potassium channel tetramerization domain containing 10*	-1.1782	0.4419
11723002_x_at	RANBP1	*RAN binding protein 1*	-1.1766	0.4424
11747606_a_at	NCAPD2	*non-SMC condensin I complex subunit D2*	-1.1766	0.4424
11750599_a_at	OSBPL6	*oxysterol binding protein like 6*	-1.1746	0.4430
11745958_a_at	CD99	*CD99 molecule*	-1.1736	0.4433
11764157_s_at	TDRP	*testis development related protein*	-1.1727	0.4436
11744003_x_at	MTHFD2	*Methylenetetrahydrofolate Dehydrogenase (NADP+ Dependent) 2, Methenyltetrahydrofolate Cyclohydrolase*	-1.1723	0.4437
11757672_s_at	MRPS17	*mitochondrial ribosomal protein S17*	-1.1707	0.4442
11719334_a_at	RCBTB1	*RCC1 and BTB domain containing protein 1*	-1.1704	0.4443
11736054_a_at	CELF1	*CUGBP, Elav-like family member 1*	-1.1701	0.4444
11754220_a_at	PWP1	*PWP1 homolog, endonuclein*	-1.1701	0.4444
11757447_s_at	CYTH3	*cytohesin 3*	-1.1694	0.4446
11756652_a_at	NTMT1	*N-terminal Xaa-Pro-Lys N-methyltransferase 1*	-1.1691	0.4447
11758633_s_at	PDCD5	*programmed cell death 5*	-1.1688	0.4448
11743613_a_at	TMOD3	*tropomodulin 3*	-1.1684	0.4449
11751994_s_at	JAG1	*jagged 1*	-1.1684	0.4449
11729387_x_at	RPL31	*ribosomal protein L31*	-1.1659	0.4457
11757013_x_at	CAV1	*caveolin 1*	-1.1646	0.4461
11721767_s_at	ATAD3A	*ATPase family, AAA domain containing 3A*	-1.1642	0.4462
11758640_s_at	FARSB	*phenylalanyl-tRNA synthetase beta subunit*	-1.1642	0.4462
11723088_a_at	GAS2L1	*growth arrest specific 2 like 1*	-1.1623	0.4468
11754470_a_at	CHTF18	*chromosome transmission fidelity factor 18*	-1.1617	0.4470
11752922_x_at	TUBB	*tubulin beta class I*	-1.1613	0.4471
11754796_a_at	SLCO3A1	*solute carrier organic anion transporter family member 3A1*	-1.1594	0.4477
11720062_s_at	IER3	*immediate early response 3*	-1.1571	0.4484
11747515_a_at	SLC38A2	*solute carrier family 38 member 2*	-1.1568	0.4485
11731896_a_at	TNFSF4	*tumor necrosis factor superfamily member 4*	-1.1565	0.4486
11733422_a_at	LRRFIP2	*LRR binding FLII interacting protein 2*	-1.1559	0.4488
11728348_a_at	RPL39L	*ribosomal protein L39 like*	-1.1559	0.4488
11754606_a_at	MIR3652	*microRNA 3652*	-1.1555	0.4489
11724558_at	GNA15	*G protein subunit alpha 15*	-1.1552	0.4490
11742740_at	GEMIN5	*gem nuclear organelle associated protein 5*	-1.1549	0.4491
11716495_a_at	MAP4	*microtubule associated protein 4*	-1.1549	0.4491
11762135_at	PTPRK	*protein tyrosine phosphatase, receptor type K*	-1.1549	0.4491
11735012_a_at	DYNLL2	*dynein light chain LC8-type 2*	-1.1546	0.4492
11758449_s_at	OGFOD1	*2-oxoglutarate and iron dependent oxygenase domain containing 1*	-1.1546	0.4492
11757372_a_at	NUDT1	*nudix hydrolase 1*	-1.1539	0.4494
11726602_at	DARS2	*aspartyl-tRNA synthetase 2, mitochondrial*	-1.1533	0.4496

11736009_a_at	RSL1D1	*ribosomal L1 domain containing 1*	-1.1526	0.4498
11746200_s_at	EHD2	*EH domain containing 2*	-1.1523	0.4499
11719330_s_at	FNDC4	*fibronectin type III domain containing 4*	-1.1498	0.4507
11736609_at	MSX1	*msh homeobox 1*	-1.1494	0.4508
11755484_a_at	NUP107	*nucleoporin 107*	-1.1491	0.4509
11729343_at	POU2F2	*POU class 2 homeobox 2*	-1.1491	0.4509
11725641_at	EFHD2	*EF-hand domain family member D2*	-1.1482	0.4512
11730331_at	BRI3BP	*BRI3 binding protein*	-1.1478	0.4513
11744892_a_at	GOLT1B	*golgi transport 1B*	-1.1472	0.4515
11744098_at	NOP58	*NOP58 ribonucleoprotein*	-1.1456	0.4520
11757855_a_at	GARS	*glycyl-tRNA synthetase*	-1.1456	0.4520
11722121_a_at	PC	*pyruvate carboxylase*	-1.1440	0.4525
11743266_a_at	RPL34	*ribosomal protein L34*	-1.1431	0.4528
11757973_x_at	NMT2	*N-myristoyltransferase 2*	-1.1424	0.4530
11745815_x_at	CDIP1	*cell death inducing p53 target 1*	-1.1421	0.4531
11744511_x_at	ITGB3BP	*integrin subunit beta 3 binding protein*	-1.1415	0.4533
11725159_a_at	FBXW2	*F-box and WD repeat domain containing 2*	-1.1411	0.4534
11719109_x_at	FHL3	*four and a half LIM domains 3*	-1.1405	0.4536
11715167_at	ARHGAP22	*Rho GTPase activating protein 22*	-1.1399	0.4538
11741252_a_at	RCC1	*regulator of chromosome condensation 1*	-1.1396	0.4539
11716219_a_at	EIF2S1	*eukaryotic translation initiation factor 2 subunit alpha*	-1.1392	0.4540
11746008_x_at	NEXN	*nexilin F-actin binding protein*	-1.1389	0.4541
11753560_s_at	RAN	*RAN, member RAS oncogene family*	-1.1386	0.4542
11733171_a_at	FBXO45	*F-box protein 45*	-1.1386	0.4542
11732322_at	FXN	*frataxin*	-1.1383	0.4543
11733799_a_at	SLC31A2	*solute carrier family 31 member 2*	-1.1380	0.4544
11735234_a_at	SLC38A5	*solute carrier family 38 member 5*	-1.1376	0.4545
11717164_a_at	RANGAP1	*Ran GTPase activating protein 1*	-1.1370	0.4547
11739303_a_at	DLC1	*DLC1 Rho GTPase activating protein*	-1.1370	0.4547
11736461_at	RAB3B	*RAB3B, member RAS oncogene family*	-1.1370	0.4547
11743041_a_at	STIP1	*stress induced phosphoprotein 1*	-1.1367	0.4548
11758106_at	NRM	*Nurim (Nuclear Envelope Membrane Protein)*	-1.1364	0.4549
11732515_x_at	BAK1	*BCL2 antagonist/killer 1*	-1.1361	0.4550
11736019_a_at	NOP2	*NOP2 nucleolar protein*	-1.1354	0.4552
11757222_at	HINT1	*histidine triad nucleotide binding protein 1*	-1.1351	0.4553
11725393_s_at	MAK16	*MAK16 homolog*	-1.1348	0.4554
11721621_a_at	KATNAL1	*katanin catalytic subunit A1 like 1*	-1.1348	0.4554
11725570_a_at	RAB7B	*RAB7B, member RAS oncogene family*	-1.1345	0.4555
11718635_at	KIF1B	*kinesin family member 1B*	-1.1345	0.4555
11718656_at	SLC16A1	*solute carrier family 16 member 1*	-1.1338	0.4557
11759673_s_at	DBF4B	*DBF4 zinc finger B*	-1.1332	0.4559
11729172_s_at	NIFK	*nucleolar protein interacting with the FHA domain of MKI67*	-1.1313	0.4565

11717017_a_at	OCIAD2	*OCIA domain containing 2*	-1.1313	0.4565
11727605_at	TMEM92	*transmembrane protein 92*	-1.1307	0.4567
11722076_a_at	DONSON	*downstream neighbor of SON*	-1.1300	0.4569
11722931_a_at	GART	*phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase*	-1.1300	0.4569
11757113_a_at	SNHG1	*small nucleolar RNA host gene 1*	-1.1294	0.4571
11719891_s_at	CRYZ	*crystallin zeta*	-1.1294	0.4571
11721530_at	ZDHHC2	*zinc finger DHHC-type containing 2*	-1.1291	0.4572
11734823_a_at	APBB2	*amyloid beta precursor protein binding family B member 2*	-1.1285	0.4574
11715571_a_at	CLSTN1	*calsyntenin 1*	-1.1275	0.4577
11726567_a_at	EIF4G1	*eukaryotic translation initiation factor 4 gamma 1*	-1.1275	0.4577
11723616_a_at	PLTP	*phospholipid transfer protein*	-1.1272	0.4578
11716173_a_at	P4HB	*prolyl 4-hydroxylase subunit beta*	-1.1263	0.4581
11739206_a_at	TTL	*tubulin tyrosine ligase*	-1.1222	0.4594
11724314_a_at	LUZP1	*leucine zipper protein 1*	-1.1212	0.4597
11742899_a_at	CGGBP1	*CGG triplet repeat binding protein 1*	-1.1209	0.4598
11726869_a_at	MFSD12	*major facilitator superfamily domain containing 12*	-1.1209	0.4598
11755702_x_at	RRP7A	*ribosomal RNA processing 7 homolog A*	-1.1206	0.4599
11749168_a_at	KRT6A	*keratin 6A*	-1.1197	0.4602
11757843_s_at	PEA15	*phosphoprotein enriched in astrocytes 15*	-1.1187	0.4605
11717257_s_at	PIM1	*Pim-1 proto-oncogene, serine/threonine kinase*	-1.1184	0.4606
11753757_a_at	NUTF2	*nuclear transport factor 2*	-1.1181	0.4607
11717812_a_at	KIF3C	*kinesin family member 3C*	-1.1175	0.4609
11723169_s_at	FOXN2	*forkhead box N2*	-1.1172	0.4610
11755448_s_at	CAPRIN2	*caprin family member 2*	-1.1172	0.4610
11732779_a_at	PSMD12	*proteasome 26S subunit, non-ATPase 12*	-1.1162	0.4613
11757939_s_at	SEPT11	*septin 11*	-1.1162	0.4613
11741437_s_at	SPRYD7	*SPRY domain containing 7*	-1.1147	0.4618
11753619_s_at	EIF5AL1	*eukaryotic translation initiation factor 5A-like 1*	-1.1147	0.4618
11758014_s_at	TGFBR1	*transforming growth factor beta receptor 1*	-1.1134	0.4622
11753941_x_at	SFR1	*SWI5 dependent homologous recombination repair protein 1*	-1.1125	0.4625
11729417_at	KRT24	*keratin 24*	-1.1115	0.4628
11749980_x_at	HOPX	*HOP homeobox*	-1.1109	0.4630
11756910_x_at	FANCD2	*Fanconi anemia complementation group D2*	-1.1109	0.4630
11717321_at	OAF	*out at first homolog*	-1.1109	0.4630
11730795_at	MRPL4	*mitochondrial ribosomal protein L4*	-1.1097	0.4634
11735788_a_at	KCNG1	*potassium voltage-gated channel modifier subfamily G member 1*	-1.1090	0.4636
11720316_s_at	SLC44A2	*solute carrier family 44 member 2*	-1.1084	0.4638
11739606_x_at	CCDC88A	*coiled-coil domain containing 88A*	-1.1081	0.4639
11716565_a_at	SDCCAG3	*serologically defined colon cancer antigen 3*	-1.1069	0.4643
11722721_a_at	CENPV	*centromere protein V*	-1.1066	0.4644
11740490_at	KRT75	*keratin 75*	-1.1066	0.4644
11763585_s_at	TMPO	*thymopoietin*	-1.1053	0.4648

11719807_x_at	**BLOC1S6**	***biogenesis of lysosomal organelles complex 1 subunit 6***	**-1.1044**	**0.4651**
11754098_a_at	**AGO2**	***argonaute 2, RISC catalytic component***	**-1.1038**	**0.4653**
11759151_at	**SPC24**	***SPC24, NDC80 kinetochore complex component***	**-1.1035**	**0.4654**
11720305_a_at	**VAT1**	***vesicle amine transport 1***	**-1.1025**	**0.4657**
11757744_s_at	**FAM171A1**	***family with sequence similarity 171 member A1***	**-1.1025**	**0.4657**
11744409_a_at	**KLHL18**	***kelch like family member 18***	**-1.1022**	**0.4658**
11725297_a_at	**MAPRE2**	***microtubule associated protein RP/EB family member 2***	**-1.1019**	**0.4659**
11745177_x_at	**TPD52L2**	***tumor protein D52 like 2***	**-1.1016**	**0.4660**
11759578_s_at	**RASSF8**	***Ras association domain family member 8***	**-1.1007**	**0.4663**
11729703_a_at	**DBN1**	***drebrin 1***	**-1.1007**	**0.4663**
11757018_a_at	**COL12A1**	***collagen type XII alpha 1 chain***	**-1.1007**	**0.4663**
11718606_a_at	**DESI1**	***desumoylating isopeptidase 1***	**-1.1004**	**0.4664**
11716242_a_at	**PES1**	***pescadillo ribosomal biogenesis factor 1***	**-1.0991**	**0.4668**
11717122_s_at	**C6orf106**	***chromosome 6 open reading frame 106***	**-1.0991**	**0.4668**
11740781_a_at	**ILF3**	***interleukin enhancer binding factor 3***	**-1.0991**	**0.4668**
11742698_at	**SCG5**	***secretogranin V***	**-1.0988**	**0.4669**
11723328_a_at	**PTRH1**	***peptidyl-tRNA hydrolase 1 homolog***	**-1.0988**	**0.4669**
11717084_a_at	**PRPS1**	***phosphoribosyl pyrophosphate synthetase 1***	**-1.0982**	**0.4671**
11724784_at	**MRPS18C**	***mitochondrial ribosomal protein S18C***	**-1.0976**	**0.4673**
11756155_a_at	**NHS**	***NHS actin remodeling regulator***	**-1.0973**	**0.4674**
11715698_a_at	**NOLC1**	***nucleolar and coiled-body phosphoprotein 1***	**-1.0963**	**0.4677**
11728077_s_at	**PRKCQ**	***protein kinase C theta***	**-1.0960**	**0.4678**
11757102_a_at	**MIR7112**	***microRNA 7112***	**-1.0948**	**0.4682**
11734724_a_at	**IRF6**	***interferon regulatory factor 6***	**-1.0948**	**0.4682**
11719725_at	**PUM3**	***pumilio RNA binding family member 3***	**-1.0948**	**0.4682**
11740499_a_at	**CBX5**	***chromobox 5***	**-1.0939**	**0.4685**
11752267_a_at	**RPS6KA4**	***ribosomal protein S6 kinase A4***	**-1.0933**	**0.4687**
11731202_a_at	**AIM1L**	***absent in melanoma 1-like***	**-1.0923**	**0.4690**
11752081_a_at	**SELENOI**	***selenoprotein I***	**-1.0914**	**0.4693**

11730635_a_at	**GRHL3**	***grainyhead like transcription factor 3***	**-1.0905**	**0.4696**
11744737_a_at	**RTKN2**	***rhotekin 2***	**-1.0905**	**0.4696**
11730206_at	**PSMD9**	***proteasome 26S subunit, non-ATPase 9***	**-1.0905**	**0.4696**
11732425_at	**ANKRD22**	***ankyrin repeat domain 22***	**-1.0893**	**0.4700**
11753904_a_at	**CDC42EP2**	***CDC42 effector protein 2***	**-1.0883**	**0.4703**
11721705_at	**COL7A1**	***collagen type VII alpha 1 chain***	**-1.0874**	**0.4706**
11725861_a_at	**MYBL1**	***MYB proto-oncogene like 1***	**-1.0862**	**0.4710**
11716148_a_at	**TRAF3IP2**	***TRAF3 interacting protein 2***	**-1.0859**	**0.4711**
11743633_a_at	**STX2**	***syntaxin 2***	**-1.0859**	**0.4711**
11748605_a_at	**POLR1B**	***RNA polymerase I subunit B***	**-1.0859**	**0.4711**
11728524_a_at	**SPOCD1**	***SPOC domain containing 1***	**-1.0850**	**0.4714**
11754810_a_at	**ITGB5**	***integrin subunit beta 5***	**-1.0844**	**0.4716**
11744306_a_at	**LRR1**	***leucine rich repeat protein 1***	**-1.0834**	**0.4719**
11729665_a_at	**STK38L**	***serine/threonine kinase 38 like***	**-1.0819**	**0.4724**
11715934_s_at	**TAGLN**	***transgelin***	**-1.0813**	**0.4726**
11727901_a_at	**HPS1**	***HPS1, biogenesis of lysosomal organelles complex 3 subunit 1***	**-1.0813**	**0.4726**
11715593_s_at	**YWHAH**	***tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta***	**-1.0810**	**0.4727**

11735273_at	**TBX18**	***T-box 18***	**-1.0807**	**0.4728**
11716140_x_at	**SMS**	***spermine synthase***	**-1.0804**	**0.4729**
11753918_a_at	**NUP85**	***nucleoporin 85***	**-1.0798**	**0.4731**
11726877_at	**GJB5**	***gap junction protein beta 5***	**-1.0798**	**0.4731**
11719746_a_at	**NF2**	***neurofibromin 2***	**-1.0798**	**0.4731**
11727036_at	**SLC9B2**	***solute carrier family 9 member B2***	**-1.0798**	**0.4731**
11719776_at	**NDST1**	***N-deacetylase and N-sulfotransferase 1***	**-1.0795**	**0.4732**
11751223_a_at	**MAPK1**	***mitogen-activated protein kinase 1***	**-1.0792**	**0.4733**
11725767_at	**CLCF1**	***cardiotrophin-like cytokine factor 1***	**-1.0789**	**0.4734**
11734684_s_at	**UMPS**	***uridine monophosphate synthetase***	**-1.0770**	**0.4740**
11731516_at	**XPO4**	***exportin 4***	**-1.0770**	**0.4740**
11722260_a_at	**EDEM1**	***ER degradation enhancing alpha-mannosidase like protein 1***	**-1.0767**	**0.4741**
11739757_a_at	**FAM57A**	***family with sequence similarity 57 member A***	**-1.0764**	**0.4742**
11719789_x_at	**TUBB2A**	***tubulin beta 2A class IIa***	**-1.0758**	**0.4744**
11758223_s_at	**GNPDA1**	***glucosamine-6-phosphate deaminase 1***	**-1.0752**	**0.4746**
11736068_x_at	**NDRG4**	***NDRG family member 4***	**-1.0731**	**0.4753**
11759746_a_at	**ARHGEF28**	***Rho guanine nucleotide exchange factor 28***	**-1.0731**	**0.4753**

11739558_at	**RFWD3**	***ring finger and WD repeat domain 3***	**-1.0722**	**0.4756**
11738456_s_at	**C20orf197**	***chromosome 20 open reading frame 197***	**-1.0719**	**0.4757**
11720621_s_at	**ACLY**	***ATP citrate lyase***	**-1.0716**	**0.4758**
11763888_at	**SNORA33**	***small nucleolar RNA, H/ACA box 33***	**-1.0713**	**0.4759**
11726245_s_at	**HIST4H4**	***histone cluster 4 H4***	**-1.0710**	**0.4760**
11725149_at	**C9orf40**	***chromosome 9 open reading frame 40***	**-1.0685**	**0.4768**
11722213_at	**NPM3**	***nucleophosmin/nucleoplasmin 3***	**-1.0682**	**0.4769**
11728763_x_at	**GAL3ST4**	***galactose-3-O-sulfotransferase 4***	**-1.0679**	**0.4770**
11744034_a_at	**VASP**	***vasodilator-stimulated phosphoprotein***	**-1.0676**	**0.4771**
11717512_a_at	**SEPT8**	***septin 8***	**-1.0676**	**0.4771**
11736716_s_at	**TMPRSS11E**	***transmembrane protease, serine 11E***	**-1.0667**	**0.4774**
11746331_a_at	**ADK**	***adenosine kinase***	**-1.0664**	**0.4775**
11758211_s_at	**PM20D2**	***peptidase M20 domain containing 2***	**-1.0664**	**0.4775**
11721806_a_at	**EMC1**	***ER membrane protein complex subunit 1***	**-1.0661**	**0.4776**
11730796_x_at	**PSPH**	***phosphoserine phosphatase***	**-1.0658**	**0.4777**
11736424_a_at	**STARD4**	***StAR related lipid transfer domain containing 4***	**-1.0655**	**0.4778**
11719539_a_at	**NEMP1**	***nuclear envelope integral membrane protein 1***	**-1.0655**	**0.4778**

11726315_a_at	**METTL22**	***methyltransferase like 22***	**-1.0655**	**0.4778**
11754814_a_at	**NUP93**	***nucleoporin 93***	**-1.0652**	**0.4779**
11725291_at	**FUT1**	***Fucosyltransferase 1 (H Blood Group)***	**-1.0646**	**0.4781**
11759557_at	**BLZF1**	***basic leucine zipper nuclear factor 1***	**-1.0622**	**0.4789**
11744169_a_at	**MYBL2**	***MYB proto-oncogene like 2***	**-1.0619**	**0.4790**
11732701_a_at	**CSGALNACT2**	***chondroitin sulfate N-acetylgalactosaminyltransferase 2***	**-1.0604**	**0.4795**
11724221_at	**NAP1L2**	***nucleosome assembly protein 1 like 2***	**-1.0598**	**0.4797**
11726842_a_at	**PDS5A**	***PDS5 cohesin associated factor A***	**-1.0595**	**0.4798**
11757658_a_at	**LZIC**	***leucine zipper and CTNNBIP1 domain containing***	**-1.0592**	**0.4799**
11739107_a_at	**SEC61A1**	***Sec61 translocon alpha 1 subunit***	**-1.0592**	**0.4799**
11721293_x_at	**GIT2**	***GIT ArfGAP 2***	**-1.0583**	**0.4802**
11720905_at	**QSER1**	***glutamine and serine rich 1***	**-1.0577**	**0.4804**
11722406_at	**PFKFB4**	***6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4***	**-1.0568**	**0.4807**
11726923_a_at	**ASB6**	***ankyrin repeat and SOCS box containing 6***	**-1.0547**	**0.4814**
11724713_at	**FAM212A**	***family with sequence similarity 212 member A***	**-1.0538**	**0.4817**
11727540_a_at	**INTS7**	***integrator complex subunit 7***	**-1.0523**	**0.4822**
11728021_a_at	**CHCHD4**	***coiled-coil-helix-coiled-coil-helix domain containing 4***	**-1.0523**	**0.4822**

11755618_a_at	**ALDH4A1**	***aldehyde dehydrogenase 4 family member A1***	**-1.0523**	**0.4822**
11751106_x_at	**NUP35**	***nucleoporin 35***	**-1.0523**	**0.4822**
11743314_a_at	**FASN**	***fatty acid synthase***	**-1.0520**	**0.4823**
11716234_s_at	**CTNNBIP1**	***catenin beta interacting protein 1***	**-1.0511**	**0.4826**
11749139_a_at	**SEMA3C**	***semaphorin 3C***	**-1.0487**	**0.4834**
11719240_at	**PANX1**	***pannexin 1***	**-1.0484**	**0.4835**
11722412_s_at	**SLC7A1**	***solute carrier family 7 member 1***	**-1.0481**	**0.4836**
11734988_s_at	**FEM1B**	***fem-1 homolog B***	**-1.0478**	**0.4837**
11741629_a_at	**POLR3H**	***RNA polymerase III subunit H***	**-1.0475**	**0.4838**
11728569_at	**GSTCD**	***glutathione S-transferase C-terminal domain containing***	**-1.0475**	**0.4838**
11721554_a_at	**COLGALT1**	***Collagen Beta(1-O)Galactosyltransferase 1***	**-1.0466**	**0.4841**
11723480_at	**SAAL1**	***serum amyloid A like 1***	**-1.0463**	**0.4842**
11743330_a_at	**PGP**	***phosphoglycolate phosphatase***	**-1.0433**	**0.4852**
11757561_s_at	**NOC2L**	***NOC2 like nucleolar associated transcriptional repressor***	**-1.0431**	**0.4853**
11732719_at	**EREG**	***epiregulin***	**-1.0428**	**0.4854**
11727353_a_at	**CENPM**	***centromere protein M***	**-1.0428**	**0.4854**
11717314_a_at	**HAUS1**	***HAUS augmin like complex subunit 1***	**-1.0425**	**0.4855**

11722455_a_at	**ZNF655**	***zinc finger protein 655***	**-1.0419**	**0.4857**
11715374_a_at	**CALR**	***calreticulin***	**-1.0419**	**0.4857**
11722085_a_at	**PDCD2L**	***programmed cell death 2 like***	**-1.0419**	**0.4857**
11739004_x_at	**HDGF**	***hepatoma-derived growth factor***	**-1.0419**	**0.4857**
11752223_x_at	**POLH**	***DNA polymerase eta***	**-1.0416**	**0.4858**
11737384_at	**PCDH7**	***protocadherin 7***	**-1.0416**	**0.4858**
11735537_s_at	**MROH6**	***maestro heat like repeat family member 6***	**-1.0413**	**0.4859**
11718399_s_at	**TGM2**	***transglutaminase 2***	**-1.0410**	**0.4860**
11742184_a_at	**LAMA3**	***laminin subunit alpha 3***	**-1.0404**	**0.4862**
11742776_s_at	**GPR161**	***G protein-coupled receptor 161***	**-1.0401**	**0.4863**
11722561_a_at	**CDK4**	***cyclin dependent kinase 4***	**-1.0392**	**0.4866**
11715280_s_at	**JUP**	***junction plakoglobin***	**-1.0392**	**0.4866**
11729295_at	**TANGO6**	***transport and golgi organization 6 homolog***	**-1.0389**	**0.4867**
11721846_a_at	**MFAP5**	***microfibrillar associated protein 5***	**-1.0389**	**0.4867**
11755100_a_at	**COL16A1**	***collagen type XVI alpha 1 chain***	**-1.0389**	**0.4867**
11757352_a_at	**TRMT1**	***tRNA methyltransferase 1***	**-1.0383**	**0.4869**
11758249_s_at	**FDPS**	***farnesyl diphosphate synthase***	**-1.0380**	**0.4870**

11718954_a_at	**FBLIM1**	***filamin binding LIM protein 1***	**-1.0377**	**0.4871**
11731269_at	**KRT31**	***keratin 31***	**-1.0371**	**0.4873**
11743018_at	**NOC3L**	***NOC3 like DNA replication regulator***	**-1.0365**	**0.4875**
11732496_a_at	**AP1S3**	***adaptor related protein complex 1 sigma 3 subunit***	**-1.0333**	**0.4886**
11718531_a_at	**CAD**	***carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase***	**-1.0330**	**0.4887**
11720045_a_at	**DNAJC10**	***DnaJ Heat Shock Protein Family (Hsp40) Member C10***	**-1.0330**	**0.4887**
11717139_a_at	**HARS**	***histidyl-tRNA synthetase***	**-1.0318**	**0.4891**
11756670_x_at	**TUBA1C**	***tubulin alpha 1c***	**-1.0294**	**0.4899**
11722451_s_at	**POLR2D**	***RNA polymerase II subunit D***	**-1.0291**	**0.4900**
11736519_x_at	**CXorf38**	***chromosome X open reading frame 38***	**-1.0289**	**0.4901**
11743596_a_at	**PTPRE**	***protein tyrosine phosphatase, receptor type E***	**-1.0283**	**0.4903**
11754044_at	**CLSPN**	***claspin***	**-1.0271**	**0.4907**
11725378_a_at	**GSTO1**	***glutathione S-transferase omega 1***	**-1.0265**	**0.4909**
11757285_a_at	**DCTN5**	***dynactin subunit 5***	**-1.0262**	**0.4910**
11723578_a_at	**SMIM13**	***small integral membrane protein 13***	**-1.0259**	**0.4911**
11749728_a_at	**LNPK**	***lunapark, ER junction formation factor***	**-1.0256**	**0.4912**
11724199_x_at	**LSS**	***Lanosterol Synthase (2,3-Oxidosqualene-Lanosterol Cyclase)***	**-1.0253**	**0.4913**

11731868_a_at	**BICD2**	***BICD cargo adaptor 2***	**-1.0247**	**0.4915**
11729695_a_at	**MVD**	***mevalonate diphosphate decarboxylase***	**-1.0244**	**0.4916**
11757791_s_at	**DUSP3**	***dual specificity phosphatase 3***	**-1.0241**	**0.4917**
11754071_x_at	**TAGLN2**	***transgelin 2***	**-1.0233**	**0.4920**
11754208_x_at	**NTAN1**	***N-terminal asparagine amidase***	**-1.0233**	**0.4920**
11726101_s_at	**CALML3**	***calmodulin like 3***	**-1.0218**	**0.4925**
11725085_a_at	**LANCL2**	***LanC like 2***	**-1.0218**	**0.4925**
11756663_a_at	**NSUN2**	***NOP2/Sun RNA methyltransferase family member 2***	**-1.0218**	**0.4925**
11725178_at	**KCTD11**	***potassium channel tetramerization domain containing 11***	**-1.0206**	**0.4929**
11742934_s_at	**POC1A**	***POC1 centriolar protein A***	**-1.0198**	**0.4932**
11751600_a_at	**DAPP1**	***dual adaptor of phosphotyrosine and 3-phosphoinositides 1***	**-1.0195**	**0.4933**
11732415_s_at	**TIAM1**	***T-cell lymphoma invasion and metastasis 1***	**-1.0192**	**0.4934**
11737409_x_at	**BTF3**	***basic transcription factor 3***	**-1.0183**	**0.4937**
11728835_a_at	**GLMN**	***glomulin, FKBP associated protein***	**-1.0180**	**0.4938**
11719587_a_at	**MICALL1**	***MICAL like 1***	**-1.0168**	**0.4942**
11721567_a_at	**POLD1**	***DNA polymerase delta 1, catalytic subunit***	**-1.0162**	**0.4944**
11752618_x_at	**MIR6884**	***microRNA 6884***	**-1.0162**	**0.4944**

11758564_s_at	**NUDT15**	***nudix hydrolase 15***	**-1.0157**	**0.4946**
11739728_a_at	**RECQL**	***RecQ like helicase***	**-1.0139**	**0.4952**
11719474_a_at	**IMP4**	***IMP4 homolog, U3 small nucleolar ribonucleoprotein***	**-1.0128**	**0.4956**
11725837_a_at	**C1orf112**	***chromosome 1 open reading frame 112***	**-1.0122**	**0.4958**
11747067_a_at	**CCT5**	***chaperonin containing TCP1 subunit 5***	**-1.0122**	**0.4958**
11726224_s_at	**HNRNPL**	***heterogeneous nuclear ribonucleoprotein L***	**-1.0119**	**0.4959**
11717350_at	**NCAPH2**	***non-SMC condensin II complex subunit H2***	**-1.0113**	**0.4961**
11720143_at	**CCSAP**	***centriole, cilia and spindle associated protein***	**-1.0107**	**0.4963**
11758619_s_at	**LIF**	***leukemia inhibitory factor***	**-1.0101**	**0.4965**
11722120_a_at	**KNTC1**	***kinetochore associated 1***	**-1.0096**	**0.4967**
11718587_x_at	**SAP30BP**	***SAP30 binding protein***	**-1.0096**	**0.4967**
11733000_at	**ICAM1**	***intercellular adhesion molecule 1***	**-1.0093**	**0.4968**
11720803_at	**S100A14**	***S100 calcium binding protein A14***	**-1.0064**	**0.4978**
11732196_x_at	**KPNA4**	***karyopherin subunit alpha 4***	**-1.0058**	**0.4980**
11752166_x_at	**PKM**	***pyruvate kinase, muscle***	**-1.0049**	**0.4983**
11725515_a_at	**ABCG1**	***ATP binding cassette subfamily G member 1***	**-1.0043**	**0.4985**
11747964_a_at	**SLC4A7**	***solute carrier family 4 member 7***	**-1.0043**	**0.4985**

11720274_x_at	**ALKBH6**	***alkB homolog 6***	**-1.0014**	**0.4995**
11760430_at	**GLA**	***galactosidase alpha***	**-1.0009**	**0.4997**
11746276_s_at	**RGS12**	***regulator of G-protein signaling 12***	**-1.0009**	**0.4997**
11745732_a_at	**SLC20A2**	***solute carrier family 20 member 2***	**-1.0006**	**0.4998**
11757850_s_at	**PA2G4**	***proliferation-associated 2G4***	**-1.0006**	**0.4998**

***Diferentially expressed mRNAs were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ([Log_2Ratio > 1] or [Log_2Ratio < -1] for both upregulated or downregulated mRNAs, respectively), followed by multiple correction using a False Discovery Rate (FDR) threshold of 1% (p-adjusted value or q < 0.01).**

TABLE S5. Differentially expressed mRNAs in hNP-BSCs compared to control hNM-BSCs at day 0 of the air-liquid interface culture.*

UPREGULATED mRNAs (164)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11736422_s_at	POSTN	*periostin*	4.4495	21.8489
11717386_s_at	MT1G	*metallothionein 1G*	3.7246	13.2196
11746283_s_at	KRTAP2-3	*keratin associated protein 2-3*	3.4402	10.8546
11731925_at	CRCT1	*cysteine rich C-terminal 1*	3.4033	10.5805
11731857_x_at	MT1H	*metallothionein 1H*	2.6520	6.2854
11732959_a_at	SPRR3	*small proline rich protein 3*	2.6436	6.2487
11728397_at	MT1M	*metallothionein 1M*	2.5305	5.7777
11731168_at	IGFL1	*IGF like family member 1*	2.5102	5.6970
11753736_s_at	MT1P3	*metallothionein 1 pseudogene 3*	2.3968	5.2664
11744141_x_at	FOLR3	*folate receptor 3*	2.3871	5.2309
11746463_a_at	IL6	*interleukin 6*	2.3463	5.0852
11757033_a_at	IL13RA2	*interleukin 13 receptor subunit alpha 2*	2.2986	4.9198
11730802_at	CRNN	*cornulin*	2.1803	4.5326
11745004_x_at	HOPX	*HOP homeobox*	2.0242	4.0677
11718904_s_at	FILIP1L	*filamin A interacting protein 1 like*	2.0055	4.0152
11736978_at	PADI3	*peptidyl arginine deiminase 3*	1.9764	3.9350
11736813_at	PDCD1LG2	*programmed cell death 1 ligand 2*	1.9691	3.9153
11728876_at	CSF2	*colony stimulating factor 2*	1.9288	3.8074
11749461_a_at	CDH11	*cadherin 11*	1.8878	3.7006
11735693_x_at	SPRR2E	*small proline rich protein 2E*	1.8875	3.6999
11744047_a_at	MAP1B	*microtubule associated protein 1B*	1.8861	3.6964
11721638_s_at	CES1	*carboxylesterase 1*	1.8656	3.6442
11724387_at	HOXB2	*homeobox B2*	1.8279	3.5503
11740349_at	RNASE7	*ribonuclease A family member 7*	1.8188	3.5279
11752384_s_at	COL6A1	*collagen type VI alpha 1 chain*	1.8120	3.5112
11723151_s_at	SUGCT	*succinyl-CoA:glutarate-CoA transferase*	1.7710	3.4129
11726206_a_at	SH2D5	*SH2 domain containing 5*	1.7696	3.4097
11732713_at	FST	*follistatin*	1.7688	3.4077
11748382_a_at	SMURF2	*SMAD specific E3 ubiquitin protein ligase 2*	1.7568	3.3794
11720353_s_at	ETV5	*ETS variant 5*	1.7316	3.3209
11719032_a_at	FADS3	*fatty acid desaturase 3*	1.7009	3.2510
11729444_a_at	SULT2B1	*sulfotransferase family 2B member 1*	1.6919	3.2309
11731653_a_at	IVL	*involucrin*	1.6678	3.1774
11724038_a_at	PTGS2	*prostaglandin-endoperoxide synthase 2*	1.6559	3.1511
11757913_x_at	TUBA1A	*tubulin alpha 1a*	1.6397	3.1160
11754824_a_at	LGALSL	*galectin like*	1.6298	3.0946
11726113_a_at	FAM46B	*family with sequence similarity 46 member B*	1.6276	3.0900
11757884_s_at	MSRB3	*methionine sulfoxide reductase B3*	1.6220	3.0781
11745249_x_at	TMEM40	*transmembrane protein 40*	1.6029	3.0376
11744584_a_at	HYI	*Hydroxypyruvate Isomerase (Putative)*	1.5934	3.0175
11736685_a_at	FGF5	*fibroblast growth factor 5*	1.5666	2.9620
11728825_at	TRNP1	*TMF1-regulated nuclear protein 1*	1.5641	2.9569
11715316_x_at	HLA-C	*major histocompatibility complex, class I, C*	1.5615	2.9517
11736716_s_at	TMPRSS11E	*transmembrane protease, serine 11E*	1.5575	2.9434
11741710_a_at	COL6A3	*collagen type VI alpha 3 chain*	1.5463	2.9206
11736440_at	INF2	*inverted formin, FH2 and WH2 domain containing*	1.5280	2.8839

11748703_a_at	C1D	*C1D nuclear receptor corepressor*	1.5223	2.8725
11738222_x_at	RAET1L	*retinoic acid early transcript 1L*	1.5186	2.8651
11754180_s_at	SPRR1A	*small proline rich protein 1A*	1.5076	2.8434
11739979_a_at	AKAP2	*A-kinase anchoring protein 2*	1.4873	2.8037
11738259_s_at	CXorf49	*chromosome X open reading frame 49*	1.4802	2.7898
11721092_a_at	THBS1	*thrombospondin 1*	1.4688	2.7680
11721841_at	GLIPR1	*GLI pathogenesis related 1*	1.4670	2.7645
11715353_s_at	COL1A2	*collagen type I alpha 2 chain*	1.4659	2.7624
11728873_s_at	RBM24	*RNA binding motif protein 24*	1.4652	2.7610
11759423_at	EPPK1	*epiplakin 1*	1.4637	2.7582
11725428_a_at	ABLIM3	*actin binding LIM protein family member 3*	1.4627	2.7563
11755975_x_at	PKIB	*protein kinase (cAMP-dependent, catalytic) inhibitor beta*	1.4494	2.7310
11715620_a_at	CRYAB	*crystallin alpha B*	1.4445	2.7217
11715934_s_at	TAGLN	*transgelin*	1.4431	2.7191
11719041_at	CYGB	*cytoglobin*	1.4424	2.7177
11730740_a_at	PDLIM4	*PDZ and LIM domain 4*	1.4404	2.7140
11729265_at	SPRR2D	*small proline rich protein 2D*	1.4312	2.6967
11729417_at	KRT24	*keratin 24*	1.4272	2.6892
11729140_x_at	SLAMF7	*SLAM family member 7*	1.4162	2.6688
11741153_a_at	NCF2	*neutrophil cytosolic factor 2*	1.3971	2.6338
11724579_a_at	L1CAM	*L1 cell adhesion molecule*	1.3852	2.6121
11726614_at	CDH2	*cadherin 2*	1.3848	2.6113
11745469_a_at	INPP4B	*inositol polyphosphate-4-phosphatase type II B*	1.3696	2.5840
11748865_a_at	TMEM139	*transmembrane protein 139*	1.3500	2.5491
11763834_a_at	PPP1R1C	*protein phosphatase 1 regulatory inhibitor subunit 1C*	1.3394	2.5305
11725169_at	MOB3B	*MOB kinase activator 3B*	1.3131	2.4847
11723753_a_at	ZFAND2A	*zinc finger AN1-type containing 2A*	1.2963	2.4560
11715350_a_at	COL1A1	*collagen type I alpha 1 chain*	1.2905	2.4461
11737557_at	AMTN	*amelotin*	1.2710	2.4133
11744880_a_at	ZNF165	*zinc finger protein 165*	1.2675	2.4075
11724322_a_at	CST6	*cystatin E/M*	1.2667	2.4061
11747193_a_at	ZNF185	*Zinc Finger Protein 185 (LIM Domain)*	1.2600	2.3950
11754593_x_at	TUBB3	*tubulin beta 3 class III*	1.2576	2.3909
11725749_a_at	GAL	*galanin and GMAP prepropeptide*	1.2544	2.3857
11737041_a_at	PHLDB2	*pleckstrin homology like domain family B member 2*	1.2443	2.3691
11718464_s_at	NEURL1B	*neuralized E3 ubiquitin protein ligase 1B*	1.2384	2.3594
11754344_s_at	SPRY4	*sprouty RTK signaling antagonist 4*	1.2374	2.3578
11739039_x_at	CEACAM5	*carcinoembryonic antigen related cell adhesion molecule 5*	1.2348	2.3535
11728612_at	ADAMTS6	*ADAM metallopeptidase with thrombospondin type 1 motif 6*	1.2304	2.3463
11716939_a_at	HMOX1	*heme oxygenase 1*	1.2209	2.3310
11727247_x_at	CHRNB1	*cholinergic receptor nicotinic beta 1 subunit*	1.2208	2.3308
11749139_a_at	SEMA3C	*semaphorin 3C*	1.2192	2.3281
11755050_s_at	PLCB4	*phospholipase C beta 4*	1.2178	2.3259
11734334_at	LINC01559	*long intergenic non-protein coding RNA 1559*	1.2156	2.3223
11726006_at	SLC30A1	*solute carrier family 30 member 1*	1.2147	2.3210
11744068_x_at	APOE	*apolipoprotein E*	1.2083	2.3106
11754438_x_at	GJC1	*gap junction protein gamma 1*	1.2075	2.3093
11754559_a_at	SBSN	*suprabasin*	1.2037	2.3033
11729665_a_at	STK38L	*serine/threonine kinase 38 like*	1.1957	2.2906
11726678_a_at	AFAP1L2	*actin filament associated protein 1 like 2*	1.1855	2.2745
11754728_a_at	MAL	*mal, T-cell differentiation protein*	1.1841	2.2722
11716131_s_at	FSTL3	*follistatin like 3*	1.1761	2.2596

11724885_at	CLIC3	chloride intracellular channel 3	1.1683	2.2474
11724401_at	HS3ST2	heparan sulfate-glucosamine 3-sulfotransferase 2	1.1661	2.2440
11741778_a_at	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	1.1638	2.2404
11727538_at	NME5	NME/NM23 family member 5	1.1636	2.2402
11720842_at	RHOD	ras homolog family member D	1.1622	2.2380
11737483_at	RAET1G	retinoic acid early transcript 1G	1.1606	2.2355
11747047_a_at	MAP3K7CL	MAP3K7 C-terminal like	1.1556	2.2277
11757698_s_at	MIG7	mig-7	1.1540	2.2253
11718704_at	IGF1R	insulin like growth factor 1 receptor	1.1468	2.2142
11730462_s_at	OTX2	orthodenticle homeobox 2	1.1466	2.2139
11735273_at	TBX18	T-box 18	1.1348	2.1959
11759746_a_at	ARHGEF28	Rho guanine nucleotide exchange factor 28	1.1341	2.1948
11743444_s_at	RHOB	ras homolog family member B	1.1340	2.1947
11725517_x_at	ABCG1	ATP binding cassette subfamily G member 1	1.1259	2.1824
11755955_a_at	FAP	fibroblast activation protein alpha	1.1174	2.1695
11726536_at	CYP1A1	cytochrome P450 family 1 subfamily A member 1	1.1138	2.1641
11722193_a_at	C12orf75	chromosome 12 open reading frame 75	1.1078	2.1551
11746427_a_at	WDR66	WD repeat domain 66	1.1071	2.1541
11728024_a_at	KLK5	kallikrein related peptidase 5	1.1045	2.1503
11733832_a_at	MAP2	microtubule associated protein 2	1.1045	2.1502
11731834_a_at	IL24	interleukin 24	1.1020	2.1465
11735576_a_at	LETM2	leucine zipper and EF-hand containing transmembrane protein 2	1.0992	2.1423
11726193_at	MARCH4	membrane associated ring-CH-type finger 4	1.0905	2.1295
11752515_a_at	ODC1	ornithine decarboxylase 1	1.0891	2.1274
11752930_a_at	GBP1	guanylate binding protein 1	1.0870	2.1243
11734993_at	SKI	SKI proto-oncogene	1.0820	2.1169
11734701_a_at	DKK3	dickkopf WNT signaling pathway inhibitor 3	1.0811	2.1157
11740032_s_at	DUSP14	dual specificity phosphatase 14	1.0809	2.1154
11719880_at	OSTM1	osteopetrosis associated transmembrane protein 1	1.0767	2.1092
11717257_s_at	PIM1	Pim-1 proto-oncogene, serine/threonine kinase	1.0743	2.1057
11722248_a_at	RASSF1	Ras association domain family member 1	1.0718	2.1020
11730635_a_at	GRHL3	grainyhead like transcription factor 3	1.0696	2.0989
11718828_s_at	ITM2C	integral membrane protein 2C	1.0674	2.0957
11746700_s_at	ITM2A	integral membrane protein 2A	1.0649	2.0920
11731263_a_at	ZNF365	zinc finger protein 365	1.0600	2.0850
11729712_at	SPRR2A	small proline rich protein 2A	1.0592	2.0838
11724779_at	PGM2L1	phosphoglucomutase 2 like 1	1.0589	2.0833
11726024_at	EDN1	endothelin 1	1.0582	2.0823
11754183_s_at	HMGB3	high mobility group box 3	1.0558	2.0788
11715776_a_at	HSPB8	heat shock protein family B (small) member 8	1.0555	2.0784
11724882_x_at	TUFT1	tuftelin 1	1.0491	2.0692
11739989_a_at	CPPED1	calcineurin like phosphoesterase domain containing 1	1.0479	2.0675
11759752_at	GALNT5	polypeptide N-acetylgalactosaminyltransferase 5	1.0455	2.0641
11744402_a_at	BLZF1	basic leucine zipper nuclear factor 1	1.0447	2.0629
11729374_at	LOC100653049	keratin, type I cuticular Ha4	1.0440	2.0619
11759444_x_at	BAX	BCL2 associated X, apoptosis regulator	1.0429	2.0604
11723147_a_at	NAV3	neuron navigator 3	1.0404	2.0568
11740490_at	KRT75	keratin 75	1.0376	2.0528
11715588_x_at	MYL9	myosin light chain 9	1.0360	2.0505
11734039_x_at	FEZ1	fasciculation and elongation protein zeta 1	1.0321	2.0450
11755278_a_at	CYP2S1	cytochrome P450 family 2 subfamily S member 1	1.0317	2.0445
11746008_x_at	NEXN	nexilin F-actin binding protein	1.0281	2.0394

11718315_at	**SLC16A2**	***solute carrier family 16 member 2***	**1.0276**	**2.0387**
11724848_a_at	**DIXDC1**	***DIX domain containing 1***	**1.0224**	**2.0313**
11734975_a_at	**CLTB**	***clathrin light chain B***	**1.0219**	**2.0306**
11724407_s_at	**CCNE1**	***cyclin E1***	**1.0193**	**2.0269**
11757747_s_at	**LPIN1**	***lipin 1***	**1.0188**	**2.0262**
11744735_a_at	**TMEM200A**	***transmembrane protein 200A***	**1.0154**	**2.0215**
11715757_a_at	**RGS2**	***regulator of G-protein signaling 2***	**1.0104**	**2.0144**
11756577_a_at	**PEA15**	***phosphoprotein enriched in astrocytes 15***	**1.0098**	**2.0137**
11718506_at	**TFF3**	***trefoil factor 3***	**1.0076**	**2.0106**
11722531_a_at	**CALD1**	***caldesmon 1***	**1.0073**	**2.0101**
11733956_at	**SPRR2F**	***small proline rich protein 2F***	**1.0072**	**2.0100**
11728565_x_at	**FAM210A**	***family with sequence similarity 210 member A***	**1.0056**	**2.0078**
11762761_a_at	**ZNF667-AS1**	***ZNF667 antisense RNA 1 (head to head)***	**1.0046**	**2.0064**
11755290_s_at	**FBXL18**	***F-box and leucine rich repeat protein 18***	**1.0017**	**2.0023**

DOWNREGULATED mRNAs (234)

Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11727454_at	**SCGB1A1**	***secretoglobin family 1A member 1***	**-4.9040**	**0.0334**
11719657_a_at	**MMP9**	***matrix metallopeptidase 9***	**-3.3674**	**0.0969**
11744331_a_at	**LOXL2**	***Lysyl Oxidase Like 2***	**-3.3321**	**0.0993**
11726981_a_at	**CP**	***ceruloplasmin***	**-3.1950**	**0.1092**
11716490_a_at	**SERPINA3**	***serpin family A member 3***	**-3.1844**	**0.1100**
11721175_at	**RARRES1**	***retinoic acid receptor responder 1***	**-3.1792**	**0.1104**
11727440_at	**LOXL4**	***lysyl oxidase like 4***	**-3.0746**	**0.1187**
11716109_a_at	**PIGR**	***polymeric immunoglobulin receptor***	**-3.0012**	**0.1249**
11738511_at	**DEFB4B**	***defensin beta 4B***	**-2.6412**	**0.1603**
11747494_a_at	**DDIT4**	***aquaporin 3 (Gill blood group)***	**-2.6367**	**0.1608**
11749912_x_at	**IGFBP3**	***insulin like growth factor binding protein 3***	**-2.5873**	**0.1664**
11743168_at	**IDO1**	***indoleamine 2,3-dioxygenase 1***	**-2.5479**	**0.1710**
11716665_s_at	**GDF15**	***growth differentiation factor 15***	**-2.5437**	**0.1715**
11744030_a_at	**MMP7**	***matrix metallopeptidase 7***	**-2.5429**	**0.1716**
11727281_a_at	**MMP28**	***matrix metallopeptidase 28***	**-2.5146**	**0.1750**
11732350_a_at	**CCNA1**	***cyclin A1***	**-2.4548**	**0.1824**
11728771_a_at	**CLCA4**	***chloride channel accessory 4***	**-2.4189**	**0.1870**
11726124_at	**TCN1**	***transcobalamin 1***	**-2.3562**	**0.1953**
11726029_a_at	**UPK1B**	***uroplakin 1B***	**-2.2976**	**0.2034**
11753201_a_at	**SERPINB3**	***serpin family B member 3***	**-2.2842**	**0.2053**
11723069_at	**UBD**	***ubiquitin D***	**-2.2807**	**0.2058**
11717582_a_at	**RGCC**	***regulator of cell cycle***	**-2.2351**	**0.2124**
11731096_at	**WNT10A**	***Wnt family member 10A***	**-2.2351**	**0.2124**
11745189_a_at	**APOL1**	***apolipoprotein L1***	**-2.2122**	**0.2158**
11730374_a_at	**FYB**	***FYN binding protein***	**-2.1838**	**0.2201**
11727243_a_at	**WNT4**	***Wnt family member 4***	**-2.1578**	**0.2241**
11727698_a_at	**VMO1**	***vitelline membrane outer layer 1 homolog***	**-2.1539**	**0.2247**
11721895_x_at	**GAS1**	***growth arrest specific 1***	**-2.1028**	**0.2328**
11733687_s_at	**STRA6**	***stimulated by retinoic acid 6***	**-2.0728**	**0.2377**
11758013_s_at	**C8orf4**	***chromosome 8 open reading frame 4***	**-2.0571**	**0.2403**
11739761_a_at	**CLDN10**	***claudin 10***	**-2.0339**	**0.2442**
11749344_a_at	**HNRNPL**	***dehydrogenase/reductase 3***	**-1.9942**	**0.2510**
11754888_a_at	**ADSSL1**	***adenylosuccinate synthase like 1***	**-1.9641**	**0.2563**
11715781_a_at	**EEF2**	***eukaryotic translation elongation factor 2***	**-1.9440**	**0.2599**
11734618_a_at	**ALOX15B**	***arachidonate 15-lipoxygenase, type B***	**-1.9357**	**0.2614**

11749217_a_at	DHRS3	*transmembrane protease, serine 4*	-1.9040	0.2672
11724692_a_at	CAPN13	*calpain 13*	-1.9008	0.2678
11734658_s_at	FOS	*Fos proto-oncogene, AP-1 transcription factor subunit*	-1.8863	0.2705
11751288_a_at	HDLBP	*lysyl oxidase like 2*	-1.8810	0.2715
11716173_a_at	P4HB	*prolyl 4-hydroxylase subunit beta*	-1.8688	0.2738
11754526_a_at	PTGES	*prostaglandin E synthase*	-1.8578	0.2759
11723326_at	CA9	*carbonic anhydrase 9*	-1.8562	0.2762
11720856_a_at	HK1	*insulin receptor*	-1.8510	0.2772
11758952_at	AGR2	*anterior gradient 2, protein disulphide isomerase family member*	-1.8458	0.2782
11720020_x_at	RTEL1-TNFRSF6B	*RTEL1-TNFRSF6B Readthrough (NMD Candidate)*	-1.8232	0.2826
11719626_at	BIRC3	*retinol dehydrogenase 10 (all-trans)*	-1.8227	0.2827
11740782_a_at	RNF128	*ring finger protein 128, E3 ubiquitin protein ligase*	-1.8120	0.2848
11741519_s_at	CD14	*CD14 molecule*	-1.7999	0.2872
11720387_a_at	MRC2	*mannose receptor C type 2*	-1.7779	0.2916
11722838_a_at	GABRP	*gamma-aminobutyric acid type A receptor pi subunit*	-1.7750	0.2922
11742699_a_at	NAD	*complement C1r*	-1.7730	0.2926
11724720_a_at	GALNT12	*polypeptide N-acetylgalactosaminyltransferase 12*	-1.7700	0.2932
11732719_at	EREG	*epiregulin*	-1.7632	0.2946
11717909_at	IGFBP6	*insulin like growth factor binding protein 6*	-1.7529	0.2967
11742378_a_at	AKR1B15	*aldo-keto reductase family 1 member B15*	-1.7341	0.3006
11744255_a_at	ACADVL	*acyl-CoA dehydrogenase, very long chain*	-1.7259	0.3023
11724196_s_at	STC1	*stanniocalcin 1*	-1.7013	0.3075
11717917_a_at	WFDC2	*WAP four-disulfide core domain 2*	-1.6887	0.3102
11757793_s_at	TFPI	*tissue factor pathway inhibitor*	-1.6693	0.3144
11744556_x_at	CYP2B7P	*cytochrome P450 family 2 subfamily B member 7, pseudogene*	-1.6570	0.3171
11715393_a_at	C3	*complement C3*	-1.6543	0.3177
11747634_a_at	PYGB	*phosphorylase, glycogen; brain*	-1.6511	0.3184
11729263_x_at	SERPINB9	*serpin family B member 9*	-1.6425	0.3203
11718201_at	HEY1	*hes related family bHLH transcription factor with YRPW motif 1*	-1.6421	0.3204
11753661_a_at	ID1	*inhibitor of DNA binding 1, HLH protein*	-1.6398	0.3209
11719899_at	C11orf96	*chromosome 11 open reading frame 96*	-1.6340	0.3222
11732437_at	RPS29	*ras homolog family member V*	-1.6326	0.3225
11718295_a_at	SEMA4B	*semaphorin 4B*	-1.6228	0.3247
11748543_a_at	TXNIP	*thioredoxin interacting protein*	-1.5916	0.3318
11721456_x_at	SERPINA1	*serpin family A member 1*	-1.5808	0.3343
11719394_a_at	FBXO32	*F-box protein 32*	-1.5743	0.3358
11724219_x_at	GSTA1	*glutathione S-transferase alpha 1*	-1.5713	0.3365
11716401_a_at	SELENBP1	*selenium binding protein 1*	-1.5628	0.3385
11748046_a_at	SLC44A4	*solute carrier family 44 member 4*	-1.5589	0.3394
11726894_a_at	C2orf74	*interleukin 1 receptor associated kinase 3*	-1.5543	0.3405
11750536_x_at	CXCL5	*mucin 1, cell surface associated*	-1.5446	0.3428
11740890_a_at	FAM46A	*ADAM metallopeptidase domain 28*	-1.5312	0.3460
11758031_s_at	BHLHE41	*basic helix-loop-helix family member e41*	-1.5299	0.3463
11745725_a_at	RHOV	*granulin precursor*	-1.5191	0.3489
11731015_at	C2CD4A	*C2 calcium dependent domain containing 4A*	-1.5154	0.3498
11752302_a_at	LAMB3	*laminin subunit beta 3*	-1.5092	0.3513
11751459_x_at	LRG1	*leucine rich alpha-2-glycoprotein 1*	-1.5031	0.3528
11722116_a_at	RARB	*retinoic acid receptor beta*	-1.5002	0.3535
11723899_a_at	DHRS9	*dehydrogenase/reductase 9*	-1.4965	0.3544
11724832_at	STS	*Steroid Sulfatase (Microsomal), Isozyme S*	-1.4808	0.3583
11722054_a_at	CYP4X1	*cytochrome P450 family 4 subfamily X member 1*	-1.4779	0.3590
11732657_a_at	CYP26A1	*cytochrome P450 family 26 subfamily A member 1*	-1.4643	0.3624

11754119_a_at	**PLAU**	***plasminogen activator, urokinase***	**-1.4560**	**0.3645**
11754637_a_at	**SYTL1**	***synaptotagmin like 1***	**-1.4379**	**0.3691**
11747427_a_at	**SEC14L2**	***SEC14 like lipid binding 2***	**-1.4259**	**0.3722**
11725225_at	**CHP2**	***calcineurin like EF-hand protein 2***	**-1.4243**	**0.3726**
11741396_s_at	**C1R**	***inactive gamma-glutamyltranspeptidase 2-like***	**-1.4239**	**0.3727**
11719227_x_at	**KCNN4**	***potassium calcium-activated channel subfamily N member 4***	**-1.4204**	**0.3736**
11723785_s_at	**LIMCH1**	***LIM and calponin homology domains 1***	**-1.4185**	**0.3741**
11749978_a_at	**NDRG1**	***major vault protein***	**-1.4181**	**0.3742**
11722850_a_at	**AKT2**	***baculoviral IAP repeat containing 3***	**-1.4173**	**0.3744**
11719307_a_at	**RASSF4**	***Ras association domain family member 4***	**-1.4162**	**0.3747**
11721503_a_at	**CNN2**	***alpha 1,4-galactosyltransferase***	**-1.4051**	**0.3776**
11719171_a_at	**AKR1C1**	***aldo-keto reductase family 1 member C1***	**-1.4013**	**0.3786**
11752754_s_at	**ADAM15**	***syndecan 1***	**-1.3940**	**0.3805**
11724558_at	**GNA15**	***G protein subunit alpha 15***	**-1.3884**	**0.3820**
11758337_s_at	**CDC42EP4**	***adenosine deaminase***	**-1.3876**	**0.3822**
11726360_a_at	**ALDH3A1**	***aldehyde dehydrogenase 3 family member A1***	**-1.3827**	**0.3835**
11727132_at	**CPD**	***carboxypeptidase D***	**-1.3730**	**0.3861**
11717707_s_at	**VPS13D**	***vacuolar protein sorting 13 homolog D***	**-1.3633**	**0.3887**
11724828_at	**CCL20**	***C-C motif chemokine ligand 20***	**-1.3622**	**0.3890**
11726051_a_at	**FMO3**	***flavin containing monooxygenase 3***	**-1.3496**	**0.3924**
11748362_s_at	**ABCC3**	***ATP binding cassette subfamily C member 3***	**-1.3492**	**0.3925**
11753829_a_at	**TMPRSS4**	***plasminogen activator, tissue type***	**-1.3489**	**0.3926**
11731722_a_at	**ALDH3B1**	***aldehyde dehydrogenase 3 family member B1***	**-1.3485**	**0.3927**
11717860_a_at	**EGR1**	***early growth response 1***	**-1.3452**	**0.3936**
11725790_at	**DPYD**	***dihydropyrimidine dehydrogenase***	**-1.3441**	**0.3939**
11754057_x_at	**A4GALT**	***cellular retinoic acid binding protein 2***	**-1.3408**	**0.3948**
11719447_s_at	**GBP2**	***guanylate binding protein 2***	**-1.3404**	**0.3949**
11729571_a_at	**FAM83A**	***family with sequence similarity 83 member A***	**-1.3401**	**0.3950**
11756056_a_at	**SDC1**	***solute carrier family 2 member 1***	**-1.3383**	**0.3955**
11727590_a_at	**IL20RB**	***interleukin 20 receptor subunit beta***	**-1.3284**	**0.3982**
11723415_s_at	**SLC12A2**	***calponin 2***	**-1.3270**	**0.3986**
11752159_a_at	**SLC2A1**	***high density lipoprotein binding protein***	**-1.3237**	**0.3995**
11747365_a_at	**GANAB**	***microRNA 6890***	**-1.3212**	**0.4002**
11720002_at	**NRARP**	***NOTCH-regulated ankyrin repeat protein***	**-1.3187**	**0.4009**
11756274_a_at	**ALDH1L1**	***aldehyde dehydrogenase 1 family member L1***	**-1.3133**	**0.4024**
11750029_a_at	**EIF4H**	***eukaryotic translation initiation factor 4H***	**-1.3101**	**0.4033**
11718026_a_at	**NCOA7**	***nuclear receptor coactivator 7***	**-1.3069**	**0.4042**
11758315_s_at	**PER2**	***period circadian clock 2***	**-1.3058**	**0.4045**
11730245_a_at	**FMO2**	***flavin containing monooxygenase 2***	**-1.3015**	**0.4057**
11719658_a_at	**TF**	***transferrin***	**-1.3001**	**0.4061**
11728477_at	**CXCL3**	***C-X-C motif chemokine ligand 3***	**-1.2955**	**0.4074**
11755287_x_at	**KRT8**	***keratin 8***	**-1.2912**	**0.4086**
11731228_a_at	**DLK2**	***delta like non-canonical Notch ligand 2***	**-1.2895**	**0.4091**
11718481_s_at	**CFI**	***complement factor I***	**-1.2852**	**0.4103**
11742813_at	**SEMA6A**	***semaphorin 6A***	**-1.2842**	**0.4106**
11745927_x_at	**F11R**	***ADAM metallopeptidase domain 15***	**-1.2814**	**0.4114**
11728163_a_at	**HSD17B3**	***hydroxysteroid 17-beta dehydrogenase 3***	**-1.2719**	**0.4141**
11731283_a_at	**PEX6**	***kallikrein related peptidase 8***	**-1.2588**	**0.4179**
11746023_a_at	**PGD**	***phosphogluconate dehydrogenase***	**-1.2522**	**0.4198**
11723845_a_at	**DEFB1**	***defensin beta 1***	**-1.2488**	**0.4208**
11725022_a_at	**VILL**	***villin like***	**-1.2474**	**0.4212**
11742423_a_at	**STEAP2**	***STEAP2 metalloreductase***	**-1.2457**	**0.4217**

11722573_a_at	NBPF10	*endoplasmic reticulum aminopeptidase 2*	-1.2396	0.4235
11756588_a_at	ST6GALNAC1	*ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1*	-1.2385	0.4238
11758938_x_at	SAA2-SAA4	*SAA2-SAA4 readthrough*	-1.2365	0.4244
11752559_a_at	TRIM2	*plexin B2*	-1.2321	0.4257
11756236_a_at	FBLN1	*fibulin 1*	-1.2318	0.4258
11747507_x_at	IL20RA	*nucleosome assembly protein 1 like 4*	-1.2287	0.4267
11753619_s_at	EIF5AL1	*eukaryotic translation initiation factor 5A-like 1*	-1.2280	0.4269
11758221_s_at	ARRDC3	*arrestin domain containing 3*	-1.2260	0.4275
11746991_a_at	ATP1B1	*ATPase Na+/K+ transporting subunit beta 1*	-1.2196	0.4294
11749525_a_at	MUC1	*AKT serine/threonine kinase 2*	-1.2102	0.4322
11717823_s_at	TNFAIP2	*TNF alpha induced protein 2*	-1.2089	0.4326
11757383_a_at	CTSH	*cathepsin H*	-1.2032	0.4343
11759310_at	FAM171B	*family with sequence similarity 171 member B*	-1.2029	0.4344
11733474_at	SOX21	*SRY-box 21*	-1.2012	0.4349
11742379_x_at	AKR1B15	*aldo-keto reductase family 1 member B15*	-1.1996	0.4354
11719067_s_at	EIF2S3	*eukaryotic translation initiation factor 2 subunit gamma*	-1.1959	0.4365
11753431_x_at	MDM2	*N-myc downstream regulated 1*	-1.1923	0.4376
11740652_x_at	GRN	*neuroblastoma breakpoint family member 10*	-1.1857	0.4396
11724372_at	ANXA10	*annexin A10*	-1.1831	0.4404
11728717_at	CFB	*C-X-C motif chemokine ligand 5*	-1.1825	0.4406
11759905_a_at	RDH10	*exonuclease 3'-5' domain containing 3*	-1.1805	0.4412
11717464_at	NCOA7	*latexin*	-1.1792	0.4416
11732569_at	SLCO1B3	*solute carrier organic anion transporter family member 1B3*	-1.1763	0.4425
11755044_x_at	GSAP	*gamma-secretase activating protein*	-1.1694	0.4446
11725474_a_at	MAP3K5	*mitogen-activated protein kinase kinase kinase 5*	-1.1575	0.4483
11746500_x_at	ELF3	*glutathione S-transferase omega 2*	-1.1575	0.4483
11754091_s_at	SMAD3	*SMAD family member 3*	-1.1542	0.4493
11743959_a_at	LOX	*microRNA 6787*	-1.1510	0.4503
11727016_s_at	PAPPA	*pappalysin 1*	-1.1507	0.4504
11723777_a_at	SUMF2	*bromodomain containing 3*	-1.1504	0.4505
11753509_a_at	FOXC1	*forkhead box C1*	-1.1475	0.4514
11725584_at	HAS3	*hyaluronan synthase 3*	-1.1466	0.4517
11758028_s_at	FOXQ1	*forkhead box Q1*	-1.1431	0.4528
11715752_at	TSPAN7	*tetraspanin 7*	-1.1415	0.4533
11717137_s_at	EXD3	*CDC42 effector protein 4*	-1.1389	0.4541
11723225_a_at	CLDN11	*claudin 11*	-1.1329	0.4560
11739004_x_at	HDGF	*hepatoma-derived growth factor*	-1.1307	0.4567
11756312_a_at	SERPINF1	*serpin family F member 1*	-1.1288	0.4573
11722310_a_at	TMC4	*transmembrane channel like 4*	-1.1285	0.4574
11720281_a_at	EVA1C	*eva-1 homolog C*	-1.1275	0.4577
11730323_at	LOC102724197	*ribosomal protein S29*	-1.1253	0.4584
11744337_a_at	ERAP2	*glutamate-ammonia ligase*	-1.1247	0.4586
11752617_a_at	MIR6884	*microRNA 6884*	-1.1241	0.4588
11719176_a_at	GPRC5B	*G protein-coupled receptor class C group 5 member B*	-1.1147	0.4618
11720154_at	NRIP1	*nuclear receptor interacting protein 1*	-1.1131	0.4623
11757871_s_at	PBX1	*PBX homeobox 1*	-1.1128	0.4624
11715537_x_at	IDH2	*Isocitrate Dehydrogenase (NADP(+)) 2, Mitochondrial*	-1.1119	0.4627
11744508_a_at	CCDC146	*coiled-coil domain containing 146*	-1.1112	0.4629
11745260_x_at	KLK8	*solute carrier family 12 member 2*	-1.1081	0.4639
11749550_a_at	SCPEP1	*serine carboxypeptidase 1*	-1.1072	0.4642
11727918_s_at	MUC20	*mucin 20, cell surface associated*	-1.1050	0.4649
11732060_a_at	LEMD1	*LEM domain containing 1*	-1.1038	0.4653

11737184_at	**SAA2**	***serum amyloid A2***	**-1.1025**	**0.4657**
11733115_a_at	**CA2**	***carbonic anhydrase 2***	**-1.1010**	**0.4662**
11732565_at	**SLC6A14**	***solute carrier family 6 member 14***	**-1.0985**	**0.4670**
11716934_a_at	**CCDC80**	***coiled-coil domain containing 80***	**-1.0930**	**0.4688**
11723404_at	**PPARGC1A**	***PPARG coactivator 1 alpha***	**-1.0908**	**0.4695**
11748907_a_at	**AQP3**	***retinoic acid receptor responder 3***	**-1.0871**	**0.4707**
11755219_a_at	**THBD**	***thrombomodulin***	**-1.0865**	**0.4709**
11740610_at	**PLXNB2**	***zinc finger protein 121***	**-1.0859**	**0.4711**
11731565_x_at	**NAP1L4**	***MDM2 proto-oncogene***	**-1.0859**	**0.4711**
11757815_s_at	**METTL7A**	***methyltransferase like 7A***	**-1.0838**	**0.4718**
11723686_s_at	**LGALS3BP**	***family with sequence similarity 46 member A***	**-1.0816**	**0.4725**
11744866_x_at	**CEL**	***carboxyl ester lipase***	**-1.0798**	**0.4731**
11722861_s_at	**LOC100507412**	***tripartite motif containing 2***	**-1.0710**	**0.4760**
11728364_a_at	**INSR**	***interleukin 20 receptor subunit alpha***	**-1.0701**	**0.4763**
11715370_s_at	**ZNF121**	***galectin 3 binding protein***	**-1.0688**	**0.4767**
11727186_a_at	**WNT5A**	***Wnt family member 5A***	**-1.0673**	**0.4772**
11761021_at	**BRD3**	***uncharacterized LOC100507412***	**-1.0670**	**0.4773**
11724528_a_at	**GCNT3**	***Glucosaminyl (N-Acetyl) Transferase 3, Mucin Type***	**-1.0601**	**0.4796**
11743972_a_at	**GLUL**	***DNA damage inducible transcript 4***	**-1.0598**	**0.4797**
11743656_a_at	**ADA**	***hydroxyprostaglandin dehydrogenase 15-***	**-1.0514**	**0.4825**
11747729_s_at	**GSTO2**	***succinate dehydrogenase complex flavoprotein subunit A pseudogene 1***	**-1.0457**	**0.4844**
11729101_a_at	**AKR1C2**	***aldo-keto reductase family 1 member C2***	**-1.0454**	**0.4845**
11752103_a_at	**SDHAP1**	***hexokinase 1***	**-1.0419**	**0.4857**
11715788_a_at	**SLC40A1**	***solute carrier family 40 member 1***	**-1.0407**	**0.4861**
11717345_a_at	**FOSB**	***FosB proto-oncogene, AP-1 transcription factor subunit***	**-1.0398**	**0.4864**
11757030_at	**ECH1**	***enoyl-CoA hydratase 1***	**-1.0353**	**0.4879**
11726793_a_at	**LXN**	***integrin subunit beta 4***	**-1.0324**	**0.4889**
11738988_a_at	**CLTB**	***glucosidase II alpha subunit***	**-1.0321**	**0.4890**
11717594_s_at	**CRABP2**	***E74 like ETS transcription factor 3***	**-1.0315**	**0.4892**
11759322_at	**BCL6**	***B-cell CLL/lymphoma 6***	**-1.0265**	**0.4909**
11753332_s_at	**CRTAP**	***heterogeneous nuclear ribonucleoprotein L***	**-1.0250**	**0.4914**
11715411_a_at	**EPAS1**	***endothelial PAS domain protein 1***	**-1.0212**	**0.4927**
11724961_a_at	**SRGAP3**	***SLIT-ROBO Rho GTPase activating protein 3***	**-1.0165**	**0.4943**
11746897_a_at	**IRAK3**	***cartilage associated protein***	**-1.0162**	**0.4944**
11720461_a_at	**DLK2**	***F11 receptor***	**-1.0157**	**0.4946**
11732862_a_at	**ADAM28**	***chromosome 2 open reading frame 74***	**-1.0151**	**0.4948**
11743856_a_at	**CTHRC1**	***collagen triple helix repeat containing 1***	**-1.0142**	**0.4951**
11730632_a_at	**OCA2**	***OCA2 melanosomal transmembrane protein***	**-1.0142**	**0.4951**
11758995_at	**MVP**	***lysyl oxidase***	**-1.0128**	**0.4956**
11741690_x_at	**ITGB4**	***sulfatase modifying factor 2***	**-1.0110**	**0.4962**
11721661_a_at	**TBXAS1**	***thromboxane A synthase 1***	**-1.0072**	**0.4975**
11729998_a_at	**B3GNT7**	***UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7***	**-1.0067**	**0.4977**
11749004_a_at	**PLAT**	***peroxisomal biogenesis factor 6***	**-1.0003**	**0.4999**

***Diferentially expressed mRNAs were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ([Log_2Ratio > 1] or [Log_2Ratio < -1] for both upregulated or downregulated mRNAs, respectively), followed by multiple correction using a False Discovery Rate (FDR) threshold of 1% (p-adjusted value or q < 0.01).**

TABLE S6. Differentially expressed mRNAs in CRSwNP compared to control NM at day 14 of the air-liquid interface culture.*

UPREGULATED mRNAs (168)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11728715_at	CXCL5	*C-X-C motif chemokine ligand 5*	2.2982	4.9183
11739536_x_at	FN1	*fibronectin 1*	2.2927	4.8997
11751020_a_at	RHCG	*Rh family C glycoprotein*	2.2768	4.8459
11751426_a_at	IL33	*interleukin 33*	2.1677	4.4932
11717566_at	EMP1	*epithelial membrane protein 1*	1.9734	3.9270
11753830_a_at	MLLT11	*myeloid/lymphoid or mixed-lineage leukemia; translocated to, 11*	1.9130	3.7660
11722530_a_at	CALD1	*caldesmon 1*	1.8713	3.6585
11725703_a_at	KLK6	*kallikrein related peptidase 6*	1.8548	3.6169
11715915_a_at	CD44	*CD44 Molecule (Indian Blood Group)*	1.8189	3.5280
11729712_at	SPRR2A	*small proline rich protein 2A*	1.7846	3.4453
11715524_a_at	COTL1	*coactosin like F-actin binding protein 1*	1.7610	3.3894
11754593_x_at	TUBB3	*tubulin beta 3 class III*	1.7242	3.3040
11721092_a_at	THBS1	*thrombospondin 1*	1.7099	3.2713
11747800_a_at	HIF1A	*hypoxia inducible factor 1 alpha subunit*	1.7066	3.2638
11736978_at	PADI3	*peptidyl arginine deiminase 3*	1.6961	3.2402
11753255_a_at	KLK7	*kallikrein related peptidase 7*	1.6866	3.2190
11721307_at	PHLDA1	*pleckstrin homology like domain family A member 1*	1.6658	3.1729
11717355_a_at	FEZ1	*fasciculation and elongation protein zeta 1*	1.6502	3.1387
11733957_x_at	SPRR2F	*small proline rich protein 2F*	1.6352	3.1064
11750242_a_at	KLK13	*kallikrein related peptidase 13*	1.6229	3.0799
11720448_at	SOX9	*SRY-box 9*	1.6070	3.0461
11729265_at	SPRR2D	*small proline rich protein 2D*	1.6070	3.0461
11715893_s_at	IFI27	*interferon alpha inducible protein 27*	1.5982	3.0276
11735693_x_at	SPRR2E	*small proline rich protein 2E*	1.5977	3.0265
11763367_at	NABP1	*nucleic acid binding protein 1*	1.5923	3.0154
11716062_a_at	TNC	*tenascin C*	1.5920	3.0147
11731925_at	CRCT1	*cysteine rich C-terminal 1*	1.5811	2.9920
11746433_a_at	CLDN1	*claudin 1*	1.5804	2.9905
11748703_a_at	C1D	*C1D nuclear receptor corepressor*	1.5661	2.9611
11750175_s_at	SVILP1	*supervillin pseudogene 1*	1.5594	2.9474
11729417_at	KRT24	*keratin 24*	1.5549	2.9381
11715716_at	MSN	*moesin*	1.5375	2.9030
11717481_s_at	FKBP10	*FK506 binding protein 10*	1.5079	2.8439
11743721_at	LGALS1	*galectin 1*	1.5009	2.8302
11737184_at	SAA2	*serum amyloid A2*	1.4958	2.8203
11751946_a_at	ARHGAP21	*Rho GTPase activating protein 21*	1.4723	2.7746
11744068_x_at	APOE	*apolipoprotein E*	1.4387	2.7108
11750102_x_at	ALDH1A3	*aldehyde dehydrogenase 1 family member A3*	1.4361	2.7059
11731394_a_at	VIM	*vimentin*	1.4205	2.6767

11716241_x_at	WTH3DI	*RAB6C-like*	1.4193	2.6745
11720972_at	TOP2A	*topoisomerase DNA II alpha*	1.4168	2.6700
11734993_at	SKI	*SKI proto-oncogene*	1.4159	2.6682
11721256_a_at	CCND1	*cyclin D1*	1.4130	2.6629
11747399_x_at	PLAT	*plasminogen activator, tissue type*	1.4058	2.6496
11749650_x_at	A2ML1	*alpha-2-macroglobulin like 1*	1.4040	2.6464
11715491_s_at	FSCN1	*fascin actin-bundling protein 1*	1.4014	2.6415
11746283_s_at	KRTAP2-3	*keratin associated protein 2-3*	1.3965	2.6327
11715306_s_at	AREG	*amphiregulin*	1.3777	2.5986
11746856_a_at	SERPINE1	*serpin family E member 1*	1.3776	2.5984
11722327_at	PGBD5	*piggyBac transposable element derived 5*	1.3711	2.5867
11748463_a_at	LOC100505984	*uncharacterized LOC100505984*	1.3685	2.5821
11748025_s_at	GJB2	*gap junction protein beta 2*	1.3651	2.5760
11719197_at	CCND2	*cyclin D2*	1.3612	2.5690
11726023_a_at	EDN1	*endothelin 1*	1.3566	2.5608
11720527_at	LTBP2	*latent transforming growth factor beta binding protein 2*	1.3563	2.5602
11720247_a_at	CEP55	*centrosomal protein 55*	1.3396	2.5308
11734956_a_at	CNTNAP2	*contactin associated protein-like 2*	1.3296	2.5133
11728810_a_at	ECHDC3	*enoyl-CoA hydratase domain containing 3*	1.3252	2.5056
11739856_s_at	TENM2	*teneurin transmembrane protein 2*	1.3233	2.5023
11720823_at	JAG1	*jagged 1*	1.3226	2.5012
11752877_x_at	TUBB	*tubulin beta class I*	1.3149	2.4879
11730096_a_at	BCL2A1	*BCL2 related protein A1*	1.3119	2.4827
11723939_a_at	CCNB1	*cyclin B1*	1.3099	2.4792
11750598_s_at	TPX2	*TPX2, microtubule nucleation factor*	1.3019	2.4656
11732997_a_at	MCM6	*minichromosome maintenance complex component 6*	1.2918	2.4484
11740744_x_at	TPM2	*tropomyosin 2 (beta)*	1.2915	2.4478
11733442_x_at	SAA1	*serum amyloid A1*	1.2822	2.4321
11747820_x_at	UPP1	*uridine phosphorylase 1*	1.2816	2.4311
11732719_at	EREG	*epiregulin*	1.2545	2.3859
11756826_a_at	ENTPD3	*ectonucleoside triphosphate diphosphohydrolase 3*	1.2507	2.3796
11758938_x_at	SAA2-SAA4	*SAA2-SAA4 readthrough*	1.2457	2.3713
11731653_a_at	IVL	*involucrin*	1.2441	2.3687
11718904_s_at	FILIP1L	*filamin A interacting protein 1 like*	1.2439	2.3683
11758619_s_at	LIF	*leukemia inhibitory factor*	1.2431	2.3671
11744047_a_at	MAP1B	*microtubule associated protein 1B*	1.2403	2.3624
11722572_at	CCNA2	*cyclin A2*	1.2395	2.3612
11740332_a_at	ATP2A2	*ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2*	1.2368	2.3567
11727658_s_at	KLK10	*kallikrein related peptidase 10*	1.2362	2.3557
11723298_s_at	AKAP2	*A-kinase anchoring protein 2*	1.2328	2.3502
11745377_x_at	PTRF	*polymerase I and transcript release factor*	1.2253	2.3380
11743969_s_at	ACTN1	*actinin alpha 1*	1.2247	2.3371
11721840_at	GLIPR1	*GLI pathogenesis related 1*	1.2159	2.3228
11727016_s_	PAPPA	*pappalysin 1*	1.2152	2.3217

at				
11762761_a_at	**ZNF667-AS1**	***ZNF667 antisense RNA 1 (head to head)***	**1.2113**	**2.3154**
11717068_a_at	**DIP2B**	***disco interacting protein 2 homolog B***	**1.2075**	**2.3093**
11755200_a_at	**DCBLD2**	***discoidin, CUB and LCCL domain containing 2***	**1.2062**	**2.3073**
11745464_x_at	**CDKN3**	***cyclin dependent kinase inhibitor 3***	**1.2036**	**2.3031**
11723104_at	**GNB4**	***G protein subunit beta 4***	**1.2018**	**2.3003**
11751805_a_at	**TYMS**	***thymidylate synthetase***	**1.2006**	**2.2984**
11723616_a_at	**PLTP**	***phospholipid transfer protein***	**1.1969**	**2.2925**
11753626_a_at	**CDA**	***cytidine deaminase***	**1.1947**	**2.2889**
11723983_at	**KRT6B**	***keratin 6B***	**1.1944**	**2.2885**
11728497_s_at	**SVIL**	***supervillin***	**1.1920**	**2.2847**
11724459_x_at	**MIR6756**	***microRNA 6756***	**1.1736**	**2.2557**
11748355_a_at	**SLC16A1**	***solute carrier family 16 member 1***	**1.1728**	**2.2545**
11755614_s_at	**FERMT1**	***fermitin family member 1***	**1.1701**	**2.2502**
11746046_a_at	**UBQLN2**	***ubiquilin 2***	**1.1688**	**2.2482**
11753008_a_at	**IL36G**	***interleukin 36, gamma***	**1.1677**	**2.2465**
11724328_a_at	**UBE2C**	***ubiquitin conjugating enzyme E2 C***	**1.1521**	**2.2223**
11753704_a_at	**STMN1**	***stathmin 1***	**1.1515**	**2.2214**
11733000_at	**ICAM1**	***intercellular adhesion molecule 1***	**1.1482**	**2.2163**
11729132_a_at	**PSME3**	***proteasome activator subunit 3***	**1.1476**	**2.2154**
11723069_at	**UBD**	***ubiquitin D***	**1.1470**	**2.2146**
11749023_a_at	**SLC16A4**	***solute carrier family 16 member 4***	**1.1442**	**2.2103**
11738996_a_at	**DPYSL2**	***dihydropyrimidinase like 2***	**1.1418**	**2.2065**
11730373_a_at	**FYB**	***FYN binding protein***	**1.1396**	**2.2032**
11752284_x_at	**ALOX15B**	***arachidonate 15-lipoxygenase, type B***	**1.1369**	**2.1991**
11747139_a_at	**RASA1**	***RAS p21 protein activator 1***	**1.1368**	**2.1990**
11725945_x_at	**TINAGL1**	***tubulointerstitial nephritis antigen like 1***	**1.1367**	**2.1988**
11740423_a_at	**PRKDC**	***protein kinase, DNA-activated, catalytic polypeptide***	**1.1367**	**2.1987**
11727782_a_at	**TPM4**	***tropomyosin 4***	**1.1364**	**2.1983**
11716495_a_at	**MAP4**	***microtubule associated protein 4***	**1.1363**	**2.1982**
11744103_at	**TLCD1**	***TLC domain containing 1***	**1.1344**	**2.1952**
11746368_a_at	**FAM222B**	***family with sequence similarity 222 member B***	**1.1343**	**2.1951**
11745219_a_at	**R3HDM1**	***R3H domain containing 1***	**1.1313**	**2.1905**
11716638_s_at	**COL4A1**	***collagen type IV alpha 1 chain***	**1.1307**	**2.1896**
11716609_a_at	**CRABP2**	***cellular retinoic acid binding protein 2***	**1.1256**	**2.1819**
11744263_s_at	**RAC2**	***Ras-Related C3 Botulinum Toxin Substrate 2 (Rho Family, Small GTP Binding Protein Rac2)***	**1.1255**	**2.1817**
11717812_a_at	**KIF3C**	***kinesin family member 3C***	**1.1243**	**2.1800**
11724478_s_at	**FOSL1**	***FOS like 1, AP-1 transcription factor subunit***	**1.1212**	**2.1753**
11753825_x_at	**FKBP1A**	***FK506 binding protein 1A***	**1.1191**	**2.1721**
11726909_at	**ZBED2**	***zinc finger BED-type containing 2***	**1.1187**	**2.1715**
11752670_a_at	**MIR1908**	***microRNA 1908***	**1.1163**	**2.1679**
11742184_a_at	**LAMA3**	***laminin subunit alpha 3***	**1.1150**	**2.1659**
11743965_s_at	**CERCAM**	***cerebral endothelial cell adhesion molecule***	**1.1094**	**2.1575**

11733997_a_at	SERPINB7	*serpin family B member 7*	1.1062	2.1528
11730194_a_at	SEC14L2	*SEC14 like lipid binding 2*	1.1035	2.1488
11723882_x_at	CECR1	*cat eye syndrome chromosome region, candidate 1*	1.0989	2.1419
11738511_at	DEFB4B	*defensin beta 4B*	1.0988	2.1417
11740957_x_at	SLC2A6	*solute carrier family 2 member 6*	1.0966	2.1385
11723192_a_at	UHRF1	*ubiquitin like with PHD and ring finger domains 1*	1.0965	2.1383
11753549_a_at	CMTM3	*CKLF like MARVEL transmembrane domain containing 3*	1.0955	2.1368
11743496_a_at	MIR6845	*microRNA 6845*	1.0947	2.1357
11715615_at	BTG2	*BTG anti-proliferation factor 2*	1.0942	2.1349
11758125_s_at	DEPDC1B	*DEP domain containing 1B*	1.0916	2.1311
11741680_a_at	SERPINE2	*serpin family E member 2*	1.0915	2.1310
11725832_s_at	OTUB2	*OTU deubiquitinase, ubiquitin aldehyde binding 2*	1.0913	2.1306
11722839_at	LYAR	*Ly1 antibody reactive*	1.0841	2.1201
11725155_at	FJX1	*four jointed box 1*	1.0795	2.1133
11755955_a_at	FAP	*fibroblast activation protein alpha*	1.0794	2.1131
11715316_x_at	HLA-C	*major histocompatibility complex, class I, C*	1.0776	2.1105
11728135_at	NIPAL4	*NIPA like domain containing 4*	1.0762	2.1085
11727454_at	SCGB1A1	*secretoglobin family 1A member 1*	1.0744	2.1059
11741032_a_at	HMMR	*hyaluronan mediated motility receptor*	1.0687	2.0976
11723274_a_at	SLC35F2	*solute carrier family 35 member F2*	1.0672	2.0954
11731602_at	TMEM154	*transmembrane protein 154*	1.0661	2.0938
11731101_at	MELTF	*melanotransferrin*	1.0636	2.0901
11724562_x_at	RHOF	*ras homolog family member F, filopodia associated*	1.0592	2.0838
11716358_s_at	PRC1	*protein regulator of cytokinesis 1*	1.0590	2.0835
11726689_a_at	STAT1	*signal transducer and activator of transcription 1*	1.0571	2.0807
11727503_at	SOX7	*SRY-box 7*	1.0533	2.0753
11716132_a_at	FSTL3	*follistatin like 3*	1.0506	2.0714
11719852_s_at	SEPT10	*septin 10*	1.0431	2.0606
11723829_s_at	ANO1	*anoctamin 1*	1.0424	2.0596
11728719_a_at	LTBP1	*latent transforming growth factor beta binding protein 1*	1.0389	2.0546
11756412_a_at	NT5DC2	*5'-nucleotidase domain containing 2*	1.0365	2.0513
11758136_s_at	SLC35G2	*solute carrier family 35 member G2*	1.0329	2.0461
11728024_a_at	KLK5	*kallikrein related peptidase 5*	1.0322	2.0452
11757698_s_at	MIG7	*mig-7*	1.0317	2.0444
11715919_a_at	SH3BGRL3	*SH3 domain binding glutamate rich protein like 3*	1.0250	2.0349
11716126_x_at	ZYX	*zyxin*	1.0219	2.0306
11755252_a_at	AMIGO2	*adhesion molecule with Ig like domain 2*	1.0218	2.0304
11754360_a_at	RRM2	*ribonucleotide reductase regulatory subunit M2*	1.0193	2.0269
11754242_a_at	TJP1	*tight junction protein 1*	1.0186	2.0260
11715452_s_at	COL4A2	*collagen type IV alpha 2 chain*	1.0124	2.0173
11756820_a_at	IFIT1	*interferon induced protein with tetratricopeptide repeats 1*	1.0101	2.0141
11735833_a_at	CEMIP	*cell migration inducing hyaluronan binding protein*	1.0072	2.0100
11730349_a_at	TLDC1	*TBC/LysM-associated domain containing 1*	1.0014	2.0019

DOWNREGULATED mRNAs (219)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11737634_a_at	UGT2A1	*UDP glucuronosyltransferase family 2 member A1 complex locus*	-2.6215	0.1625
11730779_at	ADH1C	*Alcohol Dehydrogenase 1C (Class I), Gamma Polypeptide*	-2.6100	0.1638
11725562_at	C20orf85	*chromosome 20 open reading frame 85*	-2.5986	0.1651
11720349_at	ROPN1L	*rhophilin associated tail protein 1 like*	-2.5864	0.1665
11723524_at	AGR3	*anterior gradient 3, protein disulphide isomerase family member*	-2.4812	0.1791
11734525_a_at	C11orf88	*chromosome 11 open reading frame 88*	-2.3585	0.1950
11722994_s_at	ADH1A	*Alcohol Dehydrogenase 1A (Class I), Alpha Polypeptide*	-2.3540	0.1956
11742251_s_at	CYP2A6	*cytochrome P450 family 2 subfamily A member 6*	-2.2440	0.2111
11733934_a_at	PIFO	*primary cilia formation*	-2.2338	0.2126
11729439_a_at	CAPSL	*calcyphosine like*	-2.2102	0.2161
11763989_at	LOC101927057	*uncharacterized LOC101927057*	-2.1571	0.2242
11724219_x_at	GSTA1	*glutathione S-transferase alpha 1*	-2.1297	0.2285
11716489_a_at	STATH	*statherin*	-2.0740	0.2375
11754354_s_at	PROM1	*prominin 1*	-2.0698	0.2382
11751078_s_at	CYP2F1	*cytochrome P450 family 2 subfamily F member 1*	-2.0463	0.2421
11716112_at	PIGR	*polymeric immunoglobulin receptor*	-2.0368	0.2437
11760213_a_at	TMC5	*transmembrane channel like 5*	-2.0233	0.2460
11744240_at	SNTN	*sentan, cilia apical structure protein*	-2.0186	0.2468
11732910_x_at	FAM183A	*family with sequence similarity 183 member A*	-2.0052	0.2491
11720372_at	TESC	*tescalcin*	-1.9925	0.2513
11726303_a_at	MFSD4A	*major facilitator superfamily domain containing 4A*	-1.9834	0.2529
11758196_s_at	IGFBP5	*insulin like growth factor binding protein 5*	-1.9624	0.2566
11729297_at	MMP13	*matrix metallopeptidase 13*	-1.8997	0.2680
11757612_a_at	ASRGL1	*asparaginase like 1*	-1.8943	0.2690
11719767_a_at	TPPP3	*tubulin polymerization promoting protein family member 3*	-1.8842	0.2709
11720917_a_at	BPIFB1	*BPI fold containing family B member 1*	-1.8804	0.2716
11732833_a_at	C9orf135	*chromosome 9 open reading frame 135*	-1.8778	0.2721
11726576_x_at	CYP2A6	*cytochrome P450 family 2 subfamily A member 6*	-1.8778	0.2721
11756097_s_at	ZMYND10	*zinc finger MYND-type containing 10*	-1.8720	0.2732
11727734_at	CFAP126	*cilia and flagella associated protein 126*	-1.8515	0.2771
11719818_at	PIP	*prolactin induced protein*	-1.8505	0.2773
11727921_a_at	TEKT1	*tektin 1*	-1.8181	0.2836
11730044_a_at	C9orf24	*chromosome 9 open reading frame 24*	-1.8171	0.2838
11747494_a_at	DDIT4	*aquaporin 3 (Gill blood group)*	-1.8145	0.2843
11721887_a_at	CRYM	*crystallin mu*	-1.7824	0.2907
11746662_a_at	ARMC3	*armadillo repeat containing 3*	-1.7720	0.2928
11729920_at	BBOF1	*basal body orientation factor 1*	-1.7466	0.2980
11737141_a_at	RSPH1	*radial spoke head 1 homolog*	-1.7456	0.2982
11751769_a_at	LOC100287413	*uncharacterized LOC100287413*	-1.7293	0.3016
11722863_at	SCGB2A1	*secretoglobin family 2A member 1*	-1.7293	0.3016
11718790_at	HES6	*hes family bHLH transcription factor 6*	-1.7240	0.3027
11743595_at	C5orf49	*chromosome 5 open reading frame 49*	-1.7122	0.3052

11740580_at	**ASAH1**	***N-acylsphingosine amidohydrolase 1***	**-1.7032**	**0.3071**
11722157_a_at	**CCNO**	***cyclin O***	**-1.6892**	**0.3101**
11731779_a_at	**C11orf70**	***chromosome 11 open reading frame 70***	**-1.6762**	**0.3129**
11752737_a_at	**CLEC7A**	***C-type lectin domain family 7 member A***	**-1.6702**	**0.3142**
11758272_at	**SLC34A2**	***solute carrier family 34 member 2***	**-1.6615**	**0.3161**
11733359_a_at	**CFAP45**	***cilia and flagella associated protein 45***	**-1.6520**	**0.3182**
11719321_a_at	**DNALI1**	***dynein axonemal light intermediate chain 1***	**-1.6362**	**0.3217**
11723961_s_at	**PTN**	***pleiotrophin***	**-1.6349**	**0.3220**
11756495_a_at	**SPAG6**	***sperm associated antigen 6***	**-1.6344**	**0.3221**
11724085_at	**DAPL1**	***death associated protein like 1***	**-1.6171**	**0.3260**
11756881_a_at	**LOC101926951**	***uncharacterized LOC101926951***	**-1.6069**	**0.3283**
11755403_a_at	**CHST9**	***carbohydrate sulfotransferase 9***	**-1.5968**	**0.3306**
11715994_x_at	**ID2**	***inhibitor of DNA binding 2, HLH protein***	**-1.5782**	**0.3349**
11746749_a_at	**ZBBX**	***zinc finger B-box domain containing***	**-1.5641**	**0.3382**
11753232_a_at	**NDRG1**	***N-myc downstream regulated 1***	**-1.5391**	**0.3441**
11726029_a_at	**UPK1B**	***uroplakin 1B***	**-1.5249**	**0.3475**
11724109_a_at	**C9orf116**	***chromosome 9 open reading frame 116***	**-1.4953**	**0.3547**
11756793_a_at	**VNN2**	***vanin 2***	**-1.4892**	**0.3562**
11756684_a_at	**DYNLRB2**	***dynein light chain roadblock-type 2***	**-1.4739**	**0.3600**
11717820_a_at	**SLC4A4**	***solute carrier family 4 member 4***	**-1.4699**	**0.3610**
11752898_a_at	**PPIL6**	***peptidylprolyl isomerase like 6***	**-1.4635**	**0.3626**
11721619_at	**FOXJ1**	***forkhead box J1***	**-1.4584**	**0.3639**
11721704_a_at	**CRIP1**	***cysteine rich protein 1***	**-1.4568**	**0.3643**
11757882_x_at	**GSTA1**	***glutathione S-transferase alpha 1***	**-1.4469**	**0.3668**
11759809_at	**PLEKHS1**	***pleckstrin homology domain containing S1***	**-1.4418**	**0.3681**
11719538_at	**BBOX1**	***gamma-butyrobetaine hydroxylase 1***	**-1.4297**	**0.3712**
11756274_a_at	**ALDH1L1**	***aldehyde dehydrogenase 1 family member L1***	**-1.4239**	**0.3727**
11739916_a_at	**SERPINB11**	***Serpin Family B Member 11 (Gene/Pseudogene)***	**-1.4193**	**0.3739**
11735674_a_at	**AKAP14**	***A-kinase anchoring protein 14***	**-1.4173**	**0.3744**
11731606_at	**SCIN**	***scinderin***	**-1.4013**	**0.3786**
11745736_a_at	**ACADVL**	***acyl-CoA dehydrogenase, very long chain***	**-1.3963**	**0.3799**
11715343_at	**MUC16**	***mucin 16, cell surface associated***	**-1.3933**	**0.3807**
11750860_a_at	**CMAHP**	***cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene***	**-1.3861**	**0.3826**
11716308_s_at	**CYBRD1**	***cytochrome b reductase 1***	**-1.3842**	**0.3831**
11757570_s_at	**PRR15**	***proline rich 15***	**-1.3835**	**0.3833**
11754650_a_at	**ATP10B**	***ATPase Phospholipid Transporting 10B (Putative)***	**-1.3767**	**0.3851**
11722573_a_at	**NBPF10**	***endoplasmic reticulum aminopeptidase 2***	**-1.3759**	**0.3853**
11725158_at	**STEAP1**	***STEAP family member 1***	**-1.3692**	**0.3871**
11721318_at	**PARM1**	***prostate androgen-regulated mucin-like protein 1***	**-1.3651**	**0.3882**
11750836_a_at	**EFHC1**	***EF-hand domain containing 1***	**-1.3596**	**0.3897**
11724372_at	**ANXA10**	***annexin A10***	**-1.3540**	**0.3912**
11726535_a_at	**MORN5**	***MORN repeat containing 5***	**-1.3529**	**0.3915**
11749978_a_at	**NDRG1**	***major vault protein***	**-1.3514**	**0.3919**
11755287_x_at	**KRT8**	***keratin 8***	**-1.3448**	**0.3937**

11742730_a_at	CAPS	*calcyphosine*	-1.3445	0.3938
11756356_a_at	FAM81B	*family with sequence similarity 81 member B*	-1.3292	0.3980
11724692_a_at	CAPN13	*calpain 13*	-1.3263	0.3988
11745465_x_at	METTL7A	*methyltransferase like 7A*	-1.3219	0.4000
11726981_a_at	CP	*ceruloplasmin*	-1.3201	0.4005
11720993_at	SOX2	*SRY-box 2*	-1.3183	0.4010
11757645_s_at	FIBIN	*Fin Bud Initiation Factor Homolog (Zebrafish)*	-1.3172	0.4013
11730944_a_at	CCDC65	*coiled-coil domain containing 65*	-1.3140	0.4022
11758474_s_at	COLCA1	*colorectal cancer associated 1*	-1.3101	0.4033
11758225_s_at	IQGAP2	*IQ motif containing GTPase activating protein 2*	-1.3061	0.4044
11737088_at	TLL1	*tolloid like 1*	-1.3012	0.4058
11720088_x_at	NUCB2	*nucleobindin 2*	-1.2948	0.4076
11744484_s_at	HLA-DRA	*major histocompatibility complex, class II, DR alpha*	-1.2824	0.4111
11743003_a_at	CYP4B1	*cytochrome P450 family 4 subfamily B member 1*	-1.2740	0.4135
11753810_a_at	CCL5	*C-C motif chemokine ligand 5*	-1.2737	0.4136
11734176_a_at	CFAP52	*cilia and flagella associated protein 52*	-1.2681	0.4152
11727983_a_at	LRRC46	*leucine rich repeat containing 46*	-1.2647	0.4162
11738049_a_at	ATP2C2	*ATPase secretory pathway Ca2+ transporting 2*	-1.2608	0.4173
11755588_a_at	SLC5A5	*solute carrier family 5 member 5*	-1.2605	0.4174
11755226_s_at	KLHDC7A	*kelch domain containing 7A*	-1.2557	0.4188
11715788_a_at	SLC40A1	*solute carrier family 40 member 1*	-1.2550	0.4190
11729453_s_at	CYP2B6	*cytochrome P450 family 2 subfamily B member 6*	-1.2467	0.4214
11724875_a_at	CD36	*CD36 molecule*	-1.2450	0.4219
11732241_s_at	SLITRK6	*SLIT and NTRK like family member 6*	-1.2440	0.4222
11742423_a_at	STEAP2	*STEAP2 metalloreductase*	-1.2368	0.4243
11745292_a_at	C22orf15	*chromosome 22 open reading frame 15*	-1.2362	0.4245
11721895_x_at	GAS1	*growth arrest specific 1*	-1.2362	0.4245
11723246_s_at	SFRP1	*secreted frizzled related protein 1*	-1.2358	0.4246
11735084_s_at	FREM2	*FRAS1 related extracellular matrix protein 2*	-1.2328	0.4255
11758995_at	MVP	*lysyl oxidase*	-1.2267	0.4273
11732678_a_at	DNAH12	*dynein axonemal heavy chain 12*	-1.2253	0.4277
11718723_at	ARRDC3	*arrestin domain containing 3*	-1.2203	0.4292
11757071_s_at	STEAP1B	*STEAP family member 1B*	-1.2116	0.4318
11740868_a_at	LDLRAD1	*low density lipoprotein receptor class A domain containing 1*	-1.2112	0.4319
11728727_at	CEACAM7	*carcinoembryonic antigen related cell adhesion molecule 7*	-1.2092	0.4325
11733474_at	SOX21	*SRY-box 21*	-1.2066	0.4333
11751459_x_at	LRG1	*leucine rich alpha-2-glycoprotein 1*	-1.2029	0.4344
11715708_s_at	MB	*myoglobin*	-1.2029	0.4344
11744581_a_at	KHDRBS3	*KH RNA binding domain containing, signal transduction associated 3*	-1.2026	0.4345
11741477_a_at	NPHP1	*nephrocystin 1*	-1.2026	0.4345
11731286_at	EDN2	*endothelin 2*	-1.2002	0.4352
11720901_a_at	GRAMD1C	*GRAM domain containing 1C*	-1.1989	0.4356
11735637_a_at	LRRC23	*leucine rich repeat containing 23*	-1.1966	0.4363

11744556_x_at	CYP2B7P	*cytochrome P450 family 2 subfamily B member 7, pseudogene*	-1.1963	0.4364
11735488_a_at	CASC1	*cancer susceptibility candidate 1*	-1.1923	0.4376
11726916_at	SLCO4C1	*solute carrier organic anion transporter family member 4C1*	-1.1897	0.4384
11720243_x_at	TCN2	*transcobalamin 2*	-1.1890	0.4386
11723441_a_at	EPHA4	*EPH receptor A4*	-1.1871	0.4392
11716173_a_at	P4HB	*prolyl 4-hydroxylase subunit beta*	-1.1811	0.4410
11734842_at	MPHOSPH8	*M-phase phosphoprotein 8*	-1.1805	0.4412
11721687_at	ID4	*inhibitor of DNA binding 4, HLH protein*	-1.1805	0.4412
11737857_a_at	DNAAF1	*dynein axonemal assembly factor 1*	-1.1736	0.4433
11739725_a_at	TC2N	*tandem C2 domains, nuclear*	-1.1672	0.4453
11752060_x_at	ERN2	*endoplasmic reticulum to nucleus signaling 2*	-1.1600	0.4475
11723516_a_at	CAB39L	*calcium binding protein 39 like*	-1.1562	0.4487
11721503_a_at	CNN2	*alpha 1,4-galactosyltransferase*	-1.1427	0.4529
11725494_at	RSPH9	*radial spoke head 9 homolog*	-1.1421	0.4531
11729061_a_at	DNAH5	*dynein axonemal heavy chain 5*	-1.1364	0.4549
11729137_at	UGT2B7	*UDP glucuronosyltransferase family 2 member B7*	-1.1361	0.4550
11716401_a_at	SELENBP1	*selenium binding protein 1*	-1.1338	0.4557
11721993_at	SLC6A6	*solute carrier family 6 member 6*	-1.1329	0.4560
11720031_a_at	TRIM29	*tripartite motif containing 29*	-1.1316	0.4564
11730245_a_at	FMO2	*flavin containing monooxygenase 2*	-1.1307	0.4567
11755748_s_at	PLAC8	*placenta specific 8*	-1.1282	0.4575
11744064_at	MUC5B	*mucin 5B, oligomeric mucus/gel-forming*	-1.1266	0.4580
11721917_a_at	ANKRD37	*ankyrin repeat domain 37*	-1.1244	0.4587
11721898_at	FAM3D	*family with sequence similarity 3 member D*	-1.1125	0.4625
11730469_s_at	LMO2	*LIM domain only 2*	-1.1115	0.4628
11743943_a_at	RSPH4A	*radial spoke head 4 homolog A*	-1.1090	0.4636
11715781_a_at	EEF2	*eukaryotic translation elongation factor 2*	-1.1081	0.4639
11730485_at	CAPNS2	*calpain small subunit 2*	-1.1059	0.4646
11745725_a_at	RHOV	*granulin precursor*	-1.1047	0.4650
11754879_a_at	SDR16C5	*short chain dehydrogenase/reductase family 16C, member 5*	-1.1022	0.4658
11728753_at	ADH7	*Alcohol Dehydrogenase 7 (Class IV), Mu Or Sigma Polypeptide*	-1.0991	0.4668
11750939_a_at	SLC39A7	*solute carrier family 39 member 7*	-1.0970	0.4675
11745361_a_at	CRNDE	*Colorectal Neoplasia Differentially Expressed (Non-Protein Coding)*	-1.0926	0.4689
11754806_s_at	CADPS2	*calcium dependent secretion activator 2*	-1.0905	0.4696
11724940_x_at	CDHR3	*cadherin related family member 3*	-1.0871	0.4707
11742103_a_at	TLE2	*transducin like enhancer of split 2*	-1.0853	0.4713
11749355_a_at	CFB	*complement factor B*	-1.0844	0.4716
11748328_s_at	KRT16	*keratin 16*	-1.0838	0.4718
11721614_a_at	KIT	*KIT proto-oncogene receptor tyrosine kinase*	-1.0801	0.4730
11742224_a_at	CDC20B	*cell division cycle 20B*	-1.0798	0.4731
11732569_at	SLCO1B3	*solute carrier organic anion transporter family member 1B3*	-1.0798	0.4731
11749525_a_at	MUC1	*AKT serine/threonine kinase 2*	-1.0792	0.4733
11754601_s_at	LOC100130872	*uncharacterized LOC100130872*	-1.0783	0.4736
11756688_x_at	EFCAB1	*EF-hand calcium binding domain 1*	-1.0764	0.4742

11715462_x_at	LYZ	*lysozyme*	-1.0746	0.4748
11730265_x_at	CCDC69	*coiled-coil domain containing 69*	-1.0707	0.4761
11715954_a_at	CNDP2	*CNDP dipeptidase 2 (metallopeptidase M20 family)*	-1.0707	0.4761
11725980_at	CFD	*complement factor D*	-1.0695	0.4765
11739044_s_at	SLC15A2	*solute carrier family 15 member 2*	-1.0691	0.4766
11755544_a_at	EFHB	*EF-hand domain family member B*	-1.0649	0.4780
11724558_at	GNA15	*G protein subunit alpha 15*	-1.0649	0.4780
11721430_a_at	SYBU	*syntabulin*	-1.0625	0.4788
11764029_at	CEBPD	*CCAAT/enhancer binding protein delta*	-1.0610	0.4793
11719381_a_at	PSENEN	*presenilin enhancer gamma-secretase subunit*	-1.0553	0.4812
11744374_x_at	HLA-DRB1	*major histocompatibility complex, class II, DR beta 1*	-1.0526	0.4821
11755110_a_at	LRIG1	*leucine rich repeats and immunoglobulin like domains 1*	-1.0514	0.4825
11754421_a_at	VSIG2	*V-set and immunoglobulin domain containing 2*	-1.0511	0.4826
11758595_at	NBEA	*neurobeachin*	-1.0508	0.4827
11720713_a_at	KCNE3	*potassium voltage-gated channel subfamily E regulatory subunit 3*	-1.0505	0.4828
11725676_a_at	RORA	*RAR related orphan receptor A*	-1.0490	0.4833
11740055_x_at	RAB37	*RAB37, member RAS oncogene family*	-1.0487	0.4834
11726360_a_at	ALDH3A1	*aldehyde dehydrogenase 3 family member A1*	-1.0472	0.4839
11761021_at	BRD3	*uncharacterized LOC100507412*	-1.0472	0.4839
11723063_a_at	GCHFR	*GTP cyclohydrolase I feedback regulator*	-1.0469	0.4840
11721758_at	TMEM47	*transmembrane protein 47*	-1.0451	0.4846
11717582_a_at	RGCC	*regulator of cell cycle*	-1.0413	0.4859
11756809_a_at	EFHC2	*EF-hand domain containing 2*	-1.0362	0.4876
11734264_at	CERS3	*ceramide synthase 3*	-1.0356	0.4878
11758028_s_at	FOXQ1	*forkhead box Q1*	-1.0345	0.4882
11740438_a_at	FUT6	*fucosyltransferase 6*	-1.0345	0.4882
11728507_at	LY96	*lymphocyte antigen 96*	-1.0339	0.4884
11751619_a_at	APOL1	*apolipoprotein L1*	-1.0318	0.4891
11734939_a_at	SLC16A9	*solute carrier family 16 member 9*	-1.0315	0.4892
11732862_a_at	ADAM28	*chromosome 2 open reading frame 74*	-1.0300	0.4897
11734857_at	ERO1B	*endoplasmic reticulum oxidoreductase 1 beta*	-1.0253	0.4913
11726434_at	CHL1	*cell adhesion molecule L1 like*	-1.0218	0.4925
11724063_s_at	FA2H	*fatty acid 2-hydroxylase*	-1.0209	0.4928
11749875_a_at	LAMP1	*lysosomal associated membrane protein 1*	-1.0198	0.4932
11756342_s_at	GDA	*guanine deaminase*	-1.0142	0.4951
11745260_x_at	KLK8	*solute carrier family 12 member 2*	-1.0098	0.4966
11732468_at	ATP12A	*ATPase H+/K+ transporting non-gastric alpha2 subunit*	-1.0096	0.4967
11753610_a_at	VTCN1	*V-set domain containing T cell activation inhibitor 1*	-1.0090	0.4969
11758460_s_at	FAAH2	*fatty acid amide hydrolase 2*	-1.0075	0.4974
11736050_s_at	FAM229B	*family with sequence similarity 229 member B*	-1.0058	0.4980
11744430_a_at	KIF9	*kinesin family member 9*	-1.0055	0.4981
11718919_a_at	ATP6V1B1	*ATPase H+ transporting V1 subunit B1*	-1.0049	0.4983
11726051_a_at	FMO3	*flavin containing monooxygenase 3*	-1.0035	0.4988
11718754_at	CAPN5	*calpain 5*	-1.0023	0.4992

11723163_s_at	**NR3C2**	***nuclear receptor subfamily 3 group C member 2***	**-1.0009**	**0.4997**
11754171_a_at	**TMEM37**	***transmembrane protein 37***	**-1.0009**	**0.4997**

***Diferentially expressed mRNAs were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ([Log_2Ratio > 1] or [Log_2Ratio < -1] for both upregulated or downregulated mRNAs, respectively), followed by multiple correction using a False Discovery Rate (FDR) threshold of 1% (p-adjusted value or q < 0.01).**

TABLE S7. Differentially expressed mRNAs in CRSwNP compared to control NM at day 28 of the air-liquid interface culture.*

UPREGULATED mRNAs (32)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11724398_a_at	RHCG	*Rh family C glycoprotein*	2.2622	4.7972
11740565_at	PNLIPRP3	*pancreatic lipase related protein 3*	1.8889	3.7035
11730802_at	CRNN	*cornulin*	1.7710	3.4128
11748703_a_at	C1D	*C1D nuclear receptor corepressor*	1.7405	3.3414
11717891_a_at	ECM1	*extracellular matrix protein 1*	1.6869	3.2196
11725662_a_at	SLC16A14	*solute carrier family 16 member 14*	1.6498	3.1380
11753255_a_at	KLK7	*kallikrein related peptidase 7*	1.5863	3.0028
11736855_a_at	ATP6V1C2	*ATPase H+ transporting V1 subunit C2*	1.3974	2.6342
11728810_a_at	ECHDC3	*enoyl-CoA hydratase domain containing 3*	1.3974	2.6342
11736251_at	MUC21	*mucin 21, cell surface associated*	1.3423	2.5356
11743444_s_at	RHOB	*ras homolog family member B*	1.3393	2.5302
11746433_a_at	CLDN1	*claudin 1*	1.2517	2.3813
11734956_a_at	CNTNAP2	*contactin associated protein-like 2*	1.2438	2.3682
11734993_at	SKI	*SKI proto-oncogene*	1.2235	2.3352
11745837_x_at	FN1	*fibronectin 1*	1.1830	2.2705
11746368_a_at	FAM222B	*family with sequence similarity 222 member B*	1.1478	2.2157
11727401_x_at	HOPX	*HOP homeobox*	1.1421	2.2070
11755719_a_at	MLLT11	*myeloid/lymphoid or mixed-lineage leukemia; translocated to, 11*	1.1348	2.1959
11717994_a_at	NR4A1	*nuclear receptor subfamily 4 group A member 1*	1.1322	2.1919
11715620_a_at	CRYAB	*crystallin alpha B*	1.1215	2.1757
11717127_a_at	ANPEP	*alanyl aminopeptidase, membrane*	1.1114	2.1606
11720280_at	KCNMA1	*potassium calcium-activated channel subfamily M alpha 1*	1.0945	2.1354
11755794_a_at	CAPN14	*calpain 14*	1.0922	2.1320
11736978_at	PADI3	*peptidyl arginine deiminase 3*	1.0722	2.1027
11725428_a_at	ABLIM3	*actin binding LIM protein family member 3*	1.0580	2.0820
11732959_a_at	SPRR3	*small proline rich protein 3*	1.0413	2.0581
11732719_at	EREG	*epiregulin*	1.0378	2.0531
11759316_at	NFIC	*nuclear factor I C*	1.0357	2.0501
11746046_a_at	UBQLN2	*ubiquilin 2*	1.0285	2.0399
11717765_a_at	MGLL	*monoglyceride lipase*	1.0187	2.0261
11747800_a_at	HIF1A	*hypoxia inducible factor 1 alpha subunit*	1.0125	2.0174
11721177_at	PITX1	*paired like homeodomain 1*	1.0072	2.0100
DOWNREGULATED mRNAs (420)				
Probe Set IDs	**GENE SYMBOL**	**GENE NAME**	**Log_2Ratio**	**Fold Change**
11716173_a_at	P4HB	*prolyl 4-hydroxylase subunit beta*	-2.8283	0.1408
11757882_x_at	GSTA1	*glutathione S-transferase alpha 1*	-2.5666	0.1688
11749978_a_at	NDRG1	*major vault protein*	-2.4860	0.1785

11755287_x_at	KRT8	*keratin 8*	-2.4836	0.1788
11747494_a_at	AQP3	*aquaporin 3 (Gill blood group)*	-2.4328	0.1852
11715781_a_at	EEF2	*eukaryotic translation elongation factor 2*	-2.3518	0.1959
11716112_at	PIGR	*polymeric immunoglobulin receptor*	-2.3205	0.2002
11749355_a_at	CFB	*complement factor B*	-2.2751	0.2066
11720372_at	TESC	*tescalcin*	-2.2196	0.2147
11751619_a_at	APOL1	*apolipoprotein L1*	-2.1662	0.2228
11745736_a_at	ACADVL	*acyl-CoA dehydrogenase, very long chain*	-2.1571	0.2242
11719767_a_at	TPPP3	*tubulin polymerization promoting protein family member 3*	-2.1494	0.2254
11722255_a_at	RRAD	*RRAD, Ras related glycolysis inhibitor and calcium channel regulator*	-2.1190	0.2302
11751078_s_at	CYP2F1	*cytochrome P450 family 2 subfamily F member 1*	-2.0960	0.2339
11756783_a_at	TF	*transferrin*	-2.0625	0.2394
11752302_a_at	LAMB3	*laminin subunit beta 3*	-1.9624	0.2566
11726063_a_at	C2orf40	*chromosome 2 open reading frame 40*	-1.9585	0.2573
11737634_a_at	UGT2A1	*UDP glucuronosyltransferase family 2 member A1 complex locus*	-1.9579	0.2574
11727906_at	MMP10	*matrix metallopeptidase 10*	-1.9384	0.2609
11763989_at	LOC101927057	*uncharacterized LOC101927057*	-1.9214	0.2640
11729073_a_at	TSPAN19	*tetraspanin 19*	-1.8959	0.2687
11750029_a_at	EIF4H	*eukaryotic translation initiation factor 4H*	-1.8609	0.2753
11760213_a_at	TMC5	*transmembrane channel like 5*	-1.8463	0.2781
11733761_at	TMEM190	*transmembrane protein 190*	-1.8406	0.2792
11751480_a_at	TMEM231	*transmembrane protein 231*	-1.8375	0.2798
11756684_a_at	DYNLRB2	*dynein light chain roadblock-type 2*	-1.8135	0.2845
11742730_a_at	CAPS	*calcyphosine*	-1.8089	0.2854
11742251_s_at	CYP2A6	*cytochrome P450 family 2 subfamily A member 6*	-1.8014	0.2869
11755928_s_at	MMP1	*matrix metallopeptidase 1*	-1.7999	0.2872
11761021_at	BRD3	*uncharacterized LOC100507412*	-1.7884	0.2895
11745725_a_at	RHOV	*granulin precursor*	-1.7740	0.2924
11715112_at	ERICH3	*glutamate rich 3*	-1.7597	0.2953
11733042_at	SLC7A2	*solute carrier family 7 member 2*	-1.7588	0.2955
11716665_s_at	GDF15	*growth differentiation factor 15*	-1.7544	0.2964
11726051_a_at	FMO3	*flavin containing monooxygenase 3*	-1.7529	0.2967
11724558_at	GNA15	*G protein subunit alpha 15*	-1.7524	0.2968
11752559_a_at	TRIM2	*plexin B2*	-1.7490	0.2975
11735169_at	C6orf118	*chromosome 6 open reading frame 118*	-1.7403	0.2993
11721887_a_at	CRYM	*crystallin mu*	-1.7370	0.3000
11724454_at	SLC22A4	*solute carrier family 22 member 4*	-1.7250	0.3025
11723912_at	MS4A8	*membrane spanning 4-domains A8*	-1.7169	0.3042
11748415_s_at	MIR4640	*microRNA 4640*	-1.7056	0.3066
11721758_at	TMEM47	*transmembrane protein 47*	-1.7051	0.3067
11749525_a_at	AKT2	*AKT serine/threonine kinase 2*	-1.7023	0.3073
11724196_s_at	STC1	*stanniocalcin 1*	-1.6976	0.3083
11726576_x_at	CYP2A6	*cytochrome P450 family 2 subfamily A member 6*	-1.6878	0.3104
11720031_a_at	TRIM29	*tripartite motif containing 29*	-1.6878	0.3104

11749875_a_at	**LAMP1**	***lysosomal associated membrane protein 1***	**-1.6776**	**0.3126**
11753232_a_at	**NDRG1**	***N-myc downstream regulated 1***	**-1.6776**	**0.3126**
11752166_x_at	**PKM**	***pyruvate kinase, muscle***	**-1.6730**	**0.3136**
11745609_x_at	**WDR1**	***WD repeat domain 1***	**-1.6652**	**0.3153**
11756066_a_at	**LRRC23**	***leucine rich repeat containing 23***	**-1.6638**	**0.3156**

11730633_at	**MAK**	***male germ cell associated kinase***	**-1.6466**	**0.3194**
11737141_a_at	**RSPH1**	***radial spoke head 1 homolog***	**-1.6448**	**0.3198**
11756356_a_at	**FAM81B**	***family with sequence similarity 81 member B***	**-1.6313**	**0.3228**
11732833_a_at	**C9orf135**	***chromosome 9 open reading frame 135***	**-1.6282**	**0.3235**
11739004_x_at	**HDGF**	***hepatoma-derived growth factor***	**-1.6184**	**0.3257**
11731565_x_at	**NAP1L4**	***MDM2 proto-oncogene***	**-1.6126**	**0.3270**
11729297_at	**MMP13**	***matrix metallopeptidase 13***	**-1.6109**	**0.3274**
11729061_a_at	**DNAH5**	***dynein axonemal heavy chain 5***	**-1.6030**	**0.3292**
11722534_at	**RPRM**	***reprimo, TP53 dependent G2 arrest mediator candidate***	**-1.5986**	**0.3302**
11733607_a_at	**LRRC34**	***leucine rich repeat containing 34***	**-1.5955**	**0.3309**
11735858_a_at	**RIIAD1**	***Regulatory Subunit Of Type II PKA R-Subunit (RIIa) Domain Containing 1***	**-1.5912**	**0.3319**
11726029_a_at	**UPK1B**	***uroplakin 1B***	**-1.5903**	**0.3321**
11744240_at	**SNTN**	***sentan, cilia apical structure protein***	**-1.5855**	**0.3332**
11733359_a_at	**CFAP45**	***cilia and flagella associated protein 45***	**-1.5834**	**0.3337**
11727921_a_at	**TEKT1**	***tektin 1***	**-1.5786**	**0.3348**
11743959_a_at	**SLC16A3**	***solute carrier family 16 (monocarboxylate transporter), member 3***	**-1.5675**	**0.3374**
11726233_a_at	**DRC3**	***dynein regulatory complex subunit 3***	**-1.5658**	**0.3378**
11747561_s_at	**RPS6KB2**	***ribosomal protein S6 kinase B2***	**-1.5623**	**0.3386**

11722863_at	**SCGB2A1**	***secretoglobin family 2A member 1***	**-1.5619**	**0.3387**
11729920_at	**BBOF1**	***basal body orientation factor 1***	**-1.5611**	**0.3389**
11740996_a_at	**SPAG6**	***sperm associated antigen 6***	**-1.5598**	**0.3392**
11721619_at	**FOXJ1**	***forkhead box J1***	**-1.5572**	**0.3398**
11724381_at	**FAM65B**	***family with sequence similarity 65 member B***	**-1.5551**	**0.3403**
11745465_x_at	**METTL7A**	***methyltransferase like 7A***	**-1.5547**	**0.3404**
11734176_a_at	**CFAP52**	***cilia and flagella associated protein 52***	**-1.5543**	**0.3405**
11756097_s_at	**ZMYND10**	***zinc finger MYND-type containing 10***	**-1.5505**	**0.3414**
11746250_a_at	**PIFO**	***primary cilia formation***	**-1.5454**	**0.3426**
11752898_a_at	**PPIL6**	***peptidylprolyl isomerase like 6***	**-1.5408**	**0.3437**
11745260_x_at	**KLK8**	***solute carrier family 12 member 2***	**-1.5349**	**0.3451**
11723524_at	**AGR3**	***anterior gradient 3, protein disulphide isomerase family member***	**-1.5341**	**0.3453**
11731855_at	**C10orf107**	***chromosome 10 open reading frame 107***	**-1.5324**	**0.3457**
11753619_s_at	**EIF5AL1**	***eukaryotic translation initiation factor 5A-like 1***	**-1.5224**	**0.3481**
11723414_a_at	**CNN2**	***calponin 2***	**-1.5175**	**0.3493**
11756688_x_at	**EFCAB1**	***EF-hand calcium binding domain 1***	**-1.5146**	**0.3500**
11753938_a_at	**FAM166B**	***family with sequence similarity 166 member B***	**-1.5133**	**0.3503**
11744588_a_at	**CCDC17**	***coiled-coil domain containing 17***	**-1.5117**	**0.3507**

11729418_a_at	**TEKT2**	***tektin 2***	**-1.5055**	**0.3522**
11748448_a_at	**CTTN**	***cortactin***	**-1.5035**	**0.3527**
11719381_a_at	**PSENEN**	***presenilin enhancer gamma-secretase subunit***	**-1.5010**	**0.3533**
11752329_a_at	**DNAI2**	***dynein axonemal intermediate chain 2***	**-1.5006**	**0.3534**
11732082_s_at	**STOML3**	***stomatin like 3***	**-1.4965**	**0.3544**
11747671_x_at	**CRIP2**	***cysteine rich protein 2***	**-1.4945**	**0.3549**
11756056_a_at	**SDC1**	***solute carrier family 2 member 1***	**-1.4896**	**0.3561**
11756956_a_at	**SPEF1**	***sperm flagellar 1***	**-1.4896**	**0.3561**
11758777_x_at	**RBM8A**	***RNA binding motif protein 8A***	**-1.4848**	**0.3573**
11731924_a_at	**KCNRG**	***potassium channel regulator***	**-1.4844**	**0.3574**
11729042_a_at	**DLEC1**	***deleted in lung and esophageal cancer 1***	**-1.4787**	**0.3588**
11756793_a_at	**VNN2**	***vanin 2***	**-1.4779**	**0.3590**
11752754_s_at	**ADAM15**	***syndecan 1***	**-1.4735**	**0.3601**
11741280_s_at	**CASC1**	***cancer susceptibility candidate 1***	**-1.4727**	**0.3603**
11732909_at	**FAM183A**	***family with sequence similarity 183 member A***	**-1.4639**	**0.3625**
11730044_a_at	**C9orf24**	***chromosome 9 open reading frame 24***	**-1.4620**	**0.3630**
11726535_a_at	**MORN5**	***MORN repeat containing 5***	**-1.4576**	**0.3641**

11732856_at	**CDHR4**	***cadherin related family member 4***	**-1.4572**	**0.3642**
11749809_a_at	**PLAT**	***plasminogen activator, tissue type***	**-1.4564**	**0.3644**
11743800_a_at	**DNAH2**	***dynein axonemal heavy chain 2***	**-1.4556**	**0.3646**
11755403_a_at	**CHST9**	***carbohydrate sulfotransferase 9***	**-1.4525**	**0.3654**
11716670_s_at	**RAB1B**	***RAB1B, member RAS oncogene family***	**-1.4505**	**0.3659**
11759187_at	**TNFAIP8L1**	***TNF alpha induced protein 8 like 1***	**-1.4481**	**0.3665**
11729503_at	**CFAP53**	***cilia and flagella associated protein 53***	**-1.4469**	**0.3668**
11715431_a_at	**MIR6513**	***microRNA 6513***	**-1.4418**	**0.3681**
11731273_a_at	**KCNE1**	***potassium voltage-gated channel subfamily E regulatory subunit 1***	**-1.4387**	**0.3689**
11746749_a_at	**ZBBX**	***zinc finger B-box domain containing***	**-1.4375**	**0.3692**
11726567_a_at	**EIF4G1**	***eukaryotic translation initiation factor 4 gamma 1***	**-1.4367**	**0.3694**
11721736_s_at	**TNFRSF19**	***TNF receptor superfamily member 19***	**-1.4352**	**0.3698**
11743130_a_at	**SORL1**	***sortilin related receptor 1***	**-1.4340**	**0.3701**
11723246_s_at	**SFRP1**	***secreted frizzled related protein 1***	**-1.4325**	**0.3705**
11753531_s_at	**ZNF428**	***zinc finger protein 428***	**-1.4321**	**0.3706**
11730944_a_at	**CCDC65**	***coiled-coil domain containing 65***	**-1.4305**	**0.3710**
11732437_at	**RPS29**	***ras homolog family member V***	**-1.4301**	**0.3711**
11748075_a_at	**NFE2L1**	***nuclear factor, erythroid 2 like 1***	**-1.4297**	**0.3712**

11721322_at	**UNC93B1**	***Unc-93 Homolog B1 (C. Elegans)***	**-1.4181**	**0.3742**
11726159_a_at	**IQCG**	***IQ motif containing G***	**-1.4177**	**0.3743**
11747970_a_at	**ARMC4**	***armadillo repeat containing 4***	**-1.4177**	**0.3743**
11732678_a_at	**DNAH12**	***dynein axonemal heavy chain 12***	**-1.4150**	**0.3750**
11725562_at	**C20orf85**	***chromosome 20 open reading frame 85***	**-1.4147**	**0.3751**
11724940_x_at	**CDHR3**	***cadherin related family member 3***	**-1.4139**	**0.3753**
11730700_a_at	**C11orf49**	***chromosome 11 open reading frame 49***	**-1.4131**	**0.3755**
11750836_a_at	**EFHC1**	***EF-hand domain containing 1***	**-1.4089**	**0.3766**
11749510_a_at	**SAMHD1**	***SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1***	**-1.4016**	**0.3785**
11729258_at	**MNS1**	***meiosis specific nuclear structural 1***	**-1.3997**	**0.3790**
11724109_a_at	**C9orf116**	***chromosome 9 open reading frame 116***	**-1.3990**	**0.3792**
11755544_a_at	**EFHB**	***EF-hand domain family member B***	**-1.3910**	**0.3813**
11733545_x_at	**NWD1**	***NACHT and WD repeat domain containing 1***	**-1.3895**	**0.3817**
11755831_a_at	**WDR63**	***WD repeat domain 63***	**-1.3895**	**0.3817**
11753332_s_at	**CRTAP**	***heterogeneous nuclear ribonucleoprotein L***	**-1.3887**	**0.3819**
11732932_at	**SAXO2**	***stabilizer of axonemal microtubules 2***	**-1.3887**	**0.3819**
11734396_at	**HRASLS2**	***HRAS like suppressor 2***	**-1.3868**	**0.3824**
11743952_a_at	**CFAP206**	***cilia and flagella associated protein 206***	**-1.3838**	**0.3832**

11731341_a_at	**AGBL2**	***ATP/GTP binding protein like 2***	**-1.3715**	**0.3865**
11747074_x_at	**ACTN4**	***actinin alpha 4***	**-1.3692**	**0.3871**
11724621_a_at	**WDR78**	***WD repeat domain 78***	**-1.3666**	**0.3878**
11747277_a_at	**NAP1L4**	***nucleosome assembly protein 1 like 4***	**-1.3659**	**0.3880**
11747400_a_at	**COPS7A**	***COP9 signalosome subunit 7A***	**-1.3629**	**0.3888**
11752159_a_at	**SLC2A1**	***high density lipoprotein binding protein***	**-1.3618**	**0.3891**
11723777_a_at	**SUMF2**	***bromodomain containing 3***	**-1.3577**	**0.3902**
11733635_at	**FAM92B**	***family with sequence similarity 92 member B***	**-1.3577**	**0.3902**
11722807_a_at	**WDR54**	***WD repeat domain 54***	**-1.3577**	**0.3902**
11749601_x_at	**LRTOMT**	***leucine rich transmembrane and O-methyltransferase domain containing***	**-1.3577**	**0.3902**
11763973_a_at	**CFAP157**	***cilia and flagella associated protein 157***	**-1.3570**	**0.3904**
11747692_a_at	**IQUB**	***IQ motif and ubiquitin domain containing***	**-1.3570**	**0.3904**
11750939_a_at	**SLC39A7**	***solute carrier family 39 member 7***	**-1.3570**	**0.3904**
11754354_s_at	**PROM1**	***prominin 1***	**-1.3559**	**0.3907**
11755724_a_at	**MLF1**	***myeloid leukemia factor 1***	**-1.3555**	**0.3908**
11718986_a_at	**IFI6**	***interferon alpha inducible protein 6***	**-1.3540**	**0.3912**
11738988_a_at	**CLTB**	***glucosidase II alpha subunit***	**-1.3522**	**0.3917**

11728854_at	**CCDC173**	***coiled-coil domain containing 173***	**-1.3507**	**0.3921**
11721476_a_at	**AP1S1**	***adaptor related protein complex 1 sigma 1 subunit***	**-1.3500**	**0.3923**
11751459_x_at	**LRG1**	***leucine rich alpha-2-glycoprotein 1***	**-1.3481**	**0.3928**
11743595_at	**C5orf49**	***chromosome 5 open reading frame 49***	**-1.3467**	**0.3932**
11729439_a_at	**CAPSL**	***calcyphosine like***	**-1.3456**	**0.3935**
11742990_x_at	**EZR**	***ezrin***	**-1.3441**	**0.3939**
11730456_at	**CCDC96**	***coiled-coil domain containing 96***	**-1.3419**	**0.3945**
11741956_a_at	**LRRIQ1**	***leucine rich repeats and IQ motif containing 1***	**-1.3419**	**0.3945**
11732022_a_at	**TTC25**	***tetratricopeptide repeat domain 25***	**-1.3383**	**0.3955**
11727983_a_at	**LRRC46**	***leucine rich repeat containing 46***	**-1.3375**	**0.3957**
11715650_a_at	**TXNRD1**	***thioredoxin reductase 1***	**-1.3372**	**0.3958**
11743943_a_at	**RSPH4A**	***radial spoke head 4 homolog A***	**-1.3364**	**0.3960**
11727116_a_at	**PLA1A**	***phospholipase A1 member A***	**-1.3335**	**0.3968**
11749993_a_at	**CCDC78**	***coiled-coil domain containing 78***	**-1.3321**	**0.3972**
11750079_a_at	**ADRM1**	***adhesion regulating molecule 1***	**-1.3299**	**0.3978**
11718618_a_at	**DNAJA4**	***DnaJ heat shock protein family (Hsp40) member A4***	**-1.3299**	**0.3978**
11751338_x_at	**DHCR24**	***24-dehydrocholesterol reductase***	**-1.3292**	**0.3980**
11724691_at	**RIBC2**	***RIB43A domain with coiled-coils 2***	**-1.3284**	**0.3982**

11732553_a_at	**ENKUR**	***enkurin, TRPC channel interacting protein***	**-1.3284**	**0.3982**
11731779_a_at	**C11orf70**	***chromosome 11 open reading frame 70***	**-1.3266**	**0.3987**
11715954_a_at	**CNDP2**	***CNDP dipeptidase 2 (metallopeptidase M20 family)***	**-1.3255**	**0.3990**
11737857_a_at	**DNAAF1**	***dynein axonemal assembly factor 1***	**-1.3241**	**0.3994**
11747365_a_at	**GANAB**	***microRNA 6890***	**-1.3237**	**0.3995**
11746354_a_at	**C1orf158**	***chromosome 1 open reading frame 158***	**-1.3216**	**0.4001**
11748045_x_at	**LDLR**	***low density lipoprotein receptor***	**-1.3208**	**0.4003**
11746662_a_at	**ARMC3**	***armadillo repeat containing 3***	**-1.3201**	**0.4005**
11764033_s_at	**RFC5**	***replication factor C subunit 5***	**-1.3194**	**0.4007**
11730171_a_at	**AKAP8L**	***A-kinase anchoring protein 8 like***	**-1.3190**	**0.4008**
11747387_a_at	**CTNNB1**	***catenin beta 1***	**-1.3180**	**0.4011**
11735554_at	**PPP1R42**	***protein phosphatase 1 regulatory subunit 42***	**-1.3169**	**0.4014**
11756809_a_at	**EFHC2**	***EF-hand domain containing 2***	**-1.3162**	**0.4016**
11754119_a_at	**PLAU**	***plasminogen activator, urokinase***	**-1.3137**	**0.4023**
11740868_a_at	**LDLRAD1**	***low density lipoprotein receptor class A domain containing 1***	**-1.3111**	**0.4030**
11748085_a_at	**ST14**	***suppression of tumorigenicity 14***	**-1.3104**	**0.4032**
11727734_at	**CFAP126**	***cilia and flagella associated protein 126***	**-1.3094**	**0.4035**

11727572_s_at	**KLHL6**	***kelch like family member 6***	**-1.3072**	**0.4041**
11721503_a_at	**CNN2**	***alpha 1,4-galactosyltransferase***	**-1.3054**	**0.4046**
11730936_s_at	**AKNA**	***AT-hook transcription factor***	**-1.3051**	**0.4047**
11749717_a_at	**RP1**	***RP1, Axonemal Microtubule Associated***	**-1.3051**	**0.4047**
11759102_at	**UBXN10**	***UBX domain protein 10***	**-1.3047**	**0.4048**
11738049_a_at	**ATP2C2**	***ATPase secretory pathway Ca2+ transporting 2***	**-1.3033**	**0.4052**
11736861_at	**PIH1D3**	***PIH1 domain containing 3***	**-1.3015**	**0.4057**
11757612_a_at	**ASRGL1**	***asparaginase like 1***	**-1.2994**	**0.4063**
11749217_a_at	**DHRS3**	***transmembrane protease, serine 4***	**-1.2983**	**0.4066**
11751852_a_at	**TRAF4**	***TNF receptor associated factor 4***	**-1.2969**	**0.4070**
11728981_at	**ERICH5**	***glutamate rich 5***	**-1.2909**	**0.4087**
11747634_a_at	**PYGB**	***phosphorylase, glycogen; brain***	**-1.2905**	**0.4088**
11727664_x_at	**STOX1**	***storkhead box 1***	**-1.2874**	**0.4097**
11720461_a_at	**DLK2**	***F11 receptor***	**-1.2860**	**0.4101**
11729554_at	**CFAP73**	***cilia and flagella associated protein 73***	**-1.2838**	**0.4107**
11720349_at	**ROPN1L**	***rhophilin associated tail protein 1 like***	**-1.2824**	**0.4111**
11730612_a_at	**MBOAT7**	***membrane bound O-acyltransferase domain containing 7***	**-1.2821**	**0.4112**
11750162_a_at	**WDR45B**	***WD repeat domain 45B***	**-1.2786**	**0.4122**

11750408_a_at	**ADGRE5**	***adhesion G protein-coupled receptor E5***	**-1.2775**	**0.4125**
11715721_a_at	**GOLM1**	***golgi membrane protein 1***	**-1.2772**	**0.4126**
11733164_a_at	**TTC29**	***tetratricopeptide repeat domain 29***	**-1.2765**	**0.4128**
11728342_at	**DCLK1**	***doublecortin like kinase 1***	**-1.2754**	**0.4131**
11747598_a_at	**CLPTM1**	***CLPTM1, transmembrane protein***	**-1.2754**	**0.4131**
11732523_a_at	**TMEM232**	***transmembrane protein 232***	**-1.2747**	**0.4133**
11745492_a_at	**CCNO**	***cyclin O***	**-1.2733**	**0.4137**
11752531_a_at	**MDH1B**	***malate dehydrogenase 1B***	**-1.2678**	**0.4153**
11733331_at	**CCDC170**	***coiled-coil domain containing 170***	**-1.2664**	**0.4157**
11724372_at	**ANXA10**	***annexin A10***	**-1.2647**	**0.4162**
11728604_at	**RSPH14**	***radial spoke head 14 homolog***	**-1.2629**	**0.4167**
11744374_x_at	**HLA-DRB1**	***major histocompatibility complex, class II, DR beta 1***	**-1.2622**	**0.4169**
11755814_a_at	**CFAP43**	***cilia and flagella associated protein 43***	**-1.2602**	**0.4175**
11753810_a_at	**CCL5**	***C-C motif chemokine ligand 5***	**-1.2588**	**0.4179**
11726213_x_at	**CCL15**	***C-C motif chemokine ligand 15***	**-1.2564**	**0.4186**
11741066_a_at	**SUMF2**	***sulfatase modifying factor 2***	**-1.2564**	**0.4186**
11722360_a_at	**SAFB**	***scaffold attachment factor B***	**-1.2533**	**0.4195**
11756547_a_at	**CLU**	***clusterin***	**-1.2498**	**0.4205**

11754752_a_at	**ODF3B**	***outer dense fiber of sperm tails 3B***	**-1.2498**	**0.4205**
11727185_at	**DRC1**	***dynein regulatory complex subunit 1***	**-1.2491**	**0.4207**
11739532_a_at	**DAW1**	***dynein assembly factor with WD repeats 1***	**-1.2481**	**0.4210**
11727166_a_at	**FBXO15**	***F-box protein 15***	**-1.2454**	**0.4218**
11732954_at	**CCDC153**	***coiled-coil domain containing 153***	**-1.2443**	**0.4221**
11756881_a_at	**LOC101926951**	***uncharacterized LOC101926951***	**-1.2437**	**0.4223**
11755087_a_at	**C4orf47**	***chromosome 4 open reading frame 47***	**-1.2409**	**0.4231**
11715263_at	**SPEF2**	***sperm flagellar 2***	**-1.2368**	**0.4243**
11743168_at	**IDO1**	***indoleamine 2,3-dioxygenase 1***	**-1.2351**	**0.4248**
11743799_a_at	**SPAG17**	***sperm associated antigen 17***	**-1.2351**	**0.4248**
11727029_a_at	**MAP1A**	***microtubule associated protein 1A***	**-1.2348**	**0.4249**
11758504_s_at	**FAM216B**	***family with sequence similarity 216 member B***	**-1.2334**	**0.4253**
11737119_a_at	**NEK10**	***NIMA related kinase 10***	**-1.2287**	**0.4267**
11727033_at	**PAPSS2**	***3'-phosphoadenosine 5'-phosphosulfate synthase 2***	**-1.2274**	**0.4271**
11735674_a_at	**AKAP14**	***A-kinase anchoring protein 14***	**-1.2253**	**0.4277**
11747458_a_at	**MOK**	***MOK protein kinase***	**-1.2253**	**0.4277**
11749426_a_at	**PLXNB1**	***plexin B1***	**-1.2250**	**0.4278**
11733432_at	**AK7**	***adenylate kinase 7***	**-1.2247**	**0.4279**

11740755_a_at	**LYNX1**	***Ly6/neurotoxin 1***	**-1.2247**	**0.4279**
11749921_a_at	**SDC4**	***syndecan 4***	**-1.2247**	**0.4279**
11720649_a_at	**FBXW9**	***F-box and WD repeat domain containing 9***	**-1.2240**	**0.4281**
11727115_a_at	**MARK2**	***microtubule affinity regulating kinase 2***	**-1.2240**	**0.4281**
11746743_a_at	**RUVBL2**	***RuvB like AAA ATPase 2***	**-1.2230**	**0.4284**
11745822_x_at	**SRSF6**	***serine and arginine rich splicing factor 6***	**-1.2216**	**0.4288**
11742483_a_at	**CCDC190**	***coiled-coil domain containing 190***	**-1.2210**	**0.4290**
11739916_a_at	**SERPINB11**	***Serpin Family B Member 11 (Gene/Pseudogene)***	**-1.2203**	**0.4292**
11763291_a_at	**CFAP65**	***cilia and flagella associated protein 65***	**-1.2186**	**0.4297**
11754299_a_at	**MIR4800**	***microRNA 4800***	**-1.2163**	**0.4304**
11740323_at	**TCTEX1D1**	***Tctex1 domain containing 1***	**-1.2156**	**0.4306**
11740419_a_at	**XRRA1**	***X-ray radiation resistance associated 1***	**-1.2152**	**0.4307**
11755609_a_at	**HYDIN2**	***HYDIN2, Axonemal Central Pair Apparatus Protein (Pseudogene)***	**-1.2146**	**0.4309**
11736948_at	**TEX26**	***testis expressed 26***	**-1.2132**	**0.4313**
11751723_a_at	**KRT5**	***keratin 5***	**-1.2106**	**0.4321**
11717707_s_at	**VPS13D**	***vacuolar protein sorting 13 homolog D***	**-1.2082**	**0.4328**
11757444_a_at	**EGLN3**	***egl-9 family hypoxia inducible factor 3***	**-1.2076**	**0.4330**

11726360_a_at	**ALDH3A1**	***aldehyde dehydrogenase 3 family member A1***	**-1.2009**	**0.4350**
11743089_a_at	**LRRC6**	***leucine rich repeat containing 6***	**-1.2002**	**0.4352**
11735479_x_at	**CCDC125**	***coiled-coil domain containing 125***	**-1.1969**	**0.4362**
11760972_x_at	**SPACA9**	***sperm acrosome associated 9***	**-1.1963**	**0.4364**
11720064_a_at	**GLIPR2**	***GLI pathogenesis related 2***	**-1.1956**	**0.4366**
11739033_a_at	**ACTR2**	***ARP2 actin related protein 2 homolog***	**-1.1956**	**0.4366**
11749250_a_at	**ZMYND12**	***zinc finger MYND-type containing 12***	**-1.1917**	**0.4378**
11728478_a_at	**CCDC181**	***coiled-coil domain containing 181***	**-1.1897**	**0.4384**
11718876_at	**DNER**	***delta/notch like EGF repeat containing***	**-1.1874**	**0.4391**
11721704_a_at	**CRIP1**	***cysteine rich protein 1***	**-1.1857**	**0.4396**
11753618_a_at	**ADM**	***adrenomedullin***	**-1.1825**	**0.4406**
11740239_a_at	**CFAP161**	***cilia and flagella associated protein 161***	**-1.1798**	**0.4414**
11745344_a_at	**MIR6741**	***microRNA 6741***	**-1.1795**	**0.4415**
11743041_a_at	**STIP1**	***stress induced phosphoprotein 1***	**-1.1727**	**0.4436**
11743087_at	**PPBP**	***pro-platelet basic protein***	**-1.1691**	**0.4447**
11758355_s_at	**CLDN4**	***claudin 4***	**-1.1684**	**0.4449**
11747222_a_at	**CAPN1**	***calpain 1***	**-1.1675**	**0.4452**

11734525_a_at	**C11orf88**	***chromosome 11 open reading frame 88***	**-1.1668**	**0.4454**
11724582_a_at	**TPRG1L**	***tumor protein p63 regulated 1 like***	**-1.1662**	**0.4456**
11729031_a_at	**C1orf194**	***chromosome 1 open reading frame 194***	**-1.1659**	**0.4457**
11737564_a_at	**CCDC74A**	***coiled-coil domain containing 74A***	**-1.1659**	**0.4457**
11725587_a_at	**RAB36**	***RAB36, member RAS oncogene family***	**-1.1633**	**0.4465**
11755367_s_at	**DNAAF3**	***dynein axonemal assembly factor 3***	**-1.1626**	**0.4467**
11723516_a_at	**CAB39L**	***calcium binding protein 39 like***	**-1.1623**	**0.4468**
11751448_a_at	**DDB1**	***damage specific DNA binding protein 1***	**-1.1594**	**0.4477**
11730785_a_at	**TTC21A**	***tetratricopeptide repeat domain 21A***	**-1.1591**	**0.4478**
11722507_a_at	**CLIC5**	***chloride intracellular channel 5***	**-1.1562**	**0.4487**
11745177_x_at	**TPD52L2**	***tumor protein D52 like 2***	**-1.1562**	**0.4487**
11733637_a_at	**MORN3**	***MORN repeat containing 3***	**-1.1559**	**0.4488**
11725225_at	**CHP2**	***calcineurin like EF-hand protein 2***	**-1.1546**	**0.4492**
11745857_a_at	**SGSM3**	***small G protein signaling modulator 3***	**-1.1539**	**0.4494**
11745295_a_at	**ANKRD66**	***ankyrin repeat domain 66***	**-1.1530**	**0.4497**
11723961_s_at	**PTN**	***pleiotrophin***	**-1.1530**	**0.4497**
11719306_a_at	**WRAP53**	***WD repeat containing antisense to TP53***	**-1.1520**	**0.4500**

11728116_at	**DNAH10**	***dynein axonemal heavy chain 10***	**-1.1514**	**0.4502**
11742080_a_at	**SMARCD2**	***SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2***	**-1.1510**	**0.4503**
11717933_a_at	**DNAL4**	***dynein axonemal light chain 4***	**-1.1507**	**0.4504**
11715412_a_at	**EPAS1**	***endothelial PAS domain protein 1***	**-1.1501**	**0.4506**
11733381_a_at	**OSCP1**	***organic solute carrier partner 1***	**-1.1501**	**0.4506**
11721199_a_at	**IFT122**	***intraflagellar transport 122***	**-1.1482**	**0.4512**
11749777_s_at	**TRIM16**	***tripartite motif containing 16***	**-1.1482**	**0.4512**
11735084_s_at	**FREM2**	***FRAS1 related extracellular matrix protein 2***	**-1.1469**	**0.4516**
11753491_s_at	**ERP29**	***endoplasmic reticulum protein 29***	**-1.1462**	**0.4518**
11719322_at	**DNALI1**	***dynein axonemal light intermediate chain 1***	**-1.1338**	**0.4557**
11725494_at	**RSPH9**	***radial spoke head 9 homolog***	**-1.1329**	**0.4560**
11730451_at	**SDHAF4**	***succinate dehydrogenase complex assembly factor 4***	**-1.1310**	**0.4566**
11757615_a_at	**MAP6**	***microtubule associated protein 6***	**-1.1304**	**0.4568**
11731984_at	**CERKL**	***ceramide kinase like***	**-1.1294**	**0.4571**
11741477_a_at	**NPHP1**	***nephrocystin 1***	**-1.1250**	**0.4585**
11737637_a_at	**CFAP77**	***cilia and flagella associated protein 77***	**-1.1231**	**0.4591**
11731681_a_at	**KATNAL2**	***katanin catalytic subunit A1 like 2***	**-1.1228**	**0.4592**
11724914_at	**SPATA18**	***spermatogenesis associated 18***	**-1.1206**	**0.4599**

11740580_at	**ASAH1**	***N-acylsphingosine amidohydrolase 1***	**-1.1197**	**0.4602**
11756399_x_at	**CCDC189**	***coiled-coil domain containing 189***	**-1.1197**	**0.4602**
11744430_a_at	**KIF9**	***kinesin family member 9***	**-1.1197**	**0.4602**
11728177_a_at	**DYX1C1**	***dyslexia susceptibility 1 candidate 1***	**-1.1156**	**0.4615**
11724988_a_at	**CCDC113**	***coiled-coil domain containing 113***	**-1.1134**	**0.4622**
11743570_s_at	**EML1**	***echinoderm microtubule associated protein like 1***	**-1.1119**	**0.4627**
11748332_x_at	**HLA-E**	***major histocompatibility complex, class I, E***	**-1.1119**	**0.4627**
11752020_x_at	**MAP3K19**	***mitogen-activated protein kinase kinase kinase 19***	**-1.1112**	**0.4629**
11738656_a_at	**PACRG**	***PARK2 coregulated***	**-1.1094**	**0.4635**
11763187_a_at	**NUCB2**	***nucleobindin 2***	**-1.1090**	**0.4636**
11748517_a_at	**ACP2**	***acid phosphatase 2, lysosomal***	**-1.1087**	**0.4637**
11726521_a_at	**SPATA17**	***spermatogenesis associated 17***	**-1.1084**	**0.4638**
11727957_a_at	**DNAI1**	***dynein axonemal intermediate chain 1***	**-1.1078**	**0.4640**
11725875_at	**WDR66**	***WD repeat domain 66***	**-1.1078**	**0.4640**
11731626_a_at	**CCDC186**	***coiled-coil domain containing 186***	**-1.1069**	**0.4643**
11718723_at	**ARRDC3**	***arrestin domain containing 3***	**-1.1044**	**0.4651**
11729030_a_at	**SPATS1**	***spermatogenesis associated serine rich 1***	**-1.1007**	**0.4663**
11725912_a_	**ERBB4**	***erb-b2 receptor tyrosine kinase 4***	**-1.0997**	**0.4666**

at				
11733903_a_at	**SPATA4**	***spermatogenesis associated 4***	**-1.0991**	**0.4668**
11732751_a_at	**CC2D2A**	***coiled-coil and C2 domain containing 2A***	**-1.0979**	**0.4672**
11753213_x_at	**GNAI2**	***G protein subunit alpha i2***	**-1.0954**	**0.4680**
11756271_a_at	**FANK1**	***fibronectin type III and ankyrin repeat domains 1***	**-1.0948**	**0.4682**
11721318_at	**PARM1**	***prostate androgen-regulated mucin-like protein 1***	**-1.0942**	**0.4684**
11748193_a_at	**MAEA**	***macrophage erythroblast attacher***	**-1.0936**	**0.4686**
11763606_a_at	**VAV1**	***vav guanine nucleotide exchange factor 1***	**-1.0933**	**0.4687**
11755324_a_at	**NRXN3**	***neurexin 3***	**-1.0930**	**0.4688**
11754035_a_at	**IRF1**	***interferon regulatory factor 1***	**-1.0920**	**0.4691**
11724080_x_at	**COL21A1**	***collagen type XXI alpha 1 chain***	**-1.0908**	**0.4695**
11738255_x_at	**C7orf57**	***chromosome 7 open reading frame 57***	**-1.0902**	**0.4697**
11745292_a_at	**C22orf15**	***chromosome 22 open reading frame 15***	**-1.0896**	**0.4699**
11752103_a_at	**SDHAP1**	***hexokinase 1***	**-1.0893**	**0.4700**
11727667_at	**DNAH7**	***dynein axonemal heavy chain 7***	**-1.0883**	**0.4703**
11744226_a_at	**SPA17**	***sperm autoantigenic protein 17***	**-1.0871**	**0.4707**
11731052_a_at	**CEP126**	***centrosomal protein 126***	**-1.0862**	**0.4710**
11740089_x_at	**PIK3IP1**	***phosphoinositide-3-kinase interacting protein 1***	**-1.0838**	**0.4718**

11747186_a_at	**PTGES**	***prostaglandin E synthase***	**-1.0825**	**0.4722**
11747137_x_at	**ERAP2**	***endoplasmic reticulum aminopeptidase 2***	**-1.0822**	**0.4723**
11728561_a_at	**TSNAXIP1**	***translin associated factor X interacting protein 1***	**-1.0816**	**0.4725**
11728022_a_at	**TMEM45A**	***transmembrane protein 45A***	**-1.0816**	**0.4725**
11725908_at	**LRRC10B**	***leucine rich repeat containing 10B***	**-1.0804**	**0.4729**
11756650_a_at	**CHP1**	***calcineurin like EF-hand protein 1***	**-1.0801**	**0.4730**
11715147_at	**MAATS1**	***MYCBP associated and testis expressed 1***	**-1.0798**	**0.4731**
11731956_at	**CFAP100**	***cilia and flagella associated protein 100***	**-1.0786**	**0.4735**
11752119_x_at	**SLC17A5**	***solute carrier family 17 member 5***	**-1.0786**	**0.4735**
11751128_x_at	**SHISA5**	***shisa family member 5***	**-1.0758**	**0.4744**
11732862_a_at	**ADAM28**	***chromosome 2 open reading frame 74***	**-1.0752**	**0.4746**
11735523_a_at	**FAM47E**	***family with sequence similarity 47 member E***	**-1.0728**	**0.4754**
11755547_a_at	**STK33**	***serine/threonine kinase 33***	**-1.0722**	**0.4756**
11758376_s_at	**CFAP69**	***cilia and flagella associated protein 69***	**-1.0710**	**0.4760**
11734503_x_at	**ALOX15**	***arachidonate 15-lipoxygenase***	**-1.0707**	**0.4761**
11719067_s_at	**EIF2S3**	***eukaryotic translation initiation factor 2 subunit gamma***	**-1.0695**	**0.4765**
11724589_s_at	**MMP12**	***matrix metallopeptidase 12***	**-1.0673**	**0.4772**
11724264_a_	**IFT22**	***intraflagellar transport 22***	**-1.0661**	**0.4776**

at				
11715462_x_at	**LYZ**	***lysozyme***	**-1.0646**	**0.4781**
11743993_at	**KCTD5**	***potassium channel tetramerization domain containing 5***	**-1.0643**	**0.4782**
11731377_s_at	**RABL2B**	***RAB, member of RAS oncogene family-like 2B***	**-1.0583**	**0.4802**
11718066_a_at	**TCTN1**	***tectonic family member 1***	**-1.0574**	**0.4805**
11721917_a_at	**ANKRD37**	***ankyrin repeat domain 37***	**-1.0565**	**0.4808**
11735883_a_at	**DNAH9**	***dynein axonemal heavy chain 9***	**-1.0562**	**0.4809**
11756342_s_at	**GDA**	***guanine deaminase***	**-1.0559**	**0.4810**
11749944_a_at	**GABRP**	***gamma-aminobutyric acid type A receptor pi subunit***	**-1.0556**	**0.4811**
11717820_a_at	**SLC4A4**	***solute carrier family 4 member 4***	**-1.0547**	**0.4814**
11725178_at	**KCTD11**	***potassium channel tetramerization domain containing 11***	**-1.0532**	**0.4819**
11734373_a_at	**CSPP1**	***centrosome and spindle pole associated protein 1***	**-1.0526**	**0.4821**
11749398_a_at	**B9D1**	***B9 domain containing 1***	**-1.0517**	**0.4824**
11754222_a_at	**CFAP221**	***cilia and flagella associated protein 221***	**-1.0499**	**0.4830**
11751235_a_at	**NR1H2**	***nuclear receptor subfamily 1 group H member 2***	**-1.0499**	**0.4830**
11748066_s_at	**LRRC49**	***leucine rich repeat containing 49***	**-1.0475**	**0.4838**
11745934_a_at	**LOC102724985**	***pyridoxal-dependent decarboxylase domain-containing protein 1***	**-1.0463**	**0.4842**
11718790_at	**HES6**	***hes family bHLH transcription factor 6***	**-1.0460**	**0.4843**

11727722_a_at	**MYB**	***MYB proto-oncogene, transcription factor***	**-1.0460**	**0.4843**
11728388_at	**TSPAN2**	***tetraspanin 2***	**-1.0448**	**0.4847**
11734144_s_at	**LRRC37A2**	***leucine rich repeat containing 37 member A2***	**-1.0439**	**0.4850**
11748982_a_at	**CYP2S1**	***cytochrome P450 family 2 subfamily S member 1***	**-1.0439**	**0.4850**
11746126_s_at	**STAG3**	***stromal antigen 3***	**-1.0416**	**0.4858**
11720856_a_at	**HK1**	***insulin receptor***	**-1.0413**	**0.4859**
11754238_a_at	**DYDC2**	***DPY30 domain containing 2***	**-1.0392**	**0.4866**
11716799_at	**FADD**	***Fas associated via death domain***	**-1.0380**	**0.4870**
11715554_a_at	**CYB5R3**	***cytochrome b5 reductase 3***	**-1.0374**	**0.4872**
11732667_x_at	**RSPH10B**	***radial spoke head 10 homolog B***	**-1.0353**	**0.4879**
11743998_s_at	**SSBP4**	***single stranded DNA binding protein 4***	**-1.0350**	**0.4880**
11716600_a_at	**CHMP1A**	***charged multivesicular body protein 1A***	**-1.0342**	**0.4883**
11721991_a_at	**SLC6A6**	***solute carrier family 6 member 6***	**-1.0336**	**0.4885**
11732287_at	**DZIP3**	***DAZ interacting zinc finger protein 3***	**-1.0327**	**0.4888**
11731945_a_at	**WDR38**	***WD repeat domain 38***	**-1.0327**	**0.4888**
11750355_a_at	**DYX1C1-CCPG1**	***DYX1C1-CCPG1 readthrough NMD candidate***	**-1.0280**	**0.4904**
11715165_at	**DNAJC12**	***DnaJ Heat Shock Protein Family (Hsp40) Member C12***	**-1.0241**	**0.4917**
11753449_a_at	**ABHD16A**	***abhydrolase domain containing 16A***	**-1.0241**	**0.4917**

11722711_a_at	**PPOX**	***protoporphyrinogen oxidase***	**-1.0239**	**0.4918**
11747669_x_at	**ITM2C**	***integral membrane protein 2C***	**-1.0233**	**0.4920**
11727538_at	**NME5**	***NME/NM23 family member 5***	**-1.0227**	**0.4922**
11754987_x_at	**C21orf58**	***chromosome 21 open reading frame 58***	**-1.0209**	**0.4928**
11718578_a_at	**GSTM3**	***glutathione S-transferase mu 3***	**-1.0203**	**0.4930**
11736112_a_at	**ARHGAP18**	***Rho GTPase activating protein 18***	**-1.0198**	**0.4932**
11732254_a_at	**MED18**	***mediator complex subunit 18***	**-1.0192**	**0.4934**
11739007_at	**CAPZA1**	***capping actin protein of muscle Z-line alpha subunit 1***	**-1.0183**	**0.4937**
11751116_a_at	**ACTN1**	***actinin alpha 1***	**-1.0180**	**0.4938**
11758196_s_at	**IGFBP5**	***insulin like growth factor binding protein 5***	**-1.0177**	**0.4939**
11744155_x_at	**PIN1**	***peptidylprolyl cis/trans isomerase, NIMA-interacting 1***	**-1.0168**	**0.4942**
11744994_a_at	**CHPF2**	***chondroitin polymerizing factor 2***	**-1.0154**	**0.4947**
11740055_x_at	**RAB37**	***RAB37, member RAS oncogene family***	**-1.0139**	**0.4952**
11739610_a_at	**CALML4**	***calmodulin like 4***	**-1.0026**	**0.4991**
11731723_a_at	**ALDH3B1**	***aldehyde dehydrogenase 3 family member B1***	**-1.0014**	**0.4995**
11722974_a_at	**WDR90**	***WD repeat domain 90***	**-1.0012**	**0.4996**

***Diferentially expressed mRNAs were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ([Log_2Ratio > 1] or [Log_2Ratio < -1] for both upregulated or downregulated mRNAs, respectively), followed by multiple correction using a False Discovery Rate (FDR) threshold of 1% (p-adjusted value or q < 0.01).**

TABLE S8. Differentially expressed microRNAs in control NM air-liquid interface culture after 14 days of differentiation compared to day 0 (monolayer of hNM-BSCs).*

MIMAT ID	Transcript ID	miR Family	Cluster ID (Chromosome)	log2 Ratio	P.value
Upregulated miRs (ordered by Log_2 Ratio)					
MIMAT0010251_st	hsa-miR-449c-5p	mir-449[#]	C34 (chr5)[†]	3.363	< 0.001
MIMAT0003327_st	hsa-miR-449b-5p	mir-449[#]	C34 (chr5)[†]	3.056	< 0.001
MIMAT0001541_st	hsa-miR-449a	mir-449[#]	C34 (chr5)[†]	3.034	< 0.001
MIMAT0009198_st	hsa-miR-224-3p	mir-224	C152 (chrX)	2.487	< 0.001
MIMAT0025472_st	hsa-miR-6508-5p	-	-	2.243	< 0.001
MIMAT0022720_st	hsa-miR-1304-3p	mir-1304	-	2.237	< 0.001
MIMAT0009203_st	hsa-miR-449b-3p	mir-449[#]	C34 (chr5)[†]	2.079	0.0082
MIMAT0000264_st	hsa-miR-203a	mir-203	C69 (chr14)	2.019	0.0050
MIMAT0001343_st	hsa-miR-425-3p	mir-425	C114 (chr3)[†]	1.873	0.0083
MIMAT0005593_st	hsa-miR-1238-3p	mir-1238	-	1.860	0.0080
MIMAT0000432_st	hsa-miR-141-3p	mir-8[#]	C61 (chr12)	1.843	0.0085
MIMAT0016862_st	hsa-miR-4310	-	-	1.833	0.0014
MIMAT0000097_st	hsa-miR-99a-5p	mir-10	C108 (chr21)	1.726	0.0089
MIMAT0022257_st	hsa-miR-5571-5p	-	-	1.708	0.0088
MIMAT0003221_st	hsa-miR-557	mir-557	-	1.636	0.0100
MIMAT0001618_st	hsa-miR-191-3p	mir-191	C114 (chr3)[†]	1.596	0.0160
MIMAT0000242_st	hsa-miR-129-5p	miR-129	-	1.586	0.0079
MIMAT0003218_st	hsa-miR-92b-3p	mir-25	-	1.584	0.0252
MIMAT0023705_st	hsa-miR-6080	-	-	1.582	0.0094
MIMAT0000692_st	hsa-miR-30e-5p	mir-30[#]	C42 (chr1)	1.539	0.0162
MIMAT0019755_st	hsa-miR-4673	-	-	1.457	0.0082
MIMAT0000318_st	hsa-miR-200b-3p	mir-8[#]	C21 (chr1)	1.419	0.0418
MIMAT0027583_st	hsa-miR-6840-3p	-	-	1.418	0.0073
MIMAT0015070_st	hsa-miR-3188	mir-3188	-	1.391	0.0182
MIMAT0005576_st	hsa-miR-1226-5p	mir-1226	-	1.383	0.0204
MIMAT0004284_st	hsa-miR-675-5p	mir-675	-	1.372	0.0259
MIMAT0000773_st	hsa-miR-346	mir-346	-	1.339	0.0433
MIMAT0027475_st	hsa-miR-6787-3p	-	-	1.338	0.0286
MIMAT0007890_st	hsa-miR-1914-3p	mir-1914	C106 (chr20)	1.312	0.0248
MIMAT0027645_st	hsa-miR-6872-3p	-	-	1.303	0.0204
MIMAT0019815_st	hsa-miR-4710	-	-	1.261	0.0303
MIMAT0026612_st	hsa-miR-504-3p	mir-504	-	1.258	0.0419
MIMAT0000245_st	hsa-miR-30d-5p	mir-30[#]	C139 (chr8)[†]	1.256	0.0350
MIMAT0019892_st	hsa-miR-371b-5p	mir-290	C16 (chr19)	1.252	0.0196
MIMAT0027501_st	hsa-miR-6800-3p	-	-	1.251	0.0259
MIMAT0019740_st	hsa-miR-4665-3p	-	-	1.239	0.0408
MIMAT0019021_st	hsa-miR-4487	-	-	1.232	0.0425
MIMAT0018932_st	hsa-miR-378f	-	-	1.229	0.0477
MIMAT0023709_st	hsa-miR-6084	-	-	1.228	0.0253
MIMAT0000686_st	hsa-miR-34c-5p	mir-34	C59 (chr11)	1.223	0.0450
MIMAT0005943_st	hsa-miR-1292-5p	mir-1292	-	1.216	0.0457
MIMAT0023693_st	hsa-miR-6068	-	-	1.203	0.0244
MIMAT0019011_st	hsa-miR-4479	-	-	1.189	0.0415
MIMAT0015061_st	hsa-miR-3181	-	-	1.179	0.0255
MIMAT0005873_st	hsa-miR-1208	mir-1208	-	1.169	0.0409
MIMAT0030991_st	hsa-miR-8064	-	-	1.145	0.0212
MIMAT0003237_st	hsa-miR-572	mir-572	-	1.126	0.0443
MIMAT0000414_st	hsa-let-7g-5p	let-7	-	1.091	0.0452
MIMAT0019082_st	hsa-miR-4539	-	C13 (chr14)	0.970	0.0261
MIMAT0000076_st	hsa-miR-21-5p	mir-21	-	0.945	0.0251
MIMAT0000420_st	hsa-miR-30b-5p	mir-30[#]	C139 (chr8)[†]	0.945	0.0428

MIMAT0000068_st	hsa-miR-15a-5p	mir-15	C67 (chr13)	0.938	0.0436
Downregulated miRs (ordered by Log_2 Ratio)					
MIMAT0000098_st	hsa-miR-100-5p	mir-10	C60 (chr11)	-2.771	< 0.001
MIMAT0000646_st	hsa-miR-155-5p	mir-155	-	-2.582	< 0.001
MIMAT0015021_st	hsa-miR-3148	-	-	-2.105	< 0.001
MIMAT0018936_st	hsa-miR-4423-3p	mir-4423	-	-1.838	0.0020
MIMAT0019704_st	hsa-miR-4644	-	-	-1.818	0.0017
MIMAT0019726_st	hsa-miR-4659a-5p	mir-4659	C131 (chr8)	-1.782	0.0033
MIMAT0018964_st	hsa-miR-4445-3p	-	-	-1.725	0.0014
MIMAT0031011_st	hsa-miR-8084	-	-	-1.689	0.0012
MIMAT0027379_st	hsa-miR-6739-5p	-	-	-1.682	0.0027
MIMAT0000072_st	hsa-miR-18a-5p	mir-17[#]	C6 (chr13)[†]	-1.674	< 0.001
MIMAT0014991_st	hsa-miR-3128	-	-	-1.635	0.0022
MIMAT0000765_st	hsa-miR-335-5p	mir-335	-	-1.556	0.0029
MIMAT0026638_st	hsa-miR-1468-3p	mir-1468	-	-1.546	0.0030
MIMAT0017988_st	hsa-miR-3611	-	-	-1.510	0.0191
MIMAT0018188_st	hsa-miR-3914	-	-	-1.425	0.0175
MIMAT0015086_st	hsa-miR-3201	-	-	-1.418	0.0069
MIMAT0015081_st	hsa-miR-548x-3p	mir-548[#]	-	-1.360	0.0145
MIMAT0000691_st	hsa-miR-130b-3p	mir-130	C110 (chr22)	-1.336	0.0031
MIMAT0018938_st	hsa-miR-548ac	mir-548[#]	-	-1.334	0.0139
MIMAT0017991_st	hsa-miR-3613-3p	mir-3613	-	-1.330	0.0089
MIMAT0018954_st	hsa-miR-548ae	miR-548[#]	-	-1.300	0.0188
MIMAT0000445_st	hsa-miR-126-3p	mir-126	-	-1.283	0.0144
MIMAT0019745_st	hsa-miR-4668-5p	-	-	-1.240	0.0130
MIMAT0026641_st	hsa-miR-1298-3p	mir-1298	-	-1.186	0.0197
MIMAT0022741_st	hsa-miR-3529-3p	mir-3529	C24 (chr15)	-1.183	0.0202
MIMAT0000070_st	hsa-miR-17-5p	mir-17[#]	C6 (chr13)[†]	-1.146	0.0067
MIMAT0018201_st	hsa-miR-3926	miR-3926	-	-1.144	0.0208
MIMAT0003223_st	hsa-miR-559	mir-559	-	-1.099	0.0170
MIMAT0000103_st	hsa-miR-106a-5p	mir-17[#]	C7 (chrX)[†]	-1.094	0.0132
MIMAT0018185_st	hsa-miR-3911	-	-	-1.092	0.0071
MIMAT0021086_st	hsa-miR-5094	-	-	-1.085	0.0181
MIMAT0004496_st	hsa-miR-23a-5p	mir-23	C29 (chr19)	-1.044	0.0162
MIMAT0003251_st	hsa-miR-548a-3p	miR-548[#]	-	-1.038	0.0213
MIMAT0019833_st	hsa-miR-4720-5p	-	-	-1.014	0.0411
MIMAT0001412_st	hsa-miR-18b-5p	mir-17[#]	C7 (chrX)[†]	-1.007	0.0229
MIMAT0028214_st	hsa-miR-7152-5p	-	-	-0.958	0.0183
MIMAT0015052_st	hsa-miR-3175	-	-	-0.890	0.0208
MIMAT0027562_st	hsa-miR-6831-5p	-	-	-0.885	0.0169
MIMAT0000092_st	hsa-miR-92a-3p	miR-25	-	-0.855	0.0269
MIMAT0019749_st	hsa-miR-4669	-	-	-0.843	0.0138
MIMAT0009447_st	hsa-miR-1972	-	-	-0.812	0.0177
MIMAT0028235_st	hsa-miR-7162-3p	-	-	-0.790	0.0402
MIMAT0029782_st	hsa-miR-7641	miR-7641	-	-0.751	0.0498
MIMAT0000074_st	hsa-miR-19b-3p	miR-19	-	-0.720	0.0129
MIMAT0002816_st	hsa-miR-494-3p	mir-154	C2 (chr14)	-0.701	0.0489

***, Diferentially expressed (DE) microRNAs (miRs) were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ($|Log_2Ratio| > 0.6$), followed by multiple correction using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or q < 0.05); [#], miR family represented with more than one DE miR in this dataset; [†], miR cluster represented with more than one DE miR in this dataset.**

TABLE S9. Differentially expressed microRNAs in control NM air-liquid interface culture after 28 days of differentiation compared to day 0 (monolayer of hNM-BSCs).*

MIMAT ID	Transcript ID	miR Family	Cluster ID (Chromosome)	Log_2 Ratio	P.value
Upregulated miRs (ordered by Log_2 Ratio)					
MIMAT0001541_st	hsa-miR-449a	mir-449#	C34 (chr5)†	4.476	< 0.001
MIMAT0003327_st	hsa-miR-449b-5p	mir-449#	C34 (chr5)†	4.249	< 0.001
MIMAT0010251_st	hsa-miR-449c-5p	mir-449#	C34 (chr5)†	3.955	< 0.001
MIMAT0004677_st	hsa-miR-34c-3p	mir-34#	C59 (chr11)†	3.155	< 0.001
MIMAT0000686_st	hsa-miR-34c-5p	mir-34#	C59 (chr11)†	3.086	< 0.001
MIMAT0009203_st	hsa-miR-449b-3p	mir-449#	C34 (chr5)†	2.692	0.0008
MIMAT0025472_st	hsa-miR-6508-5p	-	-	2.680	< 0.001
MIMAT0003218_st	hsa-miR-92b-3p	mir-25	-	2.661	0.0010
MIMAT0022720_st	hsa-miR-1304-3p	mir-1304	-	2.446	< 0.001
MIMAT0016862_st	hsa-miR-4310	-	-	2.353	< 0.001
MIMAT0000685_st	hsa-miR-34b-5p	mir-34#	C59 (chr11)†	2.278	0.0071
MIMAT0027583_st	hsa-miR-6840-3p	-	-	2.273	< 0.001
MIMAT0001343_st	hsa-miR-425-3p	mir-425	C114 (chr3)†	2.234	0.0019
MIMAT0005593_st	hsa-miR-1238-3p	mir-1238	-	2.220	0.0014
MIMAT0022257_st	hsa-miR-5571-5p	-	-	2.194	0.0008
MIMAT0000728_st	hsa-miR-375	mir-375	-	2.068	0.0041
MIMAT0005873_st	hsa-miR-1208	mir-1208	-	1.993	0.0009
MIMAT0000242_st	hsa-miR-129-5p	miR-129	-	1.952	0.0013
MIMAT0009198_st	hsa-miR-224-3p	mir-224	C152 (chrX)	1.863	0.0052
MIMAT0023709_st	hsa-miR-6084	-	-	1.863	0.0039
MIMAT0003221_st	hsa-miR-557	mir-557	-	1.856	0.0040
MIMAT0001618_st	hsa-miR-191-3p	mir-191	C114 (chr3)†	1.844	0.0063
MIMAT0000432_st	hsa-miR-141-3p	mir-8#	C61 (chr12)	1.809	0.0145
MIMAT0004676_st	hsa-miR-34b-3p	mir-34#	C59 (chr11)†	1.801	0.0216
MIMAT0023705_st	hsa-miR-6080	-	-	1.796	0.0048
MIMAT0018444_st	hsa-miR-642b-3p	mir-642	C95 (chr19)	1.774	0.0054
MIMAT0019892_st	hsa-miR-371b-5p	mir-290	C16 (chr19)	1.773	0.0053
MIMAT0000097_st	hsa-miR-99a-5p	mir-10	C108 (chr21)	1.726	0.0106
MIMAT0000692_st	hsa-miR-30e-5p	mir-30#	C42 (chr1)	1.722	0.0150
MIMAT0004986_st	hsa-miR-943	mir-943	-	1.719	0.0045
MIMAT0000318_st	hsa-miR-200b-3p	mir-8#	C21 (chr1)†	1.695	0.0215
MIMAT0005576_st	hsa-miR-1226-5p	mir-1226	-	1.667	0.0038
MIMAT0015070_st	hsa-miR-3188	mir-3188	-	1.658	0.0043
MIMAT0030991_st	hsa-miR-8064	-	-	1.645	0.0050
MIMAT0005458_st	hsa-miR-1224-5p	mir-1224	-	1.630	0.0059
MIMAT0004976_st	hsa-miR-933	mir-933	-	1.629	0.0160
MIMAT0005825_st	hsa-miR-1180-3p	mir-1180	-	1.588	0.0318
MIMAT0000245_st	hsa-miR-30d-5p	mir-30#	C139 (chr8)	1.572	0.0211
MIMAT0003338_st	hsa-miR-660-5p	mir-188#	C4 (chrX)†	1.570	0.0247
MIMAT0027501_st	hsa-miR-6800-3p	-	-	1.566	0.0109
MIMAT0019771_st	hsa-miR-4685-5p	-	-	1.562	0.0117
MIMAT0005939_st	hsa-miR-1281	mir-1281	-	1.556	0.0114
MIMAT0018999_st	hsa-miR-4472	-	-	1.539	0.0149
MIMAT0019082_st	hsa-miR-4539	-	C13 (chr14)	1.533	0.0042
MIMAT0015061_st	hsa-miR-3181	-	-	1.526	0.0154
MIMAT0004614_st	hsa-miR-193a-5p	mir-193	-	1.525	0.0254
MIMAT0019855_st	hsa-miR-4732-5p	-	C14 (chr17)	1.523	0.0252
MIMAT0000264_st	hsa-miR-203a	mir-203	C69 (chr14)	1.515	0.0228
MIMAT0003280_st	hsa-miR-612	mir-612	-	1.497	0.0424
MIMAT0027392_st	hsa-miR-6746-5p	-	-	1.497	0.0243
MIMAT0001620_st	hsa-miR-200a-5p	mir-8#	C21 (chr1)†	1.482	0.0416

MIMAT0019050_st	hsa-miR-4513	-	-	1.481	0.0200
MIMAT0019755_st	hsa-miR-4673	-	-	1.465	0.0160
MIMAT0004284_st	hsa-miR-675-5p	mir-675	-	1.462	0.0209
MIMAT0027385_st	hsa-miR-6742-5p	-	-	1.445	0.0354
MIMAT0023693_st	hsa-miR-6068	-	-	1.437	0.0075
MIMAT0028230_st	hsa-miR-7160-5p	-	-	1.437	0.0146
MIMAT0019221_st	hsa-miR-3677-5p	-	C25 (chr16)	1.431	0.0283
MIMAT0027645_st	hsa-miR-6872-3p	-	-	1.417	0.0175
MIMAT0000682_st	hsa-miR-200a-3p	mir-8[#]	C21 (chr1)[†]	1.416	0.0405
MIMAT0026612_st	hsa-miR-504-3p	mir-504	-	1.406	0.0261
MIMAT0000773_st	hsa-miR-346	mir-346	-	1.405	0.0342
MIMAT0019791_st	hsa-miR-4697-5p	-	-	1.392	0.0319
MIMAT0027353_st	hsa-miR-6726-5p	-	-	1.388	0.0287
MIMAT0005943_st	hsa-miR-1292-5p	mir-1292	-	1.368	0.0294
MIMAT0005583_st	hsa-miR-1228-3p	mir-1228	-	1.368	0.0260
MIMAT0000762_st	hsa-miR-324-3p	mir-324	-	1.361	0.0296
MIMAT0024617_st	hsa-miR-6133	mir-6133	-	1.357	0.0291
MIMAT0019216_st	hsa-miR-3187-5p	-	C91 (chr19)	1.355	0.0258
MIMAT0004486_st	hsa-let-7f-1-3p	let-7[#]	C39 (chr9)	1.354	0.0231
MIMAT0018104_st	hsa-miR-3679-5p	-	-	1.341	0.0296
MIMAT0027406_st	hsa-miR-6753-5p	-	-	1.337	0.0289
MIMAT0021127_st	hsa-miR-5195-3p	-	-	1.329	0.0253
MIMAT0031000_st	hsa-miR-8073	-	-	1.329	0.0257
MIMAT0018966_st	hsa-miR-4447	-	-	1.323	0.0290
MIMAT0000076_st	hsa-miR-21-5p	mir-21	-	1.322	0.0242
MIMAT0027686_st	hsa-miR-6893-5p	-	-	1.316	0.0272
MIMAT0027418_st	hsa-miR-6759-5p	-	-	1.311	0.0316
MIMAT0003237_st	hsa-miR-572	mir-572	-	1.307	0.0253
MIMAT0027498_st	hsa-miR-6799-5p	-	-	1.302	0.0418
MIMAT0027480_st	hsa-miR-6790-5p	mir-6790	C93 (chr19)	1.298	0.0252
MIMAT0024610_st	hsa-miR-6127	mir-6127	-	1.291	0.0466
MIMAT0019074_st	hsa-miR-378i	-	-	1.285	0.0425
MIMAT0017994_st	hsa-miR-3615	mir-3615	-	1.280	0.0401
MIMAT0027512_st	hsa-miR-6806-5p	-	-	1.276	0.0466
MIMAT0019844_st	hsa-miR-4725-3p	-	C83 (chr17)	1.266	0.0499
MIMAT0019740_st	hsa-miR-4665-3p	-	-	1.253	0.0456
MIMAT0019815_st	hsa-miR-4710	-	-	1.242	0.0433
MIMAT0019011_st	hsa-miR-4479	-	-	1.236	0.0420
MIMAT0027377_st	hsa-miR-6738-5p	-	-	1.232	0.0477
MIMAT0004780_st	hsa-miR-532-3p	mir-188[#]	C4 (chrX)[†]	1.231	0.0426
MIMAT0027530_st	hsa-miR-6815-5p	-	-	1.197	0.0246
MIMAT0022693_st	hsa-miR-204-3p	mir-204	-	1.163	0.0470
MIMAT0027575_st	hsa-miR-6836-3p	-	-	1.156	0.0420
MIMAT0019881_st	hsa-miR-4746-3p	-	-	1.140	0.0424
MIMAT0000753_st	hsa-miR-342-3p	mir-342	C68 (chr14)	1.127	0.0432
MIMAT0021120_st	hsa-miR-5189-5p	-	-	1.121	0.0428
MIMAT0000414_st	hsa-let-7g-5p	let-7[#]	-	1.101	0.0491
MIMAT0019779_st	hsa-miR-4690-5p	-	-	1.090	0.0480
MIMAT0018084_st	hsa-miR-3663-5p	-	-	1.060	0.0419
Downregulated miRs (ordered by Log_2 Ratio)					
MIMAT0000098_st	hsa-miR-100-5p	mir-10[#]	C60 (chr11)	-3.143	< 0.001
MIMAT0000072_st	hsa-miR-18a-5p	mir-17[#]	C6 (chr13)[†]	-2.841	< 0.001
MIMAT0000646_st	hsa-miR-155-5p	mir-155	-	-2.631	< 0.001
MIMAT0000070_st	hsa-miR-17-5p	mir-17[#]	C6 (chr13)[†]	-2.302	< 0.001
MIMAT0000103_st	hsa-miR-106a-5p	mir-17[#]	C7 (chrX)[†]	-2.264	< 0.001
MIMAT0029782_st	hsa-miR-7641	miR-7641	-	-2.102	< 0.001
MIMAT0000092_st	hsa-miR-92a-3p	miR-25	-	-1.940	< 0.001

MIMAT0018964_st	hsa-miR-4445-3p	-	-	-1.931	0.0010
MIMAT0019726_st	hsa-miR-4659a-5p	mir-4659	C131 (chr8)	-1.915	0.0006
MIMAT0026638_st	hsa-miR-1468-3p	mir-1468	-	-1.890	0.0011
MIMAT0019704_st	hsa-miR-4644	-	-	-1.846	0.0006
MIMAT0000765_st	hsa-miR-335-5p	mir-335	-	-1.786	< 0.001
MIMAT0000691_st	hsa-miR-130b-3p	mir-130	C110 (chr22)	-1.752	0.0009
MIMAT0027379_st	hsa-miR-6739-5p	-	-	-1.739	0.0029
MIMAT0015086_st	hsa-miR-3201	-	-	-1.716	0.0006
MIMAT0031011_st	hsa-miR-8084	-	-	-1.709	0.0007
MIMAT0015021_st	hsa-miR-3148	-	-	-1.695	0.0007
MIMAT0014991_st	hsa-miR-3128	-	-	-1.615	0.0026
MIMAT0017988_st	hsa-miR-3611	-	-	-1.564	0.0120
MIMAT0017991_st	hsa-miR-3613-3p	mir-3613	-	-1.558	0.0008
MIMAT0000075_st	hsa-miR-20a-5p	mir-17#	C6 (chr13)†	-1.553	0.0008
MIMAT0018936_st	hsa-miR-4423-3p	mir-4423	-	-1.552	0.0052
MIMAT0021086_st	hsa-miR-5094	-	-	-1.490	0.0027
MIMAT0000445_st	hsa-miR-126-3p	mir-126	-	-1.447	0.0025
MIMAT0018954_st	hsa-miR-548ae	miR-548#	-	-1.442	0.0046
MIMAT0018188_st	hsa-miR-3914	-	-	-1.377	0.0147
MIMAT0003223_st	hsa-miR-559	mir-559	-	-1.327	0.0005
MIMAT0019745_st	hsa-miR-4668-5p	-	-	-1.305	0.0044
MIMAT0002819_st	hsa-miR-193b-3p	mir-193	C73 (chr16)	-1.284	0.0127
MIMAT0018184_st	hsa-miR-3910	miR-3910	-	-1.281	0.0069
MIMAT0003274_st	hsa-miR-606	mir-606	-	-1.270	0.0305
MIMAT0001413_st	hsa-miR-20b-5p	mir-17#	C7 (chrX)†	-1.260	0.0020
MIMAT0001412_st	hsa-miR-18b-5p	mir-17#	C7 (chrX)†	-1.249	0.0071
MIMAT0015081_st	hsa-miR-548x-3p	mir-548#	-	-1.211	0.0131
MIMAT0000078_st	hsa-miR-23a-3p	mir-23	C29 (chr19)†	-1.190	0.0263
MIMAT0021038_st	hsa-miR-548ap-3p	mir-548#	-	-1.134	0.0370
MIMAT0003251_st	hsa-miR-548a-3p	miR-548#	-	-1.079	0.0169
MIMAT0018201_st	hsa-miR-3926	miR-3926	-	-1.037	0.0491
MIMAT0000423_st	hsa-miR-125b-5p	miR-10#	-	-1.032	0.0302
MIMAT0000084_st	hsa-miR-27a-3p	mir-27#	C29 (chr19)†	-1.022	0.0254
MIMAT0000266_st	hsa-miR-205-5p	mir-205	-	-0.959	0.0197
MIMAT0004501_st	hsa-miR-27a-5p	mir-27#	C29 (chr19)†	-0.906	0.0498
MIMAT0000074_st	hsa-miR-19b-3p	mir-19	-	-0.844	0.0126
MIMAT0028214_st	hsa-miR-7152-5p	-	-	-0.802	0.0339

***, Diferentially expressed (DE) microRNAs (miRs) were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ($|Log_2Ratio| > 0.6$), followed by multiple correction using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or $q < 0.05$); #, miR family represented with more than one DE miR in this dataset; †, miR cluster represented with more than one DE miR in this dataset.**

TABLE S10. Differentially expressed microRNAs in CRSwNP air-liquid interface culture after 14 days of differentiation compared to day 0 (monolayer of hNP-BSCs).*

MIMAT ID	Transcript ID	miR Family	Cluster ID (Chromosome)	Log_2 Ratio	P.value
Upregulated miRs (ordered by Log_2 Ratio)					
MIMAT0030991_st	hsa-miR-8064	-	-	3.004	< 0.001
MIMAT0025472_st	hsa-miR-6508-5p	-	-	2.934	< 0.001
MIMAT0019082_st	hsa-miR-4539	-	C13 (chr14)	2.645	< 0.001
MIMAT0015061_st	hsa-miR-3181	-	-	2.543	< 0.001
MIMAT0027583_st	hsa-miR-6840-3p	-	-	2.518	< 0.001
MIMAT0016862_st	hsa-miR-4310	-	-	2.467	< 0.001
MIMAT0009198_st	hsa-miR-224-3p	mir-224[#]	C152 (chrX)[†]	2.369	< 0.001
MIMAT0019755_st	hsa-miR-4673	-	-	2.363	< 0.001
MIMAT0019881_st	hsa-miR-4746-3p	-	-	2.358	< 0.001
MIMAT0027575_st	hsa-miR-6836-3p	-	-	2.346	< 0.001
MIMAT0028230_st	hsa-miR-7160-5p	-	-	2.313	< 0.001
MIMAT0005576_st	hsa-miR-1226-5p	mir-1226	-	2.294	< 0.001
MIMAT0019892_st	hsa-miR-371b-5p	mir-290	C16 (chr19)	2.241	< 0.001
MIMAT0000773_st	hsa-miR-346	mir-346	-	2.238	< 0.001
MIMAT0031119_st	hsa-miR-1199-5p	mir-1199	-	2.207	< 0.001
MIMAT0022257_st	hsa-miR-5571-5p	-	-	2.186	< 0.001
MIMAT0027375_st	hsa-miR-6737-5p	-	-	2.180	< 0.001
MIMAT0023706_st	hsa-miR-6081	-	-	2.176	< 0.001
MIMAT0023709_st	hsa-miR-6084	-	-	2.174	< 0.001
MIMAT0004762_st	hsa-miR-486-3p	miR-486	-	2.169	< 0.001
MIMAT0019011_st	hsa-miR-4479	-	-	2.154	< 0.001
MIMAT0000242_st	hsa-miR-129-5p	miR-129	-	2.153	< 0.001
MIMAT0031000_st	hsa-miR-8073	-	-	2.116	< 0.001
MIMAT0019050_st	hsa-miR-4513	-	-	2.099	< 0.001
MIMAT0003309_st	hsa-miR-639	mir-639	-	2.092	< 0.001
MIMAT0001343_st	hsa-miR-425-3p	mir-425	C114 (chr3)[†]	2.087	0.0002
MIMAT0018999_st	hsa-miR-4472	-	-	2.071	< 0.001
MIMAT0022720_st	hsa-miR-1304-3p	mir-1304	-	2.063	< 0.001
MIMAT0019853_st	hsa-miR-4731-5p	-	-	2.053	< 0.001
MIMAT0005873_st	hsa-miR-1208	mir-1208	-	2.002	< 0.001
MIMAT0017999_st	hsa-miR-3619-5p	-	-	1.968	0.0003
MIMAT0019810_st	hsa-miR-4708-3p	-	-	1.929	0.0002
MIMAT0003221_st	hsa-miR-557	mir-557	-	1.912	0.0003
MIMAT0005943_st	hsa-miR-1292-5p	mir-1292	-	1.912	0.0003
MIMAT0003237_st	hsa-miR-572	mir-572	-	1.905	0.0003
MIMAT0005458_st	hsa-miR-1224-5p	mir-1224	-	1.890	0.0006
MIMAT0001618_st	hsa-miR-191-3p	mir-191	C114 (chr3)[†]	1.868	0.0003
MIMAT0019216_st	hsa-miR-3187-5p	-	C91 (chr19)[†]	1.859	0.0008
MIMAT0016919_st	hsa-miR-4292	-	-	1.850	0.0006
MIMAT0027409_st	hsa-miR-6754-3p	-	-	1.840	0.0014
MIMAT0019919_st	hsa-miR-4767	-	-	1.839	0.0003
MIMAT0019015_st	hsa-miR-4481	-	-	1.838	0.0005
MIMAT0004561_st	hsa-miR-187-5p	mir-187	-	1.837	0.0005
MIMAT0027444_st	hsa-miR-6772-5p	-	-	1.807	0.0016
MIMAT0027383_st	hsa-miR-6741-5p	-	-	1.795	0.0006
MIMAT0023705_st	hsa-miR-6080	-	-	1.781	0.0008
MIMAT0005867_st	hsa-miR-663b	mir-663	-	1.773	0.0019
MIMAT0027574_st	hsa-miR-6836-5p	-	-	1.756	0.0022
MIMAT0018084_st	hsa-miR-3663-5p	-	-	1.755	0.0020
MIMAT0018965_st	hsa-miR-4446-3p	mir-4446	-	1.728	0.0016
MIMAT0005593_st	hsa-miR-1238-3p	mir-1238	-	1.728	0.0021

MIMAT0018958_st	hsa-miR-4440	-	-	1.726	0.0019
MIMAT0023693_st	hsa-miR-6068	-	-	1.716	0.0011
MIMAT0019836_st	hsa-miR-4722-5p	-	-	1.696	0.0022
MIMAT0019074_st	hsa-miR-378i	miR-378[#]	-	1.694	0.0022
MIMAT0027642_st	hsa-miR-6871-5p	-	-	1.647	0.0022
MIMAT0019740_st	hsa-miR-4665-3p	-	-	1.634	0.0043
MIMAT0018960_st	hsa-miR-4442	-	-	1.629	0.0031
MIMAT0027602_st	hsa-miR-6851-5p	-	-	1.612	0.0037
MIMAT0027418_st	hsa-miR-6759-5p	-	-	1.604	0.0033
MIMAT0007890_st	hsa-miR-1914-3p	mir-1914	C106 (chr20)	1.604	0.0027
MIMAT0011777_st	hsa-miR-2277-3p	-	-	1.599	0.0046
MIMAT0027424_st	hsa-miR-6762-5p	-	-	1.581	0.0054
MIMAT0000692_st	hsa-miR-30e-5p	mir-30[#]	C42 (chr1)	1.574	0.0046
MIMAT0019789_st	hsa-miR-4695-3p	-	-	1.564	0.0040
MIMAT0018360_st	hsa-miR-3944-3p	-	-	1.552	0.0041
MIMAT0007349_st	hsa-miR-1471	mir-1471	-	1.550	0.0052
MIMAT0024617_st	hsa-miR-6133	mir-6133	-	1.546	0.0042
MIMAT0019887_st	hsa-miR-4750-5p	-	-	1.538	0.0027
MIMAT0023694_st	hsa-miR-6069	-	C112 (chr22)	1.529	0.0045
MIMAT0027512_st	hsa-miR-6806-5p	-	-	1.527	0.0045
MIMAT0030998_st	hsa-miR-8071	miR-8071	-	1.503	0.0050
MIMAT0019949_st	hsa-miR-4785	-	-	1.499	0.0084
MIMAT0019788_st	hsa-miR-4695-5p	-	-	1.492	0.0036
MIMAT0019779_st	hsa-miR-4690-5p	-	-	1.481	0.0041
MIMAT0019221_st	hsa-miR-3677-5p	-	C25 (chr16)	1.478	0.0066
MIMAT0003263_st	hsa-miR-595	mir-595	-	1.477	0.0066
MIMAT0015065_st	hsa-miR-3185	-	-	1.476	0.0046
MIMAT0018005_st	hsa-miR-3622b-5p	mir-3622[#]	C132 (chr8)[†]	1.467	0.0091
MIMAT0000772_st	hsa-miR-345-5p	mir-345	-	1.464	0.0122
MIMAT0027392_st	hsa-miR-6746-5p	-	-	1.462	0.0085
MIMAT0012735_st	hsa-miR-718	mir-718	-	1.455	0.0100
MIMAT0005586_st	hsa-miR-1231	mir-1231	-	1.453	0.0049
MIMAT0027554_st	hsa-miR-6827-5p	mir-6827	-	1.452	0.0095
MIMAT0016873_st	hsa-miR-4322	-	-	1.449	0.0066
MIMAT0027612_st	hsa-miR-6856-5p	-	-	1.442	0.0110
MIMAT0017994_st	hsa-miR-3615	mir-3615	-	1.429	0.0103
MIMAT0027686_st	hsa-miR-6893-5p	-	-	1.426	0.0117
MIMAT0005866_st	hsa-miR-1203	mir-1203	-	1.420	0.0102
MIMAT0015069_st	hsa-miR-3187-3p	-	C91 (chr19)[†]	1.417	0.0065
MIMAT0004696_st	hsa-miR-323a-5p	mir-154	C2 (chr14)	1.413	0.0134
MIMAT0000762_st	hsa-miR-324-3p	mir-324[#]	-	1.408	0.0153
MIMAT0019844_st	hsa-miR-4725-3p	-	C83 (chr17)	1.395	0.0099
MIMAT0027492_st	hsa-miR-6796-5p	-	-	1.392	0.0122
MIMAT0015024_st	hsa-miR-3151-5p	mir-3151	-	1.385	0.0187
MIMAT0027484_st	hsa-miR-6792-5p	-	-	1.384	0.0117
MIMAT0027501_st	hsa-miR-6800-3p	-	-	1.379	0.0112
MIMAT0018943_st	hsa-miR-4428	mir-4428	-	1.359	0.0186
MIMAT0027498_st	hsa-miR-6799-5p	-	-	1.346	0.0133
MIMAT0000426_st	hsa-miR-132-3p	mir-132	C77 (chr17)	1.345	0.0101
MIMAT0018966_st	hsa-miR-4447	-	-	1.345	0.0195
MIMAT0019065_st	hsa-miR-4526	mir-4526	-	1.343	0.0187
MIMAT0004957_st	hsa-miR-760	mir-760	-	1.340	0.0217
MIMAT0004804_st	hsa-miR-615-5p	mir-615	-	1.338	0.0221
MIMAT0004702_st	hsa-miR-339-3p	mir-339	-	1.334	0.0087
MIMAT0021120_st	hsa-miR-5189-5p	-	-	1.332	0.0135
MIMAT0019815_st	hsa-miR-4710	-	-	1.327	0.0155
MIMAT0000438_st	hsa-miR-152-3p	mir-148	-	1.321	0.0090
MIMAT0019947_st	hsa-miR-4783-3p	-	-	1.314	0.0136

MIMAT0019957_st	hsa-miR-4787-3p	-	-	1.309	0.0188
MIMAT0004976_st	hsa-miR-933	mir-933	-	1.305	0.0348
MIMAT0000761_st	hsa-miR-324-5p	mir-324[#]	-	1.302	0.0241
MIMAT0027468_st	hsa-miR-6784-5p	-	-	1.299	0.0225
MIMAT0005939_st	hsa-miR-1281	mir-1281	-	1.295	0.0123
MIMAT0027678_st	hsa-miR-6889-5p	-	-	1.286	0.0271
MIMAT0027486_st	hsa-miR-6793-5p	-	-	1.279	0.0266
MIMAT0004486_st	hsa-let-7f-1-3p	let-7	C39 (chr9)	1.279	0.0205
MIMAT0018178_st	hsa-miR-3180	miR-3180	-	1.272	0.0221
MIMAT0019948_st	hsa-miR-4784	-	-	1.260	0.0227
MIMAT0027371_st	hsa-miR-6735-5p	-	-	1.237	0.0219
MIMAT0016882_st	hsa-miR-4253	-	-	1.236	0.0296
MIMAT0019020_st	hsa-miR-4486	-	-	1.234	0.0205
MIMAT0023711_st	hsa-miR-6086	-	-	1.233	0.0307
MIMAT0025486_st	hsa-miR-6515-5p	-	-	1.232	0.0343
MIMAT0004587_st	hsa-miR-23b-5p	mir-23	C17 (chr9)	1.229	0.0392
MIMAT0018937_st	hsa-miR-378g	-	-	1.228	0.0395
MIMAT0022297_st	hsa-miR-5589-5p	-	-	1.227	0.0267
MIMAT0018191_st	hsa-miR-3917	-	-	1.226	0.0365
MIMAT0019940_st	hsa-miR-4436b-5p	miR-4436	-	1.224	0.0218
MIMAT0005951_st	hsa-miR-1307-3p	mir-1307	-	1.219	0.0237
MIMAT0027452_st	hsa-miR-6776-5p	-	-	1.217	0.0240
MIMAT0027520_st	hsa-miR-6810-5p	-	-	1.217	0.0349
MIMAT0019075_st	hsa-miR-4535	-	-	1.213	0.0398
MIMAT0018003_st	hsa-miR-3622a-5p	mir-3622[#]	C132 (chr8)[†]	1.208	0.0433
MIMAT0027530_st	hsa-miR-6815-5p	-	-	1.206	0.0411
MIMAT0004611_st	hsa-miR-185-3p	mir-185	-	1.206	0.0251
MIMAT0000281_st	hsa-miR-224-5p	mir-224[#]	C152 (chrX)[†]	1.203	0.0243
MIMAT0018994_st	hsa-miR-4467	-	C129 (chr7)	1.202	0.0276
MIMAT0004780_st	hsa-miR-532-3p	mir-188	C4 (chrX)	1.202	0.0281
MIMAT0005826_st	hsa-miR-1181	mir-1181	-	1.201	0.0331
MIMAT0027385_st	hsa-miR-6742-5p	-	-	1.196	0.0348
MIMAT0005865_st	hsa-miR-1202	mir-1202	-	1.195	0.0415
MIMAT0026477_st	hsa-miR-128-1-5p	mir-128	-	1.187	0.0306
MIMAT0022260_st	hsa-miR-5572	-	-	1.182	0.0313
MIMAT0000731_st	hsa-miR-378a-5p	mir-378[#]	-	1.181	0.0345
MIMAT0027357_st	hsa-miR-6728-5p	-	-	1.175	0.0378
MIMAT0027353_st	hsa-miR-6726-5p	-	-	1.174	0.0378
MIMAT0003307_st	hsa-miR-637	mir-637	-	1.173	0.0417
MIMAT0028109_st	hsa-miR-7106-5p	-	-	1.170	0.0415
MIMAT0026612_st	hsa-miR-504-3p	mir-504	-	1.166	0.0396
MIMAT0004811_st	hsa-miR-33b-3p	mir-33	C81 (chr17)	1.157	0.0396
MIMAT0027622_st	hsa-miR-6860	-	-	1.145	0.0416
MIMAT0005583_st	hsa-miR-1228-3p	mir-1228	-	1.145	0.0454
MIMAT0022691_st	hsa-miR-197-5p	mir-197	-	1.144	0.0394
MIMAT0021021_st	hsa-miR-5001-5p	-	-	1.139	0.0343
MIMAT0019041_st	hsa-miR-4505	-	-	1.133	0.0382
MIMAT0004284_st	hsa-miR-675-5p	mir-675	-	1.128	0.0480
MIMAT0000430_st	hsa-miR-138-5p	miR-138	-	1.124	0.0241
MIMAT0004948_st	hsa-miR-885-3p	mir-885	-	1.124	0.0414
MIMAT0027377_st	hsa-miR-6738-5p	-	-	1.123	0.0416
MIMAT0027393_st	hsa-miR-6746-3p	-	-	1.103	0.0397
MIMAT0004792_st	hsa-miR-92b-5p	mir-25	-	1.101	0.0396
MIMAT0027475_st	hsa-miR-6787-3p	-	-	1.099	0.0480
MIMAT0019899_st	hsa-miR-4756-5p	-	-	1.099	0.0415
MIMAT0000420_st	hsa-miR-30b-5p	mir-30[#]	C139 (chr8)	1.099	0.0342
MIMAT0027500_st	hsa-miR-6800-5p	-	-	1.085	0.0417
MIMAT0024615_st	hsa-miR-6131	mir-6131	-	1.072	0.0430

MIMAT0027482_st	hsa-miR-6791-5p	-	-	1.049	0.0478
MIMAT0000449_st	hsa-miR-146a-5p	mir-146	-	0.994	0.0240
MIMAT0018932_st	hsa-miR-378f	miR-378[#]	-	0.947	0.0254
Downregulated miRs (ordered by Log_2 Ratio)					
MIMAT0022742_st	hsa-miR-1273g-3p	mir-1273	C22 (chr1)	-1.869	< 0.001
MIMAT0015052_st	hsa-miR-3175	-	-	-1.731	< 0.001
MIMAT0018961_st	hsa-miR-4443	-	-	-1.711	< 0.001
MIMAT0000072_st	hsa-miR-18a-5p	mir-17[#]	C6 (chr13)[†]	-1.710	< 0.001
MIMAT0000098_st	hsa-miR-100-5p	mir-10	C60 (chr11)	-1.642	< 0.001
MIMAT0002816_st	hsa-miR-494-3p	mir-154[#]	C2 (chr14)[†]	-1.406	< 0.001
MIMAT0031180_st	hsa-miR-7977	-	-	-1.352	0.0014
MIMAT0029782_st	hsa-miR-7641	miR-7641	-	-1.309	0.0011
MIMAT0000646_st	hsa-miR-155-5p	mir-155	-	-1.281	< 0.001
MIMAT0019745_st	hsa-miR-4668-5p	-	-	-1.275	0.0010
MIMAT0030427_st	hsa-miR-7852-3p	-	-	-1.275	0.0009
MIMAT0017991_st	hsa-miR-3613-3p	mir-3613	-	-1.269	0.0012
MIMAT0001639_st	hsa-miR-409-3p	mir-154[#]	C2 (chr14)[†]	-1.249	0.0020
MIMAT0031002_st	hsa-miR-8075	-	-	-1.171	0.0008
MIMAT0001631_st	hsa-miR-451a	mir-451	C14 (chr17)	-1.120	0.0012
MIMAT0004514_st	hsa-miR-29b-1-5p	mir-29[#]	C130 (chr7)[†]	-1.092	0.0035
MIMAT0022259_st	hsa-miR-5100	-	-	-1.079	0.0042
MIMAT0018976_st	hsa-miR-4454	-	-	-1.060	0.0050
MIMAT0016915_st	hsa-miR-4284	-	-	-1.042	0.0040
MIMAT0000086_st	hsa-miR-29a-3p	mir-29[#]	C130 (chr7)[†]	-1.013	0.0028
MIMAT0018938_st	hsa-miR-548ac	mir-548[#]	-	-0.989	0.0043
MIMAT0031178_st	hsa-miR-7975	-	-	-0.932	0.0155
MIMAT0004496_st	hsa-miR-23a-5p	mir-23	C29 (chr19)	-0.930	0.0044
MIMAT0000103_st	hsa-miR-106a-5p	mir-17[#]	C7 (chrX)[†]	-0.925	0.0101
MIMAT0005925_st	hsa-miR-1272	mir-1272	-	-0.919	0.0091
MIMAT0002176_st	hsa-miR-485-3p	mir-485	C2 (chr14)[†]	-0.918	0.0094
MIMAT0019018_st	hsa-miR-4484	mir-4484	-	-0.898	0.0076
MIMAT0031011_st	hsa-miR-8084	-	-	-0.897	0.0088
MIMAT0004767_st	hsa-miR-193b-5p	mir-193[#]	C73 (chr16)[†]	-0.881	0.0039
MIMAT0000446_st	hsa-miR-127-3p	mir-127	C3 (chr14)[†]	-0.871	0.0041
MIMAT0001412_st	hsa-miR-18b-5p	mir-17[#]	C7 (chrX)[†]	-0.863	0.0095
MIMAT0002814_st	hsa-miR-432-5p	mir-432	C3 (chr14)[†]	-0.858	0.0143
MIMAT0000070_st	hsa-miR-17-5p	mir-17[#]	C6 (chr13)[†]	-0.852	0.0187
MIMAT0018196_st	hsa-miR-3921	-	-	-0.812	0.0085
MIMAT0018936_st	hsa-miR-4423-3p	mir-4423	-	-0.810	0.0054
MIMAT0015021_st	hsa-miR-3148	-	-	-0.803	0.0039
MIMAT0015086_st	hsa-miR-3201	-	-	-0.803	0.0086
MIMAT0000691_st	hsa-miR-130b-3p	mir-130	C110 (chr22)	-0.798	0.0154
MIMAT0015041_st	hsa-miR-1260b	mir-1260b	-	-0.790	0.0276
MIMAT0018358_st	hsa-miR-3942-5p	-	-	-0.774	0.0214
MIMAT0028117_st	hsa-miR-7110-5p	-	-	-0.773	0.0160
MIMAT0000423_st	hsa-miR-125b-5p	-	-	-0.756	0.0187
MIMAT0018071_st	hsa-miR-3651	-	-	-0.750	0.0186
MIMAT0018447_st	hsa-miR-548aa	-	-	-0.748	0.0328
MIMAT0022730_st	hsa-miR-548t-3p	mir-548[#]	-	-0.748	0.0328
MIMAT0014991_st	hsa-miR-3128	-	-	-0.720	0.0092
MIMAT0018990_st	hsa-miR-548aj-3p	-	-	-0.704	0.0377
MIMAT0002819_st	hsa-miR-193b-3p	mir-193[#]	C73 (chr16)[†]	-0.703	0.0414
MIMAT0003251_st	hsa-miR-548a-3p	-	-	-0.681	0.0229
MIMAT0019019_st	hsa-miR-4485	-	-	-0.631	0.0270
MIMAT0018984_st	hsa-miR-378h	miR-378	-	-0.627	0.0324

***, Diferentially expressed (DE) microRNAs (miRs) were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio**

Expression ($|Log_2Ratio| > 0.6$), followed by multiple correction using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or $q < 0.05$); [#], miR family represented with more than one DE miR in this dataset; [†], miR cluster represented with more than one DE miR in this dataset.

TABLE S11. Differentially expressed microRNAs in CRSwNP air-liquid interface culture after 28 days of differentiation compared to day 0 (monolayer of hNP-BSCs).*

MIMAT ID	Transcript ID	miR Family	Cluster ID (Chromosome)	Log_2 Ratio	P.value
Upregulated miRs (ordered by Log_2 Ratio)					
MIMAT0001541_st	hsa-miR-449a	mir-449[#]	C34 (chr5)[†]	3.478	< 0.001
MIMAT0030991_st	hsa-miR-8064	-	-	3.267	< 0.001
MIMAT0003327_st	hsa-miR-449b-5p	mir-449[#]	C34 (chr5)[†]	3.263	< 0.001
MIMAT0025472_st	hsa-miR-6508-5p	-	-	3.245	< 0.001
MIMAT0010251_st	hsa-miR-449c-5p	mir-449[#]	C34 (chr5)[†]	3.231	< 0.001
MIMAT0009198_st	hsa-miR-224-3p	mir-224[#]	C152 (chrX)[†]	3.104	< 0.001
MIMAT0015061_st	hsa-miR-3181	-	-	3.010	< 0.001
MIMAT0016862_st	hsa-miR-4310	-	-	2.844	< 0.001
MIMAT0027583_st	hsa-miR-6840-3p	-	-	2.835	< 0.001
MIMAT0005873_st	hsa-miR-1208	mir-1208	-	2.620	< 0.001
MIMAT0000692_st	hsa-miR-30e-5p	mir-30[#]	C42 (chr1)	2.570	< 0.001
MIMAT0022720_st	hsa-miR-1304-3p	mir-1304	-	2.565	< 0.001
MIMAT0028230_st	hsa-miR-7160-5p	-	-	2.563	< 0.001
MIMAT0022257_st	hsa-miR-5571-5p	-	-	2.482	< 0.001
MIMAT0027575_st	hsa-miR-6836-3p	-	-	2.467	< 0.001
MIMAT0019881_st	hsa-miR-4746-3p	-	-	2.465	< 0.001
MIMAT0031119_st	hsa-miR-1199-5p	mir-1199[#]	-	2.460	< 0.001
MIMAT0001343_st	hsa-miR-425-3p	mir-425	C114 (chr3)[†]	2.431	< 0.001
MIMAT0019892_st	hsa-miR-371b-5p	mir-290	C16 (chr19)[†]	2.403	< 0.001
MIMAT0019755_st	hsa-miR-4673	miR-486	-	2.398	< 0.001
MIMAT0019919_st	hsa-miR-4767	-	-	2.382	< 0.001
MIMAT0000242_st	hsa-miR-129-5p	miR-129	-	2.359	< 0.001
MIMAT0000773_st	hsa-miR-346	mir-346	-	2.328	< 0.001
MIMAT0023709_st	hsa-miR-6084	-	-	2.326	< 0.001
MIMAT0019082_st	hsa-miR-4539	-	C13 (chr14)	2.325	< 0.001
MIMAT0009203_st	hsa-miR-449b-3p	mir-449[#]	C34 (chr5)[†]	2.296	< 0.001
MIMAT0005576_st	hsa-miR-1226-5p	mir-1226	-	2.290	< 0.001
MIMAT0027418_st	hsa-miR-6759-5p	-	-	2.289	< 0.001
MIMAT0019011_st	hsa-miR-4479	-	-	2.231	0.0002
MIMAT0023706_st	hsa-miR-6081	-	-	2.225	0.0002
MIMAT0027375_st	hsa-miR-6737-5p	-	-	2.212	0.0002
MIMAT0027501_st	hsa-miR-6800-3p	-	-	2.181	0.0002
MIMAT0001618_st	hsa-miR-191-3p	mir-191	C114 (chr3)[†]	2.175	0.0002
MIMAT0004677_st	hsa-miR-34c-3p	mir-34[#]	C59 (chr11)[†]	2.143	0.0001
MIMAT0019050_st	hsa-miR-4513	-	-	2.128	0.0003
MIMAT0019074_st	hsa-miR-378i	miR-378[#]	-	2.113	0.0004
MIMAT0027409_st	hsa-miR-6754-3p	-	-	2.102	0.0005
MIMAT0019789_st	hsa-miR-4695-3p	-	-	2.096	0.0004
MIMAT0005593_st	hsa-miR-1238-3p	mir-1238	-	2.095	0.0004
MIMAT0031000_st	hsa-miR-8073	-	-	2.088	0.0004
MIMAT0005458_st	hsa-miR-1224-5p	mir-1224	-	2.066	0.0006
MIMAT0003237_st	hsa-miR-572	mir-572	-	2.038	0.0004
MIMAT0003309_st	hsa-miR-639	mir-639	-	1.993	0.0008
MIMAT0018999_st	hsa-miR-4472	-	-	1.989	0.0009
MIMAT0023705_st	hsa-miR-6080	-	-	1.988	0.0004
MIMAT0016919_st	hsa-miR-4292	-	-	1.955	0.0009
MIMAT0004762_st	hsa-miR-486-3p	-	-	1.928	0.0020
MIMAT0007890_st	hsa-miR-1914-3p	mir-1914	C106 (chr20)	1.907	0.0019
MIMAT0030998_st	hsa-miR-8071	miR-8071	-	1.905	0.0019
MIMAT0000728_st	hsa-miR-375	mir-375	-	1.887	0.0018
MIMAT0019853_st	hsa-miR-4731-5p	-	-	1.884	0.0019

MIMAT0004284_st	hsa-miR-675-5p	mir-675	-	1.866	0.0024
MIMAT0000686_st	hsa-miR-34c-5p	mir-34[#]	C59 (chr11)[†]	1.864	0.0019
MIMAT0019065_st	hsa-miR-4526	mir-4526	-	1.861	0.0019
MIMAT0003221_st	hsa-miR-557	mir-557	-	1.861	0.0021
MIMAT0019221_st	hsa-miR-3677-5p	-	C25 (chr16)[†]	1.856	0.0020
MIMAT0023693_st	hsa-miR-6068	-	-	1.846	0.0009
MIMAT0019216_st	hsa-miR-3187-5p	-	C91 (chr19)[†]	1.846	0.0020
MIMAT0000762_st	hsa-miR-324-3p	mir-324[#]	-	1.821	0.0049
MIMAT0004498_st	hsa-miR-25-5p	mir-25[#]	C35 (chr7)	1.811	0.0024
MIMAT0005943_st	hsa-miR-1292-5p	mir-1292[#]	-	1.805	0.0019
MIMAT0018932_st	hsa-miR-378f	miR-378[#]	-	1.803	0.0054
MIMAT0000438_st	hsa-miR-152-3p	mir-148	-	1.800	0.0048
MIMAT0023694_st	hsa-miR-6069	-	C112 (chr22)	1.792	0.0023
MIMAT0000281_st	hsa-miR-224-5p	mir-224[#]	C152 (chrX)[†]	1.790	0.0026
MIMAT0012735_st	hsa-miR-718	mir-718	-	1.767	0.0030
MIMAT0002888_st	hsa-miR-532-5p	mir-188[#]	C4 (chrX)[†]	1.751	0.0063
MIMAT0011777_st	hsa-miR-2277-3p	-	-	1.718	0.0054
MIMAT0015024_st	hsa-miR-3151-5p	mir-3151	-	1.711	0.0049
MIMAT0000432_st	hsa-miR-141-3p	mir-8[#]	C61 (chr12)	1.709	0.0070
MIMAT0027424_st	hsa-miR-6762-5p	-	-	1.704	0.0054
MIMAT0000420_st	hsa-miR-30b-5p	mir-30[#]	C139 (chr8)[†]	1.700	0.0053
MIMAT0019810_st	hsa-miR-4708-3p	-	-	1.699	0.0026
MIMAT0004976_st	hsa-miR-933	mir-933	-	1.690	0.0069
MIMAT0005583_st	hsa-miR-1228-3p	mir-1228	-	1.687	0.0049
MIMAT0019779_st	hsa-miR-4690-5p	-	-	1.684	0.0029
MIMAT0018360_st	hsa-miR-3944-3p	-	-	1.674	0.0043
MIMAT0000772_st	hsa-miR-345-5p	mir-345	-	1.674	0.0056
MIMAT0007349_st	hsa-miR-1471	mir-1471	-	1.657	0.0050
MIMAT0022693_st	hsa-miR-204-3p	mir-204	-	1.654	0.0036
MIMAT0027602_st	hsa-miR-6851-5p	-	-	1.648	0.0063
MIMAT0004696_st	hsa-miR-323a-5p	mir-154	C2 (chr14)	1.643	0.0064
MIMAT0027686_st	hsa-miR-6893-5p	-	-	1.641	0.0064
MIMAT0016873_st	hsa-miR-4322	-	-	1.641	0.0040
MIMAT0018005_st	hsa-miR-3622b-5p	mir-3622	C132 (chr8)	1.636	0.0063
MIMAT0019740_st	hsa-miR-4665-3p	-	-	1.634	0.0072
MIMAT0004587_st	hsa-miR-23b-5p	mir-23	C17 (chr9)	1.634	0.0072
MIMAT0027444_st	hsa-miR-6772-5p	-	-	1.633	0.0063
MIMAT0027512_st	hsa-miR-6806-5p	-	-	1.628	0.0059
MIMAT0027498_st	hsa-miR-6799-5p	-	-	1.621	0.0054
MIMAT0004611_st	hsa-miR-185-3p	mir-185	-	1.620	0.0057
MIMAT0004702_st	hsa-miR-339-3p	mir-339	-	1.612	0.0054
MIMAT0000097_st	hsa-miR-99a-5p	mir-10[#]	C108 (chr21)	1.607	0.0082
MIMAT0027642_st	hsa-miR-6871-5p	-	-	1.607	0.0055
MIMAT0018960_st	hsa-miR-4442	-	-	1.604	0.0069
MIMAT0019695_st	hsa-miR-4638-5p	-	-	1.590	0.0063
MIMAT0027574_st	hsa-miR-6836-5p	-	-	1.589	0.0097
MIMAT0024617_st	hsa-miR-6133	mir-6133	-	1.586	0.0075
MIMAT0027554_st	hsa-miR-6827-5p	mir-6827	-	1.583	0.0076
MIMAT0027383_st	hsa-miR-6741-5p	-	-	1.582	0.0055
MIMAT0019887_st	hsa-miR-4750-5p	-	-	1.580	0.0051
MIMAT0016913_st	hsa-miR-4285	-	-	1.579	0.0097
MIMAT0019788_st	hsa-miR-4695-5p	-	-	1.574	0.0049
MIMAT0017994_st	hsa-miR-3615	mir-3615	-	1.563	0.0088
MIMAT0004494_st	hsa-miR-21-3p	mir-21[#]	-	1.559	0.0160
MIMAT0021033_st	hsa-miR-5006-5p	-	-	1.543	0.0097
MIMAT0004773_st	hsa-miR-500a-5p	mir-500[#]	C4 (chrX)[†]	1.538	0.0169
MIMAT0004780_st	hsa-miR-532-3p	mir-188[#]	C4 (chrX)[†]	1.533	0.0074
MIMAT0005586_st	hsa-miR-1231	mir-1231	-	1.530	0.0064

MIMAT0000731_st	hsa-miR-378a-5p	mir-378[#]	-	1.525	0.0116
MIMAT0019015_st	hsa-miR-4481	-	-	1.523	0.0098
MIMAT0019836_st	hsa-miR-4722-5p	-	-	1.517	0.0104
MIMAT0000682_st	hsa-miR-200a-3p	mir-8[#]	C21 (chr1)[†]	1.515	0.0217
MIMAT0004804_st	hsa-miR-615-5p	mir-615	-	1.512	0.0115
MIMAT0019845_st	hsa-miR-4726-5p	-	-	1.505	0.0113
MIMAT0005867_st	hsa-miR-663b	mir-663	-	1.505	0.0112
MIMAT0004986_st	hsa-miR-943	mir-943	-	1.504	0.0136
MIMAT0005866_st	hsa-miR-1203	mir-1203	-	1.500	0.0121
MIMAT0027492_st	hsa-miR-6796-5p	-	-	1.488	0.0123
MIMAT0015069_st	hsa-miR-3187-3p	-	C91 (chr19)[†]	1.488	0.0089
MIMAT0016882_st	hsa-miR-4253	-	-	1.485	0.0168
MIMAT0027558_st	hsa-miR-6829-5p	miR-4436[#]	-	1.478	0.0113
MIMAT0019844_st	hsa-miR-4725-3p	-	C83 (chr17)[†]	1.473	0.0169
MIMAT0021120_st	hsa-miR-5189-5p	-	-	1.471	0.0106
MIMAT0019815_st	hsa-miR-4710	-	-	1.469	0.0119
MIMAT0019948_st	hsa-miR-4784	-	-	1.469	0.0130
MIMAT0003336_st	hsa-miR-658	mir-658	C113 (chr22)	1.465	0.0222
MIMAT0027408_st	hsa-miR-6754-5p	-	-	1.465	0.0141
MIMAT0000245_st	hsa-miR-30d-5p	mir-30[#]	C139 (chr8)[†]	1.461	0.0257
MIMAT0018937_st	hsa-miR-378g	miR-378[#]	-	1.457	0.0161
MIMAT0000076_st	hsa-miR-21-5p	mir-21[#]	-	1.453	0.0294
MIMAT0004561_st	hsa-miR-187-5p	mir-187	-	1.452	0.0153
MIMAT0015065_st	hsa-miR-3185	-	-	1.451	0.0097
MIMAT0027377_st	hsa-miR-6738-5p	-	-	1.449	0.0201
MIMAT0001635_st	hsa-miR-452-5p	mir-452	C152 (chrX)[†]	1.445	0.0131
MIMAT0005939_st	hsa-miR-1281	mir-1281	-	1.444	0.0076
MIMAT0022297_st	hsa-miR-5589-5p	miR-138[#]	-	1.439	0.0163
MIMAT0004957_st	hsa-miR-760	mir-760	-	1.432	0.0153
MIMAT0019020_st	hsa-miR-4486	-	-	1.431	0.0113
MIMAT0019949_st	hsa-miR-4785	-	-	1.431	0.0208
MIMAT0000725_st	hsa-miR-373-5p	mir-373	C16 (chr19)[†]	1.430	0.0207
MIMAT0019056_st	hsa-miR-4519	miR-378[#]	-	1.421	0.0199
MIMAT0027357_st	hsa-miR-6728-5p	-	-	1.407	0.0264
MIMAT0026477_st	hsa-miR-128-1-5p	mir-128	-	1.406	0.0201
MIMAT0027530_st	hsa-miR-6815-5p	miR-378[#]	-	1.404	0.0208
MIMAT0018958_st	hsa-miR-4440	-	-	1.401	0.0220
MIMAT0027414_st	hsa-miR-6757-5p	miR-548	-	1.401	0.0242
MIMAT0003338_st	hsa-miR-660-5p	mir-188[#]	C4 (chrX)[†]	1.382	0.0312
MIMAT0017999_st	hsa-miR-3619-5p	-	-	1.380	0.0134
MIMAT0003263_st	hsa-miR-595	mir-595	-	1.380	0.0208
MIMAT0019771_st	hsa-miR-4685-5p	-	-	1.379	0.0285
MIMAT0027612_st	hsa-miR-6856-5p	-	-	1.377	0.0209
MIMAT0018084_st	hsa-miR-3663-5p	-	-	1.370	0.0224
MIMAT0018191_st	hsa-miR-3917	-	-	1.364	0.0257
MIMAT0028125_st	hsa-miR-7114-5p	-	-	1.362	0.0195
MIMAT0004983_st	hsa-miR-940	mir-940	C25 (chr16)[†]	1.362	0.0266
MIMAT0019843_st	hsa-miR-4725-5p	-	C83 (chr17)[†]	1.362	0.0235
MIMAT0025486_st	hsa-miR-6515-5p	-	-	1.358	0.0318
MIMAT0004775_st	hsa-miR-502-3p	mir-500[#]	C4 (chrX)[†]	1.356	0.0412
MIMAT0027353_st	hsa-miR-6726-5p	-	-	1.354	0.0209
MIMAT0027385_st	hsa-miR-6742-5p	-	-	1.353	0.0311
MIMAT0004515_st	hsa-miR-29b-2-5p	mir-29	C50 (chr1)	1.351	0.0199
MIMAT0003307_st	hsa-miR-637	mir-637	-	1.347	0.0270
MIMAT0005951_st	hsa-miR-1307-3p	mir-1307	-	1.343	0.0200
MIMAT0018966_st	hsa-miR-4447	-	-	1.341	0.0313
MIMAT0027392_st	hsa-miR-6746-5p	-	-	1.336	0.0320
MIMAT0000222_st	hsa-miR-192-5p	mir-192	C12 (chr11)	1.335	0.0381

MIMAT0004486_st	hsa-let-7f-1-3p	let-7	C39 (chr9)	1.332	0.0281
MIMAT0019075_st	hsa-miR-4535	-	-	1.330	0.0261
MIMAT0027520_st	hsa-miR-6810-5p	-	-	1.328	0.0266
MIMAT0000318_st	hsa-miR-200b-3p	mir-8[#]	C21 (chr1)[†]	1.326	0.0451
MIMAT0018965_st	hsa-miR-4446-3p	mir-4446	-	1.323	0.0223
MIMAT0019874_st	hsa-miR-4743-5p	mir-4743	-	1.320	0.0320
MIMAT0027431_st	hsa-miR-6765-3p	-	-	1.313	0.0310
MIMAT0019041_st	hsa-miR-4505	-	-	1.308	0.0246
MIMAT0004602_st	hsa-miR-125a-3p	mir-10[#]	C30 (chr19)	1.305	0.0328
MIMAT0000705_st	hsa-miR-362-5p	mir-362	C4 (chrX)[†]	1.302	0.0405
MIMAT0027678_st	hsa-miR-6889-5p	-	-	1.300	0.0404
MIMAT0005865_st	hsa-miR-1202	mir-1202	-	1.298	0.0380
MIMAT0019940_st	hsa-miR-4436b-5p	miR-4436[#]	-	1.294	0.0242
MIMAT0028109_st	hsa-miR-7106-5p	-	-	1.293	0.0381
MIMAT0019979_st	hsa-miR-4800-3p	-	-	1.289	0.0409
MIMAT0019071_st	hsa-miR-4532	-	-	1.286	0.0320
MIMAT0018178_st	hsa-miR-3180	miR-3180[#]	-	1.285	0.0282
MIMAT0031120_st	hsa-miR-1199-3p	mir-1199[#]	-	1.285	0.0311
MIMAT0027475_st	hsa-miR-6787-3p	-	-	1.277	0.0285
MIMAT0019754_st	hsa-miR-4672	mir-4672	-	1.274	0.0349
MIMAT0000761_st	hsa-miR-324-5p	mir-324[#]	-	1.269	0.0262
MIMAT0026916_st	hsa-miR-1908-3p	mir-1908	-	1.257	0.0341
MIMAT0022948_st	hsa-miR-1292-3p	mir-1292[#]	-	1.253	0.0380
MIMAT0027371_st	hsa-miR-6735-5p	-	-	1.253	0.0446
MIMAT0018994_st	hsa-miR-4467	-	C129 (chr7)	1.252	0.0312
MIMAT0019957_st	hsa-miR-4787-3p	-	-	1.248	0.0454
MIMAT0027598_st	hsa-miR-6849-5p	-	C38 (chr8)	1.243	0.0348
MIMAT0027484_st	hsa-miR-6792-5p	-	-	1.239	0.0461
MIMAT0027486_st	hsa-miR-6793-5p	-	-	1.239	0.0452
MIMAT0027462_st	hsa-miR-6781-5p	-	-	1.229	0.0396
MIMAT0004792_st	hsa-miR-92b-5p	mir-25[#]	-	1.227	0.0322
MIMAT0003227_st	hsa-miR-563	mir-563	-	1.221	0.0436
MIMAT0026612_st	hsa-miR-504-3p	mir-504	-	1.219	0.0452
MIMAT0022260_st	hsa-miR-5572	-	-	1.215	0.0410
MIMAT0019721_st	hsa-miR-4655-5p	-	-	1.214	0.0418
MIMAT0019722_st	hsa-miR-4655-3p	-	-	1.214	0.0487
MIMAT0007882_st	hsa-miR-1909-5p	mir-1909	-	1.213	0.0464
MIMAT0019033_st	hsa-miR-4498	-	-	1.210	0.0394
MIMAT0019899_st	hsa-miR-4756-5p	-	-	1.199	0.0447
MIMAT0018926_st	hsa-miR-378d	-	-	1.198	0.0387
MIMAT0015070_st	hsa-miR-3188	mir-3188	-	1.197	0.0410
MIMAT0027639_st	hsa-miR-6869-3p	-	-	1.196	0.0496
MIMAT0003228_st	hsa-miR-564	mir-564	-	1.185	0.0495
MIMAT0027406_st	hsa-miR-6753-5p	-	-	1.182	0.0457
MIMAT0019946_st	hsa-miR-4783-5p	-	-	1.178	0.0495
MIMAT0021021_st	hsa-miR-5001-5p	-	-	1.177	0.0436
MIMAT0019807_st	hsa-miR-4707-5p	-	-	1.176	0.0436
MIMAT0027500_st	hsa-miR-6800-5p	-	-	1.175	0.0414
MIMAT0015058_st	hsa-miR-3180-3p	miR-3180[#]	-	1.173	0.0462
MIMAT0019947_st	hsa-miR-4783-3p	-	-	1.172	0.0407
MIMAT0016878_st	hsa-miR-4257	-	-	1.161	0.0462
MIMAT0022977_st	hsa-miR-4632-5p	-	-	1.159	0.0478
MIMAT0019859_st	hsa-miR-4734	-	-	1.157	0.0498
MIMAT0000088_st	hsa-miR-30a-3p	mir-30[#]	-	1.055	0.0445
MIMAT0000430_st	hsa-miR-138-5p	miR-138[#]	-	1.005	0.0408
Downregulated miRs (ordered by Log_2 Ratio)					
MIMAT0000098_st	hsa-miR-100-5p	mir-10[#]	C60 (chr11)	-3.135	< 0.001

MIMAT0000072_st	hsa-miR-18a-5p	mir-17[#]	C6 (chr13)[†]	-2.819	< 0.001
MIMAT0017990_st	hsa-miR-3613-5p	mir-3613[#]	-	-2.707	< 0.001
MIMAT0000646_st	hsa-miR-155-5p	mir-155	-	-2.468	< 0.001
MIMAT0002816_st	hsa-miR-494-3p	mir-154[#]	C2 (chr14)[†]	-2.192	< 0.001
MIMAT0022742_st	hsa-miR-1273g-3p	mir-1273	C22 (chr1)	-1.995	< 0.001
MIMAT0001639_st	hsa-miR-409-3p	mir-154[#]	C2 (chr14)[†]	-1.929	< 0.001
MIMAT0001412_st	hsa-miR-18b-5p	mir-17[#]	C7 (chrX)[†]	-1.869	< 0.001
MIMAT0000446_st	hsa-miR-127-3p	mir-127	C3 (chr14)[†]	-1.837	< 0.001
MIMAT0018961_st	hsa-miR-4443	-	-	-1.687	< 0.001
MIMAT0015052_st	hsa-miR-3175	-	-	-1.656	< 0.001
MIMAT0031002_st	hsa-miR-8075	-	-	-1.525	< 0.001
MIMAT0029782_st	hsa-miR-7641	miR-7641	-	-1.496	< 0.001
MIMAT0019745_st	hsa-miR-4668-5p	-	-	-1.480	0.0003
MIMAT0017991_st	hsa-miR-3613-3p	mir-3613[#]	-	-1.435	0.0003
MIMAT0000227_st	hsa-miR-197-3p	mir-197	-	-1.433	0.0003
MIMAT0000103_st	hsa-miR-106a-5p	mir-17[#]	C7 (chrX)[†]	-1.351	0.0005
MIMAT0000691_st	hsa-miR-130b-3p	mir-130[#]	C110 (chr22)	-1.341	0.0004
MIMAT0000070_st	hsa-miR-17-5p	mir-17[#]	C6 (chr13)[†]	-1.312	0.0005
MIMAT0019018_st	hsa-miR-4484	mir-4484	-	-1.265	0.0005
MIMAT0000423_st	hsa-miR-125b-5p	miR-10[#]	-	-1.243	0.0006
MIMAT0030427_st	hsa-miR-7852-3p	-	-	-1.220	0.0015
MIMAT0000092_st	hsa-miR-92a-3p	miR-25	-	-1.191	0.0011
MIMAT0002814_st	hsa-miR-432-5p	mir-432	C3 (chr14)[†]	-1.117	0.0036
MIMAT0002819_st	hsa-miR-193b-3p	mir-193[#]	C73 (chr16)[†]	-1.112	0.0011
MIMAT0016852_st	hsa-miR-4298	-	-	-1.105	0.0037
MIMAT0031011_st	hsa-miR-8084	-	-	-1.061	0.0034
MIMAT0000733_st	hsa-miR-379-5p	mir-379	C2 (chr14)[†]	-1.051	0.0074
MIMAT0001631_st	hsa-miR-451a	mir-451	C14 (chr17)	-1.041	0.0022
MIMAT0000078_st	hsa-miR-23a-3p	mir-23[#]	C29 (chr19)[†]	-1.039	0.0035
MIMAT0028117_st	hsa-miR-7110-5p	-	-	-1.023	0.0040
MIMAT0003180_st	hsa-miR-487b-3p	mir-154[#]	C2 (chr14)[†]	-1.010	0.0156
MIMAT0030422_st	hsa-miR-7847-3p	-	-	-1.003	0.0055
MIMAT0000086_st	hsa-miR-29a-3p	mir-29[#]	C130 (chr7)[†]	-0.999	0.0034
MIMAT0016915_st	hsa-miR-4284	-	-	-0.992	0.0040
MIMAT0000266_st	hsa-miR-205-5p	mir-205	-	-0.944	0.0036
MIMAT0004514_st	hsa-miR-29b-1-5p	mir-29[#]	C130 (chr7)[†]	-0.930	0.0073
MIMAT0000450_st	hsa-miR-149-5p	mir-149	-	-0.929	0.0052
MIMAT0018938_st	hsa-miR-548ac	mir-548[#]	-	-0.919	0.0067
MIMAT0004496_st	hsa-miR-23a-5p	mir-23[#]	C29 (chr19)[†]	-0.910	0.0051
MIMAT0002176_st	hsa-miR-485-3p	mir-485	C2 (chr14)[†]	-0.907	0.0100
MIMAT0000075_st	hsa-miR-20a-5p	mir-17[#]	C6 (chr13)[†]	-0.895	0.0054
MIMAT0022741_st	hsa-miR-3529-3p	mir-3529	C24 (chr15)	-0.877	0.0091
MIMAT0018196_st	hsa-miR-3921	-	-	-0.868	0.0071
MIMAT0015086_st	hsa-miR-3201	-	-	-0.856	0.0052
MIMAT0031180_st	hsa-miR-7977	-	-	-0.850	0.0164
MIMAT0015081_st	hsa-miR-548x-3p	mir-548[#]	-	-0.844	0.0134
MIMAT0018954_st	hsa-miR-548ae	miR-548[#]	-	-0.835	0.0111
MIMAT0015021_st	hsa-miR-3148	-	-	-0.833	0.0038
MIMAT0009447_st	hsa-miR-1972	miR-1972	-	-0.822	0.0092
MIMAT0031178_st	hsa-miR-7975	-	-	-0.820	0.0242
MIMAT0014991_st	hsa-miR-3128	-	-	-0.818	0.0047
MIMAT0000257_st	hsa-miR-181b-5p	miR-181	-	-0.792	0.0186
MIMAT0018976_st	hsa-miR-4454	-	-	-0.786	0.0327
MIMAT0004784_st	hsa-miR-455-3p	mir-455	-	-0.779	0.0220
MIMAT0004926_st	hsa-miR-708-5p	mir-708	-	-0.756	0.0156
MIMAT0005915_st	hsa-miR-1263	mir-1263	-	-0.751	0.0446
MIMAT0018358_st	hsa-miR-3942-5p	-	-	-0.730	0.0447
MIMAT0000425_st	hsa-miR-130a-3p	mir-130[#]	-	-0.722	0.0035

MIMAT0022965_st	hsa-miR-3606-3p	-	-	-0.720	0.0469
MIMAT0004767_st	hsa-miR-193b-5p	mir-193[#]	C73 (chr16)[†]	-0.719	0.0074
MIMAT0016856_st	hsa-miR-4303	-	-	-0.718	0.0356
MIMAT0019359_st	hsa-miR-3974	-	-	-0.718	0.0351
MIMAT0019980_st	hsa-miR-4801	-	-	-0.715	0.0391
MIMAT0027562_st	hsa-miR-6831-5p	-	-	-0.715	0.0267
MIMAT0000091_st	hsa-miR-33a-5p	mir-33	-	-0.712	0.0400
MIMAT0018984_st	hsa-miR-378h	miR-378	-	-0.712	0.0475
MIMAT0000445_st	hsa-miR-126-3p	mir-126	-	-0.670	0.0359
MIMAT0004501_st	hsa-miR-27a-5p	mir-27	C29 (chr19)[†]	-0.668	0.0035
MIMAT0019834_st	hsa-miR-4720-3p	-	-	-0.649	0.0494
MIMAT0019837_st	hsa-miR-4722-3p	-	-	-0.647	0.0466

***, Diferentially expressed (DE) microRNAs (miRs) were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ($|Log_2Ratio| > 0.6$), followed by multiple correction using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or $q < 0.05$); [#], miR family represented with more than one DE miR in this dataset; [†], miR cluster represented with more than one DE miR in this dataset.**

TABLE S12. Differentially expressed microRNAs in CRSwNP compared to control NM air-liquid interface culture at day 0.*

MIMAT ID	Transcript ID	miR Family	Cluster ID (Chromosome)	log2 Ratio	P.value
Upregulated miRs (ordered by Log_2 Ratio)					
MIMAT0000446_st	hsa-miR-127-3p	mir-127	C3 (chr14)†	2.379	< 0.001
MIMAT0022742_st	hsa-miR-1273g-3p	mir-1273	C22 (chr1)	1.880	< 0.001
MIMAT0001639_st	hsa-miR-409-3p	mir-154#	C2 (chr14)†	1.580	0.0017
MIMAT0000086_st	hsa-miR-29a-3p	mir-29#	C130 (chr7)†	1.506	0.0119
MIMAT0000264_st	hsa-miR-203a	mir-203	C69 (chr14)	1.470	0.0070
MIMAT0004926_st	hsa-miR-708-5p	mir-708	-	1.454	0.0274
MIMAT0002816_st	hsa-miR-494-3p	mir-154#	C2 (chr14)†	1.400	0.0083
MIMAT0017990_st	hsa-miR-3613-5p	mir-3613	-	1.300	0.0071
MIMAT0018961_st	hsa-miR-4443	-	-	1.243	0.0038
MIMAT0002814_st	hsa-miR-432-5p	mir-432	C3 (chr14)†	1.199	0.0111
MIMAT0018444_st	hsa-miR-642b-3p	mir-642	C95 (chr19)	1.117	0.0211
MIMAT0000414_st	hsa-let-7g-5p	let-7	-	1.094	0.0424
MIMAT0030427_st	hsa-miR-7852-3p	-	-	1.092	0.0108
MIMAT0000733_st	hsa-miR-379-5p	mir-379	C2 (chr14)†	1.079	0.0262
MIMAT0004504_st	hsa-miR-31-3p	mir-31	-	1.069	0.0369
MIMAT0000076_st	hsa-miR-21-5p	mir-21	-	1.064	0.0105
MIMAT0002176_st	hsa-miR-485-3p	mir-485	C2 (chr14)†	1.052	0.0204
MIMAT0019021_st	hsa-miR-4487	-	-	0.989	0.0118
MIMAT0004514_st	hsa-miR-29b-1-5p	mir-29#	C130 (chr7)†	0.916	0.0462
Downregulated miRs (ordered by Log_2 Ratio)					
MIMAT0018964_st	hsa-miR-4445-3p	-	-	-2.261	< 0.001
MIMAT0027379_st	hsa-miR-6739-5p	-	-	-1.865	0.0069
MIMAT0000765_st	hsa-miR-335-5p	mir-335	-	-1.850	0.0020
MIMAT0030991_st	hsa-miR-8064	-	-	-1.836	< 0.001
MIMAT0000430_st	hsa-miR-138-5p	mir-138	-	-1.798	< 0.001
MIMAT0019726_st	hsa-miR-4659a-5p	mir-4659	C131 (chr8)	-1.788	0.0078
MIMAT0026638_st	hsa-miR-1468-3p	mir-1468	-	-1.728	0.0050
MIMAT0019704_st	hsa-miR-4644	-	-	-1.599	0.0243
MIMAT0019919_st	hsa-miR-4767	-	-	-1.532	0.0025
MIMAT0000281_st	hsa-miR-224-5p	mir-224	C152 (chrX)	-1.433	0.0071
MIMAT0021038_st	hsa-miR-548ap-3p	mir-548	-	-1.431	0.0302
MIMAT0018184_st	hsa-miR-3910	mir-3910	-	-1.327	0.0458
MIMAT0018936_st	hsa-miR-4423-3p	mir-4423	-	-1.315	0.0242
MIMAT0015061_st	hsa-miR-3181	-	-	-1.293	0.0250
MIMAT0027375_st	hsa-miR-6737-5p	-	-	-1.291	0.0220
MIMAT0021086_st	hsa-miR-5094	-	-	-1.275	0.0230
MIMAT0026641_st	hsa-miR-1298-3p	mir-1298	-	-1.230	0.0290
MIMAT0019881_st	hsa-miR-4746-3p	-	-	-1.199	0.0231
MIMAT0014991_st	hsa-miR-3128	-	-	-1.190	0.0308
MIMAT0027409_st	hsa-miR-6754-3p	-	-	-1.181	0.0316
MIMAT0019853_st	hsa-miR-4731-5p	-	-	-1.143	0.0333
MIMAT0027612_st	hsa-miR-6856-5p	-	-	-1.080	0.0463
MIMAT0004561_st	hsa-miR-187-5p	mir-187	-	-1.049	0.0300
MIMAT0004450_st	hsa-miR-297	mir-297	-	-0.946	0.0205
MIMAT0028235_st	hsa-miR-7162-3p	-	-	-0.915	0.0493
MIMAT0000761_st	hsa-miR-324-5p	mir-324	-	-0.908	0.0462
MIMAT0000449_st	hsa-miR-146a-5p	mir-146	-	-0.778	0.0274

***, Diferentially expressed (DE) microRNAs (miRs) were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ($|Log_2Ratio| > 0.6$), followed by multiple correction using a False Discovery Rate**

(FDR) threshold of 5% (p-adjusted value or q < 0.05); [#], miR family represented with more than one DE miR in this dataset; [†], miR cluster represented with more than one DE miR in this dataset.

TABLE S13. Differentially expressed microRNAs in CRSwNP compared to control NM air-liquid interface culture at day 14.*

MIMAT ID	Transcript ID	miR Family	Cluster ID (Chromosome)	log2 Ratio	P.value
Upregulated miRs (ordered by Log_2 Ratio)					
MIMAT0017990_st	hsa-miR-3613-5p	mir-3613	-	1.868	< 0.001
MIMAT0000446_st	hsa-miR-127-3p	mir-127	C3 (chr14)	1.676	< 0.001
MIMAT0005898_st	hsa-miR-1246	mir-1246	-	1.525	0.0012
MIMAT0000098_st	hsa-miR-100-5p	mir-10	C60 (chr11)	1.517	< 0.001
MIMAT0009447_st	hsa-miR-1972	mir-1972	-	1.315	0.0030
MIMAT0019746_st	hsa-miR-4668-3p	-	-	1.098	0.0443
MIMAT0000646_st	hsa-miR-155-5p	mir-155	-	1.070	0.0510
MIMAT0023706_st	hsa-miR-6081	-	-	1.054	0.0478
MIMAT0017999_st	hsa-miR-3619-5p	-	-	1.029	0.0158
MIMAT0003249_st	hsa-miR-584-5p	mir-584	-	0.901	0.0456
MIMAT0000072_st	hsa-miR-18a-5p	mir-17	C6 (chr13)	0.856	0.0495
Downregulated miRs (ordered by Log_2 Ratio)					
MIMAT0010251_st	hsa-miR-449c-5p	mir-449[#]	C34 (chr5)[†]	-3.012	< 0.001
MIMAT0001541_st	hsa-miR-449a	mir-449[#]	C34 (chr5)[†]	-2.426	< 0.001
MIMAT0003327_st	hsa-miR-449b-5p	mir-449[#]	C34 (chr5)[†]	-2.360	< 0.001
MIMAT0009203_st	hsa-miR-449b-3p	mir-449[#]	C34 (chr5)[†]	-1.678	0.0012

***, Diferentially expressed (DE) microRNAs (miRs) were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ($|Log_2Ratio| > 0.6$), followed by multiple correction using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or q < 0.05); [#], miR family represented with more than one DE miR in this dataset; [†], miR cluster represented with more than one DE miR in this dataset.**

TABLE S14. Differentially expressed microRNAs in CRSwNP compared to control NM air-liquid interface culture at day 28.*

MIMAT ID	Transcript ID	miR Family	Cluster ID (Chromosome)	Log_2 Ratio	P.value
Upregulated miRs (ordered by Log_2 Ratio)					
MIMAT0001413_st	hsa-miR-20b-5p	mir-17	C7 (chrX)	1.283	0.0367
MIMAT0023706_st	hsa-miR-6081	-	-	1.178	0.0550
MIMAT0000446_st	hsa-miR-127-3p	mir-127	C3 (chr14)	0.982	0.0550
Downregulated miRs (ordered by Log_2 Ratio)					
MIMAT0000451_st	hsa-miR-150-5p	mir-150	-	-1.339	0.0175
MIMAT0017990_st	hsa-miR-3613-5p	mir-3613	-	-1.287	0.0050
MIMAT0004676_st	hsa-miR-34b-3p	mir-34#	C59 (chr11)†	-1.232	0.0200
MIMAT0005825_st	hsa-miR-1180-3p	mir-1180	-	-1.188	0.0391
MIMAT0004677_st	hsa-miR-34c-3p	mir-34#	C59 (chr11)†	-1.097	0.0150
MIMAT0003218_st	hsa-miR-92b-3p	mir-25	-	-1.037	0.0306
MIMAT0000685_st	hsa-miR-34b-5p	mir-34#	C59 (chr11)†	-0.795	0.0320
MIMAT0000686_st	hsa-miR-34c-5p	mir-34#	C59 (chr11)†	-0.730	0.0200
MIMAT0010251_st	hsa-miR-449c-5p	mir-449	C34 (chr5)	-0.652	0.0306

***, Diferentially expressed (DE) microRNAs (miRs) were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ($|Log_2Ratio| > 0.6$), followed by multiple correction using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or $q < 0.05$); #, miR family represented with more than one DE miR in this dataset; †, miR cluster represented with more than one DE miR in this dataset.**

Table S15. List of references used to create list of genes involved related to human epithelial cell phenotypes.

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TABLE S16. Expression changes produced in Genes of Interest (GOI) related to Epithelial Cell Phenotypes during mucociliary differentiation of Nasal Polyp (NP, n = 7) and Nasal Mucosa (NM, n=7) air-liquid interface (ALI) cultures.*

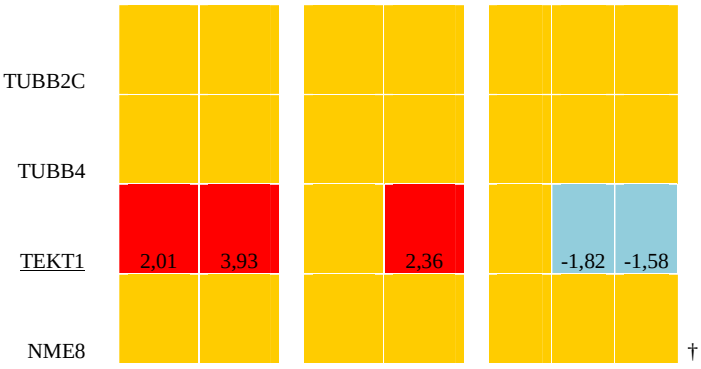
BASAL CELL SIGNATURE	NM		NP		NP vs NM		
	14 vs 0	28 vs 0	14 vs 0	28 vs 0	0	14	28
Cytoskeleton							
KRT5	-1,52			-1,29			-1,21
KRT6A		-1,10		-1,12			
KRT14		-1,64	-1,44	-1,93			
KRT16							
KRT6B	-2,41	-2,16	-1,43	-2,10		1,19	
TUBB6	-1,25	-1,48		-1,68			
EHD2	-1,21	-1,16		-1,15			
CALD1	-2,27	-1,81	-1,82	-2,45	1,01	1,87	
FSCN1	-2,22	-2,28		-1,68		1,40	
PDPN	-1,20	-1,21		-1,96			
Extracellularmatrix							
COL17A1							
ITGA6	-1,35	-1,56		-1,43			
Protease/antiprotease							
ADAMTS1	-3,04	-3,33	-2,97	-3,74			
KLK7	-2,48	-3,17	-1,33	-2,13		1,69	1,59
PLAU	-2,55	-1,78	-1,10	-1,88	-1,46		-1,31
SERPINE1	-1,48					1,38	
SERPINE2	-1,50		-1,58	-2,00		1,09	
Epidermalfunction							
SCEL							
SPRR1A		-1,88	-1,49	-2,54	1,51		
SPRR1B							
AREG	-2,76	-3,22	-1,24	-2,30		1,38	
SPRR3	2,10	1,39			2,64		1,04
Signalingligand							
EREG	-2,79	-3,84		-1,04	-1,76	1,25	1,04
NRG1	-2,04	-2,39	-2,23	-2,93			
Signaltransduction							
CAMK2N1							
DKK1	-1,46	-1,77	-2,19	-2,01			
RGS20	-1,96	-2,35	-1,29	-1,99			
STC2	-1,03		-1,16	-1,42			
CAV1	-1,26	-1,55		-1,16			
THBS1	-2,46	-1,91	-2,64	-2,77	1,47	1,71	
Transcription							
TP63	-1,30	-1,77		-1,48			
TRIB3	-1,80	-1,39	-2,06	-1,75			
BNC1	-1,58	-2,09	-1,09	-2,14			
Metabolism							
UPP1	-2,16	-2,08	-1,50	-1,94		1,28	
LIPG	-1,78	-1,42	-1,59	-2,57			
ALDH1L2							
PSAT1	-1,35		-1,37	-1,64			
Oxidation/reduction							

	LEPREL1			1,64	1,26			
Gapjunction								
	GJB2	-1,37					1,37	
	GJB6							
Cell adhesion								
	DSG3		-1,04					
Apoptosis								
	PHLDA1	-3,29	-2,89	-2,26	-2,75		1,67	
Immuneresponses								
	IL1RL1							
	IL13RA2		-1,11	-3,21	-3,33	2,30		
	IL1RN	-1,64	-1,35		-1,26			
Iontransport								
	SLC7A5	-2,62	-2,24	-2,16	-2,92			
	SLC7A11							
	SLC16A1	-1,24	-1,44		-1,13		1,17	
Water transport								
	AQP3					-2,64	-1,81	-2,43
Unknown								
	CRCT1		-1,60	-2,68	-4,25	3,40	1,58	
		NM		NP		NP	vs	NM
GOBLET CELL SIGNATURE		14 vs 0	28 vs 0	14 vs 0	28 vs 0	0	14	28
Mucins								
	MUC1	2,19	2,62	2,91	3,78	-1,54		
	MUC2							
	MUC3A							
	MUC3B							
	MUC3A							
	MUC4	1,25	1,57	2,31	2,31			
	MUC5AC							
	MUC5B	3,11	3,53	2,10	3,14		-1,13	
	MUC6							
	MUC7							
	MUC8							
	MUC9							
	MUC11							
	MUC12							
	MUC13							
	MUC14							
	MUC15	2,31	2,49	1,39	2,38			
	MUC16	3,35	3,64	2,08	3,50		-1,39	
	MUC17							
	MUC18							
	MUC19							
	MUC20			1,87	2,45	-1,11		
Genes regulating in Mucin Biosynthesis / Glycosylation								
	GALNT4							
	GALNT7							
	GALNT12			2,61	2,14	-1,77		
	GALNT15							

	GCNT1	1,15	1,05	1,39	1,42				
	GCNT2								
	GCNT3	1,81	1,89	2,35	2,95	-1,06			
	GCNT4								
	GCNT6								
	GCNT7								
Mucus Components									
	TFF1								
	TFF2								
	TFF3		1,69			1,01			
Goblet cell differentiation									
	PTGER3								
	CLCA1								
	FOXA3								
	AGR2	3,30	3,38	4,21	4,73	-1,85			
	MUC2								
	MUC16	3,35	3,64	2,08	3,50		-1,39		
	MUC5AC								
	SCGB1A1	-2,01	-2,83	3,99	1,42	-4,90	1,07		
	SPDEF								
	NOTCH1	-1,18	-1,23						
	NOTCH2								
	NOTCH3			1,32					
	NOTCH4								
	NICD1								
	NICD2								
	NICD3								
	NICD4								
Goblet cell differentiation inhibitors									
	FOXA2								
	TTF1								

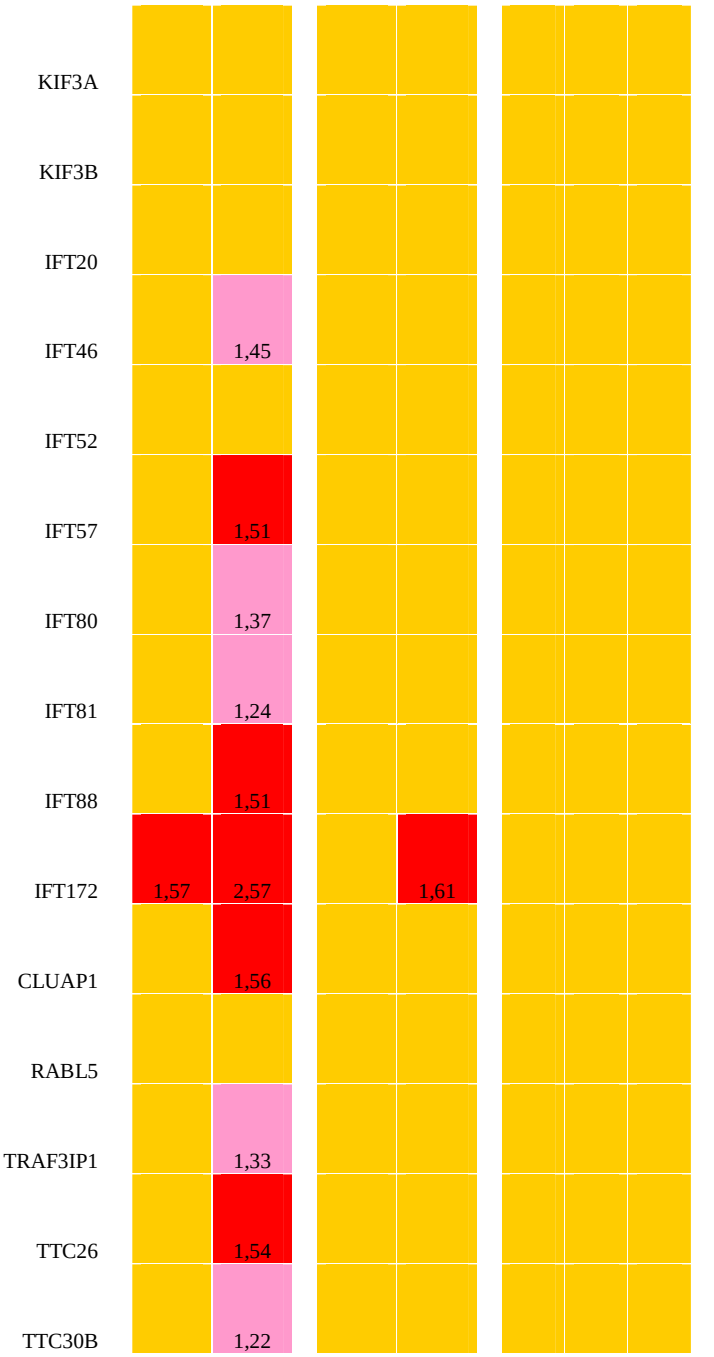
		NM		NP		NP	vs	NM	
CILIATED CELL SIGNATURE		14 vs 0	28 vs 0	14 vs 0	28 vs 0	0	14	28	
Axoneme – outer dynein arm									
	DNAH5	1,74	3,50		1,98		-1,14	-1,60	†
	DNAH9		1,65					-1,06	
	DNAH11								†
	DNAI1		2,73		1,66			-1,11	†
	DNAI2		2,69		1,20			-1,50	†
	DNAL1		1,45						†
Axoneme – inner dynein arm									
	DNAH3		1,58						
	DNAH6		2,00						
	DNAH12	1,26	3,29		2,08		-1,23	-1,42	
	DNALI1	1,77	3,57		2,60		-1,64	-1,13	
	WDR63	1,19	3,04					-1,39	
	WDR78	1,14	3,46		2,12			-1,37	
Dynein assembly and docking									
	DNAAF1	1,75	3,99		2,46		-1,17	-1,32	†
	DNAAF2								†
	DNAAF3		2,45		1,22			-1,16	†

	DYX1C1	1,06	2,68					-1,12	
	ARMC4		2,59		1,36			-1,42	
	CCDC39								†
	CCDC40								†
	CCDC103								†
	CCDC114								†
	DRC1		2,92		1,69			-1,25	†
	LRRC6		2,63		1,33			-1,20	†
	HEATR2								†
	ZMYND10	1,86	3,74		2,39		-1,87	-1,55	
Central pair									
	HYDIN							-1,21	†
	SPAG6	1,85	4,09		2,77		-1,63	-1,56	
	SPAG16								
	SPAG17		2,49					-1,24	
	SPAG1		1,35						
	PCDP1		1,89					-1,05	
Radial spoke									
	RSPH1	2,04	4,34		2,67		-1,75	-1,64	
	RSPH3		1,32						
	RSPH4A	1,26	3,43		2,13		-1,11	-1,34	†
	RSPH9	1,16	3,02		1,82		-1,14	-1,13	†
Tubulins and other microtubule-associated									
	TUB1A1								
	TUBA3								

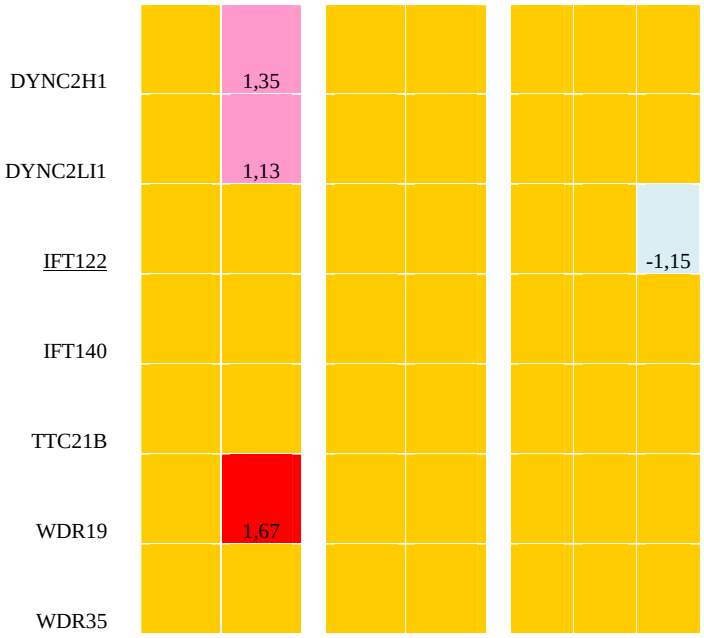


†

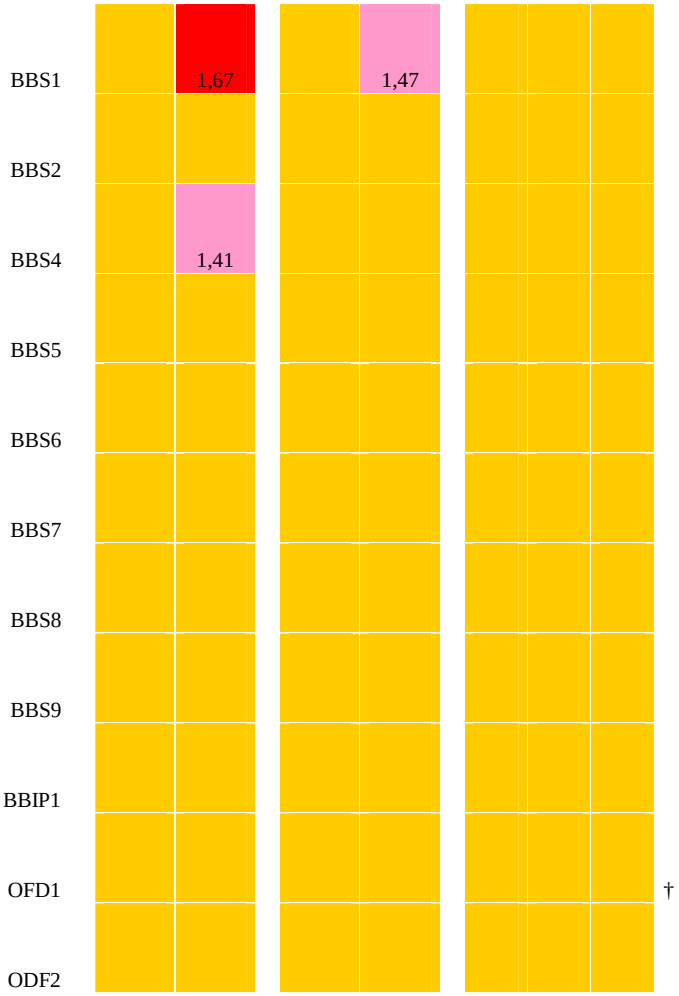
Anterograde intraflagellar transport (IFT)



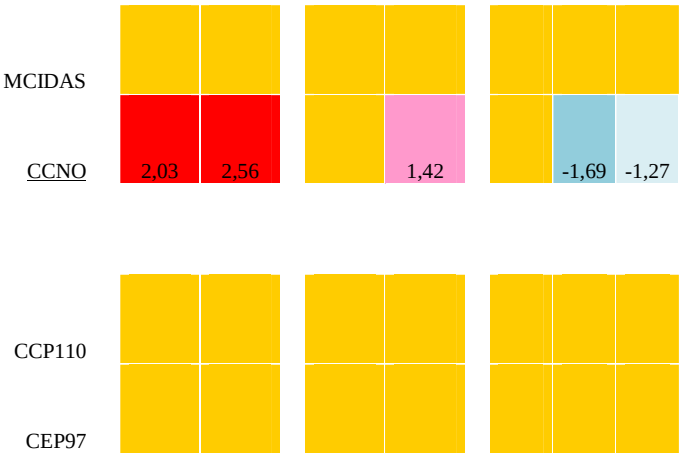
Retrograde IFT



Basal body and BBSome5




EZR
-1,34
Transition zone
NPHP1
2,66
1,59
-1,20
-1,13
RPGR
1,90
†
TMEM67
1,83
Receptors, ion channels and signaling molecules
TAS2R4
TAS2R38
TAS2R43
TAS2R46
SCNN1A
1,34
1,85
NOS3
PRKG1
AKAP14
1,50
3,60
2,44
-1,42
-1,23
PGR
SRF
Transcription factors – inducers of airway cilia formation
FOXJ1
1,68
3,31
1,76
-1,46
-1,56
RFX3
MYB
1,25
1,90
-1,05



***Diferentially expressed mRNAs were determined by using the non-parametric Rank Product test (R platform package, https://www.R-project.org/) and then filtered by Log_2Ratio Expression ([Log_2Ratio > 1] or [Log_2Ratio < -1] for both upregulated or downregulated mRNAs, respectively), followed by multiple correction using a False Discovery Rate (FDR) threshold of 1% (p-adjusted value or q < 0.01). All comparisons performed were longitudinal (day 14 and 28 versus day 0 of both NP and NM ALI) or transversal (NP compared to NM at the different days 0, 14 and 28 of ALI culture).**

† *Primary Ciliary Dyskinesia* associated genes (described in literature, Knowles et al. Am J Respir Crit Care Med 2013; 188(8), 913–922). In fully differentiated NP compared to NM, 10 of these genes are curiously downregulated (10/21 in total, 47.6% from total).

TABLE S17. Enriched Gene Ontology Biological Processes (GOTERM_BP_DIRECT) and KEGG pathways in differentiated NM air-liquid interface cultures at day 14 compared to day 0.*

GO_BP_DIRECT Term ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
GO:0051301~cell division	76	4.98	2.70	4	71	-7.74	MAD1L1, KIFC1, KNTC1, AURKA, FAM83D, CCNE2, KIF2C, CCNE1, NDE1, CDCA8, CDCA7, OIP5, CDCA2, CDCA5, CCNO, CCNA2, TUBA1B, CDCA4, CDCA3, CDK1, CDC6, KIF11, CCNF, TPX2, UBE2C, HMGA2, TACC3, PRKCE, NCAPD3, NCAPD2, CCND1, MAD2L1, SGO2, SPAG5, CCND2, ZWINT, BUB1B, CDCA7L, UBE2S, ANAPC16, GNAI2, TIPIN, LLGL2, SPC24, SPC25, VRK1, NCAPH, TUBB, SAC3D1, NCAPG2, NCAPG, BUB1, FBXO5, SKA1, ZWILCH, NSUN2, ERCC6L, PSRC1, NUF2, CENPF, NDC80, CENPE, CDC20, BIRC5, KNSTRN, SMC2, SEPT11, CDC25A, SMC4, CDC25B, CCNB1, FAM64A, CCNB2, KNL1, CKS2, MAP4	3.56E-14
GO:0000082~G1/S transition of mitotic cell cycle	32	2.10	3.91	2	30	-4.95	BCAT1, DBF4, PKMYT1, MCM10, RHOU, ITGB1, PPAT, CCNE2, PRIM1, CCNE1, TYMS, CDC45, EIF4EBP1, MCM7, POLE2, FBXO5, ORC6, CDCA5, CDC6, CDK1, SKP2, MCM2, CDKN3, MCM3, MCM4, CDC25A, MCM6, INHBA, CCND1, PLK3, RRM2, ID4	7.43E-10
GO:0007062~sister chromatid cohesion	30	1.97	3.63	0	30	-5.48	MAD1L1, KNTC1, RANGAP1, AURKB, SPC24, KIF2C, SPC25, CDCA8, NDE1, CENPA, BUB1, SKA1, ZWILCH, CDCA5, ERCC6L, CENPN, NUF2, CENPF, NDC80, BIRC5, CDC20, CENPE, CENPK, CENPH, REC8, MAD2L1, SGO2, KNL1, ZWINT, BUB1B	2.35E-08
GO:0007067~mitotic nuclear division	48	3.15	2.41	1	47	-6.64	ANAPC16, TIPIN, KNTC1, PKMYT1, ANLN, AURKA, CEP55, AURKB, SPC24, FAM83D, SPC25, KIF2C, VRK1, SAC3D1, NCAPG2, OIP5, CDCA2, BUB1, FBXO5, SKA1, ZWILCH, NSUN2, CDCA5, CCNA2, TUBB3, ASPM, CDCA3, ERCC6L, CDK1, CDC6, CENPN, KIF11, CCNF, NUF2, TPX2, CENPF, NDC80, CDC20, BIRC5, PBK, HMGA2, CDC25A, CDC25B, FAM64A, CCNB2, NOLC1, KNL1, BUB1B	4.41E-07
GO:0006260~DNA replication	35	2.29	2.81	1	34	-5.58	BLM, DBF4, TIPIN, KIAA0101, CHEK1, MCM10, DTD1, CDC45, MCM7, POLE2, ORC6, RTEL1-TNFRSF6B, EGF, FEN1, CDK1, GINS2, CDC6, CCDC88A, DTL, GINS4, RMI2, MCM2, TOP1MT, RNASEH2A, MCM3, MCM4, BRCA1, CDC25A, MCM6, RFC3, RFC2, RRM2, RRM1, CHAF1A, DSCC1	1.00E-06
GO:0008283~cell proliferation	61	4.00	2.08	13	48	-4.48	FGF5, HRAS, TSPAN1, ZAK, ELF5, UCHL1, DTYMK, AURKB, MCM10, CITED2, EDNRA, FAM83D, KIF2C, MCM7, TGFBI, TGFA, FRAT2, NRG1, MYC, IL1A, OCA2, EGFR, CDK1, CYP1A1, PDPN, BYSL, TPX2, SKP2, TACC3, TACC2, GLUL, UHRF1, PLCE1, SIX1, BUB1B, EMP1, MELK, BCAT1, GNAI2, HDGF, PRKDC, KITLG, CD74, SRC, TYMS, CSE1L, BUB1, ERCC1, TFDP1, POLR3G, CRIP1, MKI67, DLGAP5, FSCN1, CENPF, CDC25A, EPS8, LIPG, CKS2, TCF19, AREG	1.45E-06
GO:0006270~DNA replication initiation	14	0.92	5.45	0	14	-3.74	CDC6, GINS4, MCM2, MCM10, MCM3, MCM4, MCM6, PRIM1, CCNE2, CCNE1, CDC45, MCM7, POLE2, ORC6	8.28E-06
GO:0007155~cell adhesion	69	4.52	1.87	25	44	-2.29	CTNNAL1, CLSTN1, FERMT1, POSTN, EDIL3, AZGP1, SRPX, CD44, TGFBI, COL12A1, ZYX, LOXL2, ICAM1, EGFL6, EFNB1, BYSL, EFNB2, PCDHB2, ACKR3, CHST4, CERCAM, PRKCE, CD36, ANOS1, VCAN, LAMC2, HAS3, TGFB1I1, CNTN3, DST, CHL1, AMTN, TNC, ITGB4, ITGB5, KITLG, CLDN10, CX3CL1, PXN, PCDHAC2, SEMA5A, LAMB3, LPXN, SORBS2, MSLN, LAMB1, THBS1, GPNMB, FN1, PODXL, CD99, ITGA3, COL16A1, TINAGL1, COL4A6, EPHA4, CDH13, LAMA3, DSG2, ITGA6, FREM2, ITGA5, TROAP, DSC2, ABL2, THEMIS2, MUC16, FEZ1, CDH11	1.05E-05
GO:0001666~response to hypoxia	35	2.29	2.53	13	22	-1.52	CAV1, ALAD, AHCY, CLDN3, PGF, TGFB3, EGLN3, BNIP3, POSTN, ADA, ALDH3A1, CITED2, PKM, EDNRA, HMOX2, PLOD1, LOXL2, THBS1, ANGPTL4, MB, PLAT, EGR1, MUC1, CYP1A1, NR4A2, SMAD3, MMP14, ITPR1, AJUBA, VEGFC, CA9, UCP2, ETS1, HSD11B2, PLAU	1.37E-05
GO:0030198~extracellular matrix organization	38	2.49	2.42	12	26	-2.27	ELF3, PDGFA, NPNT, TNC, ITGB4, ITGB5, POSTN, SOX9, ITGB1, SPINK5, ABI3BP, LAMB3, CD44, ERO1B, TGFBI, SERPINE1, LOX, FBN2, VWA1, THBS1, LAMB1, FN1, ICAM1, COL4A2, COL4A1, EGFL6, CCDC80, NID1, ITGA3, COL16A1, COL4A6, ATP7A, LAMA3, ITGA6, ITGA5, VCAN, MFAP2, LAMC2	1.48E-05
GO:0007173~epidermal growth factor receptor signaling pathway	18	1.18	4.00	7	11	-0.94	EGFR, REPS2, HRAS, CBL, GAREM1, PIGR, SOX9, PXN, SRC, RPS6KA5, PLCE1, EPS8, EREG, TGFA, HBEGF, SHC1, AREG, EGF	1.93E-05

GO:0010811~positive regulation of cell-substrate adhesion	14	0.92	4.59	10	4	1.60	ALOX15, ITGA6, EGFL6, ITGA5, NPNT, CCDC80, PTN, HACD1, NID1, ITGA3, EDIL3, PRKCE, AGR2, ABI3BP	8.18E-05
GO:0000187~activation of MAPK activity	24	1.57	2.79	11	13	-0.41	IRAK2, CDK1, MAP2K1, MUC20, MAPKAPK3, TGFB3, TLR4, MAPK10, KIT, CD74, DUSP5, CXCL17, PLCE1, SAA1, TGFA, IL1B, SHC1, THBS1, NRG1, EGF, SHC2, DUSP7, GHR, DUSP6	1.99E-04
GO:0031581~hemidesmosome assembly	8	0.52	8.30	0	8	-2.83	LAMB3, LAMA3, ITGA6, KRT5, ITGB4, LAMC2, DST, PLEC	2.19E-04
GO:0008584~male gonad development	22	1.44	2.92	11	11	0.00	TESC, HMGB2, ARID5B, HMGCS1, FSTL3, KITLG, SIX4, TLR5, KIT, HMGA2, MMP14, SOX9, BCL2L11, CITED2, INHBA, WNT4, TNFSF10, NUPR1, RRM1, SOX15, ASPM, ERCC1	2.55E-04
GO:0055114~oxidation-reduction process	78	5.11	1.64	50	28	2.49	STEAP4, ALDH1L1, CYP2J2, DUOX2, BBOX1, MTHFD1, CRYL1, CYP39A1, PLOD1, GPX3, SRD5A3, MICAL1, LOXL4, LOX, LOXL2, IMPDH1, CYP1A1, FA2H, CYP26A1, DHRS9, ALDH3B2, CYB5A, VAT1, ALDH3B1, CYP4X1, ALOX15, NNT, ALOX15B, SQLE, RRM2, RRM1, CYBRD1, HSD11B1, CYP2A6, HSD11B2, STEAP2, DEGS2, XDH, ME3, CYP2F1, SORD, CYP2B6, EGLN3, ADH7, ALDH3A2, ALDH3A1, GPD1L, FMO4, ALDH1A1, CYP27B1, ERO1B, ALDH1A3, DHCR7, FMO3, FASN, ALDH4A1, HSD17B3, MSMO1, SCD, BCKDHB, FADS3, FADS2, CYP4F12, AAED1, P4HTM, CYP4B1, RDH10, AKR1B1, CYP4Z1, PHGDH, CYP4F3, DPYD, CP, SH3BGRL3, HPGD, DCXR, CRYM, CBS	2.90E-04
GO:0007059~chromosome segregation	18	1.18	3.30	0	18	-4.24	CENPN, KIF11, NUF2, CENPF, NDC80, CENPE, TOP1MT, KNSTRN, ESCO2, BRCA1, SPC25, NDE1, OIP5, HJURP, SPAG5, CDCA2, SKA1, TOP2A	3.52E-04
GO:0007093~mitotic cell cycle checkpoint	12	0.79	4.67	0	12	-3.46	MAD1L1, NABP1, HRAS, PLK3, MAD2L1, ZWINT, KNTC1, BUB1, TTK, BUB1B, CHEK1, ZWILCH	4.26E-04
GO:0035987~endodermal cell differentiation	11	0.72	5.08	0	11	-3.32	INHBA, COL4A2, LAMB3, LAMA3, ITGA5, COL12A1, ITGB5, MMP14, HMGA2, LAMB1, FN1	4.78E-04
GO:0008544~epidermis development	20	1.31	2.93	6	14	-1.79	KLK7, ELF3, S100A7, KLK5, SPRR2F, SPRR2E, ALDH3A2, LAMB3, LAMA3, PLOD1, KRT5, SPRR2D, SPRR2A, KRT15, IFT172, BNC1, SPRR3, LAMC2, TGM5, EMP1	6.42E-04
GO:0006268~DNA unwinding involved in DNA replication	7	0.46	8.72	0	7	-2.65	MCM7, MCM2, HMGA1, MCM4, TOP2A, RAD51, MCM6	7.87E-04
GO:0042493~response to drug	46	3.01	1.88	13	33	-2.95	ALAD, HMGB2, SORD, PGF, HMGCS1, CTPS1, PNP, CBX7, SCGB1A1, SRC, ADA, ALDH3A1, TYMS, MCM7, ACSL1, TGFA, ABCD3, PTN, LOX, THBS1, FOSL1, MYC, CCNO, ICAM1, CDK1, VAV3, CYP1A1, LGALS1, CENPF, ITGA3, DPYSL2, AK4, GAL, PPARGC1A, RAD51, CCNB1, VEGFC, INHBA, CCND1, NPC1, CA9, HSD11B2, LRP8, ABCC6, DUSP6, BCAR3	8.58E-04
GO:0006629~lipid metabolic process	29	1.90	2.30	16	13	0.56	CHKA, LDLR, ABHD5, CLU, HMGCS1, PLPP1, ACAT2, PLPP3, ASAH1, SLC16A1, SRD5A3, PLTP, PTPRN2, IL1RN, FADS3, ALDH3B2, FADS2, ACLY, GDPD3, CHPT1, ALDH3B1, GDPD1, CEL, CD36, ALOX15B, LIPG, LRP8, UGT2B7, PC	9.22E-04
GO:0042060~wound healing	19	1.25	2.96	6	13	-1.61	EGFR, DCBLD2, ERBB3, PDGFA, TNC, TGFB3, SMAD3, MAP3K5, ALOX15, CCL20, EREG, SERPINB2, SPRR3, TGFA, CNN2, SCARB1, LOX, NRG1, FN1	9.34E-04
GO:0008284~positive regulation of cell proliferation	63	4.13	1.68	16	47	-3.91	FGF5, HRAS, PRC1, PGF, PDGFA, EDN2, EDN1, TTK, TGFA, SHC1, NRG1, MYC, FOSL1, EGFR, EFNB2, VEGFC, EREG, CCND2, HAS2, LAMC2, CDCA7L, SERPINB3, EIF5A2, CSF3, FGFR2, GNAI2, CXCL5, TNC, FOXM1, CRLF1, TIPIN, KIT, SOX9, ITGB1, ALDH3A1, LIF, RAC2, XBP1, PTN, EGF, THBS1, FGFBP1, FN1, ACER3, ODC1, SHMT2, CCPG1, CRIP2, GAREM1, CDC20, BIRC5, PTGFR, ISL1, PLAC8, CDC25B, NOTCH1, ETS1, BNC1, HBEGF, ID4, PBX1, GRK5, AREG	1.00E-03
GO:0048661~positive regulation of smooth muscle cell proliferation	16	1.05	3.32	5	11	-1.50	EGFR, BMP4, FGFR2, IL18, EDN1, SKP2, CCL5, PPARGC1A, CDH13, EREG, ID2, AKR1B1, TGM2, HBEGF, THBS1, MYC	1.08E-03
GO:0030335~positive regulation of cell migration	32	2.10	2.17	9	23	-2.47	HRAS, PDGFA, EDN1, KIT, CCL5, GTSE1, SEMA5A, XBP1, GPNMB, THBS1, LAMB1, EGFR, BMP4, MYO1C, PODXL, SPHK1, SMAD3, MMP14, SNAI2, MYADM, CDH13, NOTCH1, CORO1A, ITGA6, SEMA6D, ITGA5, HBEGF, SEMA4B, HAS2, LAMC2, SERPINB3, PLAU	1.16E-03
GO:0030148~sphingolipid biosynthetic process	14	0.92	3.63	8	6	0.53	ACER3, SGPP1, FA2H, SPHK1, HACD4, ALDH3B2, CERS4, HACD1, PLPP1, ALDH3A2, PLPP3, ALDH3B1, ELOVL6, DEGS2	1.37E-03
GO:0007076~mitotic chromosome condensation	8	0.52	6.64	0	8	-2.83	NCAPH, NCAPG, NUSAP1, CDCA5, SMC2, NCAPD3, SMC4, NCAPD2	1.44E-03

GO:0022617~extracellular matrix disassembly	18	1.18	2.95	9	9	0.00	KLK7, MMP7, NID1, KIF9, CTSS, MMP14, MMP13, MMP12, MMP10, LAMB3, LAMA3, CD44, GSN, LAMC2, FBN2, LCP1, FN1, TLL1	1.62E-03
GO:0001525~angiogenesis	36	2.36	2.01	12	24	-2.00	FGFR2, CAV1, NRP1, S100A7, TNFRSF12A, PDGFA, PGF, IL18, NAA15, JAG1, RORA, MEIS1, NRCAM, TSPAN12, WARS, XBP1, TGFBI, SERPINE1, TGFA, ANGPT1, SHC1, EGF, ANGPTL4, FN1, COL4A2, VAV3, NRXN3, ACKR3, ARHGAP24, MYH9, MMP14, CXCL17, VEGFC, EREG, ITGA5, WNT7A	1.80E-03
GO:0007051~spindle organization	8	0.52	6.23	0	8	-2.83	KIF11, SPAG5, TTK, AURKA, AURKB, KNSTRN, ASPM, AUNIP	2.38E-03
GO:0006069~ethanol oxidation	7	0.46	7.27	6	1	1.89	ALDH1A1, ACSS1, ALDH1B1, ADH1C, ADH1B, ADH1A, ADH7	3.01E-03
GO:2000811~negative regulation of anoikis	8	0.52	5.86	2	6	-1.41	CAV1, NOTCH1, ITGA5, PDK4, CEACAM5, SNAI2, ITGB1, SRC	3.76E-03
GO:0050900~leukocyte migration	23	1.51	2.35	5	18	-2.71	ICAM1, HRAS, CAV1, FOXJ1, PODXL, SLC3A2, ITGA3, MYH9, SLC7A5, ITGB1, CD74, SRC, SLC16A1, THBD, ITGA6, CD44, PROCR, ITGA5, SHC1, ANGPT1, MSN, PROS1, FN1	4.84E-03
GO:0050918~positive chemotaxis	11	0.72	3.92	5	6	-0.30	SEMA5A, BMP4, VEGFC, CORO1A, HMGB2, NRP1, SAA2, SAA1, ANGPT1, CCL5, GPNMB	5.73E-03
GO:0000281~mitotic cytokinesis	10	0.66	4.30	0	10	-3.16	KIF23, KIF4A, CENPA, NUSAP1, SPTBN1, ANLN, STMN1, CEP55, RACGAP1, KIF20A	5.77E-03
GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	19	1.25	2.57	10	9	0.23	HLA-DQB1, KIF23, KIF4A, KIF11, HLA-DRB1, CENPE, CTSS, HLA-DMB, RACGAP1, HLA-DMA, KIF3C, HLA-DQA1, CD74, AP1S3, KIF2C, AP2B1, HLA-DPA1, SAR1B, HLA-DRA	6.14E-03
GO:0030855~epithelial cell differentiation	16	1.05	2.85	11	5	1.50	GSTA1, MUC1, FGFR2, CDK1, COL4A1, ELF3, ALDOC, DHRS9, TAGLN2, SPINK5, RHCG, UPK1B, SIX1, BDH2, KRT4, BMP7	6.83E-03
GO:0002576~platelet degranulation	20	1.31	2.42	10	10	0.00	TF, PDGFA, CLU, SELENOP, TGFB3, ACTN1, PCDH7, TIMP3, FLNA, VEGFC, LAMP2, CD36, SERPINE1, WDR1, THBS1, EGF, CFD, PROS1, FN1, CALM1	9.25E-03
GO:0000070~mitotic sister chromatid segregation	9	0.59	4.48	0	9	-3.00	KIFC1, MAD2L1, CENPA, SPAG5, ZWINT, NUSAP1, NDC80, KNSTRN, SMC4	9.88E-03
GO:0043627~response to estrogen	15	0.98	2.87	4	11	-1.81	CAV1, SMAD6, DTYMK, TGFB3, MMP14, GAL, CITED4, BRCA1, CITED2, SLC34A2, GSTM3, CCND1, CYP27B1, CA2, WNT7A	1.00E-02
GO:0016266~O-glycan processing	14	0.92	2.91	13	1	3.21	MUC1, ST6GAL1, GCNT3, POC1B-GALNT4, GALNT5, MUC20, CHST4, MUC4, B3GNT7, GXYLT2, MUC15, GCNT1, MUC5B, MUC16	1.47E-02
GO:0042127~regulation of cell proliferation	29	1.90	1.95	12	17	-0.93	ERBB3, FOXM1, TNC, TGFB3, EGLN3, CHEK1, JAG1, KIT, CXCL6, SOX9, SRC, CDCA7, DHCR7, CHST11, BCL6, CNN2, SGK1, CCDC88A, FA2H, RBBP9, BRCA1, TNFRSF10A, STYK1, PLA2G4A, MELTF, ACE2, DNMT1, ABL2, PLAU	1.54E-02
GO:0043066~negative regulation of apoptotic process	57	3.74	1.56	18	39	-2.78	NAA15, BNIP3, TP63, AURKA, CITED2, ATAD3A, CD44, BAG1, CHST11, TGFA, ANGPT1, CEACAM5, MYC, EGFR, CDK1, SOCS3, BCL2A1, SIX4, HMGA2, FLNA, PLAUR, SERPINB9, AMIGO2, MAP4K4, MAD2L1, CCND2, CFL1, SERPINB2, AVEN, SLC40A1, CAMK1D, PRKDC, SOX9, CD74, SRC, XBP1, TGM2, PRKAA2, THBS1, ARHGDIA, ANGPTL4, BMP4, SMAD6, SPHK1, CBL, TMBIM4, SMAD3, BIRC5, ANXA5, PTGFR, TAX1BP1, PLAC8, PLK3, UCP2, GRK5, APIP, WNT7A	1.63E-02
GO:0017144~drug metabolic process	9	0.59	4.15	7	2	1.67	FMO4, CYP1A1, CYP2B6, FMO2, EPHX2, CYP2A6, ADH1A, CAD, CYP4F12	1.75E-02
GO:0051781~positive regulation of cell division	12	0.79	3.18	4	8	-1.15	FGFR2, VEGFC, FGF5, EREG, PDGFA, PGF, GAREM1, TGFB3, TGFA, IL1B, PTN, IL1A	1.87E-02
GO:0048333~mesodermal cell differentiation	6	0.39	6.79	1	5	-1.63	FGFR2, INHBA, ITGB4, ITGA3, HMGA2, ITGB1	1.89E-02
GO:0000165~MAPK cascade	37	2.42	1.76	13	24	-1.81	FGFR2, PSMB10, FGF5, CAV1, HRAS, NDST1, PDGFA, ERBB3, IL18, MAPKAPK3, KITLG, RASGEF1A, AKAP9, FGF13, KIT, CCL5, MAP3K5, PSMD2, IL1B, SHC1, ANGPT1, SPRED1, EGF, NRG1, MYC, SHC2, EGFR, MAP2K1, ARTN, DUSP5, EREG, PSMC2, SPTBN1, HBEGF, DUSP7, DUSP6, CALM1	1.94E-02
GO:0001837~epithelial to mesenchymal transition	10	0.66	3.66	4	6	-0.63	FGFR2, S100A4, FAM83D, WNT4, NOTCH1, HMGA2, SNAI2, LOXL2, SOX9, BMP7	2.08E-02

GO:0048286~lung alveolus development	10	0.66	3.66	6	4	0.63	ATP7A, LIF, FGFR2, BMP4, PDPN, PDGFA, EDN2, TGFB3, ADA, IGFBP5	2.08E-02
GO:0006928~movement of cell or subcellular component	17	1.11	2.46	6	11	-1.21	MAP2K1, CALD1, VIM, CHST4, MYLIP, CERCAM, TPM4, TPM3, PLAUR, DNALI1, CORO1A, TUBB, ANOS1, MSN, ARHGDIA, VNN2, ARHGDIB	2.26E-02
GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	7	0.46	5.13	7	0	2.65	HLA-DQB1, HLA-DRB1, HLA-DPA1, HLA-DMB, HLA-DMA, HLA-DQA1, HLA-DRA	2.80E-02
GO:0007565~female pregnancy	17	1.11	2.38	8	9	-0.24	MUC1, PGF, TFCP2L1, BYSL, TGFB3, CAD, COL16A1, SCGB1A1, THBD, PAPPA, UCP2, ETS1, CLIC5, HSD11B2, HPGD, FOSL1, IGFBP5	3.27E-02
GO:0048538~thymus development	11	0.72	3.19	7	4	0.90	MAD1L1, CCNB2, MAP2K1, MAFB, LMO4, SIX1, PRKDC, PBX1, SIX4, BCL2L11, CITED2	3.28E-02
GO:0007018~microtubule-based movement	16	1.05	2.46	5	11	-1.50	KIF23, KIFC1, KIF4A, DNAH12, KIF11, CENPE, KIF9, RACGAP1, KIF3C, DNAH5, KIF2C, AP2B1, KIF1B, DYNLRB2, KIF20A, KIF13B	3.31E-02
GO:0098609~cell-cell adhesion	37	2.42	1.70	6	31	-4.11	STK38, SNX5, CALD1, DIAPH3, ASAP1, RANGAP1, ANLN, SFN, TAGLN2, PKM, EFHD2, FASN, CNN2, EHD1, CLINT1, PLEC, FMNL2, LAD1, MYO1B, FSCN1, CBL, SLC3A2, EIF2S3, MPP7, EEF2, FLNB, VASP, MPRIP, TMEM2, MICALL1, TMEM47, CCNB2, CGN, EIF4H, SPTBN1, PAICS, YKT6	3.51E-02
GO:0007052~mitotic spindle organization	9	0.59	3.74	0	9	-3.00	CCNB1, SPC25, KIF11, GPSM2, TTK, MAP4, NDC80, AURKA, STMN1	3.68E-02
GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	16	1.05	2.43	6	10	-1.00	CSF3, ICAM1, NRP1, KITLG, PLPP3, SRC, CD74, LIF, VEGFC, CD36, CD44, ITGA5, LRP8, ANGPT1, NRG1, GHR	3.75E-02
GO:0019373~epoxygenase P450 pathway	7	0.46	4.84	6	1	1.89	CYP2J2, CYP2F1, CYP1A1, CYP2B6, EPHX2, CYP2A6, CYP4F12	3.90E-02
GO:0007162~negative regulation of cell adhesion	10	0.66	3.37	5	5	0.00	SEMA5A, CDH13, LPXN, ERBB3, PODXL, TNC, TGFBI, ANGPT1, ARHGDIA, ARHGDIB	3.94E-02
GO:0035234~ectopic germ cell programmed cell death	5	0.33	7.79	2	3	-0.45	KITLG, IL1B, PRKDC, KIT, IL1A	4.10E-02
GO:0009168~purine ribonucleoside monophosphate biosynthetic process	6	0.39	5.75	1	5	-1.63	ADSSL1, PAICS, IMPDH1, ADA, PPAT, GART	4.53E-02
GO:0014032~neural crest cell development	6	0.39	5.75	1	5	-1.63	EDNRA, RDH10, EDN1, SNAI2, NRG1, SOX9	4.53E-02
GO:0051289~protein homotetramerization	13	0.85	2.70	4	9	-1.39	SHMT2, DNM1L, GLS, GPX3, FBP1, CDA, TP63, APIP, KCNJ2, DCXR, VASP, PPAT, TK1	4.71E-02
KEGG PATHWAY ID	Count	%	Fold Enrichment	UP	DW	Z-SCORE	Genes	real FDR
hsa04110:Cell cycle	34	2.23	2.98	1	33	-5.49	MAD1L1, DBF4, TGFB3, PKMYT1, TTK, PRKDC, CHEK1, SFN, CCNE2, CCNE1, CDC45, MCM7, BUB1, ORC6, CCNA2, MYC, TFDP1, CDK1, CDC6, SKP2, SMAD3, CDC20, MCM2, MCM3, MCM4, CDC25A, MCM6, CDC25B, CCNB1, CCND1, MAD2L1, CCNB2, CCND2, BUB1B	1.42E-07

hsa01100:Metabolic pathways	154	10.09	1.36	83	71	0.97	ALAD, GDA, B3GALT4, DTYMK, PGAM1, ADH1C, ADH1B, ADH1A, PNP, UXS1, DSE, PRIM1, GOT2, ACSS1, TRAK2, GATM, CYP1A1, FBP1, CYP26A1, CHPT1, GLCE, NME5, MGAT3, PLCE1, GLUL, NNT, ALOX15B, NME1, MGAM, HSD11B1, EXT2, XDH, CHKA, GCNT3, ME3, AHCY, SRM, NAGS, CYP2B6, ALDOC, ENPP3, HMGCS1, CTPS1, CERS4, ATP6V1B1, ACAT2, PPAT, ADA, TK1, POLE2, CDA, ALDH4A1, GCNT1, B4GALT4, ODC1, MGAT4A, ST6GAL1, ADSSL1, MSMO1, B4GALT2, SPHK1, FDPS, EPHX2, TKT, AK4, AK7, GART, CEL, PLA2G4A, GGT6, GGT7, GLS, DNMT1, NDUFC2-KCTD14, ALG11, DCXR, PC, IMPA2, CYP2J2, NDST1, ACOT2, PIP5K1B, CAD, ASAH1, PKM, MTHFD1, CRYL1, PLCB4, AGPAT5, MCEE, MCCC1, IMPDH1, NT5E, POLR1E, ALDH3B2, DHRS9, LPIN1, ALDH3B1, ST6GALNAC1, ATP6V1C2, ALOX15, ALDH1B1, SQLE, RRM2, RRM1, CYP2A6, MTAP, INPP4B, DEGS2, AMY1A, BCAT1, SORD, GALNT5, FUT6, POC1B-GALNT4, UPP1, ADH7, PLPP1, PLPP3, ALDH3A2, ALDH3A1, ALDH1A1, TYMS, ACSL1, CYP27B1, INPP5J, DHCR7, ALDH1A3, FASN, UGT2A1, HSD17B3, BDH2, FUT2, ACSL5, POLR3G, SHMT2, PLA2G16, NAT1, BCKDHB, ACLY, MAN1C1, RDH10, AKR1B1, PHGDH, LIPG, MBOAT1, CYP4F3, DPYD, PSAT1, APIP, PAICS, UGT2B7, CBS, PYGB	1.81E-04
hsa04510:Focal adhesion	39	2.56	2.06	5	34	-4.64	CAV1, HRAS, PDGFA, PGF, TNC, ITGB4, ITGB5, ITGB1, SRC, PXN, LAMB3, RAC2, SHC1, ZYX, EGF, PIK3R3, THBS1, LAMB1, SHC2, FN1, EGFR, COL4A2, VAV3, COL4A1, MAP2K1, ACTN1, ITGA3, MAPK10, FLNB, FLNA, VASP, COL4A6, VEGFC, CCND1, LAMA3, ITGA6, ITGA5, CCND2, LAMC2	2.55E-04
hsa00982:Drug metabolism - cytochrome P450	18	1.18	2.88	16	2	3.30	GSTA1, GSTA4, CYP2B6, ADH1C, ALDH3B2, ADH1B, ADH1A, ADH7, ALDH3B1, ALDH3A1, FMO4, GSTM3, ALDH1A3, FMO2, FMO3, CYP2A6, UGT2A1, UGT2B7	1.28E-03
hsa04012:ErbB signaling pathway	20	1.31	2.50	5	15	-2.24	EGFR, HRAS, MAP2K1, ERBB3, CBL, MAPK10, SRC, CBLC, EIF4EBP1, EREG, TGFA, HBEGF, SHC1, AREG, NRG1, PIK3R3, EGF, ABL2, SHC2, MYC	3.51E-03
hsa00980:Metabolism of xenobiotics by cytochrome P450	18	1.18	2.65	14	4	2.36	GSTA1, GSTA4, CYP2F1, CYP1A1, CYP2B6, ADH1C, ADH1B, ALDH3B2, ADH1A, ADH7, ALDH3B1, ALDH3A1, GSTM3, ALDH1A3, HSD11B1, CYP2A6, UGT2A1, UGT2B7	3.87E-03
hsa05323:Rheumatoid arthritis	20	1.31	2.47	14	6	1.79	HLA-DQB1, ICAM1, CXCL5, HLA-DRB1, IL18, TGFB3, TLR4, CXCL6, HLA-DMB, ATP6V1B1, CCL5, HLA-DMA, HLA-DQA1, ATP6V1C2, CCL20, IL1B, ANGPT1, HLA-DPA1, IL1A, HLA-DRA	4.10E-03
hsa05416:Viral myocarditis	15	0.98	2.86	9	6	0.77	HLA-DQB1, ICAM1, CAV1, HLA-DRB1, HLA-DMB, HLA-DMA, HLA-DQA1, HLA-F, CD55, CCND1, RAC2, HLA-DPA1, ABL2, HLA-DRA, SGCB	6.34E-03
hsa05321:Inflammatory bowel disease (IBD)	16	1.05	2.72	11	5	1.50	HLA-DQB1, HLA-DRB1, IL18, TGFB3, SMAD3, TLR4, RORA, TLR5, HLA-DMB, HLA-DMA, HLA-DQA1, STAT4, IL1B, HLA-DPA1, IL1A, HLA-DRA	6.91E-03
hsa04512:ECM-receptor interaction	19	1.25	2.38	1	18	-3.90	COL4A2, COL4A1, TNC, ITGB4, ITGB5, ITGA3, ITGB1, COL4A6, HMMR, LAMB3, CD36, LAMA3, ITGA6, CD44, ITGA5, LAMC2, THBS1, LAMB1, FN1	1.00E-02
hsa05219:Bladder cancer	12	0.79	3.18	4	8	-1.15	RPS6KA5, EGFR, HRAS, CCND1, MAP2K1, HBEGF, THBS1, DAPK2, EGF, MYC, SRC, DAPK1	1.14E-02
hsa04940:Type I diabetes mellitus	12	0.79	3.11	10	2	2.31	HLA-DQB1, CPE, HLA-DRB1, PTPRN2, IL1B, HLA-DPA1, HLA-DMB, HLA-DMA, HLA-DQA1, IL1A, HLA-DRA, HLA-F	1.42E-02
hsa03030:DNA replication	11	0.72	3.33	0	11	-3.32	PRIM1, RFC3, MCM7, POLE2, RFC2, MCM2, MCM3, RNASEH2A, MCM4, FEN1, MCM6	1.45E-02
hsa05222:Small cell lung cancer	18	1.18	2.30	1	17	-3.77	COL4A2, COL4A1, SKP2, ITGA3, ITGB1, COL4A6, CCNE2, CCNE1, LAMB3, CCND1, LAMA3, ITGA6, CKS2, LAMC2, LAMB1, PIK3R3, MYC, FN1	2.06E-02
hsa05204:Chemical carcinogenesis	17	1.11	2.31	13	4	2.18	GSTA1, GSTA4, CYP1A1, NAT1, ADH1C, ADH1B, ALDH3B2, ADH1A, ADH7, ALDH3B1, ALDH3A1, GSTM3, ALDH1A3, HSD11B1, CYP2A6, UGT2A1, UGT2B7	2.78E-02
hsa05332:Graft-versus-host disease	10	0.66	3.30	8	2	1.90	HLA-DQB1, HLA-DRB1, IL1B, HLA-DPA1, HLA-DMB, HLA-DMA, HLA-DQA1, IL1A, HLA-DRA, HLA-F	2.93E-02

hsa05200:Pathways in cancer	**54**	**3.54**	**1.50**	**16**	**38**	**-2.99**	**ADCY3, FGF5, HRAS, PGF, PDGFA, TGFB3, FGF13, EDNRA, CCNE2, CCNE1, WNT4, PLCB4, TGFA, MYC, EGFR, SKP2, DAPK2, MECOM, DAPK1, RAD51, VEGFC, CCND1, LPAR6, GNB4, LAMC2, FGFR2, GNAI2, EGLN3, KITLG, GNG11, KIT, ITGB1, TPM3, LAMB3, RAC2, LAMB1, PIK3R3, EGF, FN1, BMP4, COL4A2, COL4A1, MAP2K1, CBL, SMAD3, ITGA3, BIRC5, MAPK10, COL4A6, CBLC, LAMA3, ITGA6, CKS2, WNT7A**	**3.15E-02**
hsa00010:Glycolysis / Gluconeogenesis	**15**	**0.98**	**2.44**	**10**	**5**	**1.29**	**ALDOC, ADH1C, FBP1, PGAM1, ADH1B, ALDH3B2, ADH1A, ADH7, ALDH3A2, ALDH3B1, ALDH3A1, PKM, ACSS1, ALDH1B1, ALDH1A3**	**3.37E-02**
hsa04115:p53 signaling pathway	**15**	**0.98**	**2.44**	**1**	**14**	**-3.36**	**CDK1, CHEK1, SFN, GTSE1, CCNB1, CCNE2, CCNE1, CCND1, CCNB2, CCND2, RRM2, SERPINE1, SHISA5, THBS1, IGFBP3**	**3.37E-02**
hsa04151:PI3K-Akt signaling pathway	**48**	**3.15**	**1.51**	**15**	**33**	**-2.60**	**CSF3, FGFR2, FGF5, HRAS, PDGFA, PGF, TNC, ITGB4, KITLG, ITGB5, TLR4, GNG11, FGF13, KIT, ITGB1, CCNE2, CCNE1, LAMB3, EIF4EBP1, CREB3L1, ANGPT1, PRKAA2, EGF, PIK3R3, LAMB1, THBS1, MYB, MYC, GHR, FN1, EGFR, COL4A2, SGK1, COL4A1, MAP2K1, ITGA3, BCL2L11, BRCA1, COL4A6, VEGFC, CCND1, LAMA3, ITGA6, ITGA5, LPAR6, CCND2, GNB4, LAMC2**	**4.45E-02**

***Functional enrichment analysis of differentially expressed mRNAs (Log2Ratio > 1, Log2Ratio < 1, and q < 0.05) was done in Database for Annotation, Visualization and Integrated Discovery (DAVID, version 6.8, recently updated in Oct. 2016, https://david.ncifcrf.gov/home.jsp) and using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or q < 0.05). Enriched Gene Ontology and KEGG pathway terms are ordered in this table by FDR values. Numbers of upregulated (UP) and downregulated (DW) genes are showed in red and green, respectively. The z-score represents the overall up/down regulated genes from that term [Walter et al., 2015]. Z-score cells of this table are coloured depending on Z-score values: in red for Z >0, in blue for Z < 0 or in white for Z = 0.**

TABLE S18. Enriched Gene Ontology Biological Processes (GOTERM_BP_DIRECT) and KEGG pathways in differentiated NM air-liquid interface cultures at day 28 compared to day 0.*

GO_BP_DIRECT Term ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
GO:0060271~cilium morphogenesis	50	2.54	3.73	45	5	5.66	TTC26, STK36, CFAP221, TMEM17, TMEM231, IFT122, GSN, DYNC2H1, CCNO, TTC21A, RPGR, IFT80, FOXJ1, ARL6, PCM1, FLNA, TMEM67, BBS1, CC2D2A, RAB17, IFT81, IFT88, SNX10, IFT74, IQCB1, BBS4, CEP126, B9D1, B9D2, ASAP1, C5ORF42, DNAH5, FUZ, WDR19, IFT46, WDPCP, DNAAF1, TCTN1, IFT43, EHD1, UNC119B, ICK, NOTCH1, IFT57, DZIP1L, IFT172, CCDC113, FAM161A, RFX2, IQUB	2.11E-15
GO:0042384~cilium assembly	47	2.38	3.85	44	3	5.98	IQCB1, BBS4, CLUAP1, TTC26, CEP126, STK36, B9D1, DYNC2LI1, B9D2, C5ORF42, TMEM17, DNAH5, FUZ, CFAP53, WDR19, IFT122, TMEM231, IFT46, WDPCP, TTC30A, TTC30B, DYNC2H1, EHD1, CCNO, RPGR, IFT80, FOXJ1, DNAI2, PCM1, ARL6, FLNA, BBS1, TMEM67, NME5, TRAF3IP1, ICK, IFT57, CCDC113, DZIP1L, CC2D2A, RAB17, IFT172, FAM161A, IFT81, RFX2, SNX10, IFT74	4.22E-15
GO:0051301~cell division	84	4.26	2.44	10	73	-6.87	MAD1L1, KIFC1, STOX1, KNTC1, AURKA, CCNE2, FAM83D, KIF2C, CCNE1, CDCA8, CDCA7, OIP5, MIS18A, CDCA2, TUBA1A, CDCA5, CCNO, CCNA2, CDCA4, CDCA3, KIF14, CDK1, CDC6, KIF11, CCNF, TPX2, UBE2C, HMGA2, TACC3, PRKCE, NCAPD3, NCAPD2, MAD2L1, CCND2, ZWINT, BUB1B, CDCA7L, ANAPC7, UBE2S, CKS1B, HAUS6, TIPIN, CETN2, ENSA, LLGL2, SPC24, SPC25, VRK1, NCAPH, TUBB, SAC3D1, NCAPG2, NCAPG, BUB1, FBXO5, KLHL42, SKA2, SKA1, LMLN, ZWILCH, ERCC6L, PSRC1, NUF2, CENPF, NDC80, CENPE, CDC20, BIRC5, SPDL1, KNSTRN, SMC2, SEPT10, CDC25A, SMC4, CDC25B, CCNB1, FAM64A, CCNB2, KNL1, KIF20B, CENPV, CKS2, MAP4, CDK20	3.00E-13
GO:0007067~mitotic nuclear division	57	2.89	2.33	5	52	-6.23	STOX1, KNTC1, PKMYT1, AURKA, AURKB, FAM83D, KIF2C, OIP5, MIS18A, CDCA2, CDCA5, CCNA2, TUBB3, ASPM, CDCA3, CDC6, CDK1, KIF11, CCNF, TPX2, PBK, HMGA2, BUB1B, ANAPC7, HAUS6, TIPIN, CETN2, ANLN, CEP55, ENSA, SPC24, SPC25, VRK1, NCAPG2, SAC3D1, BUB1, FBXO5, SKA2, KLHL42, SKA1, LMLN, ZWILCH, ERCC6L, CENPN, NUF2, CENPF, NDC80, BIRC5, CDC20, CDC25A, CDC25B, FAM64A, CCNB2, NOLC1, KNL1, CENPV, KIF20B	4.06E-08
GO:0003341~cilium movement	16	0.81	6.02	16	0	4.00	CFAP100, LRRC6, DYX1C1, ARMC4, CFAP221, DNAH1, DNAI2, DNAH7, DNAH5, RSPH9, CFAP53, DNAI1, RSPH4A, CFAP73, DNAAF1, CFAP206	7.74E-08
GO:0000082~G1/S transition of mitotic cell cycle	32	1.62	3.19	3	29	-4.60	BCAT1, DBF4, PKMYT1, MCM10, RHOU, PPAT, CCNE2, PRIM1, CCNE1, TYMS, CDC45, EIF4EBP1, MCM7, CDKN2A, POLE2, FBXO5, ORC6, CDCA5, CDC6, CDK1, POLE, SKP2, MCM2, CDKN3, MCM3, MCM4, CDC25A, MCM6, INHBA, PLK3, RRM2, ID4	1.15E-07
GO:0042073~intraciliary transport	12	0.61	7.62	12	0	3.46	TRAF3IP1, ICK, RPGR, IFT46, TTC30A, TTC26, IFT57, TTC30B, IFT81, BBS12, IFT27, IFT74	4.21E-07
GO:0007062~sister chromatid cohesion	31	1.57	3.06	1	30	-5.21	MAD1L1, B9D2, KNTC1, AURKB, SPC24, KIF2C, SPC25, CDCA8, CENPA, BUB1, SKA2, SKA1, ZWILCH, CDCA5, ERCC6L, CENPN, KIF18A, NUF2, CENPF, NDC80, SPDL1, BIRC5, CDC20, CENPE, CENPK, CENPH, MAD2L1, KNL1, ZWINT, BUB1B, CENPU	5.96E-07

GO:0006260~DNA replication	39	1.98	2.56	2	37	-5.60	BLM, DBF4, TIPIN, KIAA0101, CHEK1, MCM10, DTD1, CDC45, MCM7, POLE2, ORC6, RTEL1-TNFRSF6B, FEN1, CDK1, GINS2, CDC6, CCDC88A, DTL, GINS3, POLE, GINS4, RMI2, MCM2, TOP1MT, MCM3, RNASEH2A, MCM4, CDC25A, MCM6, RFC5, RFC3, RFC4, RFC2, RRM2, RRM1, NFIA, DSCC1, DUT, REPIN1	1.60E-06
GO:0007018~microtubule-based movement	26	1.32	3.26	13	13	0.00	KIF14, KIF23, DNAH10, KIFC1, KIF4A, DNAH9, DNAH12, KIF11, DNAH3, KIF18A, CENPE, KIF9, DNAH2, RACGAP1, KIF3C, DNAH5, DNAH6, KIF2C, KIF1B, KIF20B, DYNC2H1, KIF19, DYNLRB2, DNAL4, KIF20A, KIF13B	2.38E-06
GO:0006270~DNA replication initiation	15	0.76	4.76	0	15	-3.87	CDC6, GINS4, POLE, MCM2, MCM10, MCM3, MCM4, MCM6, PRIM1, CCNE2, CCNE1, CDC45, MCM7, POLE2, ORC6	1.22E-05
GO:0035082~axoneme assembly	11	0.56	6.57	11	0	3.32	RP1, CLUAP1, C11ORF63, RSPH4A, RSPH1, CC2D2A, CFAP206, FAM179B, SPEF2, TTLL1, RSPH9	1.60E-05
GO:0003351~epithelial cilium movement	9	0.46	7.03	9	0	3.00	NME5, DNAI1, STK36, DNAH1, SPA17, TTLL1, ROPN1L, SPAG17, DPCD	1.34E-04
GO:0036159~inner dynein arm assembly	9	0.46	7.03	9	0	3.00	CFAP100, LRRC6, DYX1C1, CFAP73, DNAAF1, ZMYND10, TEKT2, DNAH1, DNAH7	1.34E-04
GO:0010811~positive regulation of cell-substrate adhesion	15	0.76	4.01	10	5	1.29	ALOX15, ITGA6, FBLN2, EGFL6, ITGA5, NPNT, CCDC80, PTN, HACD1, ITGA3, EDIL3, PRKCE, COL8A1, AGR2, ABI3BP	1.42E-04
GO:0042493~response to drug	55	2.79	1.84	19	36	-2.29	ALAD, PGF, SNCA, PPOX, SRP19, PNP, CBX7, SCGB1A1, FOS, MCM7, GATA3, TGFA, CAT, LOX, FOSL1, MYC, CCNO, ICAM1, CDK1, CYP1A1, FOSB, GAL, PPARGC1A, POR, RAD51, INHBA, VEGFC, BLMH, CA9, HSD11B2, HMGB2, SORD, HMGCS1, CTPS1, ADA, ALDH3A1, TYMS, ACSL1, ABCD3, PTN, NFATC2, THBS1, TXNIP, VAV3, LGALS1, GGH, CENPF, ITGA3, AK4, DPYSL2, CCNB1, LRP8, BCAR3, DUSP6, ABCC6	2.46E-04
GO:0008284~positive regulation of cell proliferation	75	3.81	1.63	27	48	-2.42	FGF5, STOX1, HRAS, PRC1, PGF, PDGFA, EDN2, BTC, EDN1, TTK, CTGF, TGFA, CEACAM6, SHC1, NRG1, MYC, FOSL1, KIF14, EGFR, EFNB2, VEGFC, EREG, ADM, HIPK1, CCND2, HAS2, LAMC2, CDCA7L, SERPINB3, EIF5A2, CSF3, FGFR2, KRT6A, CXCL5, ERBB4, FOXM1, CRLF1, TIPIN, KIT, SOX9, ALDH3A1, TIMP1, LIF, ZNF703, RAC2, XBP1, NPM1, PTN, THBS1, FGFBP1, FN1, ACER3, ODC1, SHMT2, CCPG1, GAREM1, CDC20, IGF2, BIRC5, HILPDA, PTGFR, ISL1, NTN1, PLAC8, CDC25B, NOTCH1, ETS1, BNC1, KIF20B, HBEGF, ID4, PBX1, AREG, GRK5, BAMBI	4.40E-04
GO:0051781~positive regulation of cell division	16	0.81	3.46	8	8	0.00	FGFR2, FGF5, PGF, PDGFA, BTC, GAREM1, TGFB3, IGF2, CSPP1, VEGFC, EREG, TGFA, PTN, IL1B, CAT, IL1A	5.00E-04
GO:0007368~determination of left/right symmetry	17	0.86	3.14	15	2	3.15	DAW1, FOXJ1, DYX1C1, DRC1, DYNC2LI1, ARMC4, DNAI2, ARL6, DNAH5, CITED2, RTTN, DPCD, NOTCH1, DNAI1, CC2D2A, DYNC2H1, IFT74	9.79E-04
GO:0000281~mitotic cytokinesis	12	0.61	4.20	2	10	-2.31	CKAP2, KIF23, BBS4, KIF4A, CENPA, ANK3, NUSAP1, ANLN, STMN1, CEP55, RACGAP1, KIF20A	9.93E-04
GO:0007155~cell adhesion	72	3.65	1.59	27	45	-2.12	CTNNAL1, MPZL3, MTSS1, FERMT1, POSTN, EDIL3, AZGP1, SRPX, CD44, CTGF, TGFBI, COL12A1, ZYX, LOXL2, ICAM1, EGFL6, EFNB1, BYSL, EFNB2, NECTIN1, PCDHB2, CHST4, CERCAM, PRKCE, CD36, VCAN, LAMC2, HAS3, TGFB1I1, CNTN3, DST, CHL1, OLFM4, AMTN, ITGB4, KITLG, CX3CL1, PCDHAC2, ALCAM, SEMA5A, LPXN, LY6D, COL7A1, SORBS2, MSLN, LMLN, COL8A1, LAMB1, THBS1, GPNMB, FN1, PODXL, EFS, CD99, ITGA3, COL16A1, TINAGL1, COL4A6, EPHA4, CDH13, LAMA3, PKP1, ITGA6, FREM2, ITGA5, TROAP, DSC3, ABL2, THEMIS2, MUC16, FEZ1, CDH11	1.50E-03
GO:0009168~purine ribonucleoside monophosphate biosynthetic process	8	0.41	6.25	1	7	-2.12	ADSSL1, GMPS, PAICS, IMPDH1, ADA, IMPDH2, PPAT, GART	1.68E-03

GO:0008584~male gonad development	23	1.17	2.49	14	9	1.04	TESC, LRRC6, HMGB2, HMGCS1, KITLG, SIX4, TLR5, KIT, HMGA2, MMP14, SOX9, BCL2L11, CITED2, INHBA, WNT4, TNFSF10, NCOA1, NUPR1, GATA3, RRM1, SOX15, PATZ1, ASPM	1.72E-03
GO:0006268~DNA unwinding involved in DNA replication	7	0.36	7.11	0	7	-2.65	MCM7, MCM2, HMGA1, MCM4, TOP2A, RAD51, MCM6	2.53E-03
GO:0035987~endodermal cell differentiation	11	0.56	4.14	0	11	-3.32	INHBA, COL4A2, LAMA3, COL7A1, ITGA5, COL12A1, MMP14, HMGA2, COL8A1, LAMB1, FN1	2.75E-03
GO:0007093~mitotic cell cycle checkpoint	12	0.61	3.81	0	12	-3.46	MAD1L1, NABP1, HRAS, PLK3, MAD2L1, ZWINT, KNTC1, BUB1, TTK, BUB1B, CHEK1, ZWILCH	2.80E-03
GO:0008544~epidermis development	21	1.07	2.51	6	15	-1.96	KLK7, SATB1, ELF3, S100A7, KLK5, SPRR2F, SPRR2E, LAMA3, COL7A1, CST6, SPRR1A, CTGF, SPRR2D, SPRR2A, KRT14, IFT172, BNC1, SPRR3, LAMC2, ZNF750, EMP1	3.27E-03
GO:0042060~wound healing	20	1.01	2.54	7	13	-1.34	EGFR, DCBLD2, KRT6A, ERBB3, PDGFA, TGFB3, TIMP1, MAP3K5, ALOX15, CCL20, EREG, FGFR1OP2, SERPINB2, SPRR3, TGFA, TFF3, CNN2, LOX, NRG1, FN1	4.13E-03
GO:0007059~chromosome segregation	18	0.91	2.69	1	17	-3.77	CENPN, KIF11, NUF2, CENPF, NEK10, NDC80, CENPE, TOP1MT, KNSTRN, ESCO2, SPC25, OIP5, HJURP, MIS18A, CDCA2, SKA2, SKA1, TOP2A	4.54E-03
GO:0007076~mitotic chromosome condensation	8	0.41	5.42	0	8	-2.83	NCAPH, NCAPG, NUSAP1, CDCA5, SMC2, NCAPD3, SMC4, NCAPD2	5.27E-03
GO:0036158~outer dynein arm assembly	8	0.41	5.42	8	0	2.83	LRRC6, DNAI1, DYX1C1, DNAAF1, ZMYND10, ARMC4, DNAI2, DNAH5	5.27E-03
GO:0044458~motile cilium assembly	8	0.41	5.42	8	0	2.83	LRRC6, DNAAF3, DNAAF1, ZMYND10, BBOF1, CC2D2A, SPATA6, RSPH9	5.27E-03
GO:0001666~response to hypoxia	33	1.67	1.95	15	18	-0.52	CAV1, ALAD, AHCY, CLDN3, PGF, TGFB3, EGLN3, BNIP3, POSTN, ADA, ALDH3A1, CITED2, EDNRA, CAT, LOXL2, THBS1, ANGPTL4, MB, PLAT, EGR1, MUC1, CYP1A1, NR4A2, MMP14, ITPR1, AJUBA, VEGFC, CA9, ADM, UCP2, ETS1, HSD11B2, PLAU	5.77E-03
GO:0008283~cell proliferation	58	2.94	1.61	14	44	-3.94	FGF5, HRAS, TSPAN1, ZAK, ELF5, UCHL1, DTYMK, AURKB, CLK1, MCM10, CITED2, EDNRA, FAM83D, KIF2C, FAM83B, MCM7, TGFBI, TGFA, RAPGEF3, NRG1, MYC, IL1A, EGFR, CDK1, CYP1A1, PDPN, BYSL, TPX2, SKP2, TACC3, TACC2, UHRF1, PLCE1, SIX1, BUB1B, EMP1, MELK, MIA, BCAT1, CKS1B, ERBB4, KITLG, CD74, TYMS, BUB1, AXIN2, POLR3G, CRIP1, MKI67, DLGAP5, FSCN1, CENPF, CDC25A, EPS8, LIPG, CKS2, TCF19, AREG	6.15E-03
GO:0022617~extracellular matrix disassembly	19	0.96	2.54	8	11	-0.69	KLK7, MMP7, KIF9, CTSS, MMP14, MMP13, MMP12, TIMP1, MMP10, LAMA3, CD44, GSN, CAPG, LAMC2, FBN2, ADAM8, LCP1, FN1, TLL1	6.22E-03
GO:0007052~mitotic spindle organization	11	0.56	3.72	2	9	-2.11	CCNB1, SPC25, EML1, KIF11, CEP126, GPSM2, TTK, MAP4, NDC80, AURKA, STMN1	7.43E-03
GO:0060972~left/right pattern formation	6	0.30	7.62	6	0	2.45	CLUAP1, FOXJ1, IFT57, DNAAF1, CITED2, DPCD	7.53E-03
GO:0009612~response to mechanical stimulus	16	0.81	2.75	9	7	0.50	TXNIP, PTGER4, CHI3L1, DNAH1, POSTN, FOSB, MMP14, CITED2, INHBB, CCNB1, MEIS2, ETS1, TRPV4, THBS1, FOSL1, SMPD2	8.52E-03
GO:0008285~negative regulation of cell proliferation	61	3.09	1.56	31	30	0.13	RARRES3, DLEC1, HRAS, RARRES1, IGFBP6, TGFB3, SKAP2, BNIPL, AZGP1, CDKN2A, GATA3, DLG3, IL1B, FOSL1, IL1A, CDC6, CLMN, HMGA1, VEGFC, INHBA, EREG, ADM, ALOX15B, NME1, SCIN, RGCC, ADAMTS1, TGFB1I1, EMP3, SMARCA2, FRK, HIST1H2AC, ERBB4, SOX7, PLPP1, FUZ, LIF, CYP27B1, BCL11B, NPM1, BCL6, GPNMB, AXIN2, FGFBP1, PINX1, BMP4, DFNA5, TESC, SMAD6, FBXO2, CDKN3, C18ORF54, RERG, CDH13, NOTCH1, IRF6, RPS6KA2, ETS1, IRF1, IGFBP3, TP53INP1	9.03E-03
GO:0006069~ethanol oxidation	7	0.36	5.93	6	1	1.89	ALDH1A1, ACSS1, ALDH1B1, ADH1C, ADH1B, ADH1A, ADH7	9.31E-03
GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	21	1.07	2.32	13	8	1.09	HLA-DQB1, KIF23, KIF4A, KIF11, HLA-DRB1, DYNC2LI1, KIF18A, CENPE, CTSS, RACGAP1, HLA-DMB, HLA-DMA, KIF3C, CD74, HLA-DQA1, KIF2C, DYNC2H1, CTSD, HLA-DPA1, SAR1B, HLA-DRA	9.93E-03

GO:0045840~positive regulation of mitotic nuclear division	10	0.51	3.91	3	7	-1.26	EREG, RGCC, EDN1, BTC, NUSAP1, TGFA, IL1B, IGF2, AURKA, IL1A	1.06E-02
GO:0007080~mitotic metaphase plate congression	12	0.61	3.29	0	12	-3.46	KIF14, CCNB1, KIFC1, KIF2C, CDCA8, PSRC1, KIF18A, CENPE, SPDL1, CEP55, CDCA5, PINX1	1.17E-02
GO:0019882~antigen processing and presentation	15	0.76	2.77	11	4	1.81	HLA-DQB1, MICB, MICA, HLA-DRB1, HLA-C, CTSS, HLA-B, HLA-DMB, CD74, HLA-DQA1, RAB32, AZGP1, RAET1L, HLA-DPA1, HLA-DRA	1.29E-02
GO:0007173~epidermal growth factor receptor signaling pathway	15	0.76	2.72	6	9	-0.77	EGFR, REPS2, HRAS, BTC, GAREM1, PIGR, SOX9, PLCE1, FAM83B, EPS8, EREG, TGFA, HBEGF, SHC1, AREG	1.56E-02
GO:0050680~negative regulation of epithelial cell proliferation	15	0.76	2.72	11	4	1.81	FGFR2, BMP4, MTSS1, IFT80, SOX2, SOX9, PBLD, IFT122, EREG, IFT57, IFT172, PTN, MCC, KRT4, IFT74	1.56E-02
GO:0001525~angiogenesis	38	1.93	1.73	15	23	-1.30	FGFR2, CAV1, NRP1, S100A7, PDGFA, PGF, EFNA1, IL18, ANPEP, JAG1, RORA, MEIS1, NRCAM, TSPAN12, OVOL2, XBP1, CTGF, TGFBI, TGFA, ANGPT1, SHC1, RAPGEF3, BCAS3, COL8A1, ADAM8, ANGPTL4, FN1, FZD8, COL4A2, VAV3, NRXN3, MMP14, MYH9, CXCL17, VEGFC, EREG, ITGA5, WNT7A	2.02E-02
GO:0030198~extracellular matrix organization	34	1.73	1.76	11	23	-2.06	MPZL3, ELF3, PDGFA, NPNT, ITGB4, POSTN, SOX9, SPINK5, ABI3BP, CD44, COL7A1, ERO1B, TGFBI, LOX, FBN2, COL8A1, THBS1, LAMB1, FN1, ICAM1, COL4A2, COL4A1, EGFL6, CCDC80, ITGA3, COL16A1, COL4A6, LAMA3, ITGA6, SERPINB5, ITGA5, FBLN5, LAMC2, VCAN	2.83E-02
GO:0034501~protein localization to kinetochore	6	0.30	6.10	0	6	-2.45	CDK1, KNL1, TTK, BUB1B, SPDL1, AURKB	2.83E-02
GO:0035721~intraciliary retrograde transport	6	0.30	6.10	6	0	2.45	ICK, WDR19, IFT122, DYNC2H1, IFT43, TTC21A	2.83E-02
GO:0043523~regulation of neuron apoptotic process	8	0.41	4.28	3	5	-0.71	KIF14, TRIM2, GATA3, NPM1, EGLN3, TP63, PCSK9, SIGMAR1	2.87E-02
GO:0000187~activation of MAPK activity	22	1.12	2.09	10	12	-0.43	IRAK2, CDK1, ADORA2B, EFNA1, MUC20, MAPKAPK3, TGFB3, TLR4, MAPK10, KIT, CD74, DUSP5, CXCL17, PLCE1, TGFA, IL1B, SHC1, THBS1, NRG1, SHC2, DUSP7, DUSP6	2.93E-02
GO:0016266~O-glycan processing	15	0.76	2.54	14	1	3.36	MUC1, GCNT3, ST6GAL1, C1GALT1C1, POC1B-GALNT4, GALNT5, MUC20, CHST4, MUC4, B3GNT7, GXYLT2, MUC15, GCNT1, MUC5B, MUC16	3.19E-02
GO:0048661~positive regulation of smooth muscle cell proliferation	15	0.76	2.54	4	11	-1.81	BMP4, FGFR2, EGFR, IL18, EDN1, SKP2, PPARGC1A, CDH13, EREG, ID2, AKR1B1, TGM2, HBEGF, THBS1, MYC	3.19E-02
GO:0000086~G2/M transition of mitotic cell cycle	26	1.32	1.93	6	20	-2.75	HAUS6, FOXM1, CETN2, PKMYT1, AKAP9, AURKA, CHEK1, ENSA, HMMR, PRKAR2B, TUBB, TUBA1A, PHLDA1, CDK1, SKP2, TPX2, BIRC5, PCM1, CDC25A, CDC25B, AJUBA, CCNB1, PLK3, CCNB2, TUBA4A, MELK	3.27E-02
GO:0015949~nucleobase-containing small molecule interconversion	9	0.46	3.66	3	6	-1.00	NME1, RRM2, DTYMK, RRM1, CTPS1, AK4, AK7, AK9, AK8	3.77E-02
GO:0006271~DNA strand elongation involved in DNA replication	7	0.36	4.74	0	7	-2.65	GINS1, PRIM1, GINS2, RFC3, RFC4, GINS3, GINS4	3.84E-02
GO:0051726~regulation of cell cycle	24	1.22	1.97	9	15	-1.22	DTL, MAK, FIGNL1, FOXM1, CCNF, PRR11, SKP2, KIAA0101, PKMYT1, CENPF, MECOM, CDC25A, CCNB1, CCNE2, CCNE1, SRSF5, ICK, ZNF703, CCNB2, OVOL2, IRF1, GRK5, CDK20, MX2	3.92E-02
GO:0007565~female pregnancy	19	0.96	2.17	10	9	0.23	MUC1, PGF, TFCP2L1, BYSL, TGFB3, FOSB, COL16A1, SCGB1A1, LGALS9, FOS, THBD, ADM, ETS1, UCP2, CLIC5, HSD11B2, FOSL1, HPGD, IGFBP5	4.32E-02
GO:0045786~negative regulation of cell cycle	11	0.56	3.02	7	4	0.90	BMP4, INHBA, BRINP1, PLA2G16, NUPR1, ALOX15B, RPS6KA2, ETS1, GMNN, GATA3, HPGD	4.47E-02
GO:0007224~smoothened signaling pathway	16	0.81	2.36	16	0	4.00	BMP4, CLUAP1, IFT80, TTC26, B9D1, TMEM17, TMEM231, HIPK1, IFT46, WDPCP, IFT57, IFT172, CC2D2A, DYRK2, IFT27, IQUB	4.66E-02
GO:1900264~positive regulation of DNA-directed DNA polymerase activity	5	0.25	7.26	0	5	-2.24	RFC5, RFC3, RFC4, RFC2, DSCC1	4.76E-02
KEGG Pathway ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR

hsa04110:Cell cycle	32	1.62	2.58	3	29	-4.60	MAD1L1, DBF4, TGFB3, PKMYT1, TTK, CHEK1, SFN, CCNE2, CCNE1, CDC45, MCM7, CDKN2A, BUB1, ORC6, CCNA2, MYC, CDK1, CDC6, SKP2, CDC20, MCM2, MCM3, MCM4, CDC25A, CDC25B, MCM6, CCNB1, CCNB2, MAD2L1, CCND2, BUB1B, ANAPC7	1.21E-05
hsa03030:DNA replication	14	0.71	3.89	0	14	-3.74	POLE, MCM2, RNASEH2A, MCM3, MCM4, MCM6, RFC5, PRIM1, RFC3, RFC4, MCM7, POLE2, RFC2, FEN1	2.99E-04
hsa04940:Type I diabetes mellitus	14	0.71	3.34	12	2	2.67	HLA-DQB1, CPE, HLA-DRB1, PTPRN2, IL1B, HLA-C, HLA-DPA1, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1, IL1A, HLA-DRA, HLA-F	1.88E-03
hsa05332:Graft-versus-host disease	12	0.61	3.64	10	2	2.31	HLA-DQB1, HLA-DRB1, IL1B, HLA-C, HLA-DPA1, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1, IL1A, HLA-DRA, HLA-F	2.93E-03
hsa05323:Rheumatoid arthritis	21	1.07	2.39	14	7	1.53	HLA-DQB1, ICAM1, CXCL5, HLA-DRB1, IL18, TGFB3, TLR4, CXCL6, HLA-DMB, ATP6V1B1, HLA-DMA, HLA-DQA1, ATP6V1C2, FOS, ATP6V0E2, CCL20, IL1B, ANGPT1, HLA-DPA1, IL1A, HLA-DRA	4.21E-03
hsa05416:Viral myocarditis	16	0.81	2.81	11	5	1.50	HLA-DQB1, ICAM1, CAV1, HLA-DRB1, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1, HLA-F, CD55, RAC2, HLA-DPA1, ABL2, HLA-DRA, SGCB	4.41E-03
hsa05166:HTLV-I infection	44	2.23	1.72	23	21	0.30	HLA-DQB1, ADCY3, HRAS, IL1R1, NRP1, ADCY7, HLA-DRB1, PDGFA, TGFB3, CHEK1, HLA-DMB, HLA-DMA, FOS, WNT4, CDKN2A, POLE2, XBP1, RRAS, NFATC2, MYB, PIK3R3, FOSL1, MYC, TCF3, EGR1, ICAM1, FZD8, SLC25A4, POLE, HLA-C, CDC20, HLA-B, HLA-DQA1, HLA-F, WNT7B, MAD2L1, CCND2, ETS1, BUB1B, HLA-DPA1, ANAPC7, WNT7A, HLA-DRA, TP53INP1	5.09E-03
hsa04115:p53 signaling pathway	16	0.81	2.39	3	13	-2.50	CDK1, RPRM, CHEK1, SFN, GTSE1, CCNB1, CCNE2, CCNE1, CDKN2A, CCNB2, CCND2, SERPINB5, RRM2, SHISA5, THBS1, IGFBP3	2.66E-02
hsa00230:Purine metabolism	31	1.57	1.76	9	22	-2.33	XDH, ADCY3, GDA, ADCY7, ENPP3, ENPP4, PNP, PPAT, ADA, PRIM1, POLE2, PDE8B, NT5E, IMPDH1, IMPDH2, POLR3G, ADSSL1, POLR1E, POLE, AK4, AK7, GMPS, AK9, AK8, GART, NME5, NME1, RRM2, ADK, RRM1, PAICS	2.94E-02
hsa05321:Inflammatory bowel disease (IBD)	15	0.76	2.35	11	4	1.81	HLA-DQB1, HLA-DRB1, IL18, TGFB3, TLR4, RORA, TLR5, HLA-DMB, HLA-DMA, HLA-DQA1, STAT4, IL1B, HLA-DPA1, IL1A, HLA-DRA	4.62E-02
hsa01100:Metabolic pathways	150	7.61	1.22	93	57	2.94	ALAD, GDA, B3GALT4, DTYMK, ADH1C, ADH1B, ADH1A, PNP, DSE, PRIM1, ACSS1, TRAK2, PHOSPHO2, C1GALT1C1, CYP1A1, POLE, FBP1, CYP26A1, CHPT1, NME5, MGAT3, PLCE1, ALOX15B, NME1, MGAM, HSD11B1, XDH, CHKA, GCNT3, ME3, AHCY, NAGS, CYP2B6, ALDOC, ENPP3, HMGCS1, CTPS1, CERS4, ATP6V1B1, PPAT, ADA, TK1, POLE2, ARG2, PLCH1, IDH2, GALC, CDA, ALDH4A1, GCNT1, B4GALT4, MGAT4A, ODC1, ST6GAL1, ADSSL1, SPHK1, EPHX2, TKT, AK4, AK7, AK9, AK8, GART, CEL, PLA2G4A, GGT6, ATP6V0E2, GGT7, GLS, GK, NDUFC2-KCTD14, PC, DUT, TM7SF2, CYP2J2, ACOT2, PIP5K1B, ANPEP, PPOX, ASAH1, CRYL1, PLCB4, MCEE, MCCC1, IMPDH1, NT5E, IMPDH2, POLR1E, PIK3C2B, NDUFC2, DHRS9, GMPS, LPIN1, ALDH3B1, ST6GALNAC1, ATP6V1C2, ALOX15, ALDH7A1, ALDH1B1, H6PD, RRM2, ADK, RRM1, GAA, CYP2A6, MTAP, DEGS2, AMY1A, BCAT1, SORD, GALNT5, FUT6, POC1B-GALNT4, UPP1, ADH7, PLPP1, ALDH3A1, ALDH1A1, TYMS, ACSL1, CYP27B1, INPP5J, FUT3, FASN, UGT2A1, FUT1, BDH2, FUT2, BDH1, ACSL5, POLR3G, SHMT2, PLA2G16, A4GALT, CES1, GMDS, NAT1, MAN1C1, IDNK, RDH10, AKR1B1, PHGDH, LIPG, MBOAT1, ALOX5, PAICS, SMPD3, UGT2B7, CBS, SMPD2	4.74E-02

***Functional enrichment analysis of differentially expressed mRNAs (Log2Ratio > 1, Log2Ratio < 1, and q < 0.05) was done in Database for Annotation, Visualization and Integrated Discovery (DAVID, version 6.8, recently updated in Oct. 2016, https://david.ncifcrf.gov/home.jsp) and using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or q < 0.05). Enriched Gene Ontology and KEGG pathway terms**

are ordered in this table by FDR values. Numbers of upregulated (UP) and downregulated (DW) genes are showed in red and green, respectively. The z-score represents the overall up/down regulated genes from that term [Walter et al., 2015]. Z-score cells of this table are coloured depending on Z-score values: in red for Z >0, in blue for Z < 0 or in white for Z = 0.

TABLE S19. Enriched Gene Ontology Biological Processes (GOTERM_BP_DIRECT) and KEGG pathways in differentiated CRSwNP air-liquid interface cultures at day 14 compared to day 0.*

GO_BP_DIRECT Term ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
GO:0051301~cell division	68	5.14	2.73	2	66	-7.76	MAD1L1, AURKA, FAM83D, CCNE2, KIF2C, CCNE1, CDCA8, CDCA7, PPP1R1C, OIP5, CDCA2, TUBA1A, CCNA1, CDCA5, CCNA2, TUBA1B, CDCA4, CDCA3, KIF14, CDK1, CDC6, KIF11, CCNF, TPX2, UBE2C, TACC3, PRKCE, HMGA2, TACC1, MAD2L1, SGO2, CCND2, ZWINT, BUB1B, CDCA7L, RUVBL1, UBE2S, CKS1B, NEK2, HAUS2, TIPIN, SPC25, VRK1, NCAPH, NCAPG, BUB1, SKA3, FBXO5, SKA1, ZWILCH, HELLS, ERCC6L, PSRC1, NUF2, CENPF, NDC80, CENPE, CDC20, BIRC5, KNSTRN, SMC2, CDC25A, SMC4, CCNB1, FAM64A, CCNB2, KNL1, CKS2	1.11E-12
GO:0000082~G1/S transition of mitotic cell cycle	28	2.12	3.86	4	24	-3.78	BCAT1, DBF4, PKMYT1, MCM10, RHOU, CDT1, CCNE2, PRIM1, CCNE1, TYMS, CDC45, CDKN2A, MCM7, POLE2, PRIM2, FBXO5, ORC6, CCNA1, CDCA5, CDC6, CDK1, SKP2, CDKN3, CDC25A, INHBA, PLK3, RRM2, ID4	2.79E-08
GO:0007067~mitotic nuclear division	47	3.56	2.66	1	46	-6.56	NEK2, HAUS2, TIPIN, PKMYT1, ANLN, AURKA, CEP55, AURKB, FAM83D, SPC25, KIF2C, VRK1, OIP5, CDCA2, BUB1, FBXO5, SKA3, SKA1, CCNA1, ZWILCH, CDCA5, CCNA2, TUBB3, HELLS, ASPM, CDCA3, ERCC6L, CDK1, CDC6, CENPN, KIF11, CCNF, NUF2, TPX2, CENPF, NDC80, CDC20, BIRC5, PBK, HMGA2, CDC25A, FAM64A, CCNB2, NUP62, KNL1, BUB1B, RUVBL1	2.95E-08
GO:0008283~cell proliferation	59	4.46	2.27	16	43	-3.52	STIL, FGF5, HRAS, ZAK, ELF5, UCHL1, DTYMK, AURKB, MCM10, CITED2, FAM83D, KIF2C, MCM7, FAM83A, CREG1, TGFA, BHLHE41, NRG1, IL1A, OCA2, CYR61, CDK1, CYP1A1, BYSL, TPX2, SKP2, PIM1, TACC3, TACC1, TACC2, GLUL, UHRF1, PLCE1, SERPINF1, KRT16, BUB1B, FOXC1, EMP1, MELK, BCAT1, CKS1B, ERBB2, KITLG, EHF, CD74, TYMS, BUB1, ERCC1, POLR3G, MKI67, DLGAP5, CENPF, GAS6, CDC25A, CSGALNACT1, LIPG, CKS2, TCF19, AREG	1.16E-07
GO:0007062~sister chromatid cohesion	27	2.04	3.68	0	27	-5.20	MAD1L1, RAD51C, AURKB, KIF2C, SPC25, CDCA8, CENPA, BUB1, SKA1, ZWILCH, CDCA5, ERCC6L, CENPN, KIF18A, NUF2, CENPF, NDC80, BIRC5, CDC20, CENPE, CENPK, CENPH, MAD2L1, SGO2, KNL1, ZWINT, BUB1B	1.67E-07
GO:0008544~epidermis development	23	1.74	3.80	6	17	-2.29	KLK7, STS, ELF3, S100A7, CRABP2, KLK5, SPRR2F, SPRR2E, ALDH3A2, CST6, SPRR1A, SPRR2D, KRT16, CTGF, SPRR2A, KRT14, BNC1, LAMC2, LOC100653049, CALML5, INSR, FABP5, EMP1	1.41E-06
GO:0042493~response to drug	48	3.63	2.22	21	27	-0.87	ALAD, SORD, ASS1, PTGS2, PGF, HMGCS1, CTPS1, PNP, MDK, SCGB1A1, ALDH3A1, TYMS, FOS, MCM7, ACSL1, PLIN2, APOD, OXCT1, TGFA, ABCD3, SEMA3C, CAT, LOX, THBS1, FOSL1, TXNIP, CDK1, IL6, HSP90AA1, VAV3, CYP1A1, LGALS1, MAOB, CENPF, ATP1A1, DPYSL2, GAL, PPARGC1A, POR, RAD51, CCNB1, VEGFC, INHBA, CA9, JUN, HSD11B2, LRP8, DUSP6	6.68E-06
GO:0006260~DNA replication	31	2.34	2.81	1	30	-5.21	BLM, DBF4, HUS1, TIPIN, KIAA0101, CHEK1, MCM10, CDT1, CDC45, MCM7, POLE2, ORC6, EGF, FEN1, EXO1, GINS2, CDC6, CDK1, DTL, GINS3, GINS4, RNASEH2A, CDC25A, RFC5, RFC3, RFC4, RFC2, RRM2, CHAF1A, TNFAIP1, DSCC1	7.84E-06
GO:0070542~response to fatty acid	9	0.68	7.44	7	2	1.67	ALAD, CD36, TBXAS1, ASS1, PTGS2, UCP2, CTGF, TLR2, CAT	1.62E-04

GO:0055114~oxidation-reduction process	72	5.45	1.71	56	16	4.71	STEAP4, ALDH1L1, PTGS2, CYP2S1, DUOX2, PGD, DUOX1, BBOX1, GPX2, AKR1C2, CRYL1, CREG1, SRD5A3, MICAL1, LOXL4, LOX, AKR1C1, CYP1A1, AIFM2, NCF2, FA2H, CYP26A1, DHRS9, ALDH3B2, CYB5A, POR, ALDH3B1, CYP4X1, ALOX15, DHRS3, NNT, AKR1B15, ALOX15B, AKR1B10, RRM2, HSD11B1, HSD11B2, STEAP2, DEGS1, ME3, CYP1B1, SORD, CYP2B6, EGLN3, ADH7, ALDH3A2, ALDH3A1, P3H2, GPD1L, ALDH1A1, CYP27B1, AKR1A1, FMO3, HSD17B3, TBXAS1, SCD, MAOA, MAOB, FADS3, IDO1, AAED1, P4HTM, MSRB3, CYP4B1, RDH10, JMJD6, CYP4F3, DPYD, CP, HPGD, DCXR, CBS	1.73E-04
GO:0016266~O-glycan processing	16	1.21	3.75	15	1	3.50	MUC1, ST6GAL1, GCNT3, POC1B-GALNT4, GALNT5, MUC20, MUC4, ST3GAL1, B3GNT7, GXYLT2, MUC15, GALNT12, GCNT1, MUC5B, B4GALT5, MUC16	2.61E-04
GO:0006271~DNA strand elongation involved in DNA replication	8	0.61	7.49	0	8	-2.83	GINS1, PRIM1, GINS2, RFC3, RFC4, GINS3, GINS4, PRIM2	6.54E-04
GO:0045840~positive regulation of mitotic nuclear division	10	0.76	5.40	4	6	-0.63	RGCC, EDN1, TGFA, NUSAP1, IL1B, IGF2, AURKA, EGF, INSR, IL1A	8.70E-04
GO:0006270~DNA replication initiation	11	0.83	4.83	0	11	-3.32	PRIM1, CCNE2, CCNE1, CDC6, CDC45, MCM7, POLE2, GINS4, PRIM2, ORC6, MCM10	9.03E-04
GO:0007093~mitotic cell cycle checkpoint	11	0.83	4.83	0	11	-3.32	MAD1L1, HRAS, PLK3, MAD2L1, ZWINT, HUS1, BUB1, TTK, BUB1B, CHEK1, ZWILCH	9.03E-04
GO:0007059~chromosome segregation	16	1.21	3.31	0	16	-4.00	CENPN, KIF11, NEK2, NUF2, CENPF, NDC80, CENPE, KNSTRN, ESCO2, SPC25, HJURP, OIP5, CDCA2, SKA3, SKA1, TOP2A	1.27E-03
GO:0030855~epithelial cell differentiation	16	1.21	3.21	12	4	2.00	GSTA1, MUC1, CDK1, COL4A1, ELF3, DHRS9, EHF, TAGLN2, SPINK5, ACADVL, AKR1C2, UPK1B, KRT14, KRT4, ID3, AKR1C1	1.81E-03
GO:0019882~antigen processing and presentation	14	1.06	3.58	9	5	1.07	HLA-DQB1, MICB, RAB3B, HLA-DRB1, HLA-C, CTSS, HLA-B, CD74, RAB32, RAB35, RAET1L, HLA-DPA1, CTSH, HLA-DRA	1.81E-03
GO:0000083~regulation of transcription involved in G1/S transition of mitotic cell cycle	9	0.68	5.50	1	8	-2.33	CCNE1, CDK1, CDC6, TYMS, CDC45, RRM2, FBXO5, CCNA1, CDT1	2.23E-03
GO:0000281~mitotic cytokinesis	10	0.76	4.85	0	10	-3.16	KIF23, KIF4A, CENPA, NUSAP1, SPTBN1, ANLN, STMN1, CEP55, RACGAP1, KIF20A	2.29E-03
GO:0045740~positive regulation of DNA replication	12	0.91	4.01	3	9	-1.73	CSF2, CDK1, IGF1R, IL6, HRAS, JUN, CACYBP, TGFB3, KITLG, AREG, INSR, TNFAIP1	2.30E-03
GO:0045429~positive regulation of nitric oxide biosynthetic process	12	0.91	3.92	5	7	-0.58	IL6, HSP90AA1, ASS1, PTGS2, EDN1, TICAM1, CLU, SMAD3, IL1B, TLR5, INSR, KLF4	2.90E-03
GO:0007080~mitotic metaphase plate congression	11	0.83	4.18	1	10	-2.71	KIF14, CCNB1, KIF2C, CDCA8, PSRC1, KIF18A, CENPE, CEP55, PDCD6IP, CDCA5, PINX1	3.51E-03
GO:0001666~response to hypoxia	27	2.04	2.21	17	10	1.35	ATP1B1, ALAD, PGF, TGFB3, EGLN3, TLR2, POSTN, ALDH3A1, CITED2, HMOX2, CYGB, CAT, THBS1, MB, MUC1, EPAS1, CYP1A1, NR4A2, SMAD3, ITPR1, AJUBA, VEGFC, CA9, ETS1, UCP2, HSD11B2, PLAU	3.84E-03
GO:0030325~adrenal gland development	8	0.61	5.92	5	3	0.71	DKK3, WNT4, FSTL3, STRA6, PBX1, HMGA2, MDK, INSR	3.97E-03
GO:0000722~telomere maintenance via recombination	10	0.76	4.39	0	10	-3.16	RFC5, PRIM1, RAD51C, RFC3, RFC4, POLE2, RFC2, PRIM2, FEN1, RAD51	5.28E-03
GO:0002576~platelet degranulation	19	1.44	2.59	12	7	1.15	TF, CLU, SELENOP, TGFB3, ACTN1, IGF2, PCDH7, GAS6, FLNA, VEGFC, CD36, PPBP, SERPINA3, TUBA4A, SERPINA1, WDR1, THBS1, EGF, PROS1	5.97E-03

GO:0008285~negative regulation of cell proliferation	48	3.63	1.70	22	26	-0.58	DLC1, RARRES3, HRAS, CYP1B1, RARRES1, PTGS2, E2F7, PPP2R5C, IGFBP6, TLR2, TGFB3, PLPP1, P3H2, CDKN2A, CYP27B1, SERPINE2, PTGES, DLG3, IL1B, BCL6, RARB, GPNMB, FOSL1, IL1A, PINX1, CEBPA, CDC6, IL6, NF2, SMAD6, FBXO2, IL24, CDKN3, C18ORF54, RERG, VEGFC, CDH13, INHBA, NUP62, ALOX15B, ETS1, JUN, SCIN, RGCC, ADAMTS1, EMP3, IGFBP3, KLF4	6.89E-03
GO:0042060~wound healing	16	1.21	2.81	8	8	0.00	WNT5A, DCBLD2, IL6, EPPK1, ERBB3, ERBB2, TGFB3, SMAD3, IL24, MAP3K5, ALOX15, FGFR1OP2, SERPINB2, TGFA, LOX, NRG1	8.48E-03
GO:0008284~positive regulation of cell proliferation	54	4.08	1.63	20	34	-1.91	FGF5, HRAS, PRC1, PGF, EDN1, TTK, AKR1C2, CTGF, TGFA, RARB, NRG1, FOSL1, INSR, KIF14, CHP2, IL24, VEGFC, CCND2, HIPK2, LAMC2, CDCA7L, SERPINB3, EIF5A2, CTSH, CSF2, TBC1D8, FOXM1, CRLF1, TIPIN, ALDH3A1, IGF1R, XBP1, THBS1, EGF, RUNX2, KLF5, ACER3, ODC1, SHMT2, IL6, TNFSF4, CCPG1, BIRC5, IGF2, CDC20, NTN1, PLAC8, ETS1, BNC1, HBEGF, ID4, PBX1, GRK5, AREG	8.54E-03
GO:0030574~collagen catabolic process	14	1.06	3.07	9	5	1.07	KLK6, MMP10, COL4A2, COL4A1, MMP9, MRC2, COL6A3, MMP7, COL6A1, CTSD, CTSS, MMP13, MMP12, COL4A5	8.99E-03
GO:0000187~activation of MAPK activity	19	1.44	2.50	9	10	-0.23	WNT5A, CDK1, MUC20, MAPKAPK3, TGFB3, MAPK10, CD74, DUSP5, PEA15, CXCL17, PLCE1, TGFA, IL1B, THBS1, NRG1, EGF, INSR, DUSP7, DUSP6	9.62E-03
GO:0001525~angiogenesis	31	2.34	1.95	17	14	0.54	CYP1B1, PTGS2, S100A7, TNFRSF12A, PGF, IL18, NAA15, MEIS1, TSPAN12, ARHGAP22, HEY1, APOD, CTGF, XBP1, TGFA, ANGPT1, ADAM8, EGF, CEACAM1, KLF5, COL4A2, VAV3, EPAS1, ACKR3, CXCL17, VEGFC, ID1, JUN, TNFAIP2, WNT7A, SEMA4A	1.03E-02
GO:0006081~cellular aldehyde metabolic process	6	0.45	7.66	6	0	2.45	ALDH1A1, AKR1A1, AKR1B10, ALDH3A2, ALDH3B1, ALDH3A1	1.08E-02
GO:0000086~G2/M transition of mitotic cell cycle	22	1.66	2.26	1	21	-4.26	CDK1, HSP90AA1, NEK2, HAUS2, PPP1R12B, FOXM1, TPX2, SKP2, PKMYT1, AURKA, BIRC5, CHEK1, CDC25A, HMMR, AJUBA, CCNB1, CCNB2, PLK3, TUBA4A, TUBA1A, MELK, PHLDA1	1.25E-02
GO:0060907~positive regulation of macrophage cytokine production	5	0.38	10.04	4	1	1.34	WNT5A, CD36, SEMA7A, GPRC5B, CD74	1.39E-02
GO:1900264~positive regulation of DNA-directed DNA polymerase activity	5	0.38	10.04	0	5	-2.24	RFC5, RFC3, RFC4, RFC2, DSCC1	1.39E-02
GO:0007052~mitotic spindle organization	9	0.68	4.22	0	9	-3.00	CCNB1, STIL, SPC25, KIF11, GPSM2, TTK, NDC80, AURKA, STMN1	1.69E-02
GO:0051726~regulation of cell cycle	20	1.51	2.27	4	16	-2.68	TRNP1, DTL, FIGNL1, FOXM1, CCNF, SKP2, KIAA0101, PKMYT1, CENPF, MECOM, CDC25A, CCNB1, CCNE2, CCNE1, CCNB2, JUN, HIPK2, PER2, ID3, GRK5	2.20E-02
GO:0045766~positive regulation of angiogenesis	19	1.44	2.32	11	8	0.69	WNT5A, SASH1, HYAL1, CYP1B1, PGF, C3, SPHK1, CX3CL1, ANXA3, SEMA5A, VEGFC, ETS1, LRG1, XBP1, HIPK2, IL1B, THBS1, CTSH, IL1A	2.28E-02
GO:0000070~mitotic sister chromatid segregation	8	0.61	4.50	0	8	-2.83	MAD2L1, CENPA, NEK2, ZWINT, NUSAP1, NDC80, KNSTRN, SMC4	2.57E-02
GO:0006955~immune response	48	3.63	1.60	31	17	2.02	HLA-DQB1, CSF2, TNFRSF21, IL1R1, HLA-DRB1, C3, IL18, CXCL3, ENPP3, TLR1, TLR2, C1R, CX3CL1, CXCL6, HLA-DMA, PNP, CD74, IGF1R, XBP1, SEMA7A, SEMA3C, IL1B, THBS1, DEFB1, IL1A, FYB, LY75, IL6, TNFSF4, SMAD6, SMAD3, HLA-C, HLA-B, IL24, CTSS, TRIM22, PDCD1LG2, TNFRSF10A, TNFSF10, TNFRSF10B, CD36, CXCL14, PPBP, ETS1, HLA-DPA1, GBP2, TNFAIP1, HLA-DRA	2.58E-02

GO:0043066~negative regulation of apoptotic process	51	3.86	1.58	19	32	-1.82	STIL, IER3, FIGNL1, MMP9, NAA15, AURKA, CITED2, ATAD3A, BAG1, CHST11, TGFA, ANGPT1, CAT, RARB, TWIST2, CYR61, KIF14, CDK1, PIM1, HMGA2, FLNA, PLAUR, AMIGO2, MAD2L1, CCND2, SERPINB2, SLC40A1, CTSH, CAMK1D, WNT5A, ASNS, CD74, IGF1R, XBP1, PRKAA2, THBS1, IL6, SMAD6, SPHK1, SMAD3, BIRC5, BIRC3, GAS6, PLAC8, PPIF, PLK3, NUP62, UCP2, ID1, GRK5, WNT7A	2.61E-02
GO:0007565~female pregnancy	16	1.21	2.53	12	4	2.00	MUC1, STS, PGF, TFCP2L1, BYSL, TGFB3, IDO1, SCGB1A1, FOS, PAPPA, UCP2, ETS1, HSD11B2, HPGD, FOSL1, IGFBP5	2.65E-02
GO:0050873~brown fat cell differentiation	9	0.68	3.95	7	2	1.67	CEBPA, PEX11A, RGS2, PTGS2, LRG1, PPARGC1A, PLAC8, ARL4A, MB	2.66E-02
GO:0051781~positive regulation of cell division	11	0.83	3.29	5	6	-0.30	VEGFC, FGF5, PPBP, PGF, TGFB3, TGFA, IL1B, IGF2, CAT, MDK, IL1A	2.70E-02
GO:0007173~epidermal growth factor receptor signaling pathway	12	0.91	3.01	6	6	0.00	RPS6KA5, NRAS, REPS2, HRAS, PLCE1, FAM83A, TGFA, HBEGF, PIGR, AREG, EGF, PXN	3.16E-02
GO:0030148~sphingolipid biosynthetic process	11	0.83	3.22	6	5	0.30	ACER3, SPTLC1, FA2H, HACD4, SPHK1, ALDH3B2, PLPP1, ALDH3A2, ALDH3B1, PLPP2, DEGS1	3.18E-02
GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	16	1.21	2.44	8	8	0.00	HLA-DQB1, KIF23, KIF2C, KIF4A, KIF11, HLA-DRB1, DYNLL2, KIF18A, CTSD, HLA-DPA1, CENPE, CTSS, RACGAP1, HLA-DMA, CD74, HLA-DRA	3.71E-02
GO:0051897~positive regulation of protein kinase B signaling	15	1.13	2.51	7	8	-0.26	IL6, IL18, AXL, IGF2, GAS6, SEMA5A, AKR1C2, XBP1, HBEGF, ANGPT1, THBS1, ADAM8, NRG1, INSR, IGFBP5	4.17E-02
GO:0060452~positive regulation of cardiac muscle contraction	5	0.38	7.81	2	3	-0.45	HSP90AA1, RGS2, CTGF, ACE2, KCNQ1	4.39E-02
KEGG Pathway ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
hsa04110:Cell cycle	27	2.04	2.67	4	23	-3.66	MAD1L1, DBF4, TGFB3, PKMYT1, TTK, CHEK1, CCNE2, CCNE1, CDC45, CDKN2A, MCM7, BUB1, ORC6, CCNA1, CCNA2, CDC6, CDK1, SKP2, SMAD3, CDC20, CDC25A, CCNB1, MAD2L1, CCNB2, YWHAH, CCND2, BUB1B	6.81E-05
hsa00980:Metabolism of xenobiotics by cytochrome P450	18	1.36	2.99	14	4	2.36	GSTA1, GSTA4, CYP1B1, CYP1A1, CYP2B6, CYP2S1, ADH1C, ALDH3B2, EPHX1, ADH1A, ADH7, ALDH3B1, ALDH3A1, UGT1A10, AKR1C2, GSTM3, HSD11B1, AKR1C1	8.82E-04
hsa05200:Pathways in cancer	54	4.08	1.69	26	28	-0.27	ADCY3, FGF5, HRAS, PTGS2, PGF, MMP9, TGFB3, CCNE2, CCNE1, FOS, WNT4, CDKN2A, TGFA, RALA, RARB, WNT10A, HSP90AA1, SKP2, MECOM, DAPK1, RAD51, VEGFC, LPAR6, NCOA4, JUN, GNB4, LAMC2, WNT5A, CKS1B, ERBB2, EGLN3, KITLG, GNG11, IGF1R, PIK3R3, EGF, CEBPA, IL6, COL4A2, COL4A1, EPAS1, SMAD3, BIRC5, MAPK10, BIRC3, FZD4, COL4A5, NRAS, WNT7B, RASSF1, BAX, CKS2, JAK1, WNT7A	1.79E-03
hsa05152:Tuberculosis	29	2.19	2.01	19	10	1.67	HLA-DQB1, HLA-DRB1, C3, IL18, TLR1, TGFB3, TLR2, HLA-DMA, CD74, CYP27B1, IL1B, CALML5, PLA2R1, IFNGR1, IL1A, IL6, MRC2, SPHK1, CTSS, MAPK10, CORO1A, PLK3, BAX, CTSD, JAK1, HLA-DPA1, CLEC7A, CD14, HLA-DRA	5.90E-03
hsa05140:Leishmaniasis	16	1.21	2.77	11	5	1.50	HLA-DQB1, PTGS2, HLA-DRB1, NCF2, C3, TLR2, TGFB3, HLA-DMA, FOS, JUN, IL1B, JAK1, HLA-DPA1, IFNGR1, IL1A, HLA-DRA	6.20E-03
hsa05321:Inflammatory bowel disease (IBD)	15	1.13	2.88	10	5	1.29	HLA-DQB1, IL6, HLA-DRB1, IL18, TGFB3, TLR2, SMAD3, TLR5, HLA-DMA, JUN, IL1B, HLA-DPA1, IFNGR1, IL1A, HLA-DRA	6.55E-03
hsa05323:Rheumatoid arthritis	18	1.36	2.51	12	6	1.41	HLA-DQB1, CSF2, IL6, HLA-DRB1, IL18, TLR2, TGFB3, CXCL6, ATP6V1B1, HLA-DMA, ATP6V1C2, FOS, JUN, IL1B, ANGPT1, HLA-DPA1, IL1A, HLA-DRA	8.04E-03
hsa00982:Drug metabolism - cytochrome P450	15	1.13	2.71	14	1	3.36	GSTA1, GSTA4, CYP2B6, MAOA, MAOB, ADH1C, ALDH3B2, ADH7, ADH1A, ALDH3B1, ALDH3A1, UGT1A10, GSTM3, FMO2, FMO3	1.24E-02

hsa05332:Graft-versus-host disease	**10**	**0.76**	**3.72**	**7**	**3**	**1.26**	**HLA-DQB1, IL6, HLA-DRB1, IL1B, HLA-C, HLA-DPA1, HLA-B, HLA-DMA, IL1A, HLA-DRA**	**1.25E-02**
hsa04145:Phagosome	**25**	**1.89**	**2.01**	**18**	**7**	**2.20**	**HLA-DQB1, HLA-DRB1, NCF2, C3, MRC2, TLR2, HLA-C, C1R, HLA-B, CTSS, ATP6V1B1, HLA-DMA, ATP6V1C2, CORO1A, CD36, TUBA4A, HLA-DPA1, CLEC7A, TUBA1A, THBS1, PLA2R1, TUBA1B, TUBB3, CD14, HLA-DRA**	**1.66E-02**
hsa05219:Bladder cancer	**11**	**0.83**	**3.29**	**6**	**5**	**0.30**	**RPS6KA5, NRAS, HRAS, CDKN2A, RASSF1, MMP9, ERBB2, HBEGF, THBS1, EGF, DAPK1**	**1.70E-02**
hsa05166:HTLV-I infection	**36**	**2.72**	**1.73**	**20**	**16**	**0.67**	**HLA-DQB1, WNT5A, ADCY3, CSF2, HRAS, IL1R1, HLA-DRB1, TGFB3, CHEK1, HLA-DMA, FOS, WNT4, CDKN2A, POLE2, XBP1, PIK3R3, FOSL1, WNT10A, IL6, SMAD3, HLA-C, CDC20, HLA-B, FZD4, NRAS, WNT7B, MAD2L1, ETS1, CCND2, JUN, BAX, JAK1, BUB1B, HLA-DPA1, WNT7A, HLA-DRA**	**1.93E-02**
hsa04940:Type I diabetes mellitus	**11**	**0.83**	**3.21**	**9**	**2**	**2.11**	**HLA-DQB1, CPE, HLA-DRB1, PTPRN2, IL1B, HLA-C, HLA-DPA1, HLA-B, HLA-DMA, IL1A, HLA-DRA**	**2.07E-02**
hsa03030:DNA replication	**10**	**0.76**	**3.41**	**0**	**10**	**-3.16**	**RFC5, PRIM1, RFC3, RFC4, MCM7, POLE2, RFC2, PRIM2, RNASEH2A, FEN1**	**2.44E-02**
hsa00561:Glycerolipid metabolism	**13**	**0.98**	**2.75**	**9**	**4**	**1.39**	**PLPP1, LPIN1, ALDH3A2, PLPP2, CEL, AGPAT5, AKR1A1, ALDH1B1, AKR1B10, LIPG, MBOAT1, GK, PNLIPRP3**	**2.69E-02**
hsa04068:FoxO signaling pathway	**22**	**1.66**	**2.02**	**13**	**9**	**0.85**	**IL6, HRAS, SGK1, SKP2, TGFB3, SMAD3, MAPK10, BCL2L11, CCNB1, IGF1R, NRAS, TNFSF10, CCNB2, PLK3, CCND2, BCL6, FBXO32, CAT, PRKAA2, PIK3R3, EGF, INSR**	**3.28E-02**

***Functional enrichment analysis of differentially expressed mRNAs (Log2Ratio > 1, Log2Ratio < 1, and q < 0.05) was done in Database for Annotation, Visualization and Integrated Discovery (DAVID, version 6.8, recently updated in Oct. 2016, https://david.ncifcrf.gov/home.jsp) and using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or q < 0.05). Enriched Gene Ontology and KEGG pathway terms are ordered in this table by FDR values. Numbers of upregulated (UP) and downregulated (DW) genes are showed in red and green, respectively. The z-score represents the overall up/down regulated genes from that term [Walter et al., 2015]. Z-score cells of this table are coloured depending on Z-score values: in red for Z >0, in blue for Z < 0 or in white for Z = 0.**

TABLE S20. Enriched Gene Ontology Biological Processes (GOTERM_BP_DIRECT) and KEGG pathways in differentiated CRSwNP air-liquid interface cultures at day 28 compared to day 0.*

GO_BP_DIRECT Term ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
GO:0051301~cell division	105	4.56	2.52	8	96	-8.59	ITGB3BP, KIFC1, KNTC1, AURKA, CDCA8, CDCA7, PPP1R1C, OIP5, CCSAP, MIS18A, CDCA2, CCNA1, CCNA2, CDCA5, CDCA4, CDCA3, RAN, TACC3, TACC1, NCAPD3, NCAPD2, MAD2L1, SGO2, SPAG5, ZWINT, CDCA7L, ANAPC16, GNAI2, NEK2, TIPIN, RCC1, LLGL2, SPC24, SPC25, VRK1, TUBB, SAC3D1, NCAPG2, FBXO5, SKA3, SKA1, HELLS, ERCC6L, NUF2, NDC80, SPDL1, CDC20, SEPT11, FAM64A, MAP4, CDK19, MAD1L1, STOX1, BORA, FAM83D, CCNE2, KIF2C, CCNE1, MASTL, TUBA1B, CCNO, TUBA1C, KIF14, CDC7, CDK1, CDC6, KIF11, CCNF, TPX2, HMGA2, PRKCE, CDK4, UBE2C, CDK2, CHMP1B, CCND2, SDCCAG3, BUB1B, MAPRE2, UBE2S, CKS1B, HAUS6, HAUS2, HAUS1, NCAPH, NCAPG, BUB1, ZWILCH, NSUN2, PDS5A, PSRC1, CENPF, CENPE, BIRC5, KNSTRN, SMC2, CDC25A, SMC4, CDC25B, CCNB1, CCNB2, KNL1, KIF20B, CENPV, CKS2	2.07E-18
GO:0000082~G1/S transition of mitotic cell cycle	41	1.78	3.37	4	37	-5.15	BCAT1, DBF4, PKMYT1, POLA2, RCC1, MCM10, RHOU, PPAT, CDT1, PRIM1, CCNE2, CCNE1, TYMS, CDC45, EIF4EBP1, MCM7, CDKN2A, POLE2, PRIM2, FBXO5, RANBP1, ORC6, CCNA1, CDCA5, CDC7, CDK1, CDC6, SKP2, MCM2, MCM3, CDK4, CDKN3, MCM4, CDK2, CDC25A, MCM6, INHBA, PLK3, DHFR, RRM2, ID4	3.10E-11
GO:0006260~DNA replication	52	2.26	2.81	4	48	-6.10	CLSPN, DBF4, MCM10, CDT1, CDC45, MCM7, ORC6, RTEL1-TNFRSF6B, CDC7, CDK1, CDC6, CCDC88A, POLH, DTL, MCM2, RNASEH2A, MCM3, MCM4, CDK2, MCM6, RFC5, RFC3, RFC4, RFC2, RRM2, RRM1, TNFAIP1, DSCC1, BLM, HUS1, TIPIN, KIAA0101, CHEK1, POLA2, DTD1, POLE2, EGF, FEN1, EXO1, GINS2, GINS3, GINS4, BRCA1, CDC25A, POLD1, CHTF18, CHAF1A, NFIA, DUT, REPIN1, NFIB, BARD1	8.31E-11
GO:0007067~mitotic nuclear division	68	2.95	2.30	3	65	-7.52	ITGB3BP, STOX1, BORA, KNTC1, PKMYT1, AURKA, AURKB, FAM83D, KIF2C, OIP5, MIS18A, CCSAP, CDCA2, MASTL, CCNA1, CDCA5, CCNA2, TUBB3, ASPM, CDCA3, CDK1, CDC6, KIF11, RAN, CCNF, TPX2, PBK, HMGA2, CDK2, BUB1B, MAPRE2, ANAPC16, HAUS6, NEK2, HAUS2, HAUS1, TIPIN, ANLN, CEP55, RCC1, SPC24, SPC25, VRK1, SAC3D1, NCAPG2, BUB1, SKA3, FBXO5, SKA1, ZWILCH, NSUN2, HELLS, ERCC6L, CENPN, NUF2, CENPF, NDC80, CDC20, BIRC5, CDC25A, CDC25B, FAM64A, CCNB2, NUP62, NOLC1, KNL1, KIF20B, CENPV	1.05E-09
GO:0007062~sister chromatid cohesion	38	1.65	3.09	0	38	-6.16	ITGB3BP, MAD1L1, RAD51C, KNTC1, RANGAP1, AURKB, SPC24, SPC25, KIF2C, CDCA8, CENPA, BUB1, SKA1, ZWILCH, CDCA5, ERCC6L, CENPN, CENPM, CENPL, PDS5A, NUF2, KIF18A, CENPF, NUP85, NDC80, SPDL1, CENPE, BIRC5, CDC20, CENPK, CENPH, MAD2L1, SGO2, KNL1, ZWINT, BUB1B, CENPU, NUP107	4.24E-09

GO:0008283~cell proliferation	84	3.65	1.93	23	61	-4.15	STIL, FGF5, HRAS, TSPAN1, ZAK, ELF5, DTYMK, UCHL1, AURKB, MCM10, CITED2, TGFB2, EDNRA, FAM83D, BAK1, KIF2C, FAM83B, BLZF1, MCM7, CREG1, TGFBI, INSIG1, TGFA, FRAT2, NRG1, BHLHE41, MYC, IL1A, OCA2, EGFR, CDK1, CYP1A1, PDPN, BYSL, PIM1, TPX2, SKP2, TACC3, TACC1, TACC2, OGFOD1, GLUL, PA2G4, UHRF1, SERPINF1, KRT16, SIX1, BUB1B, FOXC1, MAPRE2, EMP1, MELK, BCAT1, MIA, CKS1B, GNAI2, ERBB4, ERBB2, HDGF, KITLG, EHF, CD74, TYMS, CSE1L, BUB1, AXIN2, ERCC1, POLR3G, PDK1, CRIP1, MKI67, DLGAP5, FSCN1, CENPF, TNFSF9, CDC25A, GAS6, CSGALNACT1, EPS8, CKS2, LIPG, TCF19, AREG, PES1	7.37E-08
GO:0042060~wound healing	30	1.30	3.15	9	21	-2.19	DCBLD2, WNT5A, KRT6A, PDGFA, ERBB3, ERBB2, TNC, TGFB3, ELK3, TPM1, TGFB2, MAP3K5, CCL20, FGFR1OP2, TGFA, CNN2, LOX, NRG1, EGFR, IL6, EPPK1, TGFBR1, SMAD3, GRHL3, SPARC, IL24, ALOX15, EREG, SERPINB2, ENG	2.93E-07
GO:0006270~DNA replication initiation	17	0.74	4.46	0	17	-4.12	CDC7, CDC6, GINS4, POLA2, MCM2, MCM10, MCM3, MCM4, MCM6, PRIM1, CCNE2, CCNE1, CDC45, MCM7, POLE2, PRIM2, ORC6	2.76E-06
GO:0008544~epidermis development	27	1.17	2.66	6	21	-2.89	ELF3, S100A7, SPRR2F, SPRR2E, ALDH3A2, KRT5, COL7A1, SPRR2D, SPRR2A, INSR, KLK7, SATB1, STS, KLK5, KRT31, GRHL3, GJB5, PTHLH, LAMA3, SPRR1A, KRT16, IFT172, BNC1, KRT14, LAMC2, LOC100653049, EMP1	6.82E-05
GO:0008285~negative regulation of cell proliferation	79	3.43	1.67	35	44	-1.01	DLC1, RARRES3, HRAS, RARRES1, PTGS2, E2F7, PPP2R5C, TGFB3, TLR2, SKAP2, TGFB2, CTNNB1, BAK1, AZGP1, SPRY1, CDKN2A, SERPINE2, CDKN2B, PTGES, DLG3, IL1B, RARB, FOSL1, IL1A, IFNLR1, PTPRJ, CDC6, PTPRK, GTPBP4, IL24, HMGA1, PTHLH, VEGFC, INHBA, MSX1, EREG, ALOX15B, NME1, ITGB1BP1, SCIN, RGCC, TFAP2A, ADAMTS1, EMP3, SMARCA2, HIST1H2AC, CYP1B1, ERBB4, PML, SOX7, ZBTB16, PLPP1, P3H2, LIF, CYP27B1, NPM1, BCL6, GPNMB, AXIN2, FGFBP1, PINX1, BMP4, CEBPA, DFNA5, TP53I11, IL6, NF2, SMAD6, FBXO2, CDKN3, C18ORF54, RERG, CDH13, NUP62, ETS1, IRF6, RPS6KA2, PDCD5, IGFBP3	8.88E-05
GO:0030148~sphingolipid biosynthetic process	19	0.83	3.32	11	8	0.69	ACER3, FA2H, SGPP2, SPHK1, HACD4, SPTSSB, SPTSSA, ALDH3B2, HACD1, PLPP1, PLPP3, ALDH3A2, ALDH3B1, PLPP2, ELOVL4, ELOVL7, ELOVL6, DEGS2, DEGS1	8.92E-05
GO:0007049~cell cycle	50	2.17	1.93	13	36	-3.25	DBF4B, DTYMK, TP63, AURKA, AURKB, RCBTB1, PPP1R1C, KLK10, CCNO, RBL2, EGFL6, PIM1, PIM3, MCM2, PRKCE, ESCO2, AHR, TACC1, MAPK1, UHRF1, CCND2, SDCCAG3, TMPRSS11A, PDCD6IP, SIAH2, PDCD2L, ANAPC16, CKS1B, GNAI2, FOXM1, TIPIN, CYLD, HJURP, TXNIP, ERF, CCPG1, TRNP1, GMNN, SUV39H1, CDC20, CDKN3, BRCA1, SEPT11, RASSF4, NOLC1, RGS2, MAPK13, CHTF18, CHAF1A, KCTD11	1.26E-04

GO:0008284~positive regulation of cell proliferation	89	3.86	1.60	26	63	-3.92	FGF5, STOX1, HRAS, DBF4B, PRC1, PDGFA, PGF, EDN1, TTK, VIPR1, TGFB2, AKR1C2, FXN, CLCF1, TIAM1, TGFA, SHC1, RARB, NRG1, MYC, FOSL1, INSR, KIF14, EGFR, CDC7, IL24, CDK4, CDK2, EIF4G1, PTHLH, VEGFC, MAPK1, NOP2, EREG, CCND2, ITGB1BP1, HIPK2, HAS2, LAMC2, CDCA7L, SERPINB3, EIF5A2, CTSH, FGFR2, CSF2, KRT6A, TBC1D8, GNAI2, ERBB4, MVD, TNC, FOXM1, CRLF1, TIPIN, CALR, ALDH3A1, LIF, IGF1R, RAC2, XBP1, NPM1, EGF, THBS1, RUNX2, FGFBP1, KLF5, ODC1, ACER3, SHMT2, IL6, TNFSF4, CCPG1, TGFBR1, GAREM1, ROGDI, CDC20, BIRC5, PTGFR, NTN1, PLAC8, CDC25B, ETS1, BNC1, KIF20B, HBEGF, ID4, PBX1, AREG, GRK5	1.31E-04
GO:0006271~DNA strand elongation involved in DNA replication	10	0.43	5.59	0	10	-3.16	GINS1, PRIM1, GINS2, RFC3, RFC4, POLD1, GINS3, GINS4, PRIM2, POLA2	2.34E-04
GO:0045740~positive regulation of DNA replication	17	0.74	3.39	3	14	-2.67	EGFR, CDK1, CSF2, IL6, HRAS, PDGFA, TGFB3, KITLG, CALR, IGF1R, EREG, NPM1, CACYBP, SHC1, AREG, INSR, TNFAIP1	2.38E-04
GO:0007051~spindle organization	10	0.43	5.24	0	10	-3.16	KIF11, SPAG5, TTK, NTMT1, AURKA, RANBP1, AURKB, KNSTRN, ASPM, AUNIP	4.78E-04
GO:0042493~response to drug	62	2.69	1.71	23	39	-2.03	ALAD, PTGS2, PGF, SNCA, SRP19, PNP, CBX7, SCGB1A1, TGFB2, CTNNB1, BAK1, MCM7, APOD, TGFA, SEMA3C, CAT, LOX, CCNO, MYC, FOSL1, ICAM1, CDK1, CYP1A1, GAL, CDK4, PPARGC1A, POR, RAD51, INHBA, VEGFC, BLMH, HSD11B2, HMGB2, SORD, ASS1, HMGCS1, CTPS1, CALR, MDK, PFAS, ALDH3A1, TYMS, ACSL1, OXCT1, ABCD3, THBS1, TXNIP, IL6, VAV3, LGALS1, MAOB, GGH, CENPF, ITGA3, ATP1A1, DPYSL2, HDAC5, CCNB1, LRP8, BCAR3, DUSP6, ABCC6	5.27E-04
GO:0007093~mitotic cell cycle checkpoint	14	0.61	3.67	1	13	-3.21	MAD1L1, HRAS, HUS1, KNTC1, TTK, CHEK1, NABP1, PLK3, MAD2L1, CDKN2B, ZWINT, BUB1, BUB1B, ZWILCH	6.99E-04
GO:0019882~antigen processing and presentation	19	0.83	2.90	14	5	2.06	HLA-DQB1, MICB, RAB3B, MICA, HLA-DRB1, HLA-A, HLA-C, CTSS, HLA-B, HLA-DMB, HLA-DQA1, CD74, RAB32, AZGP1, RAET1L, HLA-DPA1, CTSH, HLA-DRA, RAB27A	7.74E-04
GO:0007059~chromosome segregation	21	0.91	2.59	0	21	-4.58	CENPN, KIF11, NEK2, NUF2, CENPF, NDC80, NTMT1, CENPE, RCC1, KNSTRN, ESCO2, BRCA1, SPC25, OIP5, SPAG5, HJURP, MIS18A, CDCA2, SKA3, SKA1, TOP2A	1.64E-03
GO:0007052~mitotic spindle organization	13	0.56	3.63	1	12	-3.05	CCNB1, STIL, SPC25, KIF11, CEP126, RAN, GPSM2, TTK, MAP4, NDC80, AURKA, STMN1, RCC1	1.67E-03
GO:0007050~cell cycle arrest	34	1.48	2.02	14	20	-1.03	HRAS, ZAK, SOX2, PML, RRAGD, CALR, TGFB2, PLAGL1, BRINP1, CDKN2A, CDKN2B, HBP1, PRKAA2, DDIAS, THBS1, MYC, TGFBR1, PRKAB1, SMAD3, GAS1, CDKN3, GAS6, JMY, CDKN1C, INHBA, PA2G4, IRF6, RASSF1, KIF20B, ERN2, GAS2L1, APBB2, EIF2AK4, BARD1	1.85E-03

GO:0055114~oxidation-reduction process	102	4.43	1.45	68	34	3.37	ALDH1L1, PTGS2, SNCA, PGD, HIBADH, BBOX1, LOX, CYP1A1, NCF2, FA2H, CYP26A1, POR, OGFOD1, CYP4X1, AKR1B15, NNT, ALOX15B, AKR1B10, HSD11B1, HSD11B2, ME3, CYP1B1, CYP51A1, CYP2B6, CHCHD4, P3H2, GPD1L, ALDH4A1, MSMO1, MAOA, SCD, MAOB, HGD, CRYZ, P4HTM, AAED1, CYP4B1, DHFR, CYP4Z1, DCXR, CRYM, STEAP4, CYP2S1, DUOX2, DNAJC10, DUOX1, HSD11B1L, GPX2, AKR1C2, MTHFD2, CRYL1, CYP39A1, CREG1, SRD5A3, MICAL1, LOXL4, IMPDH1, AKR1C1, KDM7A, DHRS9, ALDH3B2, CYB5A, VAT1, ALDH3B1, ALOX15, DHRS3, SQLE, RRM2, RRM1, CYP2A6, STEAP2, DEGS2, DEGS1, SORD, HSD17B2, ADH7, ALDH3A2, ALDH3A1, FMO4, ALDH1A1, CYP27B1, AKR1A1, FMO3, FASN, GSTO1, ALKBH6, TBXAS1, BCKDHB, FADS3, FADS2, IDO1, CYP4F12, MSRB3, RDH10, CHML, JMJD6, CYP4F3, ALOX5, DPYD, CP, HPGD, CBS	2.17E-03
GO:0030855~epithelial cell differentiation	21	0.91	2.52	15	6	1.96	GSTA1, MUC1, FGFR2, CDK1, COL4A1, ELF3, DHRS9, EHF, TAGLN2, SPINK5, ACADVL, AKR1C2, TAGLN, RHCG, KRT14, SIX1, UPK1B, BDH2, KRT4, ID3, AKR1C1	2.56E-03
GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	25	1.09	2.28	11	14	-0.60	HLA-DQB1, KIF23, KIF4A, KIF11, HLA-DRB1, KIF18A, DCTN5, CENPE, CTSS, RACGAP1, HLA-DMB, HLA-DMA, KIF3C, CD74, HLA-DQA1, AP1S3, KIF2C, AP1S1, AP2B1, AP1S2, DYNLL2, ACTR1B, CTSD, HLA-DPA1, HLA-DRA	2.78E-03
GO:0031581~hemidesmosome assembly	8	0.35	5.59	0	8	-2.83	LAMA3, ITGA6, KRT5, KRT14, ITGB4, LAMC2, DST, PLEC	2.98E-03
GO:0007080~mitotic metaphase plate congression	14	0.61	3.17	2	12	-2.67	KIF14, CCNB1, KIFC1, KIF2C, CDCA8, CHMP1B, PSRC1, KIF18A, SPDL1, CENPE, CEP55, PDCD6IP, CDCA5, PINX1	4.03E-03
GO:0001666~response to hypoxia	38	1.65	1.85	19	19	0.00	ATP1B1, CAV1, ALAD, AHCY, CLDN3, PGF, TLR2, TGFB3, PML, BNIP3, POSTN, TGFB2, ALDH3A1, CITED2, PKM, SLC11A2, EDNRA, HMOX2, CYGB, CAT, THBS1, ANGPTL4, MB, KCNMA1, PLAT, MUC1, CYP1A1, EPAS1, NR4A2, SMAD3, ITPR1, AJUBA, VEGFC, UCP2, ETS1, HSD11B2, ENG, PLAU	4.60E-03
GO:0001525~angiogenesis	46	2.00	1.73	22	24	-0.29	FGFR2, CAV1, CYP1B1, PTGS2, S100A7, PDGFA, PGF, TNFRSF12A, IL18, NAA15, ANPEP, JAG1, ELK3, MEIS1, TGFB2, TSPAN12, ARHGAP22, HEY1, APOD, XBP1, TGFBI, TGFA, HS6ST1, SHC1, ANGPT1, EGF, ADAM8, CEACAM1, ANGPTL4, KLF5, COL4A2, VAV3, EPAS1, ACKR3, MYH9, ANXA2, CXCL17, VEGFC, EREG, ITGA5, ID1, CLIC4, TNFSF12-TNFSF13, WNT7A, TNFAIP2, SEMA4A	4.94E-03
GO:0010628~positive regulation of gene expression	52	2.26	1.66	26	26	0.00	STOX1, HRAS, LDLR, MITF, TLR2, TGFB2, CITED2, ANK3, GSN, TRPV4, IL1B, QKI, MSN, MYC, IL1A, RAB27A, WNT10A, CDK1, PRKAB1, HMGA2, INHBA, RGCC, TFAP2A, CTSH, CSF2, CAV1, ERBB3, ERBB2, TNC, VIM, CALR, PIP, CNN2, FOXD1, PLAG1, IL6, TGFBR1, EPHX2, SMAD3, ITGA3, PTGFR, LGALS9, GAS6, BRCA1, FBLN1, ID2, RPS6KA2, ID1, DNMT1, PDCD5, AGR2, ENG	5.04E-03
GO:0000281~mitotic cytokinesis	12	0.52	3.47	1	11	-2.89	CKAP2, KIF23, KIF4A, CENPA, ANK3, NUSAP1, SPTBN1, ANLN, STMN1, CEP55, RACGAP1, KIF20A	5.72E-03

GO:0006915~apoptotic process	96	4.17	1.42	36	60	-2.45	ITGB3BP, DLC1, IER3, FAM3B, SNCA, IL19, TLR2, TP63, BNIP3, CDKN2A, CDCA7, BAG1, TIAM1, CDIP1, C8ORF4, IL1B, SEMA3A, MX1, IL1A, CDK1, EVA1A, BCL2L15, SGK1, MAGI3, BCL2L14, DFFA, PIM1, TPX2, PIM3, MCM2, IL24, MECOM, DAPK2, PRKCE, BCL2L12, TOX3, NLRP1, AHR, BCL2L11, NOC2L, DAPK1, TNS4, TNFRSF10A, EPB41L3, RNF130, MAPK1, KIF1B, TNFRSF10B, ALOX15B, CLIC4, SIX1, AVEN, BUB1B, EFNA5, PSME3, SIAH2, PDCD6IP, TNFSF12-TNFSF13, CTSH, UNC13B, TNFAIP1, MELK, FGFR2, TNFRSF21, PML, ZBTB16, FEM1B, PLAGL1, PEA15, CSE1L, BUB1, PCSK9, DDIAS, PHLDA2, TIGAR, PHLDA1, CKAP2, LGALS1, TGFBR1, BIRC5, SAP30BP, BIRC3, TNFSF9, S100A14, NTN1, GAS6, BRCA1, TNFSF10, PLK3, BAX, CYFIP2, GRK5, PDCD5, IGFBP3, DRAM1, CD14	6.57E-03
GO:0070542~response to fatty acid	9	0.39	4.44	8	1	2.33	ALAD, CD36, TBXAS1, ASS1, PTGS2, UCP2, TLR2, CAT, HMGCL	6.91E-03
GO:0006268~DNA unwinding involved in DNA replication	7	0.30	5.87	0	7	-2.65	MCM7, MCM2, HMGA1, MCM4, TOP2A, RAD51, MCM6	7.47E-03
GO:0034644~cellular response to UV	15	0.65	2.86	1	14	-3.36	PTPRK, PTGS2, TP63, PBK, AURKB, CDC25A, NOC2L, BAK1, NEDD4, BAX, POLD1, EIF2S1, MYC, EIF2AK4, PIK3R1	7.58E-03
GO:1900264~positive regulation of DNA-directed DNA polymerase activity	6	0.26	7.19	0	6	-2.45	RFC5, RFC3, RFC4, RFC2, CHTF18, DSCC1	7.83E-03
GO:0008584~male gonad development	24	1.04	2.14	13	11	0.41	WNT5A, LRRC6, HMGB2, NUDT1, TGFBR1, HMGCS1, FSTL3, KITLG, SIX4, TLR5, HMGA2, BCL2L11, CITED2, TGFB2, INHBA, WNT4, TNFSF10, NCOA4, RRM1, SOX15, PATZ1, INSR, ASPM, ERCC1	1.03E-02
GO:0043066~negative regulation of apoptotic process	79	3.43	1.46	29	50	-2.36	STIL, IER3, FIGNL1, MMP9, SNCA, NAA15, TP63, BNIP3, AURKA, CITED2, ATAD3A, CD44, FXN, BAG1, CHST11, TGFA, ANGPT1, CAT, RARB, MYC, TWIST2, KIF14, EGFR, CDK1, BCL2A1, PIM1, PIM3, SIX4, HMGA2, FLNA, PLAUR, MAP4K4, AMIGO2, PA2G4, MAD2L1, MSX1, CCND2, SERPINB2, TFAP2A, AVEN, SIAH2, CTSH, SLC40A1, CAMK1D, WNT5A, GCLC, ERBB4, CD74, IGF1R, XBP1, NPM1, TGM2, PRKAA2, THBS1, PIK3R1, ANGPTL4, BMP4, IL6, SMAD6, SPHK1, SMAD3, AHI1, MALT1, BIRC5, BIRC3, PTGFR, GAS6, PLAC8, PPIF, PLK3, NUP62, DUSP1, ID1, UCP2, CD59, GRK5, APBB2, WNT7A, BARD1	1.08E-02
GO:0007173~epidermal growth factor receptor signaling pathway	17	0.74	2.55	7	10	-0.73	EGFR, REPS2, HRAS, GAREM1, PIGR, IQGAP1, RPS6KA5, NRAS, FAM83B, EPS8, EREG, TGFA, HBEGF, SHC1, AREG, EGF, PIK3R1	1.16E-02
GO:0043407~negative regulation of MAP kinase activity	13	0.56	3.03	6	7	-0.28	BMP4, PTPRJ, STK38, UCHL1, SPRY4, IRAK3, SPRY1, RGS2, NUP62, DUSP1, APOE, IL1B, DUSP7	1.21E-02
GO:0000086~G2/M transition of mitotic cell cycle	31	1.35	1.90	4	27	-4.13	HAUS6, NEK2, HAUS2, PPP1R12B, FOXM1, BORA, HAUS1, CEP78, PKMYT1, CHEK1, AURKA, AKAP9, HMMR, PRKAR2B, TUBB, CDKN2B, MASTL, PHLDA1, CDK1, SKP2, TPX2, BIRC5, CDK2, CDC25A, CDC25B, CCNB1, AJUBA, CCNB2, PLK3, TUBA4A, MELK	1.25E-02
GO:0042476~odontogenesis	11	0.48	3.42	8	3	1.51	FGFR2, MYO5A, BMP4, WNT10A, INHBA, AQP5, TGFB3, ID3, AXIN2, LAMB1, TGFB2	1.34E-02
GO:0035987~endodermal cell differentiation	11	0.48	3.42	1	10	-2.71	INHBA, COL4A2, LAMA3, COL7A1, ITGA5, MMP9, COL12A1, ITGB5, COL6A1, HMGA2, LAMB1	1.34E-02
GO:0003341~cilium movement	11	0.48	3.42	11	0	3.32	CFAP53, LRRC6, DNAI1, RSPH4A, DNAAF1, CFAP206, ARMC4, DNAI2, DNAH7, RSPH9, DNAH5	1.34E-02
GO:0000722~telomere maintenance via recombination	12	0.52	3.15	0	12	-3.46	RFC5, PRIM1, RAD51C, RFC3, RFC4, POLE2, RFC2, POLD1, PRIM2, POLA2, FEN1, RAD51	1.51E-02

GO:0000083~regulation of transcription involved in G1/S transition of mitotic cell cycle	10	0.43	3.65	1	9	-2.53	CCNE1, CDK1, CDC6, TYMS, CDC45, DHFR, RRM2, FBXO5, CCNA1, CDT1	1.55E-02
GO:0051781~positive regulation of cell division	15	0.65	2.68	6	9	-0.77	FGFR2, FGF5, PGF, PDGFA, GAREM1, TGFB3, MDK, TGFB2, VEGFC, EREG, ITGB1BP1, TGFA, IL1B, CAT, IL1A	1.59E-02
GO:0031100~organ regeneration	15	0.65	2.68	0	15	-3.87	CDK1, MKI67, PGF, AXL, CAD, CDK4, LPIN1, PPAT, ANXA3, GAS6, PKM, BAK1, CCNA2, LCP1, PRPS1	1.59E-02
GO:0030325~adrenal gland development	9	0.39	3.97	6	3	1.00	CDKN1C, DKK3, WNT4, FSTL3, STRA6, PBX1, HMGA2, MDK, INSR	1.72E-02
GO:0007076~mitotic chromosome condensation	8	0.35	4.47	0	8	-2.83	NCAPH, NCAPG, NUSAP1, CDCA5, SMC2, NCAPD3, SMC4, NCAPD2	1.74E-02
GO:0001822~kidney development	22	0.96	2.15	9	13	-0.85	BMP4, ODC1, ASS1, TGFBR1, FSTL3, CENPF, BCL2L11, PPAT, TGFB2, CDKN1C, WNT4, SERPINF1, JMJD6, BAX, SIX1, NLE1, PCSK9, TFAP2A, ADAMTS1, HAS2, STRA6, CA2	1.80E-02
GO:0034080~CENP-A containing nucleosome assembly	14	0.61	2.73	1	14	-3.47	ITGB3BP, CENPN, CENPM, HIST4H4, CENPL, OIP5, CENPA, HJURP, KNL1, MIS18A, NPM1, CENPU, CENPK, CENPH	2.07E-02
GO:0007155~cell adhesion	78	3.39	1.43	30	48	-2.04	ITGB3BP, CTNNAL1, ATP1B1, CLSTN1, FERMT1, L1CAM, POSTN, EDIL3, CTNNB1, AZGP1, SRPX, CD44, TGFBI, COL12A1, CNTNAP2, CEACAM1, ICAM1, PTPRK, EGFL6, EFNB1, BYSL, PCDHB2, ACKR3, CHST4, CERCAM, PRKCE, JUP, CD36, VCAN, LAMC2, CNTN3, DST, CHL1, OLFM4, CYP1B1, AMTN, TNC, ITGB4, ITGB5, KITLG, CLDN10, CX3CL1, NEO1, PCDHAC2, ALCAM, SEMA5A, LPXN, LY6D, LAMB2, COL7A1, SORBS2, COL6A3, MSLN, COL6A1, LAMB1, THBS1, GPNMB, PODXL, CD99, ITGA3, SLAMF7, COL16A1, COL4A6, GAS6, EPHA4, CDH13, LAMA3, PKP1, ITGA6, ITGA5, TROAP, ABL2, THEMIS2, ENG, NTM, MUC16, FEZ1, CDH11	2.20E-02
GO:0051726~regulation of cell cycle	28	1.22	1.89	7	21	-2.65	CDK19, FIGNL1, FOXM1, PRR11, KIAA0101, PKMYT1, MYBL2, CCNE2, CCNE1, BAK1, PER2, MASTL, MX2, TRNP1, RBL2, DTL, CCNF, SKP2, CENPF, MECOM, CDC25A, CCNB1, CCNB2, HIPK2, GAS2L1, GRK5, ID3, PES1	2.47E-02
GO:0016266~O-glycan processing	17	0.74	2.38	16	1	3.64	MUC1, ST6GAL1, GCNT3, POC1B-GALNT4, GALNT5, MUC20, CHST4, MUC4, ST3GAL1, B3GNT7, GXYLT2, MUC15, GALNT12, GCNT1, MUC5B, B4GALT5, MUC16	2.62E-02
GO:0000070~mitotic sister chromatid segregation	10	0.43	3.36	0	10	-3.16	KIFC1, MAD2L1, CENPA, NEK2, SPAG5, ZWINT, NUSAP1, NDC80, KNSTRN, SMC4	3.09E-02
GO:0030335~positive regulation of cell migration	37	1.61	1.69	12	25	-2.14	HRAS, PDGFA, EDN1, GTSE1, SEMA5A, IGF1R, TIAM1, XBP1, SEMA7A, SEMA3C, RHOD, GPNMB, THBS1, LAMB1, INSR, PIK3R1, EGFR, BMP4, TGFBR1, PODXL, SPHK1, SMAD3, SNAI2, MAPK1, CDH13, CORO1A, ITGA6, ITGA5, CXCL16, CEMIP, HBEGF, HAS2, LAMC2, SERPINB3, CTSH, PLAU, SEMA4A	3.39E-02
GO:0045840~positive regulation of mitotic nuclear division	10	0.43	3.23	3	7	-1.26	EREG, RGCC, EDN1, NUSAP1, TGFA, IL1B, AURKA, EGF, INSR, IL1A	4.21E-02
GO:0006195~purine nucleotide catabolic process	7	0.30	4.52	3	4	-0.38	GDA, NUDT1, NUDT15, NT5C2, CAT, NT5E, PNP	4.37E-02
KEGG Pathway ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
hsa04110:Cell cycle	41	1.78	2.60	8	33	-3.90	MAD1L1, DBF4, TGFB3, PKMYT1, TTK, CHEK1, SFN, TGFB2, CCNE2, CCNE1, CDC45, MCM7, CDKN2A, CDKN2B, BUB1, ORC6, CCNA1, CCNA2, MYC, CDC7, CDK1, CDC6, RBL2, SKP2, SMAD3, CDC20, MCM2, MCM3, CDK4, MCM4, CDK2, CDC25A, MCM6, CDC25B, CDKN1C, CCNB1, YWHAH, CCNB2, MAD2L1, CCND2, BUB1B	1.17E-07

hsa03030:DNA replication	16	0.69	3.49	0	16	-4.00	POLA2, MCM2, RNASEH2A, MCM3, MCM4, MCM6, RFC5, PRIM1, RFC3, RFC4, MCM7, POLE2, RFC2, POLD1, PRIM2, FEN1	1.80E-04
hsa05200:Pathways in cancer	80	3.47	1.60	33	47	-1.57	ADCY3, FGF5, HRAS, PTGS2, PGF, PDGFA, MMP9, MITF, TGFB3, MMP1, TGFB2, CTNNB1, CCNE2, EDNRA, CCNE1, WNT4, CDKN2A, CDKN2B, TGFA, RALA, RARB, MYC, EGFR, WNT10A, PTGER4, SKP2, MECOM, CDK4, DAPK2, CDK2, RAD51, DAPK1, JUP, VEGFC, MAPK1, NCOA4, LPAR6, GNB4, LAMC2, WNT5A, FGFR2, CKS1B, GNAI2, ERBB2, PML, KITLG, GNG11, GNG12, ZBTB16, IGF1R, LAMB2, RAC2, EGF, PIK3R3, LAMB1, AXIN2, PIK3R1, CEBPA, BMP4, COL4A2, IL6, COL4A1, EPAS1, TGFBR1, SMAD3, BIRC5, ITGA3, MAPK10, BIRC3, FZD4, COL4A6, NRAS, WNT7B, LAMA3, ITGA6, BAX, RASSF1, CKS2, JAK1, WNT7A	1.87E-04
hsa05219:Bladder cancer	17	0.74	3.26	7	10	-0.73	EGFR, HRAS, ERBB2, MMP9, CDK4, DAPK2, MMP1, DAPK1, RPS6KA5, NRAS, MAPK1, CDKN2A, RASSF1, HBEGF, THBS1, EGF, MYC	2.52E-04
hsa04068:FoxO signaling pathway	35	1.52	2.05	19	16	0.51	HRAS, TGFB3, BNIP3, TGFB2, IGF1R, CDKN2B, HOMER3, BCL6, CAT, PRKAA2, EGF, PIK3R3, INSR, PIK3R1, EGFR, IL6, GABARAPL1, SGK1, RBL2, TGFBR1, PRKAB1, SKP2, SMAD3, MAPK10, CDK2, BCL2L11, CCNB1, MAPK1, NRAS, TNFSF10, PLK3, CCNB2, CCND2, MAPK13, FBXO32	5.90E-04
hsa05166:HTLV-I infection	56	2.43	1.72	26	30	-0.53	ADCY3, HRAS, PDGFA, TGFB3, HLA-DMB, HLA-DMA, TGFB2, CTNNB1, WNT4, CDKN2A, CDKN2B, RANBP1, FOSL1, MYC, ICAM1, WNT10A, RAN, HLA-A, HLA-C, HLA-B, CDK4, HLA-DQA1, HLA-F, MSX1, MAD2L1, CCND2, BUB1B, HLA-DPA1, HLA-DRA, HLA-DQB1, WNT5A, CSF2, IL1R1, HLA-DRB1, CHEK1, MYBL1, MYBL2, CALR, POLE2, XBP1, PIK3R3, TCF3, PIK3R1, IL6, TGFBR1, FDPS, SMAD3, CDC20, FZD4, NRAS, WNT7B, ETS1, POLD1, BAX, JAK1, WNT7A	6.10E-04
hsa05332:Graft-versus-host disease	14	0.61	3.33	11	3	2.14	HLA-DQB1, IL6, HLA-DRB1, HLA-A, IL1B, HLA-C, HLA-DPA1, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1, IL1A, HLA-DRA, HLA-F	1.37E-03

hsa01100:Metabolic pathways	197	8.55	1.26	111	86	1.78	ALAD, GDA, PTGS2, B3GALT4, PGD, HIBADH, PRIM1, PGP, PRIM2, NT5C2, CYP1A1, CYP26A1, GLCE, GLUL, NNT, ALOX15B, NME1, MGAM, HSD11B1, GATC, CHKA, ACADSB, GCNT3, AHCY, NAGS, CYP2B6, CYP51A1, ENPP3, HMGCS1, ACAT2, PPAT, TK1, IDH2, ALDH4A1, CDA, GCNT1, MGAT4A, ODC1, ST6GAL1, MAOA, SPHK1, MAOB, HGD, TKT, GART, CEL, GGT6, DHFR, GGT7, ATP6V0E2, GK, NDUFC2-KCTD14, ANPEP, ASAH1, CKB, AUH, PKM, MTHFD2, AGPAT5, PTGES, MCCC1, MCEE, NT5E, POLR1E, POLR1B, ST6GALNAC1, ATP6V1C2, ALOX15, SQLE, ADK, RRM2, RRM1, MTAP, AMY1A, DEGS2, DEGS1, BCAT1, SORD, HSD17B2, POC1B-GALNT4, FUT6, POLA2, POLR2D, PFAS, MTMR3, ACSL1, CYP27B1, FASN, FUT3, FUT1, FUT2, GALNT12, PAPSS2, PNLIPRP3, ACSL5, POLR3G, SHMT2, PLA2G16, POLR3H, TBXAS1, BCKDHB, ACLY, HYI, SDHD, MBOAT1, DPYD, PSAT1, PAICS, GNPDA1, DTYMK, ADH1C, ADH1B, ADH1A, PNP, DSE, ST3GAL1, HMGCL, FBP1, CHPT1, AKR1B10, PCCA, PRPS1, ME3, GCLC, MVD, ASS1, SRM, CTPS1, ATP6V1B1, POLE2, CSAD, PCYT1A, ADSSL1, MSMO1, EPHX2, FDPS, AK7, RIMKLB, GLS, POLD1, DNMT1, AHCYL2, DCXR, PC, DUT, IMPA2, NDST1, CYP2S1, HEXA, PIP5K1B, ACOT2, CAD, LSS, PSPH, CRYL1, IMPDH1, SELENOI, ALDH3B2, PIGT, DHRS9, PIGS, LPIN1, ALDH3B1, ACADVL, ATP6V1A, DHRS3, UMPS, ALDH1B1, GAA, CYP2A6, INPP4B, SMS, GALNT5, UPP1, ADH7, PLPP1, PLPP3, ALDH3A2, PLPP2, ALDH3A1, ALDH1A1, TYMS, AKR1A1, INPP5J, UGT2A1, BDH2, GMDS, IDO1, MAN1C1, CSGALNACT1, RDH10, CSGALNACT2, LIPG, CYP4F3, ALOX5, UGT2B7, CBS	1.92E-03
hsa04145:Phagosome	37	1.61	1.90	22	15	1.15	HLA-DQB1, RAB7B, HLA-DRB1, TUBB2A, C3, TLR2, ITGB5, HLA-DMB, CALR, ATP6V1B1, HLA-DMA, TUBB, TUBB6, THBS1, PLA2R1, TUBA1B, TUBB3, SEC61A1, TUBA1C, NCF2, HLA-A, HLA-C, HLA-B, CTSS, HLA-DQA1, HLA-F, ATP6V1A, ATP6V1C2, CORO1A, ATP6V0E2, CD36, ITGA5, TUBA4A, HLA-DPA1, CLEC7A, CD14, HLA-DRA	1.92E-03
hsa00980:Metabolism of xenobiotics by cytochrome P450	22	0.96	2.33	17	5	2.56	GSTA1, GSTA4, CYP1B1, CYP1A1, CYP2B6, CYP2S1, ADH1C, ADH1B, EPHX1, ALDH3B2, ADH1A, ADH7, ALDH3B1, ALDH3A1, AKR1C2, GSTM3, HSD11B1, CYP2A6, UGT2A1, GSTO1, AKR1C1, UGT2B7	3.23E-03
hsa04940:Type I diabetes mellitus	15	0.65	2.80	13	2	2.84	HLA-DQB1, CPE, HLA-DRB1, PTPRN2, HLA-A, IL1B, HLA-C, HLA-DPA1, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1, IL1A, HLA-DRA, HLA-F	5.84E-03
hsa05323:Rheumatoid arthritis	24	1.04	2.14	16	8	1.63	HLA-DQB1, ICAM1, CSF2, IL6, HLA-DRB1, IL18, TLR2, TGFB3, CXCL6, HLA-DMB, ATP6V1B1, HLA-DMA, HLA-DQA1, MMP1, TGFB2, ATP6V1C2, ATP6V1A, ATP6V0E2, CCL20, IL1B, HLA-DPA1, ANGPT1, IL1A, HLA-DRA	6.23E-03
hsa05416:Viral myocarditis	18	0.78	2.48	12	6	1.41	HLA-DQB1, ICAM1, CAV1, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1, HLA-F, EIF4G1, CD55, RAC2, HLA-DPA1, ABL2, HLA-DRA, SGCB	6.56E-03
hsa00982:Drug metabolism - cytochrome P450	20	0.87	2.31	18	2	3.58	GSTA1, GSTA4, CYP2B6, MAOA, MAOB, ADH1C, ADH1B, ALDH3B2, ADH1A, ADH7, ALDH3B1, ALDH3A1, FMO4, GSTM3, FMO2, FMO3, CYP2A6, UGT2A1, GSTO1, UGT2B7	7.79E-03

hsa05222:Small cell lung cancer	23	1.00	2.12	6	17	-2.29	CKS1B, COL4A2, COL4A1, PTGS2, SKP2, ITGA3, BIRC3, CDK4, COL4A6, CDK2, CCNE2, CCNE1, LAMA3, LAMB2, ITGA6, CDKN2B, CKS2, LAMC2, RARB, LAMB1, PIK3R3, MYC, PIK3R1	9.47E-03
hsa00240:Pyrimidine metabolism	26	1.13	1.96	2	24	-4.31	POLR3G, POLR3H, POLR1E, DTYMK, UPP1, CTPS1, CAD, POLA2, POLR1B, POLR2D, PNP, TK1, PRIM1, TYMS, UMPS, POLE2, NME1, POLD1, RRM2, NT5C2, RRM1, PRIM2, CDA, DPYD, NT5E, DUT	1.38E-02
hsa05205:Proteoglycans in cancer	42	1.82	1.65	16	26	-1.54	WNT5A, CAV1, HRAS, ERBB4, ERBB3, MMP9, PPP1R12B, ERBB2, TLR2, RPS6KB2, ITGB5, TIMP3, SDC2, IQGAP1, CTNNB1, TGFB2, IGF1R, WNT4, CD44, ANK3, TIAM1, MSN, PIK3R3, THBS1, MYC, TWIST2, PIK3R1, EGFR, WNT10A, FZD4, FLNB, ITPR1, FLNA, PLAUR, MAPK1, NRAS, WNT7B, ITGA5, MAPK13, HBEGF, WNT7A, PLAU	1.49E-02
hsa00480:Glutathione metabolism	16	0.69	2.46	9	7	0.50	GSTA1, ODC1, GSTA4, GCLC, SRM, PGD, ANPEP, GPX2, GGT6, GSTM3, GGT7, RRM2, RRM1, IDH2, GSTO1, SMS	1.62E-02
hsa05145:Toxoplasmosis	28	1.22	1.86	19	9	1.89	HLA-DQB1, LDLR, HLA-DRB1, GNAI2, TGFB3, TLR2, HLA-DMB, HLA-DMA, TGFB2, LAMB2, IL10RB, LAMB1, PIK3R3, PIK3R1, IFNGR1, MAPK10, BIRC3, HLA-DQA1, PPIF, MAPK1, LAMA3, ITGA6, MAPK13, JAK1, LAMC2, HLA-DPA1, ALOX5, HLA-DRA	1.95E-02
hsa05321:Inflammatory bowel disease (IBD)	18	0.78	2.21	14	4	2.36	MAF, HLA-DQB1, IL6, HLA-DRB1, IL18, TGFB3, TLR2, SMAD3, TLR5, HLA-DMB, HLA-DMA, HLA-DQA1, TGFB2, IL1B, HLA-DPA1, IFNGR1, IL1A, HLA-DRA	2.71E-02
hsa04914:Progesterone-mediated oocyte maturation	22	0.96	1.99	6	16	-2.13	ADCY3, MAD1L1, CDK1, GNAI2, CPEB3, PKMYT1, MAPK10, CDC25A, CDK2, CDC25B, CCNB1, IGF1R, MAPK1, MAD2L1, CCNB2, MAPK13, RPS6KA2, BUB1, PIK3R3, CCNA1, CCNA2, PIK3R1	3.16E-02
hsa04960:Aldosterone-regulated sodium reabsorption	13	0.56	2.62	11	2	2.50	MAPK1, ATP1B1, SGK1, NR3C2, HSD11B2, ATP1A1, NEDD4L, SFN, SCNN1B, PIK3R3, SCNN1A, INSR, PIK3R1	3.19E-02
hsa05212:Pancreatic cancer	18	0.78	2.17	10	8	0.47	EGFR, ERBB2, TGFBR1, TGFB3, SMAD3, MAPK10, CDK4, RAD51, TGFB2, MAPK1, CDKN2A, RAC2, TGFA, RALA, JAK1, PIK3R3, EGF, PIK3R1	3.24E-02
hsa04550:Signaling pathways regulating pluripotency of stem cells	31	1.35	1.74	20	11	1.62	FGFR2, WNT5A, HRAS, SOX2, MEIS1, CTNNB1, LIF, IGF1R, WNT4, AXIN2, PIK3R3, MYC, TCF3, PIK3R1, BMP4, WNT10A, SMAD3, FZD4, INHBB, MAPK1, NRAS, INHBA, WNT7B, ID2, ID1, MAPK13, JAK1, ID4, ID3, BMPR1B, WNT7A	3.26E-02
hsa05140:Leishmaniasis	19	0.83	2.10	13	6	1.61	HLA-DQB1, PTGS2, HLA-DRB1, NCF2, C3, TLR2, TGFB3, HLA-DMB, HLA-DMA, HLA-DQA1, TGFB2, MAPK1, MAPK13, IL1B, JAK1, HLA-DPA1, IFNGR1, IL1A, HLA-DRA	3.55E-02
hsa05202:Transcriptional misregulation in cancer	35	1.52	1.64	19	16	0.51	CSF2, LMO2, PDGFA, MMP9, PML, TSPAN7, ZBTB16, MEIS1, IGF1R, REL, BCL6, RUNX2, MYC, ETV5, TCF3, ETV4, PLAT, CEBPA, MAF, TMPRSS2, IL6, BCL2A1, WHSC1, SIX4, HMGA2, PROM1, JUP, ID2, CCND2, SIX1, PBX1, IGFBP3, HPGD, PLAU, CD14	4.67E-02

***Functional enrichment analysis of differentially expressed mRNAs (Log2Ratio > 1, Log2Ratio < 1, and q < 0.05) was done in Database for Annotation, Visualization and Integrated Discovery (DAVID, version 6.8, recently updated in Oct. 2016, https://david.ncifcrf.gov/home.jsp) and using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or q < 0.05). Enriched Gene Ontology and KEGG pathway terms are ordered in this table by FDR values. Numbers of upregulated (UP) and downregulated (DW) genes are showed in red and green, respectively. The z-score represents the overall up/down regulated genes from that term [Walter et al., 2015]. Z-score cells of this table are coloured depending on Z-score values: in red for Z >0, in blue for Z < 0 or in white for Z = 0.**

TABLE S21. Enriched Gene Ontology Biological Processes (GOTERM_BP_DIRECT) and KEGG pathways in differentiated hNP-BSCs compared to hNM-BSCs at day 0 of air-liquid interface culture.*

GO_BP_DIRECT Term ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
GO:0008544~epidermis development	15	3.80	8.42	10	5	1.29	STS, ELF3, KLK5, CRABP2, SPRR2F, GRHL3, SPRR2E, LAMB3, CST6, SPRR1A, SPRR2D, SPRR2A, SPRR3, LOC100653049, INSR	4.05E-08
GO:0042060~wound healing	14	3.54	8.35	6	8	-0.53	WNT5A, IL6, EPPK1, SMAD3, GRHL3, IL24, MAP3K5, SDC1, CCL20, EREG, SPRR3, TFF3, CNN2, LOX	1.80E-07
GO:0001666~response to hypoxia	18	4.56	4.99	6	12	-1.41	MUC1, PLAT, EGR1, ATP1B1, EPAS1, CYP1A1, CRYAB, SMAD3, POSTN, ADA, DDIT4, ALDH3A1, CA9, HMOX1, CYGB, THBS1, LOXL2, PLAU	2.17E-06
GO:0030855~epithelial cell differentiation	11	2.78	7.50	2	9	-2.11	GSTA1, MUC1, ACADVL, F11R, AKR1C2, CES1, ELF3, TAGLN, UPK1B, DHRS9, AKR1C1	3.17E-05
GO:0030216~keratinocyte differentiation	11	2.78	6.90	8	3	1.51	TXNIP, WNT5A, CRCT1, EREG, SPRR1A, SPRR2D, SPRR2A, SPRR3, SPRR2F, SPRR2E, IVL	6.82E-05
GO:0055114~oxidation-reduction process	31	7.85	2.50	7	24	-3.05	ALDH1L1, PTGS2, CYP2S1, PGD, ALDH3A1, AKR1C2, FMO3, HSD17B3, LOXL4, GSTO2, LOX, LOXL2, AKR1C1, TBXAS1, CYP1A1, NCF2, FADS3, DHRS9, CYP26A1, IDO1, ALDH3B1, MSRB3, CYP4X1, RDH10, DHRS3, AKR1B15, ALOX15B, HSD11B1, DPYD, CP, STEAP2	1.31E-04
GO:0018149~peptide cross-linking	9	2.28	8.59	9	0	3.00	CRCT1, SPRR1A, SPRR2D, SPRR2A, SPRR3, SPRR2F, SPRR2E, THBS1, IVL	1.46E-04
GO:0030325~adrenal gland development	6	1.52	15.06	2	4	-0.82	DKK3, WNT4, FSTL3, STRA6, PBX1, INSR	6.15E-04
GO:0071456~cellular response to hypoxia	10	2.53	4.97	3	7	-1.26	P4HB, PTGS2, EPAS1, HMOX1, RGCC, EDN1, MDM2, STC1, NDRG1, PPARGC1A	3.12E-03
GO:0030574~collagen catabolic process	8	2.03	5.96	4	4	0.00	MMP9, MRC2, COL6A3, COL1A2, MMP7, COL6A1, COL1A1, ADAM15	6.35E-03
GO:0006508~proteolysis	24	6.08	2.29	4	20	-3.27	ADAM28, PLAT, KLK8, CLCA4, CFB, C3, MMP9, KLK5, MMP7, C1R, MMP28, TMPRSS4, ADAMTS6, PAPPA, FAP, TMPRSS11E, CAPN13, UBD, ERAP2, CFI, CTSH, WFDC2, PLAU, ADAM15	6.37E-03
GO:0031424~keratinization	7	1.77	6.96	7	0	2.65	SPRR1A, SPRR2D, SPRR2A, SPRR3, SPRR2F, SPRR2E, IVL	8.09E-03
GO:0030335~positive regulation of cell migration	13	3.29	3.37	6	7	-0.28	EDN1, SMAD3, IGF1R, SEMA3C, SEMA4B, RHOD, SERPINB3, COL1A1, THBS1, INSR, CTSH, PLAU, AKT2	8.72E-03
GO:0071560~cellular response to transforming growth factor beta stimulus	7	1.77	6.81	3	4	-0.38	WNT5A, WNT10A, WNT4, EDN1, POSTN, COL1A1, PPARGC1A	9.05E-03
GO:0042542~response to hydrogen peroxide	7	1.77	6.55	3	4	-0.38	TXNIP, SDC1, CRYAB, HMOX1, EEF2, COL1A1, ADA	1.12E-02
GO:0042493~response to drug	17	4.30	2.67	7	10	-0.73	TXNIP, IL6, PTGS2, CYP1A1, FOSB, GAL, SCGB1A1, PPARGC1A, ADA, ALDH3A1, FOS, CA9, MDM2, SEMA3C, COL1A1, LOX, THBS1	1.20E-02
GO:0007568~aging	12	3.04	3.47	3	9	-1.73	FOS, IL6, CYP1A1, SLC12A2, SERPINF1, CRYAB, MMP7, EEF2, LOXL2, PPARGC1A, ADA, ALDH3A1	1.23E-02
GO:0030336~negative regulation of cell migration	9	2.28	4.52	3	6	-1.00	WNT4, EPPK1, ALOX15B, SRGAP3, RHOB, STC1, CNN2, IL24, ADAM15	1.45E-02
GO:0030198~extracellular matrix organization	13	3.29	3.16	6	7	-0.28	F11R, ELF3, CCDC80, ITGB4, POSTN, LAMB3, FBLN1, COL6A3, COL1A2, COL6A1, LOX, COL1A1, THBS1	1.52E-02
GO:0010951~negative regulation of endopeptidase activity	10	2.53	3.94	1	9	-2.53	SERPINB9, SERPINF1, LXN, C3, COL6A3, SERPINA3, TFPI, SERPINA1, SERPINB3, WFDC2	1.72E-02
GO:0048661~positive regulation of smooth muscle cell proliferation	7	1.77	5.57	5	2	1.13	IL6, EREG, PTGS2, HMOX1, EDN1, THBS1, PPARGC1A	2.65E-02
GO:0007155~cell adhesion	21	5.32	2.18	13	8	1.09	F11R, ATP1B1, AMTN, ITGB4, CLDN10, POSTN, L1CAM, SLAMF7, CDH2, LGALS3BP, LAMB3, FAP, COL6A3, RHOB, COL6A1, COL1A1, HAS3, THBS1, LOXL2, CDH11, FEZ1	2.86E-02
GO:0042476~odontogenesis	5	1.27	8.83	2	3	-0.45	WNT10A, SDC1, TUFT1, COL1A2, AQP3	3.84E-02

GO:0032496~response to lipopolysaccharide	11	2.78	3.20	3	8	-1.51	IRAK3, FOS, THBD, CYP1A1, CXCL5, PTGS2, PTGES, CXCL3, EDN1, IDO1, SCGB1A1	4.08E-02
GO:0001821~histamine secretion	3	0.76	35.78	2	1	0.58	CSF2, EDN1, ADA	4.32E-02
GO:0007565~female pregnancy	8	2.03	4.29	0	8	-2.83	MUC1, FOS, STS, THBD, PAPPA, IDO1, FOSB, SCGB1A1	4.44E-02
GO:0051591~response to cAMP	6	1.52	6.22	1	5	-1.63	FOS, SDC1, THBD, COL1A1, FOSB, ALDH3A1	4.47E-02
GO:0006954~inflammatory response	18	4.56	2.27	6	12	-1.41	F11R, IL6, ELF3, CXCL5, PTGS2, C3, LXN, CXCL3, AFAP1L2, IL24, GAL, FOS, SDC1, CCL20, SERPINA3, BCL6, THBS1, CD14	4.52E-02
KEGG PATHWAY ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
hsa04978:Mineral absorption	9	2.28	7.39	5	4	0.33	TF, ATP1B1, MT1M, SLC30A1, HMOX1, STEAP2, MT1H, SLC40A1, MT1G	2.80E-04
hsa04610:Complement and coagulation cascades	9	2.28	4.93	0	9	-3.00	PLAT, THBD, C3, CFB, TFPI, C1R, SERPINA1, CFI, PLAU	5.35E-03
hsa04668:TNF signaling pathway	11	2.78	3.92	4	7	-0.90	CSF2, FOS, MAP3K5, IL6, PTGS2, CCL20, CXCL3, MMP9, EDN1, BIRC3, AKT2	5.69E-03
hsa00980:Metabolism of xenobiotics by cytochrome P450	9	2.28	4.59	3	6	-1.00	GSTA1, AKR1C2, CYP1A1, CYP2S1, HSD11B1, GSTO2, AKR1C1, ALDH3B1, ALDH3A1	8.60E-03
hsa05202:Transcriptional misregulation in cancer	13	3.29	2.92	4	9	-1.39	PLAT, CSF2, IL6, MMP9, TSPAN7, IGF1R, MDM2, BCL6, PBX1, ETV5, IGFBP3, PLAU, CD14	1.93E-02
hsa05146:Amoebiasis	10	2.53	3.56	5	5	0.00	CSF2, SERPINB9, GNA15, IL6, LAMB3, PLCB4, COL1A2, COL1A1, SERPINB3, CD14	2.30E-02
hsa05200:Pathways in cancer	21	5.32	2.02	8	13	-1.09	WNT5A, WNT10A, FGF5, IL6, EPAS1, PTGS2, MMP9, SMAD3, BIRC3, CCNE1, IGF1R, FOS, WNT4, LAMB3, PLCB4, RASSF1, BAX, SLC2A1, MDM2, RARB, AKT2	4.20E-02
hsa00140:Steroid hormone biosynthesis	7	1.77	4.56	3	4	-0.38	AKR1C2, STS, CYP1A1, HSD11B1, SULT2B1, HSD17B3, AKR1C1	4.97E-02

***Functional enrichment analysis of differentially expressed mRNAs (Log2Ratio > 1, Log2Ratio < 1, and q < 0.05) was done in Database for Annotation, Visualization and Integrated Discovery (DAVID, version 6.8, recently updated in Oct. 2016, https://david.ncifcrf.gov/home.jsp) and using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or q < 0.05). Enriched Gene Ontology and KEGG pathway terms are ordered in this table by FDR values. Numbers of upregulated (UP) and downregulated (DW) genes are showed in red and green, respectively. The z-score represents the overall up/down regulated genes from that term [Walter et al., 2015]. Z-score cells of this table are coloured depending on Z-score values: in red for Z >0, in blue for Z < 0 or in white for Z = 0.**

TABLE S22. Enriched Gene Ontology Biological Processes (GOTERM_BP_DIRECT) and KEGG pathways in differentiated hNP-BSCs compared to hNM-BSCs at day 14 of air-liquid interface culture.*

GO_BP_DIRECT Term ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
GO:0008544~epidermis development	11	2.86	6.75	10	1	2.71	KLK7, LAMA3, ATP2A2, SPRR2D, KRT16, SPRR2A, CRABP2, KLK5, SPRR2F, SPRR2E, EMP1	8.56E-05
GO:0030216~keratinocyte differentiation	10	2.60	6.86	8	2	1.90	CRCT1, EREG, SPRR2D, KRT16, SPRR2A, SPRR2F, JAG1, CERS3, SPRR2E, IVL	2.42E-04
GO:0071456~cellular response to hypoxia	11	2.86	5.98	5	6	-0.30	CCNB1, ICAM1, P4HB, HIF1A, SFRP1, RGCC, EDN1, PTN, NDRG1, RORA, CCNA2	2.56E-04
GO:0018149~peptide cross-linking	8	2.08	8.34	8	0	2.83	CRCT1, SPRR2D, SPRR2A, SPRR2F, SPRR2E, THBS1, IVL, FN1	7.40E-04
GO:0022617~extracellular matrix disassembly	8	2.08	5.49	4	4	0.00	KLK7, CAPNS2, LAMA3, CD44, KIF9, MMP13, FN1, TLL1	1.06E-02
GO:0006928~movement of cell or subcellular component	8	2.08	4.85	6	2	1.41	TUBB, DNALI1, CALD1, VIM, MSN, CERCAM, TPM4, VNN2	2.19E-02
GO:0043616~keratinocyte proliferation	4	1.04	17.38	2	2	0.00	KLK8, EREG, FERMT1, SDR16C5	2.28E-02
GO:0030195~negative regulation of blood coagulation	4	1.04	17.38	4	0	2.00	SERPINE2, APOE, EDN1, SERPINE1	2.28E-02
GO:0006508~proteolysis	21	5.47	2.19	8	13	-1.09	ADAM28, PLAT, KLK7, KLK8, CAPNS2, CAPN5, CFB, CNDP2, KLK5, MMP13, SFRP1, PAPPA, CAPN13, FAP, PIP, ASRGL1, UBD, KLK10, CFD, TLL1, KLK13	2.69E-02
GO:0008284~positive regulation of cell proliferation	20	5.21	2.24	13	7	1.34	CXCL5, PRC1, TNC, EDN2, EDN1, KIT, SOX9, ALDH3A1, PLAC8, LIF, RAC2, SFRP1, EREG, CCND2, PTN, ID4, AREG, THBS1, FOSL1, FN1	2.80E-02
GO:0031424~keratinization	6	1.56	6.52	5	1	1.63	SPRR2D, KRT16, SPRR2A, SPRR2F, SPRR2E, IVL	3.65E-02
GO:0042493~response to drug	15	3.91	2.57	11	4	1.81	ICAM1, LGALS1, DPYSL2, STAT1, SCGB1A1, ALDH3A1, CCNB1, TYMS, TJP1, CCND1, SFRP1, PTN, THBS1, CCNO, FOSL1	3.77E-02
GO:0071347~cellular response to interleukin-1	7	1.82	5.14	4	3	0.38	ICAM1, HIF1A, SFRP1, EDN1, RORA, CCL5, SOX9	3.96E-02
GO:0007015~actin filament organization	7	1.82	5.07	7	0	2.65	RAC2, FSCN1, ACTN1, TPM2, AKAP2, RHOF, TPM4	4.25E-02
GO:0044458~motile cilium assembly	4	1.04	13.91	0	4	-2.00	DNAAF1, BBOF1, ZMYND10, RSPH9	4.46E-02
KEGG PATHWAY ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
hsa00982:Drug metabolism - cytochrome P450	12	3.13	8.90	1	11	-2.89	GSTA1, CYP2B6, FMO2, ALDH1A3, FMO3, ADH1C, UGT2A1, CYP2A6, ADH1A, ADH7, UGT2B7, ALDH3A1	8.27E-07
hsa00980:Metabolism of xenobiotics by cytochrome P450	11	2.86	7.50	1	10	-2.71	GSTA1, CYP2F1, CYP2B6, ALDH1A3, ADH1C, UGT2A1, CYP2A6, ADH1A, ADH7, UGT2B7, ALDH3A1	1.89E-05
hsa05204:Chemical carcinogenesis	9	2.34	5.67	1	8	-2.33	GSTA1, ALDH1A3, ADH1C, UGT2A1, CYP2A6, ADH1A, ADH7, UGT2B7, ALDH3A1	1.98E-03
hsa00830:Retinol metabolism	8	2.08	6.21	0	8	-2.83	CYP2B6, ADH1C, UGT2A1, CYP2A6, SDR16C5, ADH1A, ADH7, UGT2B7	3.23E-03
hsa04512:ECM-receptor interaction	9	2.34	5.22	8	1	2.33	COL4A2, LAMA3, COL4A1, CD36, CD44, TNC, THBS1, FN1, HMMR	3.55E-03
hsa04145:Phagosome	10	2.60	3.30	4	6	-0.63	LAMP1, TUBB, CD36, HLA-DRB1, HLA-C, CLEC7A, THBS1, ATP6V1B1, TUBB3, HLA-DRA	3.73E-02

***Functional enrichment analysis of differentially expressed mRNAs (Log2Ratio > 1, Log2Ratio < 1, and q < 0.05) was done in Database for Annotation, Visualization and Integrated Discovery (DAVID, version 6.8, recently updated in Oct. 2016, https://david.ncifcrf.gov/home.jsp) and using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or q < 0.05). Enriched Gene Ontology and KEGG pathway terms are ordered in this table by FDR values. Numbers of upregulated (UP) and downregulated (DW) genes are showed in red and green, respectively. The z-score represents the overall up/down regulated genes from that term [Walter et al., 2015]. Z-score cells of this table are coloured depending on Z-score values: in red for Z >0, in blue for Z < 0 or in white for Z = 0.**

TABLE S23. Enriched Gene Ontology Biological Processes (GOTERM_BP_DIRECT) and KEGG pathways in differentiated hNP-BSCs compared to hNM-BSCs at day 28 of air-liquid interface culture.*

GO_BP_DIRECT Term ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
GO:0003341~cilium movement	15	3.36	27.68	0	15	-3.87	CFAP100, LRRC6, DYX1C1, ARMC4, CFAP221, DNAI2, DNAH7, DNAH5, RSPH9, CFAP53, DNAI1, RSPH4A, CFAP73, DNAAF1, CFAP206	3.33E-16
GO:0036159~inner dynein arm assembly	8	1.79	30.66	0	8	-2.83	CFAP100, LRRC6, DYX1C1, CFAP73, DNAAF1, ZMYND10, TEKT2, DNAH7	3.16E-08
GO:0036158~outer dynein arm assembly	8	1.79	26.57	0	8	-2.83	LRRC6, DNAI1, DYX1C1, DNAAF1, ZMYND10, ARMC4, DNAI2, DNAH5	1.15E-07
GO:0044458~motile cilium assembly	7	1.57	23.25	0	7	-2.65	LRRC6, DNAAF3, DNAAF1, BBOF1, ZMYND10, CC2D2A, RSPH9	4.47E-06
GO:0035082~axoneme assembly	7	1.57	20.52	0	7	-2.65	RP1, RSPH4A, RSPH1, CC2D2A, CFAP206, SPEF2, RSPH9	1.07E-05
GO:0042384~cilium assembly	14	3.13	5.63	1	13	-3.21	CEP126, FOXJ1, ABLIM3, B9D1, DNAI2, DNAH5, ACTR2, NME5, CFAP53, TMEM231, IFT122, CC2D2A, CCDC113, CCNO	2.06E-05
GO:0060271~cilium morphogenesis	14	3.13	5.13	0	14	-3.74	CEP126, FOXJ1, B9D1, CFAP221, DNAH5, IFT122, TMEM231, DNAAF1, CC2D2A, CCDC113, TCTN1, TTC21A, CCNO, IQUB	5.87E-05
GO:0007368~determination of left/right symmetry	9	2.01	8.15	0	9	-3.00	DAW1, DNAI1, DYX1C1, FOXJ1, DRC1, CC2D2A, ARMC4, DNAI2, DNAH5	2.15E-04
GO:0022617~extracellular matrix disassembly	10	2.24	6.56	2	8	-1.90	KLK7, MMP10, LAMB3, KIF9, MMP13, MMP12, MMP1, FN1, ADAM15, CAPN1	3.43E-04
GO:0003351~epithelial cilium movement	5	1.12	19.16	0	5	-2.24	NME5, DNAI1, SPA17, ROPN1L, SPAG17	1.65E-03
GO:0007507~heart development	13	2.91	3.54	1	12	-3.05	CRIP1, ADM, DAW1, DNAI1, ERBB4, FREM2, FOXJ1, DRC1, CC2D2A, HOPX, ARMC4, PTN, DNAH5	5.47E-03
GO:0030030~cell projection organization	6	1.34	9.06	0	6	-2.45	DNAH9, SPAG6, AK7, CCDC78, PIFO, NPHP1	7.87E-03
GO:0070286~axonemal dynein complex assembly	4	0.89	19.93	0	4	-2.00	DNAAF3, DNAAF1, DRC1, PIH1D3	1.44E-02
GO:0007018~microtubule-based movement	8	1.79	4.92	0	8	-2.83	DNAH10, DNAH9, DNAH12, DNAH2, KIF9, DYNLRB2, DNAH5, DNAL4	1.98E-02
GO:0032417~positive regulation of sodium:proton antiporter activity	3	0.67	37.37	0	3	-1.73	TESC, ACTN4, CHP1	3.88E-02
GO:0001666~response to hypoxia	11	2.46	3.19	3	8	-1.51	PLAT, PKM, KCNMA1, HIF1A, ADM, ACTN4, EPAS1, CRYAB, EGLN3, PLAU, ALDH3A1	4.11E-02
GO:0006508~proteolysis	21	4.70	2.09	3	18	-3.27	ADAM28, AGBL2, PLAT, KLK7, KLK8, CFB, CNDP2, ANPEP, MMP13, MMP1, MMP12, CAPN1, MMP10, CHMP1A, SFRP1, ST14, CAPN14, ASRGL1, ERAP2, PLAU, ADAM15	4.47E-02
KEGG PATHWAY ID	Count	%	Fold Enrichment	UP	DW	Z-Score	Genes	FDR
hsa00980:Metabolism of xenobiotics by cytochrome P450	8	1.79	5.62	0	8	-2.83	GSTA1, GSTM3, CYP2F1, CYP2S1, UGT2A1, CYP2A6, ALDH3B1, ALDH3A1	6.20E-03
hsa00982:Drug metabolism - cytochrome P450	7	1.57	5.35	0	7	-2.65	GSTA1, GSTM3, FMO3, UGT2A1, CYP2A6, ALDH3B1, ALDH3A1	2.25E-02
hsa05016:Huntington's disease	11	2.46	2.98	0	11	-3.32	DNAH10, DNAH9, DNALI1, CLTB, DNAH12, DNAI1, DNAH2, DNAI2, DNAH7, DNAH5, DNAL4	4.44E-02

***Functional enrichment analysis of differentially expressed mRNAs (Log2Ratio > 1, Log2Ratio < 1, and q < 0.05) was done in Database for Annotation, Visualization and Integrated Discovery (DAVID, version 6.8, recently updated in Oct. 2016, https://david.ncifcrf.gov/home.jsp) and using a False Discovery Rate (FDR) threshold of 5% (p-adjusted value or q < 0.05). Enriched Gene Ontology and KEGG pathway terms are ordered in this table by FDR values. Numbers of upregulated (UP) and downregulated (DW) genes are showed in red and green, respectively. The z-score represents the overall up/down regulated genes from that term [Walter et al., 2015]. Z-score cells of this table are coloured depending on Z-score values: in red for Z >0, in blue for Z < 0 or in white for Z = 0.**

TABLE S24. List of mRNA-miRNA predicted interactions showing a significant inverted correlation (Spearman |rho| >0.75 and p < 0.01).

Control-NM at day 14 vs 0

mRNA	Log_2 Ratio	miR	Log_2 Ratio	ρ
MYC	-1.320	hsa-miR-449a	3.034	-0.868
STAT4	-1.069	hsa-miR-141-3p	1.843	-0.754
BCL6	2.105	hsa-miR-155-5p	-2.582	-0.793

Control-NM at day 28 vs 0

mRNA	Log_2 Ratio	miR	Log_2 Ratio	ρ
MYC	-2.125	hsa-miR-449a	4.476	-0.798
NOTCH1	-1.225	hsa-miR-34c-5p	3.086	-0.758
MYC	-2.125	hsa-miR-34c-5p	3.086	-0.851
MEIS1	1.349	hsa-miR-155-5p	-2.631	-0.771

CRSwNP at day 14 vs 0

mRNA	Log_2 Ratio	miR	Log_2 Ratio	ρ
RAB32	-1.317	hsa-miR-30e-5p	1.574	-0.763
IGF2	1.188	hsa-miR-100-5p	-1.642	-0.767
LOX	2.037	hsa-miR-29a-3p	-1.013	-0.767
RNASEL	1.365	hsa-miR-29a-3p	-1.013	-0.776
SESTD1	1.409	hsa-miR-29a-3p	-1.013	-0.767

CRSwNP at day 28 vs 0

mRNA	Log_2 Ratio	miR	Log_2 Ratio	ρ
GMNN	-1.252	hsa-miR-449b-5p	3.263	-0.908
MYBL2	-1.062	hsa-miR-30e-5p	2.570	-0.873
NRG1	-2.926	hsa-miR-125a-3p	1.305	-0.815
IL6	-2.803	hsa-miR-125a-3p	1.305	-0.789
MAPK1	-1.079	hsa-miR-129-5p	2.359	-0.771
CDC6	-2.999	hsa-miR-675-5p	1.866	-0.771
CCNE1	-2.527	hsa-miR-25-5p	1.811	-0.771
DPYSL2	-2.222	hsa-miR-452-5p	1.445	-0.767
IGF1R	-1.946	hsa-miR-375	1.887	-0.763
RASSF8	-1.101	hsa-miR-224-5p	1.790	-0.763
EPAS1	1.365	hsa-miR-17-5p	-1.312	-0.943
ANAPC16	1.343	hsa-miR-125b-5p	-1.243	-0.881
IGFBP3	4.774	hsa-miR-17-5p	-1.312	-0.859
ERBB2	1.444	hsa-miR-205-5p	-0.944	-0.859
TTC39A	1.778	hsa-miR-100-5p	-3.135	-0.824
IKZF2	1.598	hsa-miR-125b-5p	-1.243	-0.820
SATB1	1.169	hsa-miR-100-5p	-3.135	-0.815
CLU	2.690	hsa-miR-17-5p	-1.312	-0.802
ITPR1	1.485	hsa-miR-494-3p	-2.192	-0.802
BCL2L11	1.369	hsa-miR-92a-3p	-1.191	-0.802
CGN	1.052	hsa-miR-125b-5p	-1.243	-0.793

	BCL2L11	1.369	hsa-miR-181b-5p	-0.792	-0.785
	ERBB2	1.444	hsa-miR-125b-5p	-1.243	-0.780
	BCL2L11	1.369	hsa-miR-494-3p	-2.192	-0.780
	CYLD	1.135	hsa-miR-181b-5p	-0.792	-0.780
	NFIA	1.523	hsa-miR-29a-3p	-0.999	-0.776
	NEO1	1.296	hsa-miR-18a-5p	-2.819	-0.776
	SESTD1	1.464	hsa-miR-29a-3p	-0.999	-0.776
	CYLD	1.135	hsa-miR-130b-3p	-1.341	-0.767
	LOX	2.481	hsa-miR-29a-3p	-0.999	-0.763
	SCNN1A	1.847	hsa-miR-125b-5p	-1.243	-0.763

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Table S25. Epidemiological characteristics of controls (control-NM) and patients with chronic rhinosinusitis with nasal polyps (CRSwNP).

	Control-NM	CRSwNP	P value*
Study Population, n	7	7	NS
Mean Age (in years ± SEM)	48 ± 7.2	53 ± 6.0	NS
Gender (M/F)	5/2	5/2	NS
Aspirin intolerance, n (%)	0 (0)	0 (0)	NS
Bronchial Asthma, n (%)	0 (0)	0 (0)	NS
Skin Prick Test Positive, n (%)	0 (0)	3 (43)	NS
Upper respiratory tract infection (2 weeks prior to surgery), n (%)	0 (0)	0 (0)	NS
Topical CS treatment (last month prior surgery), n (%)	0 (0)	0 (0)	NS

n, sample size (no.); SEM, standard error of the mean; M, male; F, female; NS, not significant; CS, corticosteroids;
* The level of significance was evaluated by using the Fisher´s exact Test. A P value of less than .05 was considered statistically significant.

Table S26. List of primers used for validation of different mRNAs expression by Real Time PCR.

Official Gene Symbol	Gene Name	Accession Number	Primer ID	SEQUENCES
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	NM_002046	Forward	ACATCGCTCAGACACCATG
			Reverse	TGTAGTTGAGGTCAATGAAGGG
ACTB	Actin Beta	NM_001101	Forward	ACCTTCTACAATGAGCTGCG
			Reverse	CCTGGATAGCAACGTACATGG
HSP90AA1	Heat Shock Protein 90 Alpha Family Class A Member 1	NM_001017963	Forward	AGAAATGCCACCCCTTGAAG
			Reverse	GTAAGTCATCCCTCAGCCAG
AGR2	Anterior Gradient 2	NM_006408.3	Forward	AGAAGCTTGGACCGCATC
			Reverse	GGTTTGACTGTGGTATCTCTGG
SCGB1A1	Secretoglobin Family 1A Member 1	NM_003357.4	Forward	AGAGACGGAACCAGAGACAG
			Reverse	GTTTCGATGACACGCTGAAAG
MUC5AC	Mucin 5AC	NM_001304359.1	Forward	TGACACCCATGGAATTCGGG
			Reverse	AGATGCCAAAGCCAGTGGAG
MUC5B	Mucin 5B	NM_002458.2	Forward	CAAAGTGTACAAGCCATGCG
			Reverse	TGTGCGTTGAAGAGGATCTG
MUC16	Mucin 16	NM_024690.2	Forward	CTGAGACCCCAACATCCTTG
			Reverse	GGTCACTAGCGTTCCATCAG
FOXJ1	Forkhead Box J1	NM_001454.3	Forward	ACGGACAACTTCTGCTACTTC
			Reverse	TTGTTCAGAGACAGGTTGTGG
MYB	MYB Proto-Oncogene	NM_001130173.1	Forward	CATGTTCCATACCCTGTAGCG
			Reverse	TTCTCGGTTGACATTAGGAGC
CCNO	Cyclin O	NM_021147.4	Forward	GCTCATCGCTTGCAAACAG
			Reverse	AGGGTGAAGTGCAGCTTG
RFX3	Regulatory Factor X3	NM_002919.3	Forward	GCTATTCTCCCTCTACTCCAAC
			Reverse	CACAGTTACACATCCATTTCAGG
MCIDAS	Multiciliate Differentiation And DNA Synthesis Associated Cell Cycle Protein	NM_001190787.1	Forward	AGCAGGGAAGGATTTAGAAACCA
			Reverse	CCAGTGTTTCCCATTGCAGG
TP63	Tumor Protein P63	NM_003722.4	Forward	TTCGGACAGTACAAAGAACGG
			Reverse	GCATTTCATAAGTCTCACGGC
KRT5	Keratin 5	NM_000424.3	Forward	AGAGCTGAGAAACATGCAGG
			Reverse	AGCTCCACCTTGTTCATGTAG
KRT14	Keratin 14	NM_000526.4	Forward	CAATGCCAATGTCCTTCTGC
			Reverse	GTCAGTTCGTCCAGCACC
ITGA6	Integrin Subunit Alpha 6	NM_001079818.2	Forward	CCTCCCTGAGCACATATTCG
			Reverse	CACCTCCAACTTCTCCATCTC
PDPN	Podoplanin	NM_006474.4	Forward	TCAGAAAGCACAGTCCACG
			Reverse	TATGATTCCAACCAGGGTCAC