SUPPORTING INFORMATION

for

Regulation of gene expression by the BLM helicase correlates with the presence of G4 motifs

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1. SI Materials and Methods:

Cells and cell culture conditions. We analyzed mRNA and miRNA expression in primary fibroblast strains from BS patients and from matched primary human skin fibroblasts from healthy individuals (NM), as well as in primary human fibroblasts depleted for BLM protein by expression of a *BLM*-specific shRNA. Primary human skin fibroblast strains from BS patients (n=16, donor median age 11.5 years) or from control donors (n=15, donor median age 19 years) were obtained from the Coriell Cell Repositories (Camden, NJ, USA). Normal control fibroblasts (NM) were age and gender-matched to BS cases. Additional detail on these BS patient and NM fibroblasts is given in Table S1. Cells were cultured in Eagle's Minimum Essential Medium with Earle's salts, supplemented with 15% fetal bovine serum, non-essential amino acids, penicillin/streptomycin and 2mM L-glutamine (all supplied by Invitrogen, Carlsbad, CA, USA). All cells were cultured at 37°C in a humidified 5% CO_2 incubator. Passage number was calculated based on the number of passages at purchase plus the number of passages performed prior to cell harvesting. The human primary fibroblast strain 82-6 was initiated from a foreskin fibroblast preparation as previously described (1), and grown in Dulbecco-modified Eagle medium (Mediatech, Manassas, VA, USA) supplemented with 10% fetal bovine serum (HyClone, Logan, UT, USA), 100 U/mL penicillin, and 100 µg/mL streptomycin at 37ºC in a humidified 5% CO_2 incubator.

BLM depletion experiments. BLM protein was depleted from 82-6 primary human fibroblasts by lentiviral transduction with expression of a *BLM*-specific shRNA as previously described (2, 3). In brief, a *BLM*-specific shRNA (BLM-3: 5'-GTACTAAATGGCAATTTAA-3') was cloned into the lentiviral vector pLKO.1 under control of the human U6 promoter (4). Depletions were performed by transducing 10^6 primary fibroblasts cells with a *BLM*-shRNA-expressing lentivirus at a multiplicity of infection (MOI) of 10 for 2 d, followed by puromycin selection (2.0 µg/mL) for 8 d. BLM protein depletion to ≥90% was verified on day 10 by Western blot analysis, where day 0 was the start of viral transduction (2)(Figure S2). Depletions were performed in triplicate, using either the *BLM*-specific shRNA or a scrambled shRNA with no known target sequence in the human genome (plasmid 1864, Addgene, Cambridge, MA), to provide controls for comparison with untransduced cells.

RNA isolation and quality control. RNA was isolated from human diploid 82-6 primary fibroblast cultures when 75% confluent. Cells were washed in 1X PBS, scrapped off plates and collected as pellets that were stored at -80ºC. Total RNA was isolated using TRIZOL reagent, following the manufacturer's protocol (Invitrogen). Total RNA samples were isolated using Qiagen's miRNAeasy Mini Kit (Qiagen, Valencia, CA). RNA quality was assessed using the Agilent 2100 Bioanalyzer (Agilent Technologies, Palo Alto, CA), and only samples of high quality, defined by distinct 28S and 18S rRNA bands together with a RIN (RNA integrity number) >7, were used for further analyses.

mRNA expression profiling. Whole genome transcript exon profiling of BS and NM fibroblasts obtained from the Coriell collection of human primary fibroblasts, and of BLM-depleted 82-6 primary human fibroblasts were performed using the Affymetrix GeneChip Human Exon 1.0 ST Array, which contains four probes/exon and ~40 probes/gene (Affymetrix, Santa Clara, CA). RNA labeling, hybridization, washing, and image acquisition were performed at the Laboratory of Molecular Technology (NCI-Frederick) using a standard Affymetrix labeling, hybridization and wash protocol.

miRNA expression profiling. Profiling of miRNA expression in BS and NM primary fibroblasts was performed using a custom miRNA microarray chip (OSU-CCC version 4.0) that includes 898 probes to human and 704 probes to mouse mature or precursor miRNAs, spotted in duplicate (5). Briefly, total RNA (5μg) was converted to biotin-labeled complementary DNA, hybridized onto the chips, and processed by direct detection of the biotin-containing transcripts by streptavidin-Alexa 647 conjugate. Slides were subsequently scanned with the Axon 4000B Scanner (Molecular Device) and spot intensities were quantified with Genepix (version Pro 6.0.1.00). Profiling of miRNA expression in BLM-depleted primary human fibroblasts was performed using the Nanostring nCounter Human miRNA Expression Assay Kit (Nanostring, Seattle, WA). For these analyses we used 100 ng RNA and the processing protocol recommended by the manufacturer.

In order to confirm miRNA expression differences we used qPCR. RNA samples were reverse-transcribed using an Applied Biosystems High-Capacity cDNA Archive Kit (Applied Biosystems/AB, Foster City, CA) prior to assay in triplicate using miRNA-specific Taqman Gene Expression Assays (ABI). Double-stranded cDNA for each sample was amplified for 40 cycles using the TaqMan Universal PCR Master Mix using the manufacturer’s protocol on the 7500HT Sequence Detection System (ABI). For quality control, any samples with either an 18S rRNA or RNAU66 cycle value >20, or a gene or miRNA cycle value >36, were considered to be of poor quality and removed. Alternatively, PCR reactions were run following a 12-round pre-amplification on a BioMark 48.48 Dynamic Array System (Fluidigm, South San Francisco, CA). The mRNA or miRNA readings were calculated using the comparative method ($2^{-\Delta Ct}$), where Ct = threshold cycle and ΔCt = (Ct gene (or miRNA) – Ct 18S rRNA (or RNAU66)).

Identification of differentially expressed mRNAs. Raw Human Exon 1.0 ST microarray expression data were pre-processed and normalized with Affymetrix® Expression Console™ Software using RMA normalization (affymetrix.com). From normalized data, genes with significant evidence for differential expression were identified using the Bioconductor limma package using a linear fixed effects model with adjustments for age and gender for the primary fibroblast data to calculate the contrast BS-NM (6, 7). For the BLM-depleted 82-6 normal human fibroblasts, a linear fixed effects model was used to calculate three contrasts, BLM-control, NS-control, and BLM-NS. The limma methodology calculates a p-value for each gene using a modified t-test in conjunction with an empirical Bayes method to moderate the standard errors of the estimated log-fold changes. This method of detecting differentially expressed genes draws strength across genes for more robust and accurate detection of differentially expressed genes. Such an adjustment has repeatedly been shown to avoid an excess of false positives when identifying differentially expressed genes (8). We then used the p-values from limma together with the Bioconductor package qvalue (9, 10) to estimate the false discovery rate associated with our list of differentially expressed genes (DEGs). This methodology allows us to address the multiple testing problem without resorting to an excessively conservative approach that controls the familywise error, such as a Bonferroni correction. In order to directly compare the genes from the two data sets instead of probesets, we removed duplicate probesets by choosing the probesets with the maximum median variance across all the samples (11).

Exploratory analyses and visualizations were also performed for set of results using the Partek Genomics Suite version 6.6 (Partek Inc, St Louis, MO, USA) with default import para-meters. Interrogating probes were imported using the Core Meta-Probeset filter (most confident probes) with adjustment for GC content and RMA background correction, followed by Quantile Normalization and Median Polish. Gene-level data was obtained by mean summarization of the core transcripts.

Identification of differentially expressed miRNAs. Preprocessing and normalization of OSU-CCC miRNA microarrays from BS and NM primary fibroblasts were done in R (version 2.6.0). nCounter RCC files generated from BLM-depleted samples were imported into nSolver (Nanostring), quality control-verified and normalized to the geometric mean of the top 100 expressed miRNAs. Normalized probes were imported into Partek Genomics Suite. Further, miRNAs were deemed absent if intensity <10, and excluded from the analysis if they were not present in at least 40% of samples (in the case of BS-NM comparison) or at least 2 samples (in the case of BLM-depleted set), leaving 274 and 392 miRNAs, respectively. Differential expression of these miRNAs was then analyzed using ANOVA adjusted for age and gender for BS-NM samples. Exploratory analyses and visualizations were again performed using Partek.

Ingenuity pathway analysis. In order to better characterize *in vivo* roles of differentially-expressed genes, we used mRNA expression profiling results to perform an Ingenuity Pathway Analysis (IPA Ingenuity Systems, www.ingenuity.com) Core Analysis using default parameters. The output consisted of lists of Networks, Diseases, Biological Functions, and Canonical Pathways enriched within a given sample type and differentially expressed gene list. IPA also identifies potential upstream regulators (i.e., which genes affect the expression of other genes), and predicts whether putative regulatory interactions are activating or repressive based on the magnitude and direction of gene expression changes.

Gene set enrichment analyses. In order to investigate biological categories of genes and pathways altered in BS and BLM-depleted samples, we performed a Gene Set Enrichment Analysis (GSEA) on BS primary fibroblast and 82-6 cell strain data using the romer function in the limma package (7). Romer is a gene set enrichment analysis program for linear models using rotation tests (ROtation testing using MEan Ranks). Romer considers all genes in an experiment, and allows the identification of gene sets with strong cross-correlation by boosting the signal-to-noise ratio. This makes it possible to confidently detect even modest changes in gene expression. We used romer to perform GSEA using the 15 gene set collections contained in the Molecular Signature Database version 4.0 (12) (http://www.broad.mit.edu/gsea/msigdb /msigdb_index.html).

We also determined which genes that were significantly altered in both BS primary fibroblasts and BLM-depleted 82-6 cells were over-represented in statistically significant gene sets. The p-values for the intersection of the common genes with the gene sets were calculated with the R package's phyper function (13), which uses a hypergeometric distribution and sampling *without* replacement. This is the same statistical test used to test associations in Gene Ontology analysis (14).

miRNA targets analysis. In order to determine whether differentially expressed miRNAs might be modulating gene expression in BLM-deficient cells, we used our miRNA expression profiling results to search miRTarBase (15) (http://mirtarbase.mbc.nctu.edu.tw/), a curated database of miRNA-target gene interactions that have been experimentally validated. Only targets validated by strong experimental methods such as reporter assay or immunoblotting were chosen for this analysis. We searched among the miRNA target gene lists to identify genes that were significantly differentially expressed in BS and/or BLM-depleted cells. A hypergeometric test was then performed to determine the significance of the association of a given miRNA with differentially expressed genes as compared with the expectation from chance alone.

G4 enrichment statistics. In order to determine the frequency of G4 DNA motifs near TSS and in the first intron of genes in the hg19 human genome, the RefSeq Gene table and FASTA genome sequence for the hg19 human genome were downloaded from the UCSC Genome Browser Database (16) G4 motifs were located in the hg19 genome using Quadparser (17) with settings for 4 or more runs of 3 or more consecutive Gs separated by 1-12 nt loops on either strand of the genome (GC 3 4 1 12) in DAS format. Quadparser results were converted to BED format using Perl scripts. This resulted in 722,264 G4 motif annotations. R scripts were used to select regions near RefSeq TSS (-250bp to TSS, TSS to +250 bp, and the first 250 bp of the first intron), and to calculate the number of G4 motifs that overlapped these regions on each strand relative to the direction of gene transcription (template and non-template) for each gene surveyed in the expression arrays. Genes from expression arrays were matched to RefSeq regions using mRNA accessions. Of 17,318 expression array genes, 16,745 were matched to TSS in the RefSeq table (>96%). For the same 17,318 array genes, 15,728 genes were matched to Intron 1 locations (>90%).

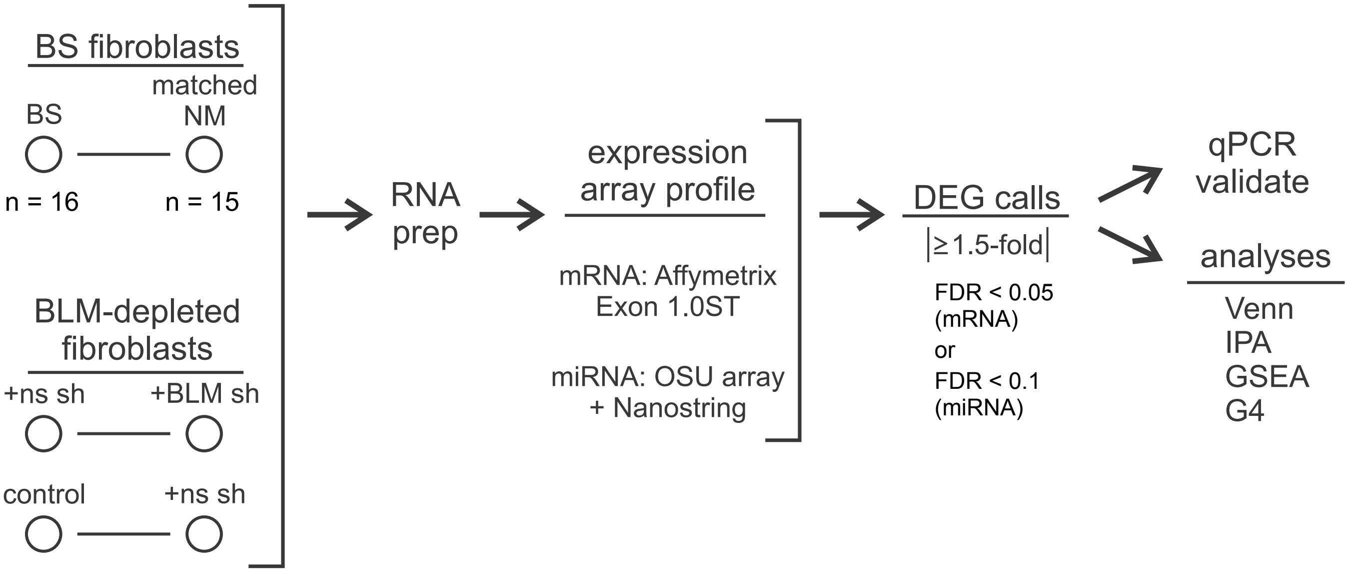
The gene sets used for G4 analysis were those with altered expression (≥1.5-fold up or down-regulated) in BS patients (BS) compared to matched normal controls (NM), or in BLM-depleted control primary fibroblasts (BLM) versus the same cells treated with a non-specific shRNA (NS). Genes up- or down-regulated ≥1.5-fold in the NS samples compared to an untreated control were excluded. For each set, we calculated the number of genes in each set with 1 or more G4 motif, the average number of G4 motifs per gene, and the total number of G4s per gene for each gene set in each region (250bp to TSS, TSS to +250bp, and 5' end of intron 1) and for G4 motifs on each strand (both, non-template, and template). We also selected a list of all genes with a G4 motif on either strand among up- or down-regulated genes (Table S7A and Table S7B).

False discovery rates of G4 motif enrichment were empirically determined for each gene set by selecting 1000 gene sets each made up of an equal number of regions selected at random from the RefSeq-based region locations described above. False discovery rates were determined by calculating the fraction of the 1000 randomly selected sets with a higher or equal value or lower or equal value compared to the results tabulated among the genes with altered expression. A result of <0.001 means that the value found in the experimental set was not observed within the range of 1000 random matching sets. In Figure 3 we present only the FDR statistics for the sum of the G4 motifs over all of the regions in each set. Statistics for the number of genes with at least one G4 motif, and the average number of motifs per G4-containing gene and their respective FDRs are available in Supplemental Table S8.

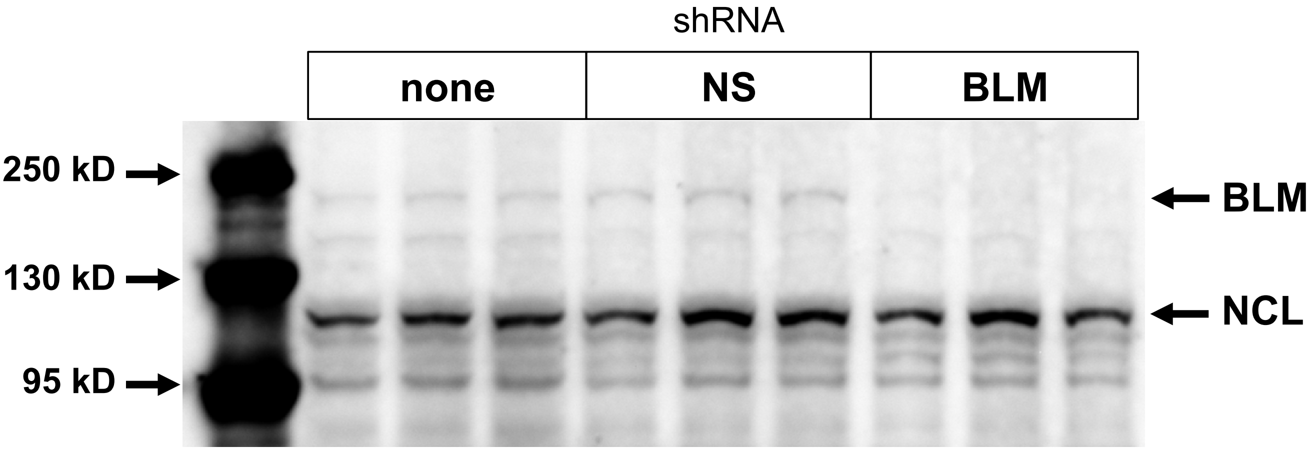
In order to generate G4 motif frequency plots we took regions 250 bp up- or downstream of the TSS and 250 bp up or downstream of the 5' end of first introns for all genes on the expression arrays. Genes in the up- or down-regulated gene sets were selected from these region tables using mRNA accessions, as described above. G4 motif BED files for each strand of the genome (+ and -) and for both strands together were converted to BEDGraph files with a value of 1 for each position that a G4 motif overlapped. These BEDGraphs were converted to bigWig format for subsequent analysis using the UCSC Kent source utility bedGraphToBigWig (18). Perl scripts that utilized the Bio::DB::BigWig library from BioPerl (19) were used to calculate the frequency of overlap for each G4 motif set, at each position relative to the TSS or 5' end of the first intron in each gene set. Frequency plots were generated using the R package ggplot2 (20)

SI Materials and Methods references:

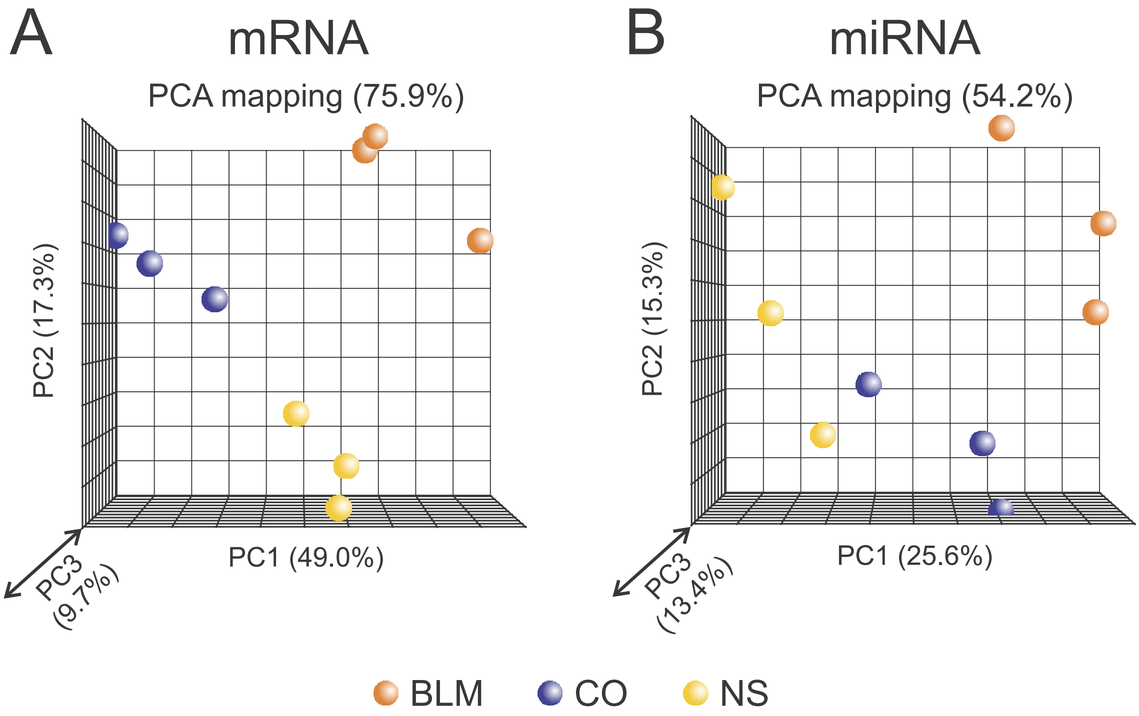
1. Dhillon KK*, et al.* (2008) Werner syndrome protein loss leads to divergent mouse and human cell phenotypes. *DNA Repair* 9:11-22.
2. Mao FJ, Sidorova JM, Lauper JM, Emond MJ, & Monnat RJ (2010) The human WRN and BLM RecQ helicases differentially regulate cell proliferation and survival after chemotherapeutic DNA damage. *Cancer Research* 70(16):6548-6555. PMCID:PMC2941797.
3. Sidorova JM, Kehrli K, Mao F, & Monnat Jr R (2013) Distinct functions of human RECQ helicases WRN and BLM in replication fork recovery and progression after hydroxyurea-induced stalling. *DNA Repair* 12(2):128-139.
4. Moffat J*, et al.* (2006) A lentiviral RNAi library for human and mouse genes applied to an arrayed viral high-content screen. *Cell (Cambridge MA)* 124(6):1283-1298.
5. Mathé EA*, et al.* (2009) MicroRNA expression in squamous cell carcinoma and adenocarcinoma of the esophagus: associations with survival. *Clinical Cancer Research* 15(19):6192-6200.
6. Smyth GK (2004) Linear models and empirical bayes methods for assessing differential expression in microarray experiments. *Stat Appl Genet Mol Biol* 3(Article 3).
7. Gentleman R*, et al.* (2004) Bioconductor: open software development for computational biology and bioinformatics. *Genome Biology* 5(10):R80.
8. Allison DB, Cui X, Page GP, & Sabripour M (2006) Microarray data analysis: from disarray to consolidation and consensus. *Nat Rev Genet* 7(1):55-65.
9. Dabney A & Storey J (2006) A reanalysis of a published Affymetrix GeneChip control dataset. *Genome Biology* 7(3):401.
10. Tusher VG, Tibshirani R, & Chu G (2001) Significance analysis of microarrays applied to the ionizing radiation response. *Proceedings of the National Academy of Sciences* 98(9):5116-5121.
11. Efron B & Tibshirani R (2007) On testing the significance of sets of genes. *Annals of Applied Statistics* 1:1070129.
12. Subramanian A*, et al.* (2005) Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. *Proceedings of the National Academy of Sciences of the United States of America* 102(43):15545-15550.
13. Johnson NL, Kotz S, & Kemp AW (1992) *Univariate Discrete Distributions* (Wiley, New York) 2 Ed.
14. Ashburner M*, et al.* (2000) Gene Ontology: tool for the unification of biology. *Nat Genet* 25(1):25-29.
15. Hsu S-D*, et al.* (2010) miRTarBase: a database curates experimentally validated microRNA–target interactions. *Nucleic Acids Research*.
16. Meyer LR*, et al.* (2013) The UCSC Genome Browser database: extensions and updates 2013. *Nucleic Acids Research* 41(D1):D64-D69.
17. Huppert JL & Balasubramanian S (2005) Prevalence of quadruplexes in the human genome. *Nucleic Acids Research* 33(9):2908-2916.
18. Kent WJ, Zweig AS, Barber G, Hinrichs AS, & Karolchik D (2010) BigWig and BigBed: enabling browsing of large distributed datasets. *Bioinformatics* 26(17):2204-2207.
19. Stajich JE*, et al.* (2002) The Bioperl Toolkit: Perl modules for the life sciences. *Genome Research* 12(10):1611-1618.
20. Wickham H (2009) *ggplot2: Elegant Graphics for Data Analysis* (Springer, New York).



Supplementary Figure S1: Study design and experimental workflow. Messenger RNA and miRNA expression profiling analyses were performed using primary fibroblasts from Bloom syndrome patients (BS) and age-, gender- and passage-matched controls (NM), and an isogenic pair of control diploid human fibroblasts (strain 82-6) expressing either a *BLM*-specific (BLM sh) or nonspecific (ns sh) shRNA from a lentiviral expression vector. Differentially expressed mRNAs and miRNAs were identified on the basis of absolute fold changes in expression of ≥1.5-fold under conditions were the false discovery rate (FDR) was <0.05 for mRNA and <0.1 for miRNA (see Methods for detail). A subset of both mRNA and miRNA expression changes were verified by quantitative PCR, prior to analyzing expression data using several different strategies (Venn overlap, gene set enrichment analyses (GSEA), analysis of expression as a function of G4 gene/miRNA content and by Ingenuity Pathway Analyses (IPA).



Supplementary Figure S2: Immunoblot verification of BLM depletion from human fibroblasts. Whole cell lysate from BLM-depleted and control 82-6 human diploid fibroblasts were immunoblotted with a human BLM-specific antibody to detect and quantify BLM protein expression. Controls included cells that were not depleted (none) or depleted with a non-specific, scrambled shRNA (NS). Each set of 3 lanes are samples from biological triplicate depletion experiments. The nuclear protein nucleolin was used as a loading control across all samples (NCL). Aliquots of the same sets of triplicate samples were used for mRNA/miRNA profiling analyses.



Supplementary Figure S3: Principal component analyses (PCA) of (A). mRNA expression and (B). miRNA expression in BLM-depleted (BLM, orange), non-specific shRNA depleted (NS, yellow) and normal control (CO, blue) primary human fibroblasts (strain 82-6) using average distance and linkage measures. Percentages indicate the portion of expression differences that can be attributed to specific principal components.

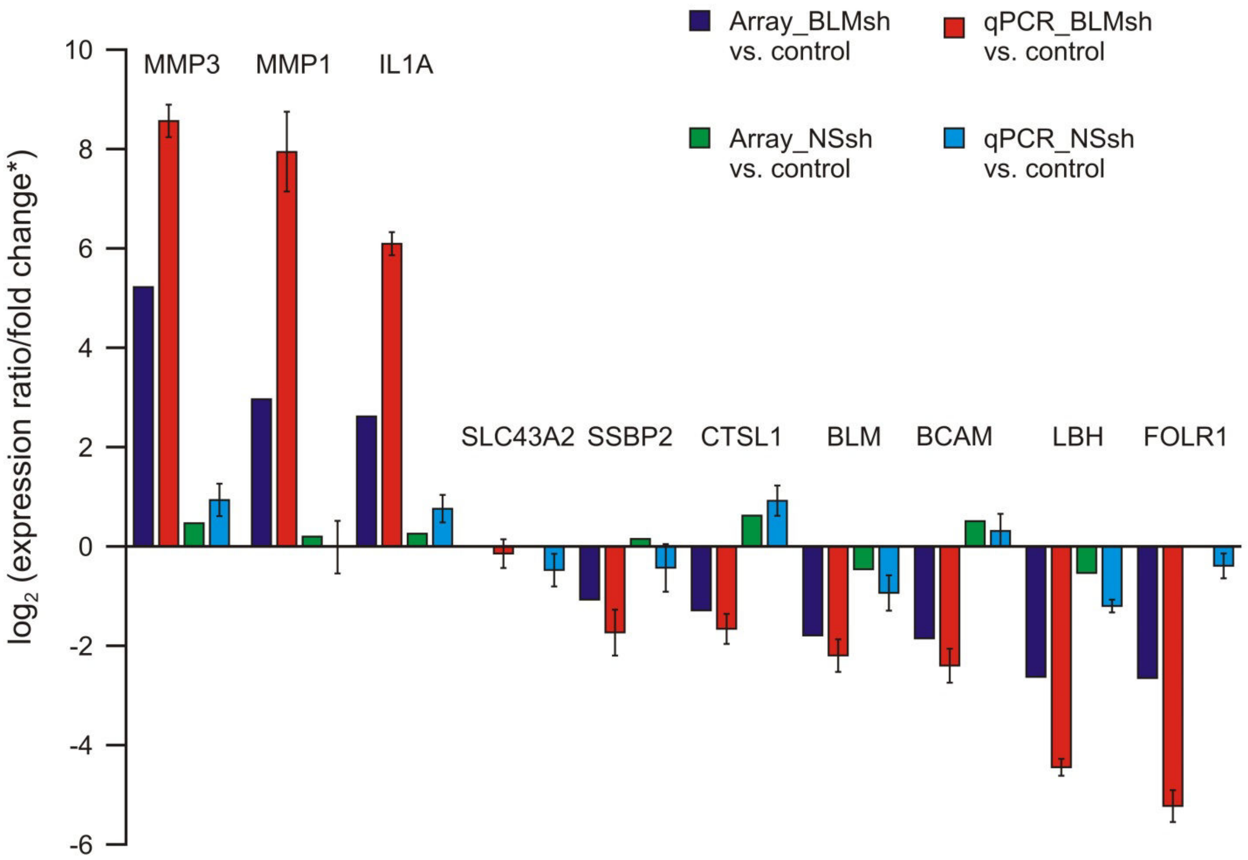


Figure S4: qPCR verification of mRNA expression levels determined by microarray. *Expression ratios are plotted for initial array-based measurements, and fold changes for qPCR confirmatory assays.

Methods: RNA was reverse-transcribed using an Applied Biosystems High-Capacity cDNA Archive Kit (Applied Biosystems/AB, Foster City, CA). Expression levels for individual genes and miRNAs were evaluated in triplicate using Taqman Gene Expression Assays (ABI). Double-stranded cDNA for each sample was amplified for 40 cycles using the TaqMan Universal PCR Master Mix using the manufacturer's protocol on the 7500HT Sequence Detection System (ABI). For quality control, any samples with either an 18S rRNA or RNAU66 cycle value >20, or a gene or miRNA cycle value >36, were considered to be of poor quality and removed. Alternatively, PCR reactions were run following a 12-round pre-amplification on a BioMark 48.48 Dynamic Array System (Fluidigm, South San Francisco, CA), or a Rotor-Gene RG-3000 PCR machine (Qiagen, Germantown, MD, USA) according to the manufacturer's instructions. The gene mRNA or miRNA readings were then calculated using the comparative method ($2^{-\Delta Ct}$), where Ct = threshold cycle and ΔCt = (Ct gene (or miRNA) – Ct 18S rRNA (or RNAU66)).

Table S1 BS patient and control detail

Coriell repositor	Genotype	Donor phenotype	Age	Gender	No. passage	miRNA array	mRNA array
(N=16)							
GM 01492	homozygous (2281delT of RECQL3) and T>G transversion resulting a transcated p53 protein	Bloom syndrome	15	M	18	included	included
GM 03498	compound heterozygous (2281delT and 3233delT of RECQL3 gene	Bloom syndrome	4	M	15	included	included
GM 03402	homozygous (2281delT of RECQL3 gene)	Bloom syndrome	30	M	12	included	included
GM 05289	homozygous (1544insA of RECQL3 gene)	Bloom syndrome	5	F	18	included	included
GM 16882	compound heterozygous (3261delT and 2281delT of RECQL3 gene	Bloom syndrome	3	F	19	included	included
GM 16886	Q700X missen mutation in BLM protein	Bloom syndrome	7	M	20	included	included
GM 16881	homozyguous (2293delC of RECQL3 gene)	Bloom syndrome	31	M	17	included	included
GM 02520	compound hererozygous (2293delC and deletion of exon 15 resulting in a frameshift)	Bloom syndrome	10	F	15	included	included
GM 02548	compound hererozygous (1544insA and T2328C transition of the RECQL3 gene)	Bloom syndrome	6	M	12	included	included
GM 00811	homozygous (6-bp del/7-bp insertion at nucleotide 2281 of REQL3 gene)	Bloom syndrome	4	M	30	included	no
GM 16883	compound heterozygous ([2015A>G] and [IVS5-2A>G] of RECQL3 gene)	Bloom syndrome	25	F	13	included	included
GM 16859	homozygous (6-bp del/7-bp ins] at nucleotide 2,281 of RECQL3 gene)	Bloom syndrome	43	F	10	included	included
GM 02932	homozygous (6-bp del/7-bp insertion at nucleotide 2281 of REQL3 gene)	Bloom syndrome	28	M	11	included	included
GM 02085	homozygous (6-bp del/7-bp insertion at nucleotide 2281 of REQL3 gene)	Bloom syndrome	2	F	30	included	included
GM 16890	homozygous (Q645X missen mutation of BLM protein)	Bloom syndrome	30	F	Unknown	included	no
GM 16891	homozygous (Q645X missen mutation of BLM protein)	Bloom syndrome	13	M	Unknown	included	included
(N=15)						included	
GM 02185	Wildtype	Not clinically affected	36	M	13	included	no
GM 07532	Wildtype	Not clinically affected	16	F	12	included	included
GM 00408	Wildtype	Not clinically affected	5	M	19	included	included
GM 00497	Wildtype	Not clinically affected	4	M	19	included	included
GM 00499	Wildtype	Not clinically affected	8	M	15	included	no
GM 00969	Wildtype	Not clinically affected	2	F	17	included	included
GM 02674	Wildtype	Not clinically affected	29	F	14	included	included
GM 03377	Wildtype	Not clinically affected	19	M	9	included	included
GM 01651	Wildtype	Not clinically affected	13	F	16	included	included
GM 03651	Wildtype	Not clinically affected	25	F	13	included	no
GM 04260	Wildtype	Not clinically affected	60	M	16	included	included
GM 08398	Wildtype	Not clinically affected	8	M	7	included	included
GM 01948	Wildtype	Not clinically affected	27	F	6	included	included
GM 08402	Wildtype	Not clinically affected	32	M	11	no	included
GM 00730	Wildtype	Not clinically affected	45	F	9	included	included

Table S2A. Significantly differentially expressed mRNAs identified in BS compared with matched control human fibroblasts

Probe Set ID	Gene Symbol	Gene Description	log$_2$(ER)	unadjusted P-Value	FDR
3919033	**SLC5A3**	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	2.59	0.000	0.004
3388807	**MMP1**	matrix metallopeptidase 1 (interstitial collagenase)	2.24	0.001	0.007
7385515	**MALAT1**	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	2.06	0.001	0.009
3770632	**SUMO2**	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	1.88	0.001	0.008
3151086	**HAS2**	hyaluronan synthase 2	1.86	0.002	0.013
3843662	**ZNF587**	zinc finger protein 587	1.76	0.000	0.003
2786322	**SLC7A11**	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	1.76	0.001	0.009
3385769	**CTSC**	cathepsin C	1.73	0.000	0.002
2857416	**IL6ST**	interleukin 6 signal transducer (gp130, oncostatin M receptor)	1.70	0.000	0.001
2646818	**ZIC1**	Zic family member 1 (odd-paired homolog, Drosophila)	1.68	0.000	0.004
2423829	**ARHGAP29**	Rho GTPase activating protein 29	1.68	0.000	0.002
2741236	**USP53**	ubiquitin specific peptidase 53	1.66	0.000	0.006
2686023	**DCBLD2**	discoidin, CUB and LCCL domain containing 2	1.64	0.000	0.001
3812074	**DSEL**	dermatan sulfate epimerase-like	1.64	0.000	0.003
2991233	**AHR**	aryl hydrocarbon receptor	1.63	0.000	0.001
2652027	**CLDN11**	claudin 11	1.63	0.002	0.012
3449068	**TMTC1**	transmembrane and tetratricopeptide repeat containing 1	1.63	0.000	0.004
3296046	**KCNMA1**	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	1.62	0.000	0.001
2816459	**F2R**	coagulation factor II (thrombin) receptor	1.59	0.000	0.002
2565902	**ANKRD36B**	ankyrin repeat domain 36B	1.56	0.004	0.016
3041122	**MGC87042**	STEAP family protein MGC87042	1.51	0.003	0.014
2720584	**SLIT2**	slit homolog 2 (Drosophila)	1.49	0.000	0.002
2649367	**PTX3**	pentraxin 3, long	1.48	0.010	0.027
3766960	**SMURF2**	SMAD specific E3 ubiquitin protein ligase 2	1.45	0.000	0.003
2733360	**FGF5**	fibroblast growth factor 5	1.42	0.000	0.006
3376556	**ATL3**	atlastin GTPase 3	1.40	0.001	0.009
2815043	**TNPO1**	transportin 1	1.37	0.000	0.002
2514566	**SSB**	Sjogren syndrome antigen B (autoantigen La)	1.34	0.003	0.015
2580802	**RND3**	Rho family GTPase 3	1.33	0.000	0.003
2992814	**GPNMB**	glycoprotein (transmembrane) nmb	1.33	0.000	0.005
3325503	**RCN1**	reticulocalbin 1, EF-hand calcium binding domain	1.32	0.005	0.018
3020302	**CAV1**	caveolin 1, caveolae protein, 22kDa	1.29	0.000	0.003
3319840	**IPO7**	importin 7	1.28	0.000	0.003
3059464	**SEMA3A**	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	1.28	0.000	0.005
3253438	**RPS24**	ribosomal protein S24	1.28	0.020	0.041
2417174	**SERBP1**	SERPINE1 mRNA binding protein 1	1.26	0.004	0.017
3890333	**TFAP2C**	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	1.26	0.000	0.006
2750594	**SC4MOL**	sterol-C4-methyl oxidase-like	1.26	0.000	0.005
3774906	**SECTM1**	secreted and transmembrane 1	1.26	0.001	0.009
3464983	**ATP2B1**	ATPase, Ca++ transporting, plasma membrane 1	1.25	0.000	0.005
2592268	**STAT1**	signal transducer and activator of transcription 1, 91kDa	1.25	0.002	0.011
3292448	**HERC4**	hect domain and RLD 4	1.25	0.000	0.001
2422722	**TGFBR3**	transforming growth factor, beta receptor III	1.24	0.011	0.030
3759335	**GJC1**	gap junction protein, gamma 1, 45kDa	1.24	0.000	0.006
2809245	**ITGA2**	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	1.23	0.006	0.022
2362394	**IFI16**	interferon, gamma-inducible protein 16	1.23	0.000	0.006
3718555	**SLFN5**	schlafen family member 5	1.23	0.000	0.005
3021158	**C7ORF58**	chromosome 7 open reading frame 58	1.22	0.000	0.004
2711644	**ATP13A3**	ATPase type 13A3	1.22	0.000	0.005
2352228	**CAPZA1**	capping protein (actin filament) muscle Z-line, alpha 1	1.22	0.000	0.003
2593670	**SF3B1**	splicing factor 3b, subunit 1, 155kDa	1.21	0.000	0.003
2512330	**MARCH7**	membrane-associated ring finger (C3HC4) 7	1.21	0.000	0.003
2473571	**RAB10**	RAB10, member RAS oncogene family	1.20	0.000	0.003
2626167	**PXK**	PX domain containing serine/threonine kinase	1.20	0.000	0.004
2434609	**CTSK**	cathepsin K	1.20	0.024	0.047
2659577	**PAK2**	p21 protein (Cdc42/Rac)-activated kinase 2	1.19	0.000	0.003
2406064	**SFPQ**	splicing factor proline/glutamine-rich	1.19	0.000	0.004
3058944	**HGF**	hepatocyte growth factor (hepapoietin A; scatter factor)	1.18	0.009	0.026
2879509	**YIPF5**	Yip1 domain family, member 5	1.18	0.000	0.003
3190659	**SET**	SET nuclear oncogene	1.18	0.000	0.006
2940551	**SSR1**	signal sequence receptor, alpha	1.18	0.000	0.002

3472755	**TBX3**	T-box 3	1.17	0.000	0.006
3353876	**OR10G9**	olfactory receptor, family 10, subfamily G, member 9	1.17	0.001	0.010
3807474	**C18ORF32**	chromosome 18 open reading frame 32	1.17	0.002	0.010
2997376	**ANLN**	anillin, actin binding protein	1.17	0.007	0.022
2584018	**DPP4**	dipeptidyl-peptidase 4	1.17	0.006	0.021
2976360	**PERP**	PERP, TP53 apoptosis effector	1.16	0.000	0.002
2500615	**TMEM87B**	transmembrane protein 87B	1.15	0.000	0.001
3729172	**CLTC**	clathrin, heavy chain (Hc)	1.15	0.000	0.002
3415046	**FLJ33996**	hypothetical protein FLJ33996	1.15	0.001	0.006
3505319	**SACS**	spastic ataxia of Charlevoix-Saguenay (sacsin)	1.15	0.000	0.005
2347096	**DR1**	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	1.14	0.000	0.005
2601414	**SERPINE2**	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	1.14	0.000	0.003
3550392	**PAPOLA**	poly(A) polymerase alpha	1.14	0.000	0.004
2571979	**SLC35F5**	solute carrier family 35, member F5	1.14	0.000	0.003
2404819	**PTP4A2**	protein tyrosine phosphatase type IVA, member 2	1.13	0.001	0.007
3715109	**WSB1**	WD repeat and SOCS box-containing 1	1.13	0.001	0.008
2831124	**MATR3**	matrin 3	1.13	0.000	0.002
3564872	**GNPNAT1**	glucosamine-phosphate N-acetyltransferase 1	1.13	0.001	0.007
2583602	**RBMS1**	RNA binding motif, single stranded interacting protein 1	1.13	0.001	0.007
3058759	**SEMA3C**	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	1.12	0.002	0.010
2930753	**C6ORF72**	chromosome 6 open reading frame 72	1.12	0.001	0.008
3462816	**PHLDA1**	pleckstrin homology-like domain, family A, member 1	1.12	0.000	0.002
2911903	**PTP4A1**	protein tyrosine phosphatase type IVA, member 1	1.12	0.000	0.003
2766456	**UGDH**	UDP-glucose 6-dehydrogenase	1.12	0.000	0.005
3103187	**TERF1**	telomeric repeat binding factor (NIMA-interacting) 1	1.11	0.000	0.003
3082590	**LOC286161**	hypothetical protein LOC286161	1.11	0.011	0.029
3429312	**HSP90B1**	heat shock protein 90kDa beta (Grp94), member 1	1.11	0.001	0.008
2714818	**CRIPAK**	cysteine-rich PAK1 inhibitor	1.11	0.003	0.015
2945677	**C6ORF62**	chromosome 6 open reading frame 62	1.11	0.000	0.004
3434393	**DYNLL1**	dynein, light chain, LC8-type 1	1.11	0.004	0.018
2911372	**BAG2**	BCL2-associated athanogene 2	1.11	0.000	0.001
3942648	**TUG1**	taurine upregulated 1 (non-protein coding)	1.11	0.000	0.006
3464747	**KITLG**	KIT ligand	1.10	0.000	0.004
3344990	**PANX1**	pannexin 1	1.10	0.000	0.001
3061651	**BET1**	blocked early in transport 1 homolog (S. cerevisiae)	1.10	0.000	0.004
3624697	**ARPP19**	cAMP-regulated phosphoprotein, 19kDa	1.10	0.001	0.010
2712632	**TFRC**	transferrin receptor (p90, CD71)	1.10	0.000	0.004
2876257	**SAR1B**	SAR1 homolog B (S. cerevisiae)	1.09	0.000	0.004
2336271	**BTF3L4**	basic transcription factor 3-like 4	1.09	0.001	0.009
3362934	**ZBED5**	zinc finger, BED-type containing 5	1.09	0.000	0.004
2643157	**CDV3**	CDV3 homolog (mouse)	1.09	0.000	0.002
3764738	**SKA2**	spindle and kinetochore associated complex subunit 2	1.09	0.002	0.010
2847967	**SEMA5A**	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	1.08	0.002	0.010
2921374	**RPF2**	ribosome production factor 2 homolog (S. cerevisiae)	1.08	0.008	0.024
3301857	**TM9SF3**	transmembrane 9 superfamily member 3	1.08	0.001	0.009
2815791	**HEXB**	hexosaminidase B (beta polypeptide)	1.08	0.000	0.001
3174816	**ANXA1**	annexin A1	1.07	0.000	0.006
3103523	**LY96**	lymphocyte antigen 96	1.07	0.000	0.002
2395177	**ERRFI1**	ERBB receptor feedback inhibitor 1	1.07	0.000	0.005
2693081	**ZNF148**	zinc finger protein 148	1.07	0.000	0.004
3002640	**EGFR**	epidermal growth factor receptor	1.07	0.000	0.001
2635641	**PVRL3**	poliovirus receptor-related 3	1.06	0.000	0.004
3764103	**SRSF1**	serine/arginine-rich splicing factor 1	1.06	0.000	0.004
2961317	**TMEM30A**	transmembrane protein 30A	1.06	0.000	0.006
2838598	**CCNG1**	cyclin G1	1.06	0.000	0.002
3107342	**PDP1**	pyruvate dehyrogenase phosphatase catalytic subunit 1	1.06	0.000	0.005
3623865	**SPPL2A**	signal peptide peptidase-like 2A	1.06	0.002	0.010
2551924	**CALM2**	calmodulin 2 (phosphorylase kinase, delta)	1.05	0.002	0.012
2813060	**PIK3R1**	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	1.05	0.000	0.006
3087167	**TUSC3**	tumor suppressor candidate 3	1.05	0.000	0.002
2492496	**NCRNA00152**	non-protein coding RNA 152	1.05	0.012	0.032
2559807	**MOBKL1B**	MOB1, Mps One Binder kinase activator-like 1B (yeast)	1.05	0.000	0.004
3610110	**NR2F2**	nuclear receptor subfamily 2, group F, member 2	1.05	0.001	0.009
3012019	**CLDN12**	claudin 12	1.04	0.000	0.003
3971877	**EIF2S3**	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	1.04	0.000	0.003
2369796	**TOR1AIP1**	torsin A interacting protein 1	1.04	0.000	0.001
2522439	**BZW1**	basic leucine zipper and W2 domains 1	1.04	0.002	0.013

3150455	**TNFRSF11B**	tumor necrosis factor receptor superfamily, member 11b	1.04	0.002	0.013
3771800	**SRSF2**	serine/arginine-rich splicing factor 2	1.04	0.000	0.002
3210808	**GNAQ**	guanine nucleotide binding protein (G protein), q polypeptide	1.04	0.001	0.007
3322048	**C11ORF58**	chromosome 11 open reading frame 58	1.04	0.006	0.022
2852333	**ZFR**	zinc finger RNA binding protein	1.04	0.000	0.002
2978026	**FBXO30**	F-box protein 30	1.03	0.000	0.003
3938817	**BMS1**	BMS1 homolog, ribosome assembly protein (yeast)	1.03	0.004	0.016
3904226	**RBM39**	RNA binding motif protein 39	1.03	0.001	0.007
2975680	**BCLAF1**	BCL2-associated transcription factor 1	1.03	0.000	0.006
3766893	**DDX5**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	1.03	0.000	0.005
3209623	**ZFAND5**	zinc finger, AN1-type domain 5	1.03	0.002	0.013
3471374	**PPP1CC**	protein phosphatase 1, catalytic subunit, gamma isozyme	1.03	0.001	0.007
2910364	**TMEM14A**	transmembrane protein 14A	1.03	0.000	0.004
3256560	**MINPP1**	multiple inositol-polyphosphate phosphatase 1	1.03	0.000	0.005
2367154	**BAT2L2**	HLA-B associated transcript 2-like 2	1.03	0.000	0.004
3012978	**GNG11**	guanine nucleotide binding protein (G protein), gamma 11	1.03	0.000	0.004
3393946	**DDX6**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	1.03	0.000	0.005
2522094	**SPATS2L**	spermatogenesis associated, serine-rich 2-like	1.02	0.000	0.004
2677653	**C3ORF63**	chromosome 3 open reading frame 63	1.02	0.000	0.005
2820925	**RHOBTB3**	Rho-related BTB domain containing 3	1.02	0.001	0.007
2649723	**MFSD1**	major facilitator superfamily domain containing 1	1.02	0.000	0.004
3751463	**NUFIP2**	nuclear fragile X mental retardation protein interacting protein 2	1.02	0.000	0.006
3425134	**TMTC3**	transmembrane and tetratricopeptide repeat containing 3	1.02	0.002	0.011
2707764	**DCUN1D1**	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	1.02	0.000	0.006
3535515	**FRMD6**	FERM domain containing 6	1.02	0.003	0.014
3580179	**HSP90AA1**	heat shock protein 90kDa alpha (cytosolic), class A member 1	1.02	0.004	0.016
2590736	**NCKAP1**	NCK-associated protein 1	1.02	0.000	0.003
2806468	**IL7R**	interleukin 7 receptor	1.02	0.002	0.011
2518428	**SSFA2**	sperm specific antigen 2	1.02	0.000	0.001
2463864	**CEP170**	centrosomal protein 170kDa	1.01	0.000	0.004
2548699	**CYP1B1**	cytochrome P450, family 1, subfamily B, polypeptide 1	1.01	0.015	0.036
2732273	**SEPT11**	septin 11	1.01	0.002	0.011
2331822	**ZMPSTE24**	zinc metallopeptidase (STE24 homolog, S. cerevisiae)	1.01	0.000	0.003
2958325	**DST**	dystonin	1.01	0.000	0.006
2738664	**SGMS2**	sphingomyelin synthase 2	1.01	0.000	0.004
3764066	**VEZF1**	vascular endothelial zinc finger 1	1.01	0.000	0.003
2378256	**SYT14**	synaptotagmin XIV	1.01	0.000	0.006
2500919	**SLC20A1**	solute carrier family 20 (phosphate transporter), member 1	1.00	0.003	0.014
3538470	**C14ORF135**	chromosome 14 open reading frame 135	1.00	0.001	0.009
3074640	**LUZP6**	leucine zipper protein 6	1.00	0.000	0.005
3445908	**EPS8**	epidermal growth factor receptor pathway substrate 8	1.00	0.000	0.006
3185063	**UGCG**	UDP-glucose ceramide glucosyltransferase	1.00	0.002	0.012
2812435	**ERBB2IP**	erbb2 interacting protein	1.00	0.000	0.006
2325593	**CLIC4**	chloride intracellular channel 4	1.00	0.004	0.017
2971801	**MAN1A1**	mannosidase, alpha, class 1A, member 1	1.00	0.000	0.002
3519309	**SPRY2**	sprouty homolog 2 (Drosophila)	1.00	0.001	0.007
2879312	**NR3C1**	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	1.00	0.000	0.004
3969855	**CA5B**	carbonic anhydrase VB, mitochondrial	1.00	0.001	0.007
3320944	**TEAD1**	TEA domain family member 1 (SV40 transcriptional enhancer factor)	1.00	0.000	0.005
2417390	**WLS**	wntless homolog (Drosophila)	0.99	0.019	0.041
3298977	**GLUD1**	glutamate dehydrogenase 1	0.99	0.000	0.006
2924898	**RNF146**	ring finger protein 146	0.99	0.002	0.011
2569908	**SEPT10**	septin 10	0.99	0.000	0.004
3988740	**PGRMC1**	progesterone receptor membrane component 1	0.99	0.000	0.006
2550522	**ZFP36L2**	zinc finger protein 36, C3H type-like 2	0.99	0.000	0.001
3105904	**CPNE3**	copine III	0.99	0.000	0.003
2417272	**GNG12**	guanine nucleotide binding protein (G protein), gamma 12	0.98	0.000	0.004
2869880	**EFNA5**	ephrin-A5	0.98	0.003	0.015
3283991	**KIF5B**	kinesin family member 5B	0.98	0.002	0.011
3628469	**RPS27L**	ribosomal protein S27-like	0.98	0.017	0.038
3364759	**PIK3C2A**	phosphoinositide-3-kinase, class 2, alpha polypeptide	0.98	0.005	0.019
3692895	**NUDT21**	nudix (nucleoside diphosphate linked moiety X)-type motif 21	0.98	0.000	0.003
2915828	**NT5E**	5'-nucleotidase, ecto (CD73)	0.98	0.000	0.003
2821761	**RGMB**	RGM domain family, member B	0.98	0.000	0.003
3143660	**MMP16**	matrix metallopeptidase 16 (membrane-inserted)	0.97	0.003	0.015
3507798	**UBL3**	ubiquitin-like 3	0.97	0.003	0.013
3299585	**LIPA**	lipase A, lysosomal acid, cholesterol esterase	0.97	0.001	0.007
3589141	**SPRED1**	sprouty-related, EVH1 domain containing 1	0.97	0.000	0.002
2588066	**ATF2**	activating transcription factor 2	0.97	0.000	0.005

2844203	**CANX**	calnexin	0.97	0.000	0.005
2997097	**SEPT7**	septin 7	0.97	0.001	0.008
3066818	**NAMPT**	nicotinamide phosphoribosyltransferase	0.97	0.004	0.016
3024275	**MKLN1**	muskelin 1, intracellular mediator containing kelch motifs	0.96	0.000	0.003
2659560	**PIGX**	phosphatidylinositol glycan anchor biosynthesis, class X	0.96	0.001	0.009
2815965	**HMGCR**	3-hydroxy-3-methylglutaryl-CoA reductase	0.96	0.000	0.005
3218067	**MRPL50**	mitochondrial ribosomal protein L50	0.96	0.000	0.006
2642887	**CCRL1**	chemokine (C-C motif) receptor-like 1	0.96	0.010	0.028
3020273	**CAV2**	caveolin 2	0.96	0.000	0.004
2684187	**GBE1**	glucan (1,4-alpha-), branching enzyme 1	0.96	0.000	0.005
3325680	**EIF3M**	eukaryotic translation initiation factor 3, subunit M	0.95	0.001	0.006
3178416	**SPIN1**	spindlin 1	0.95	0.000	0.004
2459173	**PRO2012**	hypothetical protein PRO2012	0.95	0.004	0.016
3626555	**ADAM10**	ADAM metallopeptidase domain 10	0.95	0.002	0.011
2548617	**CDC42EP3**	CDC42 effector protein (Rho GTPase binding) 3	0.95	0.001	0.010
3623424	**COPS2**	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	0.95	0.000	0.004
3452323	**SLC38A2**	solute carrier family 38, member 2	0.95	0.000	0.006
3565361	**GMFB**	glia maturation factor, beta	0.95	0.002	0.010
2593159	**STK17B**	serine/threonine kinase 17b	0.95	0.000	0.005
2649113	**TIPARP**	TCDD-inducible poly(ADP-ribose) polymerase	0.95	0.001	0.008
2819044	**RASA1**	RAS p21 protein activator (GTPase activating protein) 1	0.95	0.001	0.007
3716579	**LRRC37BP1**	leucine rich repeat containing 37B pseudogene 1	0.95	0.000	0.005
3427098	**ELK3**	ELK3, ETS-domain protein (SRF accessory protein 2)	0.95	0.000	0.003
2979056	**NUP43**	nucleoporin 43kDa	0.94	0.000	0.006
2706297	**TBL1XR1**	transducin (beta)-like 1 X-linked receptor 1	0.94	0.002	0.010
3886639	**YWHAB**	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	0.94	0.000	0.005
2423907	**F3**	coagulation factor III (thromboplastin, tissue factor)	0.94	0.008	0.025
2809831	**GPX8**	glutathione peroxidase 8 (putative)	0.94	0.000	0.006
3402315	**CD9**	CD9 molecule	0.94	0.009	0.027
3566304	**EXOC5**	exocyst complex component 5	0.94	0.000	0.005
3252036	**PLAU**	plasminogen activator, urokinase	0.94	0.000	0.003
3304624	**NT5C2**	5'-nucleotidase, cytosolic II	0.94	0.001	0.009
3628923	**FAM96A**	family with sequence similarity 96, member A	0.94	0.002	0.010
3223872	**RAB14**	RAB14, member RAS oncogene family	0.94	0.001	0.007
2835960	**G3BP1**	GTPase activating protein (SH3 domain) binding protein 1	0.94	0.000	0.005
3247818	**BICC1**	bicaudal C homolog 1 (Drosophila)	0.94	0.001	0.008
2866704	**ARRDC3**	arrestin domain containing 3	0.94	0.001	0.008
2774971	**ANTXR2**	anthrax toxin receptor 2	0.93	0.000	0.005
2687739	**CD47**	CD47 molecule	0.93	0.000	0.002
2677356	**WNT5A**	wingless-type MMTV integration site family, member 5A	0.93	0.005	0.019
3075531	**ZC3HAV1L**	zinc finger CCCH-type, antiviral 1-like	0.93	0.001	0.008
2778856	**TSPAN5**	tetraspanin 5	0.93	0.000	0.002
3130161	**GSR**	glutathione reductase	0.93	0.000	0.006
2697792	**COPB2**	coatomer protein complex, subunit beta 2 (beta prime)	0.93	0.000	0.004
2791197	**PDGFC**	platelet derived growth factor C	0.93	0.003	0.014
3996755	**BRCC3**	BRCA1/BRCA2-containing complex, subunit 3	0.93	0.001	0.010
3139882	**TRAM1**	translocation associated membrane protein 1	0.93	0.000	0.005
3463571	**PPP1R12A**	protein phosphatase 1, regulatory (inhibitor) subunit 12A	0.93	0.002	0.013
2875555	**AFF4**	AF4/FMR2 family, member 4	0.93	0.000	0.002
2520533	**OBFC2A**	oligonucleotide/oligosaccharide-binding fold containing 2A	0.93	0.001	0.007
3927480	**ADAMTS5**	ADAM metallopeptidase with thrombospondin type 1 motif, 5	0.93	0.014	0.034
2601648	**DOCK10**	dedicator of cytokinesis 10	0.93	0.000	0.003
2870889	**C5ORF13**	chromosome 5 open reading frame 13	0.92	0.012	0.031
2810458	**GPBP1**	GC-rich promoter binding protein 1	0.92	0.000	0.005
3885464	**TOP1**	topoisomerase (DNA) I	0.92	0.000	0.004
2731831	**USO1**	USO1 vesicle docking protein homolog (yeast)	0.92	0.000	0.005
3363923	**COPB1**	coatomer protein complex, subunit beta 1	0.92	0.001	0.008
2638962	**DTX3L**	deltex 3-like (Drosophila)	0.92	0.009	0.026
2349043	**SLC30A7**	solute carrier family 30 (zinc transporter), member 7	0.92	0.000	0.002
3505781	**PARP4**	poly (ADP-ribose) polymerase family, member 4	0.92	0.000	0.003
2332566	**PPCS**	phosphopantothenoylcysteine synthetase	0.92	0.000	0.002
2375810	**ZC3H11A**	zinc finger CCCH-type containing 11A	0.92	0.004	0.017
2602901	**TRIP12**	thyroid hormone receptor interactor 12	0.92	0.000	0.003
3020444	**CAPZA2**	capping protein (actin filament) muscle Z-line, alpha 2	0.92	0.000	0.005
2696764	**MSL2**	male-specific lethal 2 homolog (Drosophila)	0.92	0.000	0.004
3109191	**POLR2K**	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	0.92	0.004	0.018
3284302	**NRP1**	neuropilin 1	0.92	0.000	0.005
3429754	**KIAA1033**	KIAA1033	0.92	0.001	0.009
2830861	**EGR1**	early growth response 1	0.92	0.005	0.018

3146433	**COX6C**	cytochrome c oxidase subunit VIc	0.92	0.008	0.025
3388631	**TMEM123**	transmembrane protein 123	0.91	0.007	0.022
2364155	**UHMK1**	U2AF homology motif (UHM) kinase 1	0.91	0.000	0.003
2727226	**PDGFRA**	platelet-derived growth factor receptor, alpha polypeptide	0.91	0.000	0.004
3618333	**MEIS2**	Meis homeobox 2	0.91	0.000	0.005
3638607	**ANPEP**	alanyl (membrane) aminopeptidase	0.91	0.000	0.002
3982811	**SH3BGRL**	SH3 domain binding glutamic acid-rich protein like	0.91	0.003	0.014
3430389	**C12ORF23**	chromosome 12 open reading frame 23	0.91	0.001	0.007
3631397	**UACA**	uveal autoantigen with coiled-coil domains and ankyrin repeats	0.91	0.000	0.006
2345929	**LRRC8C**	leucine rich repeat containing 8 family, member C	0.91	0.001	0.009
3153428	**ASAP1**	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	0.90	0.000	0.005
3300350	**IDE**	insulin-degrading enzyme	0.90	0.001	0.007
3763270	**MMD**	monocyte to macrophage differentiation-associated	0.90	0.020	0.042
3126191	**PSD3**	pleckstrin and Sec7 domain containing 3	0.90	0.002	0.011
2973376	**PTPRK**	protein tyrosine phosphatase, receptor type, K	0.90	0.000	0.004
3212919	**ISCA1**	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	0.90	0.005	0.019
3352503	**ARHGEF12**	Rho guanine nucleotide exchange factor (GEF) 12	0.90	0.000	0.004
3311832	**ADAM12**	ADAM metallopeptidase domain 12	0.90	0.003	0.014
4019849	**LAMP2**	lysosomal-associated membrane protein 2	0.90	0.000	0.004
2588827	**NFE2L2**	nuclear factor (erythroid-derived 2)-like 2	0.90	0.000	0.005
3513883	**KPNA3**	karyopherin alpha 3 (importin alpha 4)	0.90	0.001	0.009
2905118	**SRSF3**	serine/arginine-rich splicing factor 3	0.90	0.001	0.010
2958670	**RAB23**	RAB23, member RAS oncogene family	0.89	0.001	0.007
3066751	**SYPL1**	synaptophysin-like 1	0.89	0.000	0.003
2742109	**FGF2**	fibroblast growth factor 2 (basic)	0.89	0.016	0.037
2458082	**WDR26**	WD repeat domain 26	0.89	0.000	0.003
3809826	**ATP8B1**	ATPase, aminophospholipid transporter, class I, type 8B, member 1	0.89	0.001	0.010
2361154	**SYT11**	synaptotagmin XI	0.89	0.001	0.010
2526980	**XRCC5**	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	0.89	0.000	0.003
2821194	**CAST**	calpastatin	0.89	0.000	0.006
2518583	**DNAJC10**	DnaJ (Hsp40) homolog, subfamily C, member 10	0.89	0.000	0.006
2342391	**TYW3**	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	0.89	0.000	0.002
2520429	**MYO1B**	myosin IB	0.89	0.002	0.011
3214668	**IARS**	isoleucyl-tRNA synthetase	0.89	0.001	0.007
2548402	**EIF2AK2**	eukaryotic translation initiation factor 2-alpha kinase 2	0.89	0.007	0.023
2648141	**MBNL1**	muscleblind-like (Drosophila)	0.88	0.000	0.005
2915133	**TPBG**	trophoblast glycoprotein	0.88	0.000	0.001
2664452	**ANKRD28**	ankyrin repeat domain 28	0.88	0.001	0.008
3408733	**RASSF8**	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	0.88	0.000	0.003
3620590	**ZFP106**	zinc finger protein 106 homolog (mouse)	0.88	0.000	0.006
2536298	**SEPT2**	septin 2	0.88	0.000	0.005
3407824	**GOLT1B**	golgi transport 1B	0.88	0.005	0.019
2994342	**TAX1BP1**	Tax1 (human T-cell leukemia virus type I) binding protein 1	0.88	0.001	0.008
2401275	**HNRNPR**	heterogeneous nuclear ribonucleoprotein R	0.88	0.000	0.006
3760625	**CDC27**	cell division cycle 27 homolog (S. cerevisiae)	0.88	0.001	0.007
3689922	**VPS35**	vacuolar protein sorting 35 homolog (S. cerevisiae)	0.88	0.000	0.006
2871821	**TMED7**	transmembrane emp24 protein transport domain containing 7	0.88	0.000	0.004
2390307	**OR2L3**	olfactory receptor, family 2, subfamily L, member 3	0.88	0.003	0.015
2823551	**MAN2A1**	mannosidase, alpha, class 2A, member 1	0.88	0.000	0.006
3446868	**LDHB**	lactate dehydrogenase B	0.88	0.000	0.005
3603408	**PSMA4**	proteasome (prosome, macropain) subunit, alpha type, 4	0.88	0.002	0.011
3327906	**API5**	apoptosis inhibitor 5	0.87	0.001	0.008
2997952	**STARD3NL**	STARD3 N-terminal like	0.87	0.000	0.004
3608113	**IQGAP1**	IQ motif containing GTPase activating protein 1	0.87	0.001	0.008
2435383	**S100A10**	S100 calcium binding protein A10	0.87	0.000	0.004
3100166	**RAB2A**	RAB2A, member RAS oncogene family	0.87	0.003	0.013
2839671	**RARS**	arginyl-tRNA synthetase	0.87	0.000	0.003
3220384	**LPAR1**	lysophosphatidic acid receptor 1	0.87	0.001	0.007
2769539	**CHIC2**	cysteine-rich hydrophobic domain 2	0.87	0.001	0.009
2870397	**PJA2**	praja ring finger 2	0.87	0.001	0.007
2588319	**KIAA1715**	KIAA1715	0.87	0.003	0.013
2883609	**CLINT1**	clathrin interactor 1	0.87	0.000	0.004
2429277	**CSDE1**	cold shock domain containing E1, RNA-binding	0.87	0.001	0.007
3510450	**LHFP**	lipoma HMGIC fusion partner	0.86	0.002	0.013
2700404	**WWTR1**	WW domain containing transcription regulator 1	0.86	0.000	0.002
2340078	**CACHD1**	cache domain containing 1	0.86	0.001	0.008
3666779	**NFAT5**	nuclear factor of activated T-cells 5, tonicity-responsive	0.86	0.000	0.005
2555490	**XPO1**	exportin 1 (CRM1 homolog, yeast)	0.86	0.000	0.005
3984779	**HNRNPH2**	heterogeneous nuclear ribonucleoprotein H2 (H')	0.86	0.001	0.008

3909354	**ADNP**	activity-dependent neuroprotector homeobox	0.86	0.000	0.004
2328465	**KHDRBS1**	KH domain containing, RNA binding, signal transduction associated 1	0.86	0.000	0.002
2462511	**HEATR1**	HEAT repeat containing 1	0.86	0.000	0.003
3409006	**MED21**	mediator complex subunit 21	0.86	0.003	0.013
2319340	**SLC25A33**	solute carrier family 25, member 33	0.86	0.002	0.010
2867693	**TTC37**	tetratricopeptide repeat domain 37	0.86	0.000	0.006
3264004	**SHOC2**	soc-2 suppressor of clear homolog (C. elegans)	0.86	0.001	0.009
3072435	**TMEM209**	transmembrane protein 209	0.85	0.000	0.006
2366028	**DCAF6**	DDB1 and CUL4 associated factor 6	0.85	0.001	0.008
2913694	**CD109**	CD109 molecule	0.85	0.003	0.013
3099750	**SDCBP**	syndecan binding protein (syntenin)	0.85	0.001	0.006
3768412	**SLC16A6**	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	0.85	0.012	0.032
3602723	**RCN2**	reticulocalbin 2, EF-hand calcium binding domain	0.85	0.010	0.027
2973694	**ARHGAP18**	Rho GTPase activating protein 18	0.85	0.000	0.001
2772968	**COX18**	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	0.85	0.000	0.005
3282213	**YME1L1**	YME1-like 1 (S. cerevisiae)	0.85	0.000	0.005
3374746	**PATL1**	protein associated with topoisomerase II homolog 1 (yeast)	0.85	0.000	0.005
2558511	**TIA1**	TIA1 cytotoxic granule-associated RNA binding protein	0.85	0.000	0.005
2556529	**SERTAD2**	SERTA domain containing 2	0.85	0.001	0.008
3014904	**ZNF655**	zinc finger protein 655	0.85	0.000	0.003
2779638	**PPP3CA**	protein phosphatase 3, catalytic subunit, alpha isozyme	0.85	0.000	0.004
3197318	**AK3**	adenylate kinase 3	0.84	0.001	0.008
4004819	**DYNLT3**	dynein, light chain, Tctex-type 3	0.84	0.003	0.014
3189311	**PBX3**	pre-B-cell leukemia homeobox 3	0.84	0.001	0.007
2377427	**CD46**	CD46 molecule, complement regulatory protein	0.84	0.001	0.007
2501697	**ACTR3**	ARP3 actin-related protein 3 homolog (yeast)	0.84	0.004	0.016
3529082	**PABPN1**	poly(A) binding protein, nuclear 1	0.84	0.000	0.004
2972310	**SERINC1**	serine incorporator 1	0.84	0.001	0.009
2960955	**SLC17A5**	solute carrier family 17 (anion/sugar transporter), member 5	0.84	0.001	0.008
2374345	**CAMSAP1L1**	calmodulin regulated spectrin-associated protein 1-like 1	0.84	0.000	0.005
3553607	**EIF5**	eukaryotic translation initiation factor 5	0.84	0.000	0.006
3886050	**SRSF6**	serine/arginine-rich splicing factor 6	0.83	0.001	0.007
2766492	**C4ORF34**	chromosome 4 open reading frame 34	0.83	0.003	0.015
3888133	**CSE1L**	CSE1 chromosome segregation 1-like (yeast)	0.83	0.002	0.010
2353881	**MAN1A2**	mannosidase, alpha, class 1A, member 2	0.83	0.000	0.004
3134511	**SNAI2**	snail homolog 2 (Drosophila)	0.83	0.005	0.019
2730673	**MOBKL1A**	MOB1, Mps One Binder kinase activator-like 1A (yeast)	0.83	0.001	0.009
3508330	**HSPH1**	heat shock 105kDa/110kDa protein 1	0.83	0.000	0.004
3061438	**SAMD9**	sterile alpha motif domain containing 9	0.83	0.008	0.025
2829416	**SEC24A**	SEC24 family, member A (S. cerevisiae)	0.83	0.000	0.003
3152220	**KIAA0196**	KIAA0196	0.83	0.000	0.003
2553282	**PSME4**	proteasome (prosome, macropain) activator subunit 4	0.83	0.000	0.004
2879105	**SPRY4**	sprouty homolog 4 (Drosophila)	0.83	0.000	0.005
2657250	**LPP**	LIM domain containing preferred translocation partner in lipoma	0.83	0.000	0.006
3306516	**SMNDC1**	survival motor neuron domain containing 1	0.83	0.000	0.004
2809399	**FST**	follistatin	0.83	0.011	0.030
2831209	**PAIP2**	poly(A) binding protein interacting protein 2	0.83	0.000	0.005
2615600	**STT3B**	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	0.83	0.001	0.009
2766893	**APBB2**	amyloid beta (A4) precursor protein-binding, family B, member 2	0.82	0.000	0.006
3039177	**ETV1**	ets variant 1	0.82	0.002	0.012
2922215	**MARCKS**	myristoylated alanine-rich protein kinase C substrate	0.82	0.003	0.016
2636185	**SLC35A5**	solute carrier family 35, member A5	0.82	0.001	0.007
2875929	**C5ORF15**	chromosome 5 open reading frame 15	0.82	0.000	0.004
2683763	**ROBO1**	roundabout, axon guidance receptor, homolog 1 (Drosophila)	0.82	0.002	0.011
4054117	**TAF13**	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	0.82	0.023	0.046
3625674	**RFX7**	regulatory factor X, 7	0.82	0.000	0.003
7385547	**CCL2**	chemokine (C-C motif) ligand 2	0.82	0.022	0.044
3136782	**NSMAF**	neutral sphingomyelinase (N-SMase) activation associated factor	0.82	0.000	0.005
2515240	**CYBRD1**	cytochrome b reductase 1	0.82	0.003	0.015
2407439	**SF3A3**	splicing factor 3a, subunit 3, 60kDa	0.82	0.002	0.011
3281621	**ARHGAP21**	Rho GTPase activating protein 21	0.82	0.002	0.010
2408855	**FOXJ3**	forkhead box J3	0.82	0.000	0.004
3448975	**ERGIC2**	ERGIC and golgi 2	0.82	0.001	0.008
3346584	**BIRC2**	baculoviral IAP repeat-containing 2	0.82	0.001	0.010
2943808	**NUP153**	nucleoporin 153kDa	0.82	0.001	0.008
3560617	**SNX6**	sorting nexin 6	0.82	0.014	0.034
2726323	**SLAIN2**	SLAIN motif family, member 2	0.82	0.000	0.005

3659858	**TMEM188**	transmembrane protein 188	0.82	0.002	0.013
3542689	**PCNX**	pecanex homolog (Drosophila)	0.82	0.001	0.009
3560673	**CFL2**	cofilin 2 (muscle)	0.81	0.004	0.016
3110317	**CTHRC1**	collagen triple helix repeat containing 1	0.81	0.010	0.027
3351315	**UBE4A**	ubiquitination factor E4A (UFD2 homolog, yeast)	0.81	0.000	0.005
2942504	**RANBP9**	RAN binding protein 9	0.81	0.001	0.008
3961664	**ST13**	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	0.81	0.000	0.003
3237088	**STAM**	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	0.81	0.000	0.005
3595096	**TCF12**	transcription factor 12	0.81	0.001	0.009
3043936	**FKBP14**	FK506 binding protein 14, 22 kDa	0.81	0.000	0.005
2412529	**NRD1**	nardilysin (N-arginine dibasic convertase)	0.81	0.000	0.004
2642791	**DNAJC13**	DnaJ (Hsp40) homolog, subfamily C, member 13	0.81	0.001	0.008
2628682	**ARL6IP5**	ADP-ribosylation-like factor 6 interacting protein 5	0.81	0.001	0.007
3468103	**GNPTAB**	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	0.81	0.001	0.008
3923426	**AGPAT3**	1-acylglycerol-3-phosphate O-acyltransferase 3	0.81	0.001	0.007
4018729	**IL13RA2**	interleukin 13 receptor, alpha 2	0.81	0.024	0.047
3809324	**TXNL1**	thioredoxin-like 1	0.81	0.000	0.003
3511031	**ELF1**	E74-like factor 1 (ets domain transcription factor)	0.81	0.000	0.004
2601995	**IRS1**	insulin receptor substrate 1	0.81	0.000	0.001
2968054	**SEC63**	SEC63 homolog (S. cerevisiae)	0.81	0.001	0.010
3061805	**SGCE**	sarcoglycan, epsilon	0.81	0.001	0.009
3999395	**MID1**	midline 1 (Opitz/BBB syndrome)	0.80	0.001	0.007
3020343	**MET**	met proto-oncogene (hepatocyte growth factor receptor)	0.80	0.006	0.020
3114358	**FAM91A1**	family with sequence similarity 91, member A1	0.80	0.000	0.006
2370991	**DHX9**	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0.80	0.000	0.005
3795733	**COLEC12**	collectin sub-family member 12	0.80	0.018	0.040
2512701	**PSMD14**	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	0.80	0.000	0.004
3422269	**RAB21**	RAB21, member RAS oncogene family	0.80	0.005	0.019
2773907	**SDAD1**	SDA1 domain containing 1	0.80	0.000	0.006
2666904	**SLC4A7**	solute carrier family 4, sodium bicarbonate cotransporter, member 7	0.80	0.000	0.006
2701927	**SLC33A1**	solute carrier family 33 (acetyl-CoA transporter), member 1	0.80	0.000	0.004
3498502	**TM9SF2**	transmembrane 9 superfamily member 2	0.80	0.005	0.018
3041294	**FAM126A**	family with sequence similarity 126, member A	0.80	0.002	0.012
2966636	**ASCC3**	activating signal cointegrator 1 complex subunit 3	0.80	0.001	0.007
2746024	**ABCE1**	ATP-binding cassette, sub-family E (OABP), member 1	0.80	0.000	0.006
3810472	**LMAN1**	lectin, mannose-binding, 1	0.80	0.002	0.011
3013255	**PEG10**	paternally expressed 10	0.80	0.001	0.010
2705748	**NCEH1**	neutral cholesterol ester hydrolase 1	0.80	0.000	0.006
3263555	**ADD3**	adducin 3 (gamma)	0.80	0.001	0.008
3248999	**REEP3**	receptor accessory protein 3	0.80	0.004	0.017
2591421	**TFPI**	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	0.80	0.001	0.010
3060051	**C7ORF23**	chromosome 7 open reading frame 23	0.80	0.001	0.008
3728964	**PRR11**	proline rich 11	0.80	0.008	0.025
3541137	**EIF2S1**	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	0.80	0.003	0.015
3421300	**MDM2**	Mdm2 p53 binding protein homolog (mouse)	0.80	0.000	0.006
2990342	**TMEM106B**	transmembrane protein 106B	0.79	0.000	0.004
2636589	**ATP6V1A**	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	0.79	0.000	0.002
2341565	**SRSF11**	serine/arginine-rich splicing factor 11	0.79	0.001	0.008
2651782	**SEC62**	SEC62 homolog (S. cerevisiae)	0.79	0.000	0.006
3765689	**MED13**	mediator complex subunit 13	0.79	0.001	0.008
3405587	**GPRC5A**	G protein-coupled receptor, family C, group 5, member A	0.79	0.013	0.033
3913712	**YTHDF1**	YTH domain family, member 1	0.79	0.000	0.003
3801943	**ZNF521**	zinc finger protein 521	0.79	0.001	0.008
3429857	**C12ORF75**	chromosome 12 open reading frame 75	0.79	0.005	0.019
3590388	**NUSAP1**	nucleolar and spindle associated protein 1	0.79	0.016	0.036
3563922	**MAP4K5**	mitogen-activated protein kinase kinase kinase kinase 5	0.79	0.001	0.010
3017547	**MLL5**	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	0.79	0.000	0.005
3114832	**SQLE**	squalene epoxidase	0.79	0.001	0.010
4021149	**SMARCA1**	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	0.79	0.001	0.007
3033209	**INSIG1**	insulin induced gene 1	0.79	0.001	0.007
2614142	**NR1D2**	nuclear receptor subfamily 1, group D, member 2	0.79	0.002	0.013
2366156	**SFT2D2**	SFT2 domain containing 2	0.79	0.001	0.010
3597476	**RAB8B**	RAB8B, member RAS oncogene family	0.78	0.000	0.003
2682436	**RYBP**	RING1 and YY1 binding protein	0.78	0.000	0.006
2496727	**MAP4K4**	mitogen-activated protein kinase kinase kinase kinase 4	0.78	0.000	0.003
2414998	**MYSM1**	Myb-like, SWIRM and MPN domains 1	0.78	0.004	0.016

2601021	**FARSB**	phenylalanyl-tRNA synthetase, beta subunit	0.78	0.000	0.006
2551786	**MCFD2**	multiple coagulation factor deficiency 2	0.78	0.000	0.005
3061456	**SAMD9L**	sterile alpha motif domain containing 9-like	0.78	0.005	0.019
2366132	**TIPRL**	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	0.78	0.001	0.007
3421630	**CCT2**	chaperonin containing TCP1, subunit 2 (beta)	0.78	0.001	0.007
3058156	**TMEM60**	transmembrane protein 60	0.78	0.002	0.012
2970532	**HDAC2**	histone deacetylase 2	0.78	0.000	0.005
3041550	**TRA2A**	transformer 2 alpha homolog (Drosophila)	0.78	0.004	0.016
3503119	**ZNF828**	zinc finger protein 828	0.78	0.000	0.005
3731826	**PRKCA**	protein kinase C, alpha	0.78	0.001	0.009
3362719	**EIF4G2**	eukaryotic translation initiation factor 4 gamma, 2	0.78	0.001	0.008
3632492	**NPTN**	neuroplastin	0.78	0.003	0.015
3273484	**LARP4B**	La ribonucleoprotein domain family, member 4B	0.78	0.003	0.014
3419641	**SRGAP1**	SLIT-ROBO Rho GTPase activating protein 1	0.78	0.000	0.005
2364231	**DDR2**	discoidin domain receptor tyrosine kinase 2	0.78	0.001	0.008
2827388	**PRRC1**	proline-rich coiled-coil 1	0.77	0.000	0.006
2614120	**RPL15**	ribosomal protein L15	0.77	0.008	0.024
3809671	**NARS**	asparaginyl-tRNA synthetase	0.77	0.003	0.014
2581430	**STAM2**	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	0.77	0.000	0.006
2336497	**ZYG11B**	zyg-11 homolog B (C. elegans)	0.77	0.001	0.008
2555277	**USP34**	ubiquitin specific peptidase 34	0.77	0.001	0.007
2703217	**KPNA4**	karyopherin alpha 4 (importin alpha 3)	0.77	0.001	0.007
3894228	**CSNK2A1**	casein kinase 2, alpha 1 polypeptide	0.77	0.001	0.008
3075566	**ZC3HAV1**	zinc finger CCCH-type, antiviral 1	0.77	0.000	0.006
3717052	**NF1**	neurofibromin 1	0.77	0.000	0.006
3045739	**HERPUD2**	HERPUD family member 2	0.77	0.000	0.006
2728448	**POLR2B**	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	0.77	0.000	0.005
3247757	**UBE2D1**	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	0.77	0.001	0.007
2515369	**HAT1**	histone acetyltransferase 1	0.77	0.001	0.008
3451375	**PRICKLE1**	prickle homolog 1 (Drosophila)	0.77	0.017	0.038
2458289	**LBR**	lamin B receptor	0.77	0.001	0.008
2881554	**DCTN4**	dynactin 4 (p62)	0.77	0.000	0.004
2691014	**GSK3B**	glycogen synthase kinase 3 beta	0.77	0.001	0.007
3422231	**TMEM19**	transmembrane protein 19	0.77	0.002	0.012
2382360	**DEGS1**	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	0.77	0.002	0.011
3804195	**SLC39A6**	solute carrier family 39 (zinc transporter), member 6	0.77	0.001	0.010
2711034	**C3ORF59**	chromosome 3 open reading frame 59	0.77	0.002	0.013
2689208	**NAA50**	N(alpha)-acetyltransferase 50, NatE catalytic subunit	0.76	0.001	0.008
2726483	**OCIAD1**	OCIA domain containing 1	0.76	0.000	0.005
2877171	**FAM13B**	family with sequence similarity 13, member B	0.76	0.000	0.006
3097152	**MCM4**	minichromosome maintenance complex component 4	0.76	0.002	0.011
2732942	**BMP2K**	BMP2 inducible kinase	0.76	0.001	0.007
3724782	**KPNB1**	karyopherin (importin) beta 1	0.76	0.001	0.006
3136413	**IMPAD1**	inositol monophosphatase domain containing 1	0.76	0.001	0.010
3146012	**NIPAL2**	NIPA-like domain containing 2	0.76	0.002	0.012
2335986	**RNF11**	ring finger protein 11	0.76	0.004	0.017
2482230	**ERLEC1**	endoplasmic reticulum lectin 1	0.76	0.001	0.009
2800906	**MTRR**	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	0.76	0.000	0.003
3042610	**SKAP2**	src kinase associated phosphoprotein 2	0.76	0.000	0.003
2325251	**TCEB3**	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	0.76	0.000	0.003
3137530	**ASPH**	aspartate beta-hydroxylase	0.76	0.001	0.009
2648873	**GMPS**	guanine monphosphate synthetase	0.76	0.002	0.011
2807359	**OSMR**	oncostatin M receptor	0.76	0.003	0.015
3406589	**MGST1**	microsomal glutathione S-transferase 1	0.75	0.006	0.021
3150663	**TAF2**	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa	0.75	0.000	0.006
2523213	**BMPR2**	bone morphogenetic protein receptor, type II (serine/threonine kinase)	0.75	0.003	0.014
2507495	**UBXN4**	UBX domain protein 4	0.75	0.000	0.006
2782545	**CAMK2D**	calcium/calmodulin-dependent protein kinase II delta	0.75	0.002	0.011
2523045	**FZD7**	frizzled homolog 7 (Drosophila)	0.75	0.000	0.005
3303255	**ERLIN1**	ER lipid raft associated 1	0.75	0.015	0.035
2668021	**CMTM6**	CKLF-like MARVEL transmembrane domain containing 6	0.75	0.000	0.005
3536663	**MAPK1IP1L**	mitogen-activated protein kinase 1 interacting protein 1-like	0.75	0.001	0.009
2400322	**HP1BP3**	heterochromatin protein 1, binding protein 3	0.75	0.000	0.006
3959203	**RBFOX2**	RNA binding protein, fox-1 homolog (C. elegans) 2	0.75	0.000	0.006
3693673	**CNOT1**	CCR4-NOT transcription complex, subunit 1	0.75	0.000	0.006
3005956	**C7ORF42**	chromosome 7 open reading frame 42	0.75	0.000	0.004
3918959	**MRPS6**	mitochondrial ribosomal protein S6	0.75	0.000	0.005
3212294	**HNRNPK**	heterogeneous nuclear ribonucleoprotein K	0.75	0.000	0.005

3732885	**PRKAR1A**	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	0.75	0.001	0.009
3666732	**CYB5B**	cytochrome b5 type B (outer mitochondrial membrane)	0.75	0.002	0.011
2902574	**LY6G5B**	lymphocyte antigen 6 complex, locus G5B	0.75	0.000	0.005
4011096	**EDA2R**	ectodysplasin A2 receptor	0.75	0.001	0.007
2806091	**RAI14**	retinoic acid induced 14	0.75	0.001	0.008
3719702	**MRPL45**	mitochondrial ribosomal protein L45	0.75	0.000	0.005
2669157	**EPM2AIP1**	EPM2A (laforin) interacting protein 1	0.74	0.001	0.009
2822407	**PPIP5K2**	diphosphoinositol pentakisphosphate kinase 2	0.74	0.000	0.004
3662612	**RSPRY1**	ring finger and SPRY domain containing 1	0.74	0.000	0.005
2510884	**ARL6IP6**	ADP-ribosylation-like factor 6 interacting protein 6	0.74	0.008	0.025
2558045	**GFPT1**	glutamine--fructose-6-phosphate transaminase 1	0.74	0.003	0.015
3136178	**PLAG1**	pleiomorphic adenoma gene 1	0.74	0.005	0.019
2329341	**ZSCAN20**	zinc finger and SCAN domain containing 20	0.74	0.002	0.010
3887635	**NCOA3**	nuclear receptor coactivator 3	0.74	0.003	0.014
2616317	**PDCD6IP**	programmed cell death 6 interacting protein	0.74	0.000	0.006
3768015	**HELZ**	helicase with zinc finger	0.74	0.001	0.009
2722151	**RBPJ**	recombination signal binding protein for immunoglobulin kappa J region	0.74	0.001	0.009
3874751	**PRNP**	prion protein	0.74	0.002	0.011
2456849	**RAB3GAP2**	RAB3 GTPase activating protein subunit 2 (non-catalytic)	0.74	0.000	0.004
3960629	**DDX17**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	0.74	0.002	0.010
3680610	**GSPT1**	G1 to S phase transition 1	0.74	0.000	0.003
3328069	**HSD17B12**	hydroxysteroid (17-beta) dehydrogenase 12	0.74	0.002	0.010
2969677	**REV3L**	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	0.74	0.002	0.011
3228007	**SETX**	senataxin	0.74	0.002	0.010
2601544	**CUL3**	cullin 3	0.74	0.000	0.005
3948898	**LOC150381**	hypothetical LOC150381	0.74	0.000	0.002
3788302	**SMAD4**	SMAD family member 4	0.74	0.001	0.009
2830638	**KIF20A**	kinesin family member 20A	0.74	0.020	0.042
2457988	**ZNF706**	zinc finger protein 706	0.74	0.001	0.009
3454331	**LIMA1**	LIM domain and actin binding 1	0.74	0.010	0.028
3490655	**CKAP2**	cytoskeleton associated protein 2	0.73	0.016	0.037
2477203	**VIT**	vitrin	0.73	0.023	0.046
2550790	**LRPPRC**	leucine-rich PPR-motif containing	0.73	0.000	0.005
3275132	**GDI2**	GDP dissociation inhibitor 2	0.73	0.001	0.007
2457261	**DUSP10**	dual specificity phosphatase 10	0.73	0.012	0.032
3060245	**SLC25A40**	solute carrier family 25, member 40	0.73	0.007	0.023
3581221	**AHNAK2**	AHNAK nucleoprotein 2	0.73	0.011	0.029
3376155	**NXF1**	nuclear RNA export factor 1	0.73	0.000	0.002
3183111	**SLC44A1**	solute carrier family 44, member 1	0.73	0.003	0.015
2544179	**SF3B14**	splicing factor 3B, 14 kDa subunit	0.73	0.001	0.007
2725332	**TMEM33**	transmembrane protein 33	0.73	0.000	0.003
3435853	**TMED2**	transmembrane emp24 domain trafficking protein 2	0.73	0.004	0.016
3682135	**C16ORF63**	chromosome 16 open reading frame 63	0.73	0.002	0.012
3100909	**YTHDF3**	YTH domain family, member 3	0.73	0.000	0.006
3724698	**NPEPPS**	aminopeptidase puromycin sensitive	0.73	0.001	0.008
3742756	**DERL2**	Der1-like domain family, member 2	0.73	0.001	0.009
3390180	**KDELC2**	KDEL (Lys-Asp-Glu-Leu) containing 2	0.73	0.003	0.014
2840002	**CCDC99**	coiled-coil domain containing 99	0.72	0.016	0.036
3256279	**FAM35A**	family with sequence similarity 35, member A	0.72	0.000	0.003
2829542	**C5ORF24**	chromosome 5 open reading frame 24	0.72	0.003	0.015
2825907	**PRR16**	proline rich 16	0.72	0.001	0.007
3653317	**RBBP6**	retinoblastoma binding protein 6	0.72	0.000	0.005
2369557	**SOAT1**	sterol O-acyltransferase 1	0.72	0.001	0.008
3205506	**FBXO10**	F-box protein 10	0.72	0.001	0.007
2646327	**C3ORF58**	chromosome 3 open reading frame 58	0.72	0.000	0.003
2531522	**CAB39**	calcium binding protein 39	0.72	0.000	0.005
3539070	**HIF1A**	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	0.72	0.019	0.040
3339167	**FAM86C**	family with sequence similarity 86, member C	0.72	0.002	0.012
3466826	**CDK17**	cyclin-dependent kinase 17	0.72	0.000	0.003
2685304	**PROS1**	protein S (alpha)	0.72	0.002	0.011
2814756	**MAP1B**	microtubule-associated protein 1B	0.72	0.002	0.013
3672830	**MAP1LC3B**	microtubule-associated protein 1 light chain 3 beta	0.72	0.002	0.011
2584134	**FAP**	fibroblast activation protein, alpha	0.72	0.004	0.016
3290785	**CCDC6**	coiled-coil domain containing 6	0.72	0.001	0.009
3145149	**TP53INP1**	tumor protein p53 inducible nuclear protein 1	0.72	0.009	0.026
3017123	**PMPCB**	peptidase (mitochondrial processing) beta	0.72	0.000	0.005
4023274	**MMGT1**	membrane magnesium transporter 1	0.72	0.001	0.008
2442134	**TMCO1**	transmembrane and coiled-coil domains 1	0.72	0.001	0.010

2890148	**HNRNPH1**	heterogeneous nuclear ribonucleoprotein H1 (H)	0.72	0.002	0.012
3395464	**ASAM**	adipocyte-specific adhesion molecule	0.72	0.002	0.011
2719361	**CPEB2**	cytoplasmic polyadenylation element binding protein 2	0.71	0.000	0.002
2979679	**ZBTB2**	zinc finger and BTB domain containing 2	0.71	0.000	0.003
3497790	**IPO5**	importin 5	0.71	0.007	0.023
3537747	**PSMA3**	proteasome (prosome, macropain) subunit, alpha type, 3	0.71	0.005	0.020
2935475	**QKI**	quaking homolog, KH domain RNA binding (mouse)	0.71	0.005	0.018
2984573	**SFT2D1**	SFT2 domain containing 1	0.71	0.003	0.015
3971329	**MBTPS2**	membrane-bound transcription factor peptidase, site 2	0.71	0.000	0.006
2890413	**RNF130**	ring finger protein 130	0.71	0.003	0.014
3249788	**CCAR1**	cell division cycle and apoptosis regulator 1	0.71	0.000	0.004
2632051	**C3ORF38**	chromosome 3 open reading frame 38	0.71	0.001	0.007
2766588	**PDS5A**	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	0.71	0.001	0.007
3991698	**HPRT1**	hypoxanthine phosphoribosyltransferase 1	0.71	0.005	0.018
3561952	**SEC23A**	Sec23 homolog A (S. cerevisiae)	0.71	0.006	0.021
3402978	**DSTNP2**	destrin (actin depolymerizing factor) pseudogene 2	0.71	0.007	0.022
3653398	**TNRC6A**	trinucleotide repeat containing 6A	0.71	0.000	0.005
3387537	**MAML2**	mastermind-like 2 (Drosophila)	0.71	0.002	0.012
2504883	**UGGT1**	UDP-glucose glycoprotein glucosyltransferase 1	0.71	0.001	0.010
2556667	**RAB1A**	RAB1A, member RAS oncogene family	0.71	0.005	0.019
3405531	**DDX47**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	0.71	0.002	0.012
3362124	**TMEM9B**	TMEM9 domain family, member B	0.71	0.001	0.008
2475209	**PPP1CB**	protein phosphatase 1, catalytic subunit, beta isozyme	0.71	0.000	0.005
2531712	**PSMD1**	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	0.71	0.001	0.008
2817386	**PAPD4**	PAP associated domain containing 4	0.71	0.000	0.005
2394784	**NOL9**	nucleolar protein 9	0.71	0.000	0.004
2652410	**FNDC3B**	fibronectin type III domain containing 3B	0.71	0.002	0.012
3716664	**SUZ12P**	suppressor of zeste 12 homolog pseudogene	0.71	0.013	0.033
3489020	**RB1**	retinoblastoma 1	0.70	0.002	0.012
3564210	**PYGL**	phosphorylase, glycogen, liver	0.70	0.026	0.049
3661718	**LPCAT2**	lysophosphatidylcholine acyltransferase 2	0.70	0.012	0.031
2702154	**SSR3**	signal sequence receptor, gamma (translocon-associated protein gamma)	0.70	0.015	0.035
3352904	**SC5DL**	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	0.70	0.003	0.015
2968232	**SNX3**	sorting nexin 3	0.70	0.003	0.013
2734629	**PTPN13**	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	0.70	0.004	0.017
3802129	**SS18**	synovial sarcoma translocation, chromosome 18	0.70	0.002	0.011
3443891	**CLEC2B**	C-type lectin domain family 2, member B	0.70	0.013	0.033
2854737	**PRKAA1**	protein kinase, AMP-activated, alpha 1 catalytic subunit	0.70	0.000	0.005
2999485	**STK17A**	serine/threonine kinase 17a	0.70	0.005	0.018
3724197	**NSF**	N-ethylmaleimide-sensitive factor	0.70	0.001	0.008
2480619	**SOCS5**	suppressor of cytokine signaling 5	0.70	0.002	0.011
2403158	**AHDC1**	AT hook, DNA binding motif, containing 1	0.70	0.000	0.003
2603460	**NCL**	nucleolin	0.70	0.001	0.008
3538324	**JKAMP**	JNK1/MAPK8-associated membrane protein	0.70	0.002	0.011
3683037	**ARL6IP1**	ADP-ribosylation factor-like 6 interacting protein 1	0.70	0.012	0.031
3054165	**SBDS**	Shwachman-Bodian-Diamond syndrome	0.70	0.010	0.028
3690193	**ITFG1**	integrin alpha FG-GAP repeat containing 1	0.70	0.005	0.019
3497270	**DNAJC3**	DnaJ (Hsp40) homolog, subfamily C, member 3	0.70	0.002	0.013
3351531	**ARCN1**	archain 1	0.70	0.002	0.011
2932360	**RBM16**	RNA binding motif protein 16	0.69	0.000	0.004
2329752	**ZMYM4**	zinc finger, MYM-type 4	0.69	0.001	0.007
3535395	**TMX1**	thioredoxin-related transmembrane protein 1	0.69	0.001	0.009
3351359	**ATP5L**	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G	0.69	0.020	0.042
3901333	**CST4**	cystatin S	0.69	0.009	0.026
3042919	**HOXA9**	homeobox A9	0.69	0.000	0.004
3717635	**ZNF207**	zinc finger protein 207	0.69	0.001	0.009
3180263	**HIATL1**	hippocampus abundant transcript-like 1	0.69	0.003	0.014
2787459	**INPP4B**	inositol polyphosphate-4-phosphatase, type II, 105kDa	0.69	0.001	0.007
2531779	**ARMC9**	armadillo repeat containing 9	0.69	0.005	0.020
2989050	**RAC1**	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	0.69	0.001	0.007
3574207	**SEL1L**	sel-1 suppressor of lin-12-like (C. elegans)	0.69	0.003	0.015
3806913	**SMAD2**	SMAD family member 2	0.69	0.001	0.007
2434438	**MCL1**	myeloid cell leukemia sequence 1 (BCL2-related)	0.69	0.003	0.015
2613386	**RAB5A**	RAB5A, member RAS oncogene family	0.69	0.002	0.011
3502710	**TFDP1**	transcription factor Dp-1	0.69	0.002	0.013
2964771	**MAP3K7**	mitogen-activated protein kinase kinase kinase 7	0.69	0.000	0.005
3346453	**YAP1**	Yes-associated protein 1	0.69	0.000	0.005

2542816	**PUM2**	pumilio homolog 2 (Drosophila)	0.69	0.001	0.009
2727793	**TMEM165**	transmembrane protein 165	0.69	0.001	0.010
2774049	**SCARB2**	scavenger receptor class B, member 2	0.69	0.002	0.012
3042421	**HNRNPA2B1**	heterogeneous nuclear ribonucleoprotein A2/B1	0.69	0.003	0.015
2648378	**RAP2B**	RAP2B, member of RAS oncogene family	0.69	0.000	0.002
3129121	**CCDC25**	coiled-coil domain containing 25	0.69	0.000	0.005
3716048	**TAOK1**	TAO kinase 1	0.69	0.001	0.008
2714644	**C4ORF42**	chromosome 4 open reading frame 42	0.69	0.000	0.006
3148582	**EIF3E**	eukaryotic translation initiation factor 3, subunit E	0.69	0.000	0.005
2363919	**ATF6**	activating transcription factor 6	0.68	0.000	0.005
3040363	**TWIST1**	twist homolog 1 (Drosophila)	0.68	0.004	0.017
2708922	**IGF2BP2**	insulin-like growth factor 2 mRNA binding protein 2	0.68	0.001	0.007
2416522	**JAK1**	Janus kinase 1	0.68	0.003	0.014
2550959	**PREPL**	prolyl endopeptidase-like	0.68	0.001	0.008
3592484	**PLDN**	pallidin homolog (mouse)	0.68	0.000	0.006
2822215	**PAM**	peptidylglycine alpha-amidating monooxygenase	0.68	0.008	0.025
3952718	**UFD1L**	ubiquitin fusion degradation 1 like (yeast)	0.68	0.003	0.014
3003193	**CCT6A**	chaperonin containing TCP1, subunit 6A (zeta 1)	0.68	0.000	0.005
3326183	**CAPRIN1**	cell cycle associated protein 1	0.68	0.002	0.011
2876046	**PPP2CA**	protein phosphatase 2, catalytic subunit, alpha isozyme	0.68	0.000	0.006
2688759	**ATG3**	ATG3 autophagy related 3 homolog (S. cerevisiae)	0.68	0.002	0.012
2769947	**CLOCK**	clock homolog (mouse)	0.68	0.000	0.005
3775686	**USP14**	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	0.68	0.001	0.007
2817053	**SCAMP1**	secretory carrier membrane protein 1	0.68	0.001	0.010
2382336	**FBXO28**	F-box protein 28	0.68	0.000	0.005
2860666	**TAF9**	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	0.68	0.000	0.004
2863885	**LHFPL2**	lipoma HMGIC fusion partner-like 2	0.68	0.001	0.009
3426215	**MRPL42**	mitochondrial ribosomal protein L42	0.68	0.005	0.019
3680524	**ZC3H7A**	zinc finger CCCH-type containing 7A	0.68	0.001	0.008
3284188	**ITGB1**	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	0.68	0.005	0.019
3740171	**CRK**	v-crk sarcoma virus CT10 oncogene homolog (avian)	0.68	0.001	0.009
2642325	**ATP2C1**	ATPase, Ca++ transporting, type 2C, member 1	0.68	0.001	0.008
2922972	**DCBLD1**	discoidin, CUB and LCCL domain containing 1	0.68	0.002	0.013
2582562	**ACVR1**	activin A receptor, type I	0.68	0.001	0.008
2842101	**SFXN1**	sideroflexin 1	0.68	0.001	0.009
2647216	**HPS3**	Hermansky-Pudlak syndrome 3	0.67	0.001	0.008
3096545	**SGK196**	protein kinase-like protein SgK196	0.67	0.002	0.010
3909395	**DPM1**	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	0.67	0.004	0.018
3147726	**SLC25A32**	solute carrier family 25, member 32	0.67	0.001	0.009
2452637	**NUCKS1**	nuclear casein kinase and cyclin-dependent kinase substrate 1	0.67	0.005	0.018
3556323	**SUPT16H**	suppressor of Ty 16 homolog (S. cerevisiae)	0.67	0.004	0.016
3570454	**COX16**	COX16 cytochrome c oxidase assembly homolog (S. cerevisiae)	0.67	0.009	0.026
2823745	**SLC25A46**	solute carrier family 25, member 46	0.67	0.000	0.004
2927506	**TNFAIP3**	tumor necrosis factor, alpha-induced protein 3	0.67	0.001	0.008
3755714	**MED1**	mediator complex subunit 1	0.67	0.001	0.008
3149754	**EIF3H**	eukaryotic translation initiation factor 3, subunit H	0.67	0.001	0.008
2418929	**PIGK**	phosphatidylinositol glycan anchor biosynthesis, class K	0.67	0.002	0.012
3847959	**TUBB4Q**	tubulin, beta 4 // tubulin, beta 4	0.67	0.007	0.023
2470654	**DDX1**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	0.67	0.001	0.009
2423264	**TMED5**	transmembrane emp24 protein transport domain containing 5	0.67	0.000	0.004
3294438	**ANXA7**	annexin A7	0.67	0.001	0.007
3850501	**LOC147727**	hypothetical LOC147727	0.67	0.009	0.026
2496962	**IL1R1**	interleukin 1 receptor, type I	0.67	0.010	0.027
2962767	**PGM3**	phosphoglucomutase 3	0.67	0.000	0.006
2615060	**RBMS3**	RNA binding motif, single stranded interacting protein 3	0.67	0.004	0.017
3533184	**SSTR1**	somatostatin receptor 1	0.67	0.007	0.024
2696252	**RYK**	RYK receptor-like tyrosine kinase	0.67	0.002	0.011
2487696	**PCYOX1**	prenylcysteine oxidase 1	0.67	0.011	0.029
3469319	**APPL2**	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	0.67	0.001	0.010
3518169	**COMMD6**	COMM domain containing 6	0.67	0.024	0.047
3998444	**HDHD1**	haloacid dehalogenase-like hydrolase domain containing 1	0.67	0.004	0.017
3400034	**WNK1**	WNK lysine deficient protein kinase 1	0.67	0.001	0.008
3509910	**FAM48A**	family with sequence similarity 48, member A	0.67	0.001	0.009
3775842	**TYMS**	thymidylate synthetase	0.66	0.017	0.038
3108433	**MTDH**	metadherin	0.66	0.002	0.010
2620641	**LIMD1**	LIM domains containing 1	0.66	0.000	0.003
3018535	**BCAP29**	B-cell receptor-associated protein 29	0.66	0.001	0.008

2768981	**SGCB**	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	0.66	0.014	0.034
3225348	**PPP6C**	protein phosphatase 6, catalytic subunit	0.66	0.006	0.022
3629103	**KIAA0101**	KIAA0101	0.66	0.019	0.040
2645764	**ATP1B3**	ATPase, Na+/K+ transporting, beta 3 polypeptide	0.66	0.000	0.005
2644155	**NCK1**	NCK adaptor protein 1	0.66	0.001	0.007
3111530	**ENY2**	enhancer of yellow 2 homolog (Drosophila)	0.66	0.005	0.019
4006841	**SLC9A7**	solute carrier family 9 (sodium/hydrogen exchanger), member 7	0.66	0.003	0.014
3074362	**CNOT4**	CCR4-NOT transcription complex, subunit 4	0.66	0.000	0.003
3223928	**STOM**	stomatin	0.66	0.008	0.024
3918574	**IFNAR1**	interferon (alpha, beta and omega) receptor 1	0.66	0.001	0.007
3695268	**NAE1**	NEDD8 activating enzyme E1 subunit 1	0.66	0.000	0.006
2960010	**LMBRD1**	LMBR1 domain containing 1	0.66	0.008	0.025
3987996	**PLS3**	plastin 3	0.66	0.010	0.028
2830010	**SMAD5**	SMAD family member 5	0.66	0.000	0.004
3930360	**RUNX1**	runt-related transcription factor 1	0.66	0.000	0.006
3426917	**METAP2**	methionyl aminopeptidase 2	0.66	0.002	0.011
2476219	**BIRC6**	baculoviral IAP repeat-containing 6	0.66	0.001	0.007
2951916	**STK38**	serine/threonine kinase 38	0.66	0.005	0.018
3010082	**PHTF2**	putative homeodomain transcription factor 2	0.66	0.000	0.006
3309215	**EIF3A**	eukaryotic translation initiation factor 3, subunit A	0.66	0.002	0.011
3445670	**WBP11**	WW domain binding protein 11	0.66	0.000	0.005
3765299	**APPBP2**	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	0.66	0.000	0.003
2380991	**IARS2**	isoleucyl-tRNA synthetase 2, mitochondrial	0.66	0.000	0.004
3252534	**SAMD8**	sterile alpha motif domain containing 8	0.66	0.001	0.009
3147591	**AZIN1**	antizyme inhibitor 1	0.66	0.001	0.009
2813364	**SLC30A5**	solute carrier family 30 (zinc transporter), member 5	0.66	0.000	0.006
2746269	**LSM6**	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.65	0.003	0.015
2688882	**C3ORF17**	chromosome 3 open reading frame 17	0.65	0.000	0.004
2455418	**PTPN14**	protein tyrosine phosphatase, non-receptor type 14	0.65	0.001	0.008
2929168	**UTRN**	utrophin	0.65	0.002	0.012
3090922	**PPP2R2A**	protein phosphatase 2, regulatory subunit B, alpha	0.65	0.000	0.003
3427767	**TMPO**	thymopoietin	0.65	0.010	0.027
3559570	**HECTD1**	HECT domain containing 1	0.65	0.003	0.014
3047660	**GLI3**	GLI family zinc finger 3	0.65	0.008	0.025
3134034	**PRKDC**	protein kinase, DNA-activated, catalytic polypeptide	0.65	0.003	0.015
3624607	**MYO5A**	myosin VA (heavy chain 12, myoxin)	0.65	0.000	0.005
2974188	**MED23**	mediator complex subunit 23	0.65	0.000	0.005
3591963	**EIF3J**	eukaryotic translation initiation factor 3, subunit J	0.65	0.004	0.018
3717395	**SUZ12**	suppressor of zeste 12 homolog (Drosophila)	0.65	0.001	0.009
3460593	**TMBIM4**	transmembrane BAX inhibitor motif containing 4	0.65	0.001	0.010
2580635	**MMADHC**	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	0.65	0.002	0.013
2412624	**RAB3B**	RAB3B, member RAS oncogene family	0.65	0.017	0.038
3087501	**ZDHHC2**	zinc finger, DHHC-type containing 2	0.65	0.000	0.001
3431376	**ANKRD13A**	ankyrin repeat domain 13A	0.65	0.005	0.018
3974838	**DDX3X**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	0.65	0.004	0.016
2610336	**VHL**	von Hippel-Lindau tumor suppressor	0.65	0.001	0.007
2921296	**AMD1**	adenosylmethionine decarboxylase 1	0.65	0.005	0.018
2957596	**ELOVL5**	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	0.65	0.003	0.016
2457496	**HHIPL2**	HHIP-like 2	0.65	0.010	0.028
3453218	**CCNT1**	cyclin T1	0.65	0.002	0.011
2371346	**RGL1**	ral guanine nucleotide dissociation stimulator-like 1	0.65	0.000	0.004
3379777	**MRGPRF**	MAS-related GPR, member F	0.65	0.001	0.008
2476116	**SLC30A6**	solute carrier family 30 (zinc transporter), member 6	0.65	0.000	0.006
2709631	**MASP1**	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	0.65	0.024	0.047
2728189	**PAICS**	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	0.64	0.000	0.004
2355615	**SEC22B**	SEC22 vesicle trafficking protein homolog B (S. cerevisiae) (gene/pseudogene)	0.64	0.002	0.013
2733287	**PRDM8**	PR domain containing 8	0.64	0.000	0.002
2404254	**PUM1**	pumilio homolog 1 (Drosophila)	0.64	0.000	0.005
3598959	**SMAD3**	SMAD family member 3	0.64	0.002	0.011
3518455	**FBXL3**	F-box and leucine-rich repeat protein 3	0.64	0.004	0.017
3497659	**RAP2A**	RAP2A, member of RAS oncogene family	0.64	0.009	0.026
3532313	**SRP54**	signal recognition particle 54kDa	0.64	0.002	0.011
3460127	**GNS**	glucosamine (N-acetyl)-6-sulfatase	0.64	0.003	0.014
3212143	**UBQLN1**	ubiquilin 1	0.64	0.001	0.009
3958005	**C22ORF30**	chromosome 22 open reading frame 30	0.64	0.000	0.003
3229943	**SDCCAG3**	serologically defined colon cancer antigen 3	0.64	0.000	0.004

3326635	**CD44**	CD44 molecule (Indian blood group)	0.64	0.000	0.003
3512527	**TPT1**	tumor protein, translationally-controlled 1	0.64	0.002	0.012
3592023	**B2M**	beta-2-microglobulin	0.64	0.005	0.019
2389789	**SCCPDH**	saccharopine dehydrogenase (putative)	0.64	0.002	0.011
2633773	**TFG**	TRK-fused gene	0.64	0.000	0.005
3535922	**STYX**	serine/threonine/tyrosine interacting protein	0.64	0.006	0.021
3956290	**PITPNB**	phosphatidylinositol transfer protein, beta	0.64	0.001	0.009
3929395	**GCFC1**	GC-rich sequence DNA-binding factor 1	0.64	0.021	0.043
2857131	**DHX29**	DEAH (Asp-Glu-Ala-His) box polypeptide 29	0.64	0.001	0.007
2515276	**DYNC1I2**	dynein, cytoplasmic 1, intermediate chain 2	0.64	0.004	0.016
2752006	**SAP30**	Sin3A-associated protein, 30kDa	0.64	0.000	0.002
3293244	**SAR1A**	SAR1 homolog A (S. cerevisiae)	0.64	0.003	0.016
2928392	**VTA1**	Vps20-associated 1 homolog (S. cerevisiae)	0.64	0.002	0.011
2424524	**DPYD**	dihydropyrimidine dehydrogenase	0.63	0.002	0.013
3162529	**C9ORF150**	chromosome 9 open reading frame 150	0.63	0.001	0.007
2553576	**RTN4**	reticulon 4	0.63	0.000	0.005
3815165	**PTBP1**	polypyrimidine tract binding protein 1	0.63	0.000	0.004
2421883	**GBP1**	guanylate binding protein 1, interferon-inducible, 67kDa	0.63	0.024	0.046
2772017	**YTHDC1**	YTH domain containing 1	0.63	0.000	0.006
2344542	**RPF1**	ribosome production factor 1 homolog (S. cerevisiae)	0.63	0.001	0.009
2373336	**CFH**	complement factor H	0.63	0.015	0.035
3778601	**VAPA**	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	0.63	0.000	0.004
3058991	**CACNA2D1**	calcium channel, voltage-dependent, alpha 2/delta subunit 1	0.63	0.001	0.009
3651955	**METTL9**	methyltransferase like 9	0.63	0.003	0.013
3456630	**CBX5**	chromobox homolog 5	0.63	0.008	0.024
3681956	**KIAA0430**	KIAA0430	0.63	0.003	0.014
3144235	**TMEM55A**	transmembrane protein 55A	0.63	0.000	0.004
2573232	**TMEM185B**	transmembrane protein 185B (pseudogene)	0.63	0.000	0.002
3974708	**USP9X**	ubiquitin specific peptidase 9, X-linked	0.63	0.008	0.024
3429460	**TXNRD1**	thioredoxin reductase 1	0.63	0.009	0.026
3762473	**TOB1**	transducer of ERBB2, 1	0.63	0.000	0.006
3567984	**PPP2R5E**	protein phosphatase 2, regulatory subunit B', epsilon isoform	0.63	0.000	0.006
3773426	**NPTX1**	neuronal pentraxin I	0.63	0.026	0.049
2356344	**RNF115**	ring finger protein 115	0.63	0.006	0.020
2866590	**LYSMD3**	LysM, putative peptidoglycan-binding, domain containing 3	0.63	0.005	0.018
3033924	**UBE3C**	ubiquitin protein ligase E3C	0.63	0.000	0.005
3954238	**MAPK1**	mitogen-activated protein kinase 1	0.63	0.001	0.009
3597521	**APH1B**	anterior pharynx defective 1 homolog B (C. elegans)	0.63	0.000	0.004
2506570	**GPR39**	G protein-coupled receptor 39	0.63	0.003	0.015
2491336	**KCMF1**	potassium channel modulatory factor 1	0.63	0.002	0.011
2496628	**C2ORF29**	chromosome 2 open reading frame 29	0.63	0.000	0.005
2676319	**GLT8D1**	glycosyltransferase 8 domain containing 1	0.63	0.002	0.011
3478457	**STX2**	syntaxin 2	0.63	0.005	0.019
2926969	**PDE7B**	phosphodiesterase 7B	0.63	0.002	0.011
2330899	**UTP11L**	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	0.63	0.001	0.007
3697799	**AP1G1**	adaptor-related protein complex 1, gamma 1 subunit	0.63	0.002	0.011
2464484	**FAM36A**	family with sequence similarity 36, member A	0.63	0.002	0.011
2639129	**DIRC2**	disrupted in renal carcinoma 2	0.63	0.003	0.014
2415084	**JUN**	jun proto-oncogene	0.63	0.000	0.005
3917155	**USP16**	ubiquitin specific peptidase 16	0.63	0.002	0.012
2419046	**ZZZ3**	zinc finger, ZZ-type containing 3	0.62	0.001	0.008
2796790	**KIAA1430**	KIAA1430	0.62	0.002	0.013
3110272	**FZD6**	frizzled homolog 6 (Drosophila)	0.62	0.010	0.028
3094778	**TACC1**	transforming, acidic coiled-coil containing protein 1	0.62	0.002	0.011
3359910	**NUP98**	nucleoporin 98kDa	0.62	0.000	0.006
3603199	**IDH3A**	isocitrate dehydrogenase 3 (NAD+) alpha	0.62	0.008	0.024
2653932	**MFN1**	mitofusin 1	0.62	0.000	0.005
2777412	**PIGY**	phosphatidylinositol glycan anchor biosynthesis, class Y	0.62	0.003	0.014
3225398	**HSPA5**	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	0.62	0.008	0.025
2319252	**SPSB1**	splA/ryanodine receptor domain and SOCS box containing 1	0.62	0.000	0.004
3545525	**C14ORF156**	chromosome 14 open reading frame 156	0.62	0.015	0.036
3592755	**SEMA6D**	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	0.62	0.004	0.016
2530599	**AGFG1**	ArfGAP with FG repeats 1	0.62	0.002	0.011
3240340	**WAC**	WW domain containing adaptor with coiled-coil	0.62	0.001	0.010
3725779	**MYST2**	MYST histone acetyltransferase 2	0.62	0.000	0.006
3067302	**LAMB1**	laminin, beta 1	0.62	0.010	0.028
2783316	**SEC24D**	SEC24 family, member D (S. cerevisiae)	0.62	0.004	0.017
3220977	**ROD1**	ROD1 regulator of differentiation 1 (S. pombe)	0.62	0.011	0.029
2808438	**NNT**	nicotinamide nucleotide transhydrogenase	0.62	0.003	0.014

4019900	**CUL4B**	cullin 4B	0.62	0.004	0.016
2784687	**ANKRD50**	ankyrin repeat domain 50	0.62	0.004	0.016
3886512	**TTPAL**	tocopherol (alpha) transfer protein-like	0.62	0.001	0.008
2863730	**AP3B1**	adaptor-related protein complex 3, beta 1 subunit	0.62	0.004	0.016
3677795	**CREBBP**	CREB binding protein	0.62	0.000	0.004
3636470	**BTBD1**	BTB (POZ) domain containing 1	0.62	0.000	0.003
2680819	**SUCLG2**	succinate-CoA ligase, GDP-forming, beta subunit	0.62	0.011	0.030
3362468	**SBF2**	SET binding factor 2	0.61	0.006	0.020
2925590	**TMEM200A**	transmembrane protein 200A	0.61	0.006	0.022
2853768	**NUP155**	nucleoporin 155kDa	0.61	0.005	0.019
3414739	**METTL7A**	methyltransferase like 7A	0.61	0.001	0.009
2446198	**TOR1AIP2**	torsin A interacting protein 2	0.61	0.000	0.006
3725392	**CALCOCO2**	calcium binding and coiled-coil domain 2	0.61	0.000	0.006
2609608	**SETD5**	SET domain containing 5	0.61	0.000	0.005
3882854	**ITCH**	itchy E3 ubiquitin protein ligase homolog (mouse)	0.61	0.001	0.009
3332015	**OR4D10**	olfactory receptor, family 4, subfamily D, member 10	0.61	0.015	0.035
3092325	**DCTN6**	dynactin 6	0.61	0.002	0.011
3167220	**UBE2R2**	ubiquitin-conjugating enzyme E2R 2	0.61	0.000	0.003
3542207	**SRSF5**	serine/arginine-rich splicing factor 5	0.61	0.003	0.015
2430370	**GDAP2**	ganglioside induced differentiation associated protein 2	0.61	0.001	0.009
2975287	**HBS1L**	HBS1-like (S. cerevisiae)	0.61	0.001	0.007
3792952	**SOCS6**	suppressor of cytokine signaling 6	0.61	0.002	0.010
2951674	**SRPK1**	SRSF protein kinase 1	0.61	0.000	0.005
2484970	**EHBP1**	EH domain binding protein 1	0.61	0.003	0.016
3348852	**DLAT**	dihydrolipoamide S-acetyltransferase	0.61	0.000	0.004
3980887	**NONO**	non-POU domain containing, octamer-binding	0.61	0.001	0.008
3149528	**TRPS1**	trichorhinophalangeal syndrome I	0.61	0.007	0.023
3474372	**PXN**	paxillin	0.61	0.000	0.003
2345196	**HS2ST1**	heparan sulfate 2-O-sulfotransferase 1	0.61	0.000	0.003
2577958	**DARS**	aspartyl-tRNA synthetase	0.61	0.000	0.005
3043165	**HIBADH**	3-hydroxyisobutyrate dehydrogenase	0.61	0.018	0.040
2608801	**EDEM1**	ER degradation enhancer, mannosidase alpha-like 1	0.61	0.001	0.009
2469910	**LPIN1**	lipin 1	0.61	0.000	0.004
2437417	**ASH1L**	ash1 (absent, small, or homeotic)-like (Drosophila)	0.61	0.003	0.014
2659918	**LRCH3**	leucine-rich repeats and calponin homology (CH) domain containing 3	0.61	0.001	0.009
3388914	**DCUN1D5**	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	0.61	0.000	0.003
2485257	**UGP2**	UDP-glucose pyrophosphorylase 2	0.61	0.005	0.018
2805581	**SUB1**	SUB1 homolog (S. cerevisiae)	0.61	0.004	0.017
3304012	**MGEA5**	meningioma expressed antigen 5 (hyaluronidase)	0.61	0.001	0.009
2763805	**DHX15**	DEAH (Asp-Glu-Ala-His) box polypeptide 15	0.61	0.001	0.008
3019981	**MDFIC**	MyoD family inhibitor domain containing	0.61	0.001	0.007
3623771	**TRPM7**	transient receptor potential cation channel, subfamily M, member 7	0.61	0.003	0.013
2335132	**CMPK1**	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	0.61	0.005	0.019
3428131	**SCYL2**	SCY1-like 2 (S. cerevisiae)	0.61	0.004	0.016
3488985	**ITM2B**	integral membrane protein 2B	0.61	0.010	0.027
2880932	**CSNK1A1**	casein kinase 1, alpha 1	0.61	0.000	0.005
3720228	**CDK12**	cyclin-dependent kinase 12	0.61	0.000	0.005
3774635	**FASN**	fatty acid synthase	0.60	0.001	0.008
3303165	**DNMBP**	dynamin binding protein	0.60	0.000	0.004
2382117	**CAPN2**	calpain 2, (m/II) large subunit	0.60	0.001	0.007
2458701	**ACBD3**	acyl-CoA binding domain containing 3	0.60	0.001	0.006
2676041	**WDR82**	WD repeat domain 82	0.60	0.015	0.035
3318009	**RRM1**	ribonucleotide reductase M1	0.60	0.024	0.047
3319937	**WEE1**	WEE1 homolog (S. pombe)	0.60	0.002	0.012
3191589	**FUBP3**	far upstream element (FUSE) binding protein 3	0.60	0.001	0.007
3670668	**ATMIN**	ATM interactor	0.60	0.001	0.007
3564919	**FERMT2**	fermitin family member 2	0.60	0.024	0.046
2828856	**HSPA4**	heat shock 70kDa protein 4	0.60	0.001	0.009
3342983	**TMEM126B**	transmembrane protein 126B	0.60	0.001	0.010
2962820	**ME1**	malic enzyme 1, NADP(+)-dependent, cytosolic	0.60	0.005	0.018
2364677	**PBX1**	pre-B-cell leukemia homeobox 1	0.60	0.010	0.028
2641263	**RAB7A**	RAB7A, member RAS oncogene family	0.60	0.002	0.012
3707352	**RNF167**	ring finger protein 167	0.60	0.000	0.003
3728889	**TMEM49**	transmembrane protein 49	0.60	0.000	0.006
3178545	**C9ORF47**	chromosome 9 open reading frame 47	0.60	0.002	0.013
2916390	**ORC3**	origin recognition complex, subunit 3	0.60	0.002	0.011
3974556	**ATP6AP2**	ATPase, H+ transporting, lysosomal accessory protein 2	0.60	0.007	0.022
3599495	**CORO2B**	coronin, actin binding protein, 2B	0.60	0.023	0.045
2807862	**C5ORF51**	chromosome 5 open reading frame 51	0.60	0.010	0.027

2894711	**TMEM14B**	transmembrane protein 14B	0.60	0.023	0.046
3181302	**NCBP1**	nuclear cap binding protein subunit 1, 80kDa	0.60	0.001	0.010
2859195	**DIMT1L**	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	0.60	0.000	0.003
3772661	**TIMP2**	TIMP metallopeptidase inhibitor 2	0.60	0.000	0.004
3253683	**ZMIZ1**	zinc finger, MIZ-type containing 1	0.60	0.000	0.006
3732230	**PITPNC1**	phosphatidylinositol transfer protein, cytoplasmic 1	0.60	0.006	0.021
2574798	**MAP3K2**	mitogen-activated protein kinase kinase kinase 2	0.60	0.000	0.005
2886130	**PANK3**	pantothenate kinase 3	0.60	0.001	0.008
2427469	**SLC16A4**	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)	0.60	0.009	0.026
3499453	**TPP2**	tripeptidyl peptidase II	0.60	0.000	0.006
3125775	**CNOT7**	CCR4-NOT transcription complex, subunit 7	0.60	0.002	0.013
3220513	**KIAA0368**	KIAA0368	0.60	0.003	0.014
3473083	**MED13L**	mediator complex subunit 13-like	0.60	0.005	0.019
2407729	**RRAGC**	Ras-related GTP binding C	0.60	0.002	0.012
3134922	**PCMTD1**	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	0.60	0.025	0.048
2772614	**GRSF1**	G-rich RNA sequence binding factor 1	0.60	0.000	0.005
3494102	**UCHL3**	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	0.60	0.002	0.013
3279108	**NMT2**	N-myristoyltransferase 2	0.60	0.007	0.023
2542737	**LAPTM4A**	lysosomal protein transmembrane 4 alpha	0.60	0.000	0.006
3552847	**DYNC1H1**	dynein, cytoplasmic 1, heavy chain 1	0.60	0.005	0.019
2369339	**RALGPS2**	Ral GEF with PH domain and SH3 binding motif 2	0.60	0.003	0.015
4022781	**FAM122B**	family with sequence similarity 122B	0.60	0.000	0.003
2982381	**TCP1**	t-complex 1	0.60	0.004	0.016
2594812	**TRAK2**	trafficking protein, kinesin binding 2	0.60	0.005	0.019
2790570	**PLRG1**	pleiotropic regulator 1 (PRL1 homolog, Arabidopsis)	0.60	0.002	0.012
2977265	**HIVEP2**	human immunodeficiency virus type I enhancer binding protein 2	0.60	0.001	0.009
2676219	**PBRM1**	polybromo 1	0.59	0.002	0.013
3026988	**LUC7L2**	LUC7-like 2 (S. cerevisiae)	0.59	0.001	0.008
3929664	**TMEM50B**	transmembrane protein 50B	0.59	0.003	0.015
3489212	**FNDC3A**	fibronectin type III domain containing 3A	0.59	0.000	0.004
2558150	**AAK1**	AP2 associated kinase 1	0.59	0.001	0.007
2349863	**NTNG1**	netrin G1	0.59	0.001	0.009
2506903	**MGAT5**	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	0.59	0.005	0.018
2418000	**ZRANB2**	zinc finger, RAN-binding domain containing 2	0.59	0.000	0.006
4012868	**RLIM**	ring finger protein, LIM domain interacting	0.59	0.009	0.026
2887633	**BOD1**	biorientation of chromosomes in cell division 1	0.59	0.001	0.008
2468811	**ASAP2**	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	0.59	0.000	0.003
2402459	**STMN1**	stathmin 1	0.59	0.017	0.038
3337618	**PPP6R3**	protein phosphatase 6, regulatory subunit 3	0.59	0.001	0.008
3237548	**ARL5B**	ADP-ribosylation factor-like 5B	0.59	0.008	0.024
3371719	**CKAP5**	cytoskeleton associated protein 5	0.59	0.007	0.022
3812206	**TMX3**	thioredoxin-related transmembrane protein 3	0.59	0.002	0.012
3591838	**CASC4**	cancer susceptibility candidate 4	0.59	0.001	0.007
3240095	**RAB18**	RAB18, member RAS oncogene family	0.59	0.020	0.041
3431483	**ATP2A2**	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0.59	0.006	0.020
3537813	**ACTR10**	actin-related protein 10 homolog (S. cerevisiae)	0.59	0.005	0.019
2712858	**UBXN7**	UBX domain protein 7	0.59	0.003	0.015
3163136	**SNAPC3**	small nuclear RNA activating complex, polypeptide 3, 50kDa	0.59	0.005	0.018
2973995	**EPB41L2**	erythrocyte membrane protein band 4.1-like 2	0.59	0.002	0.013
3246372	**NCOA4**	nuclear receptor coactivator 4	0.59	0.006	0.020
3984655	**CENPI**	centromere protein I	0.59	0.009	0.026
3467315	**IKBIP**	IKBKB interacting protein	0.59	0.001	0.007
3537264	**C14ORF101**	chromosome 14 open reading frame 101	0.59	0.000	0.005
2345617	**PKN2**	protein kinase N2	0.59	0.002	0.012
3565303	**CNIH**	cornichon homolog (Drosophila)	0.59	0.002	0.011
2529546	**ACSL3**	acyl-CoA synthetase long-chain family member 3	0.59	0.001	0.008
3414561	**DIP2B**	DIP2 disco-interacting protein 2 homolog B (Drosophila)	0.59	0.000	0.004
2402942	**SLC9A1**	solute carrier family 9 (sodium/hydrogen exchanger), member 1	0.59	0.000	0.002
2454378	**SLC30A1**	solute carrier family 30 (zinc transporter), member 1	0.59	0.001	0.007
3907234	**SDC4**	syndecan 4	0.59	0.001	0.009
3217736	**ERP44**	endoplasmic reticulum protein 44	0.59	0.002	0.011
3921391	**WRB**	tryptophan rich basic protein	0.59	0.014	0.033
3030285	**CUL1**	cullin 1	0.59	0.000	0.006
2930592	**TAB2**	TGF-beta activated kinase 1/MAP3K7 binding protein 2	0.59	0.003	0.014
2403557	**SNORA44**	small nucleolar RNA, H/ACA box 44	0.59	0.008	0.024
3462949	**OSBPL8**	oxysterol binding protein-like 8	0.59	0.015	0.035
3992354	**SLC9A6**	solute carrier family 9 (sodium/hydrogen exchanger), member 6	0.59	0.000	0.005
3506153	**MTMR6**	myotubularin related protein 6	0.59	0.002	0.013

3716411	**CPD**	carboxypeptidase D	0.59	0.023	0.045
2998333	**C7ORF36**	chromosome 7 open reading frame 36	0.59	0.013	0.032
3781531	**CABLES1**	Cdk5 and Abl enzyme substrate 1	-0.59	0.011	0.029
3337835	**IGHMBP2**	immunoglobulin mu binding protein 2	-0.59	0.002	0.010
3676262	**SEPX1**	selenoprotein X, 1	-0.59	0.002	0.011
2558736	**ADD2**	adducin 2 (beta)	-0.59	0.000	0.003
3378210	**BRMS1**	breast cancer metastasis suppressor 1	-0.59	0.020	0.042
3205033	**YBX1**	Y box binding protein 1	-0.59	0.018	0.039
3191074	**METTL11A**	methyltransferase like 11A	-0.59	0.001	0.008
3947036	**MEI1**	meiosis inhibitor 1	-0.59	0.001	0.008
3376832	**BAD**	BCL2-associated agonist of cell death	-0.59	0.001	0.009
3540398	**FNTB**	farnesyltransferase, CAAX box, beta	-0.59	0.000	0.003
3238761	**MSRB2**	methionine sulfoxide reductase B2	-0.59	0.000	0.005
2562271	**CAPG**	capping protein (actin filament), gelsolin-like	-0.60	0.021	0.043
2492783	**THNSL2**	threonine synthase-like 2 (S. cerevisiae)	-0.60	0.005	0.019
3884158	**MANBAL**	mannosidase, beta A, lysosomal-like	-0.60	0.000	0.004
2451043	**LMOD1**	leiomodin 1 (smooth muscle)	-0.61	0.023	0.045
3073981	**AKR1B1**	aldo-keto reductase family 1, member B1 (aldose reductase)	-0.61	0.014	0.033
2450668	**TMEM9**	transmembrane protein 9	-0.61	0.000	0.004
3957679	**SELM**	selenoprotein M	-0.61	0.002	0.011
3903836	**EIF6**	eukaryotic translation initiation factor 6	-0.61	0.002	0.012
2453881	**IRF6**	interferon regulatory factor 6	-0.61	0.005	0.019
3601511	**ISLR**	immunoglobulin superfamily containing leucine-rich repeat	-0.61	0.010	0.028
3936951	**SEPT5**	septin 5	-0.62	0.001	0.007
3607183	**MRPS11**	mitochondrial ribosomal protein S11	-0.62	0.001	0.007
2427208	**GSTM3**	glutathione S-transferase mu 3 (brain)	-0.62	0.005	0.020
3942838	**LIMK2**	LIM domain kinase 2	-0.62	0.000	0.005
3824874	**IFI30**	interferon, gamma-inducible protein 30	-0.62	0.013	0.033
3714659	**DHRS7B**	dehydrogenase/reductase (SDR family) member 7B	-0.62	0.000	0.004
2333658	**ATP6V0B**	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	-0.63	0.001	0.009
3837081	**NPAS1**	neuronal PAS domain protein 1	-0.63	0.000	0.006
3830189	**FXYD1**	FXYD domain containing ion transport regulator 1	-0.64	0.001	0.009
2528774	**SLC4A3**	solute carrier family 4, anion exchanger, member 3	-0.64	0.000	0.003
2545953	**FNDC4**	fibronectin type III domain containing 4	-0.64	0.009	0.026
3923764	**LRRC3**	leucine rich repeat containing 3	-0.65	0.003	0.015
3921933	**BACE2**	beta-site APP-cleaving enzyme 2	-0.65	0.011	0.029
3825823	**NDUFA13**	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	-0.65	0.001	0.007
3832292	**KCNK6**	potassium channel, subfamily K, member 6	-0.65	0.005	0.020
2875193	**P4HA2**	prolyl 4-hydroxylase, alpha polypeptide II	-0.66	0.000	0.006
2397025	**DHRS3**	dehydrogenase/reductase (SDR family) member 3	-0.66	0.016	0.036
3953524	**SCARF2**	scavenger receptor class F, member 2	-0.66	0.000	0.005
3750939	**SDF2**	stromal cell-derived factor 2	-0.66	0.001	0.010
2899171	**HIST1H1E**	histone cluster 1, H1e	-0.67	0.025	0.048
3194613	**TMEM141**	transmembrane protein 141	-0.67	0.002	0.012
3351775	**TRAPPC4**	trafficking protein particle complex 4	-0.68	0.001	0.010
4012154	**RPS4X**	ribosomal protein S4, X-linked	-0.68	0.000	0.004
3645626	**IL32**	interleukin 32	-0.68	0.015	0.035
2899216	**HIST1H4E**	histone cluster 1, H4e	-0.68	0.002	0.013
3881045	**FAM182A**	family with sequence similarity 182, member A	-0.68	0.002	0.012
3064591	**FIS1**	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)	-0.68	0.003	0.015
3771642	**CYGB**	cytoglobin	-0.69	0.012	0.032
3168255	**HRCT1**	histidine rich carboxyl terminus 1	-0.69	0.005	0.020
3638760	**IDH2**	isocitrate dehydrogenase 2 (NADP+), mitochondrial	-0.69	0.000	0.005
3708160	**ALOX12**	arachidonate 12-lipoxygenase	-0.69	0.001	0.009
3416977	**ORMDL2**	ORM1-like 2 (S. cerevisiae)	-0.70	0.000	0.002
3982462	**PGK1**	phosphoglycerate kinase 1	-0.70	0.003	0.013
3403077	**C12ORF57**	chromosome 12 open reading frame 57	-0.70	0.002	0.012
3337137	**AIP**	aryl hydrocarbon receptor interacting protein	-0.70	0.001	0.008
3436329	**FAM101A**	family with sequence similarity 101, member A	-0.71	0.001	0.009
3336680	**RHOD**	ras homolog gene family, member D	-0.71	0.002	0.012
3403015	**ENO2**	enolase 2 (gamma, neuronal)	-0.71	0.000	0.004
2491676	**VAMP5**	vesicle-associated membrane protein 5 (myobrevin)	-0.71	0.007	0.022
2950798	**C6ORF125**	chromosome 6 open reading frame 125	-0.72	0.000	0.006
3907011	**ADA**	adenosine deaminase	-0.74	0.004	0.016
3455973	**SPRYD3**	SPRY domain containing 3	-0.74	0.000	0.002
3924041	**ADARB1**	adenosine deaminase, RNA-specific, B1	-0.74	0.001	0.010
3883236	**MMP24**	matrix metallopeptidase 24 (membrane-inserted)	-0.75	0.000	0.003
3557209	**SLC7A8**	solute carrier family 7 (amino acid transporter, L-type), member 8	-0.75	0.003	0.015
3315217	**C10ORF125**	chromosome 10 open reading frame 125	-0.75	0.001	0.007
2335048	**CYP4A22**	cytochrome P450, family 4, subfamily A, polypeptide 22	-0.75	0.001	0.009

3415915	**PFDN5**	prefoldin subunit 5	-0.76	0.000	0.003
3355145	**ST3GAL4**	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	-0.76	0.000	0.002
2977690	**SF3B5**	splicing factor 3b, subunit 5, 10kDa	-0.76	0.008	0.024
2447148	**RGS16**	regulator of G-protein signaling 16	-0.76	0.003	0.015
3853108	**NOTCH3**	notch 3	-0.76	0.015	0.035
2902935	**STK19**	serine/threonine kinase 19	-0.77	0.000	0.001
3863869	**PSG8**	pregnancy specific beta-1-glycoprotein 8	-0.79	0.011	0.030
3164086	**ADAMTSL1**	ADAMTS-like 1	-0.80	0.005	0.019
3694215	**CDH8**	cadherin 8, type 2	-0.80	0.021	0.043
3555736	**NDRG2**	NDRG family member 2	-0.81	0.000	0.001
3855104	**CRLF1**	cytokine receptor-like factor 1	-0.81	0.011	0.029
3527684	**RNASE3**	ribonuclease, RNase A family, 3	-0.82	0.000	0.006
3725714	**NXPH3**	neurexophilin 3	-0.82	0.000	0.006
4007437	**SLC38A5**	solute carrier family 38, member 5	-0.82	0.006	0.021
4007216	**UXT**	ubiquitously-expressed transcript	-0.83	0.000	0.004
3865635	**DMPK**	dystrophia myotonica-protein kinase	-0.83	0.000	0.003
2450865	**CSRP1**	cysteine and glycine-rich protein 1	-0.84	0.001	0.009
3707199	**PSMB6**	proteasome (prosome, macropain) subunit, beta type, 6	-0.84	0.001	0.008
3986514	**PRPS1**	phosphoribosyl pyrophosphate synthetase 1	-0.85	0.010	0.028
3708074	**XAF1**	XIAP associated factor 1	-0.86	0.023	0.046
2805635	**NPR3**	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	-0.87	0.024	0.047
3903052	**SNTA1**	syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)	-0.88	0.000	0.003
4022370	**GPC4**	glypican 4	-0.88	0.002	0.011
3513147	**HTR2A**	5-hydroxytryptamine (serotonin) receptor 2A	-0.89	0.004	0.017
3719962	**PSMB3**	proteasome (prosome, macropain) subunit, beta type, 3	-0.91	0.001	0.009
3394315	**C1QTNF5**	C1q and tumor necrosis factor related protein 5	-0.92	0.000	0.001
3333622	**POLR2G**	polymerase (RNA) II (DNA directed) polypeptide G	-0.94	0.000	0.002
2489606	**POLE4**	polymerase (DNA-directed), epsilon 4 (p12 subunit)	-0.94	0.000	0.005
3756689	**KRTAP1-1**	keratin associated protein 1-1	-0.95	0.021	0.043
2828787	**UQCRQ**	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	-0.95	0.000	0.004
3671695	**WFDC1**	WAP four-disulfide core domain 1	-0.95	0.010	0.028
3557048	**PSMB5**	proteasome (prosome, macropain) subunit, beta type, 5	-0.96	0.000	0.004
2946232	**HIST1H1C**	histone cluster 1, H1c	-0.96	0.001	0.008
3286776	**C10ORF10**	chromosome 10 open reading frame 10	-0.97	0.000	0.003
2600089	**PTPRN**	protein tyrosine phosphatase, receptor type, N	-0.98	0.002	0.010
3816509	**GADD45B**	growth arrest and DNA-damage-inducible, beta	-0.98	0.000	0.001
2383859	**GUK1**	guanylate kinase 1	-0.99	0.000	0.004
2351004	**GSTM5**	glutathione S-transferase mu 5	-1.00	0.025	0.048
2716328	**ADRA2C**	adrenergic, alpha-2C-, receptor	-1.01	0.000	0.006
3328600	**TSPAN18**	tetraspanin 18	-1.03	0.019	0.040
3169331	**ALDH1B1**	aldehyde dehydrogenase 1 family, member B1	-1.04	0.000	0.005
2328320	**TINAGL1**	tubulointerstitial nephritis antigen-like 1	-1.04	0.005	0.019
3726252	**SGCA**	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	-1.06	0.000	0.004
3750767	**ALDOC**	aldolase C, fructose-bisphosphate	-1.08	0.000	0.003
3638819	**CIB1**	calcium and integrin binding 1 (calmyrin)	-1.08	0.000	0.003
3417457	**MYL6**	myosin, light chain 6, alkali, smooth muscle and non-muscle	-1.09	0.000	0.001
3638188	**HAPLN3**	hyaluronan and proteoglycan link protein 3	-1.10	0.010	0.028
2451693	**FMOD**	fibromodulin	-1.10	0.015	0.035
3350830	**TAGLN**	transgelin	-1.10	0.001	0.008
3756911	**KRT34**	keratin 34	-1.14	0.013	0.032
2475678	**LBH**	limb bud and heart development homolog (mouse)	-1.15	0.002	0.011
2397898	**HSPB7**	heat shock 27kDa protein family, member 7 (cardiovascular)	-1.17	0.007	0.023
2401493	**ID3**	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	-1.19	0.005	0.019
2764192	**SEL1L3**	sel-1 suppressor of lin-12-like 3 (C. elegans)	-1.20	0.000	0.004
3667508	**CALB2**	calbindin 2	-1.20	0.001	0.008
3414440	**C12ORF62**	chromosome 12 open reading frame 62	-1.21	0.000	0.005
3630736	**ITGA11**	integrin, alpha 11	-1.21	0.002	0.010
3852381	**PODNL1**	podocan-like 1	-1.23	0.000	0.001
3299970	**ANKRD1**	ankyrin repeat domain 1 (cardiac muscle)	-1.28	0.013	0.032
3391149	**FDXACB1**	ferredoxin-fold anticodon binding domain containing 1	-1.28	0.000	0.002
3821263	**CNN1**	calponin 1, basic, smooth muscle	-1.33	0.000	0.004
3349858	**NNMT**	nicotinamide N-methyltransferase	-1.35	0.000	0.001
3617712	**GJD2**	gap junction protein, delta 2, 36kDa	-1.36	0.000	0.003
3815097	**FSTL3**	follistatin-like 3 (secreted glycoprotein)	-1.39	0.000	0.003
4035833	**CD24**	CD24 molecule	-1.42	0.001	0.010
3299504	**ACTA2**	actin, alpha 2, smooth muscle, aorta	-1.46	0.003	0.013
2363618	**SDHC**	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	-1.46	0.001	0.007
3944210	**RASD2**	RASD family, member 2	-1.61	0.004	0.016

3394264	**MCAM**	melanoma cell adhesion molecule	-1.69	0.000	0.002
3443226	**MFAP5**	microfibrillar associated protein 5	-2.09	0.001	0.009
3855218	**COMP**	cartilage oligomeric matrix protein	-2.09	0.000	0.002
3607332	**ACAN**	aggrecan	-2.90	0.000	0.004
3617719	**ACTC1**	actin, alpha, cardiac muscle 1	-2.95	0.001	0.007

1153 protein coding genes (1012 up and 141 down) were identified as significantly differentially expressed in BS cells using the following cutoff: absolute expression ratio (ER) ≥ 1.5 and false discovery rate (FDR) < 0.05. Thus significantly differentially expressed genes have $\log_2$ expression values of ≥|0.59|.

Table S2B. Significantly differentially expressed mRNAs identified in BLM-depleted compared with isogenic, nonspecific shRNA-treated control human 82-6 fibroblasts

Probe Set ID	Gene Symbol	Gene Description	log$_2$(ER)	unadjusted P-Value	FDR
2931036	**ULBP1**	UL16 binding protein 1	5.05	3.3E-10	9.8E-08
2731542	**AREG**	amphiregulin	3.95	1.3E-10	7.6E-08
3998766	**KAL1**	Kallmann syndrome 1 sequence	3.81	1.4E-11	2.2E-08
3768412	**SLC16A6**	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	3.66	1.0E-10	7.6E-08
2710599	**CLDN1**	claudin 1	3.17	1.6E-09	2.1E-07
2642720	**ACPP**	acid phosphatase, prostate	2.88	1.5E-09	2.1E-07
3464276	**SLC6A15**	solute carrier family 6 (neutral amino acid transporter), member 15	2.85	5.0E-10	1.3E-07
3849894	**OLFM2**	olfactomedin 2	2.73	9.1E-11	7.6E-08
3727928	**NOG**	noggin	2.46	7.3E-07	1.3E-05
3927480	**ADAMTS5**	ADAM metallopeptidase with thrombospondin type 1 motif, 5	2.31	6.9E-08	2.5E-06
3801492	**ANKRD29**	ankyrin repeat domain 29	2.30	4.4E-09	3.8E-07
3401704	**CCND2**	cyclin D2	2.28	3.0E-09	3.1E-07
3354443	**SLC37A2**	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	2.26	3.4E-09	3.3E-07
3282974	**SVIL**	supervillin	2.19	8.3E-09	5.8E-07
2648677	**MME**	membrane metallo-endopeptidase	2.15	2.8E-08	1.3E-06
3132782	**SFRP1**	secreted frizzled-related protein 1	2.13	6.3E-10	1.3E-07
3463112	**E2F7**	E2F transcription factor 7	2.08	4.2E-09	3.7E-07
3546924	**FLRT2**	fibronectin leucine rich transmembrane protein 2	2.04	6.8E-08	2.4E-06
3262129	**INA**	internexin neuronal intermediate filament protein, alpha	2.03	4.5E-10	1.2E-07
2786322	**SLC7A11**	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	2.01	3.3E-07	7.4E-06
3285119	**FZD8**	frizzled homolog 8 (Drosophila)	2.00	8.2E-10	1.5E-07
3058944	**HGF**	hepatocyte growth factor (hepapoietin A; scatter factor)	1.99	1.3E-05	1.1E-04
3186491	**PAPPA**	pregnancy-associated plasma protein A, pappalysin 1	1.98	2.4E-08	1.2E-06
2817941	**RASGRF2**	Ras protein-specific guanine nucleotide-releasing factor 2	1.98	1.2E-08	7.1E-07
2946383	**HIST1H4H**	histone cluster 1, H4h	1.88	9.2E-06	8.6E-05
2791419	**FAM198B**	family with sequence similarity 198, member B	1.88	8.3E-07	1.5E-05
2571483	**IL1A**	interleukin 1, alpha	1.81	3.5E-06	4.1E-05
3519309	**SPRY2**	sprouty homolog 2 (Drosophila)	1.81	2.7E-09	2.8E-07
3104489	**STMN2**	stathmin-like 2	1.81	1.9E-08	1.0E-06
3908358	**SULF2**	sulfatase 2	1.80	1.4E-10	7.6E-08
3279313	**ITGA8**	integrin, alpha 8	1.80	1.7E-09	2.2E-07
2818517	**VCAN**	versican	1.79	2.4E-07	5.8E-06
2809245	**ITGA2**	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	1.76	7.5E-09	5.5E-07
3590275	**CHAC1**	ChaC, cation transport regulator homolog 1 (E. coli)	1.73	2.3E-10	9.7E-08
2930418	**UST**	uronyl-2-sulfotransferase	1.73	1.3E-08	7.8E-07
4004853	**SRPX**	sushi-repeat-containing protein, X-linked	1.73	1.0E-09	1.6E-07
2904485	**SCUBE3**	signal peptide, CUB domain, EGF-like 3	1.73	1.2E-10	7.6E-08
3790704	**PMAIP1**	phorbol-12-myristate-13-acetate-induced protein 1	1.72	3.5E-08	1.5E-06
2476510	**LTBP1**	latent transforming growth factor beta binding protein 1	1.70	4.8E-08	1.9E-06
3862873	**CYP2A6**	cytochrome P450, family 2, subfamily A, polypeptide 6	1.69	6.6E-03	1.5E-02
3356539	**NTM**	neurotrimin	1.68	1.0E-08	6.7E-07
3781531	**CABLES1**	Cdk5 and Abl enzyme substrate 1	1.67	4.2E-07	8.8E-06
3386217	**CHORDC1**	cysteine and histidine-rich domain (CHORD)-containing 1	1.66	3.9E-05	2.6E-04
3143660	**MMP16**	matrix metallopeptidase 16 (membrane-inserted)	1.65	1.2E-08	7.5E-07
2771342	**EPHA5**	EPH receptor A5	1.64	7.1E-06	7.1E-05
3020192	**TES**	testis derived transcript (3 LIM domains)	1.63	4.4E-08	1.8E-06
2913694	**CD109**	CD109 molecule	1.61	5.0E-07	9.9E-06
3801943	**ZNF521**	zinc finger protein 521	1.61	3.9E-08	1.6E-06
2474071	**MAPRE3**	microtubule-associated protein, RP/EB family, member 3	1.61	4.4E-06	4.9E-05
3819474	**ANGPTL4**	angiopoietin-like 4	1.59	9.6E-09	6.4E-07
3808745	**CCDC68**	coiled-coil domain containing 68	1.59	4.9E-07	9.8E-06
3128046	**STC1**	stanniocalcin 1	1.57	1.1E-07	3.4E-06
3073013	**PODXL**	podocalyxin-like	1.56	1.2E-07	3.7E-06
2956052	**TNFRSF21**	tumor necrosis factor receptor superfamily, member 21	1.54	9.2E-09	6.2E-07
2872047	**SEMA6A**	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	1.53	1.0E-07	3.2E-06
2671787	**TMEM158**	transmembrane protein 158 (gene/pseudogene)	1.50	4.7E-09	4.0E-07
3162529	**C9ORF150**	chromosome 9 open reading frame 150	1.49	4.9E-08	1.9E-06
2343823	**LPHN2**	latrophilin 2	1.48	1.3E-05	1.1E-04
3771642	**CYGB**	cytoglobin	1.47	5.7E-09	4.5E-07
3068097	**DOCK4**	dedicator of cytokinesis 4	1.46	7.1E-08	2.5E-06
2611056	**PPARG**	peroxisome proliferator-activated receptor gamma	1.45	2.2E-08	1.1E-06
2711610	**LRRC15**	leucine rich repeat containing 15	1.45	1.2E-08	7.5E-07
2794704	**ASB5**	ankyrin repeat and SOCS box-containing 5	1.42	1.5E-06	2.3E-05
3039177	**ETV1**	ets variant 1	1.41	2.4E-08	1.2E-06
3971806	**SAT1**	spermidine/spermine N1-acetyltransferase 1	1.41	2.4E-08	1.2E-06
4004819	**DYNLT3**	dynein, light chain, Tctex-type 3	1.40	6.6E-06	6.7E-05

2835792	**GM2A**	GM2 ganglioside activator	1.36	1.5E-09	2.1E-07
2566848	**AFF3**	AF4/FMR2 family, member 3	1.35	1.5E-07	4.2E-06
2970086	**LAMA4**	laminin, alpha 4	1.35	3.1E-07	7.1E-06
3732793	**ARSG**	arylsulfatase G	1.35	3.8E-08	1.6E-06
3844470	**PPAP2C**	phosphatidic acid phosphatase type 2C	1.34	1.3E-09	1.9E-07
2925590	**TMEM200A**	transmembrane protein 200A	1.33	3.0E-08	1.3E-06
3075778	**HIPK2**	homeodomain interacting protein kinase 2	1.32	3.8E-08	1.6E-06
2626167	**PXK**	PX domain containing serine/threonine kinase	1.32	8.7E-08	2.9E-06
2501204	**IL1RN**	interleukin 1 receptor antagonist	1.32	4.6E-07	9.4E-06
3801621	**OSBPL1A**	oxysterol binding protein-like 1A	1.32	1.6E-07	4.4E-06
2327817	**PTPRU**	protein tyrosine phosphatase, receptor type, U	1.31	8.2E-09	5.8E-07
3420316	**HMGA2**	high mobility group AT-hook 2	1.30	2.3E-08	1.1E-06
3960930	**CBX6**	chromobox homolog 6	1.29	9.6E-10	1.6E-07
3504226	**CRYL1**	crystallin, lambda 1	1.29	4.2E-08	1.7E-06
2359377	**LCE2A**	late cornified envelope 2A	1.29	7.1E-06	7.1E-05
2832459	**PCDHB14**	protocadherin beta 14	1.29	9.1E-06	8.5E-05
3594031	**TMOD2**	tropomodulin 2 (neuronal)	1.29	3.8E-06	4.4E-05
2731513	**EREG**	epiregulin	1.28	1.0E-06	1.7E-05
2946714	**HIST1H2BK**	histone cluster 1, H2bk	1.27	4.0E-07	8.4E-06
3043936	**FKBP14**	FK506 binding protein 14, 22 kDa	1.27	6.2E-06	6.4E-05
3151086	**HAS2**	hyaluronan synthase 2	1.27	5.2E-05	3.3E-04
2915420	**PRSS35**	protease, serine, 35	1.26	2.5E-06	3.2E-05
3595441	**GCOM1**	GRINL1A complex locus	1.26	1.6E-06	2.4E-05
3300115	**PPP1R3C**	protein phosphatase 1, regulatory (inhibitor) subunit 3C	1.26	5.0E-08	1.9E-06
3812074	**DSEL**	dermatan sulfate epimerase-like	1.25	6.0E-08	2.2E-06
2890660	**GFPT2**	glutamine-fructose-6-phosphate transaminase 2	1.25	2.6E-07	6.2E-06
3260985	**SFXN3**	sideroflexin 3	1.24	5.5E-09	4.5E-07
3160175	**VLDLR**	very low density lipoprotein receptor	1.24	1.6E-07	4.3E-06
3129731	**DUSP4**	dual specificity phosphatase 4	1.22	4.0E-08	1.7E-06
2671728	**CDCP1**	CUB domain containing protein 1	1.22	1.5E-06	2.2E-05
3050462	**GRB10**	growth factor receptor-bound protein 10	1.22	9.0E-08	2.9E-06
3928590	**KRTAP21-1**	keratin associated protein 21-1	1.22	6.5E-04	2.4E-03
4018729	**IL13RA2**	interleukin 13 receptor, alpha 2	1.20	1.3E-06	2.0E-05
3399004	**OPCML**	opioid binding protein/cell adhesion molecule-like	1.19	1.6E-07	4.3E-06
3061621	**TFPI2**	tissue factor pathway inhibitor 2	1.19	3.7E-05	2.6E-04
2385967	**SLC35F3**	solute carrier family 35, member F3	1.19	1.7E-08	9.3E-07
3936951	**SEPT5**	septin 5	1.19	2.2E-08	1.1E-06
3374402	**LPXN**	leupaxin	1.19	5.0E-08	1.9E-06
2554018	**EFEMP1**	EGF-containing fibulin-like extracellular matrix protein 1	1.18	9.9E-08	3.1E-06
3638607	**ANPEP**	alanyl (membrane) aminopeptidase	1.18	7.8E-10	1.5E-07
3430086	**TCP11L2**	t-complex 11 (mouse)-like 2	1.18	1.2E-06	1.9E-05
3095313	**C8ORF4**	chromosome 8 open reading frame 4	1.18	1.2E-04	6.4E-04
4002173	**RPS6KA3**	ribosomal protein S6 kinase, 90kDa, polypeptide 3	1.18	3.9E-06	4.4E-05
2356115	**TXNIP**	thioredoxin interacting protein	1.17	4.0E-08	1.7E-06
3882949	**DYNLRB1**	dynein, light chain, roadblock-type 1	1.16	6.1E-07	1.2E-05
3026216	**CHRM2**	cholinergic receptor, muscarinic 2	1.15	2.8E-03	7.6E-03
2837029	**SGCD**	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	1.14	4.8E-06	5.2E-05
3786868	**SLC14A1**	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	1.13	1.1E-05	9.8E-05
3797561	**LAMA1**	laminin, alpha 1	1.13	2.7E-08	1.3E-06
3288518	**C10ORF72**	chromosome 10 open reading frame 72	1.13	4.5E-07	9.2E-06
3429566	**CHST11**	carbohydrate (chondroitin 4) sulfotransferase 11	1.13	1.4E-08	8.2E-07
2991150	**TSPAN13**	tetraspanin 13	1.12	2.1E-07	5.3E-06
2594089	**SATB2**	SATB homeobox 2	1.12	6.0E-08	2.2E-06
3321150	**ARNTL**	aryl hydrocarbon receptor nuclear translocator-like	1.12	7.9E-06	7.7E-05
2386747	**GPR137B**	G protein-coupled receptor 137B	1.11	3.9E-07	8.3E-06
2502762	**STEAP3**	STEAP family member 3	1.11	7.0E-07	1.3E-05
3756750	**KRTAP4-12**	keratin associated protein 4-12	1.11	1.1E-04	6.0E-04
3843156	**ZNF460**	zinc finger protein 460	1.11	7.7E-06	7.6E-05
2835300	**SLC26A2**	solute carrier family 26 (sulfate transporter), member 2	1.11	9.1E-06	8.5E-05
4009288	**HSD17B10**	hydroxysteroid (17-beta) dehydrogenase 10	1.10	5.5E-08	2.0E-06
3178147	**CTSL1**	cathepsin L1	1.10	3.0E-07	6.9E-06
3942062	**NF2**	neurofibromin 2 (merlin)	1.10	4.5E-08	1.8E-06
3773241	**TBC1D16**	TBC1 domain family, member 16	1.10	1.1E-07	3.4E-06
3977299	**CLCN5**	chloride channel 5	1.10	5.2E-06	5.5E-05
3592755	**SEMA6D**	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	1.10	1.0E-05	9.2E-05
2351294	**KCNC4**	potassium voltage-gated channel, Shaw-related subfamily, member 4	1.09	1.5E-07	4.2E-06
3140213	**MSC**	musculin	1.09	8.2E-07	1.4E-05
2775214	**PRKG2**	protein kinase, cGMP-dependent, type II	1.09	3.0E-07	6.9E-06
2816494	**F2RL1**	coagulation factor II (thrombin) receptor-like 1	1.08	1.4E-08	8.2E-07
3608398	**FURIN**	furin (paired basic amino acid cleaving enzyme)	1.08	5.1E-09	4.2E-07
3240452	**BAMBI**	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	1.07	8.7E-05	4.9E-04
2378068	**G0S2**	G0/G1switch 2	1.07	2.8E-06	3.5E-05

3075531	**ZC3HAV1L**	zinc finger CCCH-type, antiviral 1-like	1.06	3.9E-06	4.4E-05
3145149	**TP53INP1**	tumor protein p53 inducible nuclear protein 1	1.06	2.6E-06	3.4E-05
3135567	**LYPLA1**	lysophospholipase I	1.06	1.2E-03	3.9E-03
3396593	**FEZ1**	fasciculation and elongation protein zeta 1 (zygin I)	1.06	3.9E-08	1.7E-06
2995254	**C7ORF41**	chromosome 7 open reading frame 41	1.06	2.0E-06	2.8E-05
3460584	**LLPH**	LLP homolog, long-term synaptic facilitation (Aplysia)	1.06	2.8E-04	1.2E-03
3921933	**BACE2**	beta-site APP-cleaving enzyme 2	1.06	2.6E-09	2.7E-07
2614120	**RPL15**	ribosomal protein L15	1.06	5.9E-06	6.2E-05
2740067	**ANK2**	ankyrin 2, neuronal	1.05	1.6E-07	4.3E-06
3457549	**ANKRD52**	ankyrin repeat domain 52	1.05	2.4E-06	3.2E-05
3664952	**PDP2**	pyruvate dehyrogenase phosphatase catalytic subunit 2	1.04	2.9E-07	6.7E-06
2816459	**F2R**	coagulation factor II (thrombin) receptor	1.04	2.3E-08	1.1E-06
3741547	**P2RX5**	purinergic receptor P2X, ligand-gated ion channel, 5	1.04	2.9E-08	1.3E-06
3630736	**ITGA11**	integrin, alpha 11	1.04	3.7E-06	4.3E-05
3175971	**PSAT1**	phosphoserine aminotransferase 1	1.03	3.3E-05	2.3E-04
4002148	**EIF1AX**	eukaryotic translation initiation factor 1A, X-linked	1.03	3.5E-05	2.4E-04
2477438	**QPCT**	glutaminyl-peptide cyclotransferase	1.02	1.4E-06	2.1E-05
2967276	**POPDC3**	popeye domain containing 3	1.02	5.4E-06	5.7E-05
3392332	**CADM1**	cell adhesion molecule 1	1.02	1.9E-06	2.7E-05
3063463	**CYP3A7**	cytochrome P450, family 3, subfamily A, polypeptide 7	1.01	1.1E-06	1.8E-05
3820571	**ATG4D**	ATG4 autophagy related 4 homolog D (S. cerevisiae)	1.01	5.6E-07	1.1E-05
3920850	**KCNJ15**	potassium inwardly-rectifying channel, subfamily J, member 15	1.01	8.0E-06	7.8E-05
2343418	**PTGFR**	prostaglandin F receptor (FP)	1.01	2.6E-06	3.3E-05
2649723	**MFSD1**	major facilitator superfamily domain containing 1	1.00	4.6E-07	9.4E-06
3917305	**BACH1**	BTB and CNC homology 1, basic leucine zipper transcription factor 1	1.00	2.2E-06	3.0E-05
3125001	**LONRF1**	LON peptidase N-terminal domain and ring finger 1	1.00	1.9E-05	1.5E-04
3721579	**NKIRAS2**	NFKB inhibitor interacting Ras-like 2	0.99	5.9E-09	4.6E-07
3759105	**FAM171A2**	family with sequence similarity 171, member A2	0.99	1.0E-06	1.7E-05
2448382	**PTGS2**	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0.99	2.9E-05	2.1E-04
2791063	**CTSO**	cathepsin O	0.99	6.7E-06	6.7E-05
3134922	**PCMTD1**	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	0.99	2.4E-04	1.1E-03
2515627	**ITGA6**	integrin, alpha 6	0.98	7.6E-07	1.4E-05
2907568	**KLHDC3**	kelch domain containing 3	0.98	1.6E-06	2.4E-05
3984468	**SRPX2**	sushi-repeat-containing protein, X-linked 2	0.98	2.0E-06	2.8E-05
3252036	**PLAU**	plasminogen activator, urokinase	0.98	8.0E-07	1.4E-05
2950629	**TAPBP**	TAP binding protein (tapasin)	0.98	9.8E-09	6.5E-07
2372858	**RGS2**	regulator of G-protein signaling 2, 24kDa	0.98	5.7E-04	2.2E-03
2731332	**IL8**	interleukin 8	0.98	6.8E-04	2.5E-03
2421753	**GTF2B**	general transcription factor IIB	0.98	4.1E-05	2.7E-04
3127745	**TNFRSF10D**	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	0.97	2.2E-07	5.5E-06
2832297	**PCDHB2**	protocadherin beta 2	0.97	5.5E-06	5.8E-05
2832403	**PCDHB9**	protocadherin beta 9	0.97	3.8E-06	4.3E-05
3599495	**CORO2B**	coronin, actin binding protein, 2B	0.97	1.7E-07	4.5E-06
3740770	**RTN4RL1**	reticulon 4 receptor-like 1	0.97	2.4E-03	6.8E-03
2352338	**FAM19A3**	family with sequence similarity 19 (chemokine (C-C motif)-like), member A3	0.97	2.9E-06	3.6E-05
3367231	**BDNF**	brain-derived neurotrophic factor	0.96	1.0E-06	1.7E-05
3766960	**SMURF2**	SMAD specific E3 ubiquitin protein ligase 2	0.96	1.8E-08	9.9E-07
3362159	**NRIP3**	nuclear receptor interacting protein 3	0.96	9.1E-07	1.6E-05
2686023	**DCBLD2**	discoidin, CUB and LCCL domain containing 2	0.95	1.3E-07	3.9E-06
3916527	**JAM2**	junctional adhesion molecule 2	0.95	1.7E-06	2.5E-05
3886294	**TOX2**	TOX high mobility group box family member 2	0.95	2.0E-08	1.1E-06
3126191	**PSD3**	pleckstrin and Sec7 domain containing 3	0.95	7.5E-06	7.3E-05
2665199	**SATB1**	SATB homeobox 1	0.94	1.8E-05	1.5E-04
3590239	**DLL4**	delta-like 4 (Drosophila)	0.94	2.9E-06	3.6E-05
3062738	**OCM2**	oncomodulin 2	0.94	3.0E-03	8.0E-03
3978760	**MAGEH1**	melanoma antigen family H, 1	0.94	1.9E-06	2.7E-05
3756668	**KRTAP3-1**	keratin associated protein 3-1	0.94	3.1E-06	3.8E-05
3650762	**TMC7**	transmembrane channel-like 7	0.93	2.3E-02	4.1E-02
3260001	**MARVELD1**	MARVEL domain containing 1	0.93	3.1E-09	3.1E-07
3443296	**M6PR**	mannose-6-phosphate receptor (cation dependent)	0.93	8.2E-09	5.8E-07
2465778	**OR6F1**	olfactory receptor, family 6, subfamily F, member 1	0.93	3.2E-04	1.4E-03
2832387	**PCDHB8**	protocadherin beta 8	0.93	4.7E-04	1.9E-03
2967249	**BVES**	blood vessel epicardial substance	0.93	1.8E-05	1.4E-04
2832467	**PCDHB18**	protocadherin beta 18 pseudogene	0.93	6.9E-04	2.5E-03
2353717	**PTGFRN**	prostaglandin F2 receptor negative regulator	0.92	3.3E-07	7.3E-06
3850501	**LOC147727**	hypothetical LOC147727	0.92	1.4E-06	2.1E-05
3898355	**FLRT3**	fibronectin leucine rich transmembrane protein 3	0.92	1.7E-04	8.4E-04
2896177	**JARID2**	jumonji, AT rich interactive domain 2	0.92	2.3E-06	3.1E-05
2461891	**B3GALNT2**	beta-1,3-N-acetylgalactosaminyltransferase 2	0.92	2.5E-06	3.3E-05
3464860	**DUSP6**	dual specificity phosphatase 6	0.92	1.7E-07	4.6E-06

3914050	**STMN3**	stathmin-like 3	0.92	1.1E-07	3.4E-06
3359121	**IGF2**	insulin-like growth factor 2 (somatomedin A)	0.91	2.0E-05	1.6E-04
3947227	**SEPT3**	septin 3	0.91	2.8E-06	3.6E-05
2499053	**LIMS1**	LIM and senescent cell antigen-like domains 1	0.91	2.5E-04	1.1E-03
3059464	**SEMA3A**	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	0.91	6.3E-05	3.8E-04
3830277	**USF2**	upstream transcription factor 2, c-fos interacting	0.91	9.0E-08	2.9E-06
3048778	**TMED4**	transmembrane emp24 protein transport domain containing 4	0.91	7.1E-08	2.5E-06
2349043	**SLC30A7**	solute carrier family 30 (zinc transporter), member 7	0.90	3.2E-06	3.9E-05
2434575	**CTSS**	cathepsin S	0.90	3.0E-04	1.3E-03
3801411	**NPC1**	Niemann-Pick disease, type C1	0.90	4.0E-07	8.4E-06
3147286	**RRM2B**	ribonucleotide reductase M2 B (TP53 inducible)	0.90	6.9E-05	4.1E-04
3846316	**PIP5K1C**	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	0.90	2.4E-08	1.2E-06
2568968	**UXS1**	UDP-glucuronate decarboxylase 1	0.90	2.0E-05	1.6E-04
3449068	**TMTC1**	transmembrane and tetratricopeptide repeat containing 1	0.89	6.9E-05	4.1E-04
3205633	**MCART1**	mitochondrial carrier triple repeat 1	0.89	5.5E-03	1.3E-02
2344984	**CLCA2**	chloride channel accessory 2	0.89	3.1E-06	3.8E-05
3246888	**PRKG1**	protein kinase, cGMP-dependent, type I	0.89	2.5E-04	1.1E-03
3560617	**SNX6**	sorting nexin 6	0.88	2.0E-07	5.2E-06
3766651	**ERN1**	endoplasmic reticulum to nucleus signaling 1	0.88	2.4E-07	5.8E-06
3296046	**KCNMA1**	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	0.88	1.3E-07	3.7E-06
2349402	**AMY2B**	amylase, alpha 2B (pancreatic)	0.88	3.3E-03	8.7E-03
3756723	**KRTAP2-4**	keratin associated protein 2-4	0.88	3.1E-07	7.0E-06
3023384	**AHCYL2**	adenosylhomocysteinase-like 2	0.88	2.2E-06	2.9E-05
2879105	**SPRY4**	sprouty homolog 4 (Drosophila)	0.88	3.0E-06	3.7E-05
2790062	**TMEM154**	transmembrane protein 154	0.88	9.5E-05	5.2E-04
2537171	**FAM150B**	family with sequence similarity 150, member B	0.88	9.2E-08	3.0E-06
2726910	**SPATA18**	spermatogenesis associated 18 homolog (rat)	0.88	1.2E-06	1.9E-05
3410056	**TSPAN11**	tetraspanin 11	0.87	2.7E-03	7.3E-03
2417390	**WLS**	wntless homolog (Drosophila)	0.87	5.7E-07	1.1E-05
3566949	**C14ORF149**	chromosome 14 open reading frame 149	0.87	1.5E-07	4.2E-06
2382467	**CNIH3**	cornichon homolog 3 (Drosophila)	0.87	5.9E-06	6.1E-05
3389353	**CASP1**	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	0.87	9.6E-04	3.2E-03
2734421	**ARHGAP24**	Rho GTPase activating protein 24	0.87	3.3E-05	2.3E-04
3238962	**KIAA1217**	KIAA1217	0.87	1.9E-07	4.9E-06
2489545	**HK2**	hexokinase 2	0.87	1.7E-06	2.4E-05
3148463	**ANGPT1**	angiopoietin 1	0.87	1.4E-05	1.2E-04
2923939	**SMPDL3A**	sphingomyelin phosphodiesterase, acid-like 3A	0.87	2.3E-06	3.1E-05
2867836	**GLRX**	glutaredoxin (thioltransferase)	0.87	1.7E-06	2.4E-05
3811459	**KDSR**	3-ketodihydrosphingosine reductase	0.87	2.3E-07	5.6E-06
2832447	**PCDHB13**	protocadherin beta 13 // protocadherin beta 13	0.86	2.3E-04	1.1E-03
2655113	**KLHL24**	kelch-like 24 (Drosophila)	0.86	7.6E-05	4.4E-04
2405036	**BSDC1**	BSD domain containing 1	0.86	7.9E-08	2.7E-06
3564790	**ERO1L**	ERO1-like (S. cerevisiae)	0.86	5.4E-06	5.7E-05
3821159	**LPPR2**	lipid phosphate phosphatase-related protein type 2	0.86	2.4E-08	1.2E-06
3741456	**TRPV1**	transient receptor potential cation channel, subfamily V, member 1	0.85	1.9E-03	5.7E-03
2727587	**KIT**	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	0.85	1.8E-05	1.4E-04
2834863	**ABLIM3**	actin binding LIM protein family, member 3	0.85	2.9E-07	6.6E-06
3814791	**PARD6G**	par-6 partitioning defective 6 homolog gamma (C. elegans)	0.85	6.1E-05	3.7E-04
3347431	**ELMOD1**	ELMO/CED-12 domain containing 1	0.85	4.4E-06	4.9E-05
3806211	**PSTPIP2**	proline-serine-threonine phosphatase interacting protein 2	0.85	2.9E-06	3.6E-05
3174121	**MAMDC2**	MAM domain containing 2	0.85	5.7E-06	5.9E-05
2960955	**SLC17A5**	solute carrier family 17 (anion/sugar transporter), member 5	0.85	2.6E-06	3.4E-05
2964231	**RRAGD**	Ras-related GTP binding D	0.85	2.2E-07	5.4E-06
3358742	**TOLLIP**	toll interacting protein	0.85	6.6E-07	1.2E-05
4008427	**NUDT11**	nudix (nucleoside diphosphate linked moiety X)-type motif 11	0.85	6.0E-04	2.3E-03
3260265	**CNNM1**	cyclin M1	0.84	1.7E-05	1.4E-04
3104260	**PKIA**	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	0.84	1.6E-07	4.3E-06
3389273	**CASP4**	caspase 4, apoptosis-related cysteine peptidase	0.84	1.7E-07	4.6E-06
3715512	**TNFAIP1**	tumor necrosis factor, alpha-induced protein 1 (endothelial)	0.84	1.3E-07	3.8E-06
3671202	**CDH13**	cadherin 13, H-cadherin (heart)	0.84	3.3E-07	7.3E-06
3141755	**HEY1**	hairy/enhancer-of-split related with YRPW motif 1	0.84	3.3E-07	7.3E-06
2359470	**IVL**	involucrin	0.83	3.3E-04	1.4E-03
3873629	**SIRPA**	signal-regulatory protein alpha	0.83	5.1E-07	1.0E-05
2575949	**TUBA3E**	tubulin, alpha 3e	0.83	8.9E-03	1.9E-02
3625539	**NEDD4**	neural precursor cell expressed, developmentally down-regulated 4	0.83	7.6E-05	4.4E-04
3186191	**ATP6V1G1**	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	0.83	6.4E-08	2.3E-06
2973232	**C6ORF174**	chromosome 6 open reading frame 174	0.83	9.3E-05	5.1E-04
3262509	**GSTO1**	glutathione S-transferase omega 1	0.83	1.9E-06	2.7E-05
3442854	**SLC2A3**	solute carrier family 2 (facilitated glucose transporter), member 3	0.82	1.5E-07	4.2E-06
2706791	**ZMAT3**	zinc finger, matrin-type 3	0.82	1.2E-05	1.1E-04
3239380	**THNSL1**	threonine synthase-like 1 (S. cerevisiae)	0.82	4.2E-04	1.7E-03

2979246	**RAET1L**	retinoic acid early transcript 1L	0.82	2.1E-02	3.8E-02
3892873	**NTSR1**	neurotensin receptor 1 (high affinity)	0.82	3.9E-06	4.4E-05
3355733	**FLI1**	Friend leukemia virus integration 1	0.82	2.1E-07	5.4E-06
3268274	**PLEKHA1**	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	0.82	1.1E-04	6.1E-04
2739755	**AP1AR**	adaptor-related protein complex 1 associated regulatory protein	0.82	1.7E-04	8.2E-04
3894601	**FKBP1A**	FK506 binding protein 1A, 12kDa	0.81	1.6E-05	1.3E-04
3042881	**HOXA7**	homeobox A7	0.81	2.6E-05	1.9E-04
2476116	**SLC30A6**	solute carrier family 30 (zinc transporter), member 6	0.81	5.4E-05	3.4E-04
2414366	**PPAP2B**	phosphatidic acid phosphatase type 2B	0.80	7.6E-08	2.6E-06
3964154	**CERK**	ceramide kinase	0.80	1.5E-06	2.2E-05
2317434	**TPRG1L**	tumor protein p63 regulated 1-like	0.80	7.7E-08	2.7E-06
3828949	**DPY19L3**	dpy-19-like 3 (C. elegans)	0.80	9.2E-05	5.1E-04
3981959	**SLC16A2**	solute carrier family 16, member 2 (monocarboxylic acid transporter 8)	0.80	3.0E-08	1.3E-06
3688079	**NCRNA00095**	non-protein coding RNA 95	0.80	2.4E-03	6.7E-03
3601051	**NEO1**	neogenin 1	0.80	3.2E-06	3.9E-05
3771675	**ST6GALNAC2**	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	0.80	6.4E-08	2.3E-06
2841491	**C5ORF41**	chromosome 5 open reading frame 41	0.80	1.1E-03	3.6E-03
3851072	**ACP5**	acid phosphatase 5, tartrate resistant	0.79	3.2E-04	1.4E-03
3147173	**NCALD**	neurocalcin delta	0.79	1.3E-06	2.0E-05
3867443	**HSD17B14**	hydroxysteroid (17-beta) dehydrogenase 14	0.79	2.1E-05	1.6E-04
2394817	**KLHL21**	kelch-like 21 (Drosophila)	0.79	3.5E-06	4.2E-05
3842755	**LOC100128252**	hypothetical LOC100128252	0.79	3.8E-05	2.6E-04
2832392	**PCDHB16**	protocadherin beta 16	0.79	6.8E-05	4.0E-04
3728571	**OR4D1**	olfactory receptor, family 4, subfamily D, member 1	0.79	5.7E-03	1.3E-02
2921296	**AMD1**	adenosylmethionine decarboxylase 1	0.78	3.4E-06	4.0E-05
3218528	**ABCA1**	ATP-binding cassette, sub-family A (ABC1), member 1	0.78	3.1E-04	1.3E-03
3738629	**SLC16A3**	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	0.78	2.4E-08	1.2E-06
3466826	**CDK17**	cyclin-dependent kinase 17	0.78	8.3E-06	8.0E-05
3706439	**RAP1GAP2**	RAP1 GTPase activating protein 2	0.78	1.2E-05	1.0E-04
2777714	**SNCA**	synuclein, alpha (non A4 component of amyloid precursor)	0.78	7.3E-08	2.6E-06
2902348	**MICB**	MHC class I polypeptide-related sequence B	0.78	2.6E-06	3.3E-05
3341539	**KCTD21**	potassium channel tetramerisation domain containing 21	0.78	7.9E-04	2.8E-03
3536706	**LGALS3**	lectin, galactoside-binding, soluble, 3	0.78	1.4E-07	3.9E-06
3222170	**TNC**	tenascin C	0.78	8.3E-07	1.5E-05
2388525	**SDCCAG8**	serologically defined colon cancer antigen 8	0.77	6.1E-04	2.3E-03
2319340	**SLC25A33**	solute carrier family 25, member 33	0.77	2.4E-03	6.8E-03
3548929	**RIN3**	Ras and Rab interactor 3	0.77	8.4E-08	2.8E-06
3972025	**PDK3**	pyruvate dehydrogenase kinase, isozyme 3	0.77	1.1E-05	9.7E-05
2912980	**OGFRL1**	opioid growth factor receptor-like 1	0.77	1.7E-04	8.4E-04
3807474	**C18ORF32**	chromosome 18 open reading frame 32	0.77	1.8E-05	1.5E-04
2823551	**MAN2A1**	mannosidase, alpha, class 2A, member 1	0.77	4.2E-04	1.7E-03
3858285	**TSHZ3**	teashirt zinc finger homeobox 3	0.77	3.6E-04	1.5E-03
3631214	**TLE3**	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	0.77	7.5E-07	1.4E-05
3895891	**ADRA1D**	adrenergic, alpha-1D-, receptor	0.76	8.7E-08	2.9E-06
3651955	**METTL9**	methyltransferase like 9	0.76	1.3E-07	3.8E-06
2545953	**FNDC4**	fibronectin type III domain containing 4	0.76	2.2E-08	1.1E-06
3870104	**ZNF415**	zinc finger protein 415	0.76	9.4E-05	5.2E-04
2969886	**FYN**	FYN oncogene related to SRC, FGR, YES	0.76	4.5E-05	2.9E-04
3575567	**FOXN3**	forkhead box N3	0.76	3.4E-06	4.0E-05
3840164	**ZNF610**	zinc finger protein 610	0.76	2.6E-06	3.3E-05
3275042	**ASB13**	ankyrin repeat and SOCS box-containing 13	0.76	4.5E-07	9.2E-06
2864849	**SSBP2**	single-stranded DNA binding protein 2	0.76	9.9E-07	1.7E-05
2563654	**EIF2AK3**	eukaryotic translation initiation factor 2-alpha kinase 3	0.75	7.9E-05	4.5E-04
3345427	**ENDOD1**	endonuclease domain containing 1	0.75	8.1E-07	1.4E-05
3151970	**MTSS1**	metastasis suppressor 1	0.75	1.5E-06	2.2E-05
3840224	**ZNF528**	zinc finger protein 528	0.75	1.2E-04	6.2E-04
3968512	**CLCN4**	chloride channel 4	0.75	2.1E-06	2.9E-05
2786732	**MAML3**	mastermind-like 3 (Drosophila)	0.75	1.3E-05	1.2E-04
3829857	**ZNF302**	zinc finger protein 302	0.75	5.7E-04	2.2E-03
2493992	**KCNIP3**	Kv channel interacting protein 3, calsenilin	0.75	7.6E-08	2.6E-06
2832310	**PCDHB3**	protocadherin beta 3	0.75	9.9E-03	2.1E-02
2660029	**LMLN**	leishmanolysin-like (metallopeptidase M8 family)	0.75	1.6E-04	7.7E-04
3410384	**C12ORF35**	chromosome 12 open reading frame 35	0.75	3.4E-04	1.4E-03
2372924	**TROVE2**	TROVE domain family, member 2	0.74	7.5E-03	1.7E-02
3752709	**MYO1D**	myosin ID	0.74	2.5E-06	3.3E-05
3422855	**GLIPR1**	GLI pathogenesis-related 1	0.74	1.7E-07	4.5E-06
2362394	**IFI16**	interferon, gamma-inducible protein 16	0.74	6.1E-05	3.7E-04
3218067	**MRPL50**	mitochondrial ribosomal protein L50	0.74	1.7E-05	1.4E-04
3405748	**EMP1**	epithelial membrane protein 1	0.74	6.1E-07	1.2E-05

2847967	**SEMA5A**	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	0.74	5.5E-05	3.4E-04
3922100	**MX1**	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	0.74	6.0E-04	2.3E-03
3654699	**NUPR1**	nuclear protein, transcriptional regulator, 1	0.74	5.4E-06	5.7E-05
3784208	**DTNA**	dystrobrevin, alpha	0.73	1.2E-06	1.9E-05
3385951	**NOX4**	NADPH oxidase 4	0.73	5.8E-06	6.0E-05
3076076	**SLC37A3**	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	0.73	1.4E-05	1.2E-04
2714644	**C4ORF42**	chromosome 4 open reading frame 42	0.73	5.3E-05	3.4E-04
2725332	**TMEM33**	transmembrane protein 33	0.73	1.3E-05	1.1E-04
3852880	**EMR2**	egf-like module containing, mucin-like, hormone receptor-like 2	0.73	4.9E-07	9.8E-06
2443120	**DPT**	dermatopontin	0.73	2.0E-05	1.6E-04
3802129	**SS18**	synovial sarcoma translocation, chromosome 18	0.73	1.2E-04	6.5E-04
3421300	**MDM2**	Mdm2 p53 binding protein homolog (mouse)	0.73	2.0E-05	1.6E-04
3148582	**EIF3E**	eukaryotic translation initiation factor 3, subunit E	0.72	6.3E-04	2.4E-03
3329793	**SLC39A13**	solute carrier family 39 (zinc transporter), member 13	0.72	3.9E-07	8.3E-06
2856995	**ESM1**	endothelial cell-specific molecule 1	0.72	1.0E-05	9.4E-05
3843275	**ZNF419**	zinc finger protein 419	0.72	7.0E-04	2.5E-03
3660213	**CYLD**	cylindromatosis (turban tumor syndrome)	0.72	8.1E-06	7.8E-05
2626802	**PTPRG**	protein tyrosine phosphatase, receptor type, G	0.72	6.1E-05	3.7E-04
2504328	**GYPC**	glycophorin C (Gerbich blood group)	0.72	1.4E-07	3.9E-06
2327391	**SESN2**	sestrin 2	0.72	3.7E-07	8.0E-06
2470165	**TRIB2**	tribbles homolog 2 (Drosophila)	0.72	9.5E-07	1.6E-05
2331903	**ZNF643**	zinc finger protein 643	0.71	2.9E-03	7.7E-03
2378019	**CAMK1G**	calcium/calmodulin-dependent protein kinase IG	0.71	2.1E-07	5.3E-06
3990727	**RAB33A**	RAB33A, member RAS oncogene family	0.71	7.0E-05	4.1E-04
3806459	**ST8SIA5**	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	0.71	4.5E-05	2.9E-04
3674199	**CPNE7**	copine VII	0.71	8.9E-07	1.5E-05
2637112	**GAP43**	growth associated protein 43	0.71	6.7E-06	6.8E-05
2371346	**RGL1**	ral guanine nucleotide dissociation stimulator-like 1	0.71	9.0E-06	8.5E-05
3901041	**THBD**	thrombomodulin	0.71	7.6E-07	1.4E-05
2832423	**PCDHB10**	protocadherin beta 10	0.71	8.8E-06	8.3E-05
2887164	**SH3PXD2B**	SH3 and PX domains 2B	0.71	2.0E-05	1.6E-04
3940099	**ADORA2A**	adenosine A2a receptor	0.71	2.8E-05	2.1E-04
3395464	**ASAM**	adipocyte-specific adhesion molecule	0.71	1.3E-06	2.0E-05
3562003	**TRAPPC6B**	trafficking protein particle complex 6B	0.71	3.1E-04	1.3E-03
3665949	**PSKH1**	protein serine kinase H1	0.71	1.1E-06	1.8E-05
3142217	**PAG1**	phosphoprotein associated with glycosphingolipid microdomains 1	0.71	3.1E-05	2.2E-04
3512874	**LCP1**	lymphocyte cytosolic protein 1 (L-plastin)	0.71	4.5E-06	4.9E-05
3860450	**ZNF566**	zinc finger protein 566	0.71	2.1E-04	9.8E-04
3227482	**FIBCD1**	fibrinogen C domain containing 1	0.71	1.4E-06	2.1E-05
3782166	**IMPACT**	Impact homolog (mouse)	0.71	6.2E-04	2.3E-03
3106243	**RIPK2**	receptor-interacting serine-threonine kinase 2	0.70	6.9E-05	4.1E-04
2515276	**DYNC1I2**	dynein, cytoplasmic 1, intermediate chain 2	0.70	2.4E-02	4.1E-02
3419849	**TBK1**	TANK-binding kinase 1	0.70	1.9E-03	5.7E-03
3788976	**RAB27B**	RAB27B, member RAS oncogene family	0.70	3.5E-04	1.5E-03
3189932	**STXBP1**	syntaxin binding protein 1	0.70	3.3E-08	1.5E-06
3569200	**ATP6V1D**	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	0.70	1.1E-04	6.0E-04
3235516	**CAMK1D**	calcium/calmodulin-dependent protein kinase ID	0.70	5.5E-06	5.8E-05
3011838	**STEAP1**	six transmembrane epithelial antigen of the prostate 1	0.70	8.2E-05	4.7E-04
3326400	**CAT**	catalase	0.70	4.1E-07	8.5E-06
3991889	**FAM127A**	family with sequence similarity 127, member A	0.70	1.3E-06	2.0E-05
3875423	**BMP2**	bone morphogenetic protein 2	0.70	7.0E-06	7.0E-05
2835848	**SLC36A1**	solute carrier family 36 (proton/amino acid symporter), member 1	0.70	1.1E-06	1.7E-05
3592401	**C15ORF48**	chromosome 15 open reading frame 48	0.70	2.6E-04	1.2E-03
3968122	**TBL1X**	transducin (beta)-like 1X-linked	0.70	4.1E-06	4.6E-05
3718555	**SLFN5**	schlafen family member 5	0.70	2.5E-05	1.8E-04
2577028	**NCKAP5**	NCK-associated protein 5	0.70	3.9E-04	1.6E-03
2487082	**ANTXR1**	anthrax toxin receptor 1	0.70	6.4E-06	6.5E-05
2960010	**LMBRD1**	LMBR1 domain containing 1	0.69	2.4E-04	1.1E-03
3225855	**ANGPTL2**	angiopoietin-like 2	0.69	3.4E-06	4.1E-05
3204987	**OR13J1**	olfactory receptor, family 13, subfamily J, member 1	0.69	2.1E-03	6.1E-03
3759849	**PLEKHM1**	pleckstrin homology domain containing, family M (with RUN domain) member 1	0.69	6.6E-07	1.2E-05
2732391	**CCNG2**	cyclin G2	0.69	2.5E-06	3.3E-05
3469180	**SLC41A2**	solute carrier family 41, member 2	0.69	8.0E-04	2.8E-03
3528864	**MMP14**	matrix metallopeptidase 14 (membrane-inserted)	0.69	3.3E-07	7.3E-06
2331158	**AKIRIN1**	akirin 1	0.69	1.3E-05	1.2E-04
3147726	**SLC25A32**	solute carrier family 25, member 32	0.69	1.7E-05	1.4E-04
3591963	**EIF3J**	eukaryotic translation initiation factor 3, subunit J	0.68	1.3E-04	6.6E-04
3839057	**TBC1D17**	TBC1 domain family, member 17	0.68	2.9E-07	6.7E-06
3049292	**IGFBP3**	insulin-like growth factor binding protein 3	0.68	1.3E-05	1.2E-04

3984907	**ARMCX1**	armadillo repeat containing, X-linked 1	0.68	6.2E-06	6.4E-05
3403414	**DPPA3**	developmental pluripotency associated 3	0.68	1.2E-03	3.8E-03
2748061	**TRIM2**	tripartite motif-containing 2	0.68	9.8E-04	3.3E-03
3778504	**RAB31**	RAB31, member RAS oncogene family	0.68	1.6E-06	2.3E-05
3261165	**BTRC**	beta-transducin repeat containing	0.68	4.1E-06	4.6E-05
3711262	**HS3ST3B1**	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	0.68	1.2E-04	6.2E-04
3567187	**DHRS7**	dehydrogenase/reductase (SDR family) member 7	0.68	1.8E-05	1.4E-04
2425400	**EXTL2**	exostoses (multiple)-like 2	0.68	3.2E-04	1.4E-03
4023467	**ARHGEF6**	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	0.68	3.6E-05	2.5E-04
2780099	**NHEDC2**	Na+/H+ exchanger domain containing 2	0.68	1.0E-05	9.2E-05
3661152	**FTO**	fat mass and obesity associated	0.68	2.0E-07	5.1E-06
3989089	**ZBTB33**	zinc finger and BTB domain containing 33	0.68	1.2E-03	3.8E-03
3353640	**GRAMD1B**	GRAM domain containing 1B	0.67	1.1E-05	9.7E-05
2532272	**ALPP**	alkaline phosphatase, placental	0.67	1.3E-02	2.6E-02
3690154	**NETO2**	neuropilin (NRP) and tolloid (TLL)-like 2	0.67	3.0E-05	2.1E-04
3917204	**C21ORF7**	chromosome 21 open reading frame 7	0.67	6.9E-07	1.3E-05
4017381	**TSC22D3**	TSC22 domain family, member 3	0.67	8.9E-06	8.4E-05
3551485	**EML1**	echinoderm microtubule associated protein like 1	0.67	2.8E-05	2.1E-04
3115504	**MYC**	v-myc myelocytomatosis viral oncogene homolog (avian)	0.67	5.9E-07	1.1E-05
3250990	**UNC5B**	unc-5 homolog B (C. elegans)	0.67	1.3E-05	1.1E-04
2777447	**NAP1L5**	nucleosome assembly protein 1-like 5	0.67	1.0E-04	5.6E-04
3645816	**ZNF75A**	zinc finger protein 75a	0.67	4.8E-04	1.9E-03
2988726	**FSCN1**	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	0.67	8.7E-07	1.5E-05
3652271	**C16ORF52**	chromosome 16 open reading frame 52	0.67	2.9E-05	2.1E-04
3326067	**C11ORF41**	chromosome 11 open reading frame 41	0.67	1.0E-03	3.3E-03
3815045	**HCN2**	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	0.67	4.1E-05	2.7E-04
3890109	**C20ORF108**	chromosome 20 open reading frame 108	0.66	2.0E-05	1.6E-04
3212008	**FRMD3**	FERM domain containing 3	0.66	3.0E-06	3.7E-05
3418492	**TSPAN31**	tetraspanin 31	0.66	5.8E-07	1.1E-05
2968652	**SESN1**	sestrin 1	0.66	4.1E-04	1.7E-03
2992814	**GPNMB**	glycoprotein (transmembrane) nmb	0.66	1.0E-06	1.7E-05
3998632	**PNPLA4**	patatin-like phospholipase domain containing 4	0.66	4.5E-05	2.9E-04
3448152	**ITPR2**	inositol 1,4,5-triphosphate receptor, type 2	0.66	1.6E-03	4.7E-03
3928538	**KRTAP19-5**	keratin associated protein 19-5	0.66	1.6E-02	3.0E-02
3462816	**PHLDA1**	pleckstrin homology-like domain, family A, member 1	0.66	6.7E-08	2.4E-06
3887635	**NCOA3**	nuclear receptor coactivator 3	0.66	5.0E-05	3.2E-04
3061651	**BET1**	blocked early in transport 1 homolog (S. cerevisiae)	0.66	2.8E-04	1.2E-03
3627422	**RORA**	RAR-related orphan receptor A	0.66	8.3E-07	1.5E-05
3419471	**RPL14**	ribosomal protein L14	0.66	2.6E-05	1.9E-04
2802696	**FAM105A**	family with sequence similarity 105, member A	0.66	8.9E-04	3.0E-03
3283920	**ARHGAP12**	Rho GTPase activating protein 12	0.66	2.2E-03	6.2E-03
3911814	**SLMO2**	slowmo homolog 2 (Drosophila)	0.66	4.4E-05	2.9E-04
3807487	**RPL17**	ribosomal protein L17	0.65	9.6E-05	5.3E-04
2972310	**SERINC1**	serine incorporator 1	0.65	1.3E-03	4.0E-03
3819200	**EVI5L**	ecotropic viral integration site 5-like	0.65	4.0E-07	8.4E-06
3565739	**ATG14**	ATG14 autophagy related 14 homolog (S. cerevisiae)	0.65	7.6E-05	4.4E-04
3192062	**BAT2L1**	HLA-B associated transcript 2-like 1	0.65	4.0E-05	2.7E-04
3250699	**EIF4EBP2**	eukaryotic translation initiation factor 4E binding protein 2	0.65	3.6E-07	7.8E-06
2913277	**KCNQ5**	potassium voltage-gated channel, KQT-like subfamily, member 5	0.65	9.8E-05	5.4E-04
3736636	**C1QTNF1**	C1q and tumor necrosis factor related protein 1	0.65	3.8E-06	4.3E-05
3984779	**HNRNPH2**	heterogeneous nuclear ribonucleoprotein H2 (H')	0.65	7.7E-05	4.5E-04
3214451	**NFIL3**	nuclear factor, interleukin 3 regulated	0.65	6.1E-04	2.3E-03
3230610	**ABCA2**	ATP-binding cassette, sub-family A (ABC1), member 2	0.65	8.7E-08	2.9E-06
3335338	**FAM89B**	family with sequence similarity 89, member B	0.65	2.8E-06	3.6E-05
3868963	**ETFB**	electron-transfer-flavoprotein, beta polypeptide	0.65	2.9E-06	3.6E-05
2977265	**HIVEP2**	human immunodeficiency virus type I enhancer binding protein 2	0.65	1.5E-03	4.5E-03
2915828	**NT5E**	5'-nucleotidase, ecto (CD73)	0.65	1.2E-05	1.0E-04
2970985	**TSPYL4**	TSPY-like 4	0.65	5.1E-07	1.0E-05
3895795	**RNF24**	ring finger protein 24	0.64	3.4E-07	7.6E-06
2643592	**EPHB1**	EPH receptor B1	0.64	7.4E-06	7.3E-05
3732230	**PITPNC1**	phosphatidylinositol transfer protein, cytoplasmic 1	0.64	2.3E-05	1.7E-04
3018866	**DNAJB9**	DnaJ (Hsp40) homolog, subfamily B, member 9	0.64	3.9E-04	1.6E-03
2949859	**PBX2**	pre-B-cell leukemia homeobox 2	0.64	1.6E-02	3.1E-02
2821347	**ERAP2**	endoplasmic reticulum aminopeptidase 2	0.64	8.8E-04	3.0E-03
3758510	**ETV4**	ets variant 4	0.64	1.2E-05	1.0E-04
3368748	**FBXO3**	F-box protein 3	0.64	1.4E-04	7.0E-04
3830051	**SCN1B**	sodium channel, voltage-gated, type I, beta	0.64	6.7E-06	6.7E-05
3145801	**TSPYL5**	TSPY-like 5	0.64	1.3E-05	1.1E-04
2792420	**TMEM192**	transmembrane protein 192	0.64	1.8E-04	8.9E-04
2649113	**TIPARP**	TCDD-inducible poly(ADP-ribose) polymerase	0.64	1.3E-05	1.2E-04
3712062	**TRPV2**	transient receptor potential cation channel, subfamily V, member 2	0.64	1.4E-06	2.1E-05
3448975	**ERGIC2**	ERGIC and golgi 2	0.64	2.6E-03	7.2E-03
3163818	**SH3GL2**	SH3-domain GRB2-like 2	0.64	3.6E-05	2.5E-04

2934308	**IGF2R**	insulin-like growth factor 2 receptor	0.64	2.0E-06	2.8E-05
3762473	**TOB1**	transducer of ERBB2, 1	0.64	2.2E-06	3.0E-05
2806468	**IL7R**	interleukin 7 receptor	0.63	1.6E-04	8.1E-04
3835467	**ZNF234**	zinc finger protein 234	0.63	5.5E-04	2.1E-03
3432514	**OAS2**	2'-5'-oligoadenylate synthetase 2, 69/71kDa	0.63	5.7E-04	2.2E-03
2583602	**RBMS1**	RNA binding motif, single stranded interacting protein 1	0.63	5.2E-04	2.0E-03
2849469	**ANKH**	ankylosis, progressive homolog (mouse)	0.63	6.2E-06	6.4E-05
2832499	**PCDHB15**	protocadherin beta 15 // protocadherin beta 15	0.63	4.0E-05	2.7E-04
3662650	**ARL2BP**	ADP-ribosylation factor-like 2 binding protein	0.63	1.3E-06	2.0E-05
3578069	**C14ORF139**	chromosome 14 open reading frame 139	0.63	7.2E-05	4.2E-04
2832325	**PCDHB5**	protocadherin beta 5	0.63	9.2E-05	5.1E-04
3859946	**HSPB6**	heat shock protein, alpha-crystallin-related, B6	0.63	3.1E-06	3.8E-05
2326496	**DHDDS**	dehydrodolichyl diphosphate synthase	0.63	2.1E-06	2.9E-05
3215146	**NINJ1**	ninjurin 1	0.63	1.4E-05	1.2E-04
3188111	**PTGS1**	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	0.63	2.5E-06	3.3E-05
3878836	**RIN2**	Ras and Rab interactor 2	0.62	5.2E-06	5.5E-05
2992963	**CCDC126**	coiled-coil domain containing 126	0.62	2.1E-04	9.9E-04
3444503	**TAS2R31**	taste receptor, type 2, member 31	0.62	5.4E-03	1.3E-02
3318666	**SMPD1**	sphingomyelin phosphodiesterase 1, acid lysosomal	0.62	2.6E-07	6.1E-06
4048764	**C6ORF35**	chromosome 6 open reading frame 35	0.62	2.6E-03	7.2E-03
2887490	**STC2**	stanniocalcin 2	0.62	7.8E-06	7.6E-05
2406139	**KIAA0319L**	KIAA0319-like	0.62	1.3E-06	2.0E-05
3845495	**REXO1**	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	0.62	2.7E-05	2.0E-04
3403567	**NECAP1**	NECAP endocytosis associated 1	0.62	2.8E-05	2.1E-04
3412345	**TMEM117**	transmembrane protein 117	0.62	6.1E-04	2.3E-03
3324713	**METT5D1**	methyltransferase 5 domain containing 1	0.62	2.8E-02	4.8E-02
2731636	**PARM1**	prostate androgen-regulated mucin-like protein 1	0.62	3.6E-06	4.2E-05
2824581	**KCNN2**	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	0.62	1.2E-04	6.4E-04
2645387	**ACPL2**	acid phosphatase-like 2	0.62	1.6E-05	1.3E-04
3496916	**GPR180**	G protein-coupled receptor 180	0.62	1.7E-03	5.1E-03
3786471	**SETBP1**	SET binding protein 1	0.62	1.8E-06	2.5E-05
3214668	**IARS**	isoleucyl-tRNA synthetase	0.61	1.8E-07	4.9E-06
3364095	**CYP2R1**	cytochrome P450, family 2, subfamily R, polypeptide 1	0.61	2.1E-05	1.6E-04
3840883	**ZNF761**	zinc finger protein 761	0.61	3.3E-04	1.4E-03
2979267	**ULBP3**	UL16 binding protein 3	0.61	1.2E-04	6.4E-04
3021158	**C7ORF58**	chromosome 7 open reading frame 58	0.61	2.3E-04	1.0E-03
3237548	**ARL5B**	ADP-ribosylation factor-like 5B	0.61	7.7E-04	2.7E-03
3729014	**GDPD1**	glycerophosphodiester phosphodiesterase domain containing 1	0.61	1.0E-04	5.5E-04
3894322	**SRXN1**	sulfiredoxin 1	0.61	2.1E-05	1.6E-04
3701297	**CDYL2**	chromodomain protein, Y-like 2	0.61	6.1E-06	6.4E-05
2645275	**SLC25A36**	solute carrier family 25, member 36	0.61	6.0E-03	1.4E-02
3127775	**TNFRSF10A**	tumor necrosis factor receptor superfamily, member 10a	0.61	1.6E-06	2.4E-05
3957207	**GATSL3**	GATS protein-like 3	0.61	2.0E-07	5.2E-06
3764872	**PTRH2**	peptidyl-tRNA hydrolase 2	0.61	1.3E-04	6.5E-04
3190659	**SET**	SET nuclear oncogene	0.61	1.0E-06	1.7E-05
3843399	**ZNF134**	zinc finger protein 134	0.61	1.5E-04	7.5E-04
3432678	**TPCN1**	two pore segment channel 1	0.61	1.4E-05	1.2E-04
2731757	**THAP6**	THAP domain containing 6	0.61	7.9E-04	2.8E-03
2709414	**TBCCD1**	TBCC domain containing 1	0.61	1.0E-03	3.3E-03
3294159	**P4HA1**	prolyl 4-hydroxylase, alpha polypeptide I	0.61	2.8E-04	1.2E-03
2473784	**EPT1**	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)	0.60	3.4E-04	1.4E-03
3352904	**SC5DL**	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	0.60	1.1E-03	3.7E-03
3542063	**SLC39A9**	solute carrier family 39 (zinc transporter), member 9	0.60	2.0E-06	2.8E-05
3695107	**TK2**	thymidine kinase 2, mitochondrial	0.60	6.1E-07	1.2E-05
3204558	**KIAA1539**	KIAA1539	0.60	4.9E-07	9.8E-06
3842724	**ZNF583**	zinc finger protein 583	0.60	2.6E-03	7.1E-03
2916345	**SLC35A1**	solute carrier family 35 (CMP-sialic acid transporter), member A1	0.60	2.1E-03	6.1E-03
3837504	**SEPW1**	selenoprotein W, 1	0.60	1.0E-05	9.5E-05
4028512	**RPS4Y1**	ribosomal protein S4, Y-linked 1	0.60	7.6E-05	4.4E-04
2867443	**MCTP1**	multiple C2 domains, transmembrane 1	0.60	5.1E-05	3.2E-04
3449700	**FAM60A**	family with sequence similarity 60, member A	0.60	5.5E-05	3.5E-04
3047660	**GLI3**	GLI family zinc finger 3	0.60	4.3E-05	2.8E-04
3019793	**FOXP2**	forkhead box P2	0.60	6.1E-06	6.3E-05
2730746	**SLC4A4**	solute carrier family 4, sodium bicarbonate cotransporter, member 4	0.60	2.1E-04	1.0E-03
3572278	**NEK9**	NIMA (never in mitosis gene a)- related kinase 9	0.60	1.4E-06	2.1E-05
3854756	**RAB3A**	RAB3A, member RAS oncogene family	0.60	5.3E-05	3.3E-04
3429460	**TXNRD1**	thioredoxin reductase 1	0.60	1.6E-05	1.3E-04
3919033	**SLC5A3**	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	0.60	6.0E-04	2.3E-03
3154317	**NDRG1**	N-myc downstream regulated 1	0.60	8.1E-06	7.8E-05
2935475	**QKI**	quaking homolog, KH domain RNA binding (mouse)	0.60	2.6E-04	1.2E-03
3744410	**KRBA2**	KRAB-A domain containing 2	0.59	1.9E-02	3.5E-02

2771718	**UBA6**	ubiquitin-like modifier activating enzyme 6	0.59	2.0E-03	5.8E-03
2650393	**PPM1L**	protein phosphatase, Mg2+/Mn2+ dependent, 1L	0.59	3.8E-05	2.6E-04
2420615	**LPAR3**	lysophosphatidic acid receptor 3	0.59	1.1E-03	3.6E-03
3230811	**DPP7**	dipeptidyl-peptidase 7	0.59	1.6E-06	2.3E-05
2492064	**KDM3A**	lysine (K)-specific demethylase 3A	0.59	5.0E-04	1.9E-03
3744800	**STX8**	syntaxin 8	0.59	1.8E-04	8.7E-04
3592023	**B2M**	beta-2-microglobulin	0.59	3.6E-06	4.2E-05
3613725	**NDN**	necdin homolog (mouse)	0.59	5.8E-05	3.6E-04
3566495	**C14ORF37**	chromosome 14 open reading frame 37	0.59	3.9E-05	2.6E-04
2977621	**PLAGL1**	pleiomorphic adenoma gene-like 1	0.59	3.0E-05	2.1E-04
3430776	**ISCU**	iron-sulfur cluster scaffold homolog (E. coli)	0.59	1.6E-05	1.3E-04
3452231	**SLC38A1**	solute carrier family 38, member 1	0.59	6.6E-05	4.0E-04
3821727	**ZNF136**	zinc finger protein 136	0.59	7.1E-05	4.2E-04
2639225	**PDIA5**	protein disulfide isomerase family A, member 5	0.59	1.1E-05	9.6E-05
3058209	**MAGI2**	membrane associated guanylate kinase, WW and PDZ domain containing 2	0.59	2.9E-05	2.1E-04
3690193	**ITFG1**	integrin alpha FG-GAP repeat containing 1	0.59	1.3E-04	6.5E-04
2519294	**FAM171B**	family with sequence similarity 171, member B	0.59	4.3E-03	1.1E-02
3774906	**SECTM1**	secreted and transmembrane 1	0.59	8.1E-06	7.8E-05
3924372	**COL6A1**	collagen, type VI, alpha 1	0.59	1.8E-06	2.5E-05
2946345	**HIST1H2BG**	histone cluster 1, H2bg	-0.59	3.0E-04	1.3E-03
3380996	**C11ORF51**	chromosome 11 open reading frame 51	-0.59	2.2E-06	3.0E-05
3250093	**KIAA1279**	KIAA1279	-0.59	3.0E-06	3.7E-05
3630450	**AAGAB**	alpha- and gamma-adaptin binding protein	-0.59	5.1E-05	3.2E-04
3355145	**ST3GAL4**	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	-0.59	2.1E-05	1.6E-04
4019486	**SEPT6**	septin 6	-0.59	3.9E-06	4.4E-05
2591906	**OSGEPL1**	O-sialoglycoprotein endopeptidase-like 1	-0.59	2.4E-04	1.1E-03
3215701	**FANCC**	Fanconi anemia, complementation group C	-0.59	1.4E-05	1.2E-04
3445908	**EPS8**	epidermal growth factor receptor pathway substrate 8	-0.59	1.2E-05	1.0E-04
3436544	**BRI3BP**	BRI3 binding protein	-0.59	1.5E-05	1.3E-04
2451593	**CHI3L1**	chitinase 3-like 1 (cartilage glycoprotein-39)	-0.59	2.6E-05	1.9E-04
3113456	**MTBP**	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein, 104kDa	-0.59	7.7E-04	2.7E-03
3249641	**MYPN**	myopalladin	-0.59	3.4E-07	7.5E-06
3623031	**FBN1**	fibrillin 1	-0.59	2.7E-05	2.0E-04
2601648	**DOCK10**	dedicator of cytokinesis 10	-0.59	8.3E-04	2.9E-03
2713555	**KIAA0226**	KIAA0226	-0.59	1.3E-06	2.0E-05
3842264	**NAT14**	N-acetyltransferase 14 (GCN5-related, putative)	-0.60	3.1E-05	2.2E-04
2510884	**ARL6IP6**	ADP-ribosylation-like factor 6 interacting protein 6	-0.60	2.4E-03	6.7E-03
2835006	**GRPEL2**	GrpE-like 2, mitochondrial (E. coli)	-0.60	2.0E-04	9.5E-04
2474977	**FOSL2**	FOS-like antigen 2	-0.60	4.4E-06	4.8E-05
3354879	**HYLS1**	hydrolethalus syndrome 1	-0.60	1.1E-04	5.8E-04
3941010	**SRR**	SRR1 domain containing	-0.60	1.5E-06	2.3E-05
3178480	**NXNL2**	nucleoredoxin-like 2	-0.60	5.1E-04	2.0E-03
2427074	**PSMA5**	proteasome (prosome, macropain) subunit, alpha type, 5	-0.60	5.0E-05	3.2E-04
3028956	**TAS2R39**	taste receptor, type 2, member 39	-0.60	1.6E-02	3.1E-02
2903285	**PSMB9**	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	-0.60	2.1E-06	2.9E-05
3329206	**CREB3L1**	cAMP responsive element binding protein 3-like 1	-0.60	1.3E-06	2.0E-05
3719210	**DHRS11**	dehydrogenase/reductase (SDR family) member 11	-0.60	8.8E-06	8.4E-05
2460325	**C1ORF198**	chromosome 1 open reading frame 198	-0.60	6.9E-06	6.9E-05
2523689	**ABI2**	abl-interactor 2	-0.60	2.5E-05	1.9E-04
3094334	**GPR124**	G protein-coupled receptor 124	-0.60	6.3E-06	6.4E-05
3703885	**SLC7A5**	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	-0.60	1.2E-07	3.6E-06
3671935	**CRISPLD2**	cysteine-rich secretory protein LCCL domain containing 2	-0.60	2.8E-05	2.0E-04
2705748	**NCEH1**	neutral cholesterol ester hydrolase 1	-0.60	2.5E-05	1.8E-04
2812435	**ERBB2IP**	erbb2 interacting protein	-0.60	4.7E-03	1.1E-02
2475710	**LCLAT1**	lysocardiolipin acyltransferase 1	-0.60	1.6E-05	1.3E-04
2427791	**DENND2D**	DENN/MADD domain containing 2D	-0.60	5.8E-06	6.1E-05
3453712	**RHEBL1**	Ras homolog enriched in brain like 1	-0.61	5.0E-04	1.9E-03
3694657	**CDH11**	cadherin 11, type 2, OB-cadherin (osteoblast)	-0.61	6.4E-06	6.6E-05
2710474	**LEPREL1**	leprecan-like 1	-0.61	8.8E-05	4.9E-04
2437801	**ARHGEF2**	Rho/Rac guanine nucleotide exchange factor (GEF) 2	-0.61	4.0E-06	4.6E-05
3485863	**EXOSC8**	exosome component 8	-0.61	5.2E-05	3.3E-04
2644461	**ARMC8**	armadillo repeat containing 8	-0.61	1.8E-04	8.9E-04
3042973	**HOXA11**	homeobox A11	-0.61	5.6E-06	5.8E-05
2785282	**SCLT1**	sodium channel and clathrin linker 1	-0.61	5.5E-04	2.1E-03
2847292	**NSUN2**	NOP2/Sun domain family, member 2	-0.61	3.2E-06	3.9E-05
3309755	**C10ORF119**	chromosome 10 open reading frame 119	-0.61	9.3E-07	1.6E-05
3417184	**SUOX**	sulfite oxidase	-0.61	1.4E-06	2.2E-05
3534785	**PPIL5**	peptidylprolyl isomerase (cyclophilin)-like 5	-0.61	1.6E-05	1.3E-04

2360206	**ATP8B2**	ATPase, class I, type 8B, member 2	-0.61	1.0E-05	9.4E-05
2584904	**SLC38A11**	solute carrier family 38, member 11	-0.61	8.0E-05	4.6E-04
3643938	**TMEM204**	transmembrane protein 204	-0.61	1.1E-06	1.8E-05
2752006	**SAP30**	Sin3A-associated protein, 30kDa	-0.61	4.3E-05	2.8E-04
3390180	**KDELC2**	KDEL (Lys-Asp-Glu-Leu) containing 2	-0.62	1.7E-04	8.2E-04
3865635	**DMPK**	dystrophia myotonica-protein kinase	-0.62	6.3E-06	6.5E-05
2697490	**CEP70**	centrosomal protein 70kDa	-0.62	7.6E-04	2.7E-03
3833757	**SNRPA**	small nuclear ribonucleoprotein polypeptide A	-0.62	4.0E-06	4.5E-05
3733065	**MAP2K6**	mitogen-activated protein kinase kinase 6	-0.62	3.0E-05	2.2E-04
3361531	**OR10A3**	olfactory receptor, family 10, subfamily A, member 3	-0.62	3.6E-03	9.2E-03
2739792	**ALPK1**	alpha-kinase 1	-0.62	1.2E-05	1.1E-04
3907524	**PLTP**	phospholipid transfer protein	-0.62	1.4E-07	4.1E-06
3505937	**CENPJ**	centromere protein J	-0.62	4.1E-04	1.7E-03
3601511	**ISLR**	immunoglobulin superfamily containing leucine-rich repeat	-0.62	1.8E-04	8.8E-04
3380901	**NUMA1**	nuclear mitotic apparatus protein 1	-0.62	1.8E-07	4.7E-06
2791894	**FSTL5**	follistatin-like 5	-0.62	7.1E-03	1.6E-02
3333247	**FADS2**	fatty acid desaturase 2	-0.63	1.4E-06	2.1E-05
3350830	**TAGLN**	transgelin	-0.63	5.3E-07	1.0E-05
2738723	**HADH**	hydroxyacyl-CoA dehydrogenase	-0.63	2.3E-05	1.7E-04
3387483	**MTMR2**	myotubularin related protein 2	-0.63	2.2E-05	1.7E-04
3744463	**MYH10**	myosin, heavy chain 10, non-muscle	-0.63	2.9E-04	1.3E-03
3904566	**DSN1**	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	-0.63	7.1E-06	7.1E-05
3199790	**PSIP1**	PC4 and SFRS1 interacting protein 1	-0.63	1.8E-04	8.8E-04
3754227	**MYO19**	myosin XIX	-0.63	4.4E-05	2.9E-04
2664452	**ANKRD28**	ankyrin repeat domain 28	-0.63	6.1E-04	2.3E-03
2407478	**FHL3**	four and a half LIM domains 3	-0.63	4.8E-06	5.2E-05
3976519	**RBM3**	RNA binding motif (RNP1, RRM) protein 3	-0.63	1.5E-07	4.2E-06
3251298	**CHST3**	carbohydrate (chondroitin 6) sulfotransferase 3	-0.63	7.2E-07	1.3E-05
3822195	**NACC1**	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing	-0.63	1.3E-07	3.9E-06
2980258	**MTRF1L**	mitochondrial translational release factor 1-like	-0.63	2.4E-03	6.7E-03
3838118	**RUVBL2**	RuvB-like 2 (E. coli)	-0.63	7.3E-06	7.3E-05
3401197	**C12ORF32**	chromosome 12 open reading frame 32	-0.63	1.9E-06	2.7E-05
3223425	**CDK5RAP2**	CDK5 regulatory subunit associated protein 2	-0.63	1.2E-04	6.2E-04
3466556	**NTN4**	netrin 4	-0.63	4.0E-03	1.0E-02
2835576	**SYNPO**	synaptopodin	-0.64	2.4E-06	3.2E-05
2359764	**SNAPIN**	SNAP-associated protein	-0.64	4.3E-05	2.8E-04
3304004	**NPM3**	nucleophosmin/nucleoplasmin 3	-0.64	4.6E-06	5.0E-05
3355056	**FOXRED1**	FAD-dependent oxidoreductase domain containing 1	-0.64	1.3E-04	6.6E-04
3417531	**COQ10A**	coenzyme Q10 homolog A (S. cerevisiae)	-0.64	1.9E-05	1.5E-04
3281703	**PRTFDC1**	phosphoribosyl transferase domain containing 1	-0.64	2.1E-06	2.9E-05
2454935	**ANGEL2**	angel homolog 2 (Drosophila)	-0.64	1.9E-05	1.5E-04
3845909	**LMNB2**	lamin B2	-0.64	1.2E-06	1.9E-05
3023149	**FLNC**	filamin C, gamma	-0.64	1.3E-06	2.0E-05
3065740	**RELN**	reelin	-0.64	2.6E-04	1.2E-03
2328868	**HDAC1**	histone deacetylase 1	-0.64	2.4E-06	3.2E-05
3322717	**GTF2H1**	general transcription factor IIH, polypeptide 1, 62kDa	-0.64	9.6E-06	8.8E-05
3373724	**SSRP1**	structure specific recognition protein 1	-0.64	3.5E-07	7.7E-06
3510066	**POSTN**	periostin, osteoblast specific factor	-0.64	6.6E-04	2.4E-03
2730714	**DCK**	deoxycytidine kinase	-0.64	2.7E-03	7.3E-03
3633048	**EDC3**	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	-0.64	1.9E-06	2.7E-05
2343231	**NEXN**	nexilin (F actin binding protein)	-0.65	4.8E-03	1.2E-02
2877314	**CDC23**	cell division cycle 23 homolog (S. cerevisiae)	-0.65	1.6E-05	1.3E-04
3388785	**MMP10**	matrix metallopeptidase 10 (stromelysin 2)	-0.65	1.4E-03	4.4E-03
2358993	**TUFT1**	tuftelin 1	-0.65	9.1E-06	8.6E-05
2885099	**NUDCD2**	NudC domain containing 2	-0.65	1.5E-05	1.3E-04
3226644	**ZDHHC12**	zinc finger, DHHC-type containing 12	-0.65	4.8E-07	9.7E-06
2890148	**HNRNPH1**	heterogeneous nuclear ribonucleoprotein H1 (H)	-0.65	1.3E-04	6.6E-04
2474681	**GPN1**	GPN-loop GTPase 1	-0.65	5.7E-06	6.0E-05
2945741	**FAM65B**	family with sequence similarity 65, member B	-0.65	4.3E-05	2.8E-04
3405440	**CDKN1B**	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-0.65	1.8E-04	8.8E-04
3235414	**SEC61A2**	Sec61 alpha 2 subunit (S. cerevisiae)	-0.65	3.6E-05	2.5E-04
3150715	**DSCC1**	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	-0.65	1.5E-04	7.3E-04
2364381	**RGS4**	regulator of G-protein signaling 4	-0.66	1.7E-05	1.4E-04
2352804	**OLFML3**	olfactomedin-like 3	-0.66	4.9E-07	9.8E-06
2769947	**CLOCK**	clock homolog (mouse)	-0.66	4.9E-04	1.9E-03
2902633	**MSH5**	mutS homolog 5 (E. coli)	-0.66	5.9E-07	1.1E-05
3653398	**TNRC6A**	trinucleotide repeat containing 6A	-0.66	4.8E-04	1.9E-03
2523045	**FZD7**	frizzled homolog 7 (Drosophila)	-0.66	9.0E-06	8.5E-05
2827057	**GRAMD3**	GRAM domain containing 3	-0.66	2.9E-05	2.1E-04
3144973	**RAD54B**	RAD54 homolog B (S. cerevisiae)	-0.66	2.3E-06	3.1E-05
2439842	**TAGLN2**	transgelin 2	-0.66	7.9E-08	2.7E-06
2948564	**MDC1**	mediator of DNA-damage checkpoint 1	-0.66	7.4E-07	1.4E-05

2742134	**SPATA5**	spermatogenesis associated 5	-0.66	2.9E-05	2.1E-04
3373845	**SLC43A3**	solute carrier family 43, member 3	-0.66	3.9E-06	4.4E-05
2943874	**KIF13A**	kinesin family member 13A	-0.67	2.6E-04	1.2E-03
2642887	**CCRL1**	chemokine (C-C motif) receptor-like 1	-0.67	2.6E-02	4.4E-02
3044129	**GGCT**	gamma-glutamylcyclotransferase	-0.67	1.7E-04	8.2E-04
2406064	**SFPQ**	splicing factor proline/glutamine-rich	-0.67	7.5E-06	7.4E-05
3665997	**DUS2L**	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	-0.67	9.4E-06	8.7E-05
3739108	**FN3KRP**	fructosamine 3 kinase related protein	-0.67	1.4E-05	1.2E-04
3991698	**HPRT1**	hypoxanthine phosphoribosyltransferase 1	-0.67	7.8E-05	4.5E-04
3628832	**DAPK2**	death-associated protein kinase 2	-0.67	1.3E-06	2.0E-05
2336650	**PODN**	podocan	-0.67	3.2E-06	3.8E-05
2961177	**COL12A1**	collagen, type XII, alpha 1	-0.67	7.7E-04	2.7E-03
2668351	**UBP1**	upstream binding protein 1 (LBP-1a)	-0.67	5.1E-06	5.5E-05
2655476	**AP2M1**	adaptor-related protein complex 2, mu 1 subunit	-0.67	1.6E-05	1.3E-04
3723005	**FZD2**	frizzled homolog 2 (Drosophila)	-0.67	3.8E-07	8.2E-06
2336539	**ZYG11A**	zyg-11 homolog A (C. elegans)	-0.67	2.1E-05	1.6E-04
2491676	**VAMP5**	vesicle-associated membrane protein 5 (myobrevin)	-0.67	1.1E-06	1.8E-05
3328389	**EXT2**	exostosin 2	-0.67	7.8E-08	2.7E-06
3529951	**NYNRIN**	NYN domain and retroviral integrase containing	-0.67	2.5E-05	1.9E-04
3176999	**RMI1**	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	-0.67	7.8E-04	2.8E-03
2452405	**NUAK2**	NUAK family, SNF1-like kinase, 2	-0.68	2.7E-05	2.0E-04
3633578	**CSPG4**	chondroitin sulfate proteoglycan 4	-0.68	8.6E-07	1.5E-05
2347023	**CCDC18**	coiled-coil domain containing 18	-0.68	1.0E-03	3.4E-03
2674526	**NICN1**	nicolin 1	-0.68	7.8E-06	7.6E-05
2379754	**SMYD2**	SET and MYND domain containing 2	-0.68	3.4E-06	4.0E-05
2531779	**ARMC9**	armadillo repeat containing 9	-0.68	7.0E-06	7.0E-05
2440476	**F11R**	F11 receptor	-0.68	2.8E-05	2.1E-04
3947096	**CCDC134**	coiled-coil domain containing 134	-0.68	1.6E-06	2.4E-05
2856634	**ARL15**	ADP-ribosylation factor-like 15	-0.68	4.0E-04	1.6E-03
2403557	**SNORA44**	small nucleolar RNA, H/ACA box 44	-0.68	2.4E-05	1.8E-04
3428783	**DRAM1**	DNA-damage regulated autophagy modulator 1	-0.68	2.8E-06	3.5E-05
3190463	**ODF2**	outer dense fiber of sperm tails 2	-0.68	1.0E-06	1.7E-05
2610707	**HRH1**	histamine receptor H1	-0.68	3.7E-05	2.5E-04
2519577	**COL3A1**	collagen, type III, alpha 1	-0.68	4.7E-05	3.0E-04
3129465	**INTS9**	integrator complex subunit 9	-0.68	3.6E-06	4.3E-05
2949471	**NEU1**	sialidase 1 (lysosomal sialidase)	-0.68	9.8E-07	1.7E-05
2944491	**MBOAT1**	membrane bound O-acyltransferase domain containing 1	-0.68	2.8E-06	3.5E-05
3860208	**ALKBH6**	alkB, alkylation repair homolog 6 (E. coli)	-0.68	2.8E-05	2.1E-04
3714896	**FAM27L**	family with sequence similarity 27-like	-0.68	1.2E-02	2.4E-02
3245682	**MAPK8**	mitogen-activated protein kinase 8	-0.68	1.8E-05	1.5E-04
3182781	**SMC2**	structural maintenance of chromosomes 2	-0.68	7.0E-04	2.5E-03
4024160	**ATP11C**	ATPase, class VI, type 11C	-0.69	8.5E-04	2.9E-03
3432467	**OAS3**	2'-5'-oligoadenylate synthetase 3, 100kDa	-0.69	9.3E-06	8.7E-05
3855358	**HOMER3**	homer homolog 3 (Drosophila)	-0.69	2.4E-06	3.2E-05
2348757	**HIAT1**	hippocampus abundant transcript 1	-0.69	1.2E-05	1.1E-04
2723710	**PGM2**	phosphoglucomutase 2	-0.69	2.3E-05	1.7E-04
2352743	**DCLRE1B**	DNA cross-link repair 1B	-0.69	4.0E-04	1.7E-03
3416278	**HOXC11**	homeobox C11	-0.69	3.5E-05	2.4E-04
3962678	**PACSIN2**	protein kinase C and casein kinase substrate in neurons 2	-0.69	2.6E-07	6.1E-06
3708961	**WRAP53**	WD repeat containing, antisense to TP53	-0.69	8.1E-06	7.8E-05
2863964	**ARSB**	arylsulfatase B	-0.69	7.0E-06	7.0E-05
3817501	**CHAF1A**	chromatin assembly factor 1, subunit A (p150)	-0.69	1.9E-05	1.5E-04
3102372	**SULF1**	sulfatase 1	-0.69	2.2E-04	1.0E-03
3088213	**SH2D4A**	SH2 domain containing 4A	-0.70	2.6E-07	6.2E-06
2344888	**CYR61**	cysteine-rich, angiogenic inducer, 61	-0.70	9.9E-07	1.7E-05
2858023	**PLK2**	polo-like kinase 2	-0.70	5.7E-05	3.6E-04
3858852	**RHPN2**	rhophilin, Rho GTPase binding protein 2	-0.70	4.4E-04	1.8E-03
3757329	**JUP**	junction plakoglobin	-0.70	1.3E-06	2.0E-05
2766492	**C4ORF34**	chromosome 4 open reading frame 34	-0.70	5.6E-05	3.5E-04
3232979	**AKR1C1**	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	-0.70	2.0E-03	5.7E-03
3236448	**SUV39H2**	suppressor of variegation 3-9 homolog 2 (Drosophila)	-0.70	5.8E-05	3.6E-04
3323052	**NAV2**	neuron navigator 2	-0.70	9.9E-07	1.7E-05
3683377	**GPRC5B**	G protein-coupled receptor, family C, group 5, member B	-0.70	2.1E-05	1.6E-04
2562198	**TGOLN2**	trans-golgi network protein 2	-0.70	1.8E-06	2.5E-05
3418610	**XRCC6BP1**	XRCC6 binding protein 1	-0.71	1.4E-07	4.1E-06
3415368	**KRT86**	keratin 86	-0.71	8.4E-05	4.7E-04
3896200	**PCNA**	proliferating cell nuclear antigen	-0.71	1.1E-05	1.0E-04
2389789	**SCCPDH**	saccharopine dehydrogenase (putative)	-0.71	6.6E-06	6.7E-05
2638467	**GTF2E1**	general transcription factor IIE, polypeptide 1, alpha 56kDa	-0.71	4.2E-05	2.8E-04
2999755	**AEBP1**	AE binding protein 1	-0.71	2.2E-07	5.5E-06
4054204	**APOD**	apolipoprotein D	-0.71	5.5E-05	3.5E-04
2880292	**DPYSL3**	dihydropyrimidinase-like 3	-0.71	5.0E-06	5.4E-05

3258260	**EXOC6**	exocyst complex component 6	-0.71	4.0E-05	2.7E-04
3707095	**ARRB2**	arrestin, beta 2	-0.71	1.0E-05	9.3E-05
2688813	**CCDC80**	coiled-coil domain containing 80	-0.71	2.6E-07	6.2E-06
3994710	**MAMLD1**	mastermind-like domain containing 1	-0.71	5.2E-06	5.5E-05
3464747	**KITLG**	KIT ligand	-0.72	4.7E-04	1.9E-03
3433538	**RNFT2**	ring finger protein, transmembrane 2	-0.72	4.0E-06	4.5E-05
3604006	**ARNT2**	aryl-hydrocarbon receptor nuclear translocator 2	-0.72	1.9E-07	4.9E-06
2394784	**NOL9**	nucleolar protein 9	-0.72	2.8E-06	3.5E-05
2458289	**LBR**	lamin B receptor	-0.72	2.0E-04	9.6E-04
2902574	**LY6G5B**	lymphocyte antigen 6 complex, locus G5B	-0.72	4.9E-06	5.3E-05
3635125	**MTHFS**	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	-0.72	5.2E-06	5.5E-05
3645253	**SRRM1**	serine/arginine repetitive matrix 2	-0.72	1.3E-05	1.1E-04
3683037	**ARL6IP1**	ADP-ribosylation factor-like 6 interacting protein 1	-0.72	2.5E-07	6.0E-06
3469319	**APPL2**	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	-0.72	5.4E-07	1.1E-05
2553911	**SMEK2**	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	-0.72	5.4E-05	3.4E-04
3367338	**KIF18A**	kinesin family member 18A	-0.72	1.5E-04	7.4E-04
3223646	**PSMD5**	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	-0.72	7.7E-07	1.4E-05
3855596	**NR2C2AP**	nuclear receptor 2C2-associated protein	-0.73	3.6E-05	2.5E-04
2413519	**HSPB11**	heat shock protein family B (small), member 11	-0.73	9.7E-06	8.9E-05
3772187	**EPR1**	effector cell peptidase receptor 1 (non-protein coding)	-0.73	3.1E-04	1.3E-03
3010082	**PHTF2**	putative homeodomain transcription factor 2	-0.73	2.8E-04	1.2E-03
3917563	**KRTAP1-5**	keratin associated protein 15-1	-0.73	1.4E-05	1.2E-04
3456081	**RARG**	retinoic acid receptor, gamma	-0.73	4.4E-07	9.1E-06
3205488	**ZBTB5**	zinc finger and BTB domain containing 5	-0.73	3.6E-06	4.2E-05
2519480	**GULP1**	GULP, engulfment adaptor PTB domain containing 1	-0.73	4.6E-05	3.0E-04
3539499	**RHOJ**	ras homolog gene family, member J	-0.73	2.6E-06	3.3E-05
2929870	**STXBP5**	syntaxin binding protein 5 (tomosyn)	-0.74	1.6E-04	8.0E-04
2560286	**LOXL3**	lysyl oxidase-like 3	-0.74	2.9E-08	1.3E-06
3929038	**C21ORF45**	chromosome 21 open reading frame 45	-0.74	8.3E-08	2.8E-06
2695941	**TOPBP1**	topoisomerase (DNA) II binding protein 1	-0.74	3.4E-04	1.4E-03
2353237	**VANGL1**	vang-like 1 (van gogh, Drosophila)	-0.74	2.3E-05	1.8E-04
3447694	**BCAT1**	branched chain amino-acid transaminase 1, cytosolic	-0.74	3.3E-04	1.4E-03
3863811	**PSG6**	pregnancy specific beta-1-glycoprotein 6	-0.74	2.0E-03	5.9E-03
2654091	**USP13**	ubiquitin specific peptidase 13 (isopeptidase T-3)	-0.74	4.9E-06	5.3E-05
2388794	**ZNF238**	zinc finger protein 238	-0.74	8.2E-06	7.9E-05
2426951	**PSRC1**	proline/serine-rich coiled-coil 1	-0.75	4.2E-06	4.7E-05
2375784	**NCRNA00260**	non-protein coding RNA 260	-0.75	3.7E-05	2.6E-04
3866276	**SLC1A5**	solute carrier family 1 (neutral amino acid transporter), member 5	-0.75	7.6E-07	1.4E-05
3904594	**C20ORF117**	chromosome 20 open reading frame 117	-0.75	2.3E-06	3.1E-05
2634058	**FAM55C**	family with sequence similarity 55, member C	-0.75	4.1E-05	2.8E-04
2844709	**CNOT6**	CCR4-NOT transcription complex, subunit 6	-0.75	4.3E-05	2.8E-04
2884623	**C1QTNF2**	C1q and tumor necrosis factor related protein 2	-0.76	8.0E-05	4.6E-04
3850676	**KANK2**	KN motif and ankyrin repeat domains 2	-0.76	2.9E-07	6.7E-06
2924330	**TPD52L1**	tumor protein D52-like 1	-0.76	2.2E-04	1.0E-03
2542795	**SDC1**	syndecan 1	-0.76	1.3E-06	2.0E-05
3268669	**BUB3**	budding uninhibited by benzimidazoles 3 homolog (yeast)	-0.76	8.4E-07	1.5E-05
2609347	**LMCD1**	LIM and cysteine-rich domains 1	-0.76	3.9E-05	2.6E-04
3960685	**DMC1**	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	-0.76	1.1E-05	9.6E-05
3080283	**XRCC2**	X-ray repair complementing defective repair in Chinese hamster cells 2	-0.76	7.0E-04	2.5E-03
3015442	**PILRB**	paired immunoglobin-like type 2 receptor beta	-0.76	1.8E-06	2.5E-05
3168255	**HRCT1**	histidine rich carboxyl terminus 1	-0.76	2.9E-05	2.1E-04
2371547	**C1ORF21**	chromosome 1 open reading frame 21	-0.76	1.5E-05	1.3E-04
2684851	**VGLL3**	vestigial like 3 (Drosophila)	-0.76	3.6E-03	9.3E-03
3770699	**MIF4GD**	MIF4G domain containing	-0.76	3.9E-07	8.4E-06
2836451	**MFAP3**	microfibrillar-associated protein 3	-0.76	2.2E-04	1.0E-03
3757917	**PTRF**	polymerase I and transcript release factor	-0.76	4.3E-08	1.8E-06
2352758	**HIPK1**	homeodomain interacting protein kinase 1	-0.76	3.8E-06	4.4E-05
2444451	**CENPL**	centromere protein L	-0.76	4.3E-06	4.8E-05
2796484	**CASP3**	caspase 3, apoptosis-related cysteine peptidase	-0.76	1.8E-05	1.5E-04
3976797	**SUV39H1**	suppressor of variegation 3-9 homolog 1 (Drosophila)	-0.76	2.7E-04	1.2E-03
3414846	**DAZAP2**	DAZ associated protein 2	-0.77	1.8E-07	4.8E-06
2786567	**C4ORF49**	chromosome 4 open reading frame 49	-0.77	2.4E-06	3.2E-05
3764738	**SKA2**	spindle and kinetochore associated complex subunit 2	-0.77	7.9E-06	7.7E-05
3625761	**MNS1**	meiosis-specific nuclear structural 1	-0.77	9.5E-05	5.2E-04
3901851	**ABHD12**	abhydrolase domain containing 12	-0.77	1.9E-06	2.7E-05
3167553	**IL11RA**	interleukin 11 receptor, alpha	-0.77	2.1E-07	5.3E-06
3465248	**LUM**	lumican	-0.77	8.1E-04	2.8E-03
3658925	**ORC6**	origin recognition complex, subunit 6	-0.77	2.0E-07	5.2E-06
3562746	**C14ORF106**	chromosome 14 open reading frame 106	-0.77	5.5E-05	3.5E-04
3726691	**ABCC3**	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	-0.77	2.2E-08	1.1E-06

3007438	**POM121**	POM121 membrane glycoprotein	-0.77	1.8E-02	3.4E-02
2944068	**DEK**	DEK oncogene	-0.78	2.7E-04	1.2E-03
2366422	**ATP1B1**	ATPase, Na+/K+ transporting, beta 1 polypeptide	-0.78	1.0E-05	9.4E-05
3907111	**TOMM34**	translocase of outer mitochondrial membrane 34	-0.78	6.8E-08	2.4E-06
3074857	**PTN**	pleiotrophin	-0.78	3.7E-04	1.6E-03
2591643	**COL5A2**	collagen, type V, alpha 2	-0.78	6.6E-05	4.0E-04
3628498	**CA12**	carbonic anhydrase XII	-0.78	1.6E-06	2.3E-05
2514122	**LASS6**	LAG1 homolog, ceramide synthase 6	-0.78	1.1E-05	9.7E-05
2857416	**IL6ST**	interleukin 6 signal transducer (gp130, oncostatin M receptor)	-0.78	7.3E-04	2.6E-03
2334319	**TOE1**	target of EGR1, member 1 (nuclear)	-0.79	3.5E-06	4.1E-05
2757319	**SLBP**	stem-loop binding protein	-0.79	1.8E-05	1.4E-04
2829947	**TGFBI**	transforming growth factor, beta-induced, 68kDa	-0.79	9.8E-08	3.1E-06
3103293	**RDH10**	retinol dehydrogenase 10 (all-trans)	-0.79	2.1E-05	1.6E-04
3854218	**HAUS8**	HAUS augmin-like complex, subunit 8	-0.79	1.8E-04	8.6E-04
2836242	**GRIA1**	glutamate receptor, ionotropic, AMPA 1	-0.79	2.7E-06	3.5E-05
3415668	**TENC1**	tensin like C1 domain containing phosphatase (tensin 2)	-0.79	9.3E-08	3.0E-06
2533493	**SH3BP4**	SH3-domain binding protein 4	-0.79	2.1E-08	1.1E-06
2429261	**NRAS**	neuroblastoma RAS viral (v-ras) oncogene homolog	-0.80	4.8E-06	5.2E-05
3318967	**OR10A2**	olfactory receptor, family 10, subfamily A, member 2	-0.80	1.2E-02	2.4E-02
3722770	**C17ORF53**	chromosome 17 open reading frame 53	-0.80	2.8E-06	3.5E-05
3923218	**RRP1B**	ribosomal RNA processing 1 homolog B (S. cerevisiae)	-0.80	8.0E-07	1.4E-05
2779486	**H2AFZ**	H2A histone family, member Z	-0.80	2.1E-07	5.3E-06
3599709	**GLCE**	glucuronic acid epimerase	-0.80	2.7E-05	2.0E-04
3677315	**PKMYT1**	protein kinase, membrane associated tyrosine/threonine 1	-0.81	1.0E-06	1.7E-05
2904663	**FANCE**	Fanconi anemia, complementation group E	-0.81	4.2E-06	4.7E-05
3168385	**GLIPR2**	GLI pathogenesis-related 2	-0.81	1.1E-07	3.4E-06
3766621	**ICAM2**	intercellular adhesion molecule 2	-0.81	3.6E-06	4.2E-05
2429466	**NGF**	nerve growth factor (beta polypeptide)	-0.81	1.1E-05	1.0E-04
2852274	**MTMR12**	myotubularin related protein 12	-0.82	3.8E-06	4.4E-05
2719617	**BST1**	bone marrow stromal cell antigen 1	-0.82	7.7E-07	1.4E-05
3557791	**FAM158A**	family with sequence similarity 158, member A	-0.82	2.0E-06	2.8E-05
2340819	**TCTEX1D1**	Tctex1 domain containing 1	-0.82	3.0E-05	2.2E-04
3403168	**C1S**	complement component 1, s subcomponent	-0.82	7.0E-06	7.0E-05
3327906	**API5**	apoptosis inhibitor 5	-0.82	1.1E-05	1.0E-04
2334646	**RAD54L**	RAD54-like (S. cerevisiae)	-0.82	5.1E-05	3.2E-04
3318009	**RRM1**	ribonucleotide reductase M1	-0.83	7.3E-06	7.2E-05
4000944	**RBBP7**	retinoblastoma binding protein 7	-0.83	2.2E-07	5.5E-06
2905069	**KCTD20**	potassium channel tetramerisation domain containing 20	-0.83	2.6E-05	1.9E-04
3593147	**DUT**	deoxyuridine triphosphatase	-0.83	2.3E-05	1.8E-04
3279058	**ACBD7**	acyl-CoA binding domain containing 7	-0.83	4.3E-05	2.8E-04
3708074	**XAF1**	XIAP associated factor 1	-0.83	3.7E-05	2.5E-04
2324341	**NBPF3**	neuroblastoma breakpoint family, member 3	-0.83	2.5E-06	3.3E-05
3308489	**KIAA1598**	KIAA1598	-0.83	5.0E-05	3.2E-04
3056414	**RFC2**	replication factor C (activator 1) 2, 40kDa	-0.83	4.0E-05	2.7E-04
3634811	**CTSH**	cathepsin H	-0.83	6.3E-06	6.5E-05
2953852	**MED20**	mediator complex subunit 20	-0.83	4.3E-05	2.8E-04
3413278	**TMEM106C**	transmembrane protein 106C	-0.84	1.9E-06	2.7E-05
3748798	**MFAP4**	microfibrillar-associated protein 4	-0.84	2.4E-08	1.2E-06
3012019	**CLDN12**	claudin 12	-0.84	5.1E-05	3.2E-04
3995633	**BGN**	biglycan	-0.84	1.4E-07	4.0E-06
3907234	**SDC4**	syndecan 4	-0.84	3.8E-08	1.6E-06
2674808	**TRAIP**	TRAF interacting protein	-0.84	1.4E-05	1.2E-04
3060245	**SLC25A40**	solute carrier family 25, member 40	-0.84	3.4E-05	2.4E-04
2907671	**PTK7**	PTK7 protein tyrosine kinase 7	-0.84	9.9E-09	6.5E-07
3645477	**PAQR4**	progestin and adipoQ receptor family member IV	-0.84	5.0E-05	3.2E-04
2549565	**SLC8A1**	solute carrier family 8 (sodium/calcium exchanger), member 1	-0.84	3.4E-05	2.4E-04
3724197	**NSF**	N-ethylmaleimide-sensitive factor	-0.85	2.7E-07	6.3E-06
3576284	**RPS6KA5**	ribosomal protein S6 kinase, 90kDa, polypeptide 5	-0.85	4.3E-06	4.8E-05
3862273	**PRR13**	proline rich 13	-0.85	2.0E-05	1.6E-04
3476012	**MPHOSPH9**	M-phase phosphoprotein 9	-0.85	5.4E-05	3.4E-04
2330075	**EIF2C1**	eukaryotic translation initiation factor 2C, 1	-0.85	3.8E-06	4.4E-05
3723071	**DBF4B**	DBF4 homolog B (S. cerevisiae)	-0.85	9.9E-07	1.7E-05
2412799	**ORC1**	origin recognition complex, subunit 1	-0.86	5.5E-05	3.5E-04
3903146	**E2F1**	E2F transcription factor 1	-0.86	7.3E-06	7.3E-05
2950277	**HLA-DMA**	major histocompatibility complex, class II, DM alpha	-0.86	4.0E-07	8.4E-06
3548152	**TDP1**	tyrosyl-DNA phosphodiesterase 1	-0.86	4.3E-07	8.8E-06
2402459	**STMN1**	stathmin 1	-0.86	7.9E-08	2.7E-06
2350922	**GSTM4**	glutathione S-transferase mu 4	-0.87	2.0E-06	2.8E-05
3250055	**DDX21**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	-0.87	1.9E-05	1.5E-04
3651018	**CP110**	CP110 protein	-0.87	6.3E-04	2.4E-03
2361154	**SYT11**	synaptotagmin XI	-0.87	1.9E-07	5.1E-06
3226592	**WDR34**	WD repeat domain 34	-0.87	1.9E-06	2.7E-05
2327482	**RCC1**	regulator of chromosome condensation 1	-0.88	3.4E-06	4.0E-05

3149843	**RAD21**	RAD21 homolog (S. pombe)	-0.88	3.0E-06	3.7E-05
3274758	**AKR1C2**	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	-0.88	2.1E-04	9.7E-04
2750594	**SC4MOL**	sterol-C4-methyl oxidase-like	-0.88	5.7E-05	3.6E-04
2696309	**AMOTL2**	angiomotin like 2	-0.88	1.3E-07	3.8E-06
2351004	**GSTM5**	glutathione S-transferase mu 5	-0.88	1.5E-04	7.4E-04
2529627	**KCNE4**	potassium voltage-gated channel, Isk-related family, member 4	-0.89	6.1E-04	2.3E-03
3866898	**LIG1**	ligase I, DNA, ATP-dependent	-0.89	4.0E-06	4.5E-05
3261923	**AS3MT**	arsenic (+3 oxidation state) methyltransferase	-0.89	4.1E-05	2.7E-04
2353773	**TTF2**	transcription termination factor, RNA polymerase II	-0.89	4.5E-06	5.0E-05
3556966	**HAUS4**	HAUS augmin-like complex, subunit 4	-0.89	3.4E-06	4.0E-05
3318390	**TRIM6-TRIM34**	TRIM6-TRIM34 readthrough	-0.89	8.7E-08	2.9E-06
3427352	**NEDD1**	neural precursor cell expressed, developmentally down-regulated 1	-0.89	2.6E-04	1.2E-03
4012142	**ERCC6L**	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	-0.89	9.6E-07	1.6E-05
3340161	**PPME1**	protein phosphatase methylesterase 1	-0.89	1.1E-08	7.0E-07
2471316	**GEN1**	Gen homolog 1, endonuclease (Drosophila)	-0.90	1.1E-04	5.8E-04
2697721	**PRR23C**	proline rich 23C	-0.90	9.9E-04	3.3E-03
3439178	**PXMP2**	peroxisomal membrane protein 2, 22kDa	-0.90	1.1E-06	1.8E-05
3435362	**KNTC1**	kinetochore associated 1	-0.90	8.3E-06	7.9E-05
3831062	**WDR62**	WD repeat domain 62	-0.90	3.2E-06	3.9E-05
4009238	**SMC1A**	structural maintenance of chromosomes 1A	-0.91	3.7E-06	4.3E-05
3394183	**H2AFX**	H2A histone family, member X	-0.91	4.5E-07	9.2E-06
3479181	**POLE**	polymerase (DNA directed), epsilon	-0.91	1.0E-05	9.3E-05
2951567	**FKBP5**	FK506 binding protein 5	-0.91	1.3E-06	2.0E-05
3852691	**DDX39**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	-0.91	7.9E-06	7.7E-05
3340269	**POLD3**	polymerase (DNA-directed), delta 3, accessory subunit	-0.91	2.9E-05	2.1E-04
3558118	**DHRS1**	dehydrogenase/reductase (SDR family) member 1	-0.91	1.2E-07	3.5E-06
3565206	**BMP4**	bone morphogenetic protein 4	-0.91	5.2E-08	2.0E-06
3414885	**SLC4A8**	solute carrier family 4, sodium bicarbonate cotransporter, member 8	-0.91	1.3E-07	3.8E-06
3192912	**C9ORF96**	chromosome 9 open reading frame 96	-0.92	1.5E-04	7.4E-04
2902844	**CFB**	complement factor B	-0.92	2.1E-07	5.3E-06
3333358	**INCENP**	inner centromere protein antigens 135/155kDa	-0.92	4.2E-06	4.7E-05
2840002	**CCDC99**	coiled-coil domain containing 99	-0.92	3.8E-05	2.6E-04
3716664	**SUZ12P**	suppressor of zeste 12 homolog pseudogene	-0.92	8.7E-06	8.2E-05
3573994	**C14ORF145**	chromosome 14 open reading frame 145	-0.92	1.1E-05	9.8E-05
3050367	**FIGNL1**	fidgetin-like 1	-0.92	3.8E-05	2.6E-04
2441043	**OLFML2B**	olfactomedin-like 2B	-0.92	2.1E-07	5.3E-06
2330687	**ZC3H12A**	zinc finger CCCH-type containing 12A	-0.92	3.1E-06	3.8E-05
3204692	**C9ORF100**	chromosome 9 open reading frame 100	-0.93	4.0E-07	8.4E-06
3601348	**LOXL1**	lysyl oxidase-like 1	-0.93	4.3E-08	1.7E-06
7385547	**CCL2**	chemokine (C-C motif) ligand 2	-0.93	5.5E-06	5.8E-05
3550485	**VRK1**	vaccinia related kinase 1	-0.93	6.8E-07	1.3E-05
3417146	**CDK2**	cyclin-dependent kinase 2	-0.93	7.8E-07	1.4E-05
3415576	**KRT18**	keratin 18	-0.93	1.6E-06	2.3E-05
2334404	**NASP**	nuclear autoantigenic sperm protein (histone-binding)	-0.93	2.8E-07	6.4E-06
3258910	**HELLS**	helicase, lymphoid-specific	-0.93	1.9E-05	1.5E-04
2966587	**SIM1**	single-minded homolog 1 (Drosophila)	-0.94	3.1E-05	2.2E-04
2402416	**C1ORF135**	chromosome 1 open reading frame 135	-0.94	6.3E-05	3.8E-04
4000370	**FANCB**	Fanconi anemia, complementation group B	-0.94	1.4E-06	2.1E-05
3598721	**ZWILCH**	Zwilch, kinetochore associated, homolog (Drosophila)	-0.94	2.2E-06	3.0E-05
2516023	**CDCA7**	cell division cycle associated 7	-0.95	2.9E-07	6.6E-06
2384268	**HIST3H2BB**	histone cluster 3, H2bb	-0.95	9.1E-05	5.1E-04
2587961	**CHN1**	chimerin (chimaerin) 1	-0.96	8.0E-07	1.4E-05
2948547	**NRM**	nurim (nuclear envelope membrane protein)	-0.96	7.7E-07	1.4E-05
3850660	**SPC24**	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-0.96	4.4E-06	4.9E-05
3399545	**NCAPD3**	non-SMC condensin II complex, subunit D3	-0.96	2.1E-06	2.9E-05
2948630	**IER3**	immediate early response 3	-0.96	5.1E-07	1.0E-05
3758317	**BRCA1**	breast cancer 1, early onset	-0.96	3.0E-06	3.7E-05
4019900	**CUL4B**	cullin 4B	-0.96	1.9E-06	2.7E-05
3905145	**TGM2**	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyl-transferase)	-0.97	7.7E-07	1.4E-05
3443226	**MFAP5**	microfibrillar associated protein 5	-0.97	3.4E-07	7.5E-06
3827218	**RPSAP58**	ribosomal protein SA pseudogene 58	-0.97	3.3E-03	8.7E-03
3468743	**NT5DC3**	5'-nucleotidase domain containing 3	-0.97	4.0E-07	8.4E-06
2625907	**FLNB**	filamin B, beta	-0.97	4.0E-08	1.7E-06
2373693	**LHX9**	LIM homeobox 9	-0.97	8.3E-08	2.8E-06
2911413	**PRIM2**	primase, DNA, polypeptide 2 (58kDa)	-0.98	2.1E-07	5.3E-06
2369339	**RALGPS2**	Ral GEF with PH domain and SH3 binding motif 2	-0.98	1.9E-05	1.5E-04
2946324	**HIST1H3D**	histone cluster 1, H3d	-0.98	3.4E-06	4.0E-05
3013255	**PEG10**	paternally expressed 10	-0.98	1.1E-05	9.6E-05
3362852	**MRVI1**	murine retrovirus integration site 1 homolog	-0.98	2.9E-06	3.6E-05
3850069	**DNMT1**	DNA (cytosine-5-)-methyltransferase 1	-0.98	8.2E-08	2.8E-06

2732844	**ANXA3**	annexin A3	-0.99	8.5E-07	1.5E-05
3875195	**MCM8**	minichromosome maintenance complex component 8	-0.99	2.2E-05	1.7E-04
2888674	**MXD3**	MAX dimerization protein 3	-0.99	5.5E-07	1.1E-05
3970476	**SCML1**	sex comb on midleg-like 1 (Drosophila)	-1.00	7.1E-06	7.1E-05
3127334	**REEP4**	receptor accessory protein 4	-1.00	7.0E-07	1.3E-05
3748400	**USP6**	ubiquitin specific peptidase 6 (Tre-2 oncogene)	-1.00	7.7E-03	1.7E-02
3410614	**FGD4**	FYVE, RhoGEF and PH domain containing 4	-1.01	4.6E-06	5.0E-05
3904747	**RBL1**	retinoblastoma-like 1 (p107)	-1.01	4.8E-06	5.2E-05
2743315	**PHF17**	PHD finger protein 17	-1.01	9.1E-08	3.0E-06
3556990	**JUB**	jub, ajuba homolog (Xenopus laevis)	-1.01	1.5E-08	8.8E-07
3607698	**C15ORF42**	chromosome 15 open reading frame 42	-1.02	2.4E-07	5.9E-06
3204463	**FANCG**	Fanconi anemia, complementation group G	-1.02	4.0E-06	4.5E-05
3137875	**GGH**	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	-1.02	4.3E-06	4.8E-05
2364155	**UHMK1**	U2AF homology motif (UHM) kinase 1	-1.02	6.6E-06	6.7E-05
2458338	**ENAH**	enabled homolog (Drosophila)	-1.02	2.1E-05	1.6E-04
3097152	**MCM4**	minichromosome maintenance complex component 4	-1.02	4.5E-07	9.2E-06
3293724	**C10ORF54**	chromosome 10 open reading frame 54	-1.02	5.7E-06	5.9E-05
2709486	**RFC4**	replication factor C (activator 1) 4, 37kDa	-1.02	1.4E-06	2.1E-05
2584134	**FAP**	fibroblast activation protein, alpha	-1.03	8.7E-05	4.9E-04
3760268	**ARL17A**	ADP-ribosylation factor-like 17A	-1.03	1.0E-03	3.4E-03
3335029	**POLA2**	polymerase (DNA directed), alpha 2 (70kD subunit)	-1.03	7.8E-06	7.7E-05
2548617	**CDC42EP3**	CDC42 effector protein (Rho GTPase binding) 3	-1.03	8.2E-07	1.4E-05
3145107	**CCNE2**	cyclin E2	-1.04	8.0E-05	4.6E-04
3383227	**GAB2**	GRB2-associated binding protein 2	-1.04	1.2E-08	7.4E-07
3240012	**MASTL**	microtubule associated serine/threonine kinase-like	-1.04	2.5E-07	6.1E-06
2571510	**IL1B**	interleukin 1, beta	-1.04	1.8E-03	5.3E-03
3770632	**SUMO2**	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	-1.05	1.4E-05	1.2E-04
3203935	**KIF24**	kinesin family member 24	-1.05	1.1E-06	1.8E-05
2522916	**CDK15**	cyclin-dependent kinase 15	-1.05	9.2E-07	1.6E-05
2477203	**VIT**	vitrin	-1.05	1.8E-06	2.6E-05
3299504	**ACTA2**	actin, alpha 2, smooth muscle, aorta	-1.05	4.0E-08	1.7E-06
2622696	**SEMA3B**	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	-1.05	2.3E-06	3.1E-05
3154185	**TMEM71**	transmembrane protein 71	-1.05	1.9E-06	2.7E-05
3367036	**CCDC34**	coiled-coil domain containing 34	-1.06	3.0E-06	3.7E-05
2511432	**GPD2**	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	-1.06	8.3E-07	1.5E-05
2715076	**WHSC1**	Wolf-Hirschhorn syndrome candidate 1	-1.07	1.7E-08	9.3E-07
3920003	**CHAF1B**	chromatin assembly factor 1, subunit B (p60)	-1.07	5.1E-06	5.5E-05
2813442	**CENPH**	centromere protein H	-1.07	2.3E-09	2.6E-07
3354210	**SPA17**	sperm autoantigenic protein 17	-1.08	4.2E-06	4.7E-05
3059667	**SEMA3D**	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	-1.08	6.4E-03	1.5E-02
3302187	**ARHGAP19**	Rho GTPase activating protein 19	-1.08	1.7E-06	2.5E-05
3415320	**KRT7**	keratin 7	-1.08	1.5E-05	1.3E-04
2649367	**PTX3**	pentraxin 3, long	-1.08	2.2E-06	3.0E-05
3817602	**TNFAIP8L1**	tumor necrosis factor, alpha-induced protein 8-like 1	-1.08	2.7E-05	2.0E-04
3484497	**FRY**	furry homolog (Drosophila)	-1.09	1.2E-05	1.0E-04
3405515	**APOLD1**	apolipoprotein L domain containing 1	-1.09	5.9E-07	1.1E-05
2634027	**CEP97**	centrosomal protein 97kDa	-1.09	1.2E-05	1.1E-04
3880827	**GINS1**	GINS complex subunit 1 (Psf1 homolog)	-1.10	6.0E-08	2.2E-06
3333226	**FEN1**	flap structure-specific endonuclease 1	-1.10	5.2E-07	1.0E-05
2518272	**ITGA4**	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	-1.10	7.9E-05	4.6E-04
3329983	**PTPRJ**	protein tyrosine phosphatase, receptor type, J	-1.10	2.2E-07	5.5E-06
2339414	**USP1**	ubiquitin specific peptidase 1	-1.11	6.0E-05	3.7E-04
3715489	**TMEM97**	transmembrane protein 97	-1.11	2.1E-07	5.3E-06
3403015	**ENO2**	enolase 2 (gamma, neuronal)	-1.12	3.7E-07	8.1E-06
2802681	**LOC100133299**	GALI1870	-1.12	7.7E-04	2.7E-03
2565902	**ANKRD36B**	ankyrin repeat domain 36B	-1.14	1.3E-02	2.6E-02
3972093	**POLA1**	polymerase (DNA directed), alpha 1, catalytic subunit	-1.14	4.5E-06	4.9E-05
3530982	**G2E3**	G2/M-phase specific E3 ubiquitin protein ligase	-1.14	1.4E-06	2.1E-05
2898597	**GMNN**	geminin, DNA replication inhibitor	-1.14	1.1E-07	3.4E-06
3464967	**GALNT4**	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactos-aminyl-transferase 4 (GalNAc-T4)	-1.15	2.3E-07	5.6E-06
3563395	**POLE2**	polymerase (DNA directed), epsilon 2 (p59 subunit)	-1.15	3.9E-07	8.4E-06
2957126	**MCM3**	minichromosome maintenance complex component 3	-1.15	7.1E-06	7.1E-05
2584787	**COBLL1**	COBL-like 1	-1.16	1.4E-05	1.2E-04
2652675	**ECT2**	epithelial cell transforming sequence 2 oncogene	-1.16	5.1E-06	5.5E-05
2720584	**SLIT2**	slit homolog 2 (Drosophila)	-1.16	2.9E-07	6.7E-06
2783715	**MAD2L1**	MAD2 mitotic arrest deficient-like 1 (yeast)	-1.16	3.2E-06	3.9E-05
2899171	**HIST1H1E**	histone cluster 1, H1e	-1.16	3.5E-08	1.5E-06
3257246	**IFIT1**	interferon-induced protein with tetratricopeptide repeats 1	-1.16	3.0E-07	6.8E-06
2406420	**CLSPN**	claspin	-1.17	8.1E-06	7.8E-05

3433747	**RFC5**	replication factor C (activator 1) 5, 36.5kDa	-1.17	1.1E-06	1.8E-05
3119213	**LY6K**	lymphocyte antigen 6 complex, locus K	-1.17	2.2E-05	1.7E-04
3311832	**ADAM12**	ADAM metallopeptidase domain 12	-1.18	1.0E-07	3.2E-06
3741997	**ANKFY1**	ankyrin repeat and FYVE domain containing 1	-1.18	2.8E-08	1.3E-06
2947081	**HIST1H4L**	histone cluster 1, H4l	-1.18	5.8E-07	1.1E-05
2674762	**UBA7**	ubiquitin-like modifier activating enzyme 7	-1.18	8.1E-10	1.5E-07
3757970	**PSMC3IP**	PSMC3 interacting protein	-1.19	2.9E-07	6.7E-06
3319937	**WEE1**	WEE1 homolog (S. pombe)	-1.19	3.3E-09	3.2E-07
3095766	**GINS4**	GINS complex subunit 4 (Sld5 homolog)	-1.20	4.3E-07	8.8E-06
2947077	**HIST1H3I**	histone cluster 1, H3i	-1.20	3.5E-07	7.6E-06
3178583	**CKS2**	CDC28 protein kinase regulatory subunit 2	-1.20	1.4E-07	4.1E-06
2462160	**NID1**	nidogen 1	-1.20	4.5E-08	1.8E-06
4022781	**FAM122B**	family with sequence similarity 122B	-1.20	1.3E-06	2.0E-05
2928461	**GPR126**	G protein-coupled receptor 126	-1.21	3.8E-06	4.3E-05
3704980	**FANCA**	Fanconi anemia, complementation group A	-1.21	9.3E-08	3.0E-06
2451043	**LMOD1**	leiomodin 1 (smooth muscle)	-1.21	1.3E-06	2.0E-05
2946353	**HIST1H1D**	histone cluster 1, H1d	-1.21	5.5E-06	5.8E-05
2754937	**TLR3**	toll-like receptor 3	-1.21	2.0E-06	2.8E-05
2661992	**OXTR**	oxytocin receptor	-1.22	1.1E-06	1.8E-05
3821908	**RNASEH2A**	ribonuclease H2, subunit A	-1.22	3.2E-07	7.3E-06
3929775	**DONSON**	downstream neighbor of SON	-1.22	9.4E-07	1.6E-05
2425118	**SASS6**	spindle assembly 6 homolog (C. elegans)	-1.22	4.7E-05	3.0E-04
2510464	**TNFAIP6**	tumor necrosis factor, alpha-induced protein 6	-1.22	3.5E-06	4.2E-05
3649811	**NDE1**	nudE nuclear distribution gene E homolog 1 (A. nidulans)	-1.23	1.2E-07	3.6E-06
3457824	**TIMELESS**	timeless homolog (Drosophila)	-1.23	1.1E-06	1.8E-05
3414739	**METTL7A**	methyltransferase like 7A	-1.23	4.3E-09	3.8E-07
3331903	**FAM111B**	family with sequence similarity 111, member B	-1.23	2.0E-05	1.6E-04
2783207	**PRSS12**	protease, serine, 12 (neurotrypsin, motopsin)	-1.24	9.5E-08	3.0E-06
3415744	**IGFBP6**	insulin-like growth factor binding protein 6	-1.24	1.3E-08	7.8E-07
2780172	**CENPE**	centromere protein E, 312kDa	-1.24	3.5E-05	2.4E-04
3455261	**KRT81**	keratin 81	-1.24	4.6E-09	4.0E-07
3802602	**CDH2**	cadherin 2, type 1, N-cadherin (neuronal)	-1.24	2.2E-08	1.1E-06
2326410	**CCDC21**	coiled-coil domain containing 21	-1.24	5.7E-07	1.1E-05
3428845	**C12ORF48**	chromosome 12 open reading frame 48	-1.25	9.9E-09	6.5E-07
3810542	**CCBE1**	collagen and calcium binding EGF domains 1	-1.26	7.7E-08	2.7E-06
2686458	**ABI3BP**	ABI family, member 3 (NESH) binding protein	-1.26	6.8E-07	1.3E-05
3817698	**UHRF1**	ubiquitin-like with PHD and ring finger domains 1	-1.26	4.7E-08	1.8E-06
3944147	**MCM5**	minichromosome maintenance complex component 5	-1.27	8.1E-07	1.4E-05
3765580	**BRIP1**	BRCA1 interacting protein C-terminal helicase 1	-1.27	1.4E-06	2.1E-05
2434129	**HIST2H2AB**	histone cluster 2, H2ab	-1.27	2.8E-06	3.6E-05
2899223	**HIST1H2AE**	histone cluster 1, H2ae	-1.27	3.9E-06	4.5E-05
3000905	**C7ORF69**	chromosome 7 open reading frame 69	-1.27	1.2E-06	1.9E-05
2709606	**RPL39L**	ribosomal protein L39-like	-1.27	2.5E-07	6.0E-06
3809826	**ATP8B1**	ATPase, aminophospholipid transporter, class I, type 8B, member 1	-1.28	8.3E-08	2.8E-06
2427007	**SORT1**	sortilin 1	-1.28	3.1E-08	1.4E-06
3458133	**PRIM1**	primase, DNA, polypeptide 1 (49kDa)	-1.28	3.8E-07	8.2E-06
4045643	**S100A16**	S100 calcium binding protein A16	-1.28	2.6E-09	2.7E-07
3748323	**SHMT1**	serine hydroxymethyltransferase 1 (soluble)	-1.28	4.8E-06	5.2E-05
3655628	**KIF22**	kinesin family member 22	-1.29	6.2E-07	1.2E-05
3887049	**UBE2C**	ubiquitin-conjugating enzyme E2C	-1.29	9.3E-07	1.6E-05
3509411	**MAB21L1**	mab-21-like 1 (C. elegans)	-1.29	1.2E-08	7.5E-07
3598959	**SMAD3**	SMAD family member 3	-1.30	2.2E-09	2.5E-07
2905404	**PIM1**	pim-1 oncogene	-1.30	2.3E-07	5.6E-06
3168409	**CCIN**	calicin	-1.30	6.5E-06	6.6E-05
3493391	**C13ORF34**	chromosome 13 open reading frame 34	-1.30	6.2E-08	2.3E-06
2980241	**FBXO5**	F-box protein 5	-1.30	1.1E-06	1.8E-05
2941784	**NEDD9**	neural precursor cell expressed, developmentally down-regulated 9	-1.31	3.1E-09	3.1E-07
2700365	**TM4SF1**	transmembrane 4 L six family member 1	-1.31	1.9E-06	2.7E-05
2748163	**MND1**	meiotic nuclear divisions 1 homolog (S. cerevisiae)	-1.32	3.1E-05	2.2E-04
2899102	**HIST1H3C**	histone cluster 1, H3c	-1.33	1.3E-07	3.9E-06
2413423	**TMEM48**	transmembrane protein 48	-1.33	4.8E-08	1.9E-06
2877257	**BRD8**	bromodomain containing 8	-1.33	3.3E-08	1.4E-06
2902178	**TCF19**	transcription factor 19	-1.33	1.5E-06	2.2E-05
2899768	**HIST1H4I**	histone cluster 1, H4i	-1.34	7.2E-06	7.1E-05
2691575	**POLQ**	polymerase (DNA directed), theta	-1.34	2.8E-07	6.5E-06
3504691	**ZDHHC20**	zinc finger, DHHC-type containing 20	-1.34	1.9E-07	5.1E-06
2435005	**SELENBP1**	selenium binding protein 1	-1.34	5.7E-09	4.5E-07
2946232	**HIST1H1C**	histone cluster 1, H1c	-1.34	4.0E-07	8.4E-06
2640855	**MCM2**	minichromosome maintenance complex component 2	-1.35	5.0E-07	9.9E-06
3499132	**ITGBL1**	integrin, beta-like 1 (with EGF-like repeat domains)	-1.35	2.9E-08	1.3E-06
3235789	**MCM10**	minichromosome maintenance complex component 10	-1.35	2.7E-07	6.3E-06
2451200	**UBE2T**	ubiquitin-conjugating enzyme E2T (putative)	-1.36	2.1E-08	1.1E-06
2879166	**FGF1**	fibroblast growth factor 1 (acidic)	-1.36	7.3E-09	5.5E-07

3757108	**KRT19**	keratin 19	-1.37	9.6E-07	1.6E-05
2434319	**ANP32E**	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	-1.37	8.5E-06	8.1E-05
2946208	**HIST1H4B**	histone cluster 1, H4b	-1.38	1.2E-05	1.0E-04
3608298	**BLM**	Bloom syndrome, RecQ helicase-like	-1.38	1.5E-07	4.1E-06
3485074	**RFC3**	replication factor C (activator 1) 3, 38kDa	-1.38	1.5E-08	8.4E-07
2598099	**BARD1**	BRCA1 associated RING domain 1	-1.38	4.1E-07	8.5E-06
2945882	**CMAH**	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	-1.38	2.2E-07	5.6E-06
3257338	**KIF20B**	kinesin family member 20B	-1.38	1.3E-06	2.0E-05
2397025	**DHRS3**	dehydrogenase/reductase (SDR family) member 3	-1.38	1.1E-08	6.9E-07
3452478	**AMIGO2**	adhesion molecule with Ig-like domain 2	-1.39	1.5E-07	4.2E-06
3405587	**GPRC5A**	G protein-coupled receptor, family C, group 5, member A	-1.40	2.2E-09	2.6E-07
2946219	**HIST1H2AB**	histone cluster 1, H2ab	-1.40	8.5E-06	8.1E-05
2899243	**HIST1H4F**	histone cluster 1, H4f	-1.40	4.7E-06	5.1E-05
2946364	**HIST1H3F**	histone cluster 1, H3f	-1.40	3.6E-06	4.2E-05
2900091	**HIST1H2AL**	histone cluster 1, H2al	-1.41	7.7E-08	2.7E-06
2981912	**EZR**	ezrin	-1.41	7.1E-08	2.5E-06
2858592	**DEPDC1B**	DEP domain containing 1B	-1.42	1.1E-07	3.2E-06
2946215	**HIST1H3B**	histone cluster 1, H3b	-1.42	1.1E-07	3.2E-06
2946194	**HIST1H1A**	histone cluster 1, H1a	-1.43	1.6E-05	1.4E-04
3063685	**MCM7**	minichromosome maintenance complex component 7	-1.43	9.3E-07	1.6E-05
2388219	**EXO1**	exonuclease 1	-1.44	2.5E-07	6.0E-06
3651509	**ERI2**	ERI1 exoribonuclease family member 2	-1.44	9.3E-09	6.2E-07
2947040	**HIST1H2AJ**	histone cluster 1, H2aj	-1.47	9.2E-04	3.1E-03
2577896	**MCM6**	minichromosome maintenance complex component 6	-1.47	7.2E-08	2.5E-06
3445028	**GPR19**	G protein-coupled receptor 19	-1.47	2.3E-04	1.1E-03
2946268	**HIST1H2BC**	histone cluster 1, H2bc	-1.47	2.5E-05	1.9E-04
3377423	**CDCA5**	cell division cycle associated 5	-1.47	1.2E-06	1.9E-05
3874438	**CDC25B**	cell division cycle 25 homolog B (S. pombe)	-1.47	7.6E-09	5.5E-07
2975655	**FAM54A**	family with sequence similarity 54, member A	-1.48	6.6E-07	1.2E-05
2742985	**PLK4**	polo-like kinase 4	-1.48	2.1E-06	2.9E-05
3962165	**CENPM**	centromere protein M	-1.48	3.3E-06	4.0E-05
2899772	**HIST1H2AH**	histone cluster 1, H2ah	-1.48	2.3E-05	1.7E-04
2473284	**CENPO**	centromere protein O	-1.48	1.2E-06	1.9E-05
2675936	**POC1A**	POC1 centriolar protein homolog A (Chlamydomonas)	-1.49	2.0E-06	2.8E-05
2900059	**HIST1H2BM**	histone cluster 1, H2bm	-1.49	2.7E-07	6.3E-06
3726375	**EME1**	essential meiotic endonuclease 1 homolog 1 (S. pombe)	-1.49	2.5E-07	6.0E-06
3728964	**PRR11**	proline rich 11	-1.49	1.2E-09	1.7E-07
2711034	**C3ORF59**	chromosome 3 open reading frame 59	-1.50	3.8E-09	3.5E-07
2652027	**CLDN11**	claudin 11	-1.50	7.7E-09	5.6E-07
2899206	**HIST1H2BF**	histone cluster 1, H2bf	-1.51	9.2E-08	3.0E-06
3706753	**GSG2**	germ cell associated 2 (haspin)	-1.51	3.6E-07	7.9E-06
3540136	**HSPA2**	heat shock 70kDa protein 2	-1.51	3.1E-10	9.8E-08
3444043	**OLR1**	oxidized low density lipoprotein (lectin-like) receptor 1	-1.51	1.1E-06	1.8E-05
2411228	**STIL**	SCL/TAL1 interrupting locus	-1.52	2.0E-08	1.1E-06
3342426	**C11ORF82**	chromosome 11 open reading frame 82	-1.52	2.0E-09	2.4E-07
3438061	**GPR133**	G protein-coupled receptor 133	-1.52	1.9E-09	2.4E-07
2900051	**HIST1H3H**	histone cluster 1, H3h	-1.53	4.0E-07	8.4E-06
3415857	**ESPL1**	extra spindle pole bodies homolog 1 (S. cerevisiae)	-1.53	7.1E-08	2.5E-06
3595979	**CCNB2**	cyclin B2	-1.53	7.6E-09	5.5E-07
3186966	**TLR4**	toll-like receptor 4	-1.53	5.7E-07	1.1E-05
2474240	**KHK**	ketohexokinase (fructokinase)	-1.53	2.0E-06	2.8E-05
3151534	**ATAD2**	ATPase family, AAA domain containing 2	-1.55	7.4E-07	1.4E-05
2600689	**EPHA4**	EPH receptor A4	-1.55	5.0E-08	1.9E-06
2739160	**CCDC109B**	coiled-coil domain containing 109B	-1.55	4.2E-07	8.7E-06
3286602	**CXCL12**	chemokine (C-X-C motif) ligand 12	-1.57	2.0E-11	2.7E-08
3591704	**WDR76**	WD repeat domain 76	-1.57	5.0E-09	4.2E-07
4007689	**KCND1**	potassium voltage-gated channel, Shal-related subfamily, member 1	-1.57	8.3E-09	5.8E-07
3044597	**PDE1C**	phosphodiesterase 1C, calmodulin-dependent 70kDa	-1.59	2.6E-08	1.2E-06
3703112	**GINS2**	GINS complex subunit 2 (Psf2 homolog)	-1.59	2.0E-07	5.2E-06
3460467	**RPSAP52**	ribosomal protein SA pseudogene 52	-1.59	3.7E-09	3.5E-07
3150289	**SAMD12**	sterile alpha motif domain containing 12	-1.60	1.2E-06	1.9E-05
2946319	**HIST1H4D**	histone cluster 1, H4d	-1.61	3.0E-06	3.7E-05
3427767	**TMPO**	thymopoietin	-1.63	2.1E-09	2.5E-07
2363852	**FCRLA**	Fc receptor-like A	-1.63	5.5E-07	1.1E-05
3401804	**RAD51AP1**	RAD51 associated protein 1	-1.63	2.6E-08	1.2E-06
2335922	**CDKN2C**	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	-1.63	4.3E-07	8.9E-06
3078348	**EZH2**	enhancer of zeste homolog 2 (Drosophila)	-1.64	9.7E-08	3.1E-06
2650199	**SMC4**	structural maintenance of chromosomes 4	-1.64	5.7E-07	1.1E-05
2946369	**HIST1H3G**	histone cluster 1, H3g	-1.64	1.1E-07	3.3E-06
2899095	**HIST1H4A**	histone cluster 1, H4a	-1.65	8.3E-05	4.7E-04
3402571	**NCAPD2**	non-SMC condensin I complex, subunit D2	-1.65	1.0E-09	1.6E-07
3791896	**SERPINB7**	serpin peptidase inhibitor, clade B (ovalbumin), member 7	-1.67	1.3E-08	7.9E-07

2859667	**CENPK**	centromere protein K	-1.67	1.2E-06	2.0E-05
3910785	**AURKA**	aurora kinase A	-1.67	2.0E-10	9.2E-08
2900116	**HIST1H2BO**	histone cluster 1, H2bo	-1.68	4.5E-08	1.8E-06
2522212	**SGOL2**	shugoshin-like 2 (S. pombe)	-1.68	1.2E-06	2.0E-05
3590086	**RAD51**	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	-1.69	5.1E-08	1.9E-06
3454223	**RACGAP1**	Rac GTPase activating protein 1	-1.69	1.5E-09	2.1E-07
3365776	**E2F8**	E2F transcription factor 8	-1.69	2.3E-09	2.6E-07
4052881	**FAM72D**	family with sequence similarity 72, member D	-1.70	9.5E-08	3.0E-06
3619945	**OIP5**	Opa interacting protein 5	-1.70	1.0E-09	1.6E-07
3710823	**MYOCD**	myocardin	-1.70	1.1E-06	1.8E-05
2877990	**TMEM173**	transmembrane protein 173	-1.71	3.2E-10	9.8E-08
2720251	**NCAPG**	non-SMC condensin I complex, subunit G	-1.71	3.1E-07	7.1E-06
2378937	**DTL**	denticleless homolog (Drosophila)	-1.73	1.4E-07	4.0E-06
3936913	**CDC45**	cell division cycle 45 homolog (S. cerevisiae)	-1.73	1.1E-07	3.5E-06
2454444	**NEK2**	NIMA (never in mitosis gene a)-related kinase 2	-1.73	8.2E-09	5.8E-07
3984655	**CENPI**	centromere protein I	-1.73	1.5E-08	8.5E-07
2687979	**KIAA1524**	KIAA1524	-1.74	2.4E-07	5.9E-06
3934695	**PTTG1**	pituitary tumor-transforming 1 interacting protein	-1.74	1.6E-07	4.3E-06
2899146	**HIST1H4C**	histone cluster 1, H4c	-1.74	3.4E-08	1.5E-06
3707950	**FAM64A**	family with sequence similarity 64, member A	-1.74	8.3E-10	1.5E-07
3644764	**CCNF**	cyclin F	-1.74	1.4E-07	3.9E-06
3290210	**ZWINT**	ZW10 interactor	-1.75	4.2E-08	1.7E-06
3821263	**CNN1**	calponin 1, basic, smooth muscle	-1.76	5.4E-10	1.3E-07
3720896	**CDC6**	cell division cycle 6 homolog (S. cerevisiae)	-1.76	2.2E-08	1.1E-06
2840036	**DOCK2**	dedicator of cytokinesis 2	-1.77	2.6E-09	2.7E-07
2571457	**CKAP2L**	cytoskeleton associated protein 2-like	-1.78	1.6E-07	4.3E-06
2798915	**TRIP13**	thyroid hormone receptor interactor 13	-1.78	8.5E-09	5.9E-07
3413875	**TROAP**	trophinin associated protein (tastin)	-1.78	4.4E-08	1.8E-06
2350714	**SYPL2**	synaptophysin-like 2	-1.78	1.2E-06	1.9E-05
3442475	**C1R**	complement component 1, r subcomponent	-1.79	7.4E-09	5.5E-07
3291435	**RTKN2**	rhotekin 2	-1.80	7.3E-07	1.3E-05
3604147	**KIAA1199**	KIAA1199	-1.80	1.0E-06	1.7E-05
3490655	**CKAP2**	cytoskeleton associated protein 2	-1.80	1.1E-08	7.0E-07
2870889	**C5ORF13**	chromosome 5 open reading frame 13	-1.81	3.5E-07	7.6E-06
2752725	**NEIL3**	nei endonuclease VIII-like 3 (E. coli)	-1.82	6.4E-09	5.0E-07
2408189	**PPT1**	palmitoyl-protein thioesterase 1	-1.82	1.4E-11	2.2E-08
3504617	**SKA3**	spindle and kinetochore associated complex subunit 3	-1.84	2.5E-08	1.2E-06
2450345	**KIF14**	kinesin family member 14	-1.84	8.0E-07	1.4E-05
2874371	**FBN2**	fibrillin 2	-1.84	4.9E-08	1.9E-06
3788049	**SKA1**	spindle and kinetochore associated complex subunit 1	-1.84	1.1E-08	7.0E-07
3881443	**TPX2**	TPX2, microtubule-associated, homolog (Xenopus laevis)	-1.85	1.5E-10	7.6E-08
3136888	**TOX**	thymocyte selection-associated high mobility group box	-1.86	1.7E-08	9.4E-07
3607510	**FANCI**	Fanconi anemia, complementation group I	-1.86	2.8E-08	1.3E-06
3949055	**GTSE1**	G-2 and S-phase expressed 1	-1.87	1.1E-08	7.1E-07
3886223	**MYBL2**	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	-1.87	3.5E-09	3.4E-07
3168508	**MELK**	maternal embryonic leucine zipper kinase	-1.87	5.7E-09	4.5E-07
3223687	**PHF19**	PHD finger protein 19	-1.88	1.8E-09	2.3E-07
3744263	**AURKB**	aurora kinase B	-1.89	5.3E-09	4.3E-07
2610241	**FANCD2**	Fanconi anemia, complementation group D2	-1.90	1.1E-08	6.9E-07
2416218	**ITGB3BP**	integrin beta 3 binding protein (beta3-endonexin)	-1.90	6.9E-07	1.3E-05
2806517	**SKP2**	S-phase kinase-associated protein 2 (p45)	-1.92	3.1E-10	9.8E-08
2914777	**TTK**	TTK protein kinase	-1.92	2.0E-07	5.2E-06
2877378	**CDC25C**	cell division cycle 25 homolog C (S. pombe)	-1.93	2.5E-06	3.2E-05
3474104	**CIT**	citron (rho-interacting, serine/threonine kinase 21)	-1.94	1.1E-09	1.6E-07
3689880	**SHCBP1**	SHC SH2-domain binding protein 1	-1.97	1.0E-09	1.6E-07
2947063	**HIST1H2AK**	histone cluster 1, H2ak	-1.98	6.4E-08	2.3E-06
3599811	**KIF23**	kinesin family member 23	-1.99	2.5E-09	2.7E-07
3082181	**NCAPG2**	non-SMC condensin II complex, subunit G2	-2.00	3.9E-09	3.6E-07
3590014	**CASC5**	cancer susceptibility candidate 5	-2.00	4.2E-08	1.7E-06
2796510	**MLF1IP**	MLF1 interacting protein	-2.01	2.2E-08	1.1E-06
3635903	**DNM1P41**	DNM1 pseudogene 41	-2.01	1.1E-02	2.3E-02
3752258	**EVI2B**	ecotropic viral integration site 2B	-2.02	3.4E-08	1.5E-06
2899090	**HIST1H3A**	histone cluster 1, H3a	-2.02	1.8E-08	9.8E-07
3250146	**SRGN**	serglycin	-2.03	1.5E-10	7.6E-08
2604254	**HJURP**	Holliday junction recognition protein	-2.04	5.4E-10	1.3E-07
2747190	**DCLK2**	doublecortin-like kinase 2	-2.05	1.1E-09	1.7E-07
2714955	**TACC3**	transforming, acidic coiled-coil containing protein 3	-2.05	6.7E-09	5.2E-07
2620256	**KIF15**	kinesin family member 15	-2.07	1.5E-08	8.8E-07
3008019	**ELN**	elastin	-2.09	1.9E-09	2.4E-07
3593575	**SLC27A2**	solute carrier family 27 (fatty acid transporter), member 2	-2.09	7.3E-10	1.5E-07
3515965	**DIAPH3**	diaphanous homolog 3 (Drosophila)	-2.09	3.1E-08	1.4E-06
2947095	**HIST1H3J**	histone cluster 1, H3j	-2.09	9.3E-07	1.6E-05
3736290	**BIRC5**	baculoviral IAP repeat-containing 5	-2.09	7.0E-09	5.3E-07

3772158	**TK1**	thymidine kinase 1, soluble	-2.10	5.2E-10	1.3E-07
2378325	**SERTAD4**	SERTA domain containing 4	-2.10	7.0E-10	1.4E-07
3776139	**NDC80**	NDC80 homolog, kinetochore complex component (S. cerevisiae)	-2.11	2.0E-08	1.1E-06
2838656	**HMMR**	hyaluronan-mediated motility receptor (RHAMM)	-2.11	4.8E-08	1.9E-06
3248289	**CDK1**	cyclin-dependent kinase 1	-2.12	9.4E-08	3.0E-06
3775842	**TYMS**	thymidylate synthetase	-2.13	3.7E-09	3.5E-07
2665572	**SGOL1**	shugoshin-like 1 (S. pombe)	-2.13	4.5E-08	1.8E-06
3587457	**ARHGAP11A**	Rho GTPase activating protein 11A	-2.13	9.9E-08	3.1E-06
3589697	**BUB1B**	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	-2.16	2.8E-10	9.8E-08
2451693	**FMOD**	fibromodulin	-2.17	9.4E-10	1.6E-07
2784113	**CCNA2**	cyclin A2	-2.17	2.2E-10	9.7E-08
3091475	**SCARA3**	scavenger receptor class A, member 3	-2.17	4.6E-12	1.4E-08
3463727	**LIN7A**	lin-7 homolog A (C. elegans)	-2.18	5.5E-10	1.3E-07
3590388	**NUSAP1**	nucleolar and spindle associated protein 1	-2.18	2.3E-09	2.6E-07
3428268	**GAS2L3**	growth arrest-specific 2 like 3	-2.18	8.7E-11	7.6E-08
3653072	**PLK1**	polo-like kinase 1	-2.19	4.5E-10	1.2E-07
3756193	**TOP2A**	topoisomerase (DNA) II alpha 170kDa	-2.19	1.8E-08	9.7E-07
2494484	**NCAPH**	non-SMC condensin I complex, subunit H	-2.23	1.7E-09	2.2E-07
3980560	**KIF4A**	kinesin family member 4A	-2.23	7.7E-10	1.5E-07
3852565	**ASF1B**	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	-2.24	9.0E-09	6.1E-07
3023883	**CPA4**	carboxypeptidase A4	-2.24	2.7E-08	1.3E-06
2449559	**ASPM**	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	-2.25	7.3E-07	1.3E-05
3884892	**FAM83D**	family with sequence similarity 83, member D	-2.25	3.8E-11	4.4E-08
3090697	**CDCA2**	cell division cycle associated 2	-2.26	2.8E-09	2.8E-07
2379863	**CENPF**	centromere protein F, 350/400kDa (mitosin)	-2.26	1.7E-07	4.5E-06
2813414	**CCNB1**	cyclin B1	-2.27	9.0E-10	1.6E-07
3639031	**PRC1**	protein regulator of cytokinesis 1	-2.28	6.1E-11	6.2E-08
3440598	**FOXM1**	forkhead box M1	-2.30	1.9E-09	2.4E-07
2334098	**KIF2C**	kinesin family member 2C	-2.31	1.4E-08	7.9E-07
2364438	**NUF2**	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-2.31	2.4E-09	2.6E-07
2827185	**LMNB1**	lamin B1	-2.31	2.2E-09	2.6E-07
3258168	**KIF11**	kinesin family member 11	-2.32	3.5E-08	1.5E-06
2333136	**CDC20**	cell division cycle 20 homolog (S. cerevisiae)	-2.34	2.5E-10	9.8E-08
2324084	**CDA**	cytidine deaminase	-2.36	9.5E-10	1.6E-07
2473991	**CENPA**	centromere protein A	-2.37	2.7E-10	9.8E-08
3129149	**PBK**	PDZ binding kinase	-2.40	4.4E-09	3.8E-07
3756911	**KRT34**	keratin 34	-2.41	3.0E-10	9.8E-08
3565663	**DLGAP5**	discs, large (Drosophila) homolog-associated protein 5	-2.42	1.4E-10	7.6E-08
3629103	**KIAA0101**	KIAA0101	-2.42	1.1E-09	1.6E-07
2997376	**ANLN**	anillin, actin binding protein	-2.44	1.5E-09	2.1E-07
2438282	**IQGAP3**	IQ motif containing GTPase activating protein 3	-2.45	5.4E-10	1.3E-07
3442322	**CDCA3**	cell division cycle associated 3	-2.45	7.3E-09	5.5E-07
2947073	**HIST1H1B**	histone cluster 1, H1b	-2.45	1.9E-08	1.0E-06
3750785	**SPAG5**	sperm associated antigen 5	-2.45	1.6E-10	8.0E-08
3312490	**MKI67**	antigen identified by monoclonal antibody Ki-67	-2.50	6.3E-10	1.3E-07
2469252	**RRM2**	ribonucleotide reductase M2	-2.52	4.2E-09	3.7E-07
2585933	**SPC25**	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-2.54	6.4E-10	1.3E-07
3945545	**APOBEC3B**	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	-2.56	2.9E-10	9.8E-08
2570616	**BUB1**	budding uninhibited by benzimidazoles 1 homolog (yeast)	-2.57	5.5E-10	1.3E-07
3258444	**CEP55**	centrosomal protein 55kDa	-2.59	4.3E-10	1.2E-07
3536336	**CDKN3**	cyclin-dependent kinase inhibitor 3	-2.63	9.0E-12	2.1E-08
2793951	**HMGB2**	high-mobility group box 2	-2.63	5.7E-09	4.5E-07
2330773	**CDCA8**	cell division cycle associated 8	-2.65	1.6E-09	2.1E-07
4041113	**KPNA2**	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	-2.72	4.6E-09	4.0E-07
2417528	**DEPDC1**	DEP domain containing 1	-2.72	5.1E-08	1.9E-06
2946225	**HIST1H2BB**	histone cluster 1, H2bb	-2.81	2.2E-06	2.9E-05
3209726	**ALDH1A1**	aldehyde dehydrogenase 1 family, member A1	-2.95	7.3E-09	5.5E-07
2830638	**KIF20A**	kinesin family member 20A	-2.96	2.8E-12	1.4E-08
3381817	**UCP2**	uncoupling protein 2 (mitochondrial, proton carrier)	-2.98	4.5E-12	1.4E-08

1153 protein coding genes (1012 up and 141 down) were identified as significantly differentially expressed in BS cells using the following cutoff: absolute expression ratio (ER) ≥ 1.5 and false discovery rate (FDR) < 0.05. Thus significantly differentially expressed genes have $\log_2$ expression values of ≥|0.59|.

Table S2C. Common significantly differentially expressed mRNAs in BS and BLM-depleted cells

Probe Set ID	Gene Symbol	Gene Description	Log_2(ER)	
			BS vs NM	BLM vs NS
3299504	**ACTA2**	actin, alpha 2, smooth muscle, aorta	-1.46	-1.05
3311832	**ADAM12**	ADAM metallopeptidase domain 12	0.90	-1.18
3927480	**ADAMTS5**	ADAM metallopeptidase with thrombospondin type 1 motif, 5	0.93	2.31
2921296	**AMD1**	adenosylmethionine decarboxylase 1	0.65	0.78
2664452	**ANKRD28**	ankyrin repeat domain 28	0.88	-0.63
2997376	**ANLN**	anillin, actin binding protein	1.17	-2.44
3638607	**ANPEP**	alanyl (membrane) aminopeptidase	0.91	1.18
3327906	**API5**	apoptosis inhibitor 5	0.87	-0.82
3469319	**APPL2**	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	0.67	-0.72
3237548	**ARL5B**	ADP-ribosylation factor-like 5B	0.59	0.61
3683037	**ARL6IP1**	ADP-ribosylation factor-like 6 interacting protein 1	0.70	-0.72
2510884	**ARL6IP6**	ADP-ribosylation-like factor 6 interacting protein 6	0.74	-0.60
2531779	**ARMC9**	armadillo repeat containing 9	0.69	-0.68
3395464	**ASAM**	adipocyte-specific adhesion molecule	0.72	0.71
3809826	**ATP8B1**	ATPase, aminophospholipid transporter, class I, type 8B, member 1	0.89	-1.28
3592023	**B2M**	beta-2-microglobulin	0.64	0.59
3921933	**BACE2**	beta-site APP-cleaving enzyme 2	-0.65	1.06
3061651	**BET1**	blocked early in transport 1 homolog (S. cerevisiae)	1.10	0.66
3807474	**C18ORF32**	chromosome 18 open reading frame 32	1.17	0.77
2711034	**C3ORF59**	chromosome 3 open reading frame 59	0.77	-1.50
2766492	**C4ORF34**	chromosome 4 open reading frame 34	0.83	-0.70
2714644	**C4ORF42**	chromosome 4 open reading frame 42	0.69	0.73
2870889	**C5ORF13**	chromosome 5 open reading frame 13	0.92	-1.81
3021158	**C7ORF58**	chromosome 7 open reading frame 58	1.22	0.61
3162529	**C9ORF150**	chromosome 9 open reading frame 150	0.63	1.49
3781531	**CABLES1**	Cdk5 and Abl enzyme substrate 1	-0.59	1.67
2840002	**CCDC99**	coiled-coil domain containing 99	0.72	-0.92
7385547	**CCL2**	chemokine (C-C motif) ligand 2	0.82	-0.93
2642887	**CCRL1**	chemokine (C-C motif) receptor-like 1	0.96	-0.67
2913694	**CD109**	CD109 molecule	0.85	1.61
2548617	**CDC42EP3**	CDC42 effector protein (Rho GTPase binding) 3	0.95	-1.03
3466826	**CDK17**	cyclin-dependent kinase 17	0.72	0.78
3984655	**CENPI**	centromere protein I	0.59	-1.73
3490655	**CKAP2**	cytoskeleton associated protein 2	0.73	-1.80
2652027	**CLDN11**	claudin 11	1.63	-1.50
3012019	**CLDN12**	claudin 12	1.04	-0.84
2769947	**CLOCK**	clock homolog (mouse)	0.68	-0.66
3821263	**CNN1**	calponin 1, basic, smooth muscle	-1.33	-1.76
3599495	**CORO2B**	coronin, actin binding protein, 2B	0.60	0.97
4019900	**CUL4B**	cullin 4B	0.62	-0.96
3771642	**CYGB**	cytoglobin	-0.69	1.47
2686023	**DCBLD2**	discoidin, CUB and LCCL domain containing 2	1.64	0.95
2397025	**DHRS3**	dehydrogenase/reductase (SDR family) member 3	-0.66	-1.38
3865635	**DMPK**	dystrophia myotonica-protein kinase	-0.83	-0.62
2601648	**DOCK10**	dedicator of cytokinesis 10	0.93	-0.59
3812074	**DSEL**	dermatan sulfate epimerase-like	1.64	1.25
2515276	**DYNC1I2**	dynein, cytoplasmic 1, intermediate chain 2	0.64	0.70
4004819	**DYNLT3**	dynein, light chain, Tctex-type 3	0.84	1.40
3148582	**EIF3E**	eukaryotic translation initiation factor 3, subunit E	0.69	0.72
3591963	**EIF3J**	eukaryotic translation initiation factor 3, subunit J	0.65	0.68
3403015	**ENO2**	enolase 2 (gamma, neuronal)	-0.71	-1.12
3445908	**EPS8**	epidermal growth factor receptor pathway substrate 8	1.00	-0.59
2812435	**ERBB2IP**	erbb2 interacting protein	1.00	-0.60
3448975	**ERGIC2**	ERGIC and golgi 2	0.82	0.64
3039177	**ETV1**	ets variant 1	0.82	1.41
2816459	**F2R**	coagulation factor II (thrombin) receptor	1.59	1.04
4022781	**FAM122B**	family with sequence similarity 122B	0.60	-1.20
2584134	**FAP**	fibroblast activation protein, alpha	0.72	-1.03
3043936	**FKBP14**	FK506 binding protein 14, 22 kDa	0.81	1.27
2451693	**FMOD**	fibromodulin	-1.10	-2.17
2545953	**FNDC4**	fibronectin type III domain containing 4	-0.64	0.76
2523045	**FZD7**	frizzled homolog 7 (Drosophila)	0.75	-0.66
3047660	**GLI3**	GLI family zinc finger 3	0.65	0.60
2992814	**GPNMB**	glycoprotein (transmembrane) nmb	1.33	0.66
3405587	**GPRC5A**	G protein-coupled receptor, family C, group 5, member A	0.79	-1.40
2351004	**GSTM5**	glutathione S-transferase mu 5	-1.00	-0.88
3151086	**HAS2**	hyaluronan synthase 2	1.86	1.27
3058944	**HGF**	hepatocyte growth factor (hepapoietin A; scatter factor)	1.18	1.99
2946232	**HIST1H1C**	histone cluster 1, H1c	-0.96	-1.34
2899171	**HIST1H1E**	histone cluster 1, H1e	-0.67	-1.16
2977265	**HIVEP2**	human immunodeficiency virus type I enhancer binding protein 2	0.60	0.65
2890148	**HNRNPH1**	heterogeneous nuclear ribonucleoprotein H1 (H)	0.72	-0.65
3984779	**HNRNPH2**	heterogeneous nuclear ribonucleoprotein H2 (H')	0.86	0.65

3991698	**HPRT1**	hypoxanthine phosphoribosyltransferase 1	0.71	-0.67
3168255	**HRCT1**	histidine rich carboxyl terminus 1	-0.69	-0.76
3214668	**IARS**	isoleucyl-tRNA synthetase	0.89	0.61
2362394	**IFI16**	interferon, gamma-inducible protein 16	1.23	0.74
4018729	**IL13RA2**	interleukin 13 receptor, alpha 2	0.81	1.20
2857416	**IL6ST**	interleukin 6 signal transducer (gp130, oncostatin M receptor)	1.70	-0.78
2806468	**IL7R**	interleukin 7 receptor	1.02	0.63
3601511	**ISLR**	immunoglobulin superfamily containing leucine-rich repeat	-0.61	-0.62
3690193	**ITFG1**	integrin alpha FG-GAP repeat containing 1	0.70	0.59
3630736	**ITGA11**	integrin, alpha 11	-1.21	1.04
2809245	**ITGA2**	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	1.23	1.76
3296046	**KCNMA1**	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	1.62	0.88
3390180	**KDELC2**	KDEL (Lys-Asp-Glu-Leu) containing 2	0.73	-0.62
3629103	**KIAA0101**	KIAA0101	0.66	-2.42
2830638	**KIF20A**	kinesin family member 20A	0.74	-2.96
3464747	**KITLG**	KIT ligand	1.10	-0.72
3756911	**KRT34**	keratin 34	-1.14	-2.41
2458289	**LBR**	lamin B receptor	0.77	-0.72
2960010	**LMBRD1**	LMBR1 domain containing 1	0.66	0.69
2451043	**LMOD1**	leiomodin 1 (smooth muscle)	-0.61	-1.21
3850501	**LOC147727**	hypothetical LOC147727	0.67	0.92
2902574	**LY6G5B**	lymphocyte antigen 6 complex, locus G5B	0.75	-0.72
2823551	**MAN2A1**	mannosidase, alpha, class 2A, member 1	0.88	0.77
3097152	**MCM4**	minichromosome maintenance complex component 4	0.76	-1.02
3421300	**MDM2**	Mdm2 p53 binding protein homolog (mouse)	0.80	0.73
3414739	**METTL7A**	methyltransferase like 7A	0.61	-1.23
3651955	**METTL9**	methyltransferase like 9	0.63	0.76
3443226	**MFAP5**	microfibrillar associated protein 5	-2.09	-0.97
2649723	**MFSD1**	major facilitator superfamily domain containing 1	1.02	1.00
3143660	**MMP16**	matrix metallopeptidase 16 (membrane-inserted)	0.97	1.65
3218067	**MRPL50**	mitochondrial ribosomal protein L50	0.96	0.74
2705748	**NCEH1**	neutral cholesterol ester hydrolase 1	0.80	-0.60
3887635	**NCOA3**	nuclear receptor coactivator 3	0.74	0.66
2394784	**NOL9**	nucleolar protein 9	0.71	-0.72
3724197	**NSF**	N-ethylmaleimide-sensitive factor	0.70	-0.85
2915828	**NT5E**	5'-nucleotidase, ecto (CD73)	0.98	0.65
3590388	**NUSAP1**	nucleolar and spindle associated protein 1	0.79	-2.18
3134922	**PCMTD1**	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	0.60	0.99
3013255	**PEG10**	paternally expressed 10	0.80	-0.98
3462816	**PHLDA1**	pleckstrin homology-like domain, family A, member 1	1.12	0.66
3010082	**PHTF2**	putative homeodomain transcription factor 2	0.66	-0.73
3732230	**PITPNC1**	phosphatidylinositol transfer protein, cytoplasmic 1	0.60	0.64
3252036	**PLAU**	plasminogen activator, urokinase	0.94	0.98
3728964	**PRR11**	proline rich 11	0.80	-1.49
3126191	**PSD3**	pleckstrin and Sec7 domain containing 3	0.90	0.95
2649367	**PTX3**	pentraxin 3, long	1.48	-1.08
2626167	**PXK**	PX domain containing serine/threonine kinase	1.20	1.32
2935475	**QKI**	quaking homolog, KH domain RNA binding (mouse)	0.71	0.60
2369339	**RALGPS2**	Ral GEF with PH domain and SH3 binding motif 2	0.60	-0.98
2583602	**RBMS1**	RNA binding motif, single stranded interacting protein 1	1.13	0.63
2371346	**RGL1**	ral guanine nucleotide dissociation stimulator-like 1	0.65	0.71
2614120	**RPL15**	ribosomal protein L15	0.77	1.06
3318009	**RRM1**	ribonucleotide reductase M1	0.60	-0.83
2752006	**SAP30**	Sin3A-associated protein, 30kDa	0.64	-0.61
2750594	**SC4MOL**	sterol-C4-methyl oxidase-like	1.26	-0.88
3352904	**SC5DL**	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	0.70	0.60
2389789	**SCCPDH**	saccharopine dehydrogenase (putative)	0.64	-0.71
3907234	**SDC4**	syndecan 4	0.59	-0.84
3774906	**SECTM1**	secreted and transmembrane 1	1.26	0.59
3059464	**SEMA3A**	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	1.28	0.91
2847967	**SEMA5A**	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	1.08	0.74
3592755	**SEMA6D**	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	0.62	1.10
3936951	**SEPT5**	septin 5	-0.62	1.19
2972310	**SERINC1**	serine incorporator 1	0.84	0.65
3190659	**SET**	SET nuclear oncogene	1.18	0.61
2406064	**SFPQ**	splicing factor proline/glutamine-rich	1.19	-0.67
3764738	**SKA2**	spindle and kinetochore associated complex subunit 2	1.09	-0.77
3768412	**SLC16A6**	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	0.85	3.66
2960955	**SLC17A5**	solute carrier family 17 (anion/sugar transporter), member 5	0.84	0.85
3147726	**SLC25A32**	solute carrier family 25, member 32	0.67	0.69
2319340	**SLC25A33**	solute carrier family 25, member 33	0.86	0.77
3060245	**SLC25A40**	solute carrier family 25, member 40	0.73	-0.84
2476116	**SLC30A6**	solute carrier family 30 (zinc transporter), member 6	0.65	0.81
2349043	**SLC30A7**	solute carrier family 30 (zinc transporter), member 7	0.92	0.90
2701927	**SLC33A1**	solute carrier family 33 (acetyl-CoA transporter), member 1	0.80	0.60

3919033	**SLC5A3**	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	2.59	0.60
2786322	**SLC7A11**	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	1.76	2.01
3718555	**SLFN5**	schlafen family member 5	1.23	0.70
2720584	**SLIT2**	slit homolog 2 (Drosophila)	1.49	-1.16
3598959	**SMAD3**	SMAD family member 3	0.64	-1.30
3766960	**SMURF2**	SMAD specific E3 ubiquitin protein ligase 2	1.45	0.96
2403557	**SNORA44**	small nucleolar RNA, H/ACA box 44	0.59	-0.68
3560617	**SNX6**	sorting nexin 6	0.82	0.88
3519309	**SPRY2**	sprouty homolog 2 (Drosophila)	1.00	1.81
2879105	**SPRY4**	sprouty homolog 4 (Drosophila)	0.83	0.88
3802129	**SS18**	synovial sarcoma translocation, chromosome 18	0.70	0.73
3355145	**ST3GAL4**	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	-0.76	-0.59
2402459	**STMN1**	stathmin 1	0.59	-0.86
3770632	**SUMO2**	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	1.88	-1.05
3716664	**SUZ12P**	suppressor of zeste 12 homolog pseudogene	0.71	-0.92
2361154	**SYT11**	synaptotagmin XI	0.89	-0.87
3350830	**TAGLN**	transgelin	-1.10	-0.63
2649113	**TIPARP**	TCDD-inducible poly(ADP-ribose) polymerase	0.95	0.64
2925590	**TMEM200A**	transmembrane protein 200A	0.61	1.33
2725332	**TMEM33**	transmembrane protein 33	0.73	0.73
3427767	**TMPO**	thymopoietin	0.65	-1.63
3449068	**TMTC1**	transmembrane and tetratricopeptide repeat containing 1	1.63	0.89
3653398	**TNRC6A**	trinucleotide repeat containing 6A	0.71	-0.66
3762473	**TOB1**	transducer of ERBB2, 1	0.63	0.64
3145149	**TP53INP1**	tumor protein p53 inducible nuclear protein 1	0.72	1.06
3429460	**TXNRD1**	thioredoxin reductase 1	0.63	0.60
3775842	**TYMS**	thymidylate synthetase	0.66	-2.13
2364155	**UHMK1**	U2AF homology motif (UHM) kinase 1	0.91	-1.02
2491676	**VAMP5**	vesicle-associated membrane protein 5 (myobrevin)	-0.71	-0.67
2477203	**VIT**	vitrin	0.73	-1.05
3319937	**WEE1**	WEE1 homolog (S. pombe)	0.60	-1.19
2417390	**WLS**	wntless homolog (Drosophila)	0.99	0.87
3708074	**XAF1**	XIAP associated factor 1	-0.86	-0.83
3075531	**ZC3HAV1L**	zinc finger CCCH-type, antiviral 1-like	0.93	1.06
3801943	**ZNF521**	zinc finger protein 521	0.79	1.61

Cutoff for significantly differentially expressed mRNAs: absolute expression ratio (ER) ≥ 1.5 and false discovery rate (FDR) < 0.05. Thus significantly differentially expressed genes have log2 expression values of ≥|0.59|.

Up-regulated mRNAs are highlighted in red and down-regulated mRNAs are highlighted in green.

Table S3. Gene Set Enrichment Analysis (GESA) detail

C2: CGP (chemical and genetic perturbations, 3402 gene sets): cut-off p-value (intersect) < 10E-8	BS vs. NM		BLM vs. NS	
	p-value (intersect)	p-value (GSEA)	p-value (intersect)	p-value (GSEA)
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_UP	3.6E-45	8.4E-03	4.4E-24	6.4E-03
SENESE_HDAC3_TARGETS_UP	9.4E-39	6.0E-04	3.5E-12	1.0E-04
CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN	2.2E-38	3.1E-03	1.3E-22	1.0E-04
SENESE_HDAC1_TARGETS_UP	1.4E-29	3.0E-04	7.2E-11	1.0E-04
ONKEN_UVEAL_MELANOMA_UP	4.5E-23	5.5E-03	n.s.	1.0E-04
NUYTTEN_NIPP1_TARGETS_DN	6.1E-23	1.0E-04	6.5E-13	1.0E-04
ACEVEDO_LIVER_CANCER_UP	8.6E-22	8.0E-03	n.s.	4.0E-04
BORCZUK_MALIGNANT_MESOTHELIOMA_UP	7.3E-21	6.1E-03	n.s.	1.0E-04
JIANG_HYPOXIA_NORMAL	1.4E-19	7.0E-04	n.s.	1.0E-04
KIM_ALL_DISORDERS_CALB1_CORR_UP	1.7E-19	9.1E-03	n.s.	1.0E-04
GENTILE_UV_HIGH_DOSE_DN	5.3E-17	3.7E-03	5.8E-12	1.0E-04
GRUETZMANN_PANCREATIC_CANCER_UP	9.2E-17	4.1E-03	1.1E-11	1.0E-04
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP	3.3E-16	4.7E-03	n.s.	1.0E-04
LAIHO_COLORECTAL_CANCER_SERRATED_UP	3.7E-16	6.3E-03	n.s.	1.0E-04
FORTSCHEGGER_PHF8_TARGETS_DN	7.1E-16	3.3E-03	n.s.	1.0E-04
THUM_SYSTOLIC_HEART_FAILURE_UP	4.2E-15	2.2E-03	n.s.	1.0E-04
MARTINEZ_RESPONSE_TO_TRABECTEDIN_DN	5.0E-14	5.3E-03	n.s.	3.3E-03
MARTINEZ_RB1_AND_TP53_TARGETS_UP	5.1E-14	3.0E-04	n.s.	1.0E-04
WANG_TUMOR_INVASIVENESS_DN	1.6E-13	1.2E-03	n.s.	1.0E-04
MARTINEZ_TP53_TARGETS_UP	1.7E-13	4.0E-04	n.s.	1.0E-04
DURCHDEWALD_SKIN_CARCINOGENESIS_DN	3.3E-13	7.0E-04	n.s.	1.0E-04
NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN	3.7E-13	9.6E-03	n.s.	1.0E-04
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN	1.2E-12	5.5E-03	n.s.	1.0E-04
TOOKER_GEMCITABINE_RESISTANCE_DN	4.1E-12	9.0E-04	n.s.	1.0E-04
JI_RESPONSE_TO_FSH_DN	5.9E-12	2.1E-03	n.s.	3.7E-03
WANG_LMO4_TARGETS_UP	1.3E-11	5.0E-03	n.s.	5.9E-03
RODRIGUES_THYROID_CARCINOMA_DN	1.6E-11	2.3E-03	n.s.	1.0E-04
ONDER_CDH1_TARGETS_1_DN	2.9E-11	1.2E-03	n.s.	1.0E-03
MARTINEZ_RB1_TARGETS_UP	4.0E-11	2.9E-03	n.s.	1.0E-04
ALONSO_METASTASIS_UP	7.7E-11	6.1E-03	n.s.	1.0E-04
BROWNE_HCMV_INFECTION_14HR_DN	3.5E-10	3.0E-03	n.s.	1.0E-04
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3	4.3E-10	7.1E-03	n.s.	8.0E-04
LU_EZH2_TARGETS_DN	2.0E-09	4.3E-03	8.3E-09	2.0E-04
DAZARD_RESPONSE_TO_UV_SCC_UP	2.1E-09	4.6E-03	n.s.	2.0E-04
HEDENFALK_BREAST_CANCER_BRCA1_VS_BRCA2	2.8E-09	5.5E-03	n.s.	1.0E-04
BENPORATH_NANOG_TARGETS	3.3E-09	5.6E-03	1.7E-11	1.0E-04
KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN	3.8E-09	3.2E-03	n.s.	1.0E-04
JIANG_HYPOXIA_VIA_VHL	4.7E-09	1.0E-03	n.s.	1.6E-03
SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_DN	1.1E-08	6.4E-03	n.s.	1.0E-04
BENPORATH_NOS_TARGETS	n.s.	1.0E-04	5.3E-11	1.0E-04

C2: CP (canonical pathways, 1320 gene sets): cut-off p-value (intersect) < 0.05	BS vs. NM		BLM vs. NS	
	p-value (intersect)	p-value (GSEA)	p-value (intersect)	p-value (GSEA)
PID_ERBB1_DOWNSTREAM_PATHWAY	5.2E-07	2.3E-03	n.s.	1.0E-04
BIOCARTA_TEL_PATHWAY	9.0E-06	1.0E-03	n.s.	1.0E-04
PID_RET_PATHWAY	1.4E-05	2.0E-04	n.s.	1.0E-04
PID_TGFBRPATHWAY	4.0E-05	3.5E-03	n.s.	6.7E-03
PID_MET_PATHWAY	4.6E-05	2.1E-03	n.s.	1.0E-04
REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	5.4E-05	1.7E-03	3.5E-02	6.3E-03
REACTOME_ACTIVATION_OF_RAC	9.8E-05	2.6E-03	n.s.	4.0E-04
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	1.1E-04	3.0E-04	3.5E-02	1.0E-04
BIOCARTA_AT1R_PATHWAY	1.3E-04	3.5E-03	n.s.	1.0E-04
REACTOME_SIGNALING_BY_NOTCH	1.6E-04	8.2E-03	1.4E-02	1.0E-04
PID_EPHBFWDPATHWAY	1.8E-04	3.3E-03	n.s.	3.6E-03
REACTOME_SEMAPHORIN_INTERACTIONS	1.8E-04	6.7E-03	4.7E-02	1.0E-04
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	2.0E-04	8.6E-03	n.s.	1.0E-04
REACTOME_PRE_NOTCH_TRANSCRIPTION_AND_TRANSLATION	2.7E-04	3.0E-04	1.5E-02	1.0E-04
BIOCARTA_AGR_PATHWAY	3.6E-04	6.7E-03	n.s.	4.0E-04
REACTOME_SIGNALING_BY_EGFR_IN_CANCER	4.3E-04	6.2E-03	n.s.	2.0E-04

PID_ILK_PATHWAY	5.1E-04	7.5E-03	n.s.	1.0E-04
PID_NFAT_3PATHWAY	5.2E-04	4.0E-04	n.s.	1.0E-04
BIOCARTA_ARF_PATHWAY	5.6E-04	1.6E-03	3.7E-02	1.0E-04
BIOCARTA_SPRY_PATHWAY	5.6E-04	2.0E-04	n.s.	1.0E-04
PID_A6B1_A6B4_INTEGRIN_PATHWAY	6.2E-04	4.8E-03	n.s.	1.0E-04
PID_FGF_PATHWAY	2.7E-03	4.1E-03	n.s.	2.0E-04
REACTOME_SPRY_REGULATION_OF_FGF_SIGNALING	4.4E-03	2.0E-03	n.s.	2.4E-03
KEGG_CHRONIC_MYELOID_LEUKEMIA	7.8E-03	9.3E-03	n.s.	1.0E-04
ST_DIFFERENTIATION_PATHWAY_IN_PC12_CELLS	8.9E-03	5.4E-03	n.s.	5.3E-03
PID_P53REGULATIONPATHWAY	1.4E-02	1.2E-03	n.s.	1.0E-04
BIOCARTA_PTDINS_PATHWAY	1.6E-02	2.8E-03	n.s.	1.0E-04
PID_INTEGRIN_A4B1_PATHWAY	1.7E-02	3.9E-03	n.s.	1.0E-04
REACTOME_METABOLISM_OF_CARBOHYDRATES	2.1E-02	5.0E-03	n.s.	1.0E-04
PID_P38GAMMADELTAPATHWAY	3.2E-02	5.8E-03	4.7E-02	1.0E-04
PID_ERBB1_INTERNALIZATION_PATHWAY	4.7E-02	6.0E-04	n.s.	1.0E-04
REACTOME_SIGNALLING_BY_NGF	n.s.	8.8E-03	1.6E-02	1.0E-04

C3: MIR (microRNA targets, 221 gene sets): cut-off p-value (intersect) < 0.05	**BS vs. NM**		**BLM vs. NS**	
	p-value (intersect)	**p-value (GSEA)**	**p-value (intersect)**	**p-value (GSEA)**
MIR-224	5.1E-14	1.0E-04	5.8E-05	1.0E-04
MIR-17-5P,MIR-20A,MIR-106A,MIR-106B,MIR-20B,MIR-519D	9.6E-11	1.2E-03	2.7E-05	1.0E-04
MIR-124A	1.2E-10	1.7E-03	n.s.	2.9E-03
MIR-1,MIR-206	2.4E-10	9.0E-04	6.2E-04	1.0E-04
MIR-9	1.0E-09	7.0E-04	4.0E-04	1.0E-04
MIR-320	5.4E-09	1.9E-03	1.7E-02	9.0E-04
MIR-409-3P	2.6E-07	6.0E-03	1.7E-02	1.0E-04
MIR-520F	8.0E-06	2.8E-03	6.7E-04	1.0E-04
MIR-520G,MIR-520H	8.0E-05	2.6E-03	4.3E-04	1.0E-04
MIR-518C	8.6E-05	6.8E-03	n.s.	1.0E-04
MIR-365	1.8E-04	2.7E-03	n.s.	8.5E-03
MIR-519E	3.2E-04	3.7E-03	3.9E-02	6.2E-03
MIR-221,MIR-222	5.8E-04	1.7E-03	n.s.	4.0E-04
MIR-199A,MIR-199B	6.1E-04	3.5E-03	n.s.	1.1E-03
MIR-93,MIR-302A,MIR-302B,MIR-302C,MIR-302D,MIR-372,MIR-373,MIR-520E,MIR-520A,MIR-526B,MIR-520B,MIR-520C,MIR-520D	2.3E-03	7.0E-04	4.2E-03	1.0E-04
MIR-212,MIR-132	3.4E-03	7.2E-03	n.s.	1.0E-04
MIR-136	9.5E-03	2.9E-03	n.s.	4.0E-04
MIR-150	1.2E-02	1.9E-03	n.s.	1.0E-04

C3: TFT (transcriptional factor targets, 615 gene sets): cut-off p-value (intersect) < 0.05	**BS vs. NM**		**BLM vs. NS**	
	p-value (intersect)	**p-value (GSEA)**	**p-value (intersect)**	**p-value (GSEA)**
MGGAAGTG_V$GABP_B	3.4E-06	6.4E-03	n.s.	3.0E-04
TTANTCA_UNKNOWN	1.2E-05	5.0E-04	1.6E-05	7.0E-04
SMTTTTGT_UNKNOWN	6.5E-05	1.6E-03	2.6E-03	1.0E-04
V$MYB_Q5_01	2.2E-04	3.1E-03	4.7E-03	1.0E-04
V$SRF_C	1.2E-03	4.2E-03	n.s.	1.0E-04
V$USF_Q6	1.3E-03	3.9E-03	n.s.	1.0E-04
GCTNWTTGK_UNKNOWN	1.4E-03	6.1E-03	7.6E-03	1.0E-04
V$CHOP_01	1.7E-03	5.2E-03	n.s.	1.2E-03
TGCGCANK_UNKNOWN	2.3E-03	9.0E-03	4.6E-02	1.0E-04
YGCGYRCGC_UNKNOWN	3.2E-03	3.8E-03	n.s.	1.0E-04
V$FOXO1_02	3.3E-03	5.8E-03	2.9E-06	1.0E-04
V$E4BP4_01	3.6E-03	7.0E-04	2.0E-02	7.6E-03
ATGGYGGA_UNKNOWN	6.4E-03	1.6E-03	4.3E-02	1.8E-03
V$CREB_Q2_01	7.2E-03	1.0E-04	n.s.	1.0E-04
V$E4F1_Q6	1.0E-02	5.1E-03	n.s.	1.0E-04
V$HTF_01	1.6E-02	4.7E-03	6.0E-03	1.0E-04
V$NRF1_Q6	3.2E-02	1.7E-03	n.s.	1.0E-04
V$HIF1_Q3	4.0E-02	7.0E-04	2.1E-02	1.0E-04
V$BRN2_01	n.s.	9.7E-03	3.1E-03	6.1E-03
V$FREAC7_01	n.s.	9.0E-04	3.8E-03	1.0E-03
V$LXR_Q3	n.s.	4.2E-03	1.3E-02	1.0E-04

C4: CM (cancer modules, 431 gene sets): cut-off p-value (intersect) < 0.05	**BS vs. NM**		**BLM vs. NS**	
	p-value (intersect)	**p-value (GSEA)**	**p-value (intersect)**	**p-value (GSEA)**
MODULE_15	9.3E-04	1.8E-03	2.9E-09	1.0E-04
MODULE_56	1.7E-02	5.6E-03	n.s.	3.7E-03
MODULE_147	3.4E-06	7.3E-03	n.s.	1.0E-04
MODULE_166	1.5E-02	3.5E-03	n.s.	9.1E-03
MODULE_256	3.1E-02	2.0E-04	n.s.	1.0E-04
MODULE_69	n.s.	9.5E-03	9.2E-03	1.0E-04
MODULE_136	n.s.	9.2E-03	4.5E-02	1.0E-04

C4: CGN (cancer gene neighborhoods, 427 gene sets): cut-off p-value (intersect) < 0.05	**BS vs. NM**		**BLM vs. NS**	
	p-value (intersect)	**p-value (GSEA)**	**p-value (intersect)**	**p-value (GSEA)**
MORF_RAB6A	8.0E-10	9.1E-03	n.s.	5.2E-03
GCM_BCL2L1	1.7E-02	2.7E-03	n.s.	1.0E-04

C5: BP (GO Biological Process Ontology, 825 gene sets): cut-off p-value (intersect) < 0.05	**BS vs. NM**		**BLM vs. NS**	
	p-value (intersect)	**p-value (GSEA)**	**p-value (intersect)**	**p-value (GSEA)**
MACROMOLECULAR_COMPLEX_ASSEMBLY	1.2E-06	2.2E-03	n.s.	1.0E-04
REGULATION_OF_METABOLIC_PROCESS	4.4E-06	3.0E-03	n.s.	1.4E-03
CELLULAR_COMPONENT_ASSEMBLY	6.1E-06	2.5E-03	n.s.	1.0E-04
REGULATION_OF_CELLULAR_METABOLIC_PROCESS	7.9E-06	2.7E-03	n.s.	2.7E-03
TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	8.5E-05	6.0E-03	n.s.	2.0E-04
REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION_AND_BIOGENESIS	8.6E-05	2.5E-03	n.s.	1.0E-04
POSITIVE_REGULATION_OF_CELLULAR_PROCESS	9.8E-05	6.9E-03	n.s.	1.0E-04
PROTEIN_KINASE_CASCADE	1.4E-04	9.4E-03	n.s.	1.0E-04
REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	1.6E-04	8.3E-03	3.0E-03	1.0E-04
ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	3.1E-04	1.0E-04	1.9E-02	1.0E-04
BIOPOLYMER_MODIFICATION	4.9E-04	5.5E-03	n.s.	1.0E-04
NEGATIVE_REGULATION_OF_TRANSCRIPTION	7.5E-04	5.3E-03	n.s.	1.0E-04
NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION_AND_BIOGENESIS	1.2E-03	6.8E-03	n.s.	1.0E-04
VESICLE_MEDIATED_TRANSPORT	1.5E-03	5.8E-03	n.s.	1.0E-04
NEGATIVE_REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	1.9E-03	8.4E-03	3.6E-02	1.0E-04
REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	5.9E-03	8.6E-03	4.0E-02	1.0E-04
POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	8.6E-03	9.7E-03	2.5E-02	1.0E-04
REGULATION_OF_TRANSFERASE_ACTIVITY	1.9E-02	2.5E-03	3.7E-02	1.0E-04
REGULATION_OF_PROTEIN_KINASE_ACTIVITY	2.6E-02	2.4E-03	n.s.	1.0E-04
REGULATION_OF_KINASE_ACTIVITY	2.9E-02	2.5E-03	n.s.	1.0E-04
REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	n.s.	9.7E-03	n.s.	1.0E-04
NEGATIVE_REGULATION_OF_CELL_ADHESION	n.s.	9.2E-03	n.s.	1.0E-04

C5: CC (GO cellular component, 233 gene sets): cut-off p-value (intersect) < 0.05	**BS vs. NM**		BLM vs. NS	
	p-value (intersect)	**p-value (GSEA)**	**p-value (intersect)**	**p-value (GSEA)**
ER_GOLGI_INTERMEDIATE_COMPARTMENT	1.3E-06	4.0E-04	n.s.	1.0E-04

C5: MF (GO molecular function, 396 gene sets): cut-off p-value (intersect) < 0.05	**BS vs. NM**		**BLM vs. NS**	
	p-value (intersect)	**p-value (GSEA)**	**p-value (intersect)**	**p-value (GSEA)**
GTPASE_ACTIVITY	1.6E-04	8.2E-03	n.s.	1.0E-04
SMAD_BINDING	6.3E-03	4.6E-03	n.s.	1.0E-04
PROTEIN_KINASE_ACTIVITY	7.2E-03	2.8E-03	1.7E-02	1.0E-04
TRANSITION_METAL_ION_BINDING	1.2E-02	7.6E-03	n.s.	1.0E-04
NUCLEOTIDE_BINDING	2.8E-02	1.0E-03	4.0E-02	1.0E-04
PURINE_NUCLEOTIDE_BINDING	2.8E-02	1.2E-03	n.s.	1.0E-04
PURINE_RIBONUCLEOTIDE_BINDING	4.1E-02	1.5E-03	n.s.	1.0E-04
S_ADENOSYLMETHIONINE_DEPENDENT_METHYLTRANSFERASE_ACTIVITY	n.s.	3.9E-03	6.6E-03	9.1E-03

C6: Oncogenic signatures (189 gene sets): cut-off p-value (intersect) < 0.05	**BS vs. NM**		**BLM vs. NS**	
	p-value (intersect)	**p-value (GSEA)**	**p-value (intersect)**	**p-value (GSEA)**
CAMP_UP.V1_DN	2.1E-10	2.0E-04	1.3E-02	8.0E-04
STK33_UP	2.3E-09	3.8E-03	2.3E-08	1.0E-04

C7: Immunologic signatures (1910 gene sets): cut-off p-value (intersect) < 0.05	**BS vs. NM**		**BLM vs. NS**	
	p-value (intersect)	**p-value (GSEA)**	**p-value (intersect)**	**p-value (GSEA)**
GSE17721_12H_VS_24H_POLYIC_BMDM_UP	1.0E-13	2.6E-03	9.2E-03	1.0E-04
GSE9006_HEALTHY_VS_TYPE_1_DIABETES_PBMC_AT_DX_UP	2.8E-11	1.8E-03	n.s.	2.0E-04
GSE22886_NAIVE_VS_MEMORY_TCELL_DN	2.8E-11	1.0E-03	1.8E-04	1.0E-04
GSE17721_CTRL_VS_GARDIQUIMOD_0.5H_BMDM_UP	3.9E-11	7.0E-04	n.s.	1.0E-04
GSE17721_0.5H_VS_4H_PAM3CSK4_BMDM_DN	4.6E-11	5.5E-03	3.4E-02	7.0E-04
GSE10239_MEMORY_VS_KLRG1HIGH_EFF_CD8_TCELL_DN	7.7E-11	9.6E-03	1.6E-07	1.0E-04
GSE20715_WT_VS_TLR4_KO_LUNG_UP	4.8E-09	8.8E-03	n.s.	4.0E-04
GSE17721_POLYIC_VS_PAM3CSK4_4H_BMDM_DN	7.4E-09	1.0E-03	n.s.	1.0E-04
GSE39820_TGFBETA3_IL6_VS_TGFBETA3_IL6_IL23A_TREATED_CD4_TCELL_UP	1.1E-08	9.1E-03	3.3E-03	9.0E-04
GSE22886_NAIVE_BCELL_VS_DC_DN	4.4E-08	7.6E-03	n.s.	1.0E-04
GSE27786_BCELL_VS_NKCELL_DN	9.6E-08	3.2E-03	n.s.	4.4E-03
GSE339_EX_VIVO_VS_IN_CULTURE_CD4POS_DC_DN	9.6E-08	3.7E-03	n.s.	3.2E-03
GSE9006_HEALTHY_VS_TYPE_1_DIABETES_PBMC_4MONTH_POST_DX_UP	9.6E-08	4.2E-03	1.9E-02	1.0E-04
GSE22886_NAIVE_CD8_TCELL_VS_MEMORY_TCELL_DN	1.2E-07	7.0E-04	5.8E-05	1.0E-04
GSE17721_LPS_VS_POLYIC_16H_BMDM_UP	1.8E-07	4.2E-03	4.7E-02	7.0E-03
GSE17721_POLYIC_VS_CPG_16H_BMDM_DN	1.8E-07	3.9E-03	n.s.	1.0E-04
GSE3982_MAST_CELL_VS_NKCELL_UP	1.8E-07	9.1E-03	n.s.	1.0E-04
GSE17721_POLYIC_VS_GARDIQUIMOD_1H_BMDM_DN	2.4E-07	4.0E-03	n.s.	2.0E-04
GSE22886_NAIVE_TCELL_VS_NEUTROPHIL_UP	2.4E-07	8.5E-03	n.s.	4.4E-03
GSE39820_TGFBETA1_IL6_VS_TGFBETA1_IL6_IL23A_TREATED_CD4_TCELL_UP	4.4E-07	3.0E-04	n.s.	1.0E-04
GSE7460_CTRL_VS_TGFB_TREATED_ACT_FOXP3_HET_TCONV_UP	4.4E-07	1.0E-04	n.s.	1.0E-04
GSE17721_LPS_VS_GARDIQUIMOD_24H_BMDM_DN	6.4E-07	1.6E-03	2.0E-04	1.0E-04
GSE17721_POLYIC_VS_GARDIQUIMOD_4H_BMDM_DN	6.4E-07	1.9E-03	n.s.	1.0E-04
GSE17721_POLYIC_VS_CPG_2H_BMDM_DN	9.3E-07	9.8E-03	n.s.	6.0E-04
GSE3982_EOSINOPHIL_VS_NKCELL_UP	1.2E-06	6.7E-03	6.6E-03	1.0E-04
GSE3982_BASOPHIL_VS_CENT_MEMORY_CD4_TCELL_UP	1.7E-06	1.5E-03	2.0E-03	1.0E-04
GSE339_EX_VIVO_VS_IN_CULTURE_CD8POS_DC_UP	2.2E-06	1.0E-03	1.7E-02	1.0E-04
GSE13484_UNSTIM_VS_YF17D_VACCINE_STIM_PBMC_UP	2.4E-06	3.9E-03	n.s.	3.0E-03
GSE17721_LPS_VS_GARDIQUIMOD_16H_BMDM_DN	2.7E-06	5.4E-03	6.1E-04	1.0E-04
GSE17721_CTRL_VS_LPS_4H_BMDM_UP	4.5E-06	8.6E-03	4.5E-02	1.0E-04
GSE9037_CTRL_VS_LPS_4H_STIM_BMDM_UP	5.0E-06	9.5E-03	n.s.	1.0E-04
GSE11057_NAIVE_VS_CENT_MEMORY_CD4_TCELL_DN	5.6E-06	9.7E-03	n.s.	1.0E-04
GSE12845_IGD_NEG_BLOOD_VS_DARKZONE_GC_TONSIL_BCELL_DN	6.2E-06	7.5E-03	n.s.	2.0E-04
GSE17580_UNINFECTED_VS_S_MANSONI_INF_TREG_DN	7.7E-06	9.0E-04	5.4E-03	1.0E-04
GSE29618_BCELL_VS_PDC_DAY7_FLU_VACCINE_DN	1.7E-05	4.6E-03	4.7E-03	1.0E-04
GSE11057_NAIVE_VS_EFF_MEMORY_CD4_TCELL_DN	1.8E-05	7.3E-03	5.0E-03	1.0E-04
GSE14308_TH17_VS_NAIVE_CD4_TCELL_UP	2.0E-05	2.5E-03	2.6E-03	2.7E-03
GSE20366_TREG_VS_NAIVE_CD4_TCELL_UP	2.0E-05	3.6E-03	2.1E-06	1.0E-04
GSE13484_12H_UNSTIM_VS_YF17D_VACCINE_STIM_PBMC_UP	2.1E-05	6.7E-03	n.s.	8.5E-03
GSE17721_CPG_VS_GARDIQUIMOD_6H_BMDM_DN	2.1E-05	6.1E-03	n.s.	1.0E-04
GSE17721_LPS_VS_PAM3CSK4_16H_BMDM_DN	2.8E-05	1.9E-03	1.6E-03	1.0E-04
GSE360_L_DONOVANI_VS_B_MALAYI_LOW_DOSE_MAC_UP	3.7E-05	1.8E-03	4.7E-02	3.9E-03
GSE7764_NKCELL_VS_SPLENOCYTE_UP	5.5E-05	7.6E-03	1.9E-02	1.0E-04
GSE39820_CTRL_VS_IL1B_IL6_CD4_TCELL_DN	8.0E-05	2.6E-03	6.3E-05	1.0E-04
GSE7764_IL15_NK_CELL_24H_VS_SPLENOCYTE_DN	9.7E-05	6.5E-03	2.0E-03	1.0E-04
GSE13484_UNSTIM_VS_3H_YF17D_VACCINE_STIM_PBMC_DN	1.1E-04	6.8E-03	n.s.	1.3E-03
GSE9037_WT_VS_IRAK4_KO_LPS_4H_STIM_BMDM_UP	1.2E-04	9.3E-03	9.2E-03	4.0E-04
GSE17721_POLYIC_VS_GARDIQUIMOD_16H_BMDM_UP	1.5E-04	7.8E-03	n.s.	2.3E-03
GSE13229_MATURE_VS_INTMATURE_NKCELL_DN	1.5E-04	3.3E-03	n.s.	9.6E-03
GSE39820_CTRL_VS_IL1B_IL6_CD4_TCELL_UP	1.5E-04	1.0E-04	n.s.	1.0E-04
GSE37416_CTRL_VS_12H_F_TULARENSIS_LVS_NEUTROPHIL_UP	2.2E-04	3.0E-03	7.6E-03	1.0E-04
GSE36476_CTRL_VS_TSST_ACT_72H_MEMORY_CD4_TCELL_YOUNG_UP	2.4E-04	8.0E-04	n.s.	1.0E-04
GSE3982_MAST_CELL_VS_CENT_MEMORY_CD4_TCELL_UP	2.6E-04	7.2E-03	4.4E-03	1.0E-04
GSE17721_LPS_VS_PAM3CSK4_6H_BMDM_UP	2.9E-04	1.4E-03	n.s.	1.0E-04
GSE27786_CD4_TCELL_VS_NKCELL_DN	2.9E-04	6.0E-04	n.s.	1.0E-04
GSE16522_MEMORY_VS_NAIVE_ANTI_CD3CD28_STIM_CD8_TCELL_UP	3.4E-04	2.8E-03	n.s.	1.0E-04

GSE9650_NAIVE_VS_EXHAUSTED_CD8_TCELL_DN	3.4E-04	5.9E-03	2.7E-03	1.0E-04
GSE24634_NAIVE_CD4_TCELL_VS_DAY10_IL4_CONV_TREG_DN	4.0E-04	1.0E-03	1.1E-10	1.0E-04
GSE3982_MAC_VS_TH2_UP	4.0E-04	3.5E-03	n.s.	2.8E-03
GSE24142_ADULT_VS_FETAL_DN3_THYMOCYTE_UP	4.7E-04	5.0E-03	7.1E-03	5.0E-04
GSE20366_CD103_KLRG1_DP_VS_DN_TREG_DN	5.3E-04	6.9E-03	1.7E-04	1.0E-04
GSE360_CTRL_VS_M_TUBERCULOSIS_MAC_UP	5.7E-04	1.9E-03	n.s.	1.0E-04
GSE17721_LPS_VS_GARDIQUIMOD_12H_BMDM_DN	6.2E-04	3.1E-03	n.s.	1.0E-04
GSE27786_NKTCELL_VS_MONO_MAC_UP	6.4E-04	8.6E-03	n.s.	1.0E-04
GSE3982_EOSINOPHIL_VS_MAC_DN	6.7E-04	2.6E-03	n.s.	1.0E-04
GSE27786_ERYTHROBLAST_VS_NEUTROPHIL_DN	8.5E-04	9.0E-04	n.s.	1.0E-04
GSE12845_IGD_POS_BLOOD_VS_NAIVE_TONSIL_BCELL_DN	9.1E-04	5.1E-03	2.1E-02	3.3E-03
GSE17721_LPS_VS_PAM3CSK4_4H_BMDM_UP	9.9E-04	3.7E-03	1.3E-02	1.0E-04
GSE360_CTRL_VS_B_MALAYI_LOW_DOSE_DC_UP	1.0E-03	4.0E-04	n.s.	2.0E-04
GSE17721_12H_VS_24H_GARDIQUIMOD_BMDM_DN	1.5E-03	4.2E-03	n.s.	1.3E-03
GSE9650_EFFECTOR_VS_EXHAUSTED_CD8_TCELL_DN	2.0E-03	2.2E-03	7.2E-04	1.0E-04
GSE27786_NKTCELL_VS_ERYTHROBLAST_UP	2.1E-03	2.6E-03	n.s.	1.0E-04
GSE24634_TREG_VS_TCONV_POST_DAY3_IL4_CONVERSION_DN	2.2E-03	3.2E-03	3.4E-03	1.0E-04
GSE17721_PAM3CSK4_VS_GADIQUIMOD_1H_BMDM_DN	3.2E-03	7.2E-03	n.s.	2.5E-03
GSE27786_ERYTHROBLAST_VS_MONO_MAC_DN	3.2E-03	8.3E-03	n.s.	1.0E-04
GSE3982_MAST_CELL_VS_MAC_DN	3.2E-03	8.3E-03	n.s.	2.0E-04
GSE3982_CTRL_VS_PMA_STIM_EOSINOPHIL_UP	3.5E-03	6.5E-03	n.s.	2.0E-04
GSE32423_IL7_VS_IL4_MEMORY_CD8_TCELL_UP	4.2E-03	8.0E-04	1.1E-04	1.0E-04
GSE17721_LPS_VS_CPG_12H_BMDM_UP	4.5E-03	9.1E-03	3.9E-02	1.0E-04
GSE13484_12H_VS_3H_YF17D_VACCINE_STIM_PBMC_UP	5.9E-03	2.0E-04	n.s.	1.0E-04
GSE17721_LPS_VS_GARDIQUIMOD_8H_BMDM_UP	5.9E-03	3.5E-03	4.7E-02	1.0E-04
GSE39820_CTRL_VS_IL1B_IL6_IL23A_CD4_TCELL_UP	5.9E-03	6.8E-03	1.8E-04	1.0E-04
GSE360_CTRL_VS_B_MALAYI_HIGH_DOSE_MAC_UP	6.2E-03	2.0E-04	n.s.	2.0E-04
GSE360_DC_VS_MAC_B_MALAYI_LOW_DOSE_UP	7.1E-03	3.7E-03	n.s.	4.0E-04
GSE32423_IL7_VS_IL7_IL4_MEMORY_CD8_TCELL_UP	7.2E-03	1.1E-03	2.3E-03	1.0E-04
GSE17721_LPS_VS_POLYIC_16H_BMDM_DN	7.5E-03	1.3E-03	n.s.	1.0E-04
GSE5463_CTRL_VS_DEXAMETHASONE_TREATED_THYMOCYTE_DN	8.0E-03	4.7E-03	2.9E-03	6.8E-03
GSE3982_NEUTROPHIL_VS_BASOPHIL_UP	8.6E-03	1.9E-03	n.s.	2.0E-04
GSE30962_ACUTE_VS_CHRONIC_LCMV_SECONDARY_INF_CD8_TCELL_UP	9.2E-03	8.1E-03	1.2E-02	1.0E-04
GSE17721_LPS_VS_CPG_4H_BMDM_DN	9.8E-03	5.1E-03	n.s.	2.0E-04
GSE36476_YOUNG_VS_OLD_DONOR_MEMORY_CD4_TCELL_72H_TSST_ACT_DN	1.0E-02	9.5E-03	n.s.	1.0E-03
GSE360_HIGH_VS_LOW_DOSE_B_MALAYI_DC_UP	1.1E-02	5.4E-03	n.s.	1.8E-03
GSE11864_CSF1_VS_CSF1_IFNG_PAM3CYS_IN_MAC_UP	1.1E-02	1.5E-03	n.s.	1.0E-04
GSE24142_EARLY_THYMIC_PROGENITOR_VS_DN3_THYMOCYTE_FETAL_UP	1.2E-02	7.0E-04	n.s.	1.0E-04
GSE36476_CTRL_VS_TSST_ACT_40H_MEMORY_CD4_TCELL_YOUNG_UP	1.4E-02	2.0E-03	1.8E-02	8.0E-04
GSE17721_LPS_VS_PAM3CSK4_8H_BMDM_DN	1.6E-02	9.1E-03	n.s.	5.0E-04
GSE27786_CD8_TCELL_VS_MONO_MAC_DN	2.0E-02	7.0E-04	3.6E-04	1.0E-04
GSE17974_0.5H_VS_72H_UNTREATED_IN_VITRO_CD4_TCELL_UP	2.8E-02	4.6E-03	n.s.	1.0E-04
GSE37416_CTRL_VS_6H_F_TULARENSIS_LVS_NEUTROPHIL_UP	4.2E-02	1.1E-03	n.s.	3.8E-03
GSE360_DC_VS_MAC_UP	4.8E-02	6.8E-03	n.s.	3.3E-03
GSE17721_CTRL_VS_POLYIC_1H_BMDM_UP	5.0E-02	6.3E-03	n.s.	1.0E-04

Note:

p-value (intersect) is the p-value of a hypergeometric test for genes that were in common between BS-NM and BLM-NS data and were represented in statistically significant genesets.

p-value (GSEA) is the p-value of the Gene Set Enrichment Analysis (GSEA).

n.s.: not significant at the cut-off p-value (intersect). Common genesets between BS vs. NM and BLM vs. NS are highlighted in bold type.

Table S4. Significantly differentially expressed miRNAs identified in BS or BLM-depleted fibroblasts

miRBase ID	BS vs. NM			BLM vs. NS		
	p-value	FDR	Expression Ratio	p-value	FDR	Expression Ratio
hsa-miR-181a-5p	5.85E-03	3.34E-02	2.60	3.42E-02	n.s.	n.s.
hsa-miR-595	8.04E-04	1.03E-02	2.13	n.s.	n.s.	n.s.
hsa-miR-30a-5p	1.93E-03	1.76E-02	2.12	n.s.	n.s.	n.s.
hsa-miR-30d-5p	2.43E-03	2.00E-02	1.90	n.s.	n.s.	n.s.
hsa-miR-155-5p	1.67E-02	6.62E-02	1.90	3.99E-02	n.s.	n.s.
hsa-miR-29b-3p	2.90E-02	9.94E-02	1.85	n.s.	n.s.	n.s.
hsa-miR-412	2.21E-03	1.89E-02	1.83	n.s.	n.s.	n.s.
hsa-miR-130a-3p	5.19E-03	3.16E-02	1.79	4.70E-03	9.23E-02	n.s.
hsa-miR-320a	5.32E-04	7.67E-03	1.75	n.s.	n.s.	n.s.
hsa-miR-484	3.17E-03	2.12E-02	1.73	n.s.	n.s.	n.s.
hsa-miR-29c-3p	1.44E-02	6.06E-02	1.72	n.s.	n.s.	n.s.
hsa-miR-634	2.77E-03	2.05E-02	1.68	1.22E-02	n.s.	n.s.
hsa-miR-26b-5p	6.29E-03	3.39E-02	1.68	n.s.	n.s.	n.s.
hsa-miR-34a-5p	1.10E-02	4.93E-02	1.67	n.s.	n.s.	n.s.
hsa-miR-199a-5p	2.14E-02	8.25E-02	1.63	1.52E-05	3.04E-03	-1.68
hsa-miR-328	1.66E-02	6.62E-02	1.63	n.s.	n.s.	n.s.
hsa-miR-29a-3p	2.38E-02	8.67E-02	1.62	4.43E-02	n.s.	n.s.
hsa-miR-130b-3p	2.69E-02	9.34E-02	1.56	n.s.	n.s.	n.s.
hsa-miR-103a-3p	5.81E-03	3.34E-02	1.51	n.s.	n.s.	n.s.
hsa-miR-143-3p	7.17E-03	3.64E-02	-2.35	5.93E-04	3.16E-02	-1.68
hsa-miR-499a-5p	2.50E-03	2.00E-02	-2.05	n.s.	n.s.	n.s.
hsa-miR-92b-3p	3.14E-03	2.12E-02	-1.92	n.s.	n.s.	n.s.
hsa-miR-145-5p	8.59E-04	1.03E-02	-1.89	3.96E-03	8.55E-02	-2.22
hsa-let-7c	6.76E-05	2.65E-03	-1.88	n.s.	n.s.	n.s.
hsa-let-7b-5p	5.27E-07	1.44E-04	-1.88	3.27E-02	n.s.	n.s.
hsa-miR-632	5.12E-04	7.67E-03	-1.87	n.s.	n.s.	n.s.
hsa-let-7e-5p	2.55E-05	1.40E-03	-1.86	5.01E-03	9.23E-02	n.s.
hsa-miR-129-5p	6.51E-03	3.43E-02	-1.85	n.s.	n.s.	n.s.
hsa-miR-636	1.88E-05	1.29E-03	-1.73	n.s.	n.s.	n.s.
hsa-let-7d-5p	7.92E-05	2.67E-03	-1.71	3.51E-03	7.79E-02	1.80
hsa-let-7g-5p	3.48E-03	2.22E-02	-1.71	n.s.	n.s.	n.s.
hsa-miR-638	2.77E-03	2.05E-02	-1.71	n.s.	n.s.	n.s.
hsa-miR-365a-3p	9.65E-03	4.48E-02	-1.70	n.s.	n.s.	n.s.
hsa-let-7a-5p	6.86E-06	9.40E-04	-1.70	n.s.	n.s.	n.s.
hsa-miR-99a-5p	9.30E-03	4.39E-02	-1.66	1.50E-03	5.03E-02	1.59
hsa-let-7f-5p	9.91E-04	1.10E-02	-1.61	n.s.	n.s.	n.s.
hsa-miR-193a-5p	4.69E-04	7.67E-03	-1.57	n.s.	n.s.	n.s.
hsa-miR-152	1.48E-02	6.14E-02	-1.55	n.s.	n.s.	n.s.
hsa-miR-221-3p	4.04E-02	n.s.	n.s.	6.18E-05	7.06E-03	2.50
hsa-miR-107	2.27E-02	8.48E-02	n.s.	2.61E-05	3.48E-03	2.37
hsa-miR-495	n.s.	n.s.	n.s.	1.51E-03	5.03E-02	2.03
hsa-miR-24-3p	n.s.	n.s.	n.s.	2.97E-04	1.83E-02	1.83
hsa-let-7i-5p	1.36E-03	1.43E-02	n.s.	2.40E-05	3.48E-03	1.67
hsa-miR-409-3p	n.s.	n.s.	n.s.	5.79E-03	9.53E-02	1.56
hsa-miR-382-5p	n.s.	n.s.	n.s.	2.59E-03	6.91E-02	1.53
hsa-miR-210	3.16E-04	6.00E-03	n.s.	3.16E-03	7.44E-02	-3.38
hsa-miR-15a-5p	n.s.	n.s.	n.s.	5.01E-03	9.23E-02	-2.69
hsa-miR-629-5p	n.s.	n.s.	n.s.	5.08E-03	9.23E-02	-2.51
hsa-miR-15b-5p	n.s.	n.s.	n.s.	1.09E-05	3.04E-03	-2.26
hsa-miR-196a-5p	3.59E-02	n.s.	n.s.	2.48E-03	6.83E-02	-1.72
hsa-miR-16-5p	n.s.	n.s.	n.s.	1.15E-05	3.04E-03	-1.70
hsa-miR-25-3p	n.s.	n.s.	n.s.	9.48E-04	4.21E-02	-1.59

A total of 38 (19 up and 19 down) miRNAS were identified as significantly differentially expressed in BS fibroblasts, and 19 (9 up and 10 down) miRNAs in BLM-depleted human fibroblasts using the following cut-off: absolute expression ratio ≥ 1.5 and false discovery rate (FDR) < 0.1.

Cancer/disease associated miRNAs annotated in MalaCards: The Human Malady Compendium (http://www.malacards.org/) are highlighted in bold italic font.

Table S5: Experimentally validated targets of miRNAs significantly altered in BS or BLM-depleted cells.

	change in miRNA expression		
miRBase ID	**BS vs NM**	**BLM vs NS**	**Validated Targets**
hsa-miR-143-3p	↓ down	↓ down	AKT1 BCL2 COL1A1 DNMT3A FHIT FNDC3B FSCN1 HK2 HRAS KRAS MACC1 MAPK7 MDM2 MMP13 MYO6 SERPINE1
hsa-miR-145-5p	↓ down	↓ down	ADAM17 BNIP3 CBFB CDH2 CDK4 CDKN1A CLINT1 CPEB4 CTGF DDX17 EIF4E ERG F11R FLI1 FSCN1 FZD7 HDAC2 HOXA9 IFNB1 IGF1R ILK IRS1 IRS2 ITGB8 KLF4 KRT7 MDM2 MUC1 MYC MYO5A MYO6 MYRF NANOG NEDD9 NRAS PAK4 POU5F1 PPM1D PPP3CA ROBO2 RTKN SERPINE1 SOCS7 SOX2 STAT1 SWAP70 TIRAP TMOD3 VEGFA YES1
hsa-miR-199a-5p	↑ up	↓ down	CAV1 DDR1 EDN1 ERBB2 EZH2 GPR78 IKBKB LIF MAP3K11 SIRT1 SMAD4 SMARCA2 SULT1E1 UNG
hsa-let-7d-5p	↓ down	↑ up	APP DICER1 HMGA2 IL13 MPL PDGFA SLC11A2
hsa-miR-99a-5p	↓ down	↑ up	FGFR3 IGR1R MTOR RAVER2 SERPINE1
hsa-miR-181a-5p	↑ up	n.s.	ATM BCL2 BCL2L11 CDKN1B CDX2 DDIT4 DUSP5 DUSP6 FOS GATA6 GPR78 HIPK2 HRAS KAT2B KLF6 MCL1 MTMR3 NLK NOTCH1 PLAG1 PRAP1 PROX1 PTPN11 PTPN22 RALA SIRT1 XIAP ZNF763
hsa-miR-595	↑ up	n.s.	PARD6A
hsa-miR-30a-5p	↑ up	n.s.	ABL1 AVEN BECN1 DTL FOXD1 NEUROD1 NOTCH1 PIK3CD PRDM1 RUNX2 SEPT7 SMAD1 TNRC6A TUBB4B
hsa-miR-30d-5p	↑ up	n.s.	CASP3 EZH2 GNAI2 GPR78 RUNX2 SMAD1 TP53
hsa-miR-155-5p	↑ up	n.s.	ACTR2 AGO4 AGTR1 ANAPC16 APAF1 APC ARFIP1 ARID2 ARL15 ARL6IP5 ARMC2 ARPC3 BACH1 BCL6 C16orf62 C17orf80 C3orf18 CAB39 CARD11 CARHSP1 CBR4 CCDC41 CCDC82 CD68 CDC40 CEBPB CEP41 CHD9 CIAPIN1 CLUAP1 CSNK1A1 CYP2U1 CYR61 DCUN1D2 DET1 DHX40 E2F2 EDN1 ETS1 EXOSC2 FAM135A FAM177A1 FAM199X FAM91A1 FGF7 FLI1 FOXO3 GABARAPL1 GATM GCFC2 GCSAM GOLT1B GPM6B HAL HBP1 HERC4 HIVEP2 ICAM1 IFNGR1 IGJ IKBKE IL13RA1 IL17RB IL8 INPP5D INPP5F INTS6 JARID2 JUN KBTBD2 KDM3A KIAA0430 KLHL5 KRAS KRCC1 LCORL LDOC1 LIN7C LNX2 LRIF1 LRRC59 MAP3K10 MAP3K14 MASTL MATR3 MBNL3 MCM8 MECP2 MEF2A MEIS1 MITF MLH1 MORC3 MPP5 MRPL18 MRPS27 MSH2 MSH6 MSI2 MYB MYBL1 MYD88 MYO10 MYO1D NARS NFATC2IP NOS3 NOVA1 OLR1 PAK2 PALD1 PBRM1 PCDH9 PDLIM5 PHC2 PHF14 PHF17 PICALM PKIA PKN2 PLS1 POLE3 PRKAR1A RAB11FIP2 RAC1 RAPGEF2 RBAK RHEB RHOA RUNX2 SAP30L SDCBP SECISBP2 SELE SKI SLC33A1 SLC35F2 SMAD1 SMAD2 SMAD3 SMAD4 SMAD5 SMARCA4 SOCS1 SPI1 SSX2IP TAB2 TAF5L TBC1D14 TBC1D8B TBCA TCF12 TLE4 TM6SF1 TOMM20 TP53INP1 TRAK1 TRIP13 TSHZ3 TSPAN14 TTF1 UBQLN1 UBTD2 UPF2 UQCRFS1 VPS18 WBP1L WEE1 WHSC1L1 WWC1 YWHAZ ZIC3 ZNF248 ZNF254 ZNF28 ZNF493 ZNF561 ZNF611 ZNF652 ZNF83
hsa-miR-29b-3p	↑ up	n.s.	ADAM12 BACE1 BCL2 BMP1 CDC42 CDK6 COL1A1 COL3A1 COL4A1 COL5A3 CTNNBIP1 DNAJB11 DNMT1 DNMT3A DNMT3B DUSP2 ESR1 FGA FGB FGG FOS GRN HDAC4 IFNG IMPDH1 MCL1 MMP15 MMP2 MMP24 MYCN NASP NCOA3 NID1 NKIRAS2 PPP1R13B PTEN RAX S100B SFPQ SP1 TBX21 TCL1A TET1 VEGFA
hsa-miR-412	↑ up	n.s.	ACVR1C
hsa-miR-130a-3p	↑ up	n.s.	APP ATG2B ATXN1 CSF1 DICER1 ESR1 HOXA10 HOXA5 IFITM1 KLF4 MAFB MEOX2 PPARG RUNX3 SMAD4 TAC1
hsa-miR-320a	↑ up	n.s.	AQP1 AQP4 HSPB6 MAPK1 MCL1 NPR1 TAC1 TFRC
hsa-miR-484	↑ up	n.s.	FIS1
hsa-miR-29c-3p	↑ up	n.s.	BACE1 BCL2 CDC42 CDK6 COL15A1 COL1A1 COL1A2 COL21A1 COL3A1 COL4A1 COL4A2 COL7A1 DNMT3A DNMT3B FBN1 FGA FGB FGG GAPDH IGFBP1 LAMC1 MCL1 MMP15 MMP24 MYCN PPP1R13B SPARC SRSF10 TDG TFAP2C WNT4
hsa-miR-634	↑ up	n.s.	not available (n.a.)
hsa-miR-26b-5p	↑ up	n.s.	ABCA1 ARL4C CCNE1 CDK6 EPHA2 PTGS2
hsa-miR-34a-5p	↑ up	n.s.	ACSL1 ACSL4 AXIN2 AXL BCL2 BMP7 CCL22 CCND1 CCND3 CCNE2 CD44 CDC25A CDK4 CDK6 CDKN2A CDKN2C CEBPB DLL1 E2F1 E2F3 EPHA5 FOSL1 FOXP1 GRM7 HDAC1 HNF4A IFNB1 IMPA1 IMPDH2 JAG1 KLB LDHA LEF1 MAGEA12 MAGEA2 MAGEA3 MAGEA6 MAP2K1 MAP3K9 MET MTA2 MYB MYC MYCN NANOG NOTCH1 NOTCH2 PDGFRA PEA15 PPP1R10 SIRT1 SOX2 SPI1 STX1A SYT1 TP53 ULBP2 VAMP2 VEGFA WNT1 YY1 ZAP70
hsa-miR-328	↑ up	n.s.	ABCG2 BACE1 CD44 H2AFX PTPRJ
hsa-miR-29a-3p	↑ up	n.s.	ABL1 ADAMTS9 BACE1 BCL2 BCL7A CD276 CDC42 CDK6 COL4A1 COL4A2 CPEB3 CPEB4 DICER1 DKK1 DNMT3A DNMT3B FGA FGB FGG GLUL HBP1 IMPDH1 ITGA11 ITIH5 KREMEN2 LPL MCL1 MYCN NASP NAV3 PIK3R1 PPM1D PPP1R13B PTEN PXDN RAN S100B SFRP2 TNFAIP3

hsa-miR-130b-3p	↑ up	n.s.	CSF1 DICER1 PPARG RUNX3 TP53INP1 UVRAG ZEB1
hsa-miR-103a-3p	↑ up	n.s.	CAV1 CCNE1 CDK2 CREB1 CYP2C8 DAPK1 DICER1 GPD1 ID2 KLF4 PTEN TIMP3
hsa-miR-499a-5p	↓ down	n.s.	FOXO4 PDCD4 SOX6
hsa-miR-92b-3p	↓ down	n.s.	CDKN1C NLK PRMT5 SLC15A1
hsa-let-7c-5p	↓ down	n.s.	BCL2L1 COPS6 COPS8 DICER1 GPS1 HMGA2 MPL MYC NRAS TGFBR1 TRIM71
hsa-let-7b-5p	↓ down	n.s.	ACTG1 CCNA1 CCNA2 CCND1 CCND2 CDC34 CDK6 CYP2J2 DICER1 HMGA2 IFNB1 LIN28A LIN28B MTPN NR2E1 PRDM1 RPIA
hsa-miR-632	↓ down	n.s.	PRDX6
hsa-let-7e-5p	↓ down	n.s.	EIF3J HMGA2 MPL MYCN SMC1A WNT1
hsa-miR-129-5p	↓ down	n.s.	FMR1 NOTCH1 UBE2F
hsa-miR-636	↓ down	n.s.	n.a.
hsa-let-7g-5p	↓ down	n.s.	BCL2L1 BMI1 CDKN2A COL1A2 HMGA2 IGF2BP1 IL13 KRAS MYC
hsa-miR-638	↓ down	n.s.	OSCP1
hsa-miR-365a-3p	↓ down	n.s.	BCL2 CCND1 IL6
hsa-let-7a-5p	↓ down	n.s.	AGO4 APP CASP3 CASP8 CASP9 CCND2 CDKN1A DICER1 E2F1 E2F2 EGFR FOXA1 HAS2 HMGA1 HMGA2 HRAS IGF2 IL6 ITGB3 KRAS LIN28A MPL MYC NF2 NKIRAS2 NR1I2 NRAS PRDM1 RAVER2 TMED7 TRIM71 UHRF2 VDR
hsa-let-7f-5p	↓ down	n.s.	COPS6 COPS8 CYP19A1 GPS1 IL13 KLK6 KLK10 MPL PRDM1 SLC5A5
hsa-miR-193a-5p	↓ down	n.s.	TP73
hsa-miR-152	↓ down	n.s.	DMNT1 HLA-G IGF1R IRS1 TGFA
hsa-miR-221-3p	n.s.	↑ up	ARIH2 BBC3 BMF BNIP3 BNIP3L BRAP CDKN1B CDKN1C CERS2 CORO1A CREBZF DDIT4 DICER1 DKK2 DVL2 ESR1 FMR1 FOS FOXO3 HMGXB4 ICAM1 KIT MEOX2 MYBL1 NAIP PTEN SELE TBK1 TCEAL1 TICAM1 TIMP3 TMED7 TNFSF10 TP53 USP18 ZEB2
hsa-miR-107	n.s.	↑ up	ARNT BACE1 CCNE1 CDCA4 CDK6 CHRM1 CRKL CYP2C8 DAPK1 DICER1 FBXW7 GRN HIF1A KLF4 MYB NFIA NOTCH2 PLAG1 PTEN RAB1B VEGFA
hsa-miR-495	n.s.	↑ up	MEIS1 PBX3
hsa-miR-24-3p	n.s.	↑ up	ACVR1B ARHGAP19 AURKB BCL2L11 BRCA1 CCNA2 CDK1 CDK4 CDKN1B CDKN2A CHEK1 CNDP2 CORO1A DEDD DHFR DHFRP1 DND1 E2F2 FAF1 FEN1 FURIN H2AFX HNF4A MAPK14 MCM10 MCM4 MLEC MYC NOTCH1 PAK4 PCNA POLD1 PTPN9 PTPRF SH3PXD2A ST7L STX16 TGFB1 TMED7 TRIB3 ZNF217
hsa-let-7i-5p	n.s.	↑ up	COPS6 COPS8 GPS1 IL13 SOCS1 TLR4
hsa-miR-409-3p	n.s.	↑ up	ANG FGA FGB FGG IFNG PHF10
hsa-miR-382-5p	n.s.	↑ up	n.a.
hsa-miR-210	n.s.	↓ down	ABCB9 ACVR1B AIFM3 APC ATP11C BDNF CASP8AP2 CBX1 CDK10 CHD9 CLASP2 CPEB2 DDAH1 DENND6A E2F3 EFNA3 ELK3 FGFRL1 GPD1L HECTD1 HOXA1 HOXA3 HOXA9 ISCU KIAA1161 MDGA1 MIB1 MID1IP1 MNT MRE11A NCAM1 NIPBL NPTX1 P4HB PIM1 PTAR1 PTPN1 RAD52 SEH1L SERTAD2 SMCHD1 TNPO1 TP53I11 UBQLN1 VMP1 XIST XPA
hsa-miR-15a-5p	n.s.	↓ down	AKT3 APP BACE1 BCL2 BMI1 BRCA1 CADM1 CCND1 CCND2 CCNE1 CDC25A CHUK DMTF1 IFNG MYB PURA RECK TMEM184B TP53 TSPYL2 UCP2 VEGFA WNT3A
hsa-miR-629-5p	n.s.	↓ down	HNF4A
hsa-miR-15b-5p	n.s.	↓ down	BCL2 CCND1 CCNE1 EIF4A1 IFNG PURA RECK VEGFA
hsa-miR-196a-5p	n.s.	↓ down	ANXA1 BACH1 CDKN1B HMOX1 HOXA5 HOXA7 HOXB7 HOXB8 HOXC8 HOXD8 KRT5 S100A9 SPRR2C
hsa-miR-16-5p	n.s.	↓ down	ACVR2A AKT3 ARL2 BCL2 BMI1 BRCA1 CADM1 CAPRIN1 CCND1 CCND3 CCNE1 CCNT2 CDK6 CHUK HMGA1 IFNG MYB NCOR2 PIM1 PPM1D PTGS2 PURA TP53 TPPP3 UNG VEGFA WNT3A ZYX
hsa-miR-25-3p	n.s.	↓ down	BCL2L11 CCL26 CDH1 CDKN1C EZH2 KAT2B KLF4 MDM2 PRMT5 SMAD7 TP53

Validated miRNA target search was performed on miRNAs significantly changed in BS or BLM-depleted human fibroblasts (Table S5) using miRTarBase (v4.4, http://mirtarbase.mbc.nctu.edu.tw/)(16). Only target genes validated by strong experimental assays such as reporter assay or Western blot were listed.

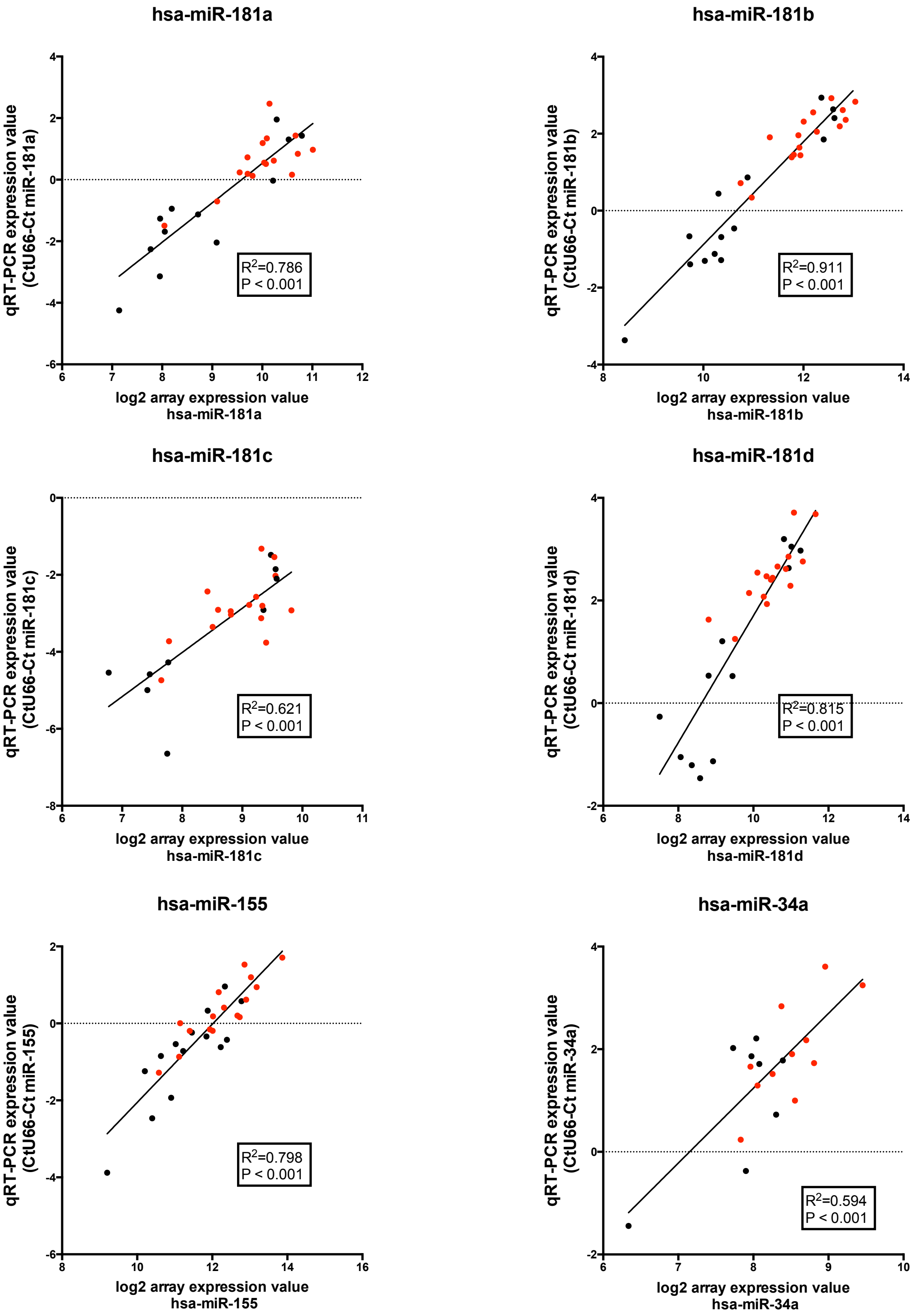
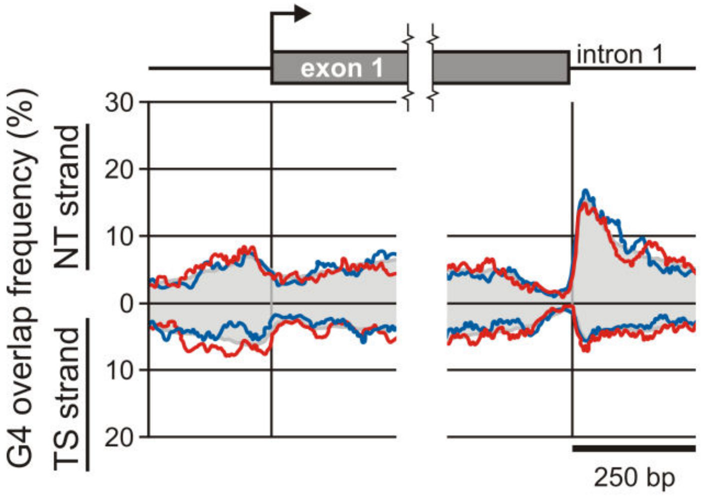


Figure S5: qPCR verification of miRNA expression levels determined by microarray. The log2expression values for indicated microRNAs are plotted against the qRT-PCR -ΔCt values ($\Delta Ct = Ct_{miRNA} - Ct_{RNU66}$). Each dot represents a primary fibroblast cell line (red = BS, black = NM). Shown are the regression line as well as the P- and R^2 values (coefficient of determination) for the correlation. Methodological details are in the Supplementary materials.



up-regulated genes (n = 547)

G4 strand	-250 bp to TSS	TSS to +250 bp	first 250 bp of intron 1
NT	ns	ns	ns
TS	ns	ns	ns

down-regulated genes (n = 520)

G4 strand	-250 bp to TSS	TSS to +250 bp	first 250 bp of intron 1
NT	ns	ns	+(0.017)
TS	ns	ns	ns

Supplementary Figure S6: G4 motif frequencies and enrichment near transcription start sites and intron 1 boundaries of genes with altered expression in BLMdepleted cells. (A) G4 motif frequencies as a function of location in genes up- and down-regulated in BLM-depleted cells. G4 motif counts are shown for non-transcribed strands (NT) and transcribed strands (TS) over the 250 bp ± gene transcription start sites (TSSs) and exon 1/intron 1 5' boundaries for genes whose expression was up- or downregulated (red and blue curves, respectively) versus the comparable distributions for 1,000 randomly-selected gene sets of equal size drawn from the pool of all genes on expression arrays. Gray areas indicate average G4 motif frequencies among all genes surveyed on expression arrays. (B) False Discovery Rates (FDR) of observed G4 motif frequencies compared to 1,000 randomly selected gene sets. ns: non-significant (FDR >0.05)

Table S6. Hypergeometric test of miRNA targeting vs. significantly altered mRNA expression

miRBase ID	BS-NM miR direction	BLM-NS miR direction	num validated targets	DEG targets DOWN in BS-NM	total DEG DOWN in BS-NM	fraction altered as predicted	p-value	intersect genes
hsa-miR-199a-5p	up	down	15	0	141		1	
hsa-miR-181a-5p	up	n.s.	28	0	141		1	
hsa-miR-595	up	n.s.	1	0	141		1	
hsa-miR-30a-5p	up	n.s.	14	0	141		1	
hsa-miR-30d-5p	up	n.s.	7	0	141		1	
hsa-miR-155-5p	up	n.s.	183	0	141		1	
hsa-miR-29b-3p	up	n.s.	44	1	141	0.023	4.985E-02	MMP24
hsa-miR-412	up	n.s.	1	0	141		1	
hsa-miR-130a-3p	up	n.s.	23	0	141		1	
hsa-miR-320a	up	n.s.	8	0	141		1	
hsa-miR-484	up	n.s.	1	1	141	1.000	0	FIS1
hsa-miR-29c-3p	up	n.s.	31	1	141	0.032	2.623E-02	MMP24
hsa-miR-26b-5p	up	n.s.	6	0	141		1	
hsa-miR-34a-5p	up	n.s.	63	0	141		1	
hsa-miR-328	up	n.s.	5	0	141		1	
hsa-miR-29a-3p	up	n.s.	47	1	141	0.021	5.608E-02	ITGA11
hsa-miR-130b-3p	up	n.s.	7	0	141		1	
hsa-miR-103a-3p	up	n.s.	12	0	141		1	
				UP in BS-NM	**UP in BS-NM**			
hsa-miR-143-3p	down	down	15	2	1012	0.133	5.346E-02	FNDC3B, MDM2
hsa-let-7d-5p	down	up	7	0	1012		1	
hsa-miR-99a-5p	down	up	5	0	1012		1	
hsa-miR-499a-5p	down	n.s.	3	0	1012		1	
hsa-miR-92b-3p	down	n.s.	4	0	1012		1	
hsa-let-7c-5p	down	n.s.	11	0	1012		1	
hsa-let-7b-5p	down	n.s.	24	2	1012	0.083	1.625E-01	BIRC6, PDGFRA
hsa-miR-632	down	n.s.	1	0	1012		1	
hsa-let-7e-5p	down	n.s.	6	1	1012	0.167	4.372E-02	EIF3J
hsa-miR-129-5p	down	n.s.	7	1	1012	0.143	5.888E-02	BMPR2
hsa-let-7g-5p	down	n.s.	10	0	1012		1	
hsa-miR-638	down	n.s.	1	0	1012		1	
hsa-miR-365a-3p	down	n.s.	3	0	1012		1	
hsa-let-7a-5p	down	n.s.	44	4	1012	0.091	1.122E-01	EGFR, HAS2, SLC20A1, TMED7
hsa-let-7f-5p	down	n.s.	15	0	1012		1	
hsa-miR-193a-5p	down	n.s.	1	0	1012		1	
hsa-miR-152	down	n.s.	5	1	1012	0.200	3.031E-02	IRS1
hsa-miR-145-5p	down	down	50	10	1012	0.200	1.169E-04	CLINT1, DDX17, FZD7, HDAC2, HOXA9, IRS1, MDM2, MYO5A,
				DOWN in BLM-NS	**DOWN in BLM-NS**			
hsa-let-7d-5p	down	up	7	0	752		1	
hsa-miR-99a-5p	down	up	5	0	752		1	
hsa-miR-221-3p	n.s.	up	38	1	752	0.026	4.959E-01	CDKN1B
hsa-miR-107	n.s.	up	21	0	752		1	
hsa-miR-495	n.s.	up	2	0	752		1	
hsa-let-7i-5p	n.s.	up	6	1	752	0.167	2.514E-02	TLR4
hsa-miR-409-3p	n.s.	up	6	0	752		1	
hsa-miR-24-3p	n.s.	up	54	12	752	0.222	3.747E-07	ARHGAP19, AURKB, BRCA1, CDK1, CDKN1B, E2F1, FEN1, H2AFX, MCM10, MCM4, PCNA, RRM2
				UP in BLM-NS	**UP in BLM-NS**			
hsa-miR-143-3p	down	down	15	2	580	0.133	1.259E-02	FSCN1, MDM2
hsa-miR-145-5p	down	down	50	4	580	0.080	2.542E-02	FLI1, FSCN1, MDM2, MYC
hsa-miR-199a-5p	up	down	15	0	580		1	
hsa-miR-210	n.s.	down	47	2	580	0.043	2.079E-01	BDNF, ISCU
hsa-miR-15a-5p	n.s.	down	29	2	580	0.069	7.176E-02	CADM1, CCND2
hsa-miR-629-5p	n.s.	down	1	0	580		1	
hsa-miR-15b-5p	n.s.	down	8	0	580		1	
hsa-miR-196a-5p	n.s.	down	14	2	580	0.143	1.032E-02	BACH1, HOXA7
hsa-miR-16-5p	n.s.	down	34	2	580	0.059	1.042E-01	CADM1, PTGS2
hsa-miR-25-3p	n.s.	down	11	1	580	0.091	5.041E-02	MDM2

Table S6a: Selected target genes differentially expressed in BS and BLM depleted cells

BS cells

	Gene	Function	mRNA expression
Apoptosis	BIRC6	anti-apoptotic	up
	FIS1	pro-apoptotic	down
p53 pathway	MDM2	negative regulator of p53	up
Growth factor receptor/oncogene	EGFR	EGF receptor	up
	PDGFRA	PDGF receptor	up
	FZD7	Wnt signaling component	up
	MYC	plays an important role in cell cycle progression, apoptosis and cellular transformation.	up
	FLI1	proto-oncogene	up
Insulin signaling	IRS1	insulin receptor signaling	up

BLM depleted cells

	Gene	Function	mRNA expression
p53 pathway	MDM2	negative regulator of p53	up
Oncogene	MYC	plays an important role in cell cycle progression, apoptosis and cellular transformation.	up
	FLI1	proto-oncogene?	up
DNA replication & DNA damage response	BRCA1	DNA damage response and repair	down
	FEN1	DNA replication and repair	down
	H2AFX	DNA damage response and repair	down
	MCM4	DNA replication	down
	MCM10	DNA replication and repair	down
	PCNA	DNA replication	down
	RRM2	DNA replication	down
Cell cycle control	CDK1	Regulation of cell cycle progression.	down
	CDKN1B	Inhibition of cell cycle progression.	down
	E2F1	Involved in cell cycle regulation or in DNA replication.	down

Table 7A: Differentially Expressed Genes in BS patients vs NM that have at least one G4 motif in each region

Region	-250 bp to TSS						TSS to +250 bp						First 250bp of Intron 1					
Regulation	Up			Down			Up			Down			Up			Down		
G4 Strand	Either	NT	T	Either	NT	T	Either	NT	T	Either	NT	T	Either	NT	T	Either	NT	T
Gene Symbols	AAK1	ACBD3	ACSL3	ACAN	ADA	ACAN	AAK1	AAK1	ACTR10	ACAN	ADA	ACAN	AAK1	AAK1	ACBD3	ADA	ADA	ADARB1
	ACBD3	ACTR10	ADAM10	ACTC1	ADARB1	ACTC1	ACTR10	ACTR3	ACVR1	ADA	ADARB1	ADAMTSL1	ACBD3	ACSL3	ACTR10	ADARB1	ADARB1	AKR1B1
	ACSL3	ACTR3	ADAMTS5	ADA	ADD2	ADAMTSL1	ACTR3	ADAM10	ADD3	ADAMTSL1	ALOX12	AKR1B1	ACSL3	ACTR3	ACTR3	ADD2	ADD2	ALOX12
	ACTR10	ADAMTS5	ADNP	ADAMTSL1	ALDH1B1	AIP	ACVR1	ADD3	ADNP	ADARB1	ATP6V0B	BAD	ACTR10	ADD3	ADAM10	AKR1B1	AKR1B1	BAD
	ACTR3	ADD3	AFF4	ADARB1	ALDOC	ALOX12	ADAM10	AGPAT3	AGFG1	AKR1B1	BACE2	C10orf10	ACTR3	AFF4	ADNP	ALOX12	ALOX12	C1QTNF5
	ADAM10	AGPAT3	AGPAT3	ADD2	ALOX12	BAD	ADD3	AHDC1	AGPAT3	ALOX12	BAD	CABLES1	ADAM10	AGFG1	AGPAT3	ATP6V0B	ATP6V0B	CABLES1
	ADD3	AHDC1	ANKRD13A	AIP	BAD	C10orf10	ADNP	AHNAK2	AHNAK2	ATP6V0B	C12orf57	CRLF1	ADD3	AGPAT3	AHNAK2	BACE2	BACE2	CALB2
	ADNP	AHNAK2	ANKRD36B	ALDH1B1	C10orf10	CABLES1	AGFG1	ANKRD13A	ANKRD13A	BACE2	C1QTNF5	CYGB	ADNP	AHDC1	AHR	BAD	C12orf57	CRLF1
	AFF4	AHR	ANXA7	ALDOC	CD24	CALB2	AGPAT3	ANPEP	ANXA7	BAD	CIB1	CYP4A22	AFF4	AHNAK2	ANKRD13A	C12orf57	CABLES1	ENO2
	AGFG1	AK3	AP1G1	ALOX12	COMP	CIB1	AHDC1	ANXA7	APH1B	C10orf10	CRLF1	DMPK	AGFG1	AK3	APH1B	C1QTNF5	CIB1	FDXACB1
	AGPAT3	ANKRD36B	APBB2	BAD	CRLF1	CYGB	AHNAK2	APPBP2	ARCN1	C12orf57	EIF6	ENO2	AGPAT3	ANKRD13A	APPL2	CABLES1	CNN1	FUOM
	AHDC1	ANKRD50	APH1B	C10orf10	DMPK	DMPK	ANKRD13A	ARHGAP21	ARHGEF12	C1QTNF5	FAM101A	FNDC4	AHDC1	ANKRD36B	ARL6IP1	CALB2	CRLF1	GPC4
	AHNAK2	ANLN	API5	CABLES1	FNDC4	ENO2	ANPEP	ARHGAP29	ARL6IP1	CABLES1	FIS1	FUOM	AHNAK2	ANKRD50	ARL6IP6	CIB1	CYGB	KCNK6
	AHR	ANPEP	ARCN1	CALB2	GSTM5	FMOD	ANXA7	ARL5B	ASAP1	CIB1	FSTL3	IDH2	AHR	ANPEP	ASAP2	CNN1	CYP4A22	LRRC3
	AK3	ARL5B	ARHGAP18	CD24	GUK1	FNDC4	APH1B	ARL6IP6	ASAP2	CRLF1	FUOM	LMOD1	AK3	ANXA7	ATMIN	CRLF1	DHRS3	MEI1
	ANKRD13A	ARL6IP6	ARHGAP29	CIB1	IFI30	FSTL3	APPBP2	ARPP19	ATG3	CYGB	FXYD1	LRRC3	ANKRD13A	AP3B1	ATP1B3	CYGB	DMPK	MRPS11
	ANKRD36B	ARPP19	ARHGEF12	COMP	LBH	FUOM	ARCN1	ASAP1	ATP6AP2	CYP4A22	GSTM5	NPAS1	ANKRD36B	APH1B	ATP8B1	CYP4A22	EIF6	MSRB2
	ANKRD50	ARRDC3	ARL6IP6	CRLF1	MANBAL	GADD45B	ARHGAP21	ASAP2	ATP6V1A	DMPK	HAPLN3	RASD2	ANKRD50	APPL2	AZIN1	DHRS3	FAM101A	NPAS1
	ANPEP	ASAP2	ASAP2	CYGB	MCAM	GJD2	ARHGAP29	ASPH	ATP8B1	EIF6	ID3	RHOD	ANPEP	ARHGAP21	BCAP29	DMPK	FIS1	NPR3
	ANXA7	ASH1L	ATF2	DMPK	MMP24	GPC4	ARHGEF12	ATMIN	BAG2	ENO2	IFI30	SCARF2	ANXA7	ARHGAP29	BMPR2	EIF6	FMOD	NTMT1
	AP3B1	ASPH	ATG3	ENO2	MSRB1	IDH2	ARL5B	ATP2C1	BCAP29	FAM101A	IRF6	SDHC	AP3B1	ARL6IP5	BTBD1	ENO2	FNDC4	NXPH3
	APH1B	ATF2	ATP6V1A	FMOD	MSRB2	ITGA11	ARL6IP1	ATP5L	BICC1	FIS1	KCNK6	SELM	APH1B	ASAP1	BTF3L4	FAM101A	FSTL3	PGK1
	APPL2	ATMIN	AZIN1	FNDC4	MYL6	KRT34	ARL6IP6	ATP6AP2	BIRC6	FNDC4	LRRC3	SEPT5	APPL2	ASH1L	C12orf23	FDXACB1	FUOM	RASD2
	ARHGAP21	ATP1B3	BICC1	FSTL3	NDRG2	LIMK2	ARPP19	ATP8B1	BMPR2	FSTL3	MANBAL	SLC38A5	ARHGAP21	ASPH	CAB39	FIS1	FXYD1	SDHC
	ARHGAP29	ATP2A2	BIRC2	FUOM	NOTCH3	LRRC3	ASAP1	BAG2	BZW1	FUOM	MMP24	SNTA1	ARHGAP29	ATMIN	CACHD1	FMOD	GADD45B	SEL1L3
	ARL6IP1	ATP2C1	BIRC6	GADD45B	NPAS1	MCAM	ASAP2	BCAP29	C12orf75	FXYD1	MSRB1	ST3GAL4	ARL6IP1	ATP1B3	CALCOCO2	FNDC4	GSTM5	SELM
	ARL6IP5	ATP8B1	BMP2K	GJD2	NPR3	MMP24	ASPH	BET1	C3orf58	GSTM5	MSRB2	TAGLN	ARL6IP5	ATP2A2	CAMK2D	FSTL3	GUK1	SEPT5
	ARL6IP6	AZIN1	BRCC3	GPC4	NXPH3	MYL6	ATG3	BIRC2	CACHD1	HAPLN3	MYL6	TMEM141	ARL6IP6	ATP5L	CAMSAP2	FUOM	HAPLN3	SLC4A3
	ASAP1	BAG2	BZW1	GSTM5	POLR2G	NDRG2	ATMIN	BMP2K	CACNA2D1	ID3	NDRG2	TMEM9	ASAP1	ATP6AP2	CAPRIN1	FXYD1	HSPB7	TMEM9
	ASAP2	BICC1	C12orf75	GUK1	PTPRN	NPAS1	ATP2C1	BTBD1	CALCOCO2	IDH2	NDUFA13	UXT	ASAP2	AZIN1	CAPZA2	GADD45B	IFI30	YBX1
	ASH1L	BMPR2	C3orf17	IDH2	RPS4X	NPR3	ATP5L	C12orf23	CAMSAP2	IFI30	NOTCH3	YBX1	ASH1L	B2M	CAV2	GPC4	IRF6	
	ASPH	BOD1	C3orf58	IFI30	SCARF2	PODNL1	ATP6AP2	C12orf75	CAST	IRF6	NXPH3		ASPH	BCAP29	CCDC6	GSTM5	ISLR	
	ATMIN	C12orf23	CACHD1	ITGA11	SEL1L3	POLE4	ATP6V1A	C3orf17	CAV1	KCNK6	ORMDL2		ATMIN	BET1	CCT6A	GUK1	LMOD1	
	ATP1B3	C12orf75	CACNA2D1	KRT34	SELM	PTPRN	ATP8B1	C5orf51	CCDC6	LMOD1	PGK1		ATP1B3	BIRC2	CEP170	HAPLN3	LRRC3	
	ATP2A2	C5orf51	CAMSAP2	LBH	SEPT5	RASD2	BAG2	CA5B	CD44	LRRC3	PODNL1		ATP2A2	BIRC6	CHAMP1	HSPB7	MMP24	
	ATP5L	CA5B	CANX	LIMK2	SLC4A3	RHOD	BCAP29	CAB39	CD9	MANBAL	POLR2G		ATP5L	BLOC1S6	CLIC4	IFI30	MSRB1	
	ATP6AP2	CALCOCO2	CCDC25	LRRC3	SPRYD3	SCARF2	BET1	CALCOCO2	CDC42EP3	MMP24	RNASE3		ATP6AP2	BMS1	CLINT1	IRF6	MYL6	
	ATP8B1	CAMSAP2	CCDC6	MANBAL	ST3GAL4	SDF2	BICC1	CAMK2D	CDV3	MSRB1	RPS4X		ATP8B1	BTBD1	CLOCK	ISLR	NDRG2	
	AZIN1	CANX	CCT6A	MCAM		SEPT5	BIRC2	CAMSAP2	CFL2	MSRB2	SCARF2		AZIN1	BZW1	CMTM6	KCNK6	NDUFA13	
	B2M	CAPZA2	CD46	MMP24		SGCA	BIRC6	CANX	CLIC4	MYL6	SGCA		B2M	C12orf23	CNEP1R1	LMOD1	NOTCH3	
	BCAP29	CAST	CDC42EP3	MSRB1		SLC38A5	BMP2K	CAST	CLMP	NDRG2	SLC4A3		BCAP29	C12orf75	CNOT4	LRRC3	NPR3	
	BET1	CAV2	CDK17	MSRB2		SLC4A3	BMPR2	CAV1	CLOCK	NDUFA13	SNTA1		BET1	C3orf17	COPB1	MEI1	NXPH3	
	BIRC2	CD47	CDV3	MYL6		SNTA1	BTBD1	CAV2	CMPK1	NOTCH3	SPRYD3		BIRC2	C3orf58	COPS2	MMP24	ORMDL2	
	BIRC6	CD9	CFL2	NDRG2		ST3GAL4	BZW1	CD44	CNEP1R1	NPAS1	ST3GAL4		BIRC6	C5orf15	COX16	MRPS11	PODNL1	
	BLOC1S6	CDK17	CHAMP1	NOTCH3		TAGLN	C12orf23	CD47	CPEB2	NXPH3	TMEM141		BLOC1S6	C5orf51	CREBBP	MSRB1	POLE4	
	BMPR2	CLMP	CHIC2	NPAS1		TMEM141	C12orf75	CDK12	CPNE3	ORMDL2	TMEM9		BMPR2	C9orf47	CSNK2A1	MSRB2	POLR2G	
	BMS1	CLOCK	CLDN11	NPR3		UXT	C3orf17	CEP170	CREBBP	PGK1	UQCRQ		BMS1	CA5B	CTBP1-AS2	MYL6	PSMB5	
	BTBD1	CNEP1R1	CLIC4	NXPH3		VAMP5	C3orf58	CFL2	CTBP1-AS2	PODNL1	UXT		BTBD1	CACNA2D1	CUL3	NDRG2	PTPRN	
	BTF3L4	COLEC12	CLMP	PODNL1			C5orf51	CHAMP1	CUL4B	POLR2G	VAMP5		BTF3L4	CAMK2D	DCUN1D1	NDUFA13	RGS16	
	BZW1	CORO2B	CLOCK	POLE4			CA5B	CLOCK	CYBRD1	RASD2			BZW1	CAPN2	DCUN1D5	NOTCH3	RHOD	
	C12orf23	COX20	CNOT11	POLR2G			CAB39	CMTM6	DCTN6	RHOD			C12orf23	CAST	DDX1	NPAS1	RNASE3	
	C12orf75	CREBBP	CNOT4	PTPRN			CACHD1	CNEP1R1	DCUN1D1	RNASE3			C12orf75	CAV1	DDX17	NPR3	RPS4X	
	C3orf17	CST4	CNOT7	RASD2			CACNA2D1	CNOT1	DDX3X	RPS4X			C3orf17	CCAR1	DDX3X	NTMT1	SCARF2	
	C3orf58	CTBP1-AS2	CPNE3	RHOD			CALCOCO2	CNOT11	DNAJC10	SCARF2			C3orf58	CCDC6	DHX9	NXPH3	SDF2	
	C5orf15	CTHRC1	CRK	RPS4X			CAMK2D	CNOT4	DNAJC3	SDHC			C5orf15	CCNG1	DNAJC3	ORMDL2	SEL1L3	
	C5orf51	CUL1	CUL3	SCARF2			CAMSAP2	CNOT7	DPP4	SELM			C5orf51	CCNT1	DYNC1H1	PGK1	SGCA	
	C9orf47	DARS	CUL4B	SDF2			CANX	COLEC12	DPYD	SEPT5			C9orf47	CCT6A	DYNLT3	PODNL1	SLC4A3	
	CA5B	DCBLD1	CYP1B1	SEL1L3			CAST	COPB1	DSTNP2	SGCA			CA5B	CD109	EDEM1	POLE4	SNTA1	

CAB39
CACHD1
CACNA2D1
CALCOCO2
CAMK2D
CAMSAP2
CAPN2
CAPRIN1
CAPZA2
CAST
CAV1
CAV2
CCAR1
CCDC6
CCNG1
CCNT1
CCT6A
CD109
CD47
CD9
CDC42EP3
CDK17
CDV3
CEP170
CFL2
CHAMP1
CHIC2
CKAP2
CKAP5
CLIC4
CLINT1
CLOCK
CLTC
CMPK1
CMTM6
CNEP1R1
CNIH1
CNOT1
CNOT4
CNOT7
COLEC12
COPB1
COPB2
COPS2
COX16
COX20
CPEB2
CREBBP
CRK
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CTBP1-AS2
CUL3
CYB5B
CYBRD1
CYP1B1
DARS
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DCBLD1
DCBLD2
DCTN6
DCUN1D1
DCUN1D5

DCTN4
DDX5
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DERL2
DNAJC13
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DPYD
DR1
DTX3L
DYNLL1
EDA2R
EDEM1
EGR1
EHBP1
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EIF3A
EIF5
ELK3
EPB41L2
F2R
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FBXO30
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FGF2
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FOXJ3
GFPT1
GLI3
GMFB
GMPS
GNAQ
GNG12
GPR39
GSK3B
GSPT1
HEATR1
HELZ
HERC4
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IGF2BP2
IL6ST
INPP4B
INSIG1
IQGAP1
ITGA2
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JUN
KCMF1
KCNMA1
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LARP4B
LBR

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DDX3X
DHX9
DIRC2
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GDAP2
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HERC4
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TAGLN
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VAMP5

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COLEC12
COPB1
COX20
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CPNE3
CREBBP
CRK
CSNK2A1
CTBP1-AS2
CTHRC1
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CUL4B
CYBRD1
DARS
DCBLD2
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DCUN1D1
DCUN1D5
DDX3X
DDX6
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DHX9
DIRC2
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EGR1
EHBP1

COX20
CRK
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CTHRC1
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EHBP1
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ERRFI1
ETV1
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FUBP3
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GDAP2
GFPT1
GJC1
GMFB
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GPR39
HDHD1
HELZ
HEXB
HHIPL2
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HPRT1

DTX3L
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LHFPL2
LIPA
LMAN1
LMBRD1
LPIN1
LRPPRC
LY6G5B
MAN1A1
MAP3K7
MAPK1
MAPK1IP1L
MB21D2
ME1
MET
MMD
MRGPRF
MRPL45
MRPS6
MSL2
MTDH
MYO1B

SLC38A5
SLC4A3
SNTA1
SPRYD3
ST3GAL4
TAGLN
TMEM141
TMEM9
UQCRQ
UXT
VAMP5
YBX1

CAB39
CACHD1
CACNA2D1
CALCOCO2
CAMK2D
CAMSAP2
CAPN2
CAPRIN1
CAPZA2
CAST
CAV1
CAV2
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CCT6A
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CDV3
CEP170
CFL2
CHAMP1
CHIC2
CKAP2
CKAP5
CLIC4
CLINT1
CLOCK
CLTC
CMPK1
CMTM6
CNEP1R1
CNIH1
CNOT1
CNOT4
CNOT7
COLEC12
COPB1
COPB2
COPS2
COX16
COX20
CPEB2
CREBBP
CRK
CSNK2A1
CTBP1-AS2
CUL3
CYB5B
CYBRD1
CYP1B1
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CD47
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CEP170
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CHAMP1
CHIC2
CKAP2
CKAP5
CLIC4
CLOCK
CLTC
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COPB2
COX20
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CYBRD1
CYP1B1
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DDX6
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DNAJC3
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DYNC1I2
DYNLT3
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EFNA5
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EHBP1
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EIF2S3
EIF3H

EGFR
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EIF2S1
ENY2
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F3
FERMT2
FGF2
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FNDC3B
G3BP1
GBE1
GJC1
GLT8D1
GLUD1
GMPS
GNAQ
GNPTAB
GNS
GSK3B
GSPT1
HELZ
HERPUD2
HGF
HIBADH
HIF1A
HNRNPA2B1
HNRNPH2
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IDE
IL6ST
ITFG1
JKAMP
KCMF1
KCNMA1
KDELC2
KHDRBS1
KIAA0196
KIAA0430
KPNB1
LARP4B
LBR
LMAN1
LMBRD1
LRPPRC
LRRC8C
LY6G5B
MAN1A1
MAN2A1
MAP3K7
MAP4K4
MAPK1
MATR3
MCFD2
MCM4
MDFIC
ME1
MEIS2
METTL9
MINPP1

POLR2G
PSMB5
PTPRN
RASD2
RGS16
RHOD
RNASE3
RPS4X
SCARF2
SDF2
SDHC
SEL1L3
SELM
SEPT5
SGCA
SLC4A3
SNTA1
SPRYD3
ST3GAL4
TMEM141
TMEM9
TRAPPC4
UQCRQ
VAMP5
WFDC1
YBX1

SPRYD3
ST3GAL4
TMEM141
TMEM9
TRAPPC4
UQCRQ
VAMP5
WFDC1
YBX1

	DDX1	LHFP	KIAA1715				EIF2AK2	HPS3	MYO5A				DDX1	EIF3J	MMADHC			
	DDX17	LHFPL2	KITLG				EIF2S1	HS2ST1	NAMPT				DDX17	EIF5	MMD			
	DDX3X	LINC00152	KPNA4				EIF2S3	HSD17B12	NCKAP1				DDX3X	ELK3	MOB1B			
	DDX47	LOC150381	KPNB1				EIF4G2	HSP90AA1	NCOA4				DDX47	ELOVL5	MYO1B			
	DDX5	LPAR1	LAMB1				EIF5	IDH3A	NF1				DDX5	EPB41L2	NABP1			
	DDX6	LPP	LAPTM4A				EPB41L2	IGF2BP2	NFAT5				DDX6	EPS8	NARS			
	DEGS1	LRRC8C	LHFP				ERLIN1	IKBIP	NNT				DEGS1	ERRFI1	NCOA4			
	DERL2	MAN2A1	LHFPL2				ERP44	IMPAD1	NONO				DERL2	EXOC5	NPTX1			
	DHX15	MAP1LC3B	LIMA1				ERRFI1	INSIG1	NPEPPS				DHX15	F2R	NR1D2			
	DHX9	MDFIC	LMAN1				ETV1	IQGAP1	NPTN				DHX9	F3	NREP			
	DIP2B	MED13	LOC150381				F2R	ITCH	NR1D2				DIP2B	FAM126A	NRP1			
	DNAJC10	MET	LPIN1				F3	ITFG1	NR3C1				DNAJC10	FAM35A	NSF			
	DNAJC13	METTL7A	LYSMD3				FAM122B	ITGB1	NREP				DNAJC13	FAM86C1	NT5C2			
	DNAJC3	MFN1	MALAT1				FAM208A	JUN	NRP1				DNAJC3	FAM91A1	NT5E			
	DNMBP	MFSD1	MAML2				FAM35A	KCMF1	NT5C2				DNMBP	FAM96A	NUCKS1			
	DPYD	MGST1	MAN1A1				FAM86C1	KIAA0430	NUP98				DPYD	FASN	NUP98			
	DYNC1H1	MMD	MAP1B				FAM91A1	KIAA1033	OCIAD1				DYNC1H1	FBXL3	PAPOLA			
	DYNC1I2	MOB1A	MAP1LC3B				FASN	KIAA1430	OSMR				DYNC1I2	FBXO10	PATL1			
	DYNLT3	MOB1B	MAP4K4				FBXL3	KIAA1715	PAK2				DYNLT3	FBXO28	PAXBP1			
	EDEM1	MRGPRF	MAP4K5				FBXO10	KITLG	PANK3				EDEM1	FERMT2	PBX3			
	EFNA5	MRPS6	MARCH7				FBXO28	KPNA4	PANX1				EFNA5	FNDC3A	PCNX			
	EGFR	MYO5A	MCL1				FBXO30	LDHB	PAPOLA				EGFR	FNDC3B	PDCD6IP			
	EGR1	NABP1	MCM4				FERMT2	LHFPL2	PATL1				EGR1	FOXJ3	PITPNB			
	EHBP1	NF1	MDFIC				FGF2	LIMA1	PBX1				EHBP1	FUBP3	PITPNC1			
	EIF2AK2	NMT2	MDM2				FOXJ3	LOC150381	PDGFC				EIF2AK2	FZD6	PKN2			
	EIF2S1	NR1D2	ME1				FUBP3	LPAR1	PITPNB				EIF2S1	G3BP1	PPP3CA			
	EIF2S3	NR3C1	MED13				FZD6	LPIN1	PITPNC1				EIF2S3	GBE1	PPP6C			
	EIF3H	NREP	MED13L				G3BP1	LRPPRC	PLS3				EIF3H	GDAP2	PPP6R3			
	EIF3J	NRP1	MET				GDAP2	LRRC37BP1	PPP1CC				EIF3J	GDI2	PREPL			
	EIF5	NT5C2	METAP2				GDI2	LRRC8C	PPP1R12A				EIF5	GFPT1	PRKAR1A			
	ELK3	NTNG1	METTL9				GFPT1	LY6G5B	PPP2CA				ELK3	GJC1	PRKCA			
	ELOVL5	OCIAD1	MKLN1				GJC1	MAN2A1	PPP2R2A				ELOVL5	GMFB	PRR14L			
	ENY2	OSBPL8	MMADHC				GLUD1	MAP4K4	PPP2R5E				ENY2	GNG12	PSMD1			
	EPB41L2	OSMR	MMD				GMFB	MAPK1IP1L	PPP3CA				EPB41L2	GNPNAT1	PTBP1			
	EPS8	PABPN1	MMGT1				GNAQ	MB21D2	PPP6R3				EPS8	GOLT1B	PXN			
	ERBB2IP	PAK2	MOB1B				GNG11	MCFD2	PREPL				ERBB2IP	GPRC5A	PYGL			
	ERRFI1	PANK3	MRPL45				GNG12	MED1	PRICKLE1				ERRFI1	GSPT1	QKI			
	EXOC5	PAPD4	MRPL50				GNPNAT1	MED13	PRKAR1A				EXOC5	HDAC2	RAB14			
	F2R	PBX1	MSL2				GNS	MED13L	PRKCA				F2R	HDHD1	RAB23			
	F3	PCYOX1	MTDH				GOLT1B	MKLN1	PRR14L				F3	HELZ	RAB3GAP2			
	FAM126A	PDGFC	MYO1B				GPBP1	MMD	PRRC2C				FAM126A	HERC4	RAB7A			
	FAM35A	PERP	NABP1				GPR39	MMP16	PSMA4				FAM35A	HERPUD2	RANBP9			
	FAM86C1	PGRMC1	NAMPT				GSPT1	MOB1A	PTBP1				FAM86C1	HHIPL2	RARS			
	FAM91A1	PHLDA1	NF1				GSR	MRGPRF	PTBP3				FAM91A1	HIATL1	RASSF8			
	FAM96A	PIGX	NFAT5				HDAC2	MSL2	PTP4A1				FAM96A	HMGCR	REV3L			
	FASN	PIK3R1	NNT				HDHD1	MTRR	PTPN14				FASN	HNRNPH2	RNF130			
	FBXL3	PLAG1	NPEPPS				HECTD1	NAE1	PTPRK				FBXL3	HNRNPK	ROBO1			
	FBXO10	PPP1R12A	NUDT21				HELZ	NAMPT	RAB10				FBXO10	HNRNPR	RRAGC			
	FBXO28	PPP3CA	NUP155				HERC4	NCKAP1	RAB3B				FBXO28	HOXA9	RTN4			
	FERMT2	PPP6C	NUP98				HEXB	NFE2L2	RAB7A				FERMT2	HPRT1	RYK			
	FGF2	PPP6R3	ORC3				HHIPL2	NOL9	RAB8B				FGF2	HSP90AA1	S100A10			
	FNDC3A	PRKDC	PAIP2				HIF1A	NR1D2	RAC1				FNDC3A	HSP90B1	SAP30			
	FNDC3B	PRR14L	PAK2				HMGCR	NRD1	RAP2A				FNDC3B	HSPH1	SCAF8			
	FOXJ3	PRRC1	PDGFC				HNRNPH2	NSF	RCN1				FOXJ3	IDE	SCAMP1			
	FUBP3	PSD3	PEG10				HNRNPK	NT5C2	RCN2				FUBP3	IDH3A	SCCPDH			
	FZD6	PSMD1	PERP				HOXA9	NTNG1	REEP3				FZD6	IFI16	SEC63			
	G3BP1	PSME4	PGM3				HPRT1	NUCKS1	REV3L				G3BP1	IFNAR1	SEPT10			
	GBE1	PTBP1	PHTF2				HPS3	NXF1	RGMB				GBE1	INPP4B	SERINC1			
	GDAP2	PTBP3	PIGX				HS2ST1	OSBPL8	RNF11				GDAP2	INSIG1	SERPINE2			
	GDI2	PTP4A2	PKN2				HSD17B12	PABPN1	RNF130				GDI2	IQGAP1	SERTAD2			
	GFPT1	PUM2	PLAG1				HSP90AA1	PAIP2	RPS27L				GFPT1	ITCH	SFT2D1			
	GJC1	PVRL3	PLS3				IARS	PANK3	RTN4				GJC1	ITGA2	SFT2D2			

	GLT8D1	PXN	PPCS				IARS2	PANX1	SCAF8				GLT8D1	ITGB1	SFXN1			
	GLUD1	PYGL	PPP1CC				IDH3A	PAPOLA	SCARB2				GLUD1	ITM2B	SGCE			
	GMFB	QKI	PPP2CA				IGF2BP2	PATL1	SCCPDH				GMFB	KCMF1	SH3BGRL			
	GMPS	RAB10	PPP2R2A				IKBIP	PBX1	SDCCAG3				GMPS	KIAA0196	SKAP2			
	GNAQ	RAB1A	PPP2R5E				IMPAD1	PCNX	SEMA3C				GNAQ	KIAA1033	SLC25A33			
	GNG12	RAB23	PRDM8				INSIG1	PIGX	SEMA5A				GNG12	KIAA1715	SLC30A1			
	GNPNAT1	RAB2A	PRICKLE1				IQGAP1	PITPNB	SEMA6D				GNPNAT1	KIF5B	SLC30A5			
	GNPTAB	RAB5A	PRKAA1				ISCA1	PITPNC1	SEPT10				GNPTAB	KITLG	SLC44A1			
	GNS	RAB8B	PRKCA				ITCH	POLR2B	SERINC1				GNS	KMT2E	SLC9A6			
	GOLT1B	RAC1	PSD3				ITFG1	POMK	SERTAD2				GOLT1B	KPNA3	SLC9A7			
	GPRC5A	RALGPS2	PSMA4				ITGB1	PPP1CB	SETD5				GPRC5A	KPNA4	SLFN5			
	GSK3B	RAP2A	PTPN14				ITM2B	PPP1CC	SFPQ				GSK3B	KPNB1	SMAD3			
	GSPT1	RAP2B	PTX3				JUN	PPP1R12A	SFT2D1				GSPT1	LAMP2	SMAD4			
	HDAC2	RASSF8	PXN				KCMF1	PPP6C	SFT2D2				HDAC2	LAPTM4A	SMAD5			
	HDHD1	RBFOX2	PYGL				KCNMA1	PPP6R3	SKAP2				HDHD1	LARP4B	SNX3			
	HELZ	REEP3	QKI				KIAA0196	PRKDC	SLC20A1				HELZ	LBR	SNX6			
	HERC4	RGL1	RAB1A				KIAA0430	PROS1	SLC35F5				HERC4	LHFPL2	SOCS5			
	HERPUD2	RHOBTB3	RAB21				KIAA1033	PRR14L	SLC5A3				HERPUD2	LIMA1	SPATS2L			
	HGF	ROBO1	RAB23				KIAA1430	PSD3	SLC9A1				HGF	LMBRD1	SPIN1			
	HHIPL2	RRAGC	RAB2A				KIAA1715	PSMD1	SLC9A6				HHIPL2	LOC150381	SPPL2A			
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	HMGCR	SAR1B	RBMS1				KPNA4	PUM2	SMAD3				HMGCR	LRCH3	STK38			
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	HOXA9	SDCBP	RFX7				LHFPL2	RAB21	SPRED1				HOXA9	LUC7L2	SUMO2			
	HPRT1	SEC63	RPS27L				LIMA1	RAB8B	SSFA2				HPRT1	LURAP1L	SUPT16H			
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	HSP90B1	SEMA5A	RYBP				LMAN1	RAP2B	STARD3NL				HSP90B1	LY6G5B	SYPL1			
	HSPH1	SERPINE2	RYK				LMBRD1	RASA1	STK38				HSPH1	MAN2A1	TBL1XR1			
	IDE	SERTAD2	SAMD8				LOC150381	RASSF8	STMN1				IDE	MAP1LC3B	TCEB3			
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	IL6ST	SFT2D2	SEC23A				LRRC37BP1	RNF11	SUPT20H				IL6ST	MAPK1IP1L	TFRC			
	INPP4B	SFXN1	SECTM1				LRRC8C	RNF146	SUZ12				INPP4B	MASP1	TGFBR3			
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	IQGAP1	SGCE	SEMA6D				MAN1A1	RPF2	TAB2				IQGAP1	MCM4	TM9SF3			
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	ITFG1	SLAIN2	SEPT11				MAP3K7	RRM1	TCF12				ITFG1	MDM2	TMEM260			
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	KIAA1033	SOCS6	SLC9A7				MKLN1	SDC4	TMEM19				KIAA1033	MTMR6	UBXN4			
	KIAA1715	SPSB1	SMAD2				MMD	SDCCAG3	TMEM243				KIAA1715	MTRR	UBXN7			
	KIF5B	SQLE	SMAD3				MMP16	SEC23A	TMEM30A				KIF5B	MYO1B	UGDH			
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	KPNA3	STK17A	SNX6				MRPL45	SEPT7	TMEM9B				KPNA3	NAE1	VEZF1			
	KPNA4	STK38	SOCS5				MRPS6	SET	TNFAIP3				KPNA4	NAMPT	VPS35			
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PIGX
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	NR3C1						PTPN14	VPS35					NR3C1	RALGPS2				
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	PATL1						RBMS1						PATL1	RYK				
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	PBX3						RCN2						PBX3	SAMD8				
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	PGRMC1						RNF146						PGRMC1	SDAD1				
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	PIGX						RPS27L						PIGX	SEC23A				
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	PITPNC1						RRM1						PITPNC1	SEC62				
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	POLR2B						RUNX1						POLR2B	SEPT7				
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	PPP2R2A						SBF2						PPP2R2A	SETD5				
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	PUM2						SGCB						PUM2	SMARCA1				
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	RAB23						SLC30A5						RAB23	SPIN1				
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	RAB3B						SLC35F5						RAB3B	SPSB1				
	RAB3GAP2						SLC5A3						RAB3GAP2	SRPK1				
	RAB5A						SLC9A1						RAB5A	SRSF2				
	RAB7A						SLC9A6						RAB7A	SRSF3				
	RAB8B						SLC9A7						RAB8B	SRSF5				
	RAC1						SLFN5						RAC1	SS18				
	RALGPS2						SMAD2						RALGPS2	SSFA2				
	RANBP9						SMAD3						RANBP9	STAT1				
	RAP2A						SMAD4						RAP2A	STEAP1B				
	RARS						SMARCA1						RARS	STK17A				
	RASSF8						SMNDC1						RASSF8	STMN1				
	RB1						SNAPC3						RB1	STX2				
	RBFOX2						SNX6						RBFOX2	SUB1				
	RBMS1						SOCS5						RBMS1	SUZ12P1				
	RCN2						SOCS6						RCN2	SYT11				
	REEP3						SPATS2L						REEP3	TAB2				
	REV3L						SPIN1						REV3L	TAF9				
	RFX7						SPRED1						RFX7	TAOK1				
	RGL1						SPSB1						RGL1	TBL1XR1				
	RNF130						SRPK1						RNF130	TCEB3				
	RNF146						SS18						RNF146	TCF12				
	ROBO1						SSFA2						ROBO1	TCP1				
	RPF2						SSR1						RPF2	TEAD1				
	RPS24						STAM2						RPS24	TERF1				
	RRAGC						STARD3NL						RRAGC	TFDP1				
	RSPRY1						STK17A						RSPRY1	TFG				
	RTN4						STK38						RTN4	TFRC				
	RUNX1						STMN1						RUNX1	TIPARP				
	RYK						STOM						RYK	TM9SF2				
	S100A10						STX2						S100A10	TMED2				
	SAMD8						STYX						SAMD8	TMEM106B				
	SAP30						SUB1						SAP30	TMEM165				
	SAR1A						SUCLG2						SAR1A	TMEM209				
	SBF2						SUPT16H						SBF2	TMEM248				
	SC5D						SUPT20H						SC5D	TMEM33				
	SCAF8						SUZ12						SCAF8	TMPO				
	SCAMP1						SUZ12P1						SCAMP1	TMTC1				
	SCCPDH						SYPL1						SCCPDH	TMX3				
	SDAD1						TAB2						SDAD1	TNFAIP3				
	SDC4						TACC1						SDC4	TNPO1				
	SDCBP						TAF9						SDCBP	TNRC6A				
	SEC23A						TAOK1						SEC23A	TOB1				
	SEC24D						TBL1XR1						SEC24D	TPP2				
	SEC62						TCEB3						SEC62	TPT1				
	SEC63						TCF12						SEC63	TRAK2				

	SECTM1						TCP1						SECTM1	TRAM1				
	SEPT10						TEAD1						SEPT10	TRIP12				
	SEPT11						TFDP1						SEPT11	TRPM7				
	SEPT7						TFRC						SEPT7	TRPS1				
	SERBP1						TGFBR3						SERBP1	TUBB4A				
	SERINC1						TIMP2						SERINC1	TUSC3				
	SERPINE2						TIPARP						SERPINE2	TYMS				
	SERTAD2						TIPRL						SERTAD2	UBE2D1				
	SET						TM9SF2						SET	UBE2R2				
	SETD5						TMED5						SETD5	UBE3C				
	SF3B14						TMED7						SF3B14	UBQLN1				
	SFPQ						TMEM123						SFPQ	UBXN7				
	SFT2D1						TMEM14B						SFT2D1	UCHL3				
	SFT2D2						TMEM165						SFT2D2	UFD1L				
	SFXN1						TMEM19						SFXN1	UGCG				
	SGCB						TMEM243						SGCB	UGDH				
	SGCE						TMEM248						SGCE	USO1				
	SGMS2						TMEM260						SGMS2	USP14				
	SH3BGRL						TMEM30A						SH3BGRL	USP34				
	SHOC2						TMEM55A						SHOC2	USP9X				
	SKA2						TMEM87B						SKA2	VAPA				
	SKAP2						TMEM9B						SKAP2	VEZF1				
	SLAIN2						TMX3						SLAIN2	VPS35				
	SLC17A5						TNFAIP3						SLC17A5	WAC				
	SLC20A1						TNFRSF11B						SLC20A1	WDR26				
	SLC25A33						TNPO1						SLC25A33	WRB				
	SLC25A40						TNRC6A						SLC25A40	WSB1				
	SLC25A46						TOB1						SLC25A46	XPO1				
	SLC30A1						TPBG						SLC30A1	XRCC5				
	SLC30A5						TPP2						SLC30A5	YAP1				
	SLC30A7						TRIP12						SLC30A7	YTHDC1				
	SLC35F5						TRPS1						SLC35F5	YTHDF1				
	SLC38A2						TSPAN5						SLC38A2	ZBTB2				
	SLC39A6						TTPAL						SLC39A6	ZC3H11A				
	SLC44A1						TUBB4A						SLC44A1	ZC3H7A				
	SLC5A3						TUSC3						SLC5A3	ZC3HAV1				
	SLC9A6						TWIST1						SLC9A6	ZC3HAV1L				
	SLC9A7						TXNL1						SLC9A7	ZFAND5				
	SLFN5						UBE2D1						SLFN5	ZFR				
	SLIT2						UBE2R2						SLIT2	ZMIZ1				
	SMAD2						UBE3C						SMAD2	ZMYM4				
	SMAD3						UBXN7						SMAD3	ZNF148				
	SMAD4						UCHL3						SMAD4	ZNF706				
	SMAD5						UFD1L						SMAD5	ZSCAN20				
	SMARCA1						UGCG						SMARCA1					
	SMNDC1						UGDH						SMNDC1					
	SMURF2						UGP2						SMURF2					
	SNX3						USP14						SNX3					
	SNX6						USP34						SNX6					
	SOAT1						USP53						SOAT1					
	SOCS5						VEZF1						SOCS5					
	SOCS6						VHL						SOCS6					
	SPATS2L						VPS35						SPATS2L					
	SPDL1						WBP11						SPDL1					
	SPIN1						WDR82						SPIN1					
	SPPL2A						WLS						SPPL2A					
	SPRED1						WNK1						SPRED1					
	SPRY2						WSB1						SPRY2					
	SPSB1						YAP1						SPSB1					
	SRGAP1						YTHDC1						SRGAP1					
	SRPK1						YTHDF1						SRPK1					
	SRSF2						ZBED5						SRSF2					

	SRSF3						ZBTB2						SRSF3					
	SRSF5						ZC3H11A						SRSF5					
	SS18						ZC3H7A						SS18					
	SSFA2						ZDHHC2						SSFA2					
	STAT1						ZFAND5						STAT1					
	STEAP1B						ZFP36L2						STEAP1B					
	STK17A						ZFR						STK17A					
	STK38						ZMIZ1						STK38					
	STMN1						ZMPSTE24						STMN1					
	STOM						ZMYM4						STOM					
	STT3B						ZNF148						STT3B					
	STX2						ZNF521						STX2					
	SUB1						ZNF655						SUB1					
	SUMO2						ZSCAN20						SUMO2					
	SUPT16H						ZYG11B						SUPT16H					
	SUZ12P1												SUZ12P1					
	SYPL1												SYPL1					
	SYT11												SYT11					
	TAB2												TAB2					
	TAF9												TAF9					
	TAOK1												TAOK1					
	TBL1XR1												TBL1XR1					
	TCEB3												TCEB3					
	TCF12												TCF12					
	TCP1												TCP1					
	TEAD1												TEAD1					
	TERF1												TERF1					
	TFDP1												TFDP1					
	TFG												TFG					
	TFRC												TFRC					
	TGFBR3												TGFBR3					
	TIMP2												TIMP2					
	TIPARP												TIPARP					
	TM9SF2												TM9SF2					
	TM9SF3												TM9SF3					
	TMED2												TMED2					
	TMEM106B												TMEM106B					
	TMEM165												TMEM165					
	TMEM209												TMEM209					
	TMEM248												TMEM248					
	TMEM260												TMEM260					
	TMEM33												TMEM33					
	TMEM50B												TMEM50B					
	TMEM9B												TMEM9B					
	TMPO												TMPO					
	TMTC1												TMTC1					
	TMX3												TMX3					
	TNFAIP3												TNFAIP3					
	TNPO1												TNPO1					
	TNRC6A												TNRC6A					
	TOB1												TOB1					
	TOP1												TOP1					
	TPBG												TPBG					
	TPP2												TPP2					
	TPT1												TPT1					
	TRA2A												TRA2A					
	TRAK2												TRAK2					
	TRAM1												TRAM1					
	TRIP12												TRIP12					
	TRPM7												TRPM7					
	TRPS1												TRPS1					
	TUBB4A												TUBB4A					

	TUSC3												TUSC3					
	TYMS												TYMS					
	UACA												UACA					
	UBE2D1												UBE2D1					
	UBE2R2												UBE2R2					
	UBE3C												UBE3C					
	UBQLN1												UBQLN1					
	UBXN4												UBXN4					
	UBXN7												UBXN7					
	UCHL3												UCHL3					
	UFD1L												UFD1L					
	UGCG												UGCG					
	UGDH												UGDH					
	UHMK1												UHMK1					
	USO1												USO1					
	USP14												USP14					
	USP34												USP34					
	USP9X												USP9X					
	VAPA												VAPA					
	VEZF1												VEZF1					
	VPS35												VPS35					
	VTA1												VTA1					
	WAC												WAC					
	WBP11												WBP11					
	WDR26												WDR26					
	WDR82												WDR82					
	WEE1												WEE1					
	WRB												WRB					
	WSB1												WSB1					
	XPO1												XPO1					
	XRCC5												XRCC5					
	YAP1												YAP1					
	YME1L1												YME1L1					
	YTHDC1												YTHDC1					
	YTHDF1												YTHDF1					
	ZBTB2												ZBTB2					
	ZC3H11A												ZC3H11A					
	ZC3H7A												ZC3H7A					
	ZC3HAV1												ZC3HAV1					
	ZC3HAV1L												ZC3HAV1L					
	ZDHHC2												ZDHHC2					
	ZFAND5												ZFAND5					
	ZFR												ZFR					
	ZMIZ1												ZMIZ1					
	ZMYM4												ZMYM4					
	ZNF148												ZNF148					
	ZNF521												ZNF521					
	ZNF655												ZNF655					
	ZNF706												ZNF706					
	ZSCAN20												ZSCAN20					
	ZYG11B												ZYG11B					

Table S7B: Differentially Expressed Genes in response to shBLM compared to shNS filtered against NS-Control that have at least one G4 motif in each region

Region	-250 bp to TSS						TSS to +250 bp						First 250bp of Intron 1					
Regulation	**Up**			**Down**			**Up**			**Down**			**Up**			**Down**		
G4 Strand	**Either**	**NT**	**T**	**Either**	**NT**	**T**	**Either**	**NT**	**T**	**Either**	**NT**	**T**	**Either**	**NT**	**T**	**Either**	**NT**	**T**
Gene Symbols	ABCA2	ABCA2	ABLIM3	AAGAB	AAGAB	ABCC3	ABCA2	ACP5	ABCA2	ABCC3	ABCC3	ABI2	ABCA2	ACP5	ABCA2	ABCC3	ABCC3	ABHD12
	ABLIM3	ACP5	ADAMTS5	ABCC3	ABCC3	ABI2	ABLIM3	ACPL2	ABLIM3	ABHD12	ABHD12	ACBD7	ABLIM3	ACPL2	ABLIM3	ABHD12	ABHD12	ACBD7
	ACP5	ACPL2	ADRA1D	ABHD12	ABHD12	AEBP1	ACP5	ADRA1D	ADRA1D	ABI2	ABI2	AEBP1	ACP5	AKIRIN1	ADRA1D	ABI2	ABI2	ANAPC15
	ACPL2	ADAMTS5	ALPP	ABI2	ABI2	ANKFY1	ACPL2	AHCYL2	AHCYL2	ACBD7	ACBD7	AJUBA	ACPL2	ANKRD29	AFF3	ACBD7	ACBD7	ANXA3
	ADRA1D	AHCYL2	ANGPTL4	AEBP1	AGO1	ANKRD36B	ADRA1D	ANKRD29	ANGPTL2	AEBP1	AGO1	ANAPC15	ADRA1D	ANPEP	ALPP	AEBP1	AEBP1	APOBEC3B
	AFF3	AKIRIN1	ANK2	AGO1	ALKBH6	API5	AHCYL2	ANPEP	ANGPTL4	AGO1	AJUBA	APOBEC3B	AFF3	ANTXR1	ANKH	AGO1	AGO1	APPL2
	AKIRIN1	ALPP	ANKH	ALKBH6	AMOTL2	ARHGEF39	ANGPTL2	AP1AR	ANKH	AJUBA	ALKBH6	ARHGEF39	AKIRIN1	ARHGAP12	ANKRD52	ALKBH6	ALKBH6	ARL6IP1
	ALPP	ANGPTL2	ANKRD29	AMOTL2	ANKRD36B	ARNT2	ANGPTL4	ARHGAP24	ANKRD52	ALKBH6	AMOTL2	ARL6IP1	ALPP	ARHGAP24	ARNTL	ALPK1	ALPK1	ARMC8
	ANKH	ANKRD52	ANTXR1	ANKFY1	ANLN	BGN	ANKH	ARL5B	ANTXR1	AMOTL2	ANKFY1	ARNT2	ANKH	ARL2BP	ATG4D	AMOTL2	AMOTL2	ARNT2
	ANKRD29	ANPEP	ARHGAP12	ANKRD36B	ANXA3	BIRC5	ANKRD29	ARNTL	AREG	ANAPC15	ANXA3	AS3MT	ANKRD29	ASB13	BDNF	ANAPC15	ANKFY1	ARSB
	ANKRD52	AP1AR	ASB13	ANLN	ARRB2	C1orf21	ANKRD52	ASB13	ASB13	ANKFY1	AP2M1	ASF1B	ANKRD52	B2M	BMP2	ANKFY1	ANKRD36B	AS3MT
	ANPEP	ARL5B	ATG14	ANXA3	AS3MT	C9orf96	ANPEP	ATP6V1D	ATG4D	ANXA3	ARHGAP19	ATP8B1	ANPEP	B3GALNT2	CABLES1	ANKRD36B	AP2M1	ASF1B
	ANTXR1	ARNTL	BACH1	API5	ATP8B1	CDA	ANTXR1	BACE2	BDNF	AP2M1	ARNT2	BGN	ANTXR1	BACE2	CBX6	ANXA3	APPL2	ATP8B1
	ARHGAP12	ATG4D	CABLES1	ARHGEF39	AUNIP	CDC20	AP1AR	BAMBI	BMP2	APOBEC3B	ARRB2	BIRC5	ARHGAP12	BAMBI	CCDC126	AP2M1	ARHGAP19	BGN
	ARHGAP24	B3GALNT2	CADM1	ARNT2	BGN	CDC23	AREG	BDNF	CABLES1	ARHGAP19	ATP8B1	BRI3BP	ARHGAP24	BDNF	CCDC68	APOBEC3B	ARHGEF2	BIRC5
	ARL2BP	BACH1	CCDC68	ARRB2	BMP4	CDC42EP3	ARHGAP24	BET1	CAMK1D	ARHGEF39	ATP8B2	C17orf53	ARL2BP	BET1	CDYL2	APPL2	ARHGEF39	C1orf21
	ARNTL	BSDC1	CDK17	AS3MT	BRI3BP	CDCA5	ARL5B	C16orf52	CBX6	ARL6IP1	AUNIP	C1orf21	ARNTL	BMP2	CHORDC1	ARHGAP19	ARL15	CASP3
	ASB13	C16orf52	CERK	ATP8B1	C1orf21	CDH11	ARNTL	CBX6	CCDC68	ARNT2	AURKA	CA12	ASB13	BTRC	CHRM2	ARHGEF2	ARMC8	CCNB2
	ATG4D	CADM1	CLMP	AUNIP	C9orf96	CDH2	ASB13	CCNG2	CERK	ARRB2	BRI3BP	CASP3	ATG4D	C16orf52	CLCN5	ARHGEF39	ARRB2	CCNF
	B2M	CAMK1D	COL6A1	BGN	CASP3	CDK5RAP2	ATG4D	CDYL2	CHRM2	AS3MT	BUB1	CDC42EP3	B2M	CABLES1	CREBRF	ARL15	ATP8B2	CDCA3
	B3GALNT2	CAT	CPNE7	BIRC5	CCNF	CENPM	ATP6V1D	CHORDC1	CLCN5	ASF1B	C10orf54	CDCA8	B3GALNT2	CADM1	CTBP1-AS2	ARL6IP1	AUNIP	CDCA8
	BACE2	CCND2	CRYL1	BMP4	CDCA3	CHST3	BACE2	CPNE7	CLDN1	ATP8B1	C1QTNF2	CDH2	BACE2	CAMK1D	CTSO	ARMC8	AURKA	CENPA
	BAMBI	CDK17	CYGB	BRI3BP	CDCA8	CIT	BAMBI	CREBRF	CLMP	ATP8B2	CCBE1	CENPA	BAMBI	CAT	CYLD	ARNT2	BRI3BP	CEP85
	BDNF	CDYL2	CYLD	C1orf21	CDH11	CKS2	BDNF	CRYL1	CPNE7	AUNIP	CCNF	CHN1	BDNF	CBX6	CYP2R1	ARRB2	BST1	CERS6
	BET1	CHORDC1	DPP7	C9orf96	CDK2	CLDN11	BET1	CYLD	CREBRF	AURKA	CDC20	CIT	BET1	CD109	DPP7	ARSB	BUB1	CHST3
	BMP2	CLCN4	DPY19L3	CASP3	CHST3	CRISPLD2	BMP2	CYP2A6	CRYL1	BGN	CDC45	COL12A1	BMP2	CDH13	DYNLT3	AS3MT	BUB3	CIT
	BTRC	CLMP	DSEL	CCNF	CNOT6	CSPG4	C16orf52	CYP2R1	CTBP1-AS2	BIRC5	CDH11	CREB3L1	BTRC	CDK17	EIF1AX	ASF1B	C10orf54	CNOT6
	C16orf52	CORO2B	EIF3J	CDA	COL5A2	CTSH	CABLES1	DCBLD2	CTSO	BRI3BP	CDK2	CUL4B	C16orf52	CDYL2	EIF4EBP2	ATP8B1	C17orf53	COL12A1
	CABLES1	CPNE7	EIF4EBP2	CDC20	CRISPLD2	CUL4B	CAMK1D	DHDDS	CYGB	BUB1	CDK5RAP2	CXCL12	CABLES1	CERK	EML1	ATP8B2	C1orf198	CYR61
	CADM1	CTBP1-AS2	ELMOD1	CDC23	CSPG4	CXCL12	CBX6	DHRS7	DPP7	C10orf54	CENPO	CYR61	CADM1	COL6A1	EPT1	AUNIP	C1orf21	DHRS11
	CAMK1D	CYP2R1	EML1	CDC42EP3	CXCL12	DAPK2	CCDC68	DSEL	EIF4EBP2	C17orf53	CFB	DMPK	CAMK1D	CPNE7	ETFB	AURKA	C1QTNF2	E2F1
	CAT	DHDDS	ENDOD1	CDCA3	DAPK2	DCLK2	CCNG2	EIF4EBP2	ELMOD1	C1orf21	CHAF1A	DNMT1	CAT	CREBRF	ETV4	BGN	CASP3	ELN
	CBX6	DOCK4	ERN1	CDCA5	DAZAP2	DHRS1	CDYL2	ERO1L	EPHB1	C1QTNF2	CIT	DOCK2	CBX6	CRYL1	FAM150B	BIRC5	CCNA2	ENAH
	CCDC126	DPP7	FAM105A	CDCA8	DHRS11	DMPK	CERK	ETFB	EPT1	CA12	CKS2	DRAM1	CCDC126	CYGB	FAM171A2	BRI3BP	CCNF	ENO2
	CCDC68	DPY19L3	FAM127A	CDH11	DMPK	E2F1	CHORDC1	ETV1	EREG	CASP3	CNOT6	ELN	CCDC68	CYLD	FAM171B	BST1	CDC20	FANCA
	CD109	DUSP4	FAM171A2	CDH2	DOCK2	ELN	CHRM2	EVI5L	ETFB	CCBE1	CSPG4	ENO2	CD109	CYP2A6	FAM210B	BUB1	CDC42EP3	FBN2
	CDH13	ELMOD1	FAM171B	CDK2	DONSON	ENAH	CLCN5	FAM105A	ETV4	CCNF	CTSH	FAM65B	CDH13	CYP2R1	FIBCD1	BUB3	CDC45	FHL3
	CDK17	EPHA5	FAM19A3	CDK5RAP2	DRAM1	ENO2	CLDN1	FAM150B	EVI5L	CDC20	DAPK2	FHL3	CDK17	DCBLD2	FLI1	C10orf54	CDCA8	FLNC
	CDYL2	EPHB1	FAM210B	CENPM	E2F1	EPS8	CLMP	FAM171A2	F2R	CDC42EP3	DBF4B	FLNC	CDYL2	DHDDS	FSCN1	C17orf53	CDH11	FOSL2
	CERK	ERAP2	FAM89B	CHST3	ELN	EZR	CPNE7	FAM210B	FAM105A	CDC45	DDX21	FOXM1	CERK	DHRS7	FYN	C1orf198	CDH2	GPR126
	CHORDC1	ERO1L	FBXL19-AS1	CIT	ENAH	FAM27L	CREBRF	FAM89B	FAM171B	CDCA8	DDX39A	FRY	CHORDC1	DNAJB9	GCOM1	C1orf21	CDK5RAP2	HADH
	CHRM2	ETV4	FNDC4	CKS2	FADS2	FAM65B	CRYL1	FBXO3	FAM210B	CDH11	DHRS11	FSTL5	CHRM2	DTNA	HCN2	C1QTNF2	CENPO	HIAT1
	CLCN5	EVI5L	FSCN1	CLDN11	FANCA	FAM83D	CTBP1-AS2	FEZ1	FIBCD1	CDH2	DOCK2	FZD2	CLCN5	DUSP6	HGF	CASP3	CHAF1A	HOXA11
	COL6A1	F2R	FTO	CNOT6	FBN1	FANCC	CTSO	FKBP1A	FNDC4	CDK2	DONSON	GAB2	COL6A1	DYNC1I2	HIPK2	CCNA2	CHN1	IER3
	CPNE7	F2RL1	FYN	COL5A2	FHL3	FANCE	CYGB	FLI1	FOXP2	CDK5RAP2	ERI2	GINS4	CPNE7	DYNLT3	HMGA2	CCNB2	CIT	IGFBP6
	CREBRF	FAM150B	G0S2	CRISPLD2	FLNB	FBN2	CYLD	GAP43	GCOM1	CENPA	ESPL1	GSG2	CREBRF	E2F7	HNRNPH2	CCNF	CKS2	INCENP
	CRYL1	FAM171A2	GCOM1	CSPG4	FLNC	FEN1	CYP2A6	GCOM1	GFPT2	CENPO	EZR	HAUS4	CRYL1	EIF2AK3	IGF2	CDC20	CNN1	INTS9
	CTBP1-AS2	FAM210B	GFPT2	CTSH	FOSL2	FLNB	CYP2R1	GM2A	GM2A	CFB	F11R	HIAT1	CTBP1-AS2	EIF3J	INA	CDC42EP3	CNOT6	KANK2
	CTSO	FAM89B	GLI3	CUL4B	FOXRED1	FLNC	DCBLD2	GRB10	GPR137B	CHAF1A	FADS2	HOXA11	CTSO	EPHA5	ISCU	CDC45	CREB3L1	KRT7
	CYGB	FBXO3	GM2A	CXCL12	FZD2	FMOD	DHDDS	GSTO1	HCN2	CHN1	FANCA	ICAM2	CYGB	EPT1	ITFG1	CDCA3	CSPG4	LBR
	CYLD	FEZ1	GRB10	DAPK2	GINS2	FN3KRP	DHRS7	GTF2B	HEY1	CIT	FBN1	IER3	CYLD	EREG	ITGA6	CDCA8	CTSH	LOXL1
	CYP2A6	FLI1	GTF2B	DAZAP2	GLIPR2	FOXM1	DPP7	HCN2	HIPK2	CKS2	FEN1	JADE1	CYP2A6	EVI5L	ITGA8	CDH11	DAPK2	LY6G5B
	CYP2R1	FNDC4	HAS2	DCLK2	GPR124	GAB2	DSEL	HEY1	HMGA2	CNOT6	FGD4	JUP	CYP2R1	F2R	ITPR2	CDH2	DAZAP2	LY6K
	DCBLD2	FOXN3	HCN2	DHRS1	GPRC5B	GALNT4	EIF4EBP2	HNRNPH2	HSD17B10	COL12A1	FN3KRP	KCND1	DCBLD2	F2RL1	KCNJ15	CDK5RAP2	DBF4B	MCM4
	DHDDS	FSCN1	HEY1	DHRS11	GSTM5	GLIPR2	ELMOD1	IMPACT	IARS	CREB3L1	FOSL2	KIAA0226	DHDDS	FAM105A	KCNMA1	CENPA	DDX21	MIF4GD
	DHRS7	GATSL3	HIPK2	DMPK	HDAC1	GPR126	EPHB1	ITFG1	IGF2	CSPG4	FOXRED1	KIAA1598	DHRS7	FAM150B	KDM3A	CENPO	DDX39A	MSH5
	DNAJB9	GCOM1	HIVEP2	DOCK2	HIAT1	GSG2	EPT1	IVL	IGF2R	CTSH	FZD2	KPNA2	DNAJB9	FAM171A2	KDSR	CEP85	DHRS11	MYBL2
	DPP7	GFPT2	HSD17B10	DONSON	HPRT1	H2AFZ	EREG	JAM2	ISCU	CUL4B	GAB2	KRT7	DPP7	FAM171B	LAMA1	CERS6	DHRS3	NEU1

DTNA	GLI3	IGF2	DRAM1	HSPB11	HAUS8	ERO1L	KCNIP3	ITGA6	CXCL12	GINS2	LBR	DTNA	FAM89B	LMBRD1	CHAF1A	DMPK	NID1
DUSP6	GPR137B	IGF2R	E2F1	IGFBP6	HOMER3	ETFB	KCNQ5	ITGA8	CYR61	GINS4	LCLAT1	DUSP6	FBXO3	LPPR2	CHN1	DNMT1	NREP
DYNC1I2	GRB10	IGFBP3	ELN	ITGA4	HOXC11	ETV1	KCTD21	JAM2	DAPK2	GLIPR2	LMNB1	DYNC1I2	FIBCD1	LTBP1	CHST3	DOCK2	NSF
DYNLT3	GSTO1	IMPACT	ENAH	KANK2	HRH1	ETV4	KDM3A	KCNC4	DBF4B	GSTM4	LMOD1	DYNLT3	FKBP1A	MAN2A1	CIT	DRAM1	NUDCD2
E2F7	HCN2	INA	ENO2	KCND1	IGFBP6	EVI5L	KIAA1217	KCNJ15	DDX21	GSTM5	LOXL1	E2F7	FLI1	MAPRE3	CKS2	DUT	NXNL2
EIF1AX	HEY1	ISCU	EPS8	KHK	JADE1	F2R	KIAA1551	KCNMA1	DDX39A	GTF2H1	LY6G5B	EIF1AX	FNDC4	METTL9	CNN1	E2F1	ORC6
EIF2AK3	HGF	ITGA11	EZR	KIAA0226	KIAA1199	FAM105A	LCE2A	KCNQ5	DHRS11	GTSE1	MB21D2	EIF2AK3	FRMD3	MICB	CNOT6	ENAH	PACSIN2
EIF3J	HIST1H4H	ITGA2	FADS2	KIAA1199	KIF13A	FAM150B	LGALS3	KDSR	DMPK	HADH	MCM7	EIF3J	FYN	MTSS1	COL12A1	EPS8	PAQR4
EIF4EBP2	HIVEP2	ITPR2	FAM27L	KIF22	KPNA2	FAM171A2	LMLN	KIAA1217	DNMT1	HAUS4	MIF4GD	EIF4EBP2	GATSL3	NEK9	CREB3L1	ERI2	PGM2
EML1	HMGA2	KCNC4	FAM65B	KRT19	KRT34	FAM171B	LPAR3	KLHDC3	DOCK2	HDAC1	MRVI1	EML1	GCOM1	NETO2	CSPG4	ESPL1	PHF19
EPHA5	HOXA7	KCNMA1	FAM83D	KRT7	KRT7	FAM210B	LPHN2	KLHL21	DONSON	HIST1H4L	MYBL2	EPHA5	GDPD1	NOX4	CTSH	EXT2	PKMYT1
EPT1	IGF2R	KCNN2	FANCA	LBR	LIG1	FAM89B	LTBP1	LAMA1	DRAM1	HJURP	NACC1	EPT1	GLRX	NT5E	CYR61	FAM64A	PLK2
EREG	IL1RN	KIAA0319L	FANCC	LMCD1	LMCD1	FBXO3	LYPLA1	LMBRD1	ELN	HLA-DMA	NAT14	EREG	GPR137B	PARD6G	DAPK2	FANCA	PLTP
ETFB	ITGA2	KLHDC3	FANCE	LOXL3	LOXL1	FEZ1	M6PR	LPAR3	ENO2	HMGB2	NAV2	ETFB	GRB10	PBX2	DAZAP2	FANCC	PODN
ETV4	ITGA6	KLHL21	FBN1	MCM2	MCM2	FIBCD1	MAN2A1	LPPR2	ERI2	HOMER3	NREP	ETV4	GSTO1	PITPNC1	DBF4B	FBN1	POLA2
EVI5L	ITGA8	KLHL24	FBN2	METTL7A	MCM4	FKBP1A	MAPRE3	LTBP1	ESPL1	HPRT1	NT5DC3	EVI5L	GTF2B	PLEKHM1	DDX21	FBN2	PPME1
F2R	JARID2	LAMA1	FEN1	MIF4GD	MCM7	FLI1	MCTP1	LYPLA1	EZR	HSPA2	NTN4	F2R	HCN2	PNPLA4	DDX39A	FEN1	PTRF
F2RL1	KCNIP3	LGALS3	FHL3	MTHFS	MCMBP	FNDC4	MICB	M6PR	F11R	HSPB11	NYNRIN	F2RL1	HIPK2	PODXL	DHRS11	FHL3	PXMP2
FAM105A	KCNMA1	LONRF1	FLNB	MTMR12	MTHFS	FOXP2	MME	MAP3K7CL	FADS2	IGFBP6	OLFML2B	FAM105A	HMGA2	POPDC3	DHRS3	FLNB	RDH10
FAM150B	KCNQ5	LPPR2	FLNC	MYH10	MTRF1L	GAP43	MMP16	MAPRE3	FAM65B	INCENP	ORC6	FAM150B	HNRNPH2	PPAP2B	DMPK	FLNC	SAMD12
FAM171A2	KIAA0319L	LTBP1	FMOD	NACC1	MXD3	GCOM1	MTURN	MCTP1	FANCA	IQGAP3	PACSIN2	FAM171A2	HOXA7	PPAP2C	DNMT1	FMOD	SAP30
FAM171B	KIT	M6PR	FN3KRP	NCAPD3	MYBL2	GFPT2	MYC	MSC	FBN1	ITGA4	PHF19	FAM171B	HSPB6	PSTPIP2	DOCK2	FN3KRP	SCCPDH
FAM210B	KLHL21	MAGEH1	FOSL2	NDE1	MYOCD	GM2A	NCALD	MTURN	FEN1	KANK2	PIM1	FAM210B	IFI16	PTGS1	DRAM1	FOXM1	SELENBP1
FAM89B	LAMA1	MAGI2	FOXM1	NEU1	NAT14	GPR137B	NEDD4	NF2	FGD4	KHK	PKMYT1	FAM89B	IGF2	QKI	DUT	GAB2	SHCBP1
FBXO3	LONRF1	MDM2	FOXRED1	NGF	NDE1	GRB10	NEK9	NFIL3	FHL3	KIAA0226	PLTP	FBXO3	IGFBP3	QPCT	E2F1	GINS2	SLBP
FIBCD1	LPAR3	METTL9	FZD2	NID1	NID1	GSTO1	NEO1	NUDT11	FLNC	KIF22	PRC1	FIBCD1	INA	RAB31	ELN	GINS4	SLC4A8
FKBP1A	LYPLA1	MRPL50	GAB2	NPM3	NT5DC3	GTF2B	NETO2	OGFRL1	FN3KRP	KIF4A	PRR23C	FKBP1A	ITGA2	REXO1	ENAH	GLCE	SMAD3
FLI1	MAN2A1	MSC	GALNT4	NRAS	NYNRIN	HCN2	NF2	P2RX5	FOSL2	KPNA2	PRSS12	FLI1	ITPR2	RGS2	ENO2	GLIPR2	SNRPA
FNDC4	MARVELD1	MTURN	GINS2	NREP	OLFML2B	HEY1	NKIRAS2	PARD6G	FOXM1	KRT18	RARG	FNDC4	IVL	RIN3	EPS8	GPR124	SORT1
FRMD3	MFSD1	MX1	GLIPR2	NSUN2	PCNA	HIPK2	NPC1	PARM1	FOXRED1	LMNB1	RDH10	FRMD3	KCNC4	RORA	ERI2	GPRC5A	SPA17
FSCN1	MICB	MYC	GPR124	NT5DC3	PEG10	HMGA2	NTSR1	PIP5K1C	FRY	LOXL3	RPL39L	FSCN1	KCNIP3	RRAGD	ESPL1	GPRC5B	SRRM2
FYN	MME	MYO1D	GPR126	NTN4	PIM1	HNRNPH2	NUPR1	PITPNC1	FSTL5	LY6G5B	RRM2	FYN	KCNN2	SCN1B	EXT2	GSTM4	STMN1
GATSL3	MX1	NDN	GPRC5B	NUAK2	POC1A	HSD17B10	OCM2	PLEKHM1	FZD2	MB21D2	SAMD12	GATSL3	KCTD21	SEMA6A	FAM64A	GSTM5	SUMO2
GCOM1	NAP1L5	NEDD4	GSG2	NUMA1	POLE	IARS	OSBPL1A	PODXL	GAB2	MCM2	SCCPDH	GCOM1	KDM3A	SEPT5	FANCA	GTF2H1	SUZ12P1
GDPD1	NCALD	NEK9	GSTM5	NXNL2	PRC1	IGF2	PARD6G	PPARG	GINS2	MCM5	SCML1	GDPD1	KIAA0319L	SEPW1	FANCC	GTSE1	SYPL2
GLRX	NETO2	NEO1	H2AFZ	NYNRIN	PTK7	IGF2R	PBX2	PPM1L	GINS4	MDC1	SDC1	GLRX	KIAA1551	SERINC1	FBN1	HAUS4	TACC3
GPR137B	NF2	NETO2	HAUS8	PCNA	PTRF	IMPACT	PDIA5	PRSS35	GLIPR2	MIF4GD	SELENBP1	GPR137B	KIT	SESN2	FBN2	HDAC1	TGOLN2
GRB10	NFIL3	NFIL3	HDAC1	PDE1C	RAD54L	ISCU	PDP2	PTPRG	GSG2	MTFR2	SFPQ	GRB10	KLHDC3	SFRP1	FEN1	HIPK1	TK1
GSTO1	NINJ1	NUDT11	HIAT1	PHF19	RARG	ITFG1	PIP5K1C	RAB31	GSTM4	MTHFS	SH2D4A	GSTO1	KLHL21	SH3PXD2B	FHL3	HJURP	TMEM204
GTF2B	NKIRAS2	PAG1	HOMER3	PKMYT1	RBBP7	ITGA6	PITPNC1	RGS2	GSTM5	MTMR12	SLC1A5	GTF2B	LAMA4	SLC16A2	FLNB	HMGB2	TMEM97
HCN2	NOG	PARD6G	HOXC11	PRSS12	RNFT2	ITGA8	PNPLA4	RIN3	GTF2H1	MXD3	SLC4A8	HCN2	LCE2A	SLC16A3	FLNC	HOMER3	TOMM34
HGF	NPC1	PBX2	HPRT1	PTK7	SAMD12	IVL	POPDC3	RRAGD	GTSE1	MYH10	SMAD3	HGF	LIMS1	SLC25A33	FMOD	HOXC11	TPD52L1
HIPK2	NRIP3	PDP2	HRH1	PTPRJ	SCARA3	JAM2	PPAP2C	SCN1B	HADH	NACC1	SSRP1	HIPK2	LMBRD1	SLC25A51	FN3KRP	HPRT1	TRIP13
HMGA2	NTSR1	PIP5K1C	HSPB11	PTRF	SCML1	KCNC4	PPARG	SEMA5A	HAUS4	NAT14	ST3GAL4	HMGA2	LMLN	SLC26A2	FOSL2	HRH1	UCP2
HNRNPH2	OSBPL1A	PLAGL1	IGFBP6	PXMP2	SDC1	KCNIP3	PRKG2	SEMA6A	HDAC1	NCAPH	STMN1	HNRNPH2	LONRF1	SLC35F3	FOXM1	HSPB11	UHMK1
HOXA7	P4HA1	PLEKHM1	ITGA4	RARG	SEC61A2	KCNJ15	PSD3	SEMA6D	HIAT1	NDC1	STXBP5	HOXA7	LPAR3	SLC37A2	GAB2	IGFBP6	VANGL1
HSPB6	PAPPA	PMAIP1	JADE1	RDH10	SEMA3B	KCNMA1	PTGFRN	SEPT5	HIST1H4L	NDE1	TACC3	HSPB6	LPHN2	SLC37A3	GINS2	INTS9	WDR62
IFI16	PARD6G	PODXL	KANK2	RHPN2	SH3BP4	KCNQ5	PTGS1	SEPW1	HJURP	NEK2	TAGLN	IFI16	LPPR2	SLC39A13	GINS4	IQGAP3	WEE1
IGF2	PARM1	POPDC3	KCND1	RPL39L	SHMT1	KCTD21	PTPRU	SERINC1	HLA-DMA	NEU1	TGFBI	IGF2	LTBP1	SLFN5	GLCE	ISLR	ZDHHC12
IGFBP3	PHLDA1	PPAP2C	KHK	RRM2	SLBP	KDM3A	PXK	SESN2	HMGB2	NGF	TK1	IGFBP3	LURAP1L	SNX6	GLIPR2	JADE1	
INA	PMAIP1	PPARG	KIAA0226	S100A16	SLC1A5	KDSR	QPCT	SFRP1	HOMER3	NID1	TNFAIP8L1	INA	LYPLA1	SPRY2	GPR124	JUP	
ISCU	PODXL	PPP1R3C	KIAA1199	SAP30	SLC4A8	KIAA1217	RAB27B	SH3GL2	HOXA11	NOL9	TOE1	ISCU	MAGI2	ST6GALNAC2	GPR126	KANK2	
ITFG1	PPM1L	PRKG2	KIF13A	SCARA3	SMAD3	KIAA1551	RAP1GAP2	SH3PXD2B	HPRT1	NPM3	TRIM6-TRIM3	ITFG1	MAML3	STEAP3	GPRC5A	KIAA0226	
ITGA2	PRKG1	PRSS35	KIF22	SDC4	SOGA1	KLHDC3	RBMS1	SIRPA	HSPA2	NRAS	UCP2	ITGA2	MAN2A1	STXBP1	GPRC5B	KIAA1598	
ITGA6	PSD3	PSD3	KPNA2	SEC61A2	ST3GAL4	KLHL21	REXO1	SLC16A3	HSPB11	NSF	VANGL1	ITGA6	MAPRE3	SULF2	GSTM4	KIF23	
ITGA8	PSTPIP2	PSKH1	KRT19	SEPT6	L5P-PVRIG2P	LAMA1	RIN3	SLC37A3	ICAM2	NT5DC3	ZDHHC12	ITGA8	MCTP1	TBC1D17	GSTM5	KPNA2	
ITPR2	PTGFRN	QKI	KRT34	SERTAD4	SUZ12P1	LCE2A	RPS6KA3	SLC38A1	IER3	NXNL2		ITPR2	MDM2	TBCCD1	GTF2H1	KRT18	
IVL	PTGS1	RBMS1	KRT7	SHCBP1	SYPL2	LGALS3	RRAGD	SLC39A13	IGFBP6	NXPE3		IVL	METTL9	TK2	GTSE1	KRT19	
KCNC4	PTGS2	REXO1	LBR	SKP2	TAGLN	LMBRD1	RRM2B	SLC5A3	INCENP	NYNRIN		KCNC4	MICB	TLE3	HADH	LBR	
KCNIP3	PTPRU	RIN3	LIG1	SLC38A11	TAGLN2	LMLN	RTN4RL1	SLC6A15	IQGAP3	ORC6		KCNIP3	MSC	TMED4	HAUS4	LMNB2	
KCNJ15	QKI	RIPK2	LMCD1	SLC43A3	TGFBI	LPAR3	SATB1	SLFN5	ITGA4	PGM2		KCNJ15	MTSS1	TMEM117	HDAC1	LMOD1	
KCNMA1	QPCT	RNF24	LOXL1	SLC7A5	TGM2	LPHN2	SC5D	SNX6	JADE1	PKMYT1		KCNMA1	MTURN	TOX2	HIAT1	LOXL3	

	KCNN2	RAB31	SATB1	LOXL3	SMAD3	TK1	LPPR2	SCN1B	SRXN1	JUP	POC1A		KCNN2	MYO1D	TPRG1L	HIPK1	LY6G5B	
	KCTD21	RAB33A	SATB2	MCM2	SNRPA	RIM6-TRIM3	LTBP1	SEPT3	ST6GALNAC2	KANK2	PODN		KCTD21	NCALD	TRAPPC6B	HJURP	MCM2	
	KDM3A	RAP1GAP2	SCN1B	MCM4	SOGA1	UCP2	LYPLA1	SEPW1	STEAP3	KCND1	PRC1		KDM3A	NEDD4	TSHZ3	HMGB2	MCM4	
	KDSR	RASGRF2	SECTM1	MCM7	SORT1	UHMK1	M6PR	SET	STMN3	KHK	PSMA5		KDSR	NEO1	TUBA3E	HOMER3	MCM5	
	KIAA0319L	RGL1	SEMA5A	MCMBP	SPA17	VAMP5	MAN2A1	SLC16A2	STXBP1	KIAA0226	PSMB9		KIAA0319L	NETO2	USF2	HOXA11	MCM7	
	KIAA1551	RNF24	SEMA6D	METTL7A	SPAG5	XRCC6BP1	MAP3K7CL	SLC16A6	TIPARP	KIAA1598	PSMC3IP		KIAA1551	NFIL3	UXS1	HOXC11	MCMBP	
	KIT	RPS6KA3	SEPT5	MIF4GD	ST3GAL4	ZBTB5	MAPRE3	SLC17A5	TMED4	KIF22	PSRC1		KIT	NINJ1	ZC3HAV1L	HPRT1	MDC1	
	KLHDC3	SEMA5A	SEPW1	MTHFS	STMN1	ZC3H12A	MCTP1	SLC25A32	TMEM158	KIF4A	PTK7		KLHDC3	NPC1	ZNF521	HRH1	MIF4GD	
	KLHL21	SEPT3	SETBP1	MTMR12	SUV39H1	ZDHHC12	MICB	SLC25A51	TOB1	KPNA2	PTPRJ		KLHL21	NTM	ZNF610	HSPB11	MTMR12	
	LAMA1	SEPT5	SIRPA	MTRF1L	SYNPO		MME	SLC2A3	TOX2	KRT18	PTTG1IP		LAMA1	OCM2		IER3	MXD3	
	LAMA4	SEPW1	SLC17A5	MXD3	TACC3		MMP16	SLC35A1	TSHZ3	KRT7	PXMP2		LAMA4	P2RX5		IGFBP6	MYBL2	
	LCE2A	SET	SLC25A33	MYBL2	TDP1		MSC	SLC37A2	TSPAN11	LBR	RACGAP1		LCE2A	PAPPA		INCENP	MYH10	
	LIMS1	SETBP1	SLC30A7	MYH10	TGFBI		MTURN	SLC37A3	TUBA3E	LCLAT1	RAD51		LIMS1	PCMTD1		INTS9	NACC1	
	LMBRD1	SH3PXD2B	SLC35F3	MYOCD	TGM2		MYC	SLC38A1	UBA6	LMNB1	RARG		LMBRD1	PDIA5		IQGAP3	NASP	
	LMLN	SLC16A2	SLC38A1	NACC1	TMEM204		NCALD	SLC39A13	USF2	LMOD1	RBBP7		LMLN	PDK3		ISLR	NAT14	
	LONRF1	SLC16A3	SLC39A13	NAT14	UBP1		NEDD4	SLC4A4	UST	LOXL1	RHPN2		LONRF1	PDP2		JADE1	NAV2	
	LPAR3	SLC16A6	SLC4A4	NCAPD3	VANGL1		NEK9	SLMO2	UXS1	LOXL3	RNASEH2A		LPAR3	PHLDA1		JUP	NBPF3	
	LPHN2	SLC5A3	SLC6A15	NDE1	WEE1		NEO1	SMPD1	VLDLR	LY6G5B	RPSAP52		LPHN2	PIP5K1C		KANK2	NCAPD3	
	LPPR2	SLC6A15	SMPD1	NEU1	ZDHHC12		NETO2	SNX6	ZNF460	MB21D2	RPSAP58		LPPR2	PITPNC1		KIAA0226	NCAPH	
	LTBP1	SLMO2	SMURF2	NGF			NF2	SRXN1	ZNF521	MCM2	RRM2		LTBP1	PMAIP1		KIAA1598	NDC1	
	LURAP1L	SMPD1	SNCA	NID1			NFIL3	SS18	ZNF583	MCM5	RUVBL2		LURAP1L	PNPLA4		KIF23	NGF	
	LYPLA1	SOGA3	SNX6	NPM3			NKIRAS2	SSBP2		MCM7	S100A16		LYPLA1	PPAP2C		KPNA2	NID1	
	MAGI2	SSBP2	SPRY2	NRAS			NPC1	ST6GALNAC2		MDC1	SDC1		MAGI2	PPARG		KRT18	NPM3	
	MAML3	STC2	SRXN1	NREP			NTSR1	STEAP3		MIF4GD	SDC4		MAML3	PRKG2		KRT19	NSF	
	MAN2A1	STEAP3	SS18	NSUN2			NUDT11	SULF2		MRVI1	SEC61A2		MAN2A1	PSD3		KRT7	NSUN2	
	MAPRE3	TBK1	ST8SIA5	NT5DC3			NUPR1	TAPBP		MTFR2	SEMA3B		MAPRE3	PTGFR		LBR	NTN4	
	MCTP1	THBD	STC2	NTN4			OCM2	TCP11L2		MTHFS	SEPT6		MCTP1	PTGFRN		LMNB2	NUMA1	
	MDM2	TMED4	STMN3	NUAK2			OGFRL1	TMC7		MTMR12	SERTAD4		MDM2	PTPRG		LMOD1	NUSAP1	
	METTL9	TMEM117	STXBP1	NUMA1			OSBPL1A	TMED4		MXD3	SH2D4A		METTL9	PXK		LOXL1	NXNL2	
	MICB	TMEM158	TAPBP	NXNL2			P2RX5	TMEM117		MYBL2	SH3BP4		MICB	QKI		LOXL3	OIP5	
	MSC	TMEM192	TBCCD1	NYNRIN			PARD6G	TMOD2		MYH10	SHCBP1		MSC	RAB33A		LY6G5B	ORC6	
	MTSS1	TMOD2	THBD	OLFML2B			PARM1	TOB1		NACC1	SHMT1		MTSS1	RAB3A		LY6K	OXTR	
	MTURN	TMTC1	TLE3	PCNA			PBX2	TOLLIP		NAT14	SLBP		MTURN	RAET1L		MCM2	PAQR4	
	MYO1D	TNC	TMEM158	PDE1C			PDIA5	TPRG1L		NAV2	SMYD2		MYO1D	RAP1GAP2		MCM4	PDE1C	
	NCALD	TOB1	TMOD2	PEG10			PDP2	TRIB2		NCAPH	SNAPIN		NCALD	RBMS1		MCM5	PGM2	
	NEDD4	TPRG1L	TNFAIP1	PHF19			PIP5K1C	TSPAN11		NDC1	SOGA1		NEDD4	RGL1		MCM7	PHF19	
	NEK9	TRIB2	TSC22D3	PIM1			PITPNC1	TUBA3E		NDE1	SORT1		NEK9	RIN3		MCMBP	PIM1	
	NEO1	TSC22D3	TSHZ3	PKMYT1			PLEKHM1	UBA6		NEK2	ST3GAL4		NEO1	RPL17		MDC1	PLK2	
	NETO2	TSPAN11	TSPAN11	POC1A			PNPLA4	ULBP3		NEU1	STMN1		NETO2	RPS6KA3		MIF4GD	POC1A	
	NFIL3	TXNIP	UBA6	POLE			PODXL	UST		NGF	SUOX		NFIL3	RRAGD		MSH5	PODN	
	NINJ1	ULBP3	UNC5B	PRC1			POPDC3	VLDLR		NID1	SUV39H1		NINJ1	RTN4RL1		MTMR12	POLE	
	NOX4	USF2	VLDLR	PRSS12			PPAP2C	VSTM4		NOL9	SUZ12P1		NOX4	SC5D		MXD3	PRC1	
	NPC1	VSTM4	ZBTB33	PTK7			PPARG	WLS		NPM3	SYPL2		NPC1	SCN1B		MYBL2	PRSS12	
	NT5E	WLS	ZC3HAV1L	PTPRJ			PPM1L	ZMAT3		NRAS	TENC1		NT5E	SECTM1		MYH10	PSMA5	
	NTM		ZNF528	PTRF			PRKG2	ZNF136		NREP	TGM2		NTM	SEPW1		NACC1	PSMB9	
	OCM2		ZNF583	PXMP2			PRSS35	ZNF566		NSF	TNRC6A		OCM2	SET		NASP	PSMC3IP	
	P2RX5		ZNF610	RAD54L			PSD3			NT5DC3	TROAP		P2RX5	SFXN3		NAT14	PSRC1	
	PAPPA			RARG			PTGFRN			NTN4	UBP1		PAPPA	SIRPA		NAV2	PTK7	
	PARD6G			RBBP7			PTGS1			NXNL2	USP6		PARD6G	SLC16A2		NBPF3	PTPRJ	
	PBX2			RDH10			PTPRG			NXPE3	VAMP5		PBX2	SLC16A3		NCAPD3	PTRF	
	PCMTD1			RHPN2			PTPRU			NYNRIN	ZBTB5		PCMTD1	SLC17A5		NCAPH	PTTG1IP	
	PDIA5			RNFT2			PXK			OLFML2B	ZC3H12A		PDIA5	SLC25A33		NDC1	PXMP2	
	PDK3			RPL39L			QPCT			ORC6	ZDHHC12		PDK3	SLC25A36		NEU1	RACGAP1	
	PDP2			RRM2			RAB27B			PACSIN2	ZWINT		PDP2	SLC25A51		NGF	RAD54L	
	PHLDA1			S100A16			RAB31			PGM2	ZYG11A		PHLDA1	SLC26A2		NID1	RBBP7	
	PIP5K1C			SAMD12			RAP1GAP2			PHF19			PIP5K1C	SLC30A7		NPM3	RDH10	
	PITPNC1			SAP30			RBMS1			PIM1			PITPNC1	SLC35A1		NREP	RFC2	
	PLEKHM1			SCARA3			REXO1			PKMYT1			PLEKHM1	SLC35F3		NSF	RHPN2	
	PMAIP1			SCML1			RGS2			PLTP			PMAIP1	SLC37A2		NSUN2	RNASEH2A	
	PNPLA4			SDC1			RIN3			POC1A			PNPLA4	SLC37A3		NTN4	RPS6KA5	
	PODXL			SDC4			RPS6KA3			PODN			PODXL	SLC38A1		NUDCD2	RPSAP52	
	POPDC3			SEC61A2			RRAGD			PRC1			POPDC3	SLC4A4		NUMA1	RPSAP58	

	PPAP2B			SEMA3B			RRM2B			PRR23C			PPAP2B	SLC5A3		NUSAP1	RRM2	
	PPAP2C			SEPT6			RTN4RL1			PRSS12			PPAP2C	SLC6A15		NXNL2	RRP1B	
	PPARG			SERTAD4			SATB1			PSMA5			PPARG	SMPDL3A		OIP5	RUVBL2	
	PRKG2			SH3BP4			SC5D			PSMB9			PRKG2	SMURF2		ORC6	S100A16	
	PSD3			SHCBP1			SCN1B			PSMC3IP			PSD3	SNX6		OXTR	SAP30	
	PSTPIP2			SHMT1			SEMA5A			PSRC1			PSTPIP2	SOGA3		PACSIN2	SCCPDH	
	PTGFR			SKP2			SEMA6A			PTK7			PTGFR	SRPX		PAQR4	SDC1	
	PTGFRN			SLBP			SEMA6D			PTPRJ			PTGFRN	SS18		PDE1C	SDC4	
	PTGS1			SLC1A5			SEPT3			PTTG1IP			PTGS1	SSBP2		PGM2	SEC61A2	
	PTPRG			SLC38A11			SEPT5			PXMP2			PTPRG	ST6GALNAC2		PHF19	SEMA3B	
	PXK			SLC43A3			SEPW1			RACGAP1			PXK	STEAP1		PIM1	SEPT6	
	QKI			SLC4A8			SERINC1			RAD51			QKI	STMN2		PKMYT1	SERTAD4	
	QPCT			SLC7A5			SESN2			RARG			QPCT	STMN3		PLK2	SFPQ	
	RAB31			SMAD3			SET			RBBP7			RAB31	TIPARP		PLTP	SH2D4A	
	RAB33A			SNRPA			SFRP1			RDH10			RAB33A	TMC7		POC1A	SH3BP4	
	RAB3A			SOGA1			SH3GL2			RHPN2			RAB3A	TMEM117		PODN	SHCBP1	
	RAET1L			SORT1			SH3PXD2B			RNASEH2A			RAET1L	TMEM192		POLA2	SHMT1	
	RAP1GAP2			SPA17			SIRPA			RPL39L			RAP1GAP2	TMEM33		POLE	SLBP	
	RBMS1			SPAG5			SLC16A2			RPSAP52			RBMS1	TMOD2		PPME1	SLC1A5	
	REXO1			ST3GAL4			SLC16A3			RPSAP58			REXO1	TMTC1		PRC1	SLC43A3	
	RGL1			STAG3L5P-PVRIG2P-PILRB			SLC16A6			RRM2			RGL1	TNFAIP1		PRSS12	SLC4A8	
	RGS2			STMN1			SLC17A5			RUVBL2			RGS2	TNFRSF10A		PSMA5	SLC7A5	
	RIN3			SUV39H1			SLC25A32			S100A16			RIN3	TNFRSF21		PSMB9	SLIT2	
	RORA			SUZ12P1			SLC25A51			SAMD12			RORA	TOB1		PSMC3IP	SMAD3	
	RPL17			SYNPO			SLC2A3			SCCPDH			RPL17	TOLLIP		PSRC1	SMYD2	
	RPS6KA3			SYPL2			SLC35A1			SCML1			RPS6KA3	TPRG1L		PTK7	SNAPIN	
	RRAGD			TACC3			SLC37A2			SDC1			RRAGD	TRIB2		PTPRJ	SOGA1	
	RTN4RL1			TAGLN			SLC37A3			SDC4			RTN4RL1	TSPAN31		PTRF	SORT1	
	SC5D			TAGLN2			SLC38A1			SEC61A2			SC5D	TUBA3E		PTTG1IP	SPAG5	
	SCN1B			TDP1			SLC39A13			SELENBP1			SCN1B	UBA6		PXMP2	SRRM2	
	SECTM1			TGFBI			SLC4A4			SEMA3B			SECTM1	ULBP3		RACGAP1	SSRP1	
	SEMA6A			TGM2			SLC5A3			SEPT6			SEMA6A	UNC5B		RAD54L	ST3GAL4	
	SEPT5			TK1			SLC6A15			SERTAD4			SEPT5	USF2		RBBP7	STMN1	
	SEPW1			TMEM204			SLFN5			SFPQ			SEPW1	VLDLR		RDH10	STXBP5	
	SERINC1			TRIM6-TRIM34			SLMO2			SH2D4A			SERINC1	VSTM4		RFC2	SUOX	
	SESN2			UBP1			SMPD1			SH3BP4			SESN2	ZBTB33		RHPN2	SUV39H1	
	SET			UCP2			SNX6			SHCBP1			SET	ZC3HAV1L		RNASEH2A	SUZ12P1	
	SFRP1			UHMK1			SRXN1			SHMT1			SFRP1	ZNF136		RPS6KA5	SYT11	
	SFXN3			VAMP5			SS18			SLBP			SFXN3	ZNF234		RPSAP52	TENC1	
	SH3PXD2B			VANGL1			SSBP2			SLC1A5			SH3PXD2B	ZNF566		RPSAP58	TGFBI	
	SIRPA			WEE1			ST6GALNAC2			SLC4A8			SIRPA			RRM2	TGM2	
	SLC16A2			XRCC6BP1			STEAP3			SMAD3			SLC16A2			RRP1B	TIMELESS	
	SLC16A3			ZBTB5			STMN3			SMYD2			SLC16A3			RUVBL2	TNRC6A	
	SLC17A5			ZC3H12A			STXBP1			SNAPIN			SLC17A5			S100A16	TROAP	
	SLC25A33			ZDHHC12			SULF2			SOGA1			SLC25A33			SAMD12	TYMS	
	SLC25A36						TAPBP			SORT1			SLC25A36			SAP30	VAMP5	
	SLC25A51						TCP11L2			SSRP1			SLC25A51			SCCPDH	WDR34	
	SLC26A2						TIPARP			ST3GAL4			SLC26A2			SDC1	XRCC6BP1	
	SLC30A7						TMC7			STMN1			SLC30A7			SDC4	ZC3H12A	
	SLC35A1						TMED4			STXBP5			SLC35A1			SEC61A2	ZWINT	
	SLC35F3						TMEM117			SUOX			SLC35F3			SELENBP1		
	SLC37A2						TMEM158			SUV39H1			SLC37A2			SEMA3B		
	SLC37A3						TMOD2			SUZ12P1			SLC37A3			SEPT6		
	SLC38A1						TOB1			SYPL2			SLC38A1			SERTAD4		
	SLC39A13						TOLLIP			TACC3			SLC39A13			SFPQ		
	SLC4A4						TOX2			TAGLN			SLC4A4			SH2D4A		
	SLC5A3						TPRG1L			TENC1			SLC5A3			SH3BP4		
	SLC6A15						TRIB2			TGFBI			SLC6A15			SHCBP1		
	SLFN5						TSHZ3			TGM2			SLFN5			SHMT1		
	SMPDL3A						TSPAN11			TK1			SMPDL3A			SLBP		
	SMURF2						TUBA3E			TNFAIP8L1			SMURF2			SLC1A5		
	SNX6						UBA6			TNRC6A			SNX6			SLC43A3		

	SOGA3						ULBP3			TOE1			SOGA3			SLC4A8		
	SPRY2						USF2			TRIM6-TRIM34			SPRY2			SLC7A5		
	SRPX						UST			TROAP			SRPX			SLIT2		
	SS18						UXS1			UBP1			SS18			SMAD3		
	SSBP2						VLDLR			UCP2			SSBP2			SMYD2		
	ST6GALNAC2						VSTM4			USP6			ST6GALNAC2			SNAPIN		
	STEAP1						WLS			VAMP5			STEAP1			SNRPA		
	STEAP3						ZMAT3			VANGL1			STEAP3			SOGA1		
	STMN2						ZNF136			ZBTB5			STMN2			SORT1		
	STMN3						ZNF460			ZC3H12A			STMN3			SPA17		
	STXBP1						ZNF521			ZDHHC12			STXBP1			SPAG5		
	SULF2						ZNF566			ZWINT			SULF2			SRRM2		
	TBC1D17						ZNF583			ZYG11A			TBC1D17			SSRP1		
	TBCCD1												TBCCD1			ST3GAL4		
	TIPARP												TIPARP			STMN1		
	TK2												TK2			STXBP5		
	TLE3												TLE3			SUMO2		
	TMC7												TMC7			SUOX		
	TMED4												TMED4			SUV39H1		
	TMEM117												TMEM117			SUZ12P1		
	TMEM192												TMEM192			SYPL2		
	TMEM33												TMEM33			SYT11		
	TMOD2												TMOD2			TACC3		
	TMTC1												TMTC1			TENC1		
	TNFAIP1												TNFAIP1			TGFBI		
	TNFRSF10A												TNFRSF10A			TGM2		
	TNFRSF21												TNFRSF21			TGOLN2		
	TOB1												TOB1			TIMELESS		
	TOLLIP												TOLLIP			TK1		
	TOX2												TOX2			TMEM204		
	TPRG1L												TPRG1L			TMEM97		
	TRAPPC6B												TRAPPC6B			TNRC6A		
	TRIB2												TRIB2			TOMM34		
	TSHZ3												TSHZ3			TPD52L1		
	TSPAN31												TSPAN31			TRIP13		
	TUBA3E												TUBA3E			TROAP		
	UBA6												UBA6			TYMS		
	ULBP3												ULBP3			UCP2		
	UNC5B												UNC5B			UHMK1		
	USF2												USF2			VAMP5		
	UXS1												UXS1			VANGL1		
	VLDLR												VLDLR			WDR34		
	VSTM4												VSTM4			WDR62		
	ZBTB33												ZBTB33			WEE1		
	ZC3HAV1L												ZC3HAV1L			XRCC6BP1		
	ZNF136												ZNF136			ZC3H12A		
	ZNF234												ZNF234			ZDHHC12		
	ZNF521												ZNF521			ZWINT		
	ZNF566												ZNF566					
	ZNF610												ZNF610					

Table S8: G4 statistic for genes significantly altered in BS and BLM-depleted cells

Extended G4 Statistics for genes regulated in BS patients compared to Normal control

Region	-250bp to TSS								
Regulation	Up or Down N=1138								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	575	870	1.51	350	442	1.26	326	428	1.31
Random Genes	531.78	807.26	1.52	322.23	407.13	1.26	310.25	398.93	1.29
SD(Random)	16.41	30.03	0.03	15.33	20.99	0.03	14.5	21.39	0.03
FDR Rand > Reg	0.006	0.021	0.57	0.045	0.05	0.495	0.147	0.081	0.18
FDR Rand < Reg	0.994	0.982	0.43	0.962	0.955	0.506	0.871	0.922	0.821

Region	-250bp to TSS								
Regulation	Up N=1000								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	505	741	1.47	302	371	1.23	288	370	1.28
Random Genes	467.86	710.25	1.52	282.76	356.71	1.26	273.63	351.42	1.28
SD(Random)	15.44	27.7	0.03	14.12	20.38	0.03	13.54	19.34	0.03
FDR Rand > Reg	0.004	0.145	0.935	0.087	0.228	0.855	0.164	0.189	0.491
FDR Rand < Reg	0.998	0.864	0.065	0.919	0.785	0.145	0.854	0.828	0.509

Region	-250bp to TSS								
Regulation	Down N=138								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	70	129	1.84	48	71	1.48	38	58	1.53
Random Genes	64.52	98.06	1.52	38.68	48.74	1.26	37.66	48.42	1.29
SD(Random)	5.73	10.31	0.09	5.03	7.24	0.09	5.27	7.42	0.09
FDR Rand > Reg	0.188	0.001	0.001	0.042	0.003	0.004	0.514	0.109	0.003
FDR Rand < Reg	0.844	0.999	0.999	0.972	0.998	0.996	0.562	0.918	0.997

Region	TSS to +250								
Regulation	Up or Down N=1138								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	577	829	1.44	303	359	1.18	377	470	1.25
Random Genes	536.45	771.84	1.44	262.73	319.64	1.22	365.46	454.18	1.24
SD(Random)	16.32	27.08	0.03	13.37	17.71	0.03	16.06	21.57	0.02
FDR Rand > Reg	0.007	0.019	0.525	0.001	0.013	0.868	0.256	0.243	0.424
FDR Rand < Reg	0.993	0.982	0.475	0.999	0.989	0.132	0.76	0.776	0.577

Region	TSS to +250								
Regulation	Up N=1000								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	507	721	1.42	272	319	1.17	328	402	1.23
Random Genes	472.1	679.64	1.44	231.06	280.98	1.22	320.73	398.9	1.24
SD(Random)	15.58	26.87	0.03	12.95	17.77	0.03	14.35	19.57	0.03
FDR Rand > Reg	0.015	0.068	0.724	0.001	0.024	0.912	0.329	0.458	0.767
FDR Rand < Reg	0.987	0.934	0.276	0.999	0.978	0.088	0.692	0.564	0.233

Region	TSS to +250								
Regulation	Down N=138								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	70	108	1.54	31	40	1.29	49	68	1.39
Random Genes	64.94	93.33	1.44	31.73	38.61	1.22	44.41	55.15	1.24
SD(Random)	5.75	9.83	0.08	4.83	6.58	0.09	5.5	7.59	0.07
FDR Rand > Reg	0.222	0.084	0.089	0.599	0.429	0.183	0.235	0.06	0.031
FDR Rand < Reg	0.825	0.938	0.913	0.477	0.636	0.824	0.818	0.953	0.969

Region	First 250bp of Intron 1								
Regulation	Up or Down N=1117								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	689	1110	1.61	288	355	1.23	541	755	1.4
Random Genes	621.33	958.77	1.54	251.32	314.89	1.25	476.63	645.96	1.36
SD(Random)	16.11	30.78	0.03	13.42	18.83	0.03	16.55	26	0.03
FDR Rand > Reg	0.001	<0.001	0.013	0.002	0.015	0.735	<0.001	<0.001	0.076
FDR Rand < Reg	1	1	0.987	0.999	0.986	0.265	1	1	0.924

Region	TSS to +250								
Regulation	Up N=987								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	605	973	1.61	258	317	1.23	474	656	1.38
Random Genes	548.96	847.84	1.54	222.21	278.74	1.25	421.25	570.87	1.36
SD(Random)	15.21	29.55	0.03	13.23	18.25	0.03	14.84	23.96	0.03
FDR Rand > Reg	0.001	<0.001	0.018	0.002	0.021	0.76	<0.001	<0.001	0.177
FDR Rand < Reg	0.999	1	0.982	0.998	0.983	0.24	1	1	0.823

Region	TSS to +250								
Regulation	Down N=130								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	84	137	1.63	30	38	1.27	67	99	1.48
Random Genes	72.45	112.03	1.55	29.49	36.99	1.25	55.78	75.7	1.36
SD(Random)	5.78	11.18	0.09	4.75	6.66	0.1	5.5	8.7	0.08
FDR Rand > Reg	0.027	0.018	0.177	0.489	0.447	0.438	0.02	0.002	0.083
FDR Rand < Reg	0.981	0.986	0.823	0.599	0.6	0.57	0.985	0.999	0.917

Extended G4 Statistics for genes with altered regulation in BLM-depleted compared to NS shRNA depleted human fibroblasts filtered to remove NS shRNA vs Control

Region	-250bp to TSS								
Regulation	Up or Down N=1067								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	508	777	1.53	296	381	1.29	303	396	1.31
Random Genes	498.04	756.25	1.52	302.94	382	1.26	292.01	375.44	1.29
SD(Random)	15.93	28.62	0.03	14.61	20.8	0.03	13.61	20.13	0.03
FDR Rand > Reg	0.286	0.231	0.357	0.701	0.538	0.187	0.218	0.146	0.247
FDR Rand < Reg	0.734	0.776	0.644	0.32	0.492	0.813	0.806	0.866	0.754

Region	-250bp to TSS								
Regulation	Up N=547								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	281	425	1.51	167	216	1.29	164	209	1.27
Random Genes	255.3	387.14	1.52	155.32	195.94	1.26	150.09	193.22	1.29
SD(Random)	11.22	20.47	0.05	10.27	13.87	0.04	10.06	14.39	0.04
FDR Rand > Reg	0.007	0.034	0.533	0.137	0.088	0.213	0.087	0.144	0.626
FDR Rand < Reg	0.996	0.971	0.467	0.884	0.92	0.787	0.924	0.874	0.377

Region	-250bp to TSS								
Regulation	Down N=520								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	227	352	1.55	129	165	1.28	139	187	1.35
Random Genes	243.04	369.82	1.52	147.49	186.43	1.26	142.16	182.93	1.29
SD(Random)	11.06	20.1	0.05	10.65	14.55	0.04	10.12	14.51	0.05
FDR Rand > Reg	0.928	0.823	0.258	0.962	0.942	0.35	0.643	0.395	0.113
FDR Rand < Reg	0.081	0.188	0.742	0.049	0.066	0.651	0.39	0.624	0.887

Region	TSS to +250								
Regulation	Up or Down N=1067								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	515	722	1.4	256	307	1.2	341	415	1.22
Random Genes	504.37	726.39	1.44	246.26	299.79	1.22	342.37	425.46	1.24
SD(Random)	15.1	26.31	0.03	13.76	17.88	0.03	15.25	21.14	0.03
FDR Rand > Reg	0.233	0.564	0.906	0.259	0.334	0.742	0.55	0.692	0.84
FDR Rand < Reg	0.786	0.449	0.094	0.767	0.68	0.261	0.48	0.325	0.16

Region	TSS to +250								
Regulation	Up N=547								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	258	369	1.43	142	174	1.23	166	195	1.17
Random Genes	257.97	372.22	1.44	126.71	154.17	1.22	175.93	219.15	1.25
SD(Random)	11.16	19.37	0.04	10.3	13.18	0.04	11.18	14.93	0.03
FDR Rand > Reg	0.531	0.586	0.625	0.079	0.072	0.414	0.828	0.952	0.983
FDR Rand < Reg	0.501	0.439	0.378	0.933	0.931	0.586	0.197	0.054	0.017

Region	TSS to +250								
Regulation	Down N=520								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	257	353	1.37	114	133	1.17	175	220	1.26
Random Genes	245.38	353.43	1.44	120.16	146.26	1.22	166.94	207.55	1.24
SD(Random)	11.27	19.18	0.04	9.95	13.11	0.04	10.56	14.49	0.04
FDR Rand > Reg	0.167	0.523	0.943	0.742	0.854	0.885	0.242	0.213	0.361
FDR Rand < Reg	0.861	0.501	0.057	0.283	0.16	0.122	0.783	0.81	0.643

Region	First 250bp of Intron 1								
Regulation	Up or Down N=997								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	586	900	1.54	236	294	1.25	454	606	1.33
Random Genes	554.75	858.11	1.55	224.01	280.62	1.25	424.97	575.54	1.35
SD(Random)	15.56	29.17	0.03	12.86	17.74	0.03	14.98	23.61	0.03
FDR Rand > Reg	0.024	0.074	0.642	0.193	0.237	0.569	0.029	0.094	0.748
FDR Rand < Reg	0.98	0.928	0.358	0.83	0.779	0.432	0.975	0.915	0.253

Region	TSS to +250								
Regulation	Up N=514								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	294	451	1.53	129	162	1.26	222	289	1.3
Random Genes	286.33	442.69	1.55	115.36	144.55	1.25	220.07	298.6	1.36
SD(Random)	10.52	19.96	0.04	9.33	12.77	0.05	11.01	17.38	0.04
FDR Rand > Reg	0.237	0.35	0.602	0.082	0.095	0.463	0.445	0.729	0.932
FDR Rand < Reg	0.79	0.667	0.398	0.932	0.917	0.538	0.582	0.293	0.069

Region	TSS to +250								
Regulation	Down N=483								
G4 Motif Strand	Either			T			NT		
Statistics	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene	# With G4	Total # G4s	G4s per gene
Regulated Genes	292	449	1.54	107	132	1.23	232	317	1.37
Random Genes	268.24	414.51	1.55	109.12	136.8	1.25	206.07	278.79	1.35
SD(Random)	10.81	21.07	0.05	8.7	12.28	0.05	10.64	16.86	0.04
FDR Rand > Reg	0.012	0.048	0.558	0.627	0.664	0.656	0.007	0.017	0.373
FDR Rand < Reg	0.99	0.955	0.442	0.419	0.361	0.346	0.994	0.986	0.627