Supplementary Information

The histone methyltransferase MLL3 contributes to genome-scale circadian transcription

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Materials & Methods

Chromatin immunoprecipitation (ChIP)

All animal experimentation was licensed by the Home Office under the Animals (Scientific Procedures) Act, 1987. Liver tissue was harvested from *n*=4 adult male C57Bl/6 mice once every 3 hours on the second cycle after transfer from 12L:12DR to DR:DR (L, light [220 µW cm^{-2}] and DR, dim red light [< 5 µW cm^{-2}]) and immediately frozen and then stored at -80°C prior to use. Prior to sampling, animals were stably entrained to a 12 h L: 12 h DR cycle for 3-4 weeks.

Liver tissue (30mg per final ChIP) was rapidly chopped into small (approx. 5 mm x 5mm x 2.5mm cubes) whilst defrosting using a sterile scalpel and immediately submerged in 4% formaldehyde (Sigma) and incubated at room temperature with gentle shaking for 10 mins. Glycine (1.25M) was added to a final concentration of 125 mM and incubated for a further 10 mins to quench the formaldehyde. Tissue was then dounce homogenised briefly to break up the tissue and then passed through a 100 µm cell strainer (BD Biosciences) and a cell suspension harvested. The cells were washed in ice cold phosphate-buffered saline (PBS) and then incubated with 2ml Farnham Lysis Buffer (5 mM PIPES pH 8.0, 85 mM KCl, 0.5% NP40, Roche Complete Protease Inhibitor Cocktail) at 4^{o}C for 15 mins to release nuclei. After spinning down, pelleted nuclei were then lysed with 1ml RIPA Buffer (1xPBS, 1% NP40, 0.5% Sodium Deoxycholate, 0.1% SDS, Roche Complete Protease Inhibitor Cocktail) and incubated for a further 15 mins at 4^{o}C. Chromatin was sheared using a Diagenode Bioruptor at 4^{o}C, using conditions optimised to produce 150-300bp fragments with the use of 15 ml Falcon tubes holding 2ml of lysate each (30 cycles of 30 secs on HIGH, 30 secs OFF). Sheared chromatin was transferred to 1.5 ml microcentrifuge tubes and spun at 14,000 rpm for 15 min at 4°C to pellet debris. Cleared supernatants were transferred to clean microcentrifuge tubes and 100 µl from each sample lysate was saved for use as an input control for sequencing and to check fragment size distribution.

For each liver from *n*=4 animals per time-point, duplicate ChIPs were performed with each antibody. ChIP-grade antibodies were purchased from Abcam (UK): anti-H3K4me3 (ab8580), anti-H3K9me3 (ab8898) and anti-Histone H3 (ab1791). 50 µl of Protein G magnetic beads (Dynal/Invitrogen) were washed three times (in 1 ml 1XPBS/1% BSA) and then incubated with 5 µg antibody in 300 µl volumes (diluted in PBS/BSA) for 4 hours at 4°C on a rotator. Excess, or non-specifically bound, antibody was removed by washing a further three times in PBS/BSA. The beads were then added to 900 µl of sheared chromatin in 1.5 ml DNA Lo-bind tubes (Eppendorf) and incubated at 4°C overnight with gentle rotation. Beads were washed six times in 1 ml LiCl Wash Buffer (100 mM Tris, 500 mM LiCl, 1% NP40, 1% Sodium Deoxycholate) for 3 min each, followed by a brief wash in Tris-EDTA (TE) buffer, pH 7.4. The beads were then suspended in TE, transferred to a clean microcentrifuge tube, and TE was removed. 200 µl of IP Elution Buffer (1% SDS and 100 mM $NaHCO_3$) was added at room temperature and then the beads were incubated for 45 mins at 65°C with continuous shaking on a thermomixer (at 800 rpm). The eluate was then removed from the beads and incubated overnight at 65°C to reverse cross-linking. DNA was extracted using a Qiagen Minelute PCR purification kit (using 12 µl of Buffer EB to elute DNA) and then quantified using Picogreen assays (Invitrogen) in a microplate as per the manufacturer's instructions. Input chromatin was reverse cross-linked in parallel and assayed with a Nanodrop spectrophotometer (because of the much higher DNA concentration) and a sample was run on a 2% agarose gel to check fragment size distributions were correct.

Multiplex Library Preparation & Sequencing

For H3K4me3, H3K9me3, Histone H3 and input DNA samples, these were prepared for sequencing on an Illumina Genome Analyzer II following the manufacturer's recommended library preparation protocol using 50 ng of ChIPed DNA, except that a custom adapter was used, the PCR was performed using indexed reverse primers in a high-efficiency amplification step, and the size selection step was performed after the PCR (1-3). For MLL3 ChIP in liver tissue or mouse embryonic fibroblasts (MEFs), standard Illumina indexing primers were used, as per the manufacturer's instructions. All libraries were multiplexed, and 4 indexed pooled samples (corresponding to four time-points, CT0, 6, 12, 18) sequenced per lane.

Bioinformatics: Alignment and Peak Detection

Analysis was performed using the Darwin Supercomputer of the University of Cambridge High Performance Computing Service (http://www.hpc.cam.ac.uk/), provided by Dell Inc. using Strategic Research Infrastructure Funding from the Higher Education Funding Council for England. Raw paired-end 50bp reads (in FASTQ format) were aligned to the UCSC mm9 genome build with Bowtie (http://bowtie-bio.sourceforge.net/index.shtml) using pre-built indexes downloaded from the host website (4-6). Parameters were optimised to utilise the software's multi-threading capabilities (we typically used a 128-core cluster for alignments). Alignment files were then converted from the standard Bowtie output format to ALN files (for use with Cisgenome) using a custom Perl script. Alignments were then analysed using a 2-sample comparison (ChIPed sample vs. Input control for each time-point) with Cisgenome v1, using a cut-off false discovery rate of 10% and a sliding window size of 100 (7-9). Output files were converted into various formats for browsing datasets and to display data. The Cisgenome and UCSC browsers were used for data visualisation, using custom tracks (1, 7, 10). Raw sequence data (FASTQ format), alignments (Bowtie format) and peak data (as Cisgenome/Affymetrix BAR format) are deposited on the NCBI GEO database (Accessions: GSE23550 and GSE37396) and are MINSEQE-compliant.

Microarrays

Total RNA was isolated from liver samples of C57/Bl6 mice over a circadian time course as previously described (4). Per time point, *n*=3 biological replicate samples were collected and processed individually. RNA from each individual biological replicate sample was hybridized on an Affymetrix mouse Gene ST1.0 microarray (Accession: GSE37396), using the manufacturer's protocol.

Microarray Data Analysis

Microarray analysis was performed using GeneSpring GX 11, with intensity values being normalized using the Robust Multi-array Average (RMA) algorithm. Data from a recent high-temporal resolution microarray study performed by the Hogenesch and Panda laboratories was used to determine the transcriptional profiles of genes with rhythmic histone methylation patterns (7). Genes with statistically significant ChIP-seq peaks at each time-point were checked against a list of rhythmic transcripts and their Affymetrix IDs, COSOPT/Fisher G-test q-values and period estimates were obtained (see Supplementary Table 1). Data were obtained from the NCBI GEO database (Accession: GSE11923) and the associated paper (2, 7).

Validation of ChIP with Real-time PCR (qPCR)

We performed ChIP on a separate set of liver samples (from animals from the same cohort) using 5 μg per ChIP of the anti-histone antibodies above, and also normal rabbit IgG (Cell Signaling Technology #2729) as a negative control for comparison. We performed real-time

PCR using SYBR green master mix (Applied Biosystems) with primers as below. Compared to IgG and input chromatin, all gave a significant (approx. 5-10 fold) enrichment at the positive loci examined, and no enrichment at selected negative loci. Primers were designed with Primer3Plus software using its standard parameters for qPCR, with an amplicon length of 75-125 bp:

Histone	Time-point	Forward Primer	Reverse Primer	Closest Gene	Amplicon size
H3K4me3	CT0	TACATGCCAGCGAACAAGAC	GCCTAATTGCAGGGAGAAAC	Defb7	122
H3K4me3	CT0	TCTGCCTCCTTCAGCAAATC	CATCGTTGGTACGGTTCAAG	Pdia4	92
H3K4me3	CT6	CCTCCGTTGCCTGAGAGAC	GGAGACATAGCTGGGTGGTC	Tmem64	94
H3K4me3	CT6	TACACAGATCCTGGGCCTTC	CAGCAAAACGCTGAGAACAA	A930016P21Rik	96
H3K4me3	CT12	TCATCTAGATTGCGCGACAC	TAGATAGTGGCGGGGTTCTG	Ipo9	76
H3K4me3	CT12	GCAAGGAGGGAGAAGACACA	CGAAGGGTCTCTGAATGCTC	Aftph	112
H3K4me3	CT18	CGTGGACCTCACAACATCAT	TGGGCTGAACCCAACTTTAC	Ndufb5	102
H3K4me3	CT18	GAGGAAGAGGGACCAAAACC	GGTTGTTGACACGGACTCCT	Tcf25	79
H3K9me3	CT0	CCCTGTCTCGAAAAACCAAA	TGGCCATGACAATACCAAAA	Zc3h7a	95
H3K9me3	CT0	TGCCTTGAGGAAATGAGCTT	CCAGACCACCCAAGCTTAAA	3110007F17Rik	79
H3K9me3	CT6	TCCTTGCCATATTCCAGGTC	GAGAAACATCCACTTGACAACG	Alkbh8	97
H3K9me3	CT6	GAGGTCCTTGGTCCTGTGAA	TCCTCCATCCACCCATTTTA	Rbmy1a1	82
H3K9me3	CT12	GACATGAGAGGGAGGGACTG	TATGCCCTCATTGCACTTCA	C230081A13Rik	93
H3K9me3	CT12	GCCATGCATGTCTAAGTACGC	GCGACCAAAGGAACCATAAC	Pgk2	81
H3K9me3	CT18	GCATCCATCCCTGAAAAGAC	CTGAGACTCACGTTTTCCTTCC	Sp110	100
H3K9me3	CT18	TCGGAGGGAACCAGCTACTA	CCAGAGGAAACTCTGGTGGA	4631422O05Rik	113

Real-time PCR (qPCR) for gene expression analysis

RNA from individual livers (see above ChIP methods) was extracted with TRIzol reagent (Invitrogen) and purified with RNAeasy Mini Kits (Qiagen). Total RNA was then used for reverse transcription via a High Capacity cDNA Archive Kit (Applied Biosystems). The resulting cDNA was then diluted 1:5 and used in duplicate 10 µl PCR reactions according to the manufacturer's protocol (TaqMan Gene Expression Master Mix, Applied Biosystems) with validated Taqman Gene Expression Assays (Applied Biosystems). For control reactions, mouse β-actin mRNA was amplified from the same samples. Real-time PCR was performed with an ABI 7900HT (Applied Biosystems) system. The relative levels of each mRNA were calculated by the $2^{-\Delta\Delta Ct}$ method (Ct stands for the cycle number at which the signal reaches the threshold of detection) and normalized to the corresponding β-actin mRNA levels. One-way ANOVA analysis was performed on data for each gene profile by Graphpad Prism v5 software, and post hoc Bonferroni tests were performed as required. The following assays were employed:

Gene	Taqman Assay Number
Arntl (Bmal1)	Mm_00500226_m1
Mll3	Mm_01156964_m1
Actb (β-actin)	Mm_00607939_s1

For mouse embryonic fibroblast (MEF) time courses, pre-mRNA and mature mRNA were assayed in duplicate reactions, for three biological replicate samples, as described previously (5, 11).

Gel Electrophoresis and Immunoblotting

Wild-type and *mCry1 –/– mCry2 –/–* animals (C57Bl/6 background, 12 weeks old) were individually housed under 12-hour light, 12-hour dark cycles (LD 12:12) and constant temperature (21±2°C). Livers from animals were harvested every 4 hours over the 24h cycle (ZT0, 4, 8, 12, 16, 20), flash-frozen and stored at -80°C. Lysates from ground-up livers were prepared using Chaps/Urea buffer (8M Urea, 4% Chaps, 5mM Magnesium Acetate, 10mM Tris pH6). Total protein abundance was determined using RC/DC reagents (Bio-rad) and concentration corrected to 4 $\mu g\ \mu l^{-1}$ for all samples. Lysates were diluted with denaturing LDS sample buffer (Invitrogen) with 1:10 β-mercaptoethanol to a final protein concentration 2 $\mu g\ \mu l^{-1}$, and heated to 70°C for 10 mins prior to loading on gels. 10 µg protein per lane was loaded for immunoblotting.

We used NuPAGE Novex 4–12% Bis-Tris gradient gels for Bmal1 and β-actin analyses, and 3-8% Tris-Acetate gels for MLL3 (Life Technologies). Gels were run according to the manufacturer's protocol with a non-reducing MES SDS buffer system (for Bis-Tris gels), or Tris-Acetate SDS Buffer (for Tris-Acetate gels). Protein transfer to nitrocellulose for blotting was performed using the iBlot system (Life Technologies), with a standard (P3, 7 min) protocol for Bis-Tris gels, or an optimised protocol for transferring high-molecular mass proteins from Tris-Acetate gels (P3, 10 min). Nitrocellulose was then washed briefly, and then blocked for 30 min in 0.5% w/w BSA/non-fat dried milk (Marvel) in Tris buffered saline/0.05% Tween-20 (TBST). After three brief washes in TBST, membranes were incubated in antibody diluted in blocking buffer (0.5% milk/BSA) overnight at 4 °C. The following day, membranes were washed for 5 min three times (in TBST) and then incubated with 1:10,000 HRP-conjugated secondary antibody (Sigma-Aldrich) for 30 min. Four more 10-min washes were then performed before performing chemiluminescence detection using Immobilon Western Chemiluminescent HRP Substrate (Millipore). To check protein loading was even in the gels, they were stained with Coomassie SimplyBlue (Life Technologies). The following antibodies were used:

Antigen	Manufacturer	Catalogue Number	Dilution used
Bmal1	Santa Cruz	sc-48790	1:2,000
MLL3	Abcam	ab71200	1:1,000
β-actin	Santa Cruz	sc-47778	1:5,000

Bioluminescence reporter vectors

Promoter regions from mouse *Bmal1* and *Per2* (8, 12) were amplified by PCR, or digested directly from the parent vector for *Cry1* (1, 3), and subcloned into the pGL4.20 vector (Promega) between the *Kpn*I and *Hind*III restriction enzyme sites. For *Rev-erbα* (*Nr1d1*), a 1,003 bp fragment (mouse chromosome 11:98636454-98637456, mm9 annotation) was amplified by PCR from BAC clone RP23-395E10 and then cloned into pGL4.20 using restriction-free cloning (4, 6). Clones were sequence-verified to confirm correct insert sequences. The following primers were used for cloning PCRs:

Gene Promoter	Forward Primer	Reverse Primer
Bmal1	`CGGCGGGTACCGAGGGATGGGCGAAGAGATG`	`CGGCGAAGCTTGATCCCGCGGCGGCGGCGGCA`
mPer2	`CGGCGGGTACCGCCCGAAGTGGACGAGCCTA`	`CGGCGAAGCTTAGCCGCTAGTCCCAGTAGCG`
Rev-erbα	`GCCAAGCTTGGCAATCCGGTACTGTTGGTAAAGCCACCTGCCAATTCGGGGAGTTGAGGGGT`	`TGGCGCTGGGCCCTTCTTAATGTTTTTGGCATCTTCCATGCAACCAGGAAGTAAGTAGGTGATGGA`

Cell culture & bioluminescence assays

Mouse embryonic fibroblasts (MEFs) were cultured in Dulbecco's modified Eagle medium (DMEM) containing 4.5 g l^{-1} glucose, 10% (v/v) fetal bovine serum (FBS), 1X Glutamax-I (Invitrogen 35050-038), 100 U penicillin/ml and 100 μg ml^{-1} streptomycin (Penicillin – Streptomycin Solution, Sigma P0781-100ML). Cells were cultured at 37°C, 5% CO$_2$ in a standard humidified incubator. To create stable luciferase reporter lines, 1 μg of each vector was transfected using GeneJuice® Transfection Reagent (Novagen Cat# 70967-3) and then cells selected for approx. 2 weeks with Puromycin-supplemented medium (final concentration of 2 μg ml^{-1}) in 35 mm diameter cell culture dishes.

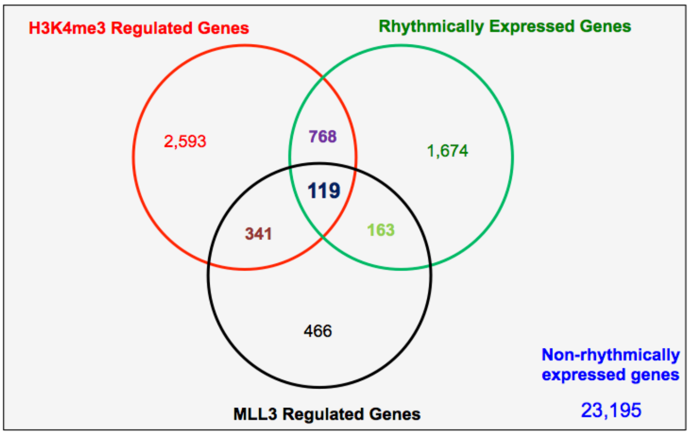
Bioluminescence assays were performed at 37^{o}C using 96-well plate reader (Berthold CentroLIA LB 960), with an integration time of 56 secs / well, every 90 mins, using a standard protocol (7, 9). Briefly, cells were seeded into white 96-well plates and allowed to grow until fully confluent in supplemented medium (as above), before being synchronised with a dexamethasone shock, at a final concentration of 100 nM for 15 minutes at 37^{o}C (7, 10). After this, cells were incubated in ‘air medium’ supplemented with luciferin substrate and puromycin for data collection (2, 7, 9, 13). Bioluminescence data traces were analysed with BRASS software (http://millar.bio.ed.ac.uk/PEBrown/BRASS/BrassPage.htm).

Statistical analysis

Parametric statistics (1-way and 2-way ANOVA) and χ^2 tests were performed using Graphpad Prism v5 software.

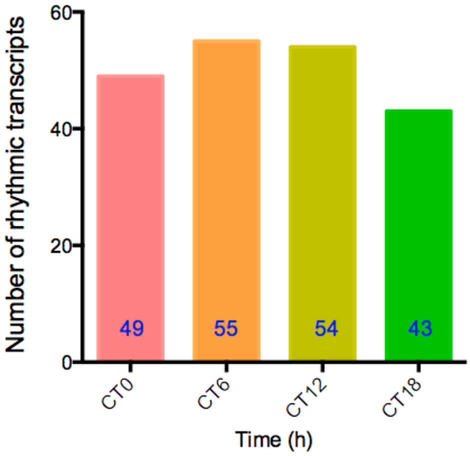
Supplementary Figures

a

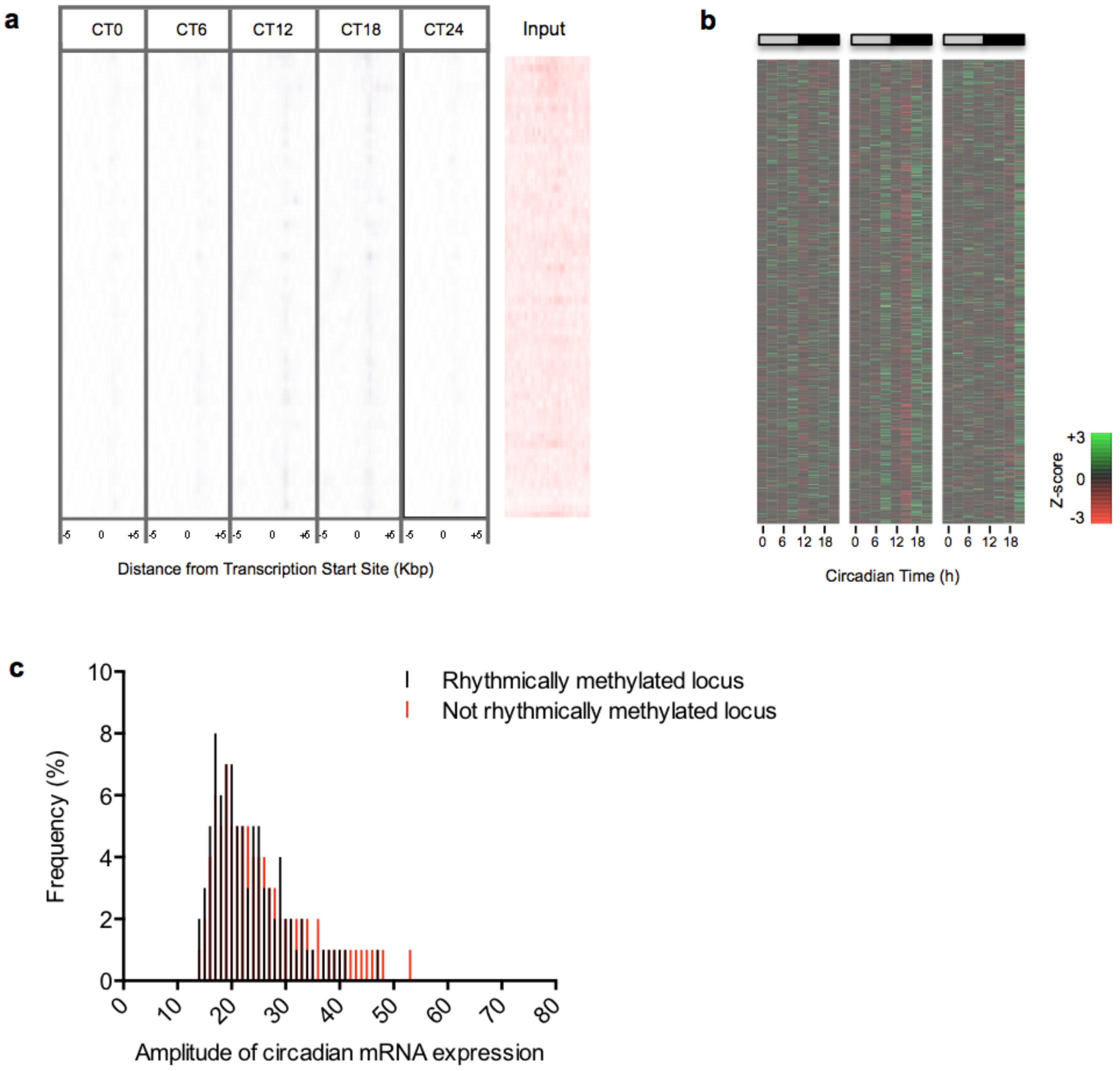


Percentage of total H3K4me sites that are rhythmic = (2593+768+119+341)/(23195+2593+768+119+341+1837) = **13.2%**

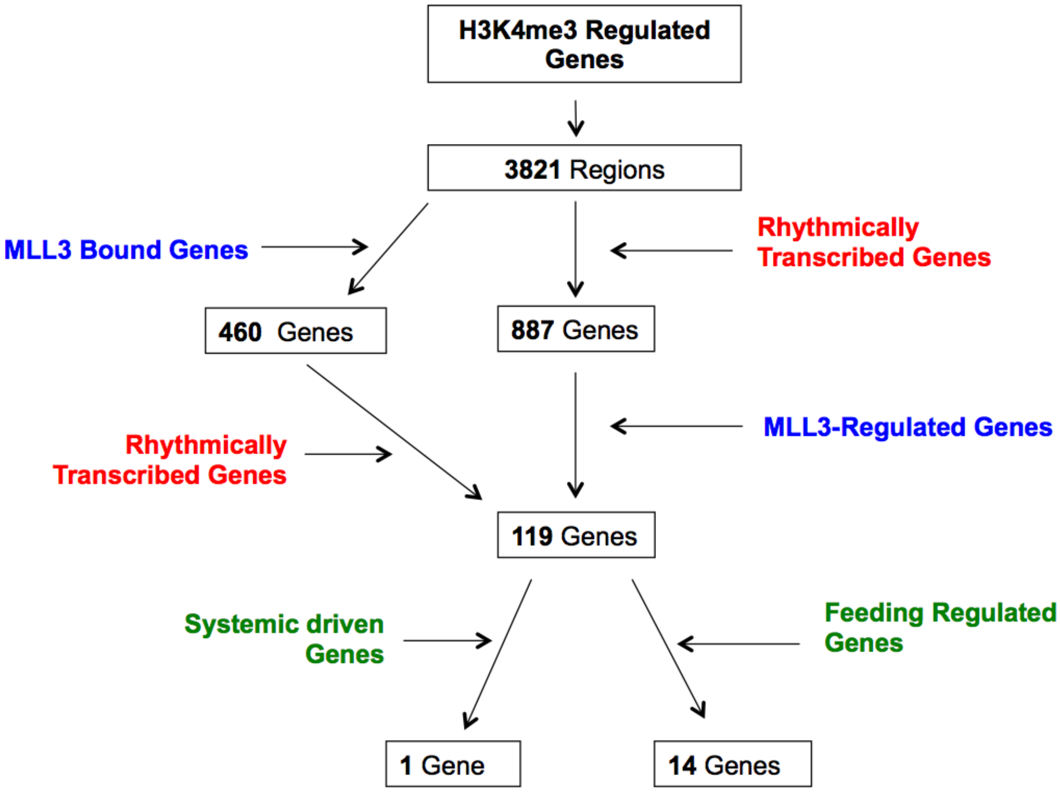
b



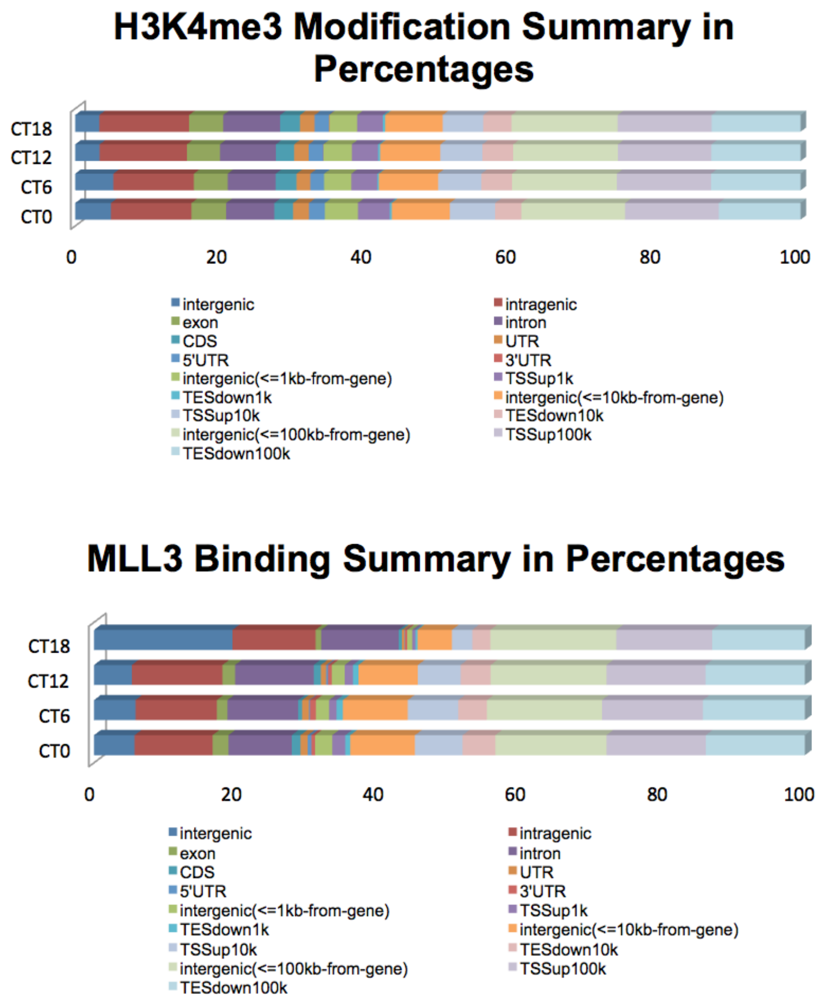
Supplementary Figure S1 **a,** Comparison of loci that exhibit rhythmic histone methylation with circadian transcripts. Venn Diagram showing the number of rhythmically bound H3K4me3 genomic loci and overlap with transcripts that exhibit circadian oscillation in liver tissue, and those bound by MLL3. **b**, Phase distribution of rhythmic transcripts. The numbers of transcripts peaking at each time-point is shown at the base of the respective column.



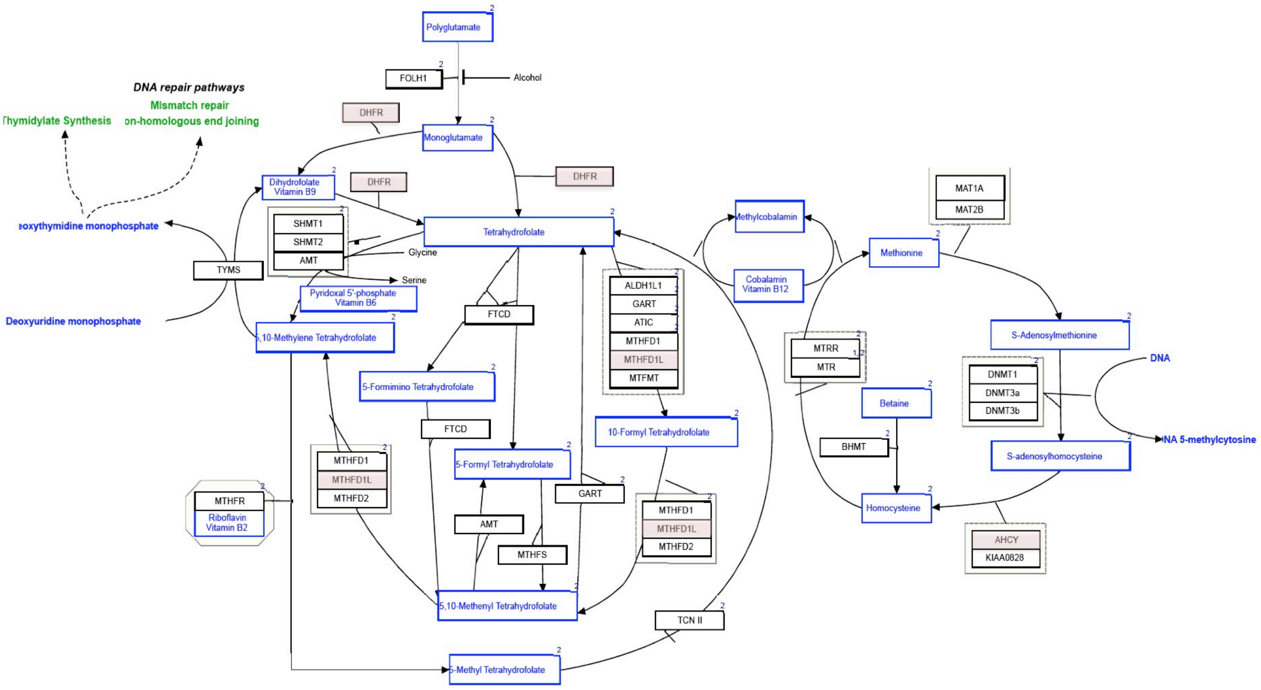
Supplementary Figure S2 Non-rhythmic H3K4me3 sites correlate with non-rhythmic gene expression and no difference in amplitude distributions for rhythmically-methylated loci. a, Heat map of H3K4me3 binding signal at CT0-18 (with CT0 re-plotted as CT24) from –5 kb to +5 kb surrounding the centre of all the binding sites. Each line represents a single H3K4me3 binding region. The cluster of loci (*n*=900) shown did not show significant H3K4me3 binding peaks at any of the time-points. CT, Circadian Time (animals maintained in constant darkness, with subjective dawn represented by CT0, and dusk represented by CT12). The Input (non-enriched) DNA signal is shown for comparison. **b,** Heat map of the respective genes shown in **a**. Normalized expression is shown for three independent biological replicate sets of liver, sampled every 3 hours in constant conditions. Light grey bars indicate circadian daytime; black bars signify circadian night. **c,** Comparison of amplitudes of circadian mRNAs in the liver that were associated with rhythmic H3K4 trimethylation or not. Amplitudes showed a similar distribution in both cases, as illustrated.



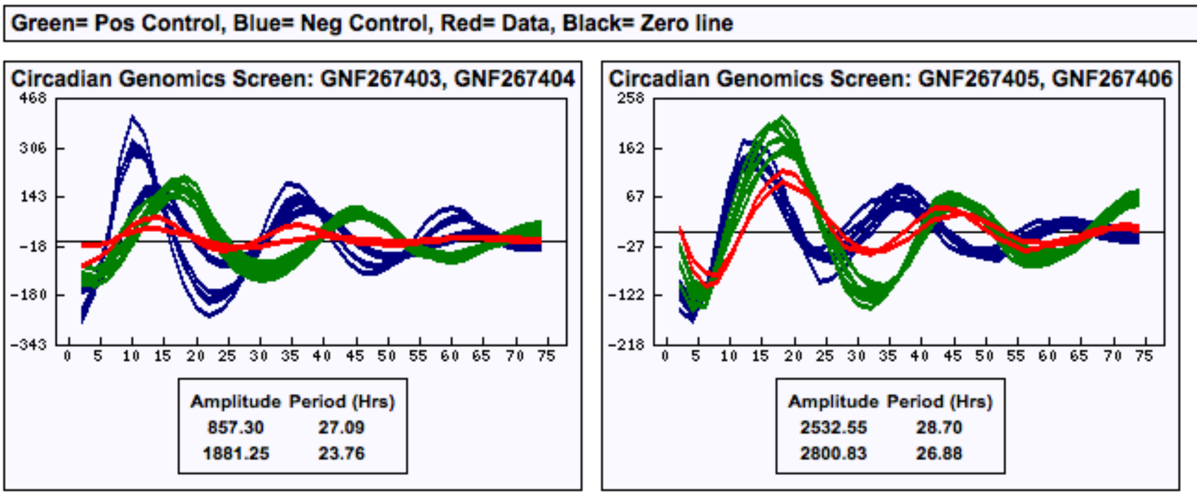
Supplementary Figure S3 Categorisation of H3K4me3 binding sites in relation to MLL3 binding sites across the genome. The flow chart shows a series of filtering steps to focus on MLL3-regulated, rhythmic transcripts. Cross-correlation with systemic-driven (5, 14) and feeding-regulated genes (8, 15) are shown (see main text for further details).



Supplementary Figure S4 Genomic distribution of H3K4me3 and MLL3 binding sites. Localization of binding sites relative to the annotated gene is shown. CT, Circadian Time (animals maintained in constant darkness, with subjective dawn represented by CT0, and dusk represented by CT12). Data are presented as percentages of all binding sites for H3K4me3 or MLL3 at each time-point.



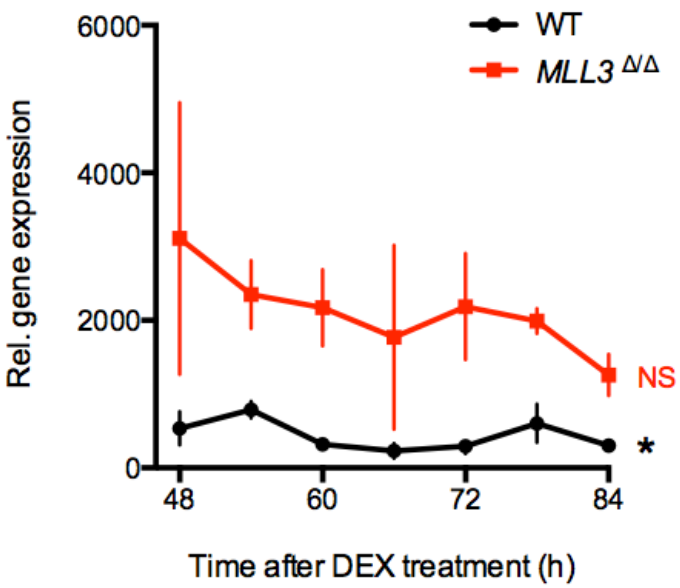
Supplementary Figure S5 Multiple steps in one-carbon metabolism are under circadian regulation through MLL3. Dihydrofolate reductase (DHFR), *S*-adenosylhomocysteine hydrolase (AHCY) and Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (MTHFD1L) are highlighted with red shading. The human one-carbon pathway was redrawn from Wikipathways. (http://wikipathways.org/index.php/Pathway:WP241)



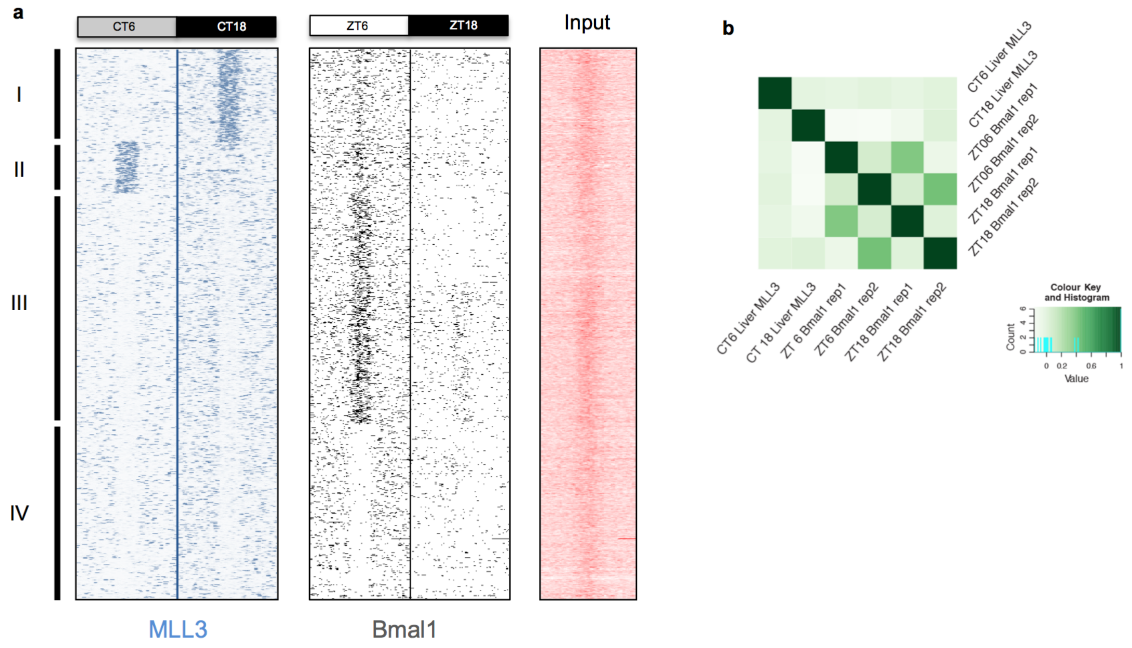
Amplitude	Period (Hrs)
857.30	27.09
1881.25	23.76

Amplitude	Period (Hrs)
2532.55	28.70
2800.83	26.88

Supplementary Figure S6 Knockdown of MLL3 affects the transcriptional clockwork in a human cell line. Circadian rhythms of *Bmal1::luciferase* reporter expression in human U2OS cells are affected by siRNAs specifically directed against *MLL3* (red line). Data were obtained from BioGPS, http://biogps.org/ (1, 13). Data for a negative control (scrambled siRNA, blue line) and a positive control (*mCry2* siRNA, green line) are also shown for comparison. Circadian parameters are shown below each profile.



Supplementary Figure S7 Gene expression of *MLL3* in mouse embryonic fibroblasts (MEFs). Following synchronisation with dexamethasone (DEX), wild type (WT) or methyltransferase-deficient (*MLL3*$^{\Delta/\Delta}$) MEFs were harvested and assayed by quantitative real-time PCR using primers specific for mature *MLL3* mRNA. Data are mean ± s.e.m. for three biological replicates per time-point. Two-way ANOVA revealed a significant genotype effect ($P < 0.001$). For each respective genotype, there was a clear time effect for wild type (WT) MEFs ($P < 0.05$), which was not seen in *MLL3*$^{\Delta/\Delta}$ MEFs (NS = not significant) when assessed by one-way ANOVA.



Supplementary Figure S8 Bmal1 and MLL3 binding at transcription start sites do not correlate well. **a,** Heat maps showing MLL3 and Bmal1 binding signal at hundreds of promoter regions, from –5 kb to +5 kb surrounding the centre of transcription start sites of genes. Each line represents the same genomic locus. CT, Circadian Time (animals maintained in constant darkness, with subjective dawn represented by CT0, and dusk represented by CT12). For CT samples, animals were kept in constant darkness; light grey bars indicate subjective daytime and black bars signify subjective night. ZT, Zeitgeber Time (animals maintained in 12h:12h light:dark cycles, with lights on represented by ZT0, and lights off by ZT12). For ZT samples, white bars indicate daytime (animals were in the light); black bars signify night (animals were in darkness). The Input (non-enriched) DNA signal is shown for comparison. Cluster I: MLL3 binding enriched at CT18; Cluster II: MLL3 binding sites enriched at CT6; Cluster III: Bmal1 binding enriched at ZT6; Cluster IV: No MLL3 or Bmal1 binding (negative control regions). **b,** Heat map representing clustering of MLL3 binding events compared to those of Bmal1. For each of the differentially bound sites, the RPKM-fold (RPKM of ChIP divided by RPKM of control) was calculated for each sample, and a Pearson correlation value for each sample pair computed using DiffBind (4, 16). The Heat map shows the correlation scores. RPKM, Reads Per Kilobase per Million mapped reads. Bmal1 binding signals were re-analyzed using data from Rey et al. 2011 (7, 11).

Supplementary Table Legends

Supplementary Table S1
Annotated list of *n*=887 genomic loci that exhibit circadian variation in H3K4me3 binding and also generate rhythmic transcripts in mouse liver.

Supplementary Table S2
Circwave Batch v3.3 harmonic regression analysis of microarray gene expression profiling data for *n*=3 biological replicates over the circadian cycle. We transcriptionally profiled the *n*=887 genomic loci that exhibit circadian variation in H3K4me3 binding and also generate rhythmic transcripts (see Supplementary Table S1) using a different microarray platform (Affymetrix Mouse Gene 1.0 ST Array) to that initially used to characterise these genes' circadian profiles (Affymetrix Mouse Genome 430 2.0 Array).

Supplementary Table S3
Annotated list of *n*=460 genomic loci that exhibit circadian variation in H3K4me3 and MLL3 binding, and also generate rhythmic transcripts in mouse liver.

Supplementary Table S4
Annotated list of *n*=119 genomic loci that exhibit circadian variation in H3K4me3 binding, are regulated by MLL3 methyltransferase activity, and also generate rhythmic transcripts in mouse liver.

Supplementary Table S5
Functional analysis of MLL3-regulated circadian loci (see Supplementary Table S4 for list). Genes are listed by functional category or by the relevant pathway that they fall into. Analysis was performed using DAVID (2, 7, 17).

Supplementary Table S6
List of genes driven by systemic cues, derived from Kornmann et al. 2007 (5, 11, 14). Gaps in the table arise because the genes listed are not annotated in the latest mouse genome annotation used to map their loci (mouse genome version NCBI37/mm9, July 2007). MLL3-regulated genes are highlighted in bold red lettering.

Supplementary Table S7
List of genes driven by feeding cues, derived from Vollmers et al. 2009 (8, 12, 15). Gaps in the table arise because the genes listed are not annotated in the latest mouse genome annotation used to map their loci (mouse genome version NCBI37/mm9, July 2007). MLL3-regulated genes are highlighted in bold red lettering.

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16. Ross-Innes CS et al. (2012) Differential oestrogen receptor binding is associated with clinical outcome in breast cancer. *Nature*:1–6.

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Table S1	Gene symbol	Refseq ID	Chromosome	Start Position	End Position	Strand	Genbank ID	Gene Description
1	0610007C21Rik	NM_027855|N	chr5	31350844	31356996	+	AB009018	RIKEN cDNA 0610007C21 gene
2	0610010F05Rik	NM_027860	chr11	23440495	23533621	-	BC079876	RIKEN cDNA 0610010F05 gene
3	0610038F07Rik	NM_025333	chr19	10576130	10599699	-	BC085277	RIKEN cDNA 0610038F07 gene
4	0910001L09Rik	NM_00108110	chr5	138696959	138700612	+	BC056178	RIKEN cDNA 0910001L09 gene
5	1110008P14Rik		chr2	32232617	32237404	-	BC024615|B	RIKEN cDNA 1110008P14 gene
6	1110020P15Rik	NM_197979	chr11	4601971	4604347	-	BC087874	RIKEN cDNA 1110020P15 gene
7	1110034B05Rik	NR_004860|N	chr1	57445088	57463529	-	BC058590	RIKEN cDNA 1110034B05 gene
8	1110038D17Rik		chr10	74969028	74980125	-	BC024851|B	RIKEN cDNA 1110038D17 gene
9	1600002H07Rik		chr17	24351999	24357714	-	BC072612|B	RIKEN cDNA 1600002H07 gene
10	1600014C10Rik	NM_00108538	chr7	38968305	38982587	+	BC085480	RIKEN cDNA 1600014C10 gene
11	1700017B05Rik	NM_028820	chr9	57100129	57110406	+		
12	1700023B02Rik|Sp	NM_025854	chr2	73121929	73150624	-	BC099444	RIKEN cDNA 1700023B02 gene | trans-acting transcription factor 9
13	1700123O20Rik		chr14	55305053	55309581	+	BC011283|AB	RIKEN cDNA 1700123O20 gene
14	1810013L24Rik		chr16	8830194	8856289	+	BC116778|B	RIKEN cDNA 1810013L24 gene
15	1810063B05Rik		chr8	128946415	128949334	+	BC038634|B	RIKEN cDNA 1810063B05 gene
16	2010209O12Rik	NM_133913	chr5	24092559	24098305	+	AK122504	RIKEN cDNA 2010209O12 gene
17	2010305A19Rik	NM_027250	chr4	108000757	108013323	+	BC012391	RIKEN cDNA 2010305A19 gene
18	2310016E02Rik	NM_024460	chr5	31208258	31210098	-	BC002177	RIKEN cDNA 2310016E02 gene
19	2310035C23Rik	NM_173187|N	chr1	107560490	107651697	+	BC117949	RIKEN cDNA 2310035C23 gene
20	2310037I24Rik		chr15	98349239	98364669	-	BC125631|B	RIKEN cDNA 2310037I24 gene
21	2310047O13Rik	NM_024185	chr2	12268891	12341087	-	BC027202	RIKEN cDNA 2310047O13 gene
22	2410002O22Rik	NM_025879|N	chr13	104932234	104968519	-	BC021756	RIKEN cDNA 2410002O22 gene | hypothetical protein LOC100040518 | hypothetical protein LOC10004447
23	2510002D24Rik	NM_00103316	chr16	18836684	18840036	+		RIKEN cDNA 2510002D24 gene
24	2610101N10Rik	NM_00111497	chr9	95360821	95412415	-	BC068265	RIKEN cDNA 2610101N10 gene
25	2610507B11Rik	NM_00100200	chr11	78075258	78104127	+	BC075633	RIKEN cDNA 2610507B11 gene
26	2700038C09Rik	NM_025598	chr2	180922010	180923209	+	BC058516	RIKEN cDNA 2700038C09 gene
27	4833426J09Rik	NM_00102460	chr8	107115368	107120766	+	BC094946	RIKEN cDNA 4833426J09 gene
28	4833439L19Rik		chr13	54652584	54666722	-	BC033445	RIKEN cDNA 4833439L19 gene
29	4933403F05Rik	NM_153794	chr18	68426332	68459874	-	BC038695	RIKEN cDNA 4933403F05 gene
30	4933407H18Rik	NM_00108110	chr5	33721198	33760513	+		RIKEN cDNA 4933407H18 gene
31	5430407P10Rik	NM_144883	chr2	6018653	6051192	-	BC025867	RIKEN cDNA 5430407P10 gene
32	6330409N04Rik	NM_025697	chr14	62153142	62175723	-	BC037015	RIKEN cDNA 6330409N04 gene
33	9030612M13Rik	NM_172458	chr17	32908181	32924492	-	BC043671	RIKEN cDNA 9030612M13 gene
34	9130011J15Rik	NM_172396	chr8	75089097	75094948	-	BC055692	RIKEN cDNA 9130011J15 gene
35	9530058B02Rik		chr17	26000643	26005683	-	BC024332	RIKEN cDNA 9530058B02 gene
36	9530068E07Rik	NM_153117	chr11	52209930	52222225	+	BC034829	RIKEN cDNA 9530068E07 gene
37	A230067G21Rik	NM_00103334	chr2	146086112	146337742	-	BC053994	RIKEN cDNA A230067G21 gene
38	A430005L14Rik		chr4	153331346	153336023	+	BC052148	RIKEN cDNA A430005L14 gene
39	A530082C11Rik	NM_177186	chr4	154975525	154997449	+	BC058728	RIKEN cDNA A530082C11 gene
40	Abat	NM_172961	chr16	8513582	8621661	+	BC058079	4-aminobutyrate aminotransferase
41	Abce1	NM_015751	chr8	82207341	82235639	-	BC005422	ATP-binding cassette, sub-family E (OABP), member 1
42	Abhd13	NM_00108111	chr8	9977864	9990221	+	BC043690	abhydrolase domain containing 13
43	Abhd6	NM_025341	chr14	8835416	8889069	+	BC027011	abhydrolase domain containing 6
44	Abi1	NM_00107719	chr2	22805705	22895585	-	AF420251	abl-interactor 1
45	Abtb1	NM_030251	chr6	88785910	88791894	-	AB053477	ankyrin repeat and BTB (POZ) domain containing 1
46	Abtb2	NM_178890	chr2	103406467	103558580	+	BC054399	ankyrin repeat and BTB (POZ) domain containing 2
47	Acad8	NM_025862	chr9	26781720	26807131	-	BC037644	acyl-Coenzyme A dehydrogenase family, member 8
48	Acly	NM_134037	chr11	100337670	100389215	-	BC056378	ATP citrate lyase
49	Acn9	NM_00107771	chr6	6906011	6991770	+	BC118927	ACN9 homolog (S. cerevisiae)
50	Acss2	NM_019811	chr2	155342695	155411460	+	BC051432	acyl-CoA synthetase short-chain family member 2
51	Actn1	NM_134156	chr12	81268532	81361303	-	BC054830	actinin, alpha 1
52	Acvr1b	NM_007395	chr15	101004556	101043032	+	BC059832	activin A receptor, type 1B
53	Add1	NM_00110244	chr5	34916461	34974957	+	AF096839	adducin 1 (alpha)
54	Adfp	NM_007408	chr4	86302469	86315963	-	M93275	adipose differentiation related protein
55	Adss	NM_007422	chr1	179693309	179726640	-	L24554	adenylosuccinate synthetase, non muscle
56	Aftph	NM_181411	chr11	20585087	20641502	-	BC052036	aftiphilin
57	Agl	NM_00108132	chr3	116445969	116510327	-	BC044780	amylo-1,6-glucosidase, 4-alpha-glucanotransferase
58	Agpat6	NM_018743	chr8	24283418	24318818	-	BC031767	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)
59	Ahcy	NM_016661	chr2	154885046	154900169	-	BC086781	S-adenosylhomocysteine hydrolase
60	Ahsa1	NM_146036	chr12	88607658	88614930	+	BC025552	AHA1, activator of heat shock protein ATPase homolog 1 (yeast)
61	AI597468		chr10	84565488	84583363	+	BC086492	
62	Aifm2	NM_00103919	chr10	61178036	61202008	+	BC038129	apoptosis-inducing factor, mitochondrion-associated 2
63	Ak2	NM_016895|N	chr4	128670509	128689056	+	BC008610	adenylate kinase 2
64	Ak3	NM_021299	chr19	29095322	29122445	-	BC058191	adenylate kinase 3
65	Akap9	NM_194462	chr5	3928178	4080204	+		A kinase (PRKA) anchor protein (yotiao) 9
66	Alas1	NM_020559	chr9	106136258	106150187	-	BC022110	aminolevulinic acid synthase 1
67	Alcam	NM_009655	chr16	52251003	52454187	-	BC027280	activated leukocyte cell adhesion molecule
68	Aldh1l1	NM_027406	chr6	90500812	90549165	+	BC030722	aldehyde dehydrogenase 1 family, member L1
69	Aldob	NM_144903	chr4	49548867	49562361	-	BC036132	aldolase 2, B isoform
70	Amd1|Amd2|Amd-p	NM_009665|N	chr10	40008969	40021992	-	BC092072	S-adenosylmethionine decarboxylase 1 | S-adenosylmethionine decarboxylase 2 | S-adenosylmethionine d
71	Angel2	NM_021421	chr1	192752424	192770372	+	BC024907	angel homolog 2 (Drosophila)
72	Ankhd1|Eif4ebp3	NM_175375	chr18	36753736	36818562	+	AK129284	ankyrin repeat and KH domain containing 1 | eukaryotic translation initiation factor 4E binding protein 3
73	Ankrd17	NM_030886|N	chr5	90656191	90795590	-	AF130371	ankyrin repeat domain 17
74	Ankrd56	NM_175270	chr5	93470197	93473977	-		ankyrin repeat domain 56
75	Ankzf1	NM_026187	chr1	75188709	75195962	+	BC071240	ankyrin repeat and zinc finger domain containing 1
76	Anp32a	NM_009672	chr9	62189235	62226609	+	BC062899	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
77	Anxa5	NM_009673	chr3	36347845	36374620	-	U29396	annexin A5
78	Anxa7	NM_009674|N	chr14	21274499	21299162	-	L13129	annexin A7
79	Ap3m1	NM_018829	chr14	21854032	21871649	-	BC010667	adaptor-related protein complex 3, mu 1 subunit
80	Aph1a|LOC100039	NM_146104	chr3	95697919	95702226	+	BC012406	anterior pharynx defective 1a homolog (C. elegans) | similar to Aph1a protein
81	Aqp11	NM_175105	chr7	104874889	104886757	-	AB028148	aquaporin 11
82	Arfgap1	NM_145760	chr2	180701970	180717165	+	BC052922	ADP-ribosylation factor GTPase activating protein 1
83	Arhgap12	NM_00103969	chr18	6024446	6136096	-	BC024633	Rho GTPase activating protein 12
84	Arl1	NM_025859	chr10	88194111	88206839	+	BC096684	ADP-ribosylation factor-like 1
85	Arl6ip4	NM_144509	chr5	124565815	124568205	+	AB035383	ADP-ribosylation factor-like 6 interacting protein 4
86	Armc1	NM_028840	chr3	19032144	19063065	-	BC021451	armadillo repeat containing 1
87	Arrdc3	NM_00104259	chr13	81022673	81035303	+	BC054844	arrestin domain containing 3
88	Asl	NM_133768	chr5	130487134	130500215	-	BC016670	argininosuccinate lyase
89	Atf2|LOC10004799	NM_00102509	chr2	73654566	73730685	-	BC079883	activating transcription factor 2 | similar to Cyclic AMP-dependent transcription factor ATF-2 (Activating trans
90	Atf4	NM_009716	chr15	80085614	80087971	+	BC085169	activating transcription factor 4
91	Atg3|D930048N14	NM_026402	chr16	45158942	45188651	+	BC010809|B	autophagy-related 3 (yeast) | RIKEN cDNA D930048N14 gene
92	Atp1a1	NM_144900	chr3	101380146	101408607	-	BC042435	ATPase, Na+/K+ transporting, alpha 1 polypeptide
93	Atp5h|LOC100039	NM_027862	chr11	115277011	115281233	-	BC081431	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d | ATP synthase, H+ transporting, mitoc
94	Atp6v0b	NM_033617	chr4	117556931	117559934	-	BC030393	ATPase, H+ transporting, lysosomal V0 subunit B
95	Atp6v1c1	NM_025494	chr15	38591688	38621953	+	AB088407	ATPase, H+ transporting, lysosomal V1 subunit C1
96	Atp6v1d	NM_023721	chr12	79943969	79962625	-	BC033457	ATPase, H+ transporting, lysosomal V1 subunit D
97	Atp6v1e1	NM_007510	chr6	120745262	120772719	-	BC003421	VATPase, H+ transporting, lysosomal V1 subunit E1
98	Atxn2l	NM_183020	chr7	133635222	133646816	-	BC054483	ataxin 2-like
99	B3galnt2	NM_178640	chr13	14046941	14091353	+	BC085110	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2
100	Bag4	NM_026121	chr8	26875008	26895681	-	AF332863	BCL2-associated athanogene 4
101	Baiap2	NM_130862|N	chr11	119804406	119868144	+	BC006620	brain-specific angiogenesis inhibitor 1-associated protein 2
102	Bat1a	NM_019693	chr17	35378759	35390628	+	BC024859	HLA-B-associated transcript 1A
103	BC013529	NM_145418	chr10	7487745	7500715	-	BC013529	
104	BC016495	NM_145497	chr19	18706506	18726681	+	BC016495	
105	BC048355	NM_207161	chr17	46633717	46636567	+	BC048355	
106	Bcar1	NM_009954	chr8	114234374	114267709	-	BC057578	breast cancer anti-estrogen resistance 1
107	Becn1	NM_019584	chr11	101147266	101163581	-	BC005770	beclin 1, autophagy related
108	Bet1	NM_009748	chr6	4026904	4036927	-	BC005572	blocked early in transport 1 homolog (S. cerevisiae)
109	Blcap	NM_016916	chr2	157382098	157392097	-	BC083339	bladder cancer associated protein homolog (human)
110	Blvrb	NM_144923	chr7	28232997	28251494	+	BC006617	biliverdin reductase B (flavin reductase (NADPH))
111	Bmf	NM_138313	chr2	118354493	118375414	-	BC079650	Bcl2 modifying factor
112	Bnip3l	NM_009761	chr14	67604076	67627701	-	AY057069	BCL2/adenovirus E1B interacting protein 3-like
113	Brd4	NM_020508|N	chr17	32333219	32421054	-	AF461395	bromodomain containing 4
114	Brd8	NM_030147	chr18	34758269	34784464	-	BC025644	bromodomain containing 8
115	Brd9	NM_00102450	chr13	74075286	74098343	+	BC031484	bromodomain containing 9
116	Brp44l	NM_018819	chr12	112096436	112097144	-	BC103767	brain protein 44-like
117	Bsdc1	NM_133889	chr4	129138923	129165685	+	BC049111	BSD domain containing 1
118	Bst2	NM_198095	chr8	74057851	74061336	-	BC087949	bone marrow stromal cell antigen 2
119	Bzw1	NM_025824	chr1	58449971	58463397	+	BC028865	basic leucine zipper and W2 domains 1
120	C330023M02Rik		chr5	121847991	121890122	+	BC132172|B	RIKEN cDNA C330023M02 gene
121	C630028N24Rik	NM_177351	chr9	54765090	54795289	+	BC038618	RIKEN cDNA C630028N24 gene
122	C77080	NM_00103318	chr4	128896822	128925687	-	AK129382	
123	Cabc1	NM_023341	chr1	182095271	182126143	-	BC030937	chaperone, ABC1 activity of bc1 complex like (S. pombe)
124	Cacybp	NM_009786	chr1	162132500	162142908	-	BC025948	calcyclin binding protein
125	Calm1|Calm2|Calm	NM_009790	chr12	101437738	101448016	+	BC054805	calmodulin 1 | calmodulin 2 | calmodulin 3
126	Camk2g	NM_178597|N	chr14	21554097	21613310	-	AF395884	calcium/calmodulin-dependent protein kinase II gamma
127	Cars	NM_013742	chr7	150743133	150785961	-	BC054717	cysteinyl-tRNA synthetase
128	Cbfa2t2	NM_172860|N	chr2	154262229	154365092	+	BC145679	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human)
129	Cblb	NM_00103323	chr16	52033136	52208154	+		Casitas B-lineage lymphoma b
130	Cbs	NM_144855|N	chr17	31749585	31774110	-	BC013480	cystathionine beta-synthase
131	Cbx3	NM_007624	chr13	65995145	65995681	-	BC018354|B	chromobox homolog 3 (Drosophila HP1 gamma)
132	Ccbl2	NM_173763	chr3	142364039	142407874	+	AF363737	cysteine conjugate-beta lyase 2
133	Ccdc142|Mrpl53	NM_00108126	chr6	83051688	83059933	+	BC065995	coiled-coil domain containing 142 | mitochondrial ribosomal protein L53
134	Ccng2	NM_007635	chr5	93696283	93705251	+	BC060180	cyclin G2
135	Ccnh	NM_023243	chr13	85329042	85353328	+	AF287135	cyclin H
136	Cct7	NM_007638	chr6	85402067	85418466	+	BC008255	chaperonin subunit 7 (eta)
137	Cd2ap	NM_009847	chr17	42929900	43013338	-	AF077003	CD2-associated protein
138	Cd302	NM_025422	chr2	60090050	60122475	-	BC005501	CD302 antigen
139	Cd9	NM_007657	chr6	125410284	125444778	-	BC070474	CD9 antigen
140	Cdadc1	NM_027986	chr14	60178225	60216781	-	BC006901	cytidine and dCMP deaminase domain containing 1
141	Cdc37l1	NM_025950	chr19	29064857	29092061	+	BC031761	cell division cycle 37 homolog (S. cerevisiae)-like 1
142	Cdk6	NM_009873	chr5	3344312	3522225	+	AF132483	cyclin-dependent kinase 6
143	Cdk8	NM_153599	chr5	147043251	147114450	+	BC025046	cyclin-dependent kinase 8
144	Cebpb	NM_009883	chr2	167514415	167515918	+	M61007	CCAAT/enhancer binding protein (C/EBP), beta
145	Cebpd	NM_007679	chr16	15887379	15889638	+	X61800	CCAAT/enhancer binding protein (C/EBP), delta
146	Cgrrf1	NM_026832	chr14	47451906	47473873	+	BC037677	cell growth regulator with ring finger domain 1
147	Chchd1	NM_025366	chr14	21522270	21523647	+	BC092216	coiled-coil-helix-coiled-coil-helix domain containing 1
148	Chchd4	NM_133928	chr6	91414270	91423417	-	BC019405	coiled-coil-helix-coiled-coil-helix domain containing 4
149	Chd1	NM_007690	chr17	15841938	15907328	+	BC115822	chromodomain helicase DNA binding protein 1
150	Chid1	NM_026522	chr7	148679037	148725715	-	BC006876	chitinase domain containing 1
151	Chmp1a	NM_145606	chr8	125728164	125736759	-	BC036138	chromatin modifying protein 1A
152	Chmp2a	NM_026885	chr7	13617363	13620093	-	BC012230	chromatin modifying protein 2A
153	Chmp7	NM_134078	chr14	70116807	70132348	-	BC033365	CHMP family, member 7
154	Chordc1	NM_025844	chr9	18096711	18118445	+	BC018374	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1
155	Chpt1	NM_144807	chr10	87936058	87966670	-	AY445814	choline phosphotransferase 1
156	Churc1	NM_206534	chr12	77866560	77884167	+	BC076499	churchill domain containing 1
157	Cisd1	NM_134007	chr10	70793242	70807623	-	BC013522	CDGSH iron sulfur domain 1
158	Cisd2	NM_025902	chr3	135069376	135086397	-	BC058279|A	CDGSH iron sulfur domain 2
159	Cited2	NM_010828	chr10	17443052	17445462	+	BC057126	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
160	Cks2|LOC1000394	NM_025415	chr13	51740694	51746023	+	BC022647	CDC28 protein kinase regulatory subunit 2 | similar to Cyclin-dependent kinases regulatory subunit 2 (CKS-
161	Clec2d	NM_053109	chr6	129130633	129136552	+	AF321553	C-type lectin domain family 2, member d
162	Clint1	NM_00104552	chr11	45665466	45724125	+	AB093212	clathrin interactor 1
163	Clmn	NM_053155|N	chr12	106001324	106103286	-	AB059648	calmin

164	Cln8	NM_012000	chr8	14888536	14901720	+	BC021625	ceroid-lipofuscinosis, neuronal 8
165	Clpx	NM_011802|N	chr9	65142102	65178465	+	AF134983	caseinolytic peptidase X (E.coli)
166	Clta	NM_00108038	chr4	44025555	44045718	+	U91848	clathrin, light polypeptide (Lca)
167	Cltc	NM_0010039	chr11	86508153	86570994	-	BC079897	clathrin, heavy polypeptide (Hc)
168	Cmtm6	NM_026036	chr9	114640320	114658462	+	AY241868	CKLF-like MARVEL transmembrane domain containing 6
169	Cmtm8	NM_027294	chr9	114698463	114753270	-	AY243513	CKLF-like MARVEL transmembrane domain containing 8
170	Cnn3	NM_028044	chr3	121129458	121161123	+	BC055711	calponin 3, acidic
171	Cnot4	NM_016877	chr6	34972065	35083715	-	BC058778	CCR4-NOT transcription complex, subunit 4
172	Cobll1	NM_177025	chr2	64926408	65077460	-	AY308746	Cobl-like 1
173	Col18a1	NM_009929|N	chr10	76514924	76629246	-	BC064817	collagen, type XVIII, alpha 1
174	Commd7	NM_133850	chr2	153442669	153458475	-	BC092215	COMM domain containing 7
175	Cp	NM_0010426	chr3	19857054	19908792	+	BC062957	ceruloplasmin
176	Cpeb2	NM_175937	chr5	43625198	43677429	+	BC107349	cytoplasmic polyadenylation element binding protein 2
177	Cpeb3	NM_198300	chr19	37095781	37281952	-	AB093274	cytoplasmic polyadenylation element binding protein 3
178	Cpsf3	NM_018813	chr12	21292260	21320695	+	BC023297	cleavage and polyadenylation specificity factor 3
179	Cpt1a	NM_013495	chr19	3323320	3385733	+	BC046383	carnitine palmitoyltransferase 1a, liver
180	Crebbp	NM_0010254	chr16	4084048	4213404	-		CREB binding protein
181	Crebzf	NM_145151	chr7	97591535	97593285	+	AF408398	CREB/ATF bZIP transcription factor
182	Crem	NM_00111085	chr18	3266354	3327525	-	AY738721	cAMP responsive element modulator
183	Crip2	NM_024223	chr12	114378742	114383717	+	BC002096	cysteine rich protein 2
184	Crot	NM_023733	chr5	8966038	8997161	-	BC012308	carnitine O-octanoyltransferase
185	Cs	NM_026444	chr10	127774873	127799535	+	BC029754	citrate synthase
186	Csde1	NM_144901	chr3	102824533	102862106	+	BC062097	cold shock domain containing E1, RNA binding
187	Csnk1a1	NM_146087	chr18	61714987	61748428	+	BC019740	casein kinase 1, alpha 1
188	Csnk2a1|LOC1000	NM_007788	chr2	152052621	152107583	+	BC060742	casein kinase 2, alpha 1 polypeptide | similar to Casein kinase 2, alpha 1 polypeptide
189	Ctage5	NM_146034	chr12	60230733	60291163	+	BC026864	CTAGE family, member 5
190	Ctdsp1|LOC10004	NM_153088	chr1	74438173	74443859	+	AY028804	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1 | similar to golli-inte
191	Ctr9	NM_009431	chr7	118172519	118199891	+	L49502	
192	Ctsh	NM_007801	chr9	89949347	89970927	+	U06119	cathepsin H
193	Ctsl	NM_009984	chr13	64464522	64471614	-	BC068163	cathepsin L
194	Cttn	NM_007803	chr7	151621629	151656642	-	U03184	cortactin
195	Cugbp1	NM_017368|N	chr2	90780615	90857212	+	AF267535	CUG triplet repeat, RNA binding protein 1
196	Cul1	NM_012042	chr6	47404323	47476138	+	BC029260	cullin 1
197	Cul2	NM_029402	chr18	3383029	3436372	+	BC026779	cullin 2
198	Cxcl12	NM_0010124	chr6	117118581	117213445	+	D43804	chemokine (C-X-C motif) ligand 12
199	Cxxc5	NM_133687	chr18	35989472	36021347	+	BC089314	CXXC finger 5
200	Cycs	NM_007808	chr6	50512562	50516473	-		cytochrome c, somatic
201	Cyld	NM_173369	chr8	91220974	91272367	+	BC042438	cylindromatosis (turban tumor syndrome)
202	Cyp2u1		chr3	130994057	131006145	-		cytochrome P450, family 2, subfamily u, polypeptide 1
203	Cyp8b1	NM_010012	chr9	121823474	121825415	-	BC010973	cytochrome P450, family 8, subfamily b, polypeptide 1
204	D030074E01Rik	NM_029491	chr18	20975813	21054579	-	AK173085	RIKEN cDNA D030074E01 gene
205	D10Ertd322e	NM_026065	chr10	94943440	94964561	-	BC024337	DNA segment, Chr 10, ERATO Doi 322, expressed
206	D10Ertd641e	NM_025514	chr10	59450657	59465860	-	BC025117	DNA segment, Chr 10, ERATO Doi 641, expressed
207	D10Jhu81e|LOC10	NM_138601	chr10	77624812	77632513	-	BC013475	DNA segment, Chr 10, Johns Hopkins University 81 expressed | similar to es1 protein
208	D10Wsu102e		chr10	82822983	82831580	+	BC094241	DNA segment, Chr 10, Wayne State University 102, expressed
209	D15Ertd621e		chr15	58247037	58289295	+	BC070426|D	DNA segment, Chr 15, ERATO Doi 621, expressed
210	D16Ertd472e	NM_025967	chr16	78543775	78576892	-	BC019957	DNA segment, Chr 16, ERATO Doi 472, expressed
211	D17Wsu104e	NM_080837	chr17	56315964	56323343	-	AY038184	DNA segment, Chr 17, Wayne State University 104, expressed
212	D2hgdh	NM_178882	chr1	95721838	95814696	+	BC023277	D-2-hydroxyglutarate dehydrogenase
213	D4Ertd22e	NM_0010256	chr4	140668926	140695711	-	BC066992	DNA segment, Chr 4, ERATO Doi 22, expressed
214	Dad1|LOC100044	NM_010015|N	chr14	54855160	54873589	-	BC058116	defender against cell death 1 | hypothetical protein LOC100044173
215	Daxx	NM_007829	chr17	34046443	34052534	+	BC128373	Fas death domain-associated protein
216	Dazap1	NM_133188|N	chr10	79727819	79751153	+	BC049355	DAZ associated protein 1
217	Dazap2	NM_011873	chr15	100446072	100451192	+	AF085348	DAZ associated protein 2
218	Dbp	NM_016974	chr7	52960602	52965521	+	BC018323	D site albumin promoter binding protein
219	Dctn2	NM_027151	chr10	126703455	126718863	+	BC004613	dynactin 2
220	Dctn4	NM_026302	chr18	60685875	60718416	+	BC034725	dynactin 4
221	Dctn5	NM_021608	chr7	129276568	129292558	+	BC010834	dynactin 5
222	Dcun1d2	NM_0010245	chr8	13255963	13288126	-		DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)
223	Dcun1d4	NM_178896	chr5	73872294	73952029	+	BC108346	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)
224	Ddef2	NM_0010981	chr12	21117617	21276034	+	BC096022	development and differentiation enhancing factor 2
225	Ddit4	NM_029083	chr10	59412423	59414518	-	BC132645	DNA-damage-inducible transcript 4
226	Ddx17	NM_199080|N	chr15	79358126	79377171	-	BC096036	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
227	Ddx39	NM_197982	chr8	86239098	86247247	+	BC020134	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
228	Ddx42	NM_028074	chr11	106078240	106110453	+	BC043036	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42
229	Ddx46	NM_145975	chr13	55736412	55780492	+	BC092240	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46
230	Ddx6	NM_00111082	chr9	44412981	44445274	+	BC021452	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
231	Deb1	NM_026794	chr9	121619504	121622506	+	BC027548	differentially expressed in B16F10 1
232	Dedd	NM_011615	chr1	173261384	173271749	+	BC023668	death effector domain-containing
233	Depdc6	NM_0010379	chr15	54943879	55085757	+		DEP domain containing 6
234	Dhdh	NM_027903	chr7	52728933	52744166	-	BC116414	dihydrodiol dehydrogenase (dimeric)
235	Dhfr	NM_010049	chr13	93124738	93159008	+	BC005796	dihydrofolate reductase
236	Dhrs3	NM_011303	chr4	144482730	144518112	+	BC010972	dehydrogenase/reductase (SDR family) member 3
237	Dhx36	NM_028136	chr3	62274005	62310910	-	AF448804	DEAH (Asp-Glu-Ala-His) box polypeptide 36
238	Dhx9	NM_007842	chr1	155302943	155334772	-	U91922	DEAH (Asp-Glu-Ala-His) box polypeptide 9
239	Dlat	NM_145614	chr9	50442740	50467885	-	BC031495	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)
240	Dmap1	NM_023178	chr4	117347286	117354858	-	AF438610	DNA methyltransferase 1-associated protein 1
241	Dnaja1	NM_008298	chr4	40669566	40681997	+	AF055664	DnaJ (Hsp40) homolog, subfamily A, member 1
242	Dnaja2	NM_019794	chr8	88061539	88079243	-	AB028853	DnaJ (Hsp40) homolog, subfamily A, member 2
243	Dnajb1	NM_018808	chr8	86132092	86135802	+	AB028272	DnaJ (Hsp40) homolog, subfamily B, member 1
244	Dnajb6	NM_0010379	chr5	30062480	30113018	+		DnaJ (Hsp40) homolog, subfamily B, member 6
245	Dnmt3b	NM_0010039	chr2	153475190	153555633	+	AY078427	DNA methyltransferase 3B
246	Dock4	NM_172803	chr12	41172640	41573082	+		dedicator of cytokinesis 4
247	Dpp9	NM_172624	chr17	56326105	56358311	-	BC057631	dipeptidylpeptidase 9
248	Dvl1	NM_010091	chr4	155221521	155233412	+	U10115	dishevelled, dsh homolog 1 (Drosophila)
249	Dym	NM_027727	chr18	75178420	75446622	+	BC038276	dymeclin
250	Dynll2	NM_026556	chr11	87793027	87801007	-	BC040822	dynein light chain LC8-type 2
251	Ece2	NM_025462|N	chr16	20611674	20619080	+	BC115542	endothelin converting enzyme 2
252	Edem1	NM_138677	chr6	108778646	108809345	+	AB042828	ER degradation enhancer, mannosidase alpha-like 1
253	Efhd2	NM_025994	chr4	141414057	141430867	-	BC125303	EF hand domain containing 2
254	Efna1	NM_010107	chr3	89075657	89083563	-	BC002046	ephrin A1
255	Egln2	NM_053208	chr7	27943677	27951792	-	AF453879	EGL nine homolog 2 (C. elegans)
256	Eif1a	NM_010120	chr18	46757358	46769862	+	AF026481	eukaryotic translation initiation factor 1A
257	Eif1ad	NM_027236	chr19	5366813	5371511	+	BC024640	eukaryotic translation initiation factor 1A domain containing
258	Eif3j	NM_144545	chr2	121854419	121877831	+	BC080788	eukaryotic translation initiation factor 3, subunit J
259	Eif4a1	NM_144958	chr1	60760761	60762537	+	X03040|AK1	eukaryotic translation initiation factor 4A1
260	Eif4a2	NM_013506|N	chr16	23107829	23114020	+	BC094422	eukaryotic translation initiation factor 4A2
261	Eif4b	NM_145625	chr15	101904361	101927604	+	BC007171	eukaryotic translation initiation factor 4B
262	Eif4e	NM_007917	chr3	138189155	138220563	+	BC085087	eukaryotic translation initiation factor 4E
263	Eif4ebp1	NM_007918	chr8	28370831	28387140	+	U28656	eukaryotic translation initiation factor 4E binding protein 1
264	Eif4ebp2	NM_010124	chr10	60895228	60915521	-	BC015082	eukaryotic translation initiation factor 4E binding protein 2
265	Eif5|LOC10004765	NM_173363|N	chr12	112776416	112784959	+	BC039275	eukaryotic translation initiation factor 5 | similar to Eukaryotic translation initiation factor 5
266	Elf1	NM_007920	chr14	79881001	79982283	+	U19617	E74-like factor 1
267	Elk4	NM_007923	chr1	133904453	133929182	+	BC004798	ELK4, member of ETS oncogene family
268	Elovl5	NM_134255	chr9	77765175	77832323	+	BC022911	ELOVL family member 5, elongation of long chain fatty acids (yeast)
269	Elovl6	NM_130450	chr3	129235304	129341413	+	AY053453	ELOVL family member 6, elongation of long chain fatty acids (yeast)
270	Elp4	NM_023876	chr2	105540266	105744657	-		elongation protein 4 homolog (S. cerevisiae)
271	Epm2aip1	NM_175266	chr9	111174345	111181593	+	BC018474	EPM2A (laforin) interacting protein 1
272	Erap1	NM_030711	chr13	74777321	74850794	+	AF227511	endoplasmic reticulum aminopeptidase 1
273	Erbb3	NM_010153	chr10	128005702	128026708	-	BC106091	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
274	Erf	NM_010155	chr7	26027573	26035684	-	BC063092	Ets2 repressor factor
275	Ergic1	NM_026170	chr17	26698457	26793881	+	BC005516	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1
276	Erh|LOC10004277	NM_007951	chr12	81735015	81744794	-	BC083141	enhancer of rudimentary homolog (Drosophila) | similar to human protein homologous to DROER protein
277	Erp29	NM_026129	chr5	121894760	121902483	-	BC017125|A	endoplasmic reticulum protein 29
278	Esrra	NM_007953	chr19	6985467	6996308	-	U85259	estrogen related receptor, alpha
279	Etf1	NM_144866	chr18	35063573	35091607	-	BC013717	eukaryotic translation termination factor 1
280	Etfdh	NM_025794	chr3	79407723	79432642	-	BC057670	electron transferring flavoprotein, dehydrogenase
281	Ethe1	NM_023154	chr7	25372562	25393944	+	BC094044	ethylmalonic encephalopathy 1
282	Etnk2|LOC100044	NM_175443	chr1	135260341	135275956	+	BC152310	ethanolamine kinase 2 | hypothetical protein LOC100044148
283	Ewsr1	NM_007968	chr11	4969691	4999080	-	BC068226	Ewing sarcoma breakpoint region 1
284	Exoc4	NM_009148	chr6	33199124	33922943	+	BC034644	exocyst complex component 4
285	Exosc2	NM_144886	chr2	31526235	31536840	+	BC021807	exosome component 2
286	Extl2	NM_021388	chr3	115710395	115731878	+	AF200973	exostoses (multiple)-like 2
287	F2r	NM_010169	chr13	96371744	96388429	-	BC031516	coagulation factor II (thrombin) receptor
288	Fads2	NM_019699	chr19	10137270	10257902	-	AF126798	fatty acid desaturase 2
289	Fahd1	NM_023480	chr17	24972079	24987247	-	BC026949	fumarylacetoacetate hydrolase domain containing 1
290	Faim	NM_00112285	chr9	98886792	98902438	+	BC079662	Fas apoptotic inhibitory molecule
291	Farsb	NM_011811	chr1	78414533	78485472	-	AF123263	phenylalanyl-tRNA synthetase, beta subunit
292	Fbxl20	NM_028149	chr11	97943868	98010930	-	EF649694	F-box and leucine-rich repeat protein 20
293	Fbxl3	NM_015822	chr14	103479456	103498735	-	BC067203	F-box and leucine-rich repeat protein 3
294	Fbxo3	NM_212433|N	chr2	103867956	103903394	+	BC058253	F-box protein 3
295	Fbxo33	NM_0010331	chr12	60301643	60320466	-		F-box protein 33
296	Fbxw9	NM_026791	chr8	87584027	87591020	+	BC053694	F-box and WD-40 domain protein 9
297	Fdps	NM_134469	chr3	88897510	88905867	-	BC048497	farnesyl diphosphate synthetase
298	Fdx1	NM_007996	chr9	51751412	51771659	-	L29123	ferredoxin 1
299	Fech	NM_007998	chr18	64616202	64648720	-	BC006746	ferrochelatase
300	Fgd6	NM_053072	chr10	93498746	93608083	+		FYVE, RhoGEF and PH domain containing 6
301	Fis1	NM_025562	chr5	137437956	137442104	+	BC010783	fission 1 (mitochondrial outer membrane) homolog (yeast)
302	Fkbp4	NM_010219	chr6	128379556	128388674	-	BC003447	FK506 binding protein 4
303	Flcn	NM_146018	chr11	59604910	59623275	-	BC025820	folliculin
304	Flnb	NM_134080	chr14	8650666	8784099	+		filamin, beta
305	Flot1	NM_008027	chr17	35960292	35969732	+	BC004647	flotillin 1
306	Fndc3a	NM_207636	chr14	72937758	73109810	-	DQ192036	fibronectin type III domain containing 3a
307	Fnip1	NM_173753	chr11	54251691	54331738	+	BC079892	folliculin interacting protein 1
308	Frg1	NM_013522	chr8	42482812	42502428	-	U62105	FSHD region gene 1
309	Fusip1	NM_0010803	chr13	20086890	20087672	-	BC083082	FUS interacting protein (serine-arginine rich) 1
310	Fzd4	NM_008055	chr7	96552876	96558595	+	BC015256	frizzled homolog 4 (Drosophila)
311	G3bp2	NM_011816|N	chr5	92481189	92512731	-	AF145285	GTPase activating protein (SH3 domain) binding protein 2
312	Gab1	NM_021356	chr8	83288330	83404378	-	BC007483	growth factor receptor bound protein 2-associated protein 1
313	Gabarap	NM_019749	chr11	69804866	69808453	+	BC024621	gamma-aminobutyric acid receptor associated protein
314	Gabarapl1	NM_020590	chr6	129483183	129492349	+	AF180518	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1
315	Gadd45a	NM_007836	chr6	66985090	66987401	-	BC011141	growth arrest and DNA-damage-inducible 45 alpha
316	Galt	NM_016658	chr4	41702376	41705555	+	BC010985	galactose-1-phosphate uridyl transferase
317	Gas2l3	NM_0010333	chr10	88874272	88906721	-		growth arrest-specific 2 like 3
318	Gbf1	NM_178930	chr19	46227048	46361000	+	BC076569	golgi-specific brefeldin A-resistance factor 1
319	Gcap14	NM_027045|N	chr14	37688122	37781950	-	BC048641	granule cell antiserum positive 14
320	Gch1	NM_008102	chr14	47773570	47809081	-	BC005643	GTP cyclohydrolase 1
321	Gclm	NM_008129	chr3	121948510	121969566	+	U95053	glutamate-cysteine ligase , modifier subunit
322	Gcnt2	NM_023887|N	chr13	40955137	41056267	+	BC094572	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme
323	Ggnbp2	NM_153144	chr11	84646231	84684240	-	AB064543	gametogenetin binding protein 2
324	Glo1	NM_025374|N	chr17	30729806	30749560	-	BC024663	glyoxalase 1
325	Glrx3	NM_023140	chr7	144629331	144660277	+	BC087885	glutaredoxin 3
326	Glrx5	NM_028419	chr12	106270879	106280438	+	BC058371	glutaredoxin 5 homolog (S. cerevisiae)
327	Gna13	NM_010303	chr11	109224108	109262683	+	M63660	guanine nucleotide binding protein, alpha 13

328	Gnaq	NM_008139	chr19	16207321	16461943	+	BC057583	guanine nucleotide binding protein, alpha q polypeptide
329	Gne	NM_015828	chr4	44049698	44097038	-	BC015277	glucosamine
330	Gnl2	NM_145552	chr4	124707282	124732616	+	BC003262	guanine nucleotide binding protein-like 2 (nucleolar)
331	Gnpda1	NM_011937	chr18	38487204	38498605	-	AF160355	glucosamine-6-phosphate deaminase 1
332	Golga5	NM_013747	chr12	103707345	103736117	+	BC016883	golgi autoantigen, golgin subfamily a, 5
333	Golim4	NM_175193	chr3	75680105	75760871	-	BC089354	golgi integral membrane protein 4
334	Gprc5c	NM_00111033	chr11	114731933	114733674	+	BC005757	G protein-coupled receptor, family C, group 5, member C
335	Gprin3	NM_183183	chr6	59298190	59376288	-	AK173336	GPRIN family member 3
336	Grk5	NM_018869	chr19	60966243	61168245	+	AF040746	G protein-coupled receptor kinase 5
337	Gsk3a	NM_00103166	chr7	26013278	26022870	-		glycogen synthase kinase 3 alpha
338	Gss	NM_008180	chr2	155388917	155418448	-	U35456	glutathione synthetase
339	Gsta3	NM_00107735	chr1	21230670	21255640	+	M73483	glutathione S-transferase, alpha 3
340	Gstz1	NM_010363	chr12	88488668	88505673	+	BC031777	glutathione transferase zeta 1 (maleylacetoacetate isomerase)
341	Gtf2f1	NM_133801	chr17	57142825	57150841	-	BC031123	general transcription factor IIF, polypeptide 1
342	Gtf3c2|Mpv17	NM_027901	chr5	31458378	31482517	-	BC043100	general transcription factor IIIC, polypeptide 2, beta | Mpv17 transgene, kidney disease mutant
343	H3f3b|LOC100045	NM_008211	chr11	115883226	115885818	-	BC021768	H3 histone, family 3B | similar to H3 histone, family 3A
344	Hars2	NM_080636	chr18	36942934	36952223	+	BC004596	histidyl-tRNA synthetase 2, mitochondrial (putative)
345	Hectd3	NM_175244	chr4	116667953	116677882	+	BC070411	HECT domain containing 3
346	Herpud1	NM_022331	chr8	96910400	96919259	+	BC013523	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
347	Hes6	NM_019479	chr1	93308059	93309799	-	AF260236	hairy and enhancer of split 6 (Drosophila)
348	Hexim1	NM_138753	chr11	102977639	102981039	+	AY090614	hexamethylene bis-acetamide inducible 1
349	Hfe	NM_010424	chr13	23793908	23802680	-	U66849	hemochromatosis
350	Hipk3	NM_010434	chr2	104269913	104334401	-	AF077660	homeodomain interacting protein kinase 3
351	Hist1h1c	NM_015786	chr13	23830676	23832236	+	BC089604|AK	histone cluster 1, H1c
352	Hist2h2aa1|Hist1h2	NM_013549|N	chr3	96049420	96050038	+	BC089519|BC	histone cluster 2, H2aa1 | histone cluster 1, H2an | histone cluster 2, H2aa2 | histone cluster 2, H2ac | histo
353	Hmbs	NM_013551|N	chr9	44144344	44152261	-	BC003861	hydroxymethylbilane synthase
354	Hmg20b	NM_010440	chr10	80808796	80813163	-	BC071217	high mobility group 20 B
355	Hn1l|ENSMUSG00	NM_029288	chr14	7242025	7245512	-	EF651808|CT	hematological and neurological expressed 1-like | predicted gene, ENSMUSG00000068790 | predicted gen
356	Hnrnpa1|EG43485	NM_00103912	chr15	103070848	103075388	+	BC089340	heterogeneous nuclear ribonucleoprotein A1 | predicted gene, EG434858 | heterogeneous nuclear ribonucl
357	Hnrnpc	NM_016884	chr14	52693226	52723679	-	AF095257	heterogeneous nuclear ribonucleoprotein C
358	Hnrnpu	NM_016805	chr1	180258699	180267916	-	BC018353	heterogeneous nuclear ribonucleoprotein U
359	Hras1	NM_008284	chr7	148375006	148379893	-	BC050837	Harvey rat sarcoma virus oncogene 1
360	Hsd17b12	NM_019657	chr2	93872854	93998066	-	BC090659	hydroxysteroid (17-beta) dehydrogenase 12
361	Hsp90aa1	NM_010480	chr11	77106957	77109931	+	BC094024	heat shock protein 90, alpha (cytosolic), class A member 1
362	Hspa2	NM_00100201	chr12	77505163	77507925	+	BC052350	heat shock protein 2
363	Hspa4	NM_008300	chr11	53073316	53113981	-	BC003770	heat shock protein 4
364	Hspa4l	NM_011020	chr3	40549418	40594373	+	BC110662	heat shock protein 4 like
365	Htatip2	NM_016865	chr7	57014523	57029370	+	BC004083	HIV-1 tat interactive protein 2, homolog (human)
366	Idh3a	NM_029573	chr9	54434285	54452469	+	BC034273	isocitrate dehydrogenase 3 (NAD+) alpha
367	Ifnar2	NM_010509|N	chr16	91373144	91405834	+	AF013274	interferon (alpha and beta) receptor 2
368	Ifrd1	NM_013562	chr12	40928154	40949772	-	BC043723	interferon-related developmental regulator 1
369	Igf1	NM_010512|N	chr10	87321813	87394870	+	BC012409	insulin-like growth factor 1
370	Il15ra	NM_008358|N	chr2	11627070	11655621	+	BC022705	interleukin 15 receptor, alpha chain
371	Il1rap	NM_008364|N	chr16	26581794	26725350	+	BC021159	interleukin 1 receptor accessory protein
372	Il6ra	NM_010559	chr3	89673246	89717084	-		interleukin 6 receptor, alpha
373	Ing2	NM_023503	chr8	48752532	48760512	-	BC096433	inhibitor of growth family, member 2
374	Ing4	NM_133345	chr6	124989861	124999283	+	BC009127	inhibitor of growth family, member 4
375	Inmt	NM_009349	chr6	55120620	55125032	-	BC013518	indolethylamine N-methyltransferase
376	Insig2	NM_133748|N	chr1	123200930	123229157	-	BC023067	insulin induced gene 2
377	Insr	NM_010568	chr8	3153235	3154602	-		insulin receptor
378	Ints10	NM_027590	chr8	71317853	71353307	+	BC031923	integrator complex subunit 10
379	Itpa	NM_025922	chr2	130493543	130507350	+	BC094466	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)
380	Ivns1abp	NM_054102|N	chr1	153191628	153211575	+	DQ914523	influenza virus NS1A binding protein
381	Iws1	NM_173441	chr18	32227393	32258102	+	BC068184	IWS1 homolog (S. cerevisiae)
382	Jph1	NM_020604	chr1	16987445	17087970	-	AB024445	junctophilin 1
383	Junb	NM_008416	chr8	87500809	87502647	-	BC092302	Jun-B oncogene
384	Kcnk5	NM_021542	chr14	20959279	21001006	-	BC034012	potassium channel, subfamily K, member 5
385	Kctd3	NM_172650	chr1	190794974	190831719	-	BC061458	potassium channel tetramerisation domain containing 3
386	Keap1	NM_016679|N	chr9	21034175	21043776	-	AB020063	kelch-like ECH-associated protein 1
387	Kif1b	NM_207682|N	chr4	148550428	148681807	-	AF131865	kinesin family member 1B
388	Klf1	NM_010635	chr8	87425827	87429190	+	M97200	Kruppel-like factor 1 (erythroid)
389	Klf12	NM_010636	chr14	100269851	100549015	-	BC067408	Kruppel-like factor 12
390	Klf13	NM_021366	chr7	71036253	71083801	-	AF251796	Kruppel-like factor 13
391	Klf6	NM_011803	chr13	5860735	5869639	+	BC020042	Kruppel-like factor 6
392	Klf9|2310051E17R	NM_010638	chr19	23215716	23241401	+	Y14296	Kruppel-like factor 9 | RIKEN cDNA 2310051E17 gene
393	Klhl17	NM_145671	chr4	155604075	155608889	-		
394	Klhl21	NM_00103335	chr4	151383000	151391786	+		kelch-like 21 (Drosophila)
395	Kpnb1	NM_008379	chr11	97021024	97049206	-	BC055115	karyopherin (importin) beta 1
396	L2hgdh	NM_145443	chr12	70786736	70825805	-	BC016226	L-2-hydroxyglutarate dehydrogenase
397	l7Rn6	NM_026304	chr7	97067199	97089695	-	DQ196315	lethal, Chr 7, Rinchik 6
398	Lars2	NM_153168	chr9	123276058	123371784	+	AJ428066	leucyl-tRNA synthetase, mitochondrial
399	Lasp1	NM_010688	chr11	97660986	97700078	+	BC010840	LIM and SH3 protein 1
400	Lcp1	NM_008879	chr14	75536232	75630615	+	BC022943	lymphocyte cytosolic protein 1
401	Leprot	NM_175036	chr4	101320388	101331969	+	BC010289	leptin receptor overlapping transcript
402	Lias	NM_024471	chr5	65782736	65801662	+	BC002141	lipoic acid synthetase
403	Lig3	NM_010716	chr11	82594637	82617776	+	BC083500	ligase III, DNA, ATP-dependent
404	Lin52|EG629959	NM_173756	chr11	104434861	104435211	+	BC120496	lin-52 homolog (C. elegans) | predicted gene, EG629959
405	Lin54	NM_00111501	chr5	100871060	100929658	-	AK220225	lin-54 homolog (C. elegans)
406	Litaf	NM_019980	chr16	10958952	10993400	-	BC018559	LPS-induced TN factor
407	Lonp2	NM_025827	chr8	89148006	89240535	+	BC049090	lon peptidase 2, peroxisomal
408	Lpgat1	NM_172266	chr1	193541902	193603856	+	AK172914	lysophosphatidylglycerol acyltransferase 1
409	Lpin1	NM_172950|N	chr12	16542763	16617772	-	AF180471	lipin 1
410	Lpp	NM_178665	chr16	24393576	24981130	+	BC085321	LIM domain containing preferred translocation partner in lipoma
411	Lrrc28	NM_175124	chr7	74658296	74790117	-	BC086694	leucine rich repeat containing 28
412	Lsm14b	NM_177727	chr2	179759692	179770166	+	BC099395	LSM14 homolog B (SCD6, S. cerevisiae)
413	Ltbr	NM_010736	chr6	125256594	125263872	-	U29173	lymphotoxin B receptor
414	Luc7l2	NM_138680	chr6	38501465	38559444	+	AF318301	LUC7-like 2 (S. cerevisiae)
415	Lyrm4	NM_201358	chr13	36070666	36209226	-	BC034664	LYR motif containing 4
416	Mad2l2	NM_027985	chr4	147505029	147519805	+	BC011282	MAD2 mitotic arrest deficient-like 2 (yeast)
417	Mafb	NM_010658	chr2	160189497	160192738	-	BC038256	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)
418	Mak10	NM_030153	chr13	59686772	59736159	+	BC056435	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)
419	Map2k3	NM_008928	chr11	60745557	60766309	+	BC007467	mitogen-activated protein kinase kinase 3
420	Map2k7	NM_00104255	chr8	4238828	4251420	+	BC070467	mitogen-activated protein kinase kinase 7
421	Map3k1	NM_011945	chr13	112536641	112599191	-	AF117340	mitogen-activated protein kinase kinase kinase 1
422	Map3k7ip2	NM_138667	chr10	7625917	7644660	-	BC004813	mitogen-activated protein kinase kinase kinase 7 interacting protein 2
423	Marcks	NM_008538	chr10	36853049	36858732	-	BC046601	myristoylated alanine rich protein kinase C substrate
424	Masp1	NM_008555	chr16	23449490	23520676	-	D16492	mannan-binding lectin serine peptidase 1
425	Mat2a	NM_145569	chr6	72382790	72389552	-	BC058360	methionine adenosyltransferase II, alpha
426	Mbtd1	NM_134012	chr11	93747531	93806635	+	BC064014	mbt domain containing 1
427	Mcart1	NM_00100994	chr4	45332949	45421633	-	BC089000	mitochondrial carrier triple repeat 1
428	Mcfd2	NM_176808|N	chr17	87653783	87665255	-	AF475283	multiple coagulation factor deficiency 2
429	Mcl1	NM_008562	chr3	95462710	95467106	+	BC021638	myeloid cell leukemia sequence 1
430	Mcm10	NM_027290	chr2	4911770	4933837	-	BC094576	minichromosome maintenance deficient 10 (S. cerevisiae)
431	Med28	NM_025895	chr5	45911491	45920523	+	BC024941	mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)
432	Med8	NM_020000|N	chr4	118081942	118088387	+	BC021870	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)
433	Mef2a	NM_00103371	chr7	74376970	74517744	-	BC096598	myocyte enhancer factor 2A
434	Metap2	NM_019648	chr10	93321234	93353947	-	AB003144	methionine aminopeptidase 2
435	Mfsd1	NM_025813	chr3	67386690	67408155	+	BC024891	major facilitator superfamily domain containing 1
436	Mgea5|E330018D0	NM_023799|N	chr19	45824749	45858269	-	AK129188	meningioma expressed antigen 5 (hyaluronidase) | RIKEN cDNA E330018D03 gene
437	Mgll	NM_011844	chr6	88674478	88778351	+	BC057965	monoglyceride lipase
438	Mitf	NM_00111319	chr6	97757178	97968701	+	BC108976	microphthalmia-associated transcription factor
439	Mkks	NM_021527	chr2	136699519	136717118	-	BC080765	McKusick-Kaufman syndrome protein
440	Mknk2	NM_021462	chr10	80128072	80138619	-	AB164081	MAP kinase-interacting serine/threonine kinase 2
441	Mkrn1	NM_018810	chr6	39347819	39370437	-	AF192785	makorin, ring finger protein, 1
442	Mll3	NM_00108138	chr5	24777616	25004520	-		myeloid/lymphoid or mixed-lineage leukemia 3
443	Mllt10	NM_010804	chr2	17976898	18134017	+	BC070475	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10
444	Mlx	NM_011550	chr11	100948624	100953521	+	BC038004	MAX-like protein X
445	Mn1	NM_00108123	chr5	111847186	111883811	+		meningioma 1
446	Mobkl1a	NM_026735	chr5	89149922	89187014	+	BC104403	MOB1, Mps One Binder kinase activator-like 1A (yeast)
447	Mobkl2b	NM_178061	chr4	34899953	35104715	-	BC020028	MOB1, Mps One Binder kinase activator-like 2B (yeast)
448	Mocos	NM_026779	chr18	24802897	24860072	+	BC113786	molybdenum cofactor sulfurase
449	Morf4l1	NM_00103914	chr9	89986507	90009600	-	AF319621	mortality factor 4 like 1
450	Mpdz	NM_010820	chr4	80925497	81088576	-	AF326528	multiple PDZ domain protein
451	Mpi	NM_025837	chr9	57392068	57400559	-	AF244360	mannose phosphate isomerase
452	Mrpl15	NM_025300	chr1	4763290	4775791	-	BC027233	mitochondrial ribosomal protein L15
453	Mrpl19	NM_026490	chr6	81907820	81915943	-	BC043921	mitochondrial ribosomal protein L19
454	Mrpl20	NM_025570	chr4	155177727	155184084	+	BC039985	mitochondrial ribosomal protein L20
455	Mrpl34	NM_053162	chr8	73988825	73989652	+	BC052086	mitochondrial ribosomal protein L34
456	Mrps22	NM_025485	chr9	98489149	98502078	-	BC051198	mitochondrial ribosomal protein S22
457	Mrps24	NM_026080	chr11	5603986	5607688	-	BC029262	mitochondrial ribosomal protein S24
458	Mrps25	NM_025578	chr6	92119506	92134017	-	BC022953	mitochondrial ribosomal protein S25
459	Mrps27	NM_173757	chr13	100114741	100185516	+	BC049149	mitochondrial ribosomal protein S27
460	Mrps9	NM_023514	chr1	42908128	42962528	+	BC116437	mitochondrial ribosomal protein S9
461	Mrto4	NM_023536	chr12	21831738	21832686	-	BC005734	MRT4, mRNA turnover 4, homolog (S. cerevisiae)
462	Msi2|LOC1000389	NM_054043	chr11	88152962	88579543	-	BC111809	Musashi homolog 2 (Drosophila) | similar to Musashi homolog 2 (Drosophila)
463	Mta3	NM_054082	chr17	84105539	84217859	+	AF288138	metastasis associated 3
464	Mterfd2	NM_178051	chr1	95195788	95202447	-	BC055877	MTERF domain containing 2
465	Mthfd1l	NM_172308	chr10	6190430	6373423	-	BC030437	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
466	Mtif2	NM_133767	chr11	29426457	29445279	+	BC066819	mitochondrial translational initiation factor 2
467	Mtmr10	NM_172742	chr7	71442454	71485160	+	BC055074	myotubularin related protein 10
468	Mtmr2	NM_023858	chr9	13552854	13610925	+	BC063050	myotubularin related protein 2
469	Mtpn	NM_008098	chr6	35458906	35489819	-	BC054811	myotrophin
470	Myo1b	NM_010863	chr1	51806609	51972796	-	BC054786	myosin IB
471	N6amt1	NM_026366	chr16	87354430	87368894	+	AY456393	N-6 adenine-specific DNA methyltransferase 1 (putative)
472	Nab1	NM_008667	chr1	52514720	52557292	-	BC016886	Ngfi-A binding protein 1
473	Naca	NM_00111319	chr10	127472629	127485693	+	U48364	nascent polypeptide-associated complex alpha polypeptide
474	Nadk	NM_138671	chr4	154936513	154965106	+	BC004012	NAD kinase
475	Nagk	NM_019542	chr6	83745038	83752550	+	BC004689	N-acetylglucosamine kinase
476	Narg2	NM_145618	chr9	69245782	69280885	+	BC068183	NMDA receptor-regulated gene 2
477	Nat13	NM_028108	chr16	44139922	44163479	+	BC057117	N-acetyltransferase 13
478	Nbr1	NM_008676	chr11	101413469	101443267	+	U73039	neighbor of Brca1 gene 1
479	Ncbp2	NM_026554	chr16	31948701	31958433	+	BC118926	nuclear cap binding protein subunit 2
480	Nck1	NM_010878	chr9	100395422	100446553	-	BC002015	non-catalytic region of tyrosine kinase adaptor protein 1
481	Ncl	NM_010880	chr1	88255651	88256536	+		nucleolin
482	Ncoa2	NM_008678|N	chr1	13131366	13364145	-	U39060	nuclear receptor coactivator 2
483	Ncor1	NM_011308	chr11	62130192	62271308	-	BC086657	nuclear receptor co-repressor 1
484	Ndufa9	NM_025358	chr6	126771973	126799143	-	BC058378	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9
485	Ndufb5	NM_025316	chr3	32635984	32650486	+	BC025155	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5
486	Ndufb6	NM_00103330	chr4	40217696	40226401	-		NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6
487	Ndufb9	NM_023172	chr15	58765365	58771044	+	BC031539	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9
488	Ndufc2|LOC67585	NM_024220	chr7	104548587	104556309	+	BC002097	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 | similar to NADH dehydrogenase (ubiquino
489	Ndufs8	NM_144870	chr19	3908867	3912735	-	BC086766	NADH dehydrogenase (ubiquinone) Fe-S protein 8
490	Nek4	NM_011849	chr14	31764672	31800635	+	BC057939	NIMA (never in mitosis gene a)-related expressed kinase 4
491	Nelf	NM_00103938	chr2	24909899	24918401	+	BC006642	nasal embryonic LHRH factor

492	Nfe2l2	NM_010902	chr2	75513573	75542720	-	BC026943	nuclear factor, erythroid derived 2, like 2
493	Nfix	NM_00108198	chr8	87232513	87324039	-	BC003766	nuclear factor I/X
494	Nfkbia	NM_010907	chr12	56590588	56593582	-	BC046754	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
495	Nfx1	NM_023739	chr4	40917976	40973025	+	AF223576	nuclear transcription factor, X-box binding 1
496	Ninj1	NM_013610	chr13	49282898	49291620	+	U91513	ninjurin 1
497	Nob1	NM_026277	chr8	109936386	109948941	-	BC103793	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)
498	Nr1d1|Thra	NM_145434	chr11	98629246	98636556	-	BC008989|B	nuclear receptor subfamily 1, group D, member 1 | thyroid hormone receptor alpha
499	Nr1d2	NM_011584	chr14	19036571	19071609	-	BC096461	nuclear receptor subfamily 1, group D, member 2
500	Nr3c2	NM_00108390	chr8	79432171	79766429	+	BC133713	nuclear receptor subfamily 3, group C, member 2
501	Nr6a1	NM_010264	chr2	38578890	38783208	-	AF390896	nuclear receptor subfamily 6, group A, member 1
502	Nras	NM_010937	chr3	102862152	102871837	+	BC051443	neuroblastoma ras oncogene
503	Nudt19	NM_033080	chr7	36332204	36340947	-	X04097	nudix (nucleoside diphosphate linked moiety X)-type motif 19
504	Nufip2	NM_00102420	chr11	77499657	77555294	+		nuclear fragile X mental retardation protein interacting protein 2
505	Nup133	NM_172288	chr8	126423200	126473165	-	BC026845	nucleoporin 133
506	Nup88	NM_172394|N	chr11	70756560	70783475	-	BC032929	nucleoporin 88
507	Oaz1	NM_008753	chr10	80289401	80292035	+	BC094287	ornithine decarboxylase antizyme 1
508	Odc1	NM_013614	chr12	17551778	17557890	+	BC083122	ornithine decarboxylase, structural 1
509	Ola1	NM_025942|N	chr2	72930858	73052504	-	BC011318	Obg-like ATPase 1
510	ORF19	NM_00103775	chr17	66460886	66469843	+	BC025839	open reading frame 19
511	Ormdl3	NM_025661	chr11	98442575	98451175	-	BC046594	ORM1-like 3 (S. cerevisiae)
512	Osgin1	NM_027950	chr8	121958932	121970156	+	BC022135	oxidative stress induced growth inhibitor 1
513	Ostf1	NM_017375	chr19	18655245	18706299	-	BC060986	osteoclast stimulating factor 1
514	Oxr1	NM_130885	chr15	41280573	41692594	+	BC098491	oxidation resistance 1
515	Oxsm	NM_027695	chr14	17071173	17082322	-	BC119793	3-oxoacyl-ACP synthase, mitochondrial
516	Pah	NM_008777	chr10	86984682	87046880	+	BC013458	phenylalanine hydroxylase
517	Paip1	NM_145457|N	chr13	120217729	120246198	+	BC051042	polyadenylate binding protein-interacting protein 1
518	Pan3	NM_028291	chr5	148242465	148364518	+	BC082547	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)
519	Pank1	NM_023792|N	chr19	34885384	34953945	-	AF200357	pantothenate kinase 1
520	Papd4	NM_133905	chr13	93917355	93962238	-	BC016629	PAP associated domain containing 4
521	Paqr9	NM_198414	chr9	95460236	95462540	+	AY424298	progestin and adipoQ receptor family member IX
522	Parp12	NM_172893	chr6	39036412	39068348	-	BC120733	poly (ADP-ribose) polymerase family, member 12
523	Parp14	NM_00103953	chr16	35832960	35871586	-	DQ372930	poly (ADP-ribose) polymerase family, member 14
524	Parp16	NM_177460	chr9	65043160	65087031	+	BC055447	poly (ADP-ribose) polymerase family, member 16
525	Pawr	NM_054056	chr10	107769245	107850810	+	DQ363525	PRKC, apoptosis, WT1, regulator
526	Pcmtd2	NM_153594	chr2	181572608	181592157	+	BC040385	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2
527	Pcsk4	NM_008793	chr10	79784028	79792218	-	D01093	proprotein convertase subtilisin/kexin type 4
528	Pdcd2	NM_008799	chr17	15658525	15664245	-	U10903	programmed cell death 2
529	Pdcl3	NM_026850	chr1	39044649	39054081	+	BC005601	phosducin-like 3
530	Pde9a	NM_008804	chr17	31523196	31613254	+	AF031147	phosphodiesterase 9A
531	Pdhx	NM_175094	chr2	102861234	102913668	-	BC061231	pyruvate dehydrogenase complex, component X
532	Pdia6	NM_027959	chr12	17273401	17291576	+	BC006865	protein disulfide isomerase associated 6
533	Pdk1	NM_172665	chr2	71711281	71740731	+	BC027196	pyruvate dehydrogenase kinase, isoenzyme 1
534	Pdk4	NM_013743	chr6	5433351	5446309	-	BC026134	pyruvate dehydrogenase kinase, isoenzyme 4
535	Pdrg1	NM_178939	chr2	152834626	152841119	-	BC031699	p53 and DNA damage regulated 1
536	Pdss2	NM_027772	chr10	42941323	43159763	+	AB210840	prenyl (solanesyl) diphosphate synthase, subunit 2
537	Pex11a	NM_011068	chr7	86882135	86887911	-	AF093669	peroxisomal biogenesis factor 11a
538	Pex16	NM_145122	chr2	92212261	92221440	+	BC010822	peroxisome biogenesis factor 16
539	Pex26	NM_028730	chr6	121133685	121148855	+	BC019144	peroxisome biogenesis factor 26
540	Pex6	NM_145488	chr17	46848412	46862490	+	BC003424	peroxisomal biogenesis factor 6
541	Pfdn2	NM_011070	chr1	173275830	173288301	+	BC049606	prefoldin 2
542	Pfkfb3	NM_133232	chr2	11393062	11423694	-	BC052400	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
543	Phf17	NM_172303	chr3	41359654	41420779	+	BC020316	PHD finger protein 17
544	Phldb2	NM_153412	chr16	45746356	45844491	-	BC050915|A	pleckstrin homology-like domain, family B, member 2
545	Pigl	NM_00103953	chr11	62271788	62327402	+	BC096678	phosphatidylinositol glycan anchor biosynthesis, class L
546	Pih1d1	NM_029406	chr7	52409724	52415435	+	BC068254	PIH1 domain containing 1
547	Pik3r1	NM_00107749	chr13	102450716	102538172	-	BC026146	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)
548	Pim1	NM_008842	chr17	29627757	29632429	+	BC042885	proviral integration site 1
549	Pim3	NM_145478	chr15	88692624	88696159	+	BC017621	proviral integration site 3
550	Pip5k1a	NM_008847	chr3	94862473	94910780	-	BC031774	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha
551	Pitpnb	NM_019640	chr5	111759783	111817379	+	BC034676	phosphatidylinositol transfer protein, beta
552	Pitpnc1	NM_145823	chr11	107069206	107332034	-	AB077281	phosphatidylinositol transfer protein, cytoplasmic 1
553	Pla2g12b	NM_023530	chr10	58866410	58884738	+	BC021592	phospholipase A2, group XIIB
554	Plcg1	NM_021280	chr2	160557046	160601496	+	BC065091	phospholipase C, gamma 1
555	Plekha3	NM_031256	chr2	76513352	76534630	+	BC031110	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3
556	Plxna2	NM_008882	chr1	196446023	196643063	+	D86949	plexin A2
557	Pnkd	NM_00103950	chr17	88368161	88368544	-	BC058945	paroxysmal nonkinesiogenic dyskinesia
558	Pnpla2	NM_025802	chr7	148641105	148646642	+	BC019188	patatin-like phospholipase domain containing 2
559	Pnrc2	NM_026383	chr4	135426844	135429742	-	BC006598	proline-rich nuclear receptor coactivator 2
560	Ppa1	NM_026438	chr10	61111369	61136916	+	BC010468	pyrophosphatase (inorganic) 1
561	Ppara	NM_011144|N	chr15	85566206	85633249	+	BC016892	peroxisome proliferator activated receptor alpha
562	Ppargc1b	NM_133249	chr18	61457790	61560085	-	AF453324	peroxisome proliferative activated receptor, gamma, coactivator 1 beta
563	Ppib	NM_011149	chr9	65907976	65914436	+	M60456	peptidylprolyl isomerase B
564	Ppm1k	NM_175523	chr6	57456496	57485420	-	BC092238	protein phosphatase 1K (PP2C domain containing)
565	Ppp1cc	NM_013636	chr5	122608288	122625278	+	BC021646	protein phosphatase 1, catalytic subunit, gamma isoform
566	Ppp1r14b	NM_008889	chr19	7049538	7051814	+	BC082545	protein phosphatase 1, regulatory (inhibitor) subunit 14B
567	Ppp1r3b	NM_177741	chr8	36438795	36451199	+	BC079666	protein phosphatase 1, regulatory (inhibitor) subunit 3B
568	Ppp2r1a	NM_016891	chr17	21082418	21102870	+	BC052678	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform
569	Ppp2r1b	NM_00103408	chr9	50665040	50702334	+	BC056218	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform
570	Ppp2r5a|LOC1000	NM_144880	chr1	193175860	193220920	-	BC059026	protein phosphatase 2, regulatory subunit B (B56), alpha isoform | similar to Protein phosphatase 2, regulat
571	Ppp3ca	NM_008913	chr3	136333734	136600350	+	J05479	protein phosphatase 3, catalytic subunit, alpha isoform
572	Ppp3cb	NM_008914	chr14	21319262	21365766	-	BC066000	protein phosphatase 3, catalytic subunit, beta isoform
573	Pqlc1	NM_025861	chr18	80450031	80489455	+	BC043686	PQ loop repeat containing 1
574	Pqlc2	NM_145384	chr4	138849945	138866600	-	BC019216	PQ loop repeat containing 2
575	Prdx6	NM_007453	chr1	163170243	163181297	-	AF093852	peroxiredoxin 6
576	Prei4	NM_028802|N	chr2	132354819	132403986	-	BC033408	preimplantation protein 4
577	Prkar1a	NM_021880	chr11	109511558	109530970	+	BC003461	protein kinase, cAMP dependent regulatory, type I, alpha
578	Prkci	NM_008857	chr3	30894669	30951660	+	AK220517	protein kinase C, iota
579	Prkrir	NM_028410	chr7	105851873	105866572	+	BC049103	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)
580	Prpf19	NM_134129	chr19	10962646	10980022	+	BC004070	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)
581	Prpf6	NM_133701	chr2	181336078	181390366	+	BC014869	PRP6 pre-mRNA splicing factor 6 homolog (yeast)
582	Prr14	NM_145589	chr7	134615128	134620272	+	BC055033	proline rich 14
583	Prr16	NM_00108122	chr18	51277392	51579698	+	BC132481	proline rich 16
584	Psmb10	NM_013640	chr8	108459639	108462015	-	U77784	proteasome (prosome, macropain) subunit, beta type 10
585	Psmd1	NM_027357	chr1	87961194	88035870	+		proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
586	Psmd13	NM_011875	chr7	148068293	148084541	+	AF107838	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13
587	Psmd2	NM_134101	chr10	30968078	30970684	+	BC028851	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2
588	Psmd4	NM_008951	chr3	94836619	94846467	-	AB029144	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
589	Psmd8	NM_026545	chr7	29959271	29965550	-	BC004075	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
590	Psmd9	NM_026000	chr5	123678255	123700140	+	BC051930	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9
591	Psme2	NM_011190|N	chr14	56206277	56209938	-	BC005680	proteasome (prosome, macropain) 28 subunit, beta
592	Pstpip2	NM_013831	chr18	78033042	78120553	+	CT010308	proline-serine-threonine phosphatase-interacting protein 2
593	Ptbp1	NM_00107736	chr10	79317350	79327178	+	BC007472	polypyrimidine tract binding protein 1
594	Ptcd2	NM_026873	chr13	100089604	100114642	-	BC025110	pentatricopeptide repeat domain 2
595	Ptcd3	NM_027275	chr6	71830628	71858756	-	BC115434	pentatricopeptide repeat domain 3
596	Ptplad1	NM_021345	chr9	64834790	64869520	-	BC031755	protein tyrosine phosphatase-like A domain containing 1
597	Ptpmt1	NM_025576	chr2	90750870	90758197	-	BC026750	protein tyrosine phosphatase, mitochondrial 1
598	Pxmp4	NM_021534	chr2	154412762	154429409	-	BC025796	peroxisomal membrane protein 4
599	Pycrl	NM_025412	chr15	75746904	75752064	-	BC026536	pyrroline-5-carboxylate reductase-like
600	Qars	NM_133794	chr9	108410390	108418268	+	BC079854	glutaminyl-tRNA synthetase
601	Rab11a	NM_017382	chr9	64563107	64585563	-	BC010722	RAB11a, member RAS oncogene family
602	Rab14	NM_026697	chr2	35035721	35056640	-	BC009085	RAB14, member RAS oncogene family
603	Rab17	NM_008998	chr1	92854710	92866197	-	BC051071	RAB17, member RAS oncogene family
604	Rab1b	NM_029576	chr19	5099205	5106996	-	BC016408	RAB1B, member RAS oncogene family
605	Rab3gap1	NM_178690	chr1	129765363	129840445	+	BC046297	RAB3 GTPase activating protein subunit 1
606	Rab43	NM_00103939	chr6	87738847	87761773	-	BC010248	RAB43, member RAS oncogene family
607	Rab5a	NM_025887	chr17	53618559	53647005	+	BC096481	RAB5A, member RAS oncogene family
608	Rabac1	NM_010261	chr7	25754767	25757747	-	AF252856	Rab acceptor 1 (prenylated)
609	Rabepk	NM_145522	chr2	34634186	34655311	-	BC019800	Rab9 effector protein with kelch motifs
610	Rabgap1	NM_146121|N	chr2	37298805	37422300	+	BC031714	RAB GTPase activating protein 1
611	Ranbp10	NM_145824	chr8	108291845	108351250	-	AY337314	RAN binding protein 10
612	Rapgef6	NM_175258	chr11	54336349	54512787	+	BC059847	Rap guanine nucleotide exchange factor (GEF) 6
613	Rassf3	NM_138956	chr10	120847406	120913361	-	BC011511	Ras association (RalGDS/AF-6) domain family member 3
614	Rb1cc1	NM_009826	chr1	6204743	6265656	+	AB070619	RB1-inducible coiled-coil 1
615	Rbbp5	NM_172517	chr1	134329764	134402236	+	BC057632	retinoblastoma binding protein 5
616	Rbbp7	NM_009031	chrX	159198365	159217022	+	BC003785	retinoblastoma binding protein 7
617	Rbks	NM_153196	chr5	31926399	32000000	-	BC023339	ribokinase
618	Rbm17	NM_152824	chr2	11507066	11524826	-	BC034896	RNA binding motif protein 17
619	Rbm25	NM_027349	chr12	84973210	85009462	+	BC010792	RNA binding motif protein 25
620	Rbm26	NM_134077	chr14	105513682	105576481	-	BC066051	RNA binding motif protein 26
621	Rbm43	NM_030243	chr2	51779968	51790683	-	BC003333	RNA binding motif protein 43
622	Rbm5	NM_148930	chr9	107642702	107673318	-	BC031899	RNA binding motif protein 5
623	Rbpj	NM_009035|N	chr5	53980824	54047374	+	BC051387	recombination signal binding protein for immunoglobulin kappa J region
624	Rbpms	NM_019733|N	chr8	34893116	35040313	-	BC030397	RNA binding protein gene with multiple splicing
625	Rcl1	NM_021525	chr19	29175865	29218419	+	BC004574	RNA terminal phosphate cyclase-like 1
626	Rell1	NM_145923	chr5	64300315	64360115	-	BC031198	RELT-like 1
627	Rfc5	NM_028128	chr5	117829154	117839042	-	BC089001	replication factor C (activator 1) 5
628	Rfk	NM_019437	chr19	17468573	17475839	+	BC051021	riboflavin kinase
629	Rfwd3	NM_146218	chr7	137487026	137497918	-	BC096602	ring finger and WD repeat domain 3
630	Rfxank	NM_011266|N	chr8	72654705	72663096	-	BC010971	regulatory factor X-associated ankyrin-containing protein
631	Rhbdd1	NM_029777|N	chr1	82313172	82441941	+	BC005518	rhomboid domain containing 1
632	Ric8	NM_053194	chr7	148043296	148049630	+	BC022917	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)
633	Riok2	NM_025934	chr17	17511536	17530935	+	BC010781	RIO kinase 2 (yeast)
634	Ripk1	NM_009068	chr13	34094310	34127039	+	BC054542	receptor (TNFRSF)-interacting serine-threonine kinase 1
635	Rlf	NM_00108101	chr4	120818963	120887666	-		rearranged L-myc fusion sequence
636	Rnaseh2a	NM_027187	chr8	87480509	87489984	-	BC029252	ribonuclease H2, large subunit
637	Rnaseh2b	NM_026001	chr14	62950941	62991829	+	BC047997	ribonuclease H2, subunit B
638	Rnd1	NM_172612	chr15	98499636	98507892	-	BC048531	Rho family GTPase 1
639	Rnf125	NM_026301	chr18	21103126	21142349	+	BC116883	ring finger protein 125
640	Rnf167	NM_027445	chr11	70460789	70465382	+	BC010777	ring finger protein 167
641	Rnf4	NM_011278	chr5	34679039	34696085	+	AF169300	ring finger protein 4
642	Rnf6	NM_028774	chr5	147020780	147033013	-	AY039004	ring finger protein (C3H2C3 type) 6
643	Rnps1	NM_00108012	chr6	7932358	7933386	-	AK182396	ribonucleic acid binding protein S1
644	Rock1	NM_009071	chr18	10067465	10181315	-	U58512	Rho-associated coiled-coil containing protein kinase 1
645	Rorc	NM_011281	chr3	94176708	94202510	+	U43508	RAR-related orphan receptor gamma
646	Rpa1	NM_026653	chr11	75113763	75161812	-	BC019119	replication protein A1
647	Rpia	NM_009075	chr6	70715695	70742169	-	L35034	ribose 5-phosphate isomerase A
648	Rpl13|LOC100039	NM_016738	chr14	59512343	59512966	+	BC055358	ribosomal protein L13 | similar to ribosomal protein L13
649	Rpl13a	NM_009438	chr7	52381146	52384107	-	BC065799	ribosomal protein L13a
650	Rpl22|mCG_13005	NM_009079	chr4	151699835	151708180	+	BC021344	ribosomal protein L22 | ribosomal protein L22 pseudogene
651	Rpn1	NM_133933	chr6	88034505	88055298	+	BC016080	ribophorin I
652	Rrm2	NM_009104	chr12	25393119	25398973	+	BC085136	ribonucleotide reductase M2
653	Rtn3	NM_00100393	chr19	7500391	7557779	-	AY750849	reticulon 3
654	Rwdd4a	NM_203507	chr8	48619046	48638179	+	BC016198	RWD domain containing 4A
655	Rxrb	NM_011306	chr17	34168797	34175344	+	BC049773	retinoid X receptor beta

656	Sar1b	NM_025535	chr11	51577189	51605428	+	BC085178	SAR1 gene homolog B (S. cerevisiae)
657	Sars	NM_011319	chr3	108227783	108248087	-	BC008612	seryl-aminoacyl-tRNA synthetase
658	Sbk1	NM_145587	chr7	133416133	133438530	+	BC031759	SH3-binding kinase 1
659	Scamp1	NM_029153	chr13	94971388	95055236	-	BC034283	secretory carrier membrane protein 1
660	Scap	NM_00100114	chr9	110235831	110287450	+	BC070437	SREBF chaperone
661	Scaper	NM_00108134	chr9	55398057	55767412	-		S phase cyclin A-associated protein in the ER
662	Scarb1	NM_016741	chr5	125757460	125824887	-	BC004656	scavenger receptor class B, member 1
663	Scyl3	NM_028776	chr1	165859921	165885257	+	BC043085	SCY1-like 3 (S. cerevisiae)
664	Sdc2	NM_008304	chr15	32850478	32964476	+	U00674	syndecan 2
665	Sdc4	NM_011521	chr2	164249747	164268688	-	D89571	syndecan 4
666	Sdhd	NM_025848	chr9	50404451	50411922	-	BC145731	succinate dehydrogenase complex, subunit D, integral membrane protein
667	Sec23a	NM_009147	chr12	60059371	60113004	-	BC034610	SEC23A (S. cerevisiae)
668	Seh1l	NM_00103908	chr18	67934468	67955141	+	BC027244	SEH1-like (S. cerevisiae
669	Senp5	NM_177103	chr16	31962592	32003257	-	BC080830	SUMO/sentrin specific peptidase 5
670	Sep-10	NM_00102491	chr10	58604375	58684595	-	BC053752	septin 10
671	Sepx1	NM_013759	chr17	24873587	24879723	+	BC090646	selenoprotein X 1
672	Serbp1	NM_025814|N	chr6	67216973	67235957	+	BC013665	Serpine1 mRNA binding protein 1
673	Serinc3	NM_012032	chr2	163449009	163470867	-	AB029499	serine incorporator 3
674	Serinc5	NM_172588	chr13	93381093	93499751	+	BC062131	serine incorporator 5
675	Serpinf2	NM_008878	chr11	75245238	75253005	-	BC026756	serine (or cysteine) peptidase inhibitor, clade F, member 2
676	Sf1	NM_00111079	chr19	6363943	6377196	+	BC009091	splicing factor 1
677	Sf3b1	NM_031179	chr1	55042013	55084323	-	AB037890	splicing factor 3b, subunit 1
678	Sfrs1|LOC1000485	NM_173374|N	chr11	87861173	87867259	+	BC046773	splicing factor, arginine/serine-rich 1 (ASF/SF2) | similar to splicing factor, arginine/serine-rich 1 (splicing fac
679	Sfrs11	NM_00109375	chr3	157673608	157699575	-	BC037053	splicing factor, arginine/serine-rich 11
680	Sfrs3	NM_013663	chr17	29169618	29180311	+	BC071196	splicing factor, arginine/serine-rich 3 (SRp20)
681	Sfrs5	NM_00107969	chr4	129576193	129577696	+	BC082593	splicing factor, arginine/serine-rich 5 (SRp40, HRS)
682	Sft2d1|LOC100038	NM_134114	chr11	45865317	45865796	-	BC091770	SFT2 domain containing 1 | hypothetical protein LOC100038858 | hypothetical protein LOC100044184
683	Sgpl1	NM_009163	chr10	60561390	60610347	-	BC026135	sphingosine phosphate lyase 1
684	Sh3glb1	NM_019464	chr3	144347972	144383287	-	AF272946	SH3-domain GRB2-like B1 (endophilin)
685	Sh3yl1	NM_013709	chr12	31596534	31645022	+	BC110043	Sh3 domain YSC-like 1
686	Shprh	NM_172937|N	chr10	10869257	10935067	+	AY162264	SNF2 histone linker PHD RING helicase
687	Sin3a	NM_011378|N	chr9	56924183	56976175	+	U22394	transcriptional regulator, SIN3A (yeast)
688	Slc10a1	NM_011387	chr12	82054172	82069692	-	AB003303	solute carrier family 10 (sodium/bile acid cotransporter family), member 1
689	Slc20a1	NM_015747	chr2	129024536	129037351	+	M73696	solute carrier family 20, member 1
690	Slc22a5	NM_011396	chr11	53678030	53705162	-	BC031118	solute carrier family 22 (organic cation transporter), member 5
691	Slc25a22	NM_026646	chr7	148615648	148623726	-	BC050887	solute carrier family 25 (mitochondrial carrier, glutamate), member 22
692	Slc25a40	NM_178766	chr5	8422838	8459978	+	BC083103	solute carrier family 25, member 40
693	Slc2a9	NM_00110241	chr5	38740545	38893391	-	AF469480	solute carrier family 2 (facilitated glucose transporter), member 9
694	Slc30a10	NM_00103328	chr1	187278727	187292641	+	BC054548	solute carrier family 30, member 10
695	Slc31a1	NM_175090	chr4	62021783	62052801	+	BC034674	solute carrier family 31, member 1
696	Slc35a3	NM_144902	chr3	116373716	116415198	-	BC024110	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3
697	Slc35b1	NM_016752	chr11	95246236	95252983	+	D87990	solute carrier family 35, member B1
698	Slc35c2	NM_144893	chr2	165102054	165113327	-	BC094025	solute carrier family 35, member C2
699	Slc37a4	NM_008063	chr9	44206259	44211051	+	BC075655	solute carrier family 37 (glucose-6-phosphate transporter), member 4
700	Slc46a3	NM_027872	chr5	148690017	148706391	-	BC006902	solute carrier family 46, member 3
701	Slc5a3	NM_017391	chr16	92077302	92079458	+		solute carrier family 5 (inositol transporters), member 3
702	Slc9a3r1	NM_012030	chr11	115024655	115042493	+	BC085141	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
703	Slmo2	NM_025531	chr2	174290592	174298442	-	BC026968	slowmo homolog 2 (Drosophila)
704	Smad3	NM_016769	chr9	63494574	63605801	-	BC066850	MAD homolog 3 (Drosophila)
705	Smarca2	NM_011416|N	chr19	26679650	26852811	+	BC075641	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
706	Smc4	NM_133786	chr3	68808894	68838551	+	BC061481	structural maintenance of chromosomes 4
707	Smek2	NM_134034	chr11	29072967	29119680	+	BC006870	SMEK homolog 2, suppressor of mek1 (Dictyostelium)
708	Sntb1	NM_016667	chr15	55470709	55738504	-	U89997	syntrophin, basic 1
709	Snw1	NM_025507	chr12	88790860	88809727	-	BC049245	SNW domain containing 1
710	Snx4	NM_080557	chr16	33251530	33300355	+	BC016599	sorting nexin 4
711	Snx5	NM_024225	chr2	144075862	144096607	-	BC002242	sorting nexin 5
712	Sp1	NM_013672	chr15	102236759	102263102	+	AF022363	trans-acting transcription factor 1
713	Sp4	NM_009239	chr12	119473406	119539843	-	BC076630	trans-acting transcription factor 4
714	Spag9	NM_027569|N	chr11	93857405	93987694	+	BC094670	sperm associated antigen 9
715	Spc25	NM_025565	chr2	69031952	69044214	-	BC033605	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)
716	Spnb2	NM_175836|N	chr11	29999722	30168144	-	M74773	spectrin beta 2
717	Spnb3	NM_021287	chr19	4711223	4752352	+	BC079860	spectrin beta 3
718	Spred2	NM_033523	chr11	19824375	19922600	+	BC066013	sprouty-related, EVH1 domain containing 2
719	Spry4	NM_011898	chr18	38745915	38761069	-	BC050944	sprouty homolog 4 (Drosophila)
720	Sqstm1	NM_011018	chr11	50013654	50024469	-	U57413	sequestosome 1
721	Sra1	NM_025291	chr18	36826900	36829952	-	BC048362	steroid receptor RNA activator 1
722	Srpk2	NM_009274	chr5	23009174	23182266	-	BC062941	serine/arginine-rich protein specific kinase 2
723	Srrm2	NM_175229	chr17	23940193	23961704	+	BC019803	serine/arginine repetitive matrix 2
724	St13	NM_133726	chr15	81195470	81230124	-	BC003843	suppression of tumorigenicity 13
725	St3gal1	NM_009177	chr15	66934437	67008444	-	BC099693	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
726	St3gal4	NM_009178	chr9	34854161	34924395	-	BC050773	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
727	Stam	NM_011484	chr2	13995739	14069965	+	BC044666	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1
728	Stard3nl	NM_024270	chr13	19449545	19487621	-	BC003334	STARD3 N-terminal like
729	Stard4	NM_133774	chr18	33361075	33373470	-	BC005642	StAR-related lipid transfer (START) domain containing 4
730	Stard7	NM_139308	chr2	127095975	127124676	+	BC017524	START domain containing 7
731	Stk24	NM_145465	chr14	121685563	121778455	-	AY188357	serine/threonine kinase 24 (STE20 homolog, yeast)
732	Stk4	NM_021420	chr2	163899888	163981260	+	BC054521	serine/threonine kinase 4
733	Strap	NM_011499	chr6	137683645	137699786	+	AF096285	serine/threonine kinase receptor associated protein
734	Stt3a	NM_008408	chr9	36538958	36575239	-	AK129027	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)
735	Stub1	NM_019719	chr17	25967579	25970306	-	BC027427	STIP1 homology and U-Box containing protein 1
736	Stx4a	NM_009294	chr7	134985322	134992497	+	BC005791	syntaxin 4A (placental)
737	Sub1	NM_011294	chr15	11911094	11925762	-	J03750	SUB1 homolog (S. cerevisiae)
738	Suds3	NM_178622|N	chr5	117541689	117565955	-	BC055764	suppressor of defective silencing 3 homolog (S. cerevisiae)
739	Sumo1	NM_009460	chr1	59696281	59727653	-	BC083158	SMT3 suppressor of mif two 3 homolog 1 (yeast)
740	Sumo3	NM_019929	chr10	77068979	77081076	+	AF063847	SMT3 suppressor of mif two 3 homolog 3 (yeast)
741	Taok1	NM_144825	chr11	77343551	77345076	-	BC019960	TAO kinase 1
742	Tardbp	NM_145556|N	chr4	147986491	148001105	-	BC025544	TAR DNA binding protein
743	Tars	NM_033074	chr15	11313418	11329413	-	BC055371	threonyl-tRNA synthetase
744	Tars2	NM_027931	chr3	95543897	95558785	-	BC008995	threonyl-tRNA synthetase 2, mitochondrial (putative)
745	Tax1bp1	NM_025816	chr6	52663742	52716484	+	BC014798	Tax1 (human T-cell leukemia virus type I) binding protein 1
746	Tbc1d17	NM_00104265	chr7	52096146	52104449	-	BC017607	TBC1 domain family, member 17
747	Tbc1d20	NM_024196	chr2	152119608	152139730	+	BC034504	TBC1 domain family, member 20
748	Tbcb	NM_025548	chr7	31009150	31016805	-	BC010684	tubulin folding cofactor B
749	Tbce	NM_178337	chr13	14090218	14131905	-	AY082332	tubulin-specific chaperone e
750	Tbcel	NM_173038	chr9	42220400	42280309	-		tubulin folding cofactor E-like
751	Tcp1	NM_013686	chr17	13109331	13117933	+	M12899	t-complex protein 1
752	Tcp11l2	NM_146008	chr10	84039692	84077104	+	BC029663	t-complex 11 (mouse) like 2
753	Tef	NM_017376|N	chr15	81633209	81657293	+	BC036982	thyrotroph embryonic factor
754	Tex2	NM_198292	chr11	106363448	106474244	-	BC057406	testis expressed gene 2
755	Tfrc	NM_011638	chr16	32609103	32632876	+	BC054522	transferrin receptor
756	Tgif1	NM_009372	chr17	71193551	71202835	-	BC005724	TG interacting factor 1
757	Tgm2	NM_009373	chr2	157942138	157972128	-	BC016492	transglutaminase 2, C polypeptide
758	Thap4	NM_025920	chr1	95601967	95651441	-	BC063758|AK	THAP domain containing 4
759	Thoc3	NM_028597	chr13	54560879	54570180	-	BC019603	THO complex 3
760	Timm10|Timm13	NM_013899	chr2	84667178	84670370	+	BC031448	translocase of inner mitochondrial membrane 10 homolog (yeast) | translocase of inner mitochondrial memb
761	Timm17a	NM_011590	chr1	137198112	137210314	-	BC098216	translocase of inner mitochondrial membrane 17a
762	Timm44	NM_011592	chr8	4259734	4275903	-	U69898	translocase of inner mitochondrial membrane 44
763	Timm9	NM_013896|N	chr12	72224159	72237662	-	BC024370	translocase of inner mitochondrial membrane 9 homolog (yeast)
764	Tiparp	NM_178892	chr3	65332369	65359440	+	BC068173	TCDD-inducible poly(ADP-ribose) polymerase
765	Tirap	NM_054096	chr9	34994345	35006906	-	AF378130	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein
766	Tle1	NM_011599	chr4	71778176	71861896	-	BC057573	transducin-like enhancer of split 1, homolog of Drosophila E(spl)
767	Tm7sf3	NM_026281	chr6	146552011	146583062	-	DQ104329	transmembrane 7 superfamily member 3
768	Tm9sf2	NM_080556	chr14	122506304	122558825	+	BC003862	transmembrane 9 superfamily member 2
769	Tm9sf3	NM_133352	chr19	41285332	41338494	-	AF269151	transmembrane 9 superfamily member 3
770	Tmed5|LOC10004	NM_028876	chr5	108546680	108561610	-	BC132023	transmembrane emp24 protein transport domain containing 5 | similar to Transmembrane emp24 protein tra
771	Tmem120a	NM_172541	chr5	136211359	136220042	-	BC046757	transmembrane protein 120A
772	Tmem126b	NM_026734	chr7	97617333	97624505	-	BC049680	transmembrane protein 126B
773	Tmem134	NM_00107864	chr19	4125959	4132285	+	BC026765	transmembrane protein 134
774	Tmem183a	NM_020588|N	chr1	136242674	136258576	-	BC003210	transmembrane protein 183A
775	Tmem33	NM_028975|N	chr5	67651891	67682700	+	BC016570	transmembrane protein 33
776	Tmem41a	NM_025693	chr16	21934399	21947617	-	BC019770	transmembrane protein 41a
777	Tmem41b	NM_153525	chr7	117115701	117129768	-	BC086759	transmembrane protein 41B
778	Tmem51	NM_145402	chr4	141586907	141640219	-	BC003277	transmembrane protein 51
779	Tmem57	NM_025382	chr4	134358674	134409260	-	AY846873	transmembrane protein 57
780	Tmem69	NM_177670	chr4	116224133	116228541	-	BC106178	transmembrane protein 69
781	Tmem85	NM_026519	chr2	112203166	112208184	-	BC051926	transmembrane protein 85
782	Tmem87b	NM_028248	chr2	128644047	128677528	+		transmembrane protein 87B
783	Tmem93	NM_025318	chr11	72989021	72990539	-	BC022104	transmembrane protein 93
784	Tmod3	NM_016963	chr9	75345587	75407464	-	BC082595	tropomodulin 3
785	Tmtc4	NM_028651	chr14	123318193	123382483	-	BC031368	transmembrane and tetratricopeptide repeat containing 4
786	Tmub2	NM_028076	chr11	102146275	102150738	+	BC029841	transmembrane and ubiquitin-like domain containing 2
787	Tnrc6b	NM_144812|N	chr15	80541743	80771516	+	BC068158	trinucleotide repeat containing 6b
788	Tob2	NM_020507	chr15	81678700	81689226	-	AK122537	transducer of ERBB2, 2
789	Tomm20|LOC1000	NM_024214|X	chr8	129458452	129469730	-	BC002087	translocase of outer mitochondrial membrane 20 homolog (yeast) | translocase of outer mitochondrial meml
790	Top1mt	NM_028404	chr15	75487463	75509220	-	AF362952	DNA topoisomerase 1, mitochondrial
791	Topors	NM_134097	chr4	40206639	40216874	-	AB072395	topoisomerase I binding, arginine/serine-rich
792	Tor1a	NM_144884	chr2	30816147	30823411	-	BC017683	torsin family 1, member A (torsin A)
793	Tpd52	NM_00102526	chr3	8929436	9004515	-	AY048852	tumor protein D52
794	Tpd52l1	NM_009413	chr10	31052186	31165727	-	AF004428	tumor protein D52-like 1
795	Tpi1	NM_009415	chr6	124760733	124764430	-	BC046761	triosephosphate isomerase 1
796	Tpm3	NM_022314	chr3	89876603	89904528	+	AF317223	tropomyosin 3, gamma
797	Tppp	NM_182839	chr13	74146926	74173201	+	BC054803	tubulin polymerization promoting protein
798	Tprgl	NM_026388	chr4	153531594	153534793	-	BC019544	transformation related protein 63 regulated like
799	Trafd1	NM_172275	chr5	121821739	121835580	-	BC038396	TRAF type zinc finger domain containing 1
800	Trim11	NM_053168	chr11	58791617	58804960	+	BC020102	tripartite motif-containing 11
801	Trim25	NM_009546	chr11	88860747	88881607	+	BC006908	tripartite motif-containing 25
802	Trim37	NM_197987	chr11	86940579	87034184	+	BC058678	tripartite motif-containing 37
803	Trit1	NM_025873	chr4	122693840	122732179	+	BC019812	tRNA isopentenyltransferase 1
804	Tsku	NM_00102461	chr7	105499187	105509798	-	BC116311	tsukushin
805	Tspan4	NM_053082	chr7	148661139	148679321	+	BC083070	tetraspanin 4
806	Tspan9	NM_175414	chr6	127911418	128093596	-	BC052503	tetraspanin 9
807	Tssc1	NM_201357	chr12	29436731	29552356	+	BC031458	tumor suppressing subtransferable candidate 1
808	Ttc1	NM_133795	chr11	43543014	43561487	-	BC010236	tetratricopeptide repeat domain 1
809	Tuba1b|Tuba1c	NM_011654	chr15	98761858	98764855	-	BC083120|M	tubulin, alpha 1B | tubulin, alpha 1C
810	Tuba4a	NM_009447	chr1	75211549	75215828	-	BC019959	tubulin, alpha 4A
811	Tubb2c	NM_146116	chr2	25077682	25080164	-	BC083319	tubulin, beta 2c
812	Tubb6	NM_026473	chr18	67550373	67562403	+	BC008225	tubulin, beta 6
813	Tubgcp2	NM_133755	chr7	147181895	147222165	-	BC012519	tubulin, gamma complex associated protein 2
814	Txn2	NM_019913	chr15	77745477	77759424	-	BC068182|AK	thioredoxin 2
815	Txndc15	NM_175150	chr13	55816011	55827594	+	BC062180	thioredoxin domain containing 15
816	Txnl1	NM_016792	chr18	63822455	63852040	-	BC061123	thioredoxin-like 1
817	Tymp|Sco2	NM_138302|N	chr15	89202068	89207470	-	AB060274|BC	thymidine phosphorylase | SCO cytochrome oxidase deficient homolog 2 (yeast)
818	Uba6	NM_172712	chr5	86539742	86601768	-	BC063048	ubiquitin-like modifier activating enzyme 6
819	Ubac1	NM_133835	chr2	25854067	25877231	-	BC021811	ubiquitin associated domain containing 1

820	Ube2b	NM_009458	chr11	51799064	51813889	-	U57690	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)
821	Ube2e2	NM_144839	chr14	19406091	19726141	-	BC016265	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)
822	Ube2f	NM_026454	chr1	93147143	93182501	+	BC016117	ubiquitin-conjugating enzyme E2F (putative)
823	Ube2k	NM_016786	chr5	65928510	65990167	+	AB011081	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)
824	Ube2n	NM_080560	chr10	94977796	95008292	+	BC067069	ubiquitin-conjugating enzyme E2N
825	Ube2q1	NM_027315	chr3	89577538	89587922	+	BC082275	ubiquitin-conjugating enzyme E2Q (putative) 1
826	Ube4b	NM_022022	chr4	148702525	148800858	-	AF260926	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)
827	Ubqln1	NM_152234|N	chr13	58277523	58316997	-	BC026847	ubiquilin 1
828	Ubr1	NM_009461	chr2	120687382	120796451	-	AF061555	ubiquitin protein ligase E3 component n-recognin 1
829	Uchl5	NM_019562	chr1	145624442	145654075	+	AF175903	ubiquitin carboxyl-terminal esterase L5
830	Ufd1l	NM_011672	chr16	18812402	18835348	+	BC006630	ubiquitin fusion degradation 1 like
831	Ugcg	NM_011673	chr4	59202331	59235705	+	BC050828	UDP-glucose ceramide glucosyltransferase
832	Uhrf1bp1l	NM_029166	chr10	89207771	89281145	+	BC132134	UHRF1 (ICBP90) binding protein 1-like
833	Unc84b	NM_194342	chr15	79554500	79572960	-	BC098208	unc-84 homolog B (C. elegans)
834	Uqcrc2	NM_025899	chr7	127778703	127803037	+	BC003423	ubiquinol cytochrome c reductase core protein 2
835	Usp12	NM_011669	chr5	147546385	147606532	-	BC049274	ubiquitin specific peptidase 12
836	Usp32	NM_00102993	chr11	84797992	84917463	-		ubiquitin specific peptidase 32
837	Usp47	NM_133758	chr7	119167020	119254900	+	BC108425	ubiquitin specific peptidase 47
838	Utrn	NM_011682	chr10	12101986	12581533	-	X83506	utrophin
839	Uxs1	NM_026430	chr1	43806132	43884593	-	BC037049	UDP-glucuronate decarboxylase 1
840	Vav2	NM_009500	chr2	27117628	27282432	-	BC053060	vav 2 oncogene
841	Vdac2	NM_011695	chr14	22650783	22665101	+	U30838	voltage-dependent anion channel 2
842	Vezf1	NM_016686	chr11	87881781	87898231	+	AF104410	vascular endothelial zinc finger 1
843	Vps11	NM_027889	chr9	44156175	44169753	-	BC029004	vacuolar protein sorting 11 (yeast)
844	Vps36	NM_027338	chr8	23303332	23329069	+	BC010811	vacuolar protein sorting 36 (yeast)
845	Vps4b	NM_009190	chr1	108666015	108693253	-	U10119	vacuolar protein sorting 4b (yeast)
846	Vti1a	NM_016862	chr19	55390547	55701799	+	BC089321	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)
847	Wac|LOC1000447	NM_153085	chr18	7869237	7927076	+	BC080851	WW domain containing adaptor with coiled-coil | similar to WW domain-containing adapter protein with coile
848	Wasl	NM_028459	chr6	24563803	24614988	-	BC055045	Wiskott-Aldrich syndrome-like (human)
849	Wbscr27	NM_024479	chr5	135408243	135418507	+	AY354925	Williams Beuren syndrome chromosome region 27 (human)
850	Wdr26|LOC100045	NM_145514	chr1	183107492	183142109	-		WD repeat domain 26 | similar to myocardial ischemic preconditioning upregulated protein 2
851	Wdr36	NM_00111001	chr18	32996894	33025687	+	BC094453	WD repeat domain 36
852	Wdr37	NM_172445|N	chr13	8802214	8870976	-	BC046236	WD repeat domain 37
853	Wdr42a	NM_153555	chr1	174078215	174126520	+	BC078641	WD repeat domain 42A
854	Wdr45l	NM_025793	chr11	121188548	121215723	-	BC004595	Wdr45 like
855	Wdr6	NM_031392	chr9	108474642	108481070	-	BC050894	WD repeat domain 6
856	Wee1	NM_009516	chr7	117265573	117286813	+	BC006852	wee 1 homolog (S. pombe)
857	Whsc2	NM_011914	chr5	34240571	34278971	-	BC038003	Wolf-Hirschhorn syndrome candidate 2 (human)
858	Wnt5b	NM_009525	chr6	119382551	119494336	-	BC010775	wingless-related MMTV integration site 5B
859	Wwtr1	NM_133784	chr3	57259571	57379802	-	BC014727	WW domain containing transcription regulator 1
860	Xrn2	NM_011917	chr2	146838755	146903736	+	BC054743	5'-3' exoribonuclease 2
861	Ypel5	NM_027166	chr17	73186044	73200535	+	BC085109	yippee-like 5 (Drosophila)
862	Ywhaq	NM_011739	chr12	21396190	21423297	-	BC090838	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
863	Yy1	NM_009537	chr12	110031521	110054842	+	M73963	YY1 transcription factor
864	Zc3hav1	NM_028864	chr6	38257198	38304603	-	BC029090	zinc finger CCCH type, antiviral 1
865	Zcchc6	NM_153538	chr13	59873237	59924462	-	BC043111	zinc finger, CCHC domain containing 6
866	Zdhhc20	NM_029492	chr14	58451539	58509116	-	BC019536	zinc finger, DHHC domain containing 20
867	Zfand2b	NM_026846	chr1	75165284	75168199	+	BC011495	zinc finger, AN1 type domain 2B
868	Zfand3	NM_148926	chr17	30142032	30346967	+	BC083124	zinc finger, AN1-type domain 3
869	Zfand5|LOC10004	NM_009551	chr19	21346768	21356779	+	BC119124	zinc finger, AN1-type domain 5 | similar to zinc finger protein ZNF216
870	Zfhx3	NM_007496	chr8	111238544	111485536	+	D26046	zinc finger homeobox 3
871	Zfp187	NM_00101378	chr13	21534099	21541324	-	BC068174	zinc finger protein 187
872	Zfp192	NM_139141	chr13	21605091	21622980	-		zinc finger protein 192
873	Zfp260	NM_011981	chr7	30880095	30892633	+	BC085180	zinc finger protein 260
874	Zfp277	NM_172575|N	chr12	41041633	41172367	-	BC043453	zinc finger protein 277
875	Zfp295	NM_175428|N	chr16	98168997	98183786	-	BC051176	zinc finger protein 295
876	Zfp36	NM_011756	chr7	29161803	29165272	-	M58691	zinc finger protein 36
877	Zfp36l1	NM_007564	chr12	81208747	81214000	-	M58566	zinc finger protein 36, C3H type-like 1
878	Zfp518	NM_028319	chr19	40986119	40990552	+		zinc finger protein 518
879	Zfp523	NM_172617	chr17	28314152	28342831	+	BC060611	zinc finger protein 523
880	Zfp622	NM_144523	chr15	25914121	25928237	+	BC006964	zinc finger protein 622
881	Zfp707	NM_00108106	chr15	75799649	75806176	+	BC026404	zinc finger protein 707
882	Zfp810	NM_145612	chr9	22081192	22112082	-	BC005471	zinc finger protein 810
883	Zfr	NM_011767	chr15	12047608	12115198	+	AF071059	zinc finger RNA binding protein
884	Zfyve26	NM_00100855	chr12	80333334	80397269	-	BC048379	zinc finger, FYVE domain containing 26
885	Zh2c2	NM_026250	chr1	99666772	99690285	+	BC033572	zinc finger, H2C2 domain containing
886	Zkscan1	NM_133906|N	chr5	138526312	138549050	+	BC052441	zinc finger with KRAB and SCAN domains 1
887	Znhit1	NM_027318	chr5	137458068	137463752	-	BC026751	zinc finger, HIT domain containing 1

Table S2		Alpha	0.05	Alphanew	0.03948	Alphaused	0.03948													
Gene Symbol	**Tau**	**FAnova**	**pAnova**	**R2Anova**	**TotSSCW**	**ResSSCW**	**R2CW**	**Const**	**Sin1**	**Cos1**	**Rsq1**	**Fstat1**	**p1**	**Sin2**	**Cos2**	**Rsq2**	**Fstat2**	**p2**	**dFstat2**	**dp2**
0610007C21Rik	25	1.27	0.3248	0.3572	0.002	0.0018	0.1018	0.9802	0.0039	-0.0013	0.1018	1.1902	0.3239							
0610010F05Rik	23	2.6551	0.0501	0.5374	0.0179	0.0131	0.266	0.9339	-0.0026	-0.0194	0.266	3.8043	0.0389							
0610038F07Rik	23	2.461	0.0644	0.5185	0.0047	0.004	0.1513	0.9796	-0.0019	-0.0074	0.1513	1.8719	0.1786							
0910001L09Rik	23	0.2764	0.9543	0.1079	0.0064	0.0064	0.0018	0.9741	-0.001	-0.0002	0.0018	0.0193	0.9809							
1110008P14Rik	23	1.1015	0.4079	0.3252	0.0066	0.0059	0.1106	0.9638	-0.0027	0.0072	0.1106	1.306	0.292							
1110020P15Rik	23.4	2.3937	0.0703	0.5115	0.004	0.0023	0.4291	0.9716	-0.0116	-0.0037	0.4291	7.8915	0.0028							
1110034B05Rik	25	1.183	0.3656	0.3411	0.0105	0.0101	0.0382	0.9625	0.0014	0.0056	0.0382	0.4168	0.6645							
1110038D17Rik	23	7.2212	0.0005	0.7596	0.0083	0.0021	0.7452	0.9708	-0.0046	0.0205	0.618	16.985	0	0.0076	-0.0053	0.7452	13.8936	0	4.7446	0.0213
1600002H07Rik	23	30.8587	0	0.931	0.0285	0.0021	0.9251	0.9396	-0.0404	-0.0256	0.9251	129.684	0							
1600014C10Rik	24.8	3.2713	0.0235	0.5887	0.0084	0.0043	0.4845	0.9595	0.0096	-0.0162	0.4845	9.8694	0.001							
1700023B02Rik	24.6	8.8919	0.0002	0.7955	0.0176	0.005	0.718	0.9379	0.0314	-0.0079	0.718	26.7366	0							
1700123O20Rik	23	1.6318	0.1971	0.4165	0.0039	0.0028	0.2707	0.9767	-0.0085	-0.0045	0.2707	3.8965	0.0364							
1810013L24Rik	23	6.9413	0.0007	0.7523	0.0114	0.0042	0.6303	0.9655	0.0186	-0.0157	0.6303	17.9024	0							
1810063B05Rik	25	3.508	0.0178	0.6055	0.0068	0.003	0.5555	0.9714	-0.0161	-0.0064	0.5555	13.1204	0.0002							
2010209O12Rik	23	1.3845	0.2775	0.3772	0.0057	0.0048	0.1505	0.9594	0.0075	0.0041	0.1505	1.8609	0.1803							
2010305A19Rik	25	3.2894	0.023	0.59	0.0067	0.0061	0.0947	0.9679	0.0062	-0.004	0.0947	1.0988	0.3517							
2310016E02Rik	25	1.2715	0.3241	0.3574	0.0044	0.0034	0.2273	0.9695	-0.0083	-0.0032	0.2273	3.0886	0.0667							
2310035C23Rik	25	3.1387	0.0275	0.5786	0.0154	0.0089	0.4184	0.9587	0.0166	0.0155	0.4184	7.5548	0.0034							
2310037I24Rik	25	6.8063	0.0008	0.7486	0.0081	0.0027	0.6724	0.9571	0.013	-0.0134	0.5319	11.9324	0.0003	-0.003	0.0094	0.6724	9.7515	0.0002	4.0755	0.0337
2310047O13Rik	23	1.2739	0.3231	0.3579	0.002	0.0017	0.1604	0.9856	-0.0032	0.004	0.1604	2.006	0.1595							
2410002O22Rik	23	0.9075	0.5249	0.2842	0.0079	0.0072	0.0816	0.9582	-0.0066	-0.0035	0.0816	0.9331	0.409							
2510002D24Rik	23	2.2333	0.0869	0.4942	0.0125	0.007	0.4383	0.965	0.0218	0.0002	0.4383	8.1948	0.0023							
2610101N10Rik	25	1.271	0.3244	0.3573	0.0083	0.0079	0.0428	0.9651	0.0053	-0.001	0.0428	0.4691	0.632							
2610507B11Rik	23	0.4447	0.8595	0.1629	0.0021	0.0021	0.0342	0.9785	-0.0003	-0.0024	0.0342	0.3718	0.694							
2700038C09Rik	25	4.4776	0.0062	0.662	0.0084	0.0032	0.6181	0.9718	-0.0071	0.0148	0.3955	6.8685	0.0051	-0.0007	-0.0123	0.6181	7.6866	0.0007	5.537	0.0127
4833426J09Rik	23	2.8899	0.0373	0.5584	0.0087	0.0046	0.4654	0.959	0.0175	-0.006	0.4654	9.1424	0.0014							
4833439L19Rik	25	12.2688	0	0.843	0.0139	0.0024	0.824	0.9579	-0.0281	-0.0112	0.824	49.1448	0							
4933403F05Rik	25	5.5512	0.0022	0.7083	0.0058	0.0022	0.6227	0.9736	0.0128	0.0111	0.6227	17.3265	0							
4933407H18Rik	23	4.3671	0.007	0.6564	0.0059	0.0035	0.4066	0.9724	0.0061	-0.0124	0.4066	7.1955	0.0042							
5430407P10Rik	24.6	9.0897	0.0001	0.7991	0.0208	0.0053	0.7437	0.9548	-0.0303	0.0129	0.6395	18.624	0	0.0133	0.0019	0.7437	13.7842	0	3.8642	0.0391
6330409N04Rik	23	3.2121	0.0252	0.5842	0.0034	0.0017	0.4898	0.9818	-0.0039	0.0108	0.4898	10.0793	0.0009							
9030612M13Rik	23	4.7686	0.0046	0.676	0.0149	0.0079	0.4661	0.9519	0.0137	-0.0193	0.4661	9.1669	0.0014							
9130011J15Rik	23	3.7881	0.013	0.6237	0.0042	0.0021	0.5094	0.9752	0.0116	-0.0067	0.5094	10.9028	0.0006							
9530058B02Rik	23.4	13.8693	0	0.8585	0.0125	0.0023	0.8179	0.9667	-0.0282	-0.0088	0.8179	47.1527	0							
9530068E07Rik	24.1	2.5285	0.059	0.5252	0.0035	0.0024	0.3021	0.9785	0.0093	0.0002	0.3021	4.5453	0.0229							
A230067G21Rik	23	4.4936	0.0061	0.6628	0.0228	0.0089	0.6085	0.9379	0.0165	-0.029	0.6085	16.3207	0.0001							
A430005L14Rik	25	1.556	0.2189	0.405	0.0034	0.0033	0.015	0.9754	0	0.0021	0.015	0.1596	0.8535							
A530082C11Rik	23	4.3536	0.0071	0.6557	0.0071	0.0029	0.5913	0.975	0.0116	-0.0144	0.5913	15.1924	0.0001							
Abat	25	12.5238	0	0.8457	0.0041	0.0008	0.7999	0.9719	0.0103	0.0099	0.6435	18.9521	0	0.0037	-0.0064	0.7999	18.9822	0	7.4216	0.0042
Abce1	23	5.5275	0.0023	0.7075	0.0048	0.0017	0.6401	0.9733	-0.0163	0.0003	0.6401	18.675	0							
Abhd13	23	2.2212	0.0883	0.4928	0.0075	0.0049	0.3493	0.9707	-0.0112	-0.0099	0.3493	5.6374	0.011							
Abhd6	23	7.0544	0.0006	0.7553	0.0221	0.0069	0.6885	0.9423	-0.0316	-0.0179	0.6885	23.2034	0							
Abi1	23.1	3.5772	0.0165	0.6101	0.004	0.0017	0.5649	0.9646	0.0136	-0.0023	0.5649	13.6302	0.0002							
Abtb1	25	5.4841	0.0023	0.7058	0.0078	0.0026	0.664	0.9682	0.0203	-0.0037	0.664	20.7478	0							
Abtb2	23	27.1147	0	0.9223	0.0538	0.0057	0.8932	0.9335	-0.0126	0.0567	0.7276	28.048	0	0.0217	-0.0157	0.8932	39.7407	0	14.7374	0.0001
Acad8	25	2.0926	0.1049	0.478	0.0052	0.0036	0.3026	0.9584	0.0102	0.0045	0.3026	4.5551	0.0227							
Acly	25	8.4834	0.0002	0.7878	0.019	0.0044	0.7693	0.9532	-0.0224	0.0223	0.6548	19.9178	0	0.0078	-0.0114	0.7693	15.8385	0	4.714	0.0218
Acn9	23	1.8854	0.139	0.452	0.0051	0.0032	0.3766	0.974	-0.0128	0.0014	0.3766	6.3425	0.007							
Acss2	23	12.0934	0	0.841	0.0215	0.0075	0.6496	0.9375	0.0131	0.0314	0.6496	19.4626	0							
Actn1	24.7	4.0637	0.0096	0.64	0.014	0.0055	0.6099	0.9633	0.0203	-0.0178	0.6099	16.4154	0.0001							
Acvr1b	23	3.67	0.0148	0.6162	0.0076	0.0031	0.5898	0.9682	0.0147	-0.0063	0.4022	7.0636	0.0045	-0.0093	-0.0063	0.5898	6.8289	0.0014	4.3443	0.0279
Add1	23	6.3279	0.0011	0.7346	0.0081	0.0023	0.7105	0.9549	0.0213	0.0068	0.7105	25.7639	0							
Adfp	23	12.3853	0	0.8442	0.0172	0.0032	0.816	0.9534	0.0246	0.0206	0.7	24.504	0	-0.0109	-0.0077	0.816	21.0664	0	5.9881	0.0096
Adss	23	0.869	0.5507	0.2755	0.006	0.0056	0.0754	0.9713	-0.0023	-0.0057	0.0754	0.8557	0.4393							
Aftph	25	1.7727	0.1623	0.4368	0.0049	0.0038	0.2242	0.9766	0.0093	0.001	0.2242	3.035	0.0695							
Agl	23	5.4923	0.0023	0.7061	0.017	0.0102	0.3993	0.9545	0.0042	-0.0229	0.3993	6.9797	0.0047							
Agpat6	23	3.5789	0.0164	0.6103	0.0134	0.006	0.5519	0.9285	-0.0166	-0.0188	0.5519	12.9302	0.0002							
Ahcy	25	15.6268	0	0.8724	0.0012	0.0003	0.7793	0.9859	-0.008	-0.0027	0.7793	37.0661	0							
Ahsa1	23	7.0738	0.0006	0.7558	0.0106	0.0028	0.7334	0.9652	-0.0212	0.0043	0.4883	10.0199	0.0009	0.0077	-0.0121	0.7334	13.0646	0	8.7314	0.002
AI597468	23	1.9924	0.1201	0.4657	0.0098	0.0086	0.115	0.9533	-0.0023	0.0092	0.115	1.3647	0.2772							
Aifm2	23	8.5445	0.0002	0.7889	0.0097	0.0026	0.7324	0.957	-0.0101	-0.022	0.7324	28.7429	0							
Ak2	23	39.4503	0	0.9452	0.0066	0.0006	0.9123	0.9669	-0.0032	-0.0218	0.9123	109.177	0							
Ak3	23	0.4809	0.8347	0.1738	0.0007	0.0007	0.0702	0.9879	-0.0012	-0.0017	0.0702	0.7927	0.4657							
Akap9	25	5.1705	0.0031	0.6934	0.0108	0.0051	0.5307	0.9578	0.0198	-0.0098	0.5307	11.8751	0.0004							
Alas1	23	6.6805	0.0008	0.7451	0.0934	0.0297	0.6817	0.8921	-0.0421	-0.0599	0.6817	22.4929	0							
Alcam	25	8.1921	0.0003	0.7819	0.013	0.0038	0.7028	0.9525	0.0217	-0.0074	0.5256	11.6318	0.0004	-0.0069	0.0124	0.7028	11.2344	0.0001	5.667	0.0117
Aldh1l1	23	2.4579	0.0646	0.5181	0.0018	0.0013	0.3029	0.9778	0.0023	0.0063	0.3029	4.5621	0.0226							
Aldob	23	6.6462	0.0009	0.7441	0.0008	0.0003	0.6859	0.9902	-0.0054	-0.0044	0.6859	22.9327	0							
Amd1	25	12.0332	0	0.8404	0.0457	0.0097	0.7872	0.9155	-0.0219	-0.0433	0.6413	18.7737	0	0.0015	0.0232	0.7872	17.5682	0	6.5103	0.007
Angel2	23	1.2525	0.3327	0.354	0.0116	0.0089	0.235	0.9619	-0.0119	-0.0097	0.235	3.2261	0.06							
Ankhd1	25	1.4559	0.2514	0.3891	0.0125	0.0103	0.1765	0.9432	0.0116	-0.0073	0.1765	2.2507	0.1301							
Ankrd17	23	3.9765	0.0106	0.635	0.0099	0.0055	0.4414	0.9579	0.0122	-0.0143	0.4414	8.298	0.0022							
Ankrd56	23	2.6152	0.0528	0.5336	0.0079	0.0051	0.3537	0.962	0.0058	0.0141	0.3537	5.7465	0.0102							
Ankzf1	25	0.9851	0.4753	0.3012	0.0073	0.0063	0.1359	0.9533	0.0089	-0.002	0.1359	1.6507	0.2159							
Anp32a	23	16.4416	0	0.8779	0.0185	0.0028	0.8496	0.9576	0.0146	0.0316	0.7703	35.2019	0	-0.0038	-0.0105	0.8496	26.8414	0	5.0162	0.0178
Anxa5	23.6	5.3879	0.0026	0.7021	0.006	0.0023	0.6117	0.9753	0.0111	0.0037	0.2666	3.8167	0.0386	0.013	0.0024	0.6117	7.4823	0.0009	8.4426	0.0024
Anxa7	25	8.6984	0.0002	0.7919	0.0151	0.0043	0.716	0.9541	0.016	-0.0263	0.716	26.4745	0							
Ap3m1	23	16.8832	0	0.8808	0.0175	0.0026	0.8527	0.9489	-0.0056	-0.0343	0.8527	60.8007	0							
Aph1a	25	0.4794	0.8357	0.1734	0.0027	0.0027	0.0124	0.977	0.0016	-0.0002	0.0124	0.132	0.8771							
Aqp11	25	10.5833	0.0001	0.8224	0.0094	0.0025	0.7399	0.9599	-0.0109	-0.0213	0.7399	29.8689	0							
Arfgap1	23	5.2658	0.0029	0.6973	0.0046	0.0015	0.667	0.9761	0.013	-0.0025	0.4494	8.5689	0.0019	0.0093	-0.0005	0.667	9.5152	0.0002	6.2099	0.0084
Arhgap12	25	4.1044	0.0092	0.6423	0.0055	0.0024	0.559	0.9732	0.015	0.0048	0.559	13.3085	0.0002							
Arl1	25	0.7647	0.6243	0.2507	0.0012	0.0011	0.0377	0.9857	0.0018	-0.0007	0.0377	0.4114	0.668							
Arl6ip4	23	2.017	0.1162	0.4688	0.006	0.004	0.3352	0.9811	-0.0017	-0.0127	0.3352	5.2949	0.0137							
Armc1	23	3.0418	0.031	0.571	0.0089	0.0043	0.5224	0.967	-0.0135	-0.0146	0.5224	11.4861	0.0004							
Arrdc3	25	4.3916	0.0068	0.6577	0.0625	0.0322	0.4847	0.8835	0.0488	-0.0113	0.4847	9.8766	0.0009							
Asl	25	24.9053	0	0.9159	0.0104	0.001	0.904	0.9617	-0.0251	-0.011	0.904	98.8195	0							
Atf2	23.9	2.8606	0.0387	0.5559	0.0069	0.0033	0.5288	0.9702	0.0115	-0.0065	0.3035	4.5762	0.0224	0.0069	0.0091	0.5288	5.3299	0.0047	4.5405	0.0244
Atf4	25	3.981	0.0105	0.6353	0.0081	0.0054	0.3329	0.9646	-0.0023	0.0151	0.3329	5.2391	0.0143							
Atg3	23	1.7165	0.1753	0.4289	0.005	0.0042	0.1479	0.974	-0.0063	-0.0049	0.1479	1.8227	0.1862							
Atp1a1	23.2	20.2726	0	0.8987	0.0049	0.0006	0.8728	0.9784	-0.009	-0.0166	0.8728	72.0634	0							
Atp5h	23	2.9963	0.0327	0.5673	0.0018	0.0017	0.0252	0.9794	-0.0019	0.0004	0.0252	0.2714	0.765							
Atp6v0b	24.9	4.1905	0.0084	0.6471	0.0053	0.0026	0.5152	0.9683	-0.0093	-0.0115	0.5152	11.1574	0.0005							
Atp6v1c1	23	4.839	0.0043	0.6792	0.0076	0.0036	0.5244	0.961	0.0055	-0.017	0.5244	11.5759	0.0004							
Atp6v1d	23	7.981	0.0003	0.7774	0.0173	0.0061	0.646	0.9492	-0.0262	-0.0168	0.646	19.1626	0							
Atp6v1e1	23	3.7883	0.013	0.6237	0.0096	0.005	0.4777	0.9662	0.0057	-0.0182	0.4777	9.6034	0.0011							
Atxn2l	25	0.8939	0.5339	0.2811	0.0123	0.0102	0.1688	0.9506	0.0127	-0.0035	0.1688	2.133	0.1434							
B3galnt2	24.4	4.3269	0.0073	0.6543	0.0111	0.0041	0.6261	0.9518	-0.019	-0.0022	0.4031	7.0912	0.0044	0.0134	0.0049	0.6261	7.9555	0.0006	5.6676	0.0117
Bag4	23	3.6139	0.0158	0.6126	0.0063	0.0031	0.5099	0.9654	0.0128	-0.01	0.5099	10.9233	0.0006							
Baiap2	23	1.128	0.3937	0.3304	0.0166	0.0155	0.066	0.9397	-0.0092	0.0029	0.066	0.7417	0.4884							
Bat1a	23	0.6496	0.71	0.2213	0.0019	0.0016	0.1739	0.985	0.0041	0.0034	0.1739	2.2105	0.1345							
BC013529	23	2.0483	0.1114	0.4726	0.0146	0.0104	0.2854	0.9473	-0.0145	-0.0122	0.2854	4.1937	0.0293							
BC016495	23	15.1967	0	0.8693	0.0684	0.0142	0.793	0.8923	-0.0498	-0.0466	0.793	40.2151	0							
BC048355	25	3.3376	0.0217	0.5935	0.0139	0.0078	0.4417	0.9647	-0.0188	0.0132	0.4417	8.3064	0.0022							
Bcar1	23	4.8003	0.0045	0.6774	0.0065	0.0022	0.6598	0.9648	0.0153	0.0008	0.4195	7.5872	0.0033	-0.0108	-0.0049	0.6598	9.2124	0.0003	6.7109	0.0062
Becn1	23	3.6897	0.0145	0.6175	0.0037	0.0021	0.4298	0.9677	-0.0069	-0.0093	0.4298	7.9159	0.0027							
Bet1	23	1.8568	0.1445	0.4482	0.0221	0.0174	0.2117	0.9403	-0.0148	0.0129	0.2117	2.8195	0.0823							
Blcap	23	11.3214	0	0.832	0.0119	0.0033	0.726	0.9672	-0.006	0.0256	0.726	27.8201	0							
Blvrb	23	0.0811	0.9987	0.0343	0.0076	0.0076	0.0049	0.9707	-0.0017	0.0005	0.0049	0.0517	0.9497							
Bmf	23	2.4721	0.0634	0.5196	0.0224	0.0137	0.387	0.9471	0.0205	-0.0171	0.387	6.6279	0.0059							
Bnip3l	25	7.5864	0.0004	0.7685	0.0032	0.0009	0.7307	0.9754	0.003	-0.0127	0.6058	16.1349	0.0001	0.0033	0.0045	0.7307	12.888	0	4.4065	0.0268
Brd4	23	1.1663	0.374	0.3379	0.004	0.003	0.2528	0.9698	0.0051	-0.0074	0.2528	3.5526	0.0469							
Brd8	23	2.3573	0.0737	0.5077	0.0076	0.0041	0.4673	0.9567	0.0173	0.0038	0.4673	9.2106	0.0013							
Brd9	24.2	2.8137	0.041	0.5518	0.0039	0.0019	0.51	0.9736	0.0086	-0.0039	0.2756	3.9955	0.0338	0.0059	0.0063	0.51	4.9436	0.0067	4.5434	0.0244
Brp44l	25	3.1813	0.0262	0.5819	0.0045	0.0032	0.2715	0.9838	0.0071	-0.0074	0.2715	3.9131	0.0359							
Bsdc1	23	1.2059	0.3545	0.3454	0.0038	0.0027	0.3032	0.9744	0.0074	-0.0063	0.3032	4.5696	0.0225							
Bst2	23	1.6689	0.1872	0.422	0.0025	0.0018	0.2623	0.9782	-0.0075	-0.0003	0.2623	3.7343	0.041							
Bzw1	23	1.2187	0.3483	0.3478	0.0038	0.0028	0.2667	0.9774	-0.0076	-0.0055	0.2667	3.8189	0.0385							
C330023M02Rik	23	0.5227	0.8047	0.1861	0.0042	0.0038	0.1064	0.9718	-0.0054	-0.0032	0.1064	1.2502	0.3069							
C630028N24Rik	23	2.6774	0.0487	0.5395	0.0235	0.0126	0.4634	0.9132	0.0281	-0.0115	0.4634	9.0673	0.0015							
C77080	23	2.354	0.074	0.5074	0.0113	0.0077	0.3185	0.9493	0.0176	-0.0012	0.3185	4.9069	0.0178							
Cabc1	23	215.045	0	0.9895	0.0512	0.0008	0.9852	0.9397	0.0155	0.061	0.9082	103.918	0	0.0049	-0.017	0.9852	316.881	0	49.5316	0
Cacybp	23	11.2523	0	0.8312	0.011	0.002	0.8156	0.9431	-0.025	-0.0018	0.648	19.3273	0	0.0103	-0.0065	0.8156	21.0137	0	8.639	0.0021
Calm1	23	2.3546	0.074	0.5074	0.0015	0.0009	0.4214	0.987	-0.0014	0.0069	0.4214	7.6485	0.0032							
Camk2g	23	6.8333	0.0007	0.7493	0.0079	0.0038	0.5197	0.9592	0.0189	-0.0009	0.5197	11.3623	0.0005							
Cars	25	4.4887	0.0061	0.6626	0.0131	0.0062	0.5269	0.944	0.0197	0.0128	0.5269	11.6956	0.0004							
Cbfa2t2	25	1.7079	0.1774	0.4277	0.0152	0.0111	0.2714	0.959	0.0155	-0.0106	0.2714	3.9107	0.036							
Cblb	23	1.8228	0.1514	0.4437	0.0085	0.0051	0.4007	0.961	0.0126	-0.0109	0.4007	7.0218	0.0046							
Cbs	24.5	13.4399	0	0.8547	0.0155	0.0033	0.7843	0.9588	0.0259	0.018	0.7843	38.1721	0							
Cbx3	23	0.8489	0.5645	0.2708	0.014	0.013	0.071	0.9566	0.0009	-0.0089	0.071	0.8024	0.4615							
Ccbl2	24.3	5.7511	0.0018	0.7156	0.0104	0.0037	0.6452	0.9612	-0.0196	-0.0066	0.4987	10.4439	0.0007	0.0103	0.0043	0.6452	8.6371	0.0004	3.9229	0.0375
Ccdc142	23	0.5336	0.7968	0.1893	0.0023	0.002	0.1275	0.9769	-0.0031	-0.0039	0.1275	1.534	0.2389							
Ccng2	23	5.4547	0.0024	0.7047	0.039	0.0167	0.5729	0.9361	0.0036	0.0423	0.5729	14.0867	0.0001							
Ccnh	25	2.1823	0.093	0.4884	0.008	0.007	0.1189	0.9738	-0.0001	0.009	0.1189	1.4162	0.2649							
Cct7	23	1.7447	0.1686	0.4329	0.0045	0.0029	0.351	0.9788	-0.0116	0.0015	0.351	5.6799	0.0107							
Cd2ap	25	2.0585	0.1098	0.4739	0.01	0.0081	0.192	0.963	0.0125	-0.0002	0.192	2.4953	0.1066							
Cd302	23	4.5642	0.0057	0.6663	0.0034	0.0023	0.3218	0.9815	-0.0091	-0.0037	0.3218	4.9826	0.0169							
Cd9	23.7	9.9307	0.0001	0.8129	0.0384	0.0096	0.7511	0.9261	0.043	0.0076	0.5878	14.9704	0.0001	0.0185	0.0138	0.7511	14.3338	0	6.2343	0.0083
Cdadc1	23	1.3001	0.3117	0.3626	0.0045	0.0034	0.2438	0.9759	-0.0047	-0.0083	0.2438	3.3845	0.0532							
Cdc37l1	23	1.2628	0.328	0.3559	0.0043	0.0033	0.2326	0.9616	-0.0085	-0.0039	0.2326	3.1828	0.062							
Cdk6	24	3.0757	0.0297	0.5737	0.0092	0.0051	0.4404	0.9655	0.0167	-0.0075	0.4404	8.2623	0.0023							
Cdk8	25	3.6859	0.0146	0.6172	0.0081	0.0038	0.5293	0.9564	0.014	-0.0132	0.5293	11.8056	0.0004							
Cebpb	23	3.0276	0.0315	0.5698	0.023	0.0145	0.3696	0.9381	0.0014	-0.0261	0.3696	6.1554	0.0079							
Cebpd	23	1.0179	0.4555	0.3081	0.0077	0.0059	0.2341	0.9601	-0.0054	-0.0109	0.2341	3.2088	0.0608							
Cgrrf1	23	3.04	0.031	0.5708	0.0165	0.0095	0.427	0.9566	-0.0104	-0.0218	0.427	7.8239	0.0029							
Chchd1	23	0.9796	0.4788	0.3	0.006	0.0056	0.0652	0.9693	-0.0058	-0.0001	0.0652	0.7328	0.4924							
Chchd4	23	4.5405	0.0058	0.6652	0.024	0.0115	0.5203	0.9225	-0.0213	-0.0246	0.5203	11.3864	0.0004							
Chd1	23	4.9793	0.0038	0.6854	0.008	0.0038	0.5258	0.9662	-0.0019	-0.0183	0.5258	11.6428	0.0004							
Chid1	23	2.4234	0.0676	0.5146	0.0139	0.0086	0.385	0.9499	-0.0099	0.0182	0.385	6.5726	0.0061							
Chmp1a	25	0.9318	0.509	0.2896	0.0067	0.0066	0.0089	0.9695	0.0022	-0.0002	0.0089	0.0938	0.9108							
Chmp2a	25	1.8567	0.1446	0.4482	0.0036	0.0033	0.0724	0.9817	0.0035	-0.0032	0.0724	0.8191	0.4544							
Chmp7	24.7	1.7398	0.1698	0.4322	0.0027	0.0016	0.3872	0.9828	0.0084	-0.0041	0.3872	6.634	0.0058							
Chordc1	25	13.2645	0	0.853	0.0585	0.0114	0.8057	0.8843	-0.0428	-0.0235	0.506	10.7543	0.0006	0.0331	0.018	0.8057	19.6974	0	14.6548	0.0001
Chpt1	25	0.9284	0.5112	0.2889	0.0044	0.0044	0.0098	0.9726	0.0012	-0.0016	0.0098	0.1044	0.9013							
Churc1	25	0.5264	0.802	0.1872	0.0099	0.0096	0.0345	0.9646	0.0053	-0.0002	0.0345	0.375	0.6918							
Cisd1	23	2.552	0.0572	0.5275	0.0071	0.0041	0.4252	0.9652	0.0161	0.002	0.4252	7.7684	0.003							
Cisd2	25	3.3298	0.0219	0.593	0.0044	0.0031	0.2867	0.9708	-0.0029	-0.0099	0.2867	4.2199	0.0288							
Cited2	23	4.029	0.01	0.638	0.0095	0.0057	0.3994	0.9634	0.0033	0.0173	0.3994	6.9817	0.0047							
Cks2	23.1	2.2458	0.0854	0.4956	0.0153	0.0099	0.3536	0.9599	0.0024	0.0208	0.3536	5.743	0.0102							
Clec2d	23	2.3798	0.0716	0.5101	0.0132	0.0124	0.0585	0.9635	-0.001	-0.0078	0.0585	0.6524	0.531							
Clint1	25	4.0936	0.0093	0.6417	0.0047	0.0031	0.3545	0.9714	0.0051	0.0106	0.3545	5.7667	0.0101							
Clmn	23	5.5677	0.0022	0.709	0.0282	0.0099	0.6499	0.9414	0.0233	-0.0307	0.6499	19.494	0							
Cln8	23	6.8296	0.0007	0.7492	0.0169	0.0049	0.7103	0.9467	-0.0047	-0.0308	0.7103	25.7483	0							
Clpx	23	165.807	0	0.9864	0.0984	0.0052	0.9475	0.9108	0.0122	0.0855	0.9339	148.232	0	0.015	-0.0078	0.9651	131.401	0	8.5125	0.0023
Clta	25	1.4605	0.2498	0.3899	0.003	0.0021	0.3005	0.9809	0.0085	0.0002	0.3005	4.5113	0.0234							
Cltc	25	0.6003	0.7471	0.208	0.0013	0.0012	0.0894	0.9856	0.0027	0.0015	0.0894	1.0314	0.3739							
Cmtm6	23	3.672	0.0148	0.6163	0.0065	0.0029	0.5507	0.9728	0.0012	0.0169	0.5507	12.8709	0.0002							
Cmtm8	23	0.8911	0.5358	0.2805	0.01	0.0077	0.2261	0.9593	0.0112	-0.0078	0.2261	3.0671	0.0678							
Cnn3	23	3.4205	0.0197	0.5994	0.0168	0.0158	0.0567	0.953	0.0006	-0.0087	0.0567	0.6308	0.542							
Cnot4	23	2.0981	0.1041	0.4786	0.0174	0.015	0.1371	0.954	-0.0118	-0.0083	0.1371	1.6687	0.2125							
Cobll1	23.5	8.9457	0.0002	0.7965	0.015	0.0031	0.7962	0.9523	0.0193	-0.0226	0.6939	23.8056	0	-0.0039	0.0105	0.7962	18.5601	0	4.7691	0.021
Col18a1	23	3.3168	0.0223	0.592	0.0116	0.005	0.5712	0.954	0.0208	0.0121	0.5712	13.9872	0.0001							

Commd7	23	10.3653	0.0001	0.8193	0.0194	0.0041	0.7913	0.9476	0.0077	0.0345	0.7913	39.809	0							
Cp	25	1.6078	0.2038	0.4129	0.0008	0.0006	0.2437	0.9898	0.0021	0.0033	0.2437	3.3826	0.0533							
Cpeb2	23	3.4085	0.02	0.5986	0.0165	0.0109	0.3372	0.9524	0.0212	0.0062	0.3372	5.3428	0.0133							
Cpeb3	23	2.8164	0.0409	0.552	0.0153	0.0094	0.3862	0.958	0.0018	-0.0217	0.3862	6.6053	0.006							
Cpsf3	25	0.9055	0.5262	0.2837	0.0023	0.002	0.1268	0.9765	0.0049	-0.0002	0.1268	1.5244	0.2409							
Cpt1a	23	29.7347	0	0.9286	0.0265	0.0023	0.9114	0.9517	0.0214	-0.0384	0.9114	107.983	0							
Crebbp	23	1.5941	0.2077	0.4109	0.0097	0.0093	0.0394	0.9624	0.0054	-0.0018	0.0394	0.431	0.6555							
Crebzf	25	2.8957	0.0371	0.5589	0.0119	0.0062	0.4766	0.9642	0.012	0.0178	0.4766	9.5606	0.0011							
Crem	23	2.0389	0.1128	0.4715	0.015	0.0107	0.2864	0.9581	-0.0105	0.0154	0.2864	4.2139	0.0289							
Crip2	23.8	24.9237	0	0.916	0.0403	0.0039	0.9029	0.9435	0.0006	0.0526	0.82	47.837	0	0.0139	-0.009	0.9029	44.166	0	8.1087	0.0028
Crot	24	27.3051	0	0.9228	0.0191	0.0015	0.919	0.9653	0.0302	0.0218	0.8692	69.7916	0	-0.0073	0.0051	0.919	53.923	0	5.8457	0.0105
Cs	23.5	9.2345	0.0001	0.8016	0.0068	0.0021	0.6959	0.964	0.0141	0.0142	0.6959	24.0337	0							
Csde1	23	1.2095	0.3527	0.3461	0.0076	0.0059	0.2267	0.9744	-0.0063	-0.0102	0.2267	3.0789	0.0672							
Csnk1a1	23.2	4.2103	0.0082	0.6481	0.0015	0.0008	0.4486	0.9839	0.006	0.0047	0.4486	8.5428	0.0019							
Csnk2a1	25	1.5766	0.2127	0.4082	0.0032	0.0025	0.1989	0.9798	0.0071	-0.0012	0.1989	2.6069	0.0974							
Ctage5	23	4.8227	0.0044	0.6785	0.0087	0.0048	0.4413	0.9631	0.0084	-0.0154	0.4413	8.2921	0.0022							
Ctdsp1	23	5.0313	0.0036	0.6876	0.0069	0.0025	0.633	0.9592	0.0176	0.0084	0.633	18.1138	0							
Ctr9	23	1.4969	0.2376	0.3957	0.0055	0.0046	0.1589	0.963	-0.0077	-0.0042	0.1589	1.9834	0.1625							
Ctsh	23	2.1041	0.1033	0.4793	0.0021	0.0018	0.1329	0.9806	-0.0001	-0.0047	0.1329	1.61	0.2236							
Ctsl	24.4	6.5015	0.001	0.7399	0.0029	0.0009	0.6756	0.9783	0.0124	0.0027	0.6756	21.8665	0							
Cttn	25	1.5598	0.2178	0.4056	0.003	0.0022	0.2715	0.9703	0.0064	-0.0055	0.2715	3.9125	0.036							
Cugbp1	23	5.6761	0.002	0.7129	0.0017	0.0009	0.4405	0.98	0.0029	-0.0071	0.4405	8.2656	0.0023							
Cul1	25	1.8681	0.1423	0.4497	0.0048	0.0034	0.2983	0.9677	0.0096	0.0048	0.2983	4.4634	0.0242							
Cul2	25	1.7052	0.1781	0.4273	0.0057	0.0041	0.2799	0.9692	-0.005	0.0107	0.2799	4.0808	0.0318							
Cxcl12	23	3.2007	0.0256	0.5834	0.0042	0.0032	0.2447	0.97	-0.0051	-0.0078	0.2447	3.4015	0.0525							
Cxxc5	23	4.2104	0.0082	0.6481	0.0061	0.0036	0.4015	0.9691	0.0128	0.0069	0.4015	7.0433	0.0046							
Cycs	25	0.4852	0.8316	0.1751	0.0382	0.0331	0.1332	0.9272	0.0004	-0.0209	0.1332	1.6138	0.2229							
Cyld	23	1.7894	0.1586	0.4391	0.015	0.0115	0.2358	0.9642	0.002	-0.0167	0.2358	3.2398	0.0594							
Cyp2u1	23	8.7417	0.0002	0.7927	0.0127	0.0041	0.6789	0.966	0.0258	0.0094	0.6789	22.2011	0							
Cyp8b1	25	9.3039	0.0001	0.8028	0.0273	0.0062	0.773	0.955	0.0108	0.034	0.5743	14.1658	0.0001	-0.003	-0.0207	0.773	16.1771	0	8.3169	0.0025
D030074E01Rik	25	1.9593	0.1256	0.4616	0.0085	0.0058	0.3235	0.9646	-0.0026	0.0152	0.3235	5.0209	0.0165							
D10Ertd322e	23	2.3611	0.0733	0.5081	0.016	0.0119	0.2562	0.9398	-0.0188	0.0012	0.2562	3.6159	0.0447							
D10Ertd641e	23	1.4804	0.2431	0.3931	0.0027	0.0019	0.293	0.9778	-0.0078	0.0022	0.293	4.3506	0.0263							
D10Jhu81e	23	0.4019	0.8874	0.1495	0.0054	0.0051	0.0435	0.9724	0.0032	0.0031	0.0435	0.4774	0.6269							
D10Wsu102e	25	1.7789	0.1609	0.4377	0.0052	0.0045	0.133	0.9603	0.0064	-0.0044	0.133	1.6109	0.2234							
D15Ertd621e	23	4.3139	0.0074	0.6537	0.0061	0.0031	0.4831	0.9722	0.0032	-0.015	0.4831	9.814	0.001							
D16Ertd472e	23	5.1774	0.0031	0.6937	0.0248	0.0105	0.5786	0.9329	-0.0297	-0.019	0.5786	14.4149	0.0001							
D17Wsu104e	24.4	4.5203	0.0059	0.6642	0.0098	0.0036	0.6273	0.9739	-0.0118	0.0082	0.2661	3.8073	0.0388	0.0172	-0.001	0.6273	7.9933	0.0006	9.2044	0.0016
D2hgdh	23	1.3091	0.3079	0.3642	0.0101	0.0091	0.0928	0.9355	-0.0038	-0.0079	0.0928	1.0735	0.3598							
D4Ertd22e	24	2.3501	0.0744	0.5069	0.0034	0.0021	0.402	0.979	-0.0061	0.0089	0.402	7.0573	0.0045							
Dad1	23	5.831	0.0017	0.7184	0.0047	0.0017	0.6307	0.9764	-0.0124	0.0043	0.4143	7.4266	0.0036	0.008	-0.0042	0.6307	8.1106	0.0005	5.5654	0.0125
Daxx	23	1.9789	0.1223	0.464	0.0049	0.0031	0.3741	0.9702	0.0114	0.0056	0.3741	6.2755	0.0073							
Dazap1	23	0.5748	0.7663	0.2009	0.0031	0.0028	0.1156	0.9765	0.0025	-0.0047	0.1156	1.3729	0.2752							
Dazap2	25	1.173	0.3706	0.3391	0.0054	0.0041	0.2287	0.9715	0.0082	0.0055	0.2287	3.1134	0.0654							
Dbp	23	26.4748	0	0.9205	0.3171	0.0434	0.8632	0.8282	0.0561	-0.1369	0.8632	66.2611	0							
Dctn2	25	4.7633	0.0047	0.6757	0.0041	0.0018	0.5647	0.9725	0.0136	-0.003	0.5647	13.6217	0.0002							
Dctn4	25	3.5716	0.0166	0.6098	0.0054	0.0035	0.3608	0.979	0.0126	-0.001	0.3608	5.9268	0.0091							
Dctn5	23	2.8076	0.0414	0.5512	0.0059	0.0052	0.121	0.9691	-0.005	0.0057	0.121	1.4451	0.2582							
Dcun1d2	25	5.4054	0.0025	0.7028	0.0204	0.0072	0.6486	0.9369	-0.0134	-0.0241	0.446	8.4532	0.002	0.0121	0.0134	0.6486	8.7669	0.0003	5.4765	0.0132
Dcun1d4	25	5.5187	0.0023	0.7071	0.0279	0.0112	0.5976	0.9382	0.0307	-0.0222	0.5976	15.5929	0.0001							
Ddef2	23	60.1498	0	0.9634	0.0598	0.0036	0.9401	0.9108	0.0186	0.0652	0.9401	164.825	0							
Ddit4	24.2	6.8502	0.0007	0.7498	0.0232	0.0069	0.7014	0.9174	-0.0326	0.0172	0.7014	24.6599	0							
Ddx17	23	3.8152	0.0126	0.6253	0.009	0.0051	0.4379	0.9759	0.0141	0.0118	0.4379	8.1808	0.0024							
Ddx39	23	0.7772	0.6153	0.2537	0.0062	0.0057	0.0867	0.9664	-0.0061	0.0029	0.0867	0.9969	0.3858							
Ddx42	25	2.5394	0.0581	0.5263	0.0131	0.0099	0.244	0.9617	0.0132	-0.01	0.244	3.3892	0.053							
Ddx46	25	14.7916	0	0.8662	0.02	0.0031	0.845	0.9458	0.0227	-0.0236	0.6622	20.5792	0	-0.0035	0.0172	0.845	25.903	0	11.212	0.0006
Ddx6	23	3.6533	0.0151	0.6151	0.0045	0.0022	0.5087	0.9715	-0.0009	-0.0135	0.5087	10.8736	0.0006							
Deb1	23	8.3389	0.0002	0.7849	0.0064	0.0018	0.7212	0.9677	-0.0103	-0.0142	0.5862	14.8761	0.0001	0.0087	0.0003	0.7212	12.2847	0	4.5971	0.0235
Dedd	25	1.3523	0.2901	0.3717	0.0035	0.0034	0.0377	0.9811	0.0033	0	0.0377	0.4118	0.6677							
Depdc6	23	3.6577	0.015	0.6154	0.0032	0.0016	0.5081	0.9836	-0.0006	-0.0114	0.5081	10.8468	0.0006							
Dhdh	23	8.8711	0.0002	0.7951	0.0028	0.0011	0.6061	0.9775	0.0097	-0.0068	0.6061	16.1567	0.0001							
Dhfr	25	6.2485	0.0012	0.7322	0.0202	0.0086	0.5763	0.9512	0.0189	-0.0257	0.5763	14.2835	0.0001							
Dhrs3	23	41.3689	0	0.9476	0.0199	0.0011	0.944	0.9571	0.0139	0.0366	0.9109	107.31	0	0.0013	-0.0072	0.944	80.0899	0	5.6229	0.0121
Dhx36	25	0.4571	0.8512	0.1666	0.0114	0.011	0.0389	0.9573	0.006	-0.0001	0.0389	0.4255	0.659							
Dhx9	25	14.4955	0	0.8638	0.0124	0.0021	0.8296	0.9626	0.0073	-0.0241	0.6105	16.459	0.0001	0.0028	0.0145	0.8296	23.1184	0	12.2084	0.0004
Dlat	25	2.2445	0.0856	0.4955	0.0074	0.0057	0.2318	0.9771	0.0117	0.0009	0.2318	3.1675	0.0628							
Dmap1	23	3.819	0.0125	0.6256	0.005	0.0042	0.1628	0.9783	0.0076	0.0037	0.1628	2.0419	0.1548							
Dnaja1	23	9.1253	0.0001	0.7997	0.0241	0.0064	0.7339	0.9262	-0.0317	-0.0166	0.6233	17.3729	0	0.0134	-0.0063	0.7339	13.0984	0	3.9473	0.0368
Dnaja2	25	8.5235	0.0002	0.7885	0.0042	0.0011	0.7333	0.9689	0.0039	-0.014	0.6139	16.6959	0	-0.0015	0.0063	0.7333	13.0608	0	4.253	0.0298
Dnajb1	23	13.9264	0	0.859	0.0628	0.0129	0.7951	0.8908	-0.0535	-0.0229	0.6285	17.7631	0	0.0269	-0.0116	0.7951	18.4311	0	7.724	0.0035
Dnajb6	25	10.016	0.0001	0.8142	0.0093	0.0024	0.7384	0.9608	-0.0056	-0.0201	0.5682	13.8147	0.0001	0.0026	0.0109	0.7384	13.408	0	6.1826	0.0085
Dnmt3b	23	13.822	0	0.8581	0.0247	0.0044	0.8216	0.9344	-0.0069	0.0397	0.8216	48.3598	0							
Dock4	25	4.4819	0.0062	0.6623	0.0125	0.0056	0.5479	0.9552	0.0236	-0.002	0.5479	12.7246	0.0002							
Dpp9	23	5.3493	0.0027	0.7006	0.0178	0.0064	0.6413	0.9612	0.0096	0.0291	0.6413	18.7689	0							
Dvl1	23	0.4339	0.8667	0.1596	0.0038	0.0034	0.0977	0.9776	-0.0037	0.004	0.0977	1.1374	0.3396							
Dym	25	1.3196	0.3035	0.366	0.0066	0.0055	0.1681	0.9701	0.0041	-0.009	0.1681	2.1211	0.1449							
Dynll2	23	2.4553	0.0648	0.5179	0.0075	0.0054	0.2751	0.9672	-0.005	0.0118	0.2751	3.9846	0.0341							
Ece2	23	3.0818	0.0295	0.5742	0.0136	0.0072	0.47	0.9475	-0.0235	0.001	0.47	9.3126	0.0013							
Edem1	25	9.2117	0.0001	0.8012	0.0068	0.0014	0.7943	0.9728	-0.0083	0.0098	0.3557	5.7959	0.0099	0.0147	-0.0072	0.7943	18.3395	0	20.2547	0
Efhd2	23	27.6168	0	0.9236	0.0245	0.0026	0.8927	0.9373	-0.0184	-0.0384	0.8927	87.3923	0							
Efna1	25	4.5995	0.0055	0.668	0.0471	0.0316	0.3296	0.9347	0.0138	0.033	0.3296	5.1615	0.015							
Egln2	25	1.7269	0.1728	0.4304	0.0024	0.0018	0.2437	0.9744	-0.0005	-0.0071	0.2437	3.3828	0.0533							
Eif1a	23	2.2974	0.0798	0.5013	0.0116	0.0095	0.1832	0.9645	-0.0082	0.0102	0.1832	2.3544	0.1195							
Eif1ad	25	9.6259	0.0001	0.8081	0.0069	0.0018	0.7365	0.9614	-0.01	-0.0129	0.4571	8.8394	0.0016	0.0124	0.003	0.7365	13.2734	0	10.071	0.001
Eif3j	23	2.2592	0.0839	0.4971	0.0033	0.0024	0.2815	0.9686	-0.0067	-0.0059	0.2815	4.1146	0.0311							
Eif4a1	25	8.5822	0.0002	0.7897	0.0016	0.0005	0.7058	0.9843	-0.0029	-0.0055	0.3288	5.1447	0.0152	-0.0024	0.0067	0.7058	11.3977	0.0001	12.1752	0.0004
Eif4a2	25	10.6063	0.0001	0.8227	0.0047	0.0018	0.6116	0.9688	0.0154	-0.0004	0.6116	16.5307	0							
Eif4b	23.8	10.6078	0.0001	0.8227	0.0102	0.0022	0.7882	0.9665	0.021	-0.0115	0.6725	21.5577	0	0.0044	0.009	0.7882	17.6753	0	5.1901	0.0159
Eif4e	23	1.3442	0.2933	0.3703	0.0236	0.0212	0.0989	0.9323	-0.008	-0.0115	0.0989	1.1521	0.3351							
Eif4ebp1	23	0.6938	0.6767	0.2329	0.0069	0.0054	0.2114	0.9682	0.0049	-0.0096	0.2114	2.8152	0.0826							
Eif4ebp2	25	0.9183	0.5178	0.2866	0.0065	0.0057	0.1162	0.9611	0.0078	0.0003	0.1162	1.38	0.2735							
Eif5	25	1.1155	0.4004	0.328	0.0398	0.0378	0.048	0.9347	0.011	-0.0064	0.048	0.5294	0.5966							
Elf1	23	6.179	0.0013	0.73	0.0098	0.0031	0.679	0.9641	0.017	0.013	0.5317	11.923	0.0003	0.011	0.0022	0.679	10.0495	0.0002	4.3603	0.0276
Elk4	23	2.8424	0.0396	0.5543	0.0061	0.0034	0.4475	0.9692	0.0033	-0.0144	0.4475	8.503	0.002							
Elovl5	23	20.7253	0	0.9007	0.017	0.0018	0.8953	0.9473	0.0295	0.0176	0.7841	38.1231	0	0.0064	-0.0105	0.8953	40.6037	0	10.088	0.001
Elovl6	23	11.1443	0	0.8298	0.0382	0.0109	0.7157	0.9303	-0.0338	-0.0345	0.7157	26.4309	0							
Elp4	25	6.5334	0.0009	0.7408	0.0208	0.0078	0.6234	0.9452	0.0124	0.0303	0.6234	17.3813	0							
Epm2aip1	23	3.1613	0.0268	0.5804	0.0151	0.0085	0.4354	0.942	-0.0155	0.0171	0.4354	8.0978	0.0025							
Erap1	23	2.8376	0.0398	0.5539	0.0042	0.0031	0.2668	0.9777	-0.0079	-0.0058	0.2668	3.8209	0.0384							
Erbb3	23	7.8115	0.0003	0.7736	0.0336	0.0099	0.7055	0.9363	0.0402	0.0093	0.5854	14.8238	0.0001	0.0032	-0.0177	0.7055	11.3792	0.0001	3.8753	0.0388
Erf	23	6.1386	0.0013	0.7287	0.0151	0.007	0.5398	0.9615	0.0239	-0.0108	0.5398	12.3162	0.0003							
Ergic1	25	5.6862	0.0019	0.7133	0.0055	0.0017	0.6879	0.9778	-0.0023	0.0152	0.5402	12.3373	0.0003	0.0038	-0.0075	0.6879	10.4686	0.0001	4.4942	0.0252
Erh	23	3.5193	0.0176	0.6063	0.0064	0.0038	0.4124	0.9585	-0.0145	-0.0046	0.4124	7.3685	0.0038							
Erp29	23	2.5426	0.0579	0.5266	0.0069	0.0044	0.3676	0.974	-0.0091	0.0111	0.3676	6.1044	0.0081							
Esrra	25	0.9797	0.4787	0.3	0.0046	0.0039	0.1529	0.971	-0.0047	-0.0059	0.1529	1.8958	0.175							
Etf1	25	9.0334	0.0001	0.7981	0.0067	0.0023	0.6538	0.9638	0.0096	-0.0125	0.4479	8.5193	0.002	0.0022	0.0102	0.6538	8.9698	0.0003	5.6486	0.0119
Etfdh	23.7	0.6431	0.7149	0.2196	0.0062	0.0052	0.1646	0.9669	0.0092	0.0014	0.1646	2.0683	0.1514							
Ethe1	23	13.7851	0	0.8578	0.0615	0.0094	0.8473	0.9126	0.0279	0.0595	0.8473	58.2413	0							
Etnk2	25	5.5262	0.0023	0.7074	0.0093	0.0046	0.4994	0.9625	0.0012	-0.0199	0.4994	10.4741	0.0007							
Ewsr1	23	1.878	0.1404	0.451	0.0024	0.002	0.18	0.9825	0.0011	-0.0058	0.18	2.3054	0.1244							
Exoc4	23.6	2.6776	0.0487	0.5395	0.0091	0.0044	0.5142	0.9572	0.0199	0.0009	0.5142	11.1159	0.0005							
Exosc2	23	2.1573	0.0961	0.4856	0.0042	0.003	0.2789	0.9735	-0.0095	0.003	0.2789	4.061	0.0323							
Extl2	23	1.2918	0.3152	0.3611	0.0079	0.0079	0.0064	0.9706	-0.0008	0.0018	0.0064	0.0678	0.9347							
F2r	23	1.259	0.3297	0.3552	0.0066	0.0053	0.1978	0.9702	-0.0003	0.0102	0.1978	2.5891	0.0988							
Fads2	25	8.5957	0.0002	0.7899	0.011	0.0033	0.7024	0.9438	0.0103	-0.0239	0.7024	24.7804	0							
Fahd1	23	2.6017	0.0537	0.5323	0.0128	0.0098	0.2391	0.9543	-0.0077	0.0137	0.2391	3.2996	0.0567							
Faim	23	2.3938	0.0703	0.5116	0.0146	0.0123	0.1615	0.9523	0.0058	0.0128	0.1615	2.0231	0.1572							
Farsb	23.1	0.4761	0.838	0.1724	0.0077	0.0068	0.1163	0.9722	-0.0061	0.006	0.1163	1.3819	0.273							
Fbxl20	23	10.0754	0.0001	0.8151	0.0279	0.0078	0.722	0.9429	0.0339	-0.0228	0.722	27.2697	0							
Fbxl3	23.5	4.4018	0.0067	0.6582	0.0051	0.0023	0.5486	0.9762	0.0132	0.0082	0.5486	12.759	0.0002							
Fbxo3	25	1.8264	0.1507	0.4441	0.0029	0.0026	0.0916	0.9731	0	0.0048	0.0916	1.0586	0.3647							
Fbxo33	25	9.1194	0.0001	0.7996	0.0269	0.0068	0.7468	0.9437	-0.0286	-0.0238	0.6426	18.8813	0	0.003	0.0146	0.7468	14.0085	0	3.9074	0.0379
Fbxw9	23	4.262	0.0078	0.6509	0.0063	0.0025	0.6067	0.9633	-0.0149	0.0009	0.4041	7.1217	0.0044	0.0095	-0.0038	0.6067	7.3265	0.001	4.8917	0.0193
Fdps	25	4.8502	0.0043	0.6797	0.0155	0.0057	0.6315	0.9539	-0.0009	0.0219	0.4107	7.318	0.0039	0.0103	-0.014	0.6315	8.139	0.0005	5.6908	0.0116
Fdx1	25	3.019	0.0318	0.5691	0.0039	0.0025	0.373	0.973	-0.0015	-0.011	0.373	6.2457	0.0074							
Fech	23	2.9612	0.0342	0.5644	0.0081	0.0047	0.421	0.9707	0.0009	-0.0166	0.421	7.6358	0.0032							
Fgd6	25	3.144	0.0274	0.579	0.0197	0.0106	0.4621	0.9513	0.0259	-0.0098	0.4621	9.0195	0.0015							
Fis1	25	1.1349	0.3901	0.3318	0.002	0.0015	0.2408	0.9823	-0.0036	-0.0051	0.2408	3.3298	0.0555							
Fkbp4	23.4	12.6536	0	0.847	0.0175	0.0028	0.8385	0.9539	-0.0268	0.0179	0.6871	23.0532	0	0.0079	-0.0122	0.8385	24.659	0	8.9063	0.0019
Flcn	25	15.434	0	0.871	0.0323	0.0059	0.818	0.945	0.0408	-0.0166	0.7344	29.0392	0	-0.0144	-0.0041	0.818	21.3501	0	4.3622	0.0276
Flnb	23	4.2947	0.0075	0.6526	0.0126	0.0051	0.5939	0.9486	-0.0075	-0.0236	0.5939	15.3527	0.0001							
Flot1	23.4	13.8243	0	0.8581	0.0105	0.0019	0.8174	0.9697	0.0209	-0.0116	0.6673	21.0569	0	0.0115	-0.0003	0.8174	21.2611	0	7.8094	0.0033
Fndc3a	23	3.9945	0.0103	0.636	0.0066	0.0054	0.1882	0.9633	-0.0082	-0.0063	0.1882	2.4346	0.112							
Fnip1	23	6.0396	0.0014	0.7255	0.0209	0.0071	0.6617	0.9411	0.018	-0.0281	0.6617	20.5352	0							
Frg1	25	1.3261	0.3008	0.3672	0.0055	0.0039	0.2986	0.9731	0.0113	-0.0029	0.2986	4.4691	0.0242							
Fusip1	23	3.1599	0.0268	0.5803	0.0052	0.0034	0.3533	0.9653	-0.0089	0.0084	0.3533	5.7354	0.0103							
Fzd4	23	6.2862	0.0012	0.7333	0.0264	0.0074	0.7195	0.9317	-0.0105	-0.038	0.7195	26.9367	0							
G3bp2	23	3.9621	0.0107	0.6342	0.003	0.002	0.3197	0.9829	-0.0016	0.0086	0.3197	4.9353	0.0175							
Gab1	23	2.0094	0.1174	0.4678	0.0155	0.0089	0.4254	0.9596	0	-0.023	0.4254	7.7725	0.003							
Gabarap	23	0.3552	0.9151	0.1345	0.0012	0.0012	0.0129	0.9876	-0.0004	0.001	0.0129	0.137	0.8728							
Gabarapl1	24	18.0836	0	0.8878	0.0252	0.0037	0.8523	0.9499	0.0418	-0.0066	0.8523	60.5706	0							
Gadd45a	25	2.5551	0.057	0.5278	0.0573	0.0301	0.4742	0.9074	0.0333	-0.0354	0.4742	9.4694	0.0012							
Galt	23	18.2826	0	0.8889	0.0123	0.0014	0.8835	0.9471	0.0118	0.027	0.8318	51.9212	0	0.0067	-0.0028	0.8835	36.0368	0	4.2217	0.0304
Gas2l3	23	3.2286	0.0247	0.5855	0.0184	0.0104	0.4338	0.9358	-0.0156	-0.0208	0.4338	8.0452	0.0025							
Gbf1	23	3.637	0.0154	0.6141	0.0083	0.0042	0.4948	0.9541	0.0071	0.017	0.4948	10.2844	0.0008							
Gcap14	23	2.5699	0.0559	0.5293	0.0034	0.0019	0.4311	0.9715	-0.0074	-0.0084	0.4311	7.9578	0.0027							
Gch1	24.6	21.7673	0	0.905	0.0397	0.0048	0.8795	0.9351	0.0403	-0.0367	0.8795	76.6015	0							
Gclm	25	3.0136	0.0321	0.5687	0.0041	0.0026	0.3786	0.9788	0.011	-0.0032	0.3786	6.3964	0.0068							
Gcnt2	23	3.2882	0.023	0.5899	0.0191	0.0096	0.4984	0.9303	0.0073	-0.0266	0.4984	10.4345	0.0007							
Ggnbp2	24.3	1.7392	0.1699	0.4321	0.0044	0.0028	0.3514	0.9643	0.0112	0.0012	0.3514	5.6876	0.0106							
Glo1	25	17.3479	0	0.8836	0.0071	0.0011	0.8473	0.9727	0.0141	0.017	0.8473	58.2524	0							
Glrx3	23	0.694	0.6766	0.2329	0.0051	0.0045	0.1172	0.9692	-0.0071	0.0013	0.1172	1.3944	0.27							
Glrx5	25	0.9417	0.5026	0.2918	0.0059	0.005	0.1599	0.9612	-0.0037	-0.008	0.1599	1.9987	0.1605							
Gna13	25	1.2938	0.3144	0.3614	0.0028	0.0026	0.0911	0.9782	0.003	-0.0036	0.0911	1.052	0.3669							
Gnaq	25	1.3121	0.3066	0.3647	0.0023	0.0021	0.0788	0.9822	0.0025	-0.0031	0.0788	0.8982	0.4224							
Gne	23	21.1171	0	0.9023	0.0199	0.0025	0.8766	0.9525	0.0045	-0.0371	0.8766	74.6018	0							
Gnl2	23	5.0227	0.0036	0.6872	0.0077	0.0059	0.2309	0.9624	0.005	-0.0108	0.2309	3.1522	0.0635							
Gnpda1	25	3.0399	0.031	0.5708	0.0188	0.0137	0.2677	0.9399	0.018	-0.0102	0.2677	3.8382	0.038							
Golga5	25	4.2447	0.0079	0.65	0.0055	0.0044	0.2006	0.9655	0.0058	-0.0079	0.2006	2.6351	0.0953							
Golim4	23	1.393	0.2743	0.3787	0.0041	0.0034	0.1721	0.9677	-0.0054	-0.0055	0.1721	2.1826	0.1377							
Gprc5c	23	4.7183	0.0049	0.6737	0.0062	0.0026	0.5785	0.9684	0.0166	-0.0054	0.5785	14.4102	0.0001							
Gprin3	25	5.2882	0.0028	0.6982	0.0092	0.0035	0.6153	0.9674	0.0148	-0.0103	0.4439	8.3823	0.0021	-0.0114	-0.0017	0.6153	7.5964	0.0008	4.231	0.0302
Grk5	23	27.3855	0	0.923	0.0616	0.0053	0.914	0.8745	0.0156	0.0602	0.7412	30.0648	0	0.0302	0.0041	0.914	50.5074	0	19.1062	0
Gsk3a	24.1	1.6657	0.1881	0.4215	0.0048	0.0029	0.3982	0.9735	0.0114	-0.0053	0.3982	6.9487	0.0048							
Gss	25	18.0689	0	0.8877	0.0147	0.0024	0.839	0.9455	0.0158	-0.0261	0.7466	30.9424	0	0.0005	0.0105	0.839	24.7544	0	5.4507	0.0135
Gsta3	24.4	3.9678	0.0107	0.6345	0.0014	0.0007	0.5244	0.987	-0.0057	0.001	0.2836	4.1566	0.0301	0.0034	0.004	0.5244	5.2364	0.0051	4.8086	0.0204
Gstz1	23	0.8421	0.5692	0.2692	0.0011	0.0011	0.0025	0.9822	-0.0001	0.0005	0.0025	0.0259	0.9745							
Gtf2f1	23	6.4531	0.001	0.7384	0.0134	0.0011	0.9154	0.9379	-0.0208	-0.003	0.3915	6.7548	0.0054	0.0164	0.0019	0.6047	7.266	0.001	5.1241	0.0166
Gtf3c2	24.8	2.656	0.0501	0.5375	0.0058	0.0035	0.399	0.9725	0.0119	-0.0074	0.399	6.971	0.0048							
H3f3b	25	3.2968	0.0228	0.5906	0.004	0.0029	0.2656	0.9731	0.0068	0.0062	0.2656	3.7975	0.0391							
Hars2	23	2.4887	0.0621	0.5213	0.0034	0.003	0.121	0.9789	-0.0019	0.0054	0.121	1.4456	0.2581							
Hectd3	24.6	8.4016	0.0002	0.7861	0.0088	0.0024	0.7275	0.9668	0.0221	-0.0066	0.7275	28.0315	0							
Herpud1	23	22.7607	0	0.9087	0.018	0.0033	0.8191	0.9581	-0.0057	-0.0342	0.8191	47.5434	0							
Hes6	25	3.8762	0.0118	0.6291	0.0127	0.0052	0.5886	0.9386	-0.0181	-0.0075	0.3799	6.4336	0.0066	0.0143	0.0041	0.5886	6.7964	0.0014	4.8192	0.0203
Hexim1	23.9	7.0782	0.0006	0.7559	0.0246	0.0073	0.7027	0.9272	-0.0339	-0.0066	0.5802	14.5112	0.0001	0.014	0.0074	0.7027	11.2267	0.0001	3.9145	0.0377

Hfe	23	2.2713	0.0826	0.4984	0.0045	0.0037	0.1727	0.9717	-0.0042	0.0067	0.1727	2.1921	0.1366							
Hipk3	25	6.3757	0.0011	0.7361	0.0074	0.0023	0.6927	0.9647	0.0133	-0.012	0.5463	12.6452	0.0002	-0.0065	0.0074	0.6927	10.7078	0.0001	4.5251	0.0247
Hist1h1c	25	12.6629	0	0.8471	0.0456	0.011	0.7593	0.9347	-0.04	0.0197	0.5648	13.6253	0.0002	0.0272	-0.007	0.7593	14.9815	0	7.6754	0.0036
Hist2h2aa1	23	1.6742	0.1859	0.4228	0.0038	0.0032	0.1638	0.9773	-0.0052	0.0049	0.1638	2.0563	0.1529							
Hmbs	24.4	2.5143	0.0601	0.5238	0.0059	0.0038	0.3602	0.9718	0.0095	0.0092	0.3602	5.9104	0.0092							
Hmg20b	25	0.9866	0.4744	0.3015	0.0037	0.0034	0.0721	0.9789	-0.004	-0.0022	0.0721	0.8158	0.4558							
Hn1l	23.4	6.2524	0.0012	0.7323	0.0125	0.0035	0.7235	0.9499	-0.0077	0.0193	0.3853	6.5806	0.006	0.0133	-0.0128	0.7235	12.4259	0	11.6172	0.0005
Hnrnpa1	25	3.8842	0.0117	0.6295	0.0057	0.0029	0.4925	0.9749	0.0146	0.0034	0.4925	10.1884	0.0008							
Hnrnpc	25	2.701	0.0473	0.5416	0.0103	0.0057	0.4452	0.9707	-0.0134	0.0148	0.4452	8.425	0.0021							
Hnrnpu	25	1.6488	0.1925	0.4191	0.0022	0.0016	0.272	0.9734	0.0013	0.007	0.272	3.9226	0.0357							
Hras1	23	0.5161	0.8096	0.1842	0.0087	0.0076	0.1262	0.9711	-0.0095	0.0019	0.1262	1.5168	0.2425							
Hsd17b12	23	1.6921	0.1813	0.4254	0.0028	0.002	0.2801	0.982	0.0024	0.0076	0.2801	4.0861	0.0317							
Hsp90aa1	24	26.8868	0	0.9216	0.0389	0.0041	0.8947	0.9321	-0.0483	0.0107	0.7559	32.5217	0	0.0157	-0.0143	0.8947	40.3544	0	12.5166	0.0003
Hspa2	23	3.7239	0.0139	0.6197	0.0183	0.0088	0.5172	0.9437	-0.0238	-0.0159	0.5172	11.2502	0.0005							
Hspa4	25	0.8327	0.5758	0.267	0.0008	0.0007	0.0998	0.9923	0.0023	0.0011	0.0998	1.1643	0.3315							
Hspa4l	23.5	30.3152	0	0.9299	0.0535	0.005	0.9068	0.9006	-0.0551	0.018	0.7292	28.2704	0	0.0092	-0.0262	0.9068	46.2182	0	18.1069	0
Htatip2	23	6.9774	0.0007	0.7532	0.0075	0.0025	0.6626	0.9521	0.0141	0.0052	0.3327	5.2361	0.0143	0.0143	0.0038	0.6626	9.3275	0.0002	9.2866	0.0015
Idh3a	23	5.7256	0.0019	0.7147	0.016	0.0056	0.6495	0.9453	-0.0164	-0.0246	0.6495	19.4592	0							
Ifnar2	25	1.3886	0.276	0.3779	0.0025	0.0019	0.2534	0.9721	0.0069	-0.0022	0.2534	3.5628	0.0465							
Ifrd1	23	4.6825	0.005	0.672	0.0264	0.0129	0.5121	0.9437	-0.0069	-0.0324	0.5121	11.0187	0.0005							
Igf1	24.2	0.8454	0.5669	0.27	0.0019	0.0016	0.1392	0.9808	-0.0038	-0.0028	0.1392	1.6986	0.2071							
Il15ra	23	24.9137	0	0.916	0.019	0.0023	0.8781	0.9479	0.0128	-0.0342	0.8781	75.6562	0							
Il1rap	23	2.0459	0.1117	0.4723	0.0028	0.0024	0.1734	0.9739	-0.0058	-0.003	0.1734	2.2023	0.1354							
Il6ra	23.5	7.5231	0.0004	0.767	0.0397	0.0138	0.6517	0.9313	-0.0085	-0.0454	0.6517	19.6424	0							
Ing2	25	3.3327	0.0219	0.5932	0.0099	0.0056	0.4298	0.9658	0.0183	-0.0043	0.4298	7.914	0.0027							
Ing4	23	3.4253	0.0196	0.5998	0.0063	0.0032	0.4875	0.965	0.0087	0.009	0.268	3.8437	0.0378	0.0072	-0.0076	0.4875	4.5179	0.0098	4.0687	0.0338
Inmt	23	4.5251	0.0059	0.6644	0.0034	0.0017	0.5006	0.9808	-0.0107	-0.0056	0.5006	10.5271	0.0007							
Insig2	23	35.4312	0	0.9394	0.0649	0.0057	0.9117	0.9206	0.0213	0.0659	0.8749	73.4404	0	0.0038	-0.0133	0.9117	49.0662	0	3.9636	0.0364
Insr	23	2.2775	0.0819	0.4991	0.0059	0.0034	0.4279	0.9609	0.0106	-0.0097	0.4279	7.8536	0.0028							
Ints10	23	3.8799	0.0117	0.6293	0.0102	0.0052	0.4951	0.9639	-0.0098	0.0176	0.4951	10.2956	0.0008							
Itpa	23	1.7407	0.1696	0.4323	0.0072	0.0063	0.1226	0.9715	-0.0084	-0.0027	0.1226	1.4677	0.2531							
Ivns1abp	25	41.0451	0	0.9472	0.0137	0.0009	0.9365	0.9543	-0.0112	-0.0271	0.7691	34.9742	0	0.002	0.0134	0.9365	70.0998	0	25.0657	0
Iws1	25	3.0386	0.0311	0.5707	0.0071	0.0036	0.4985	0.9606	0.0155	-0.0078	0.4985	10.4362	0.0007							
Jph1	23	4.5936	0.0055	0.6677	0.0267	0.0166	0.3789	0.9179	-0.0085	-0.0275	0.3789	6.4051	0.0067							
Junb	23	2.3445	0.075	0.5063	0.0132	0.0089	0.3292	0.9456	0.0191	-0.0028	0.3292	5.1522	0.0151							
Kcnk5	24.7	5.7661	0.0018	0.7161	0.0553	0.016	0.7107	0.8605	0.0132	-0.0498	0.5934	15.3212	0.0001	-0.0162	0.0174	0.7107	11.6684	0.0001	3.8529	0.0394
Kctd3	23	0.3079	0.9399	0.1187	0.0057	0.0055	0.021	0.9702	0.0029	-0.0013	0.021	0.2252	0.8003							
Keap1	25	0.4842	0.8323	0.1748	0.0016	0.0015	0.1062	0.9878	-0.0023	-0.0029	0.1062	1.2481	0.3075							
Kif1b	25	9.0372	0.0001	0.7981	0.0181	0.0049	0.7316	0.9501	0.0326	-0.0061	0.7316	28.6174	0							
Klf1	23	1.5717	0.2142	0.4075	0.0044	0.0031	0.3002	0.9699	0.0053	-0.0089	0.3002	4.5049	0.0236							
Klf12	23	1.9406	0.1289	0.4592	0.0194	0.0126	0.3506	0.9517	0.0165	0.0175	0.3506	5.6697	0.0107							
Klf13	23.2	15.3079	0	0.8701	0.0233	0.0046	0.8021	0.9423	-0.0063	-0.0385	0.8021	42.5483	0							
Klf6	25	3.8866	0.0116	0.6297	0.0091	0.0059	0.3489	0.9606	0.0157	0.0029	0.3489	5.6265	0.011							
Klf9	23	3.6797	0.0147	0.6168	0.0283	0.0153	0.4588	0.9257	0.0332	-0.0043	0.4588	8.8997	0.0016							
Klhl21	23	5.6503	0.002	0.712	0.0211	0.0069	0.6722	0.9389	0.0119	-0.0315	0.6722	21.5282	0							
Kpnb1	23	7.0825	0.0006	0.756	0.0081	0.0029	0.6412	0.9756	-0.0061	0.0195	0.6412	18.7665	0							
L2hgdh	23.7	5.8454	0.0017	0.7189	0.0112	0.0037	0.6749	0.9567	0.0015	-0.0158	0.2663	3.8104	0.0387	0.0088	0.0176	0.6749	9.8588	0.0002	11.9379	0.0004
l7Rn6	23	6.1191	0.0013	0.728	0.0112	0.0036	0.6784	0.9685	-0.0189	0.0134	0.5477	12.7164	0.0002	0.0082	-0.007	0.6784	10.0177	0.0002	3.8579	0.0393
Lars2	23	1.0669	0.4271	0.3182	0.0045	0.004	0.0999	0.9782	0.0016	0.0058	0.0999	1.1655	0.3311							
Lasp1	23	45.4075	0	0.9521	0.0222	0.0012	0.9476	0.9687	0.0051	0.0387	0.8115	45.2026	0	-0.0054	-0.0151	0.9476	85.9077	0	24.6781	0
Lcp1	25	3.3624	0.0211	0.5953	0.0055	0.0028	0.5017	0.9692	0.0109	-0.0111	0.5017	10.5727	0.0007							
Leprot	25	1.619	0.2006	0.4146	0.0085	0.0059	0.3032	0.9679	0.0145	-0.0003	0.3032	4.5682	0.0225							
Lias	25	0.3623	0.9111	0.1368	0.0052	0.0051	0.021	0.9741	0.003	-0.0003	0.021	0.225	0.8004							
Lig3	25	1.9393	0.1291	0.459	0.0072	0.0061	0.1449	0.9756	-0.0005	0.0094	0.1449	1.7788	0.1934							
Lin52	23	5.3297	0.0027	0.6999	0.0084	0.0038	0.5423	0.9598	-0.0027	-0.019	0.5423	12.4413	0.0003							
Lin54	25	3.2874	0.0231	0.5899	0.0107	0.0052	0.5152	0.955	0.0176	-0.0129	0.5152	11.157	0.0005							
Litaf	23	6.5713	0.0009	0.7419	0.017	0.0057	0.6667	0.9641	0.0016	0.0302	0.6667	21.0042	0							
Lonp2	25	16.3972	0	0.8777	0.0088	0.0012	0.8667	0.9714	0.0217	0.0094	0.8062	43.6831	0	-0.0057	0.0039	0.8667	30.8967	0	4.3157	0.0285
Lpgat1	25	1.3754	0.281	0.3757	0.0021	0.0016	0.2321	0.9749	-0.0042	-0.0047	0.2321	3.1731	0.0625							
Lpin1	23	16.5754	0	0.8788	0.1179	0.0016	0.9863	0.8351	-0.0208	-0.0821	0.7217	27.2237	0	-0.005	0.0295	0.8112	20.4058	0	4.5037	0.0251
Lpp	23.3	0.5472	0.7867	0.1932	0.0055	0.0048	0.1391	0.9717	0.006	0.0054	0.1391	1.6959	0.2076							
Lrrc28	23	17.6091	0	0.8851	0.0527	0.0072	0.8638	0.9121	-0.0414	-0.0465	0.8638	66.6128	0							
Lsm14b	25	1.7108	0.1767	0.4281	0.0069	0.0056	0.1973	0.9626	0.0105	0.0004	0.1973	2.5816	0.0994							
Ltbr	25	4.5111	0.006	0.6637	0.0079	0.003	0.6261	0.9596	0.0155	-0.0137	0.6261	17.5807	0							
Luc7l2	23	2.2876	0.0808	0.5002	0.0039	0.0028	0.2978	0.9702	0.0093	-0.0036	0.2978	4.4524	0.0244							
Lyrm4	25	3.7142	0.0141	0.619	0.0062	0.003	0.5153	0.9706	0.0096	-0.007	0.3074	4.6612	0.0211	-0.0079	0.0073	0.5153	5.0492	0.0061	4.073	0.0337
Mad2l2	23	31.46	0	0.9323	0.0303	0.0025	0.9174	0.9487	0.0157	0.0452	0.9174	116.598	0							
Mafb	23	6.2387	0.0012	0.7319	0.076	0.0303	0.6017	0.8741	0.0089	-0.0598	0.6017	15.8597	0.0001							
Mak10	23.7	1.179	0.3676	0.3403	0.0044	0.0033	0.2451	0.9647	0.0075	-0.0058	0.2451	3.4096	0.0522							
Map2k3	23.5	12.3805	0	0.8442	0.0105	0.0029	0.7199	0.9606	-0.0125	-0.0219	0.7199	26.9845	0							
Map2k7	23.2	3.2795	0.0233	0.5893	0.0084	0.0042	0.5028	0.9656	0.019	-0.001	0.5028	10.6168	0.0007							
Map3k1	25	5.0584	0.0035	0.6888	0.014	0.0072	0.4856	0.9414	0.0108	0.0209	0.4856	9.9124	0.0009							
Map3k7ip2	23.8	22.7823	0	0.9088	0.0127	0.0024	0.8087	0.9669	0.0121	0.0267	0.8087	44.3755	0							
Marcks	25	1.8558	0.1447	0.4481	0.0112	0.0104	0.0728	0.9624	0.0052	0.0062	0.0728	0.8242	0.4523							
Masp1	25	1.4743	0.2451	0.3921	0.0016	0.0011	0.3241	0.9801	0.0051	-0.0045	0.3241	5.0356	0.0164							
Mat2a	23.1	10.2717	0.0001	0.818	0.0128	0.0035	0.7264	0.9584	-0.021	-0.019	0.7264	27.8791	0							
Mbtd1	23	4.8973	0.0041	0.6818	0.0177	0.0102	0.4235	0.9444	0.0228	-0.0106	0.4235	7.7135	0.0031							
Mcart1	23	5.4289	0.0025	0.7037	0.0253	0.0093	0.6317	0.9252	-0.0135	-0.0337	0.6317	18.0109	0							
Mcfd2	23	4.7814	0.0046	0.6766	0.006	0.0024	0.5939	0.9736	-0.0141	0.0098	0.5939	15.3569	0.0001							
Mcl1	25	1.3925	0.2745	0.3786	0.0028	0.0025	0.1146	0.9769	0.0011	-0.0052	0.1146	1.3591	0.2786							
Mcm10	23	4.7001	0.005	0.6728	0.0262	0.0167	0.3608	0.9204	0.0021	-0.0275	0.3608	5.9271	0.0091							
Med28	23	1.4733	0.2455	0.3919	0.0097	0.008	0.1765	0.9638	0.0051	0.0108	0.1765	2.2502	0.1302							
Med8	25	3.4192	0.0198	0.5993	0.005	0.002	0.5957	0.9718	-0.0017	0.0106	0.3115	4.7508	0.0199	0.0109	0.0012	0.5957	6.9984	0.0012	6.6772	0.0064
Mef2a	23	2.0885	0.1055	0.4775	0.0063	0.0038	0.4064	0.9603	0.013	-0.0068	0.4064	7.1884	0.0042							
Metap2	23	1.8291	0.1501	0.4445	0.0028	0.0024	0.148	0.9809	-0.0014	-0.0056	0.148	1.8239	0.186							
Mfsd1	25	0.8038	0.5962	0.2602	0.0054	0.0045	0.1638	0.9564	0.0053	-0.007	0.1638	2.0572	0.1528							
Mgea5	23	3.9103	0.0113	0.6311	0.0084	0.0035	0.5889	0.9614	0.0182	-0.0092	0.5889	15.0382	0.0001							
Mgll	23.1	6.2842	0.0012	0.7333	0.0111	0.0045	0.5947	0.9615	-0.0096	-0.0213	0.5947	15.4061	0.0001							
Mitf	25	2.323	0.0771	0.504	0.0104	0.0091	0.1248	0.9567	0.0014	0.0104	0.1248	1.4973	0.2467							
Mkks	23.1	1.8711	0.1417	0.4501	0.0084	0.0048	0.4285	0.9457	-0.0173	-0.0036	0.4285	7.8725	0.0028							
Mknk2	25	9.9497	0.0001	0.8132	0.035	0.009	0.7426	0.9277	-0.0046	-0.0467	0.7426	30.2862	0							
Mkrn1	23	2.4464	0.0656	0.517	0.0087	0.0057	0.3483	0.9533	0.0151	0.0059	0.3483	5.6114	0.0112							
Mll3	25	0.9957	0.4689	0.3034	0.0142	0.0126	0.1076	0.9533	0.009	-0.0071	0.1076	1.2657	0.3027							
Mllt10	23	1.5139	0.2321	0.3984	0.0115	0.009	0.2212	0.9559	0.0108	-0.0096	0.2212	2.9826	0.0724							
Mlx	25	5.6491	0.002	0.7119	0.0059	0.0022	0.6317	0.9638	-0.0135	-0.0033	0.4111	7.3284	0.0039	0.0077	0.0066	0.6317	8.1461	0.0005	5.6902	0.0116
Mn1	23.1	5.4841	0.0023	0.7058	0.0223	0.0076	0.6606	0.9291	0.033	0.0139	0.6606	20.4391	0							
Mobkl1a	25	3.3396	0.0217	0.5937	0.0075	0.0038	0.4983	0.9659	0.0153	-0.0093	0.4983	10.428	0.0007							
Mobkl2b	23	1.5268	0.228	0.4005	0.0209	0.0141	0.3245	0.9349	0.0239	0.0043	0.3245	5.0444	0.0163							
Mocos	24.4	5.5446	0.0022	0.7081	0.0177	0.0061	0.655	0.9493	0.0102	0.024	0.4776	9.6005	0.0011	0.0155	-0.0053	0.655	9.0168	0.0003	4.8829	0.0194
Morf4l1	23	2.2295	0.0873	0.4938	0.0045	0.0033	0.273	0.9726	0.0065	-0.0076	0.273	3.9427	0.0352							
Mpdz	24.1	4.8357	0.0043	0.679	0.0117	0.0043	0.6307	0.9404	0.0245	-0.003	0.6307	17.9317	0							
Mpi	23	5.3251	0.0027	0.6997	0.007	0.0034	0.5069	0.9543	-0.0131	0.0016	0.2878	4.2421	0.0284	0.0113	0.0027	0.5069	4.8836	0.007	4.223	0.0304
Mrpl15	23	12.5366	0	0.8458	0.0079	0.0026	0.6771	0.9693	-0.0215	0.0012	0.6771	22.0179	0							
Mrpl19	23	1.7307	0.1719	0.4309	0.0064	0.0046	0.2709	0.9716	-0.0116	0.0035	0.2709	3.9009	0.0363							
Mrpl20	23	1.7947	0.1574	0.4398	0.0089	0.0062	0.2962	0.9721	-0.0148	-0.0033	0.2962	4.4188	0.025							
Mrpl34	23	1.1138	0.4013	0.3276	0.0091	0.0074	0.183	0.9634	-0.0085	0.008	0.183	2.3522	0.1197							
Mrps22	23	1.4284	0.2612	0.3846	0.0032	0.0031	0.0435	0.9774	-0.0017	0.0029	0.0435	0.4774	0.627							
Mrps24	25	0.2863	0.9499	0.1113	0.0043	0.0042	0.0195	0.9788	0.0015	-0.0023	0.0195	0.2087	0.8133							
Mrps25	23	2.3043	0.0791	0.502	0.0073	0.0056	0.2308	0.9707	-0.0033	0.0111	0.2308	3.1503	0.0636							
Mrps27	23.8	4.5979	0.0055	0.6679	0.0112	0.0042	0.6218	0.9647	-0.0085	0.0154	0.3217	4.9799	0.017	0.014	-0.0089	0.6218	7.8079	0.0007	7.536	0.0039
Mrps9	25	9.5339	0.0001	0.8066	0.0057	0.0013	0.7693	0.9605	0.0135	-0.0064	0.5142	11.1158	0.0005	-0.007	0.0089	0.7693	15.8359	0	10.4995	0.0008
Mrto4	23	2.8159	0.0409	0.552	0.007	0.0041	0.4208	0.957	-0.012	-0.0106	0.4208	7.6273	0.0032							
Msi2	23	3.736	0.0138	0.6204	0.0062	0.0033	0.4678	0.9665	0.0142	0.0072	0.4678	9.2279	0.0013							
Mta3	25	1.9003	0.1362	0.454	0.0063	0.0046	0.267	0.965	0.0111	0.0033	0.267	3.8243	0.0383							
Mterfd2	25	1.553	0.2198	0.4046	0.011	0.0084	0.2315	0.9506	0.0136	0.0041	0.2315	3.1627	0.063							
Mthfd1l	23	4.6175	0.0054	0.6689	0.0336	0.0171	0.4903	0.8873	-0.0155	-0.0336	0.4903	10.101	0.0008							
Mtif2	25	3.9208	0.0112	0.6317	0.0078	0.0039	0.5073	0.9703	0.0151	0.0095	0.5073	10.8122	0.0006							
Mtmr10	23	5.5009	0.0023	0.7065	0.0132	0.0065	0.5069	0.9662	0.0059	-0.0223	0.5069	10.7928	0.0006							
Mtmr2	25	0.6666	0.6972	0.2258	0.0041	0.0035	0.1626	0.9811	0.0047	-0.006	0.1626	2.0382	0.1552							
Mtpn	23	2.9015	0.0368	0.5594	0.0009	0.0007	0.2297	0.9897	-0.002	-0.0036	0.2297	3.1315	0.0645							
Myo1b	23	3.1191	0.0282	0.5771	0.0055	0.0028	0.4825	0.9699	0.0001	0.0146	0.4825	9.7886	0.001							
N6amt1	25	3.6512	0.0151	0.615	0.0104	0.0048	0.5407	0.9457	0.0198	-0.009	0.5407	12.3609	0.0003							
Nab1	25	4.7341	0.0048	0.6744	0.017	0.0071	0.5823	0.9553	0.0166	-0.0143	0.3473	5.5871	0.0113	0.003	0.0176	0.5823	6.6209	0.0016	5.3436	0.0144
Naca	25	2.4459	0.0656	0.5169	0.0045	0.0034	0.2498	0.9788	0.0085	-0.0048	0.2498	3.4965	0.0489							
Nadk	23	1.9916	0.1202	0.4656	0.0036	0.0024	0.3324	0.9643	-0.0039	-0.0092	0.3324	5.2269	0.0144							
Nagk	23	3.7094	0.0142	0.6187	0.0061	0.0049	0.2075	0.973	0.0099	-0.0031	0.2075	2.7498	0.087							
Narg2	23	0.8814	0.5423	0.2783	0.0111	0.0101	0.086	0.9632	-0.0022	0.0084	0.086	0.9885	0.3888							
Nat13	23	2.7325	0.0454	0.5445	0.0116	0.0061	0.4785	0.9585	-0.0048	-0.0208	0.4785	9.6338	0.0011							
Nbr1	25	1.8586	0.1442	0.4485	0.0037	0.0023	0.3758	0.9697	0.0085	-0.0069	0.3758	6.3209	0.0071							
Ncbp2	23	4.3001	0.0075	0.6529	0.0092	0.0045	0.5104	0.964	-0.0191	0.0061	0.5104	10.9456	0.0006							
Nck1	23	5.5032	0.0023	0.7065	0.0103	0.0083	0.1955	0.9457	-0.0108	-0.0076	0.1955	2.5516	0.1019							
Ncl	25	1.0639	0.4288	0.3176	0.0084	0.0082	0.0286	0.9544	-0.0018	-0.0041	0.0286	0.309	0.7374							
Ncoa2	24.5	5.0875	0.0034	0.69	0.0046	0.0017	0.6235	0.9736	0.0153	-0.0008	0.6235	17.3905	0							
Ncor1	25	1.2454	0.3359	0.3527	0.0043	0.0034	0.205	0.9735	0.0084	0	0.205	2.707	0.09							
Ndufa9	23	1.285	0.3182	0.3599	0.0016	0.0015	0.0032	0.9881	-0.0006	0.0003	0.0032	0.0338	0.9668							
Ndufb5	23	3.1706	0.0265	0.5811	0.0027	0.0025	0.0805	0.9827	-0.0033	0.0027	0.0805	0.9189	0.4144							
Ndufb6	23	1.4314	0.2601	0.3851	0.0028	0.0027	0.0606	0.9793	-0.0029	0.0023	0.0606	0.6774	0.5187							
Ndufb9	25	0.1891	0.9836	0.0764	0.0095	0.0095	0.0023	0.9688	0.0009	0.001	0.0023	0.0244	0.9759							
Ndufc2	24.7	1.1135	0.4015	0.3276	0.0014	0.0011	0.1924	0.9884	-0.0025	-0.0039	0.1924	2.5016	0.1061							
Ndufs8	25	1.5591	0.218	0.4055	0.0022	0.0016	0.2716	0.9814	-0.007	0.0002	0.2716	3.9145	0.0359							
Nek4	23.7	8.2042	0.0003	0.7821	0.0111	0.0034	0.6938	0.9689	-0.0057	0.0191	0.4208	7.6278	0.0032	0.0151	-0.0047	0.6938	10.7605	0.0001	8.468	0.0023
Nelf	23	1.9686	0.1241	0.4627	0.0062	0.0038	0.3922	0.9636	0.0081	0.0118	0.3922	6.7759	0.0054							
Nfe2l2	25	2.3533	0.0741	0.5073	0.0088	0.0077	0.129	0.961	0.0089	-0.004	0.129	1.5558	0.2344							
Nfix	23	2.5555	0.057	0.5279	0.0045	0.0024	0.4638	0.9718	0.0087	-0.0096	0.4638	9.0822	0.0014							
Nfkbia	23	6.2832	0.0012	0.7333	0.0212	0.0074	0.6535	0.94	0.0162	-0.0292	0.6535	19.8072	0							
Nfx1	23	3.4985	0.018	0.6048	0.0116	0.0064	0.4478	0.9599	0.0164	-0.0126	0.4478	8.5144	0.002							
Ninj1	23	1.9773	0.1226	0.4638	0.0058	0.0035	0.389	0.977	-0.0002	0.0134	0.389	6.6857	0.0057							
Nob1	23	3.6153	0.0158	0.6127	0.0106	0.0047	0.5582	0.9569	-0.0227	-0.0003	0.5582	13.2675	0.0002							
Nr1d1	23.8	33.2004	0	0.9356	0.3771	0.046	0.878	0.8167	0.1558	-0.0579	0.878	75.5668	0							
Nr1d2	25	15.8668	0	0.8741	0.1677	0.025	0.8507	0.8856	0.0663	-0.0899	0.8507	59.815	0							
Nr3c2	23	3.1005	0.0288	0.5756	0.0355	0.0207	0.417	0.9181	0.0287	-0.02	0.417	7.5116	0.0035							
Nr6a1	23	2.6293	0.0518	0.535	0.0123	0.0092	0.2556	0.9512	0.0165	0	0.2556	3.6058	0.0451							
Nras	23	1.7197	0.1746	0.4293	0.009	0.0069	0.2369	0.9593	0.0038	-0.0125	0.2369	3.2597	0.0585							
Nudt19	24.5	0.9861	0.4747	0.3014	0.0077	0.0071	0.0795	0.9589	0.0071	0.0005	0.0795	0.9063	0.4192							
Nufip2	23	3.016	0.032	0.5689	0.0096	0.0058	0.3962	0.9536	-0.0105	-0.0146	0.3962	6.8904	0.005							
Nup133	25	3.8993	0.0115	0.6304	0.0135	0.0057	0.5741	0.9608	0.025	-0.0035	0.5741	14.1561	0.0001							
Nup88	25	1.8194	0.1522	0.4432	0.0101	0.0091	0.1016	0.9571	0.0071	-0.0062	0.1016	1.1872	0.3247							
Oaz1	25	3.1482	0.0272	0.5794	0.0023	0.0018	0.2208	0.9761	0.0064	-0.001	0.2208	2.975	0.0729							
Odc1	23	13.5654	0	0.8558	0.0258	0.0046	0.8203	0.924	-0.0421	0.007	0.8203	47.9465	0							
Ola1	23	1.1549	0.3798	0.3357	0.0056	0.0046	0.1706	0.9556	-0.008	0.004	0.1706	2.1593	0.1403							
ORF19	23.3	3.0585	0.0303	0.5723	0.0061	0.0032	0.4703	0.9681	0.0149	0.0051	0.4703	9.3217	0.0013							
Ormdl3	23	8.5613	0.0002	0.7893	0.0145	0.0034	0.7647	0.9641	-0.0067	0.0276	0.6621	20.5757	0	-0.0026	-0.0108	0.7647	15.4403	0	4.144	0.0321
Osgin1	25	7.9809	0.0003	0.7774	0.0325	0.0111	0.6586	0.9329	-0.0013	0.0429	0.6586	20.2595	0							
Ostf1	23	1.3309	0.2988	0.368	0.0052	0.0035	0.3259	0.9739	-0.0045	-0.011	0.3259	5.0763	0.0159							
Oxr1	25	1.8309	0.1498	0.4448	0.0043	0.0032	0.238	0.9694	0.0081	0.0039	0.238	3.2792	0.0576							
Oxsm	23	2.0931	0.1048	0.478	0.0063	0.0045	0.2833	0.9627	0.0085	0.009	0.2833	4.1507	0.0303							
Pah	24	8.3017	0.0002	0.7841	0.0017	0.0004	0.7495	0.9825	-0.0045	-0.0092	0.7495	31.4178	0							
Paip1	23	3.4589	0.0189	0.6021	0.0067	0.0042	0.3739	0.9741	-0.0024	-0.0141	0.3739	6.2703	0.0073							
Pan3	23	3.2193	0.025	0.5848	0.0078	0.0055	0.2943	0.9574	0.0028	-0.0132	0.2943	4.3797	0.0257							
Pank1	24.7	2.2421	0.0859	0.4952	0.0169	0.0142	0.16	0.9313	0.0147	-0.0031	0.16	2	0.1603							
Papd4	24.7	7.2281	0.0005	0.7597	0.0059	0.0017	0.7121	0.9667	0.0156	0.0098	0.7121	25.965	0							
Paqr9	24.7	7.4477	0.0005	0.7652	0.0223	0.0055	0.7556	0.9523	0.0031	0.0346	0.6558	20.0074	0	0.0003	-0.0136	0.7556	14.6877	0	3.8801	0.0386
Parp12	25	3.1177	0.0282	0.577	0.0075	0.0037	0.5087	0.9577	0.0158	0.0075	0.5087	10.8734	0.0006							
Parp14	25	2.8188	0.0408	0.5522	0.008	0.0062	0.2244	0.957	0.012	0.001	0.2244	3.038	0.0694							
Parp16	23	2.2096	0.0896	0.4915	0.0052	0.0034	0.3512	0.9615	-0.0119	0.0036	0.3512	5.6831	0.0107							

Pawr	25	3.5306	0.0174	0.607	0.0145	0.0074	0.4914	0.9542	0.0049	-0.0171	0.2668	3.8206	0.0385	0.003	0.0158	0.4914	4.5892	0.0092	4.1953	0.031
Pcmtd2	23	2.0643	0.109	0.4746	0.011	0.0071	0.3575	0.9316	0.0173	-0.0058	0.3575	5.8426	0.0096							
Pcsk4	23	2.7887	0.0423	0.5496	0.0079	0.0044	0.4443	0.9667	0.0123	-0.0116	0.4443	8.3935	0.0021							
Pdcd2	23	1.5799	0.2118	0.4087	0.0054	0.0044	0.1829	0.969	-0.0004	-0.0089	0.1829	2.3503	0.1199							
Pdcl3	25	3.585	0.0163	0.6107	0.0092	0.0051	0.4511	0.9551	0.0021	0.0187	0.4511	8.6283	0.0018							
Pde9a	23	25.396	0	0.9174	0.0419	0.0038	0.9092	0.9491	-0.0009	0.0516	0.729	28.2401	0	0.0103	-0.0222	0.9092	47.5499	0	18.8504	0
Pdhx	23.6	7.6637	0.0004	0.7703	0.0065	0.0017	0.7448	0.9614	-0.0059	-0.0176	0.6403	18.6903	0	0.0065	0.004	0.7448	13.8631	0	3.8906	0.0383
Pdia6	23	3.6457	0.0152	0.6146	0.0067	0.0031	0.5427	0.9711	-0.007	0.0156	0.5427	12.4608	0.0003							
Pdk1	23	1.1285	0.3935	0.3305	0.0087	0.0081	0.0681	0.9706	-0.0065	0.0026	0.0681	0.7671	0.4769							
Pdk4	25	16.8612	0	0.8806	0.1491	0.0186	0.8755	0.8497	-0.0112	0.0931	0.7195	26.9284	0	0.0408	0.0159	0.8755	33.4106	0	11.9108	0.0004
Pdrg1	25	0.7233	0.6548	0.2404	0.0046	0.0046	0.019	0.9788	0.0009	0.0025	0.019	0.2031	0.8178							
Pdss2	25	3.2831	0.0232	0.5895	0.0111	0.0063	0.4338	0.9684	0.0088	0.0178	0.4338	8.045	0.0025							
Pex11a	23	2.6574	0.05	0.5376	0.0085	0.0047	0.4512	0.961	-0.0023	-0.0175	0.4512	8.6341	0.0018							
Pex16	25	4.9808	0.0038	0.6854	0.0103	0.0034	0.6699	0.9554	0.018	0.0106	0.5262	11.6631	0.0004	-0.0038	-0.0101	0.6699	9.6395	0.0002	4.1343	0.0323
Pex26	24.7	3.8061	0.0127	0.6248	0.0218	0.0103	0.5286	0.9261	-0.02	-0.0233	0.5286	11.7763	0.0004							
Pex6	25	0.5713	0.7688	0.2	0.0063	0.0054	0.1402	0.9628	0.0084	0.0007	0.1402	1.7118	0.2048							
Pfdn2	23	2.1132	0.102	0.4804	0.0076	0.0045	0.4122	0.9646	-0.0085	-0.0138	0.4122	7.3645	0.0038							
Pfkfb3	23	19.8789	0	0.8969	0.1417	0.0281	0.8019	0.8213	-0.0388	-0.0811	0.6445	19.0331	0	-0.018	0.038	0.8019	19.2228	0	7.5462	0.0039
Phf17	24.9	21.0223	0	0.9019	0.027	0.0037	0.8638	0.9361	0.0404	-0.0184	0.8638	66.6018	0							
Phldb2	25	2.4471	0.0655	0.517	0.0153	0.0091	0.4062	0.9497	0.0223	0.0022	0.4062	7.1836	0.0042							
Pigl	23	3.5793	0.0164	0.6103	0.0071	0.0035	0.5135	0.9634	0.0069	0.016	0.5135	11.0823	0.0005							
Pih1d1	25	1.3918	0.2747	0.3785	0.0057	0.0047	0.1715	0.9719	0.0078	-0.0048	0.1715	2.1731	0.1388							
Pik3r1	23	3.631	0.0155	0.6137	0.0234	0.0149	0.3644	0.9376	-0.0216	-0.0164	0.3644	6.0193	0.0086							
Pim1	23	15.8051	0	0.8737	0.0469	0.0073	0.844	0.9259	0.0551	-0.001	0.7606	33.3517	0	-0.0067	-0.017	0.844	25.7082	0	5.086	0.017
Pim3	23	3.1121	0.0284	0.5766	0.0236	0.0133	0.4349	0.9241	0.0099	-0.0269	0.4349	8.082	0.0025							
Pip5k1a	23	1.3924	0.2745	0.3786	0.0052	0.0044	0.1535	0.9703	0.0032	-0.0073	0.1535	1.9044	0.1738							
Pitpnb	25	2.267	0.0831	0.4979	0.0015	0.0013	0.1432	0.9813	0.0017	0.0038	0.1432	1.7554	0.1973							
Pitpnc1	23	20.1619	0	0.8982	0.0283	0.0036	0.8721	0.9305	0.0104	-0.0431	0.8721	71.6217	0							
Pla2g12b	24.6	7.5227	0.0004	0.767	0.0138	0.0037	0.7313	0.9647	0.0137	0.0254	0.7313	28.58	0							
Plcg1	23	2.9455	0.0348	0.5631	0.0095	0.0047	0.5084	0.9594	0.0047	-0.0191	0.5084	10.8587	0.0006							
Plekha3	23	3.7287	0.0139	0.62	0.0047	0.0022	0.5395	0.9719	-0.0079	-0.0123	0.5395	12.3014	0.0003							
Plxna2	25	5.6486	0.002	0.7119	0.0441	0.0157	0.6434	0.908	0.0128	0.047	0.6434	18.9413	0							
Pnkd	23	40.7472	0	0.9469	0.0613	0.0037	0.9403	0.94	-0.0063	0.0666	0.8685	69.3303	0	0.0048	-0.0181	0.9403	74.8241	0	11.4326	0.0006
Pnpla2	25	22.5775	0	0.9081	0.0277	0.0027	0.9039	0.9406	0.0322	-0.0309	0.8632	66.2748	0	-0.0098	0.0015	0.9039	44.6687	0	4.0174	0.0351
Pnrc2	23	3.6875	0.0145	0.6173	0.0134	0.0076	0.4331	0.9606	0.0081	0.0203	0.4331	8.0225	0.0026							
Ppa1	23	2.795	0.042	0.5501	0.0061	0.0035	0.4215	0.9776	-0.0047	0.0135	0.4215	7.6515	0.0032							
Ppara	24	16.6787	0	0.8795	0.0215	0.0037	0.8294	0.9544	0.0204	-0.0327	0.8294	51.0566	0							
Ppargc1b	23	8.9317	0.0002	0.7962	0.0167	0.0035	0.7879	0.9417	0.0223	-0.0188	0.6171	16.9237	0	-0.0143	-0.0071	0.7879	17.6413	0	7.6464	0.0037
Ppib	23	1.7842	0.1597	0.4384	0.0029	0.002	0.3198	0.982	-0.0022	0.0084	0.3198	4.9374	0.0175							
Ppm1k	23	4.08	0.0094	0.6409	0.0194	0.0095	0.5084	0.9277	0.0284	-0.0061	0.5084	10.8589	0.0006							
Ppp1cc	23	2.337	0.0757	0.5056	0.0051	0.0033	0.357	0.9728	0.0019	-0.012	0.357	5.8297	0.0097							
Ppp1r14b	23	1.1667	0.3738	0.3379	0.0168	0.0123	0.2662	0.9558	-0.0186	-0.0067	0.2662	3.8087	0.0388							
Ppp1r3b	23.1	15.0824	0	0.8684	0.0668	0.0097	0.8551	0.9419	-0.0606	0.0272	0.7958	40.9199	0	0.0127	0.0136	0.8551	28.0233	0	3.8847	0.0385
Ppp2r1a	23	13.0996	0	0.8514	0.0027	0.0097	-2.5612	0.9768	0.0108	0.0062	0.6589	20.2814	0	-0.0003	-0.0047	0.7599	15.0345	0	3.9976	0.0356
Ppp2r1b	23	1.4421	0.2563	0.3869	0.0091	0.0077	0.1584	0.9371	0.0108	0.0031	0.1584	1.9766	0.1635							
Ppp2r5a	25	3.3988	0.0202	0.5979	0.0034	0.0016	0.5187	0.9752	0.0119	0.0009	0.5187	11.3161	0.0005							
Ppp3ca	25	4.6942	0.005	0.6725	0.0069	0.0032	0.5348	0.9663	0.0145	-0.0105	0.5348	12.072	0.0003							
Ppp3cb	25	2.318	0.0776	0.5035	0.0045	0.0035	0.2226	0.9731	0.0091	0	0.2226	3.0064	0.0711							
Pqlc1	23	2.3912	0.0705	0.5113	0.0118	0.0093	0.213	0.9513	-0.0148	0.0002	0.213	2.8423	0.0808							
Pqlc2	25	2.5107	0.0603	0.5235	0.0091	0.008	0.1167	0.9729	0.0088	0.0027	0.1167	1.3869	0.2718							
Prdx6	23	0.9811	0.4779	0.3003	0.0025	0.0025	0.0066	0.9836	-0.0009	0.0008	0.0066	0.07	0.9326							
Prei4	23	13.3081	0	0.8534	0.0933	0.0221	0.7626	0.892	0.0316	-0.0686	0.7626	33.7301	0							
Prkar1a	25	2.6863	0.0482	0.5403	0.0029	0.0017	0.4096	0.9754	0.009	0.0037	0.4096	7.2835	0.004							
Prkci	25	2.6235	0.0522	0.5344	0.0038	0.0018	0.5243	0.9783	-0.0082	0.0057	0.3269	5.0995	0.0157	0.0069	0.0036	0.5243	5.2346	0.0051	3.9413	0.037
Prkrir	23	3.2616	0.0238	0.588	0.0081	0.0051	0.3655	0.9709	-0.0156	-0.0037	0.3655	6.0477	0.0084							
Prpf19	25	1.8344	0.1491	0.4452	0.0037	0.0022	0.4001	0.973	0.0109	0.0014	0.4001	7.003	0.0047							
Prpf6	25	1.3392	0.2954	0.3694	0.005	0.004	0.2056	0.9755	-0.0062	0.0072	0.2056	2.7181	0.0892							
Prr14	25	3.3454	0.0215	0.5941	0.003	0.002	0.336	0.9785	0.009	0.0007	0.336	5.3123	0.0136							
Prr16	23	0.9192	0.5172	0.2868	0.0023	0.0018	0.1966	0.981	-0.0045	-0.0042	0.1966	2.57	0.1004							
Psmb10	23	3.6539	0.0151	0.6152	0.0122	0.006	0.508	0.9616	-0.0142	-0.0179	0.508	10.8394	0.0006							
Psmd1	24	2.2633	0.0835	0.4975	0.0024	0.0016	0.3391	0.9836	0.0075	0.0035	0.3391	5.3885	0.0129							
Psmd13	23	0.7931	0.6038	0.2576	0.0031	0.0026	0.1385	0.984	-0.003	-0.0052	0.1385	1.688	0.209							
Psmd2	25	2.6959	0.0476	0.5412	0.0016	0.0009	0.4408	0.9858	0.0066	0.0037	0.4408	8.2766	0.0022							
Psmd4	23	5.8444	0.0017	0.7189	0.0034	0.0011	0.685	0.9788	0.01	0.0056	0.4245	7.7456	0.003	0.0081	-0.0029	0.685	10.3315	0.0001	7.8583	0.0033
Psmd8	25	0.6229	0.7301	0.2142	0.0091	0.0082	0.0956	0.9726	0.0076	0.0034	0.0956	1.1103	0.348							
Psmd9	25	3.6099	0.0159	0.6123	0.0065	0.0033	0.4968	0.9611	0.0038	-0.0164	0.4968	10.3673	0.0007							
Psme2	23	0.9051	0.5265	0.2837	0.0049	0.0042	0.1393	0.9807	-0.0057	-0.0051	0.1393	1.6987	0.2071							
Pstpip2	23	1.8284	0.1503	0.4444	0.0235	0.0169	0.2787	0.9591	0.0117	0.0203	0.2787	4.0566	0.0324							
Ptbp1	23	3.166	0.0266	0.5807	0.0032	0.0016	0.5151	0.9817	0.0105	-0.0054	0.5151	11.153	0.0005							
Ptcd2	23	2.3393	0.0755	0.5058	0.0104	0.0093	0.1115	0.9464	-0.01	-0.0013	0.1115	1.3179	0.2889							
Ptcd3	23	1.9453	0.1281	0.4598	0.0098	0.0068	0.305	0.9543	-0.0161	-0.0013	0.305	4.609	0.0219							
Ptplad1	23	3.0456	0.0308	0.5713	0.005	0.0026	0.4702	0.9737	-0.0021	-0.0136	0.4702	9.3196	0.0013							
Ptpmt1	25	5.9769	0.0015	0.7234	0.005	0.0026	0.4857	0.9781	-0.0099	-0.0098	0.4857	9.9175	0.0009							
Pxmp4	23	21.2415	0	0.9028	0.022	0.003	0.8632	0.9446	-0.0021	0.0389	0.8632	66.2703	0							
Pycrl	23	4.2318	0.008	0.6493	0.0065	0.0024	0.6321	0.977	-0.0139	0.0055	0.3793	6.4163	0.0067	0.008	-0.0081	0.6321	8.1594	0.0005	6.5257	0.007
Qars	25	1.9621	0.1252	0.4619	0.0049	0.0038	0.234	0.9668	0.0041	-0.0092	0.234	3.2084	0.0608							
Rab11a	25	2.2707	0.0827	0.4984	0.0085	0.0061	0.2821	0.963	0.0123	-0.0074	0.2821	4.1257	0.0308							
Rab14	23	1.2437	0.3367	0.3524	0.0025	0.0019	0.2588	0.9819	0.0067	0.0035	0.2588	3.6666	0.0431							
Rab17	23	3.6533	0.0151	0.6151	0.0127	0.0054	0.5718	0.9589	0.0224	0.0114	0.5718	14.021	0.0001							
Rab1b	25	1.592	0.2083	0.4106	0.0021	0.0018	0.154	0.9759	0.0027	-0.0046	0.154	1.9114	0.1727							
Rab3gap1	24	2.6622	0.0497	0.538	0.006	0.0042	0.3118	0.9667	0.0056	-0.0112	0.3118	4.7576	0.0198							
Rab43	23	7.267	0.0005	0.7607	0.011	0.0034	0.6934	0.9603	0.0054	-0.0241	0.6934	23.7477	0							
Rab5a	25	0.7744	0.6173	0.2531	0.0073	0.0057	0.2202	0.9625	0.008	-0.0088	0.2202	2.9656	0.0734							
Rabac1	25	1.5722	0.2141	0.4075	0.0025	0.002	0.2151	0.9727	-0.0051	-0.0042	0.2151	2.8772	0.0786							
Rabepk	23	3.3793	0.0207	0.5965	0.0101	0.006	0.4094	0.9606	-0.0186	0.0032	0.4094	7.2782	0.004							
Rabgap1	25	2.5376	0.0583	0.5261	0.006	0.0045	0.2535	0.9696	0.0099	-0.0056	0.2535	3.5651	0.0465							
Ranbp10	24.9	9.6421	0.0001	0.8084	0.0101	0.0024	0.766	0.9561	0.0212	0.0096	0.6684	21.1688	0	-0.0011	-0.0088	0.766	15.5533	0	3.9634	0.0364
Rapgef6	25	2.2832	0.0813	0.4997	0.0119	0.0083	0.3057	0.9683	0.0167	-0.0052	0.3057	4.6225	0.0217							
Rassf3	25	7.8159	0.0003	0.7737	0.0282	0.0084	0.7017	0.9392	0.0376	-0.0159	0.7017	24.7021	0							
Rb1cc1	23	4.198	0.0083	0.6475	0.0165	0.0076	0.5402	0.9485	0.0075	-0.0256	0.5402	12.334	0.0003							
Rbbp5	23	1.3745	0.2814	0.3755	0.0048	0.0035	0.2788	0.9628	-0.0088	0.0058	0.2788	4.0596	0.0323							
Rbbp7	23.8	2.9102	0.0364	0.5601	0.0042	0.0021	0.501	0.9642	0.0069	-0.0073	0.2976	4.4487	0.0245	0.0084	0.0008	0.501	4.7685	0.0078	3.8717	0.0389
Rbks	23	1.5253	0.2284	0.4002	0.0063	0.0057	0.0992	0.9666	-0.0029	-0.0066	0.0992	1.1562	0.3339							
Rbm17	25	2.7622	0.0438	0.5472	0.0214	0.0159	0.2563	0.9551	0.0168	-0.0138	0.2563	3.6183	0.0446							
Rbm25	25	5.2066	0.003	0.6949	0.0132	0.0045	0.6552	0.9535	-0.0163	-0.0165	0.5075	10.8203	0.0006	0.0046	0.0115	0.6552	9.0273	0.0003	4.0703	0.0338
Rbm26	25	0.7806	0.6128	0.2546	0.0119	0.0118	0.0151	0.9495	0.0037	-0.0013	0.0151	0.1611	0.8523							
Rbm43	25	2.69	0.048	0.5406	0.0115	0.0082	0.2886	0.9401	0.0099	0.013	0.2886	4.2587	0.028							
Rbm5	23	1.0766	0.4216	0.3202	0.0028	0.0022	0.1905	0.9822	-0.0053	0.0039	0.1905	2.4712	0.1087							
Rbpj	25	1.7731	0.1622	0.4369	0.0082	0.0069	0.163	0.9653	-0.0103	0.0022	0.163	2.0453	0.1543							
Rbpms	23	8.195	0.0003	0.7819	0.0068	0.0023	0.6623	0.9648	0.0168	0.0105	0.6623	20.589	0							
Rcl1	24.5	12.9685	0	0.8502	0.0173	0.0032	0.8136	0.9489	0.0331	-0.0085	0.8136	45.8305	0							
Rell1	23.1	4.5262	0.0059	0.6645	0.015	0.0084	0.4384	0.9438	0.0234	0.0047	0.4384	8.1974	0.0023							
Rfc5	23	2.795	0.042	0.5501	0.0101	0.0059	0.421	0.9629	0.0164	0.0101	0.421	7.6354	0.0032							
Rfk	25	6.601	0.0009	0.7428	0.004	0.0024	0.4031	0.9781	-0.0114	-0.0005	0.4031	7.092	0.0044							
Rfwd3	23.7	4.7817	0.0046	0.6766	0.0029	0.0012	0.5669	0.9811	0.0075	0.0053	0.3462	5.5606	0.0115	0.0073	0.0006	0.5669	6.2165	0.0023	4.8392	0.02
Rfxank	23	12.6486	0	0.8469	0.0357	0.0067	0.813	0.9293	-0.0165	0.0452	0.813	45.641	0							
Rhbdd1	25	1.6941	0.1808	0.4257	0.0094	0.0059	0.38	0.9706	0.0157	0.0063	0.38	6.4359	0.0066							
Ric8	25	1.2885	0.3167	0.3605	0.0041	0.0029	0.2955	0.9793	0.007	-0.0075	0.2955	4.404	0.0253							
Riok2	23.5	5.8669	0.0017	0.7196	0.0282	0.0093	0.6703	0.934	-0.014	-0.0331	0.5353	12.0964	0.0003	-0.0054	0.0168	0.6703	9.6566	0.0002	3.8888	0.0384
Ripk1	23	3.7138	0.0141	0.619	0.0042	0.0034	0.2046	0.9764	-0.0063	-0.0058	0.2046	2.7002	0.0904							
Rlf	23	3.0188	0.0318	0.5691	0.0242	0.016	0.3393	0.9345	-0.0236	-0.0126	0.3393	5.3921	0.0129							
Rnaseh2a	23	2.2558	0.0843	0.4967	0.006	0.0042	0.303	0.9628	-0.0095	-0.0081	0.303	4.5639	0.0226							
Rnaseh2b	23	5.5461	0.0022	0.7082	0.0133	0.0046	0.6565	0.9575	-0.0209	-0.0177	0.6565	20.0635	0							
Rnd1	23	3.5104	0.0178	0.6056	0.0351	0.0308	0.1226	0.9257	0.0042	0.0182	0.1226	1.4677	0.2532							
Rnf125	23	47.9102	0	0.9545	0.0894	0.0073	0.9179	0.9101	0.0377	0.0735	0.9179	117.368	0							
Rnf167	23.3	2.2856	0.081	0.5	0.0102	0.0074	0.2755	0.9528	0.0153	0.0025	0.2755	3.9934	0.0339							
Rnf4	24.2	3.4898	0.0182	0.6042	0.0035	0.0018	0.494	0.9678	0.0109	-0.0049	0.494	10.2508	0.0008							
Rnf6	23	0.6632	0.6998	0.2249	0.0018	0.0015	0.1931	0.9766	0.0055	-0.0005	0.1931	2.5131	0.1051							
Rnps1	25	1.5101	0.2333	0.3978	0.0047	0.0043	0.0869	0.9757	-0.0055	-0.0017	0.0869	0.999	0.3851							
Rock1	25	1.1652	0.3745	0.3376	0.0083	0.0078	0.0689	0.9603	0.0052	-0.0048	0.0689	0.7773	0.4724							
Rorc	24.4	62.9527	0	0.965	0.075	0.0031	0.9584	0.9197	-0.0763	0.0022	0.9385	160.341	0	-0.0111	-0.0008	0.9584	109.535	0	4.548	0.0243
Rpa1	25	4.2777	0.0076	0.6517	0.0036	0.0033	0.098	0.9794	0.0019	0.0051	0.098	1.1409	0.3385							
Rpia	23	4.3872	0.0068	0.6575	0.0229	0.0165	0.2789	0.9349	-0.0222	0.007	0.2789	4.0608	0.0323							
Rpl13	23	1.4606	0.2498	0.3899	0.0213	0.0167	0.2162	0.9302	-0.0174	-0.0099	0.2162	2.8958	0.0775							
Rpl13a	23	0.2272	0.9728	0.0904	0.0036	0.0036	0.0108	0.9721	-0.0018	0.0004	0.0108	0.1141	0.8927							
Rpl22	25	1.9612	0.1253	0.4618	0.0074	0.0056	0.2354	0.9621	0.0112	0.0035	0.2354	3.233	0.0597							
Rpn1	25	5.9011	0.0016	0.7208	0.0079	0.0023	0.7063	0.9644	-0.0144	0.0111	0.5292	11.8018	0.0004	0.011	0	0.7063	11.4249	0.0001	5.7307	0.0113
Rrm2	25	21.8751	0	0.9054	0.038	0.0039	0.8963	0.9187	-0.0132	-0.0502	0.8505	59.7423	0	0.0049	0.0106	0.8963	41.0717	0	4.1991	0.0309
Rtn3	25	0.4664	0.8448	0.1695	0.0027	0.0026	0.0314	0.9827	-0.002	-0.0016	0.0314	0.3408	0.7151							
Rwdd4a	25	5.7385	0.0019	0.7151	0.0104	0.0034	0.6747	0.9575	-0.0071	-0.0186	0.4484	8.5341	0.0019	0.0101	0.0092	0.6747	9.8503	0.0002	6.6083	0.0066
Rxrb	25	0.2031	0.98	0.0816	0.0081	0.0079	0.0216	0.9669	0.0037	-0.0007	0.0216	0.2316	0.7953							
Sar1b	25	1.6445	0.1937	0.4184	0.0024	0.0017	0.2865	0.9882	-0.007	0.0032	0.2865	4.217	0.0289							
Sars	24.6	2.9467	0.0348	0.5632	0.0047	0.002	0.5613	0.9783	0.0098	-0.0034	0.267	3.824	0.0384	0.0095	0.0047	0.5613	6.0769	0.0025	6.373	0.0076
Sbk1	25	2.0087	0.1175	0.4677	0.0174	0.0132	0.2389	0.9434	0.005	-0.0183	0.2389	3.2965	0.0569							
Scamp1	23	14.8913	0	0.8669	0.0201	0.0029	0.853	0.9518	0.0164	-0.0326	0.7897	39.4336	0	-0.0024	0.0098	0.853	27.573	0	4.0937	0.0332
Scap	25	9.3183	0.0001	0.803	0.0127	0.0026	0.7949	0.9506	0.0234	0.0126	0.6944	23.8565	0	-0.0019	-0.0099	0.7949	18.4108	0	4.6567	0.0226
Scaper	25	6.5834	0.0009	0.7423	0.0173	0.0065	0.627	0.9395	0.022	0.0197	0.627	17.649	0							
Scarb1	23	5.4552	0.0024	0.7047	0.0052	0.0023	0.5676	0.9711	0.0096	0.0126	0.5676	13.781	0.0002							
Scyl3	23	4.3492	0.0071	0.6555	0.0074	0.0039	0.4783	0.9722	0.0149	-0.0086	0.4783	9.6279	0.0011							
Sdc2	25	1.8407	0.1478	0.4461	0.0037	0.0032	0.1386	0.9761	0.005	0.004	0.1386	1.6898	0.2087							
Sdc4	23	3.6063	0.0159	0.6121	0.0046	0.0026	0.435	0.9751	0.0126	-0.0032	0.435	8.0842	0.0025							
Sdhd	23	1.1321	0.3916	0.3312	0.0016	0.0013	0.1547	0.9779	-0.0039	-0.0024	0.1547	1.9221	0.1712							
Sec23a	23	3.2527	0.024	0.5873	0.0072	0.0035	0.521	0.9644	-0.0022	-0.0173	0.521	11.4224	0.0004							
Seh1l	25	2.48	0.0628	0.5204	0.0042	0.0035	0.1628	0.9714	0.0061	-0.0046	0.1628	2.0416	0.1548							
Senp5	23	2.48	0.0628	0.5204	0.0062	0.0042	0.3127	0.9686	0.002	-0.0123	0.3127	4.7782	0.0195							
Sep-10	25	1.7627	0.1645	0.4354	0.009	0.0063	0.3064	0.9543	0.0149	0.0008	0.3064	4.6381	0.0215							
Sepx1	23	1.8658	0.1428	0.4494	0.0005	0.0004	0.196	0.9878	0.003	0	0.196	2.5602	0.1012							
Serbp1	23	2.3262	0.0768	0.5044	0.0024	0.0021	0.1227	0.9839	-0.0029	-0.0041	0.1227	1.4679	0.2531							
Serinc3	23	2.2803	0.0816	0.4994	0.0013	0.0008	0.3759	0.9817	-0.0058	-0.0032	0.3759	6.3237	0.0071							
Serinc5	23	5.1969	0.0031	0.6945	0.0048	0.0016	0.6614	0.9639	0.0158	0.0053	0.6614	20.5145	0							
Serpinf2	25	33.4171	0	0.936	0.0047	0.0003	0.9292	0.98	0.0132	0.0129	0.8889	83.9721	0	-0.0025	-0.003	0.9292	62.3832	0	5.4229	0.0137
Sf1	25	0.8834	0.541	0.2787	0.0044	0.0038	0.1367	0.9784	0.0068	0.0017	0.1367	1.663	0.2136							
Sf3b1	25	6.1882	0.0013	0.7303	0.0045	0.0015	0.6723	0.9769	0.0104	-0.0078	0.4647	9.1137	0.0014	-0.0001	0.0088	0.6723	9.7458	0.0002	6.0204	0.0094
Sfrs1	23	2.115	0.1018	0.4806	0.0077	0.0046	0.4029	0.9715	-0.0114	0.0111	0.4029	7.0838	0.0045							
Sfrs11	25	2.3924	0.0704	0.5114	0.0054	0.0037	0.3092	0.971	0.0094	-0.0074	0.3092	4.7007	0.0206							
Sfrs3	23	1.0377	0.4439	0.3122	0.0099	0.0074	0.2503	0.9671	-0.0138	0.0045	0.2503	3.5058	0.0486							
Sfrs5	23.5	6.7298	0.0008	0.7465	0.0155	0.0051	0.6682	0.9538	0.0297	0.0001	0.6682	21.1461	0							
Sft2d1	25	6.933	0.0007	0.7521	0.0082	0.0029	0.6508	0.9679	0.0208	-0.0001	0.6508	19.5719	0							
Sgpl1	23	6.7598	0.0008	0.7473	0.0149	0.0051	0.659	0.9601	-0.0076	0.027	0.659	20.2898	0							
Sh3glb1	23	4.2714	0.0077	0.6514	0.0025	0.0013	0.4951	0.9755	0.0028	-0.0096	0.4951	10.2979	0.0008							
Sh3yl1	25	1.5221	0.2294	0.3997	0.0138	0.0119	0.1379	0.9454	0.0116	-0.005	0.1379	1.6792	0.2106							
Shprh	25	2.8892	0.0374	0.5583	0.0104	0.0069	0.3367	0.9543	0.0155	-0.0075	0.3367	5.3308	0.0134							
Sin3a	25	5.1954	0.0031	0.6945	0.0063	0.0023	0.6296	0.9666	0.016	-0.0092	0.6296	17.8471	0							
Slc10a1	23	1.3476	0.292	0.3709	0.0019	0.0013	0.3143	0.9846	0.004	-0.0058	0.3143	4.8134	0.019							
Slc20a1	23	14.4627	0	0.8635	0.0548	0.0178	0.6745	0.9117	-0.0099	-0.0539	0.6745	21.7586	0							
Slc22a5	23	4.3604	0.007	0.6561	0.0273	0.0104	0.6212	0.9347	0.0036	-0.0367	0.6212	17.2169	0							
Slc25a22	23	6.7392	0.0008	0.7467	0.023	0.0076	0.669	0.9333	0.0295	-0.02	0.669	21.2202	0							
Slc25a40	25	2.5687	0.056	0.5292	0.018	0.0137	0.2414	0.9456	0.0183	-0.0055	0.2414	3.3413	0.055							
Slc2a9	24.5	3.6991	0.0143	0.6181	0.0124	0.0058	0.5289	0.9459	0.0196	-0.013	0.5289	11.7874	0.0004							
Slc30a10	25	36.4601	0	0.941	0.0582	0.0039	0.9326	0.9358	-0.0208	0.0616	0.8755	73.8427	0	0.016	-0.0065	0.9326	65.6839	0	8.0369	0.003
Slc31a1	23	2.0084	0.1175	0.4677	0.0036	0.0033	0.0708	0.9702	-0.0042	-0.0021	0.0708	0.8005	0.4623							
Slc35a3	23	1.5653	0.2161	0.4065	0.0118	0.0092	0.2208	0.9566	-0.0058	-0.0135	0.2208	2.976	0.0728							
Slc35b1	23	2.0919	0.105	0.4779	0.0187	0.0132	0.2924	0.9578	-0.0149	0.015	0.2924	4.339	0.0265							
Slc35c2	23	1.19	0.3622	0.3424	0.0032	0.0025	0.2063	0.9786	0.0074	0.0018	0.2063	2.7285	0.0884							
Slc37a4	23.9	12.9385	0	0.8499	0.0233	0.0037	0.8403	0.9434	-0.0227	-0.0335	0.8403	55.2509	0							

Slc46a3	25	4.5386	0.0058	0.6651	0.0211	0.0102	0.5178	0.9448	-0.0254	-0.0151	0.5178	11.2759	0.0005							
Slc5a3	23	5.8883	0.0016	0.7204	0.0378	0.0118	0.6868	0.9021	-0.0402	-0.0115	0.5336	12.0146	0.0003	0.0192	-0.0102	0.6868	10.4161	0.0001	4.6459	0.0228
Slc9a3r1	25	5.0654	0.0035	0.6891	0.0045	0.0016	0.6497	0.9741	-0.0097	-0.0119	0.6497	19.4727	0							
Slmo2	25	7.6258	0.0004	0.7694	0.007	0.0022	0.6872	0.9671	-0.0116	-0.0135	0.5582	13.267	0.0002	0.0058	0.0061	0.6872	10.4354	0.0001	3.9176	0.0376
Smad3	25	1.682	0.1839	0.4239	0.0107	0.0099	0.076	0.9525	0.0078	0.0022	0.076	0.8637	0.436							
Smarca2	23	4.0886	0.0093	0.6414	0.0124	0.0049	0.6049	0.9537	-0.0099	-0.0229	0.6049	16.0783	0.0001							
Smc4	25	2.2833	0.0813	0.4997	0.0165	0.0118	0.2814	0.941	0.0159	-0.0122	0.2814	4.1118	0.0311							
Smek2	23	1.7177	0.175	0.4291	0.0115	0.0091	0.2085	0.9632	0.0003	-0.0139	0.2085	2.7654	0.0859							
Sntb1	23	2.8778	0.0379	0.5573	0.0043	0.0026	0.3932	0.9755	0.008	0.009	0.3932	6.8042	0.0053							
Snw1	23	4.4928	0.0061	0.6628	0.0054	0.0037	0.3135	0.9678	-0.0064	-0.01	0.3135	4.7951	0.0193							
Snx4	25	0.4315	0.8684	0.1588	0.0062	0.0058	0.0717	0.9687	0.0058	-0.0019	0.0717	0.8109	0.4579							
Snx5	23	4.6259	0.0053	0.6693	0.0023	0.0016	0.2756	0.9799	-0.0027	-0.0067	0.2756	3.9957	0.0338							
Sp1	25	3.348	0.0215	0.5943	0.0041	0.0035	0.1358	0.9771	0.0052	0.0042	0.1358	1.6502	0.216							
Sp4	25	1.3879	0.2762	0.3778	0.016	0.0145	0.0917	0.9466	0.0104	0.0029	0.0917	1.0597	0.3644							
Spag9	25	3.7088	0.0142	0.6187	0.0056	0.0029	0.4801	0.9704	0.0146	0.0021	0.4801	9.6968	0.001							
Spc25	25	10.2234	0.0001	0.8173	0.0351	0.0079	0.7735	0.9038	0.0068	-0.0426	0.6089	16.3504	0.0001	0.0123	0.0174	0.7735	16.22	0	6.9008	0.0056
Spnb2	25	2.9362	0.0352	0.5623	0.0024	0.0019	0.2047	0.9819	0.0062	0.0009	0.2047	2.7022	0.0903							
Spnb3	23.4	17.8656	0	0.8866	0.0168	0.002	0.8786	0.9458	0.0306	-0.0046	0.6676	21.086	0	-0.0173	-0.001	0.8786	34.3711	0	16.5097	0.0001
Spred2	23	3.528	0.0174	0.6068	0.0113	0.006	0.4683	0.9671	0.0206	0.0062	0.4683	9.2471	0.0013							
Spry4	23	5.7614	0.0018	0.716	0.0154	0.0085	0.4511	0.9309	0.0244	-0.0022	0.4511	8.6284	0.0018							
Sqstm1	23	16.1611	0	0.8761	0.004	0.0006	0.8385	0.9765	0.0141	0.0078	0.7374	29.4866	0	0.003	-0.0048	0.8385	24.6638	0	5.9474	0.0099
Sra1	23	3.2926	0.0229	0.5902	0.0027	0.0014	0.4573	0.9732	-0.0053	-0.0086	0.4573	8.8465	0.0016							
Srpk2	25	0.8724	0.5484	0.2762	0.0095	0.0072	0.2402	0.9584	0.0123	-0.0065	0.2402	3.3196	0.0559							
Srrm2	25	2.0849	0.106	0.477	0.0072	0.0042	0.4136	0.9754	0.0156	-0.0009	0.4136	7.4062	0.0037							
St13	23	2.842	0.0396	0.5542	0.0025	0.0015	0.4023	0.98	-0.0088	0.0028	0.4023	7.0679	0.0045							
St3gal1	23.3	7.3437	0.0005	0.7626	0.0211	0.0052	0.752	0.9587	-0.0089	0.0347	0.752	31.8345	0							
St3gal4	23	3.4252	0.0196	0.5998	0.0075	0.0056	0.25	0.9541	-0.0073	-0.0102	0.25	3.4994	0.0488							
Stam	25	2.3283	0.0766	0.5046	0.0075	0.0067	0.105	0.9759	0.0079	0.0012	0.105	1.2321	0.3119							
Stard3nl	23	1.025	0.4513	0.3096	0.0112	0.0091	0.1871	0.9508	-0.0055	0.0117	0.1871	2.416	0.1137							
Stard4	23	2.1795	0.0933	0.4881	0.0057	0.0035	0.3792	0.979	0.0076	-0.0108	0.3792	6.415	0.0067							
Stard7	25	6.9747	0.0007	0.7532	0.0035	0.0023	0.3468	0.9723	0.0077	-0.0068	0.3468	5.5737	0.0114							
Stk24	25	1.9491	0.1274	0.4603	0.0074	0.0046	0.3817	0.976	0.0149	0.0024	0.3817	6.4815	0.0064							
Stk4	25	2.0652	0.1088	0.4747	0.0037	0.0036	0.0358	0.9776	0.0033	-0.0001	0.0358	0.3904	0.6816							
Strap	25	6.407	0.001	0.7371	0.0018	0.0006	0.6461	0.9786	0.0004	-0.0075	0.4093	7.2769	0.004	-0.003	0.0053	0.6461	8.6706	0.0004	6.3538	0.0077
Stt3a	23	0.9824	0.477	0.3006	0.0026	0.0025	0.0674	0.9774	-0.0039	-0.0003	0.0674	0.7592	0.4805							
Stub1	25	0.4119	0.881	0.1527	0.002	0.002	0.0261	0.9863	0.002	0.0004	0.0261	0.2816	0.7574							
Stx4a	23.2	22.4759	0	0.9077	0.0172	0.0022	0.8734	0.9604	0.0186	0.0292	0.8139	45.9195	0	0.0088	-0.0027	0.8734	32.7716	0	4.466	0.0257
Sub1	23	1.6723	0.1864	0.4225	0.0012	0.0008	0.3008	0.9788	0.0038	0.0039	0.3008	4.5182	0.0233							
Suds3	25	1.4676	0.2474	0.391	0.0051	0.0037	0.2596	0.9758	0.0081	-0.007	0.2596	3.681	0.0426							
Sumo1	23	1.7058	0.1779	0.4274	0.0271	0.0244	0.0974	0.9125	-0.0044	-0.014	0.0974	1.1326	0.3411							
Sumo3	23.7	16.3998	0	0.8777	0.0115	0.0019	0.8344	0.9679	-0.0026	0.0256	0.6822	22.5388	0	0.0119	-0.0023	0.8344	23.9338	0	8.7319	0.002
Taok1	25	1.7222	0.174	0.4297	0.0239	0.0205	0.1413	0.9398	0.0144	-0.009	0.1413	1.7271	0.2021							
Tardbp	25	8.7067	0.0002	0.7921	0.014	0.0043	0.6932	0.9685	-0.0165	0.024	0.6932	23.7284	0							
Tars	24	28.1662	0	0.9249	0.0239	0.0022	0.9087	0.9544	-0.0063	0.0396	0.8096	44.6595	0	0.0137	-0.0029	0.9087	47.2761	0	10.3071	0.0009
Tars2	25	4.1943	0.0083	0.6473	0.0037	0.0013	0.6436	0.9838	-0.002	0.0088	0.2961	4.4176	0.025	0.0025	-0.0101	0.6436	8.5783	0.0004	9.2628	0.0016
Tax1bp1	25	2.3669	0.0728	0.5087	0.0049	0.0035	0.2854	0.9746	0.0099	-0.0043	0.2854	4.1926	0.0294							
Tbc1d17	23	11.3929	0	0.8329	0.0144	0.0034	0.7627	0.957	0.03	-0.0062	0.7627	33.7473	0							
Tbc1d20	25	3.6736	0.0148	0.6164	0.0101	0.0041	0.5982	0.9678	0.0201	-0.0105	0.5982	15.6342	0.0001							
Tbcb	23	2.0764	0.1072	0.476	0.0075	0.0054	0.2873	0.9707	-0.0042	0.0125	0.2873	4.2325	0.0285							
Tbce	24.4	2.7671	0.0435	0.5476	0.0071	0.0037	0.4806	0.9695	0.0117	0.004	0.2665	3.815	0.0386	0.0056	0.0097	0.4806	4.3958	0.011	3.9168	0.0376
Tbcel	23	17.9805	0	0.8872	0.016	0.0033	0.7916	0.9487	0.0271	-0.0118	0.6217	17.2567	0	-0.014	0.0054	0.7916	18.0409	0	7.743	0.0035
Tcp1	25	1.494	0.2385	0.3953	0.0127	0.0108	0.145	0.9353	-0.0116	-0.0034	0.145	1.7802	0.1931							
Tcp11l2	23	9.6692	0.0001	0.8088	0.0781	0.0295	0.6224	0.9155	0.0649	-0.001	0.6224	17.3094	0							
Tef	23	47.9817	0	0.9545	0.0809	0.0041	0.9496	0.9174	-0.0098	-0.0771	0.9064	101.711	0	-0.0173	-0.0026	0.9496	89.4776	0	8.1345	0.0028
Tex2	23.7	5.9474	0.0015	0.7224	0.0059	0.0019	0.6871	0.9743	0.0104	0.0152	0.6871	23.0614	0							
Tfrc	23	3.0182	0.0319	0.5691	0.0629	0.0429	0.3181	0.9048	-0.0375	-0.0183	0.3181	4.8971	0.018							
Tgif1	23.1	5.1602	0.0032	0.693	0.0124	0.0045	0.6346	0.9566	0.0172	0.0142	0.4484	8.5342	0.0019	0.0135	-0.0033	0.6346	8.2488	0.0005	4.8413	0.02
Tgm2	24.7	17.2303	0	0.8829	0.0069	0.0018	0.7377	0.97	-0.0052	0.0203	0.7377	29.5375	0							
Thap4	23	0.9414	0.5028	0.2917	0.0038	0.0035	0.0561	0.9809	0.0019	0.0037	0.0561	0.6235	0.5457							
Thoc3	23	5.0438	0.0035	0.6882	0.0033	0.0012	0.6448	0.9812	0.0057	-0.0076	0.3686	6.1296	0.008	0.0088	0.0006	0.6448	8.6232	0.0004	7.3878	0.0042
Timm10	23	1.0212	0.4536	0.3088	0.0205	0.0167	0.1874	0.9517	0.0007	-0.0176	0.1874	2.4221	0.1131							
Timm17a	23	9.5381	0.0001	0.8067	0.0072	0.0026	0.6408	0.9611	0.0069	-0.018	0.6408	18.7352	0							
Timm44	25	1.9838	0.1215	0.4646	0.0069	0.0042	0.3809	0.9717	0.0138	-0.0056	0.3809	6.4594	0.0065							
Timm9	25	6.6667	0.0008	0.7447	0.0168	0.0049	0.7079	0.935	-0.0043	-0.027	0.5526	12.971	0.0002	-0.0012	0.0146	0.7079	11.509	0.0001	5.0472	0.0175
Tiparp	23	1.589	0.2091	0.4101	0.0113	0.0088	0.22	0.9334	-0.0061	-0.013	0.22	2.9615	0.0736							
Tirap	23	1.8289	0.1502	0.4445	0.0128	0.0088	0.3145	0.9454	-0.0168	0.0076	0.3145	4.817	0.019							
Tle1	23	2.2168	0.0888	0.4923	0.0082	0.0067	0.1865	0.9572	-0.0008	-0.0111	0.1865	2.4074	0.1145							
Tm7sf3	23	3.9125	0.0113	0.6312	0.0049	0.0021	0.5683	0.9716	0.0146	0.0056	0.5683	13.8216	0.0001							
Tm9sf2	23	1.417	0.2653	0.3827	0.0044	0.0033	0.2558	0.9687	-0.0055	-0.008	0.2558	3.6092	0.0449							
Tm9sf3	23	0.6486	0.7107	0.221	0.0018	0.0014	0.2081	0.9833	-0.0013	-0.0054	0.2081	2.7596	0.0863							
Tmed5	23	12.1131	0	0.8413	0.0322	0.0077	0.7602	0.9373	-0.0001	-0.0444	0.7602	33.2929	0							
Tmem120a	25	0.9966	0.4683	0.3036	0.0258	0.0218	0.1517	0.9365	0.0171	-0.0059	0.1517	1.8774	0.1778							
Tmem126b	23	2.3685	0.0726	0.5089	0.014	0.0124	0.1118	0.9513	-0.0105	-0.0052	0.1118	1.3222	0.2878							
Tmem134	25	0.2983	0.9445	0.1154	0.0059	0.0059	0.0046	0.9733	-0.0014	-0.0003	0.0046	0.0482	0.9531							
Tmem183a	23	0.9705	0.4844	0.298	0.0016	0.0013	0.1743	0.9885	0.0016	-0.0045	0.1743	2.2163	0.1339							
Tmem33	23.5	4.6525	0.0052	0.6706	0.0134	0.0051	0.6216	0.9527	-0.026	0.0051	0.6216	17.2476	0							
Tmem41a	25	3.8817	0.0117	0.6294	0.0072	0.0042	0.4173	0.9743	-0.0085	-0.0132	0.4173	7.5198	0.0034							
Tmem41b	23	2.5098	0.0604	0.5234	0.014	0.008	0.4259	0.9281	-0.0227	0.0016	0.4259	7.7906	0.0029							
Tmem51	23	1.7594	0.1653	0.4349	0.0092	0.0091	0.0193	0.9675	0.0032	-0.0022	0.0193	0.2066	0.815							
Tmem57	23	15.2252	0	0.8695	0.0144	0.0028	0.8039	0.964	-0.025	-0.0194	0.8039	43.046	0							
Tmem69	23	0.5489	0.7855	0.1937	0.0213	0.0204	0.0394	0.9091	-0.0083	-0.002	0.0394	0.4312	0.6554							
Tmem85	25	3.9415	0.011	0.6329	0.002	0.0008	0.6102	0.9772	-0.0045	-0.0069	0.397	6.9129	0.0049	0.0061	-0.0008	0.6102	7.4371	0.0009	5.1978	0.0158
Tmem87b	25	3.4435	0.0192	0.601	0.0166	0.01	0.3959	0.9509	0.0151	-0.0186	0.3959	6.882	0.005							
Tmem93	23	4.5957	0.0055	0.6678	0.0044	0.0025	0.438	0.9744	-0.0123	-0.0041	0.438	8.1817	0.0024							
Tmod3	25	3.1449	0.0273	0.5791	0.0042	0.0038	0.1038	0.9764	0.0043	0.004	0.1038	1.2162	0.3164							
Tmtc4	23	4.8313	0.0044	0.6788	0.0087	0.0032	0.6339	0.9603	-0.0074	-0.0155	0.4305	7.9359	0.0027	0.0123	0.002	0.6339	8.2231	0.0005	5.2774	0.015
Tmub2	23	1.6409	0.1946	0.4179	0.0048	0.0038	0.1995	0.9606	0.0081	-0.0039	0.1995	2.6176	0.0966							
Tnrc6b	25	0.9173	0.5184	0.2864	0.0055	0.004	0.2746	0.9759	0.0101	-0.0052	0.2746	3.974	0.0344							
Tob2	25	7.1038	0.0006	0.7566	0.0188	0.005	0.7334	0.9467	0.0102	-0.0247	0.4994	10.473	0.0007	-0.0185	0.0073	0.7334	13.0699	0	8.3428	0.0025
Tomm20	25	8.3932	0.0002	0.786	0.0075	0.0026	0.6507	0.9623	-0.0061	-0.0143	0.384	6.5463	0.0062	0.0074	0.0102	0.6507	8.8476	0.0003	7.2514	0.0046
Top1mt	25	2.1397	0.0984	0.4835	0.0077	0.0048	0.3758	0.9667	0.0093	0.0122	0.3758	6.3223	0.0071							
Topors	23	3.1202	0.0282	0.5772	0.0106	0.0071	0.3328	0.9617	0.0152	-0.0079	0.3328	5.2375	0.0143							
Tor1a	23	4.464	0.0063	0.6614	0.0047	0.0025	0.4714	0.9799	0.0044	-0.0125	0.4714	9.3629	0.0012							
Tpd52	23.8	2.019	0.1159	0.469	0.0084	0.0059	0.3005	0.9643	-0.0118	-0.0084	0.3005	4.5104	0.0235							
Tpd52l1	23	1.6879	0.1824	0.4248	0.0078	0.0055	0.2964	0.9575	0.0097	-0.0097	0.2964	4.424	0.0249							
Tpi1	23.8	4.9096	0.004	0.6823	0.0015	0.0006	0.5887	0.9861	-0.002	0.0071	0.4217	7.6564	0.0032	0.0028	-0.0036	0.5887	6.7986	0.0014	3.8573	0.0393
Tpm3	23	1.3514	0.2905	0.3716	0.002	0.0013	0.3336	0.9788	0.0044	0.0061	0.3336	5.2573	0.0141							
Tppp	23	4.2046	0.0083	0.6478	0.0418	0.0204	0.513	0.9063	-0.0371	-0.0221	0.513	11.062	0.0005							
Tprgl	25	0.5298	0.7995	0.1882	0.0034	0.0029	0.1425	0.9825	0.0055	0.0029	0.1425	1.7442	0.1992							
Trafd1	23	5.2615	0.0029	0.6971	0.0064	0.0021	0.6712	0.9737	0.0191	0.0037	0.6712	21.4318	0							
Trim11	23	3.835	0.0123	0.6266	0.0083	0.0071	0.1416	0.9658	0.0087	0.0051	0.1416	1.7318	0.2013							
Trim25	25	4.3625	0.007	0.6562	0.0059	0.003	0.4964	0.9687	0.0127	-0.0095	0.4964	10.3479	0.0007							
Trim37	23	4.8837	0.0041	0.6812	0.0083	0.0036	0.5691	0.9561	-0.0163	0.0024	0.3763	6.3338	0.007	0.0117	0.0002	0.5691	6.2724	0.0022	4.2503	0.0298
Trit1	23	1.1724	0.3709	0.339	0.0104	0.0096	0.0753	0.9641	-0.0069	0.0042	0.0753	0.8545	0.4398							
Tsku	23	69.9739	0	0.9684	0.1113	0.0097	0.9132	0.8691	-0.0565	-0.0728	0.8915	86.2445	0	-0.015	0.0176	0.945	81.564	0	9.2359	0.0016
Tspan4	23.7	34.7318	0	0.9383	0.0479	0.0036	0.9258	0.9356	-0.0545	-0.0279	0.9258	131.022	0							
Tspan9	23	7.2967	0.0005	0.7615	0.0069	0.0019	0.7223	0.9703	0.012	0.0167	0.7223	27.3078	0							
Tssc1	25	8.3765	0.0002	0.7856	0.0069	0.0016	0.7728	0.9705	-0.0106	0.0137	0.5638	13.5706	0.0002	0.0092	-0.0068	0.7728	16.1593	0	8.742	0.002
Ttc1	23	2.9577	0.0343	0.5641	0.0065	0.0049	0.2452	0.9723	-0.0016	-0.0112	0.2452	3.4116	0.0521							
Tuba1b	25	3.9025	0.0114	0.6306	0.007	0.0026	0.627	0.9725	-0.0064	0.0109	0.3096	4.7082	0.0204	0.0139	-0.0002	0.627	7.9858	0.0006	8.0861	0.0029
Tuba4a	23	6.6151	0.0009	0.7432	0.0174	0.0057	0.671	0.9614	0	0.0307	0.671	21.4159	0							
Tubb2c	25	7.9456	0.0003	0.7766	0.0145	0.0051	0.6483	0.9533	-0.0009	0.0284	0.6483	19.3554	0							
Tubb6	23	3.4846	0.0183	0.6039	0.0154	0.0113	0.2672	0.9684	-0.0078	0.0164	0.2672	3.8285	0.0382							
Tubgcp2	25	2.1424	0.0981	0.4838	0.0066	0.0047	0.2913	0.9754	0.0125	-0.0012	0.2913	4.3159	0.0269							
Txn2	25	3.4378	0.0193	0.6006	0.0033	0.0016	0.5136	0.9818	-0.0111	-0.0036	0.5136	11.0866	0.0005							
Txndc15	23	1.5868	0.2098	0.4098	0.0055	0.0039	0.2874	0.9759	0.0011	0.0112	0.2874	4.2354	0.0285							
Txnl1	23	3.4895	0.0182	0.6042	0.0049	0.0043	0.1242	0.9691	-0.0052	0.0048	0.1242	1.4893	0.2484							
Uba6	24.1	3.9072	0.0114	0.6309	0.0368	0.0178	0.5157	0.9208	-0.028	-0.005	0.266	3.8061	0.0389	0.0273	0.0045	0.5157	5.057	0.006	4.8957	0.0193
Ubac1	23	7.3502	0.0005	0.7628	0.0135	0.0067	0.5006	0.9405	-0.0059	-0.0227	0.5006	10.5246	0.0007							
Ube2b	23.8	3.9017	0.0115	0.6306	0.0031	0.0018	0.415	0.9703	0.0099	0.003	0.415	7.4479	0.0036							
Ube2e2	25	7.396	0.0005	0.7639	0.0085	0.0032	0.6259	0.9711	0.0195	-0.0081	0.6259	17.5677	0							
Ube2f	23	3.0861	0.0293	0.5745	0.0108	0.0056	0.4871	0.9443	-0.0213	-0.0023	0.4871	9.9722	0.0009							
Ube2k	25	0.8028	0.5968	0.2599	0.0019	0.0017	0.137	0.9827	0.0046	0	0.137	1.6666	0.2129							
Ube2n	23	2.0415	0.1124	0.4718	0.0146	0.0119	0.187	0.9421	-0.0101	0.011	0.187	2.4151	0.1138							
Ube2q1	25	2.1726	0.0942	0.4873	0.0045	0.0025	0.453	0.9759	0.0119	-0.0055	0.453	8.6947	0.0018							
Ube4b	23	2.4918	0.0618	0.5216	0.0062	0.0036	0.4159	0.9626	0.0129	-0.007	0.4159	7.4749	0.0035							
Ubqln1	25	4.894	0.0041	0.6816	0.0045	0.0015	0.6699	0.9797	-0.0032	0.0127	0.4973	10.3851	0.0007	0.0062	-0.0055	0.6699	9.6398	0.0002	4.9689	0.0184
Ubr1	25	2.6862	0.0482	0.5403	0.0088	0.006	0.3227	0.9695	0.0127	-0.0092	0.3227	5.0023	0.0167							
Uchl5	23	2.3306	0.0764	0.5049	0.0105	0.0091	0.132	0.9495	-0.0034	-0.0101	0.132	1.5963	0.2263							
Ufd1l	23	0.7112	0.6638	0.2373	0.0093	0.0087	0.0696	0.9605	-0.0047	-0.0057	0.0696	0.7853	0.4689							
Ugcg	25	5.4488	0.0024	0.7045	0.0231	0.0118	0.4897	0.9474	0.0226	-0.0218	0.4897	10.0763	0.0009							
Uhrf1bp1l	23.3	3.869	0.0119	0.6286	0.0116	0.0045	0.6153	0.9635	0.0054	-0.0181	0.3706	6.1837	0.0077	0.0103	0.0119	0.6153	7.598	0.0008	6.0427	0.0093
Unc84b	25	3.9214	0.0112	0.6318	0.0124	0.005	0.5951	0.9445	0.0184	0.0012	0.3361	5.3161	0.0136	-0.0094	-0.0128	0.5951	6.9803	0.0012	6.0751	0.0091
Uqcrc2	23	1.022	0.4531	0.309	0.0008	0.0006	0.2289	0.9891	-0.0019	-0.0034	0.2289	3.1171	0.0653							
Usp12	23	1.5285	0.2274	0.4007	0.0083	0.0059	0.2907	0.9672	-0.0128	-0.0068	0.2907	4.3029	0.0272							
Usp32	23	0.5795	0.7627	0.2023	0.0058	0.0052	0.1006	0.9678	0.0069	-0.0015	0.1006	1.1748	0.3284							
Usp47	25	2.3115	0.0783	0.5028	0.0022	0.0018	0.1823	0.9831	0.0044	-0.0039	0.1823	2.3413	0.1208							
Utrn	25	2.4261	0.0674	0.5149	0.0144	0.0088	0.3865	0.9642	0.0197	-0.0091	0.3865	6.6147	0.0059							
Uxs1	23	0.9634	0.4889	0.2965	0.0067	0.0051	0.2346	0.9673	-0.0113	0.0026	0.2346	3.2187	0.0604							
Vav2	25	1.7233	0.1737	0.4299	0.0078	0.0049	0.375	0.9623	0.0142	-0.007	0.375	6.3011	0.0072							
Vdac2	25	8.2494	0.0003	0.783	0.0061	0.0018	0.7117	0.967	0.0032	-0.0169	0.5393	12.293	0.0003	0.0064	0.0066	0.7117	11.7271	0.0001	5.6809	0.0116
Vezf1	23	0.3347	0.9263	0.1277	0.0054	0.0052	0.0369	0.9743	0.0042	0.0003	0.0369	0.4024	0.6737							
Vps11	23	9.2922	0.0001	0.8026	0.0045	0.0014	0.6916	0.9792	0.0101	-0.0068	0.4069	7.2045	0.0041	0.0105	0.0019	0.6916	10.652	0.0001	8.7689	0.002
Vps36	25	1.723	0.1738	0.4298	0.0039	0.0035	0.1002	0.9727	0.0037	0.0043	0.1002	1.1691	0.3301							
Vps4b	23.7	5.7422	0.0019	0.7153	0.0041	0.0013	0.6723	0.9766	0.0148	-0.0031	0.6723	21.5424	0							
Vti1a	25	2.756	0.0441	0.5466	0.0094	0.0067	0.2863	0.9589	0.0135	-0.0068	0.2863	4.2127	0.029							
Wac	25	4.0559	0.0097	0.6396	0.0016	0.0009	0.4377	0.9826	0.0076	0.0004	0.4377	8.1723	0.0024							
Wasl	23	0.8244	0.5816	0.2651	0.0038	0.0031	0.197	0.9739	0.0055	-0.0056	0.197	2.5761	0.0999							
Wbscr27	23	10.0619	0.0001	0.8149	0.0339	0.009	0.7344	0.9282	0.0442	0.0149	0.7344	29.0301	0							
Wdr26	23.8	4.3851	0.0068	0.6574	0.0046	0.0016	0.6437	0.9725	0.0116	-0.0052	0.4178	7.5355	0.0034	0.0015	0.0092	0.6437	8.5828	0.0004	6.0243	0.0094
Wdr36	23	3.5615	0.0168	0.6091	0.0114	0.0055	0.5184	0.9585	-0.0202	-0.0103	0.5184	11.3044	0.0005							
Wdr37	23	2.0953	0.1045	0.4783	0.0167	0.01	0.4027	0.9399	-0.0239	0.0024	0.4027	7.0788	0.0045							
Wdr42a	24.6	7.9372	0.0003	0.7764	0.0028	0.0009	0.679	0.9809	0.0105	-0.0072	0.679	22.2077	0							
Wdr45l	23	2.4513	0.0652	0.5175	0.0273	0.024	0.1188	0.9329	-0.0113	-0.0122	0.1188	1.415	0.2652							
Wdr6	23	9.1726	0.0001	0.8005	0.0133	0.0036	0.73	0.9649	0.024	-0.0153	0.73	28.3894	0							
Wee1	23	28.5628	0	0.9259	0.1459	0.0145	0.9008	0.8864	-0.0385	-0.0956	0.8555	62.1893	0	-0.0195	0.0124	0.9008	43.1429	0	4.3363	0.0281
Whsc2	23	6.7852	0.0008	0.748	0.013	0.004	0.6916	0.9637	-0.0193	0.0189	0.6916	23.5446	0							
Wnt5b	25	4.8513	0.0043	0.6797	0.0099	0.0049	0.5003	0.9645	-0.0198	-0.0028	0.5003	10.5139	0.0007							
Wwtr1	24.7	0.9252	0.5133	0.2881	0.0073	0.0054	0.2603	0.962	0.0071	-0.0106	0.2603	3.6946	0.0422							
Xrn2	25	5.418	0.0025	0.7033	0.0135	0.007	0.4833	0.9513	0.0207	-0.0113	0.4833	9.8208	0.001							
Ypel5	23	4.1874	0.0084	0.6469	0.0112	0.0045	0.6011	0.9603	0.0106	-0.0206	0.6011	15.825	0.0001							
Ywhaq	23	0.7078	0.6663	0.2364	0.0101	0.0089	0.1203	0.9556	-0.0102	0.0004	0.1203	1.4363	0.2602							
Yy1	25	5.4948	0.0023	0.7062	0.0046	0.0018	0.6109	0.9664	0.0094	-0.0083	0.4429	8.3485	0.0021	-0.006	0.0058	0.6109	7.4562	0.0009	4.0995	0.0331
Zc3hav1	25	2.9185	0.036	0.5608	0.0082	0.0038	0.5278	0.972	0.0181	0.0043	0.5278	11.7349	0.0004							
Zcchc6	25	4.2158	0.0082	0.6484	0.0082	0.0038	0.5387	0.9633	0.019	-0.0009	0.5387	12.2638	0.0003							
Zdhhc20	25	1.4201	0.2642	0.3832	0.0026	0.0022	0.1473	0.9729	0.0025	-0.0052	0.1473	1.8133	0.1877							
Zfand2b	23	1.8064	0.1549	0.4414	0.004	0.003	0.257	0.9762	0.0093	0.0018	0.257	3.6328	0.0442							
Zfand3	25	4.3435	0.0071	0.6552	0.0099	0.0043	0.5665	0.9661	0.0209	-0.0055	0.5665	13.7197	0.0002							
Zfand5	25	4.7178	0.0049	0.6736	0.0166	0.0073	0.5615	0.9612	0.0238	0.0133	0.5615	13.4441	0.0002							
Zfhx3	23	1.7827	0.16	0.4382	0.0045	0.0039	0.1149	0.9762	0.0064	0.0019	0.1149	1.3631	0.2776							
Zfp187	25	1.3593	0.2873	0.3729	0.007	0.0056	0.1996	0.9629	0.0105	-0.0023	0.1996	2.619	0.0965							
Zfp192	25	1.7485	0.1677	0.4334	0.0054	0.0039	0.2722	0.9672	0.0061	0.0091	0.2722	3.9273	0.0356							
Zfp260	23	1.4199	0.2643	0.3832	0.0122	0.0118	0.0394	0.944	-0.006	-0.0024	0.0394	0.4304	0.6559							
Zfp277	25	6.5397	0.0009	0.741	0.0133	0.0056	0.5744	0.9572	0.0249	-0.0005	0.5744	14.1708	0.0001							
Zfp295	23.6	20.4046	0	0.8993	0.0268	0.0029	0.893	0.9505	-0.0314	0.03	0.849	59.0503	0	0.0097	0.0025	0.893	39.6514	0	3.9065	0.0379

Zfp36	25	2.063	0.1092	0.4744	0.0276	0.0158	0.4272	0.9442	0.0309	-0.0036	0.4272	7.8305	0.0029							
Zfp36l1	24.6	5.92	0.0016	0.7214	0.038	0.011	0.7111	0.9381	-0.0144	0.0382	0.5439	12.5217	0.0003	0.0226	-0.0059	0.7111	11.6912	0.0001	5.4974	0.0131
Zfp518	23	3.4499	0.0191	0.6015	0.0294	0.0118	0.5969	0.9248	-0.0177	0.0236	0.3228	5.0043	0.0167	0.0221	-0.0129	0.5969	7.0333	0.0012	6.46	0.0072
Zfp523	25	1.2778	0.3213	0.3586	0.0058	0.0053	0.0856	0.9652	0.0063	0.0005	0.0856	0.9828	0.3908							
Zfp622	23	0.9176	0.5182	0.2865	0.0045	0.0041	0.087	0.9613	0.005	0.003	0.087	1.001	0.3844							
Zfp707	23	4.006	0.0102	0.6367	0.0175	0.0069	0.6059	0.9394	0.0202	0.0151	0.4028	7.0809	0.0045	0.0135	-0.0101	0.6059	7.3032	0.001	4.8973	0.0193
Zfp810	25	1.7148	0.1757	0.4286	0.0119	0.0084	0.295	0.9545	0.0028	0.017	0.295	4.3939	0.0255							
Zfr	23	3.5143	0.0177	0.6059	0.0058	0.003	0.4806	0.9715	-0.0108	0.0106	0.4806	9.7146	0.001							
Zfyve26	25	12.0843	0	0.8409	0.0135	0.0025	0.8185	0.9547	0.0242	0.0126	0.6862	22.957	0	-0.0024	-0.0117	0.8185	21.4186	0	6.9252	0.0055
Zh2c2	23	4.5656	0.0057	0.6664	0.0154	0.0064	0.5822	0.9437	-0.0074	-0.0201	0.3531	5.732	0.0103	0.0113	0.0134	0.5822	6.6198	0.0016	5.2095	0.0157
Zkscan1	25	0.9946	0.4696	0.3032	0.007	0.0056	0.1975	0.9675	0.0082	0.0066	0.1975	2.5842	0.0992							
Znhit1	23	1.7912	0.1582	0.4394	0.0037	0.0032	0.1532	0.9769	-0.0041	0.0054	0.1532	1.899	0.1746							

Table S3	Gene symbol	Refseq ID	Chromosome	Start Position	End Position	Strand	Genbank ID	Gene Description
1	0610012D14Rik	NM_026690	chr7	51720263	51723122	+	BC019451	RIKEN cDNA 0610012D14 gene
2	1600012F09Rik	NM_025904	chr13	18080035	18085171	-	BC083111	RIKEN cDNA 1600012F09 gene
3	2610019A05Rik	NM_028126	chr11	106024644	106054876	-	BC052063	RIKEN cDNA 2610019A05 gene
4	2810008M24Rik		chr13	108834640	108839366	+	BC004049|BC	RIKEN cDNA 2810008M24 gene | hypothetical protein LOC100046418
5	Aarsd1	NM_144829	chr11	101268151	101278747	-	BC005711	alanyl-tRNA synthetase domain containing 1
6	Adfp	NM_007408	chr4	86302469	86315963	-	M93275	adipose differentiation related protein
7	Adh5	NM_007410	chr3	138106128	138118463	+	BC090978	alcohol dehydrogenase 5 (class III), chi polypeptide
8	Agl	NM_001081326	chr3	116445969	116510327	-	BC044780	amylo-1,6-glucosidase, 4-alpha-glucanotransferase
9	Alas1	NM_020559	chr9	106136258	106150187	-	BC022110	aminolevulinic acid synthase 1
10	Ankrd25							
11	Ap1m1	NM_007456	chr8	74764031	74781278	+	M62419	adaptor-related protein complex AP-1, mu subunit 1
12	Armc5	NM_146205	chr7	135380871	135388614	+	BC089363	armadillo repeat containing 5
13	Atg2b	NM_029654	chr12	106853933	106885039	-	BC046427	ATG2 autophagy related 2 homolog B (S. cerevisiae)
14	Atp6v1e1	NM_007510	chr6	120745262	120772719	-	BC003421	VATPase, H+ transporting, lysosomal V1 subunit E1
15	Atxn2l	NM_183020	chr7	133635222	133646816	-	BC054483	ataxin 2-like
16	Bcl2l1	NM_009743	chr2	152584468	152657418	-	BC089016	Bcl2-like 1
17	C230096C10Rik	NM_146157|NM	chr4	138908508	139045143	+	BC129804|AB	RIKEN cDNA C230096C10 gene | ubiquitin protein ligase E3 component n-recognin 4
18	Cd2bp2	NM_027353	chr7	134335174	134339514	-	BC006920	CD2 antigen (cytoplasmic tail) binding protein 2
19	Dhps	NM_001039514	chr8	87595656	87599060	+	BC061234	deoxyhypusine synthase
20	Dpys	NM_022722	chr15	39600031	39689013	-	AF249296	dihydropyrimidinase
21	Egln2	NM_053208	chr7	27943677	27951792	-	AF453879	EGL nine homolog 2 (C. elegans)
22	Etfdh	NM_025794	chr3	79407723	79432642	-	BC057670	electron transferring flavoprotein, dehydrogenase
23	Fbxl20	NM_028149	chr11	97943868	98010930	-	EF649694	F-box and leucine-rich repeat protein 20
24	Ganc							
25	Gnpat	NM_010322	chr8	127386730	127413957	+	BC025972	glyceronephosphate O-acyltransferase
26	Gpsn2	NM_134118	chr8	86095597	86118376	-	BC094046|BC	glycoprotein, synaptic 2 | RIKEN cDNA 1600014K23 gene
27	Hars	NM_008214	chr18	36926184	36942830	-	BC020088	histidyl-tRNA synthetase
28	Hebp1	NM_013546	chr6	135087546	135118585	-	AF117613	heme binding protein 1
29	Hnrpm	NM_029804|NM	chr17	33783181	33823805	-	BC054785	heterogeneous nuclear ribonucleoprotein M | membrane-associated ring finger (C3HC4) 2
30	Hspd1	NM_010477	chr1	55134679	55144689	-	BC016400	heat shock protein 1 (chaperonin)
31	Itpa	NM_025922	chr2	130493543	130507350	+	BC094466	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)
32	Lyrm4	NM_201358	chr13	36070666	36209226	-	BC034664	LYR motif containing 4
33	Map3k1	NM_011945	chr13	112536641	112599191	-	AF117340	mitogen-activated protein kinase kinase kinase 1
34	Mcm3	NM_008563	chr1	20793054	20810341	-	BC031700	minichromosome maintenance deficient 3 (S. cerevisiae)
35	Me1		chr13	62915449	62916150	+	BC094028	malic enzyme 1, NADP(+)-dependent, cytosolic
36	Mrpl37	NM_025500	chr4	106728487	106739473	-	BC028257	mitochondrial ribosomal protein L37
37	Nmt1	NM_008707	chr11	102889865	102927419	+	BC021635	N-myristoyltransferase 1
38	Ntn2l	NM_010947	chr17	24340776	24346332	-	BC094362	netrin 2-like (chicken)
39	Pigq	NM_011822	chr17	26063369	26078907	-	BC014287	phosphatidylinositol glycan anchor biosynthesis, class Q
40	Pigv	NM_178698	chr4	133216302	133228535	-	BC055060	phosphatidylinositol glycan anchor biosynthesis, class V
41	Pomt1	NM_145145	chr2	32092143	32110525	+	BC027325	protein-O-mannosyltransferase 1
42	Pqlc2	NM_145384	chr4	138849945	138866600	-	BC019216	PQ loop repeat containing 2
43	Psmg3	NM_025604	chr5	140299548	140302839	-	BC058692	proteasome (prosome, macropain) assembly chaperone 3
44	Ptma	NM_008972	chr1	88423300	88427273	+	BC085171	prothymosin alpha
45	Rexo2	NM_024233	chr9	48276617	48288716	-	BC003445	REX2, RNA exonuclease 2 homolog (S. cerevisiae)
46	Riok3	NM_024182	chr18	12287268	12315876	+	BC033271	RIO kinase 3 (yeast)
47	Rpl29	XR_002091|XR_	chr1	136414607	136415258	+	L08651|BC081	ribosomal protein L29
48	Sdccag3	NM_026563|NM	chr2	26238322	26244826	-	BC031199	serologically defined colon cancer antigen 3
49	Setd3	NM_028262	chr12	109344641	109417473	-	AY513271	SET domain containing 3
50	Slc25a30	NM_026232	chr14	76160883	76186844	-	BC022676	solute carrier family 25, member 30
51	Srp54a							
52	St13	NM_133726	chr15	81195470	81230124	-	BC003843	suppression of tumorigenicity 13
53	Stk24	NM_145465	chr14	121685563	121778455	-	AY188357	serine/threonine kinase 24 (STE20 homolog, yeast)
54	Tex2	NM_198292	chr11	106363448	106474244	-	BC057406	testis expressed gene 2
55	Txn1		chr1	44520758	44521076	-	BC094415	thioredoxin 1
56	Txndc1	NM_028339	chr12	71554123	71568611	+	BC017603	thioredoxin domain containing 1
57	Ube2z	NM_172300	chr11	95908744	95926678	-	BC054412	ubiquitin-conjugating enzyme E2Z (putative)
58	Ubl7	NM_001122873|	chr9	57758793	57777777	+	BC094047	ubiquitin-like 7 (bone marrow stromal cell-derived)
59	Wasf1	NM_031877	chr10	40603379	40658375	+	BC016896	WASP family 1
60	Zfp313	NM_030743	chr2	167318145	167341673	+	BC085146|AK	zinc finger protein 313
61	Zfp592	NM_178707	chr7	88138570	88187604	+	BC094321	zinc finger protein 592
62	2500003M10Rik		chr3	90302878	90313384	-	BC120651|BC	RIKEN cDNA 2500003M10 gene
63	5730427N09Rik		chr18	64240419	64241074	-		RIKEN cDNA 5730427N09 gene
64	A530082C11Rik	NM_177186	chr4	154975525	154997449	+	BC058728	RIKEN cDNA A530082C11 gene
65	Ahcy		chr1	7167820	7169118	+	L32836	S-adenosylhomocysteine hydrolase
66	Ak3	NM_021299	chr19	29095322	29122445	-	BC058191	adenylate kinase 3
67	BC008163		chr4	132456518	132478426	-	BC008163	
68	BC016423	NM_134063	chr13	3565281	3610342	-	BC016423	
69	Bckdha	NM_007533	chr7	26414965	26443766	-	BC003787	branched chain ketoacid dehydrogenase E1, alpha polypeptide
70	Cat	NM_009804	chr2	103294064	103325280	-	BC013447	catalase
71	Cep68	NM_172260	chr11	20127040	20149427	-	BC027174	centrosomal protein 68
72	Crk	NM_133656	chr11	75492812	75519596	+	BC012216	v-crk sarcoma virus CT10 oncogene homolog (avian)
73	Cttn	NM_007803	chr7	151621629	151656642	-	U03184	cortactin
74	Dhdh	NM_027903	chr7	52728933	52744166	-	BC116414	dihydrodiol dehydrogenase (dimeric)
75	Dnaja1	NM_008298	chr4	40669566	40681997	+	AF055664	DnaJ (Hsp40) homolog, subfamily A, member 1
76	Hnrpll	NM_144802	chr17	80428827	80461674	-	BC012849	heterogeneous nuclear ribonucleoprotein L-like
77	Lasp1	NM_010688	chr11	97660986	97700078	+	BC010840	LIM and SH3 protein 1
78	Map2k1	NM_008927	chr9	64033588	64101412	-	L02526	mitogen-activated protein kinase kinase 1
79	Mrpl18	NM_026310	chr17	13104221	13108957	-	BC011425	mitochondrial ribosomal protein L18
80	Myd116	NM_008654	chr7	52778290	52781583	-		myeloid differentiation primary response gene 116
81	Nup54	NM_183392	chr5	92844566	92864225	-	BC068114	nucleoporin 54
82	Ranbp9	NM_019930	chr13	43498748	43576342	-	AF006465	RAN binding protein 9
83	Rhbdf2	NM_172572	chr11	116459479	116488333	-	BC052182	rhomboid 5 homolog 2 (Drosophila)
84	Rpl22	NM_009079	chr4	151699835	151708180	+	BC021344	ribosomal protein L22 | ribosomal protein L22 pseudogene
85	Rps6ka4	NM_019924	chr19	6903574	6915117	-	AF074714	ribosomal protein S6 kinase, polypeptide 4
86	Sdc4	NM_011521	chr2	164249747	164268688	-	D89571	syndecan 4
87	Tmco1	NM_001039483	chr1	169238801	169264109	+	BC020098	transmembrane and coiled-coil domains 1
88	Tmem33	NM_028975|NM	chr5	67651891	67682700	+	BC016570	transmembrane protein 33
89	Ttbk2	NM_001024856|	chr2	120558552	120676340	-	AB046593	tau tubulin kinase 2
90	Ube2b	NM_009458	chr11	51799064	51813889	-	U57690	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)
91	Ypel5	NM_027166	chr17	73186044	73200535	+	BC085109	yippee-like 5 (Drosophila)
92	0610007L01Rik	NM_001081394	chr5	130698295	130719535	+	BC033455	RIKEN cDNA 0610007L01 gene
93	2010005J08Rik	NM_178623|NM	chr11	5614188	5662260	-	BC066994	RIKEN cDNA 2010005J08 gene
94	2310047O13Rik	NM_024185	chr2	12268891	12341087	-	BC027202	RIKEN cDNA 2310047O13 gene
95	2410018G20Rik	NM_029354	chr16	15848534	15863462	-	BC027550	RIKEN cDNA 2410018G20 gene
96	5230400G24Rik		chr1	82721493	82748969	+	BC059229|BC	RIKEN cDNA 5230400G24 gene
97	9130023H24Rik	NM_177001	chr7	135379920	135380933	-		RIKEN cDNA 9130023H24 gene
98	A530054K11Rik	NM_183146	chr13	67717938	67738728	-	BC098180	RIKEN cDNA A530054K11 gene
99	AI987944		chr7	48629142	48648749	-	BC099396|BC	
100	Akap8l	NM_017476	chr17	32458369	32487522	-	BC051015	A kinase (PRKA) anchor protein 8-like
101	Alkbh6	NM_198027	chr7	31093772	31099323	+	BC029805	alkB, alkylation repair homolog 6 (E. coli)
102	Als2cr2	NM_172656	chr1	59030415	59052559	+	BC055814	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 (human)
103	Atp5g3	NM_175015	chr2	73746506	73749360	-	BC116218	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 3
104	Atp5j	NM_016755|NR	chr16	84828111	84835819	-	BC010766	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F | ATP synthase, H+ transporting, mitochond
105	B4galt7	NM_146045	chr13	55701257	55711804	+	BC055703	xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)
106	BC022224	NM_177564	chr11	84634228	84642488	-	BC022224	
107	Bmpr1a	NM_009758	chr14	35224252	35315732	-	BC042611	bone morphogenetic protein receptor, type 1A
108	C330011K17Rik		chr13	67527195	67552547	-	BC080824	RIKEN cDNA C330011K17 gene
109	Ccdc104	NM_025740	chr11	29121536	29147306	-	BC005731	coiled-coil domain containing 104
110	Ccdc115	NM_027159	chr1	34493521	34496517	-	BC019430	coiled-coil domain containing 115
111	Ccdc61	NM_001033314	chr7	19476233	19495753	-		coiled-coil domain containing 61
112	Ccdc71	NM_133744	chr9	108362858	108368269	+	BC018518	coiled-coil domain containing 71
113	Cdc37l1	NM_025950	chr19	29064857	29092061	+	BC031761	cell division cycle 37 homolog (S. cerevisiae)-like 1
114	Cfdp1	NM_011801	chr8	114292373	114378210	-	BC005589	craniofacial development protein 1
115	Cnot6l	NM_178854|NM	chr5	96504608	96591009	-	BC018506	CCR4-NOT transcription complex, subunit 6-like
116	Copb2	NM_015827	chr9	98464150	98488801	+	BC006675	coatomer protein complex, subunit beta 2 (beta prime)
117	Dctn6	NM_011722	chr8	35153474	35171512	-	BC029249	dynactin 6
118	Dhx36	NM_028136	chr3	62274005	62310910	-	AF448804	DEAH (Asp-Glu-Ala-His) box polypeptide 36
119	Dynll2	NM_026556	chr11	87793027	87801007	-	BC040822	dynein light chain LC8-type 2
120	Eif1a	NM_010120	chr18	46757358	46769862	+	AF026481	eukaryotic translation initiation factor 1A
121	Eps15l1	NM_007944|NM	chr8	74864902	74945359	-	U29156	epidermal growth factor receptor pathway substrate 15-like 1
122	Fbxo38	NM_134136	chr18	62663805	62708368	-	BC056348	F-box protein 38
123	Gorasp1	NM_028976	chr9	119834791	119846676	-	BC012251	golgi reassembly stacking protein 1
124	Hnrpul1	NM_144922|NM	chr7	26506501	26539769	-	BC021506	heterogeneous nuclear ribonucleoprotein U-like 1
125	Hspa4	NM_008300	chr11	53073316	53113981	-	BC003770	heat shock protein 4
126	Igf1	NM_010512|NM	chr10	87321813	87394870	+	BC012409	insulin-like growth factor 1
127	LOC100041835							
128	Lsg1	NM_178069	chr16	30560580	30587675	-	BC043724	large subunit GTPase 1 homolog (S. cerevisiae)
129	Morf4l1	NM_001039147|	chr9	89986507	90009600	-	AF319621	mortality factor 4 like 1
130	Mpdu1	NM_011900	chr11	69470199	69476144	-	BC026776	mannose-P-dolichol utilization defect 1
131	Mphosph8	NM_023773	chr14	57194494	57316761	+	BC145700|AK	M-phase phosphoprotein 8 | poly (ADP-ribose) polymerase family, member 4 | RIKEN cDNA C030027K23 gene
132	Mrpl1	NM_053158|NM	chr5	96639134	96695728	+	BC061042	mitochondrial ribosomal protein L1
133	Mrpl13	NM_026759	chr15	55365649	55388873	-	BC060968	mitochondrial ribosomal protein L13
134	Ncl	NM_010880	chr1	88255651	88256536	+		nucleolin
135	Nipa2	NM_023647	chr7	63186957	63217838	-	BC038499	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)
136	Nol14	NM_029278	chr5	34981185	35002797	-	BC043043	nucleolar protein 14
137	Nsl1	NM_198654	chr1	192886903	192908437	+	BC029086	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)
138	Orc5l	NM_011959	chr5	21992307	22056176	-	BC006927	origin recognition complex, subunit 5-like (S. cerevisiae)
139	Pebp1	NM_018858	chr10	28749901	28751106	+	BC008169	phosphatidylethanolamine binding protein 1
140	Pigy	NM_025574	chr6	57636570	57642064	-	BC029232	phosphatidylinositol glycan anchor biosynthesis, class Y
141	Plekhf2	NM_175175	chr4	10915809	10934717	-	BC016134	pleckstrin homology domain containing, family F (with FYVE domain) member 2
142	Prim2	NM_008922	chr1	33510656	33726625	-	BC019500	DNA primase, p58 subunit
143	Psmd8	NM_026545	chr7	29959271	29965550	-	BC004075	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
144	Rbpms	NM_019733|NM	chr8	34893116	35040313	-	BC030397	RNA binding protein gene with multiple splicing
145	Rfxank	NM_011266|NM	chr8	72654705	72663096	-	BC010971	regulatory factor X-associated ankyrin-containing protein
146	Rpia	NM_009075	chr6	70715695	70742169	-	L35034	ribose 5-phosphate isomerase A
147	Rps18	NM_011296|XR_	chr13	28349496	28350006	+	M76763	ribosomal protein S18 | similar to ribosomal protein S18 | predicted gene, OTTMUSG00000000655
148	Sergef	NM_013789	chr7	53698529	53895160	-	BC119533	secretion regulating guanine nucleotide exchange factor
149	Ski	NM_011385	chr4	154528184	154596644	-	BC068305	ski sarcoma viral oncogene homolog (avian)
150	Slc30a7	NM_023214	chr3	115648861	115710297	-	BC017136	solute carrier family 30 (zinc transporter), member 7
151	Srp72	NM_025691	chr5	77403733	77428957	+	BC058769	signal recognition particle 72
152	Ssh2	NM_177710	chr11	77029927	77269050	+	AB099288	slingshot homolog 2 (Drosophila)
153	Tatdn2	NM_001033463	chr6	113647493	113661062	+	AK220217	TatD DNase domain containing 2
154	Tm7sf3	NM_026281	chr6	146552011	146583062	-	DQ104329	transmembrane 7 superfamily member 3
155	Tmem109	NM_134142	chr19	10945150	10956233	-	BC025033	transmembrane protein 109
156	Tollip	NM_023764	chr7	149060718	149088320	-	BC062139	toll interacting protein
157	Trip12	NM_133975	chr1	84717764	84835879	-	BC034113	thyroid hormone receptor interactor 12
158	Tubb6	NM_026473	chr18	67550373	67562403	+	BC008225	tubulin, beta 6
159	Ubac2	NM_026861	chr14	122277828	122420257	+	BC024467	ubiquitin associated domain containing 2

160	Ubap2	NM_026872	chr4	41141348	41222168	-	BC007179	ubiquitin-associated protein 2
161	Ube2e2	NM_144839	chr14	19406091	19726141	-	BC016265	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)
162	Usp32	NM_001029934	chr11	84797992	84917463	-		ubiquitin specific peptidase 32
163	Wdr22	NM_177267	chr12	81436835	81537526	-	AK122561	WD repeat domain 22
164	Wdr51b	NM_027740	chr10	98569805	98660622	+	BC050888	WD repeat domain 51B
165	Zbtb37	NM_173424	chr1	162938931	162964966	-	BC113763	zinc finger and BTB domain containing 37
166	Zfp27	NM_001037707|	chr7	30678356	30691123	-	BC059037	zinc finger protein 27
167	Zfp472	NM_153063	chr17	33102787	33116006	+	BC027407	zinc finger protein 472
168	Zhx3	NM_177263	chr2	160596183	160698726	-	BC058111	zinc fingers and homeoboxes 3
169	37681	NM_177115	chr18	56921370	57085202	-	BC107232	membrane-associated ring finger (C3HC4) 3
170	0610009B22Rik	NM_025319	chr11	51498886	51502136	-	BC024353	RIKEN cDNA 0610009B22 gene
171	1110049F12Rik	NM_025411	chr4	135531517	135543160	-	BC052695	RIKEN cDNA 1110049F12 gene
172	1200016B10Rik	NM_025819	chr1	153214829	153275566	-	BC060204	RIKEN cDNA 1200016B10 gene
173	1700021F05Rik	NM_026411	chr10	43244927	43260800	-	BC013506	RIKEN cDNA 1700021F05 gene
174	2210009G21Rik	NM_001038641|	chr2	136585351	136897686	+	BC067037	RIKEN cDNA 2210009G21 gene
175	2210010L05Rik	NM_133829|NM	chr1	52713148	52784162	-	BC017534	RIKEN cDNA 2210010L05 gene
176	2210018M11Rik	NM_172280	chr7	105739101	105805079	-	BC089304	RIKEN cDNA 2210018M11 gene
177	2210412D01Rik	NM_133722	chr7	91257866	91300403	-	BC018511	RIKEN cDNA 2210412D01 gene
178	2610024E20Rik		chr18	34600225	34666477	-	BC031465|BC	RIKEN cDNA 2610024E20 gene
179	2610101N10Rik	NM_001114977|	chr9	95360821	95412415	-	BC068265	RIKEN cDNA 2610101N10 gene
180	2610528E23Rik	NM_025599	chr16	57302113	57606979	-	BC038891	RIKEN cDNA 2610528E23 gene
181	3930401K13Rik	NM_001079814|	chr16	5014030	5049953	-	BC006893	RIKEN cDNA 3930401K13 gene
182	4632411B12Rik	NM_172652	chr1	36392575	36426026	-	BC132293	RIKEN cDNA 4632411B12 gene
183	4930473A06Rik	NM_001081012	chr4	83171500	83510635	+	BC039810	RIKEN cDNA 4930473A06 gene
184	4930535B03Rik	NM_001081293	chr3	95565563	95622699	-	BC067054	RIKEN cDNA 4930535B03 gene
185	5830418K08Rik	NM_176976	chr9	15107787	15162148	-	AK220270	RIKEN cDNA 5830418K08 gene | similar to KIAA1731 protein
186	9030612M13Rik	NM_172458	chr17	32908181	32924492	-	BC043671	RIKEN cDNA 9030612M13 gene
187	A230067G21Rik	NM_001033348	chr2	146086112	146337742	-	BC053994	RIKEN cDNA A230067G21 gene
188	Aatf	NM_019816	chr11	84236358	84327003	-	BC025080	apoptosis antagonizing transcription factor
189	Abca1	NM_013454	chr4	53043660	53172767	-		ATP-binding cassette, sub-family A (ABC1), member 1
190	Abcc10	NM_145140|NM	chr17	46440161	46464972	-	AF406642	ATP-binding cassette, sub-family C (CFTR/MRP), member 10
191	Abcf2	NM_013853	chr5	24064464	24083186	-	BC003300	ATP-binding cassette, sub-family F (GCN20), member 2
192	Abi1	NM_001077190|	chr2	22805705	22895585	-	AF420251	abl-interactor 1
193	Acly	NM_134037	chr11	100337670	100389215	-	BC056378	ATP citrate lyase
194	Acox1	NM_015729	chr11	116033202	116060359	-	BC056448	acyl-Coenzyme A oxidase 1, palmitoyl
195	Actn1	NM_134156	chr12	81268532	81361303	-	BC054830	actinin, alpha 1
196	Aff1	NM_001080798|	chr5	104183358	104280142	+	BC131665	AF4/FMR2 family, member 1
197	AI847670	NM_177869	chr5	20930882	20987942	+	BC055342	
198	Alcam	NM_009655	chr16	52251003	52454187	-	BC027280	activated leukocyte cell adhesion molecule
199	Aldh6a1	NM_134042	chr12	85771667	85791953	-	BC033440	aldehyde dehydrogenase family 6, subfamily A1
200	Alg2	NM_019998	chr4	47482705	47487197	-	BC051951	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase)
201	Ampd2	NM_028779	chr3	107876980	107889545	-	BC049119	adenosine monophosphate deaminase 2 (isoform L)
202	Ankrd13c	NM_001013806	chr3	157610215	157669801	+	BC065088	ankyrin repeat domain 13c
203	Ankrd17	NM_030886|NM	chr5	90656191	90795590	-	AF130371	ankyrin repeat domain 17
204	Ankrd44	NM_001081433	chr1	54710593	54983000	-		ankyrin repeat domain 44
205	Apaf1	NM_001042558|	chr10	90452056	90545515	-	BC131683	apoptotic peptidase activating factor 1
206	Apob	NM_009693	chr12	7984479	8023641	+	BC100607	apolipoprotein B
207	App	NM_007471	chr16	84954688	85173948	-	BC070409	amyloid beta (A4) precursor protein
208	Arfip1	NM_001081093	chr3	84301658	84351938	-	BC132291	ADP-ribosylation factor interacting protein 1
209	Arhgap12	NM_001039692|	chr18	6024446	6136096	-	BC024633	Rho GTPase activating protein 12
210	Arhgap17	NM_144529|NM	chr7	130419361	130513398	-	AB060553	Rho GTPase activating protein 17
211	Arid5b	NM_023598	chr10	67558341	67741488	-	AF280065	AT rich interactive domain 5B (Mrf1 like)
212	Arih1	NM_019927	chr9	59240403	59334421	-	BC057680	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)
213	Arl5a	NM_182994	chr2	52253467	52280394	-	BC048170	ADP-ribosylation factor-like 5A
214	Asah1	NM_019734	chr8	42426004	42460587	-	AF352179	N-acylsphingosine amidohydrolase 1
215	Atad1	NM_026487	chr19	32747050	32786812	-	BC029085	ATPase family, AAA domain containing 1
216	Atf6	NM_001081304	chr1	172637345	172797899	-		activating transcription factor 6
217	Atg5	NM_053069	chr10	43988164	44084097	+	BC002166	autophagy-related 5 (yeast)
218	Bad	NM_007522	chr19	7016351	7026388	+	BC006762	Bcl-associated death promoter
219	Bag4	NM_026121	chr8	26875008	26895681	-	AF332863	BCL2-associated athanogene 4
220	Bard1	NM_007525	chr1	71074294	71074611	-		BRCA1 associated RING domain 1
221	BC011248		chr17	46804391	46811236	-	BC011248	
222	BC029169		chr11	109534237	109583570	-	BC029169|BC	
223	Brip1	NM_178309	chr11	85871638	86014695	-	BC094252	BRCA1 interacting protein C-terminal helicase 1
224	Bst2	NM_198095	chr8	74057851	74061336	-	BC087949	bone marrow stromal cell antigen 2
225	Btbd9	NM_172618	chr17	30357025	30713110	-	BC057897	BTB (POZ) domain containing 9
226	Btf3	NM_145455	chr13	99079850	99086922	-	BC064010	basic transcription factor 3
227	Bxdc5	NM_027371|NM	chr3	146169308	146184382	-	BC089369	brix domain containing 5
228	C130022K22Rik	NM_172730	chr6	91828053	91849842	+	BC051147	RIKEN cDNA C130022K22 gene
229	C230094A16Rik	NM_146016	chr11	29644134	29925940	-	BC024726	RIKEN cDNA C230094A16 gene
230	C3	NM_009778	chr17	57343396	57367514	-	BC043338	complement component 3
231	Canx	NM_007597|NM	chr11	50107965	50139094	-	BC040244	calnexin
232	Ccdc49	NM_026186	chr11	97606795	97627870	-	BC079553	coiled-coil domain containing 49
233	Ccdc55	NM_001012309	chr11	76857794	76891937	-	BC089560	coiled-coil domain containing 55
234	Ccny	NM_026484	chr18	9314042	9450148	-	BC023321	cyclin Y | similar to cyclin fold protein 1
235	Cenpc1	NM_007683	chr5	86441049	86494496	-	U03113	centromere protein C1
236	Cep152	NM_001081091	chr2	125388826	125450849	-		centrosomal protein 152
237	Chchd4	NM_133928	chr6	91414270	91423417	-	BC019405	coiled-coil-helix-coiled-coil-helix domain containing 4
238	Chmp7	NM_134078	chr14	70116807	70132348	-	BC033365	CHMP family, member 7
239	Cltc	NM_001003908	chr11	86508153	86570994	-	BC079897	clathrin, heavy polypeptide (Hc)
240	Cmtm8	NM_027294	chr9	114698463	114753270	-	AY243513	CKLF-like MARVEL transmembrane domain containing 8
241	Cndp2	NM_023149	chr18	84836857	84855025	-	BC005532	CNDP dipeptidase 2 (metallopeptidase M20 family)
242	Cnot4	NM_016877	chr6	34972065	35083715	-	BC058778	CCR4-NOT transcription complex, subunit 4
243	Cobll1	NM_177025	chr2	64926408	65077460	-	AY308746	Cobl-like 1
244	Cox4nb	NM_010926	chr8	123177814	123192012	-	BC009103|AF	COX4 neighbor
245	Cradd	NM_009950	chr10	94637373	94786731	-	BC005608	CASP2 and RIPK1 domain containing adaptor with death domain
246	Creb3l2	NM_178661	chr6	37281021	37392139	-	BC043466	cAMP responsive element binding protein 3-like 2
247	Cs	NM_026444	chr10	127774873	127799535	+	BC029754	citrate synthase
248	Csnk1a1	NM_146087	chr18	61714987	61748428	+	BC019740	casein kinase 1, alpha 1
249	Ctage5	NM_146034	chr12	60230733	60291163	+	BC026864	CTAGE family, member 5
250	Ctdp1	NM_026295	chr18	80604698	80666406	-	BC053435	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1
251	Cux1	NM_009986|NM	chr5	136724005	137043301	-	BC079570	cut-like homeobox 1
252	Cyp4f14	NM_022434	chr17	33042015	33054274	-	AB037540	cytochrome P450, family 4, subfamily f, polypeptide 14
253	D2Wsu81e	NM_172660	chr2	30028973	30033975	-	BC078441	DNA segment, Chr 2, Wayne State University 81, expressed
254	D630037F22Rik	NM_001033385	chr10	55767975	55948408	-		RIKEN cDNA D630037F22 gene
255	Daam1	NM_026102|NM	chr12	72932065	73093354	+	BC076585	dishevelled associated activator of morphogenesis 1
256	Dad1	NM_010015|NM	chr14	54855160	54873589	-	BC058116	defender against cell death 1 | hypothetical protein LOC100044173
257	Dak	NM_145496	chr19	10666687	10678748	-	BC021917	dihydroxyacetone kinase 2 homolog (yeast)
258	Dcps	NM_027030	chr9	34931996	34983600	-	BC016273	decapping enzyme, scavenger
259	Dhfr	NM_010049	chr13	93124738	93159008	+	BC005796	dihydrofolate reductase
260	Dhrs3	NM_011303	chr4	144482730	144518112	+	BC010972	dehydrogenase/reductase (SDR family) member 3
261	Donson	NM_021720	chr16	91679510	91688998	-	BC043316	downstream neighbor of SON
262	Dpp9	NM_172624	chr17	56326105	56358311	-	BC057631	dipeptidylpeptidase 9
263	Dullard	NM_026017	chr11	69794670	69804103	+	BC018265	Dullard homolog (Xenopus laevis) | similar to Dullard homolog (Xenopus laevis)
264	Dync1li2	NM_001013380	chr8	106943029	106966905	-	BC058645	dynein, cytoplasmic 1 light intermediate chain 2
265	Ebag9	NM_019480	chr15	44450859	44472573	+	BC108397	estrogen receptor-binding fragment-associated gene 9
266	Eea1	NM_001001932	chr10	95403297	95508152	+	BC075637	early endosome antigen 1
267	Egfr	NM_207655|NM	chr11	16652206	16813912	+	AF275367	epidermal growth factor receptor
268	Ehd1	NM_010119	chr19	6276734	6300096	+	BC043332	EH-domain containing 1
269	Elovl2	NM_019423	chr13	41277864	41315762	-	BC098215	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
270	Erbb4	NM_010154	chr1	68086625	69154330	-	AF059177	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
271	Esco1	NM_001081222	chr18	10566600	10610107	-	BC008220	establishment of cohesion 1 homolog 1 (S. cerevisiae)
272	Etfa	NM_145615	chr9	55302315	55360050	-	BC096645	electron transferring flavoprotein, alpha polypeptide
273	F2r	NM_010169	chr13	96371744	96388429	-	BC031516	coagulation factor II (thrombin) receptor
274	Fbxl3	NM_015822	chr14	103479456	103498735	-	BC067203	F-box and leucine-rich repeat protein 3
275	Fbxo30	NM_027968	chr10	11001172	11016763	+	BC037691	F-box protein 30
276	Fbxw11	NM_134015	chr11	32542748	32646816	+	BC034261	F-box and WD-40 domain protein 11
277	Fech	NM_007998	chr18	64616202	64648720	-	BC006746	ferrochelatase
278	Foxa1	NM_008259	chr12	58641615	58647108	-	BC096524	forkhead box A1 | similar to Hepatocyte nuclear factor 3-alpha (HNF-3A) (Forkhead box protein A1)
279	Foxo3a		chr10	41905020	41905238	-		forkhead box O3a
280	Fryl	NM_028194	chr5	73412435	73467184	-	BC051118	furry homolog-like (Drosophila)
281	Fyco1	NM_148925|NM	chr9	123698628	123760687	-		FYVE and coiled-coil domain containing 1
282	Garnl1		chr12	56921651	56922567	+	AK015025	GTPase activating RANGAP domain-like 1
283	Gc	NM_008096	chr5	89846547	89886790	-	BC010762	group specific component
284	Gch1	NM_008102	chr14	47773570	47809081	-	BC005643	GTP cyclohydrolase 1
285	Gm672	NM_201354	chr18	75590859	75857208	-	BC058104	gene model 672, (NCBI)
286	Gss	NM_008180	chr2	155388917	155418448	-	U35456	glutathione synthetase
287	Gtf2f1	NM_133801	chr17	57142825	57150841	-	BC031123	general transcription factor IIF, polypeptide 1
288	Gtf2f2	NM_026816	chr14	76296744	76410672	-	BC027173	general transcription factor IIF, polypeptide 2
289	Hdlbp	NM_133808	chr1	95302517	95375385	-	BC027788	high density lipoprotein (HDL) binding protein
290	Hexim1	NM_138753	chr11	102977639	102981039	+	AY090614	hexamethylene bis-acetamide inducible 1
291	Hibadh	NM_145567	chr6	52496224	52590294	-	BC003914	3-hydroxyisobutyrate dehydrogenase
292	Hivep2	NM_010437	chr10	13686185	13871184	+		human immunodeficiency virus type I enhancer binding protein 2
293	Hps3	NM_080634	chr3	19895945	19935302	-	BC058235	Hermansky-Pudlak syndrome 3 homolog (human)
294	Id3	NM_008321	chr4	135699737	135701305	+	M60523	inhibitor of DNA binding 3
295	Ikzf5		chr3	46854304	46855563	-	BC089455	IKAROS family zinc finger 5
296	Inoc1	NM_026574	chr2	119198773	119303365	-	BC061495	INO80 complex homolog 1 (S. cerevisiae)
297	Ints6	NM_008715	chr14	63295157	63397198	-	BC059263	integrator complex subunit 6
298	Ipo11	NM_029665	chr13	107584519	107726995	-	BC031900	importin 11
299	Iqgap2	NM_027711	chr13	96397130	96661654	-		IQ motif containing GTPase activating protein 2
300	Irf2	NM_008391	chr8	47825127	47932820	+	J03168	interferon regulatory factor 2
301	Itpr1	NM_010585	chr6	108163112	108501104	+	BC003271	inositol 1,4,5-triphosphate receptor 1
302	Kazald1	NM_178929	chr19	45150629	45153772	+	BC115642	Kazal-type serine peptidase inhibitor domain 1
303	Klf9	NM_010638	chr19	23215716	23241401	+	Y14296	Kruppel-like factor 9 | RIKEN cDNA 2310051E17 gene
304	Larp7	NM_138593	chr3	127239632	127256267	-	BC023165	La ribonucleoprotein domain family, member 7
305	Lcorl	NM_172153|NM	chr5	46090530	46248745	-	AB076078	ligand dependent nuclear receptor corepressor-like
306	Lipa	NM_021460|NM	chr19	34566804	34601912	-	BC058564	lysosomal acid lipase A
307	Lrpprc	NM_028233	chr17	85104587	85189898	-	BC059862	leucine-rich PPR-motif containing
308	Man2a1	NM_008549	chr17	64950989	65104450	+		mannosidase 2, alpha 1
309	Mapkapk2	NM_008551	chr1	132950281	132994144	-	BC063064	MAP kinase-activated protein kinase 2
310	Mccc1	NM_023644	chr3	35858234	35899553	-	AF310338	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)
311	Med8	NM_020000|NM	chr4	118081942	118088387	+	BC021870	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)
312	Mef2a	NM_001033713	chr7	74376970	74517744	-	BC096598	myocyte enhancer factor 2A
313	Meis2	NM_010825	chr2	115688349	115890849	-	U57343	Meis homeobox 2
314	Mfsd8	NM_028140	chr3	40621992	40697924	-	BC113790	major facilitator superfamily domain containing 8
315	Mif	NM_010798|NM	chr10	75322099	75322995	-	BC024895	macrophage migration inhibitory factor | macrophage migration inhibitory factor-like | similar to macrophage migr
316	Mitf	NM_001113198|	chr6	97757178	97968701	+	BC108976	microphthalmia-associated transcription factor
317	Mllt3	NM_027326|NM	chr4	87415829	87679311	-	BC021420	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3
318	Mrpl15	NM_025300	chr1	4763290	4775791	-	BC027233	mitochondrial ribosomal protein L15
319	Mtdh	NM_026002	chr15	34012474	34072140	+	AF501309	Metadherin

320	Mthfd1l	NM_172308	chr10	6190430	6373423	-	BC030437	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
321	Mtmr2	NM_023858	chr9	13552854	13610925	+	BC063050	myotubularin related protein 2
322	Nab1	NM_008667	chr1	52514720	52557292	-	BC016886	Ngfi-A binding protein 1
323	Napb	NM_019632	chr2	148520378	148558203	-	BC038362	N-ethylmaleimide sensitive fusion protein attachment protein beta
324	Nek1	NM_175089	chr8	63471992	63610141	+	AK173292	NIMA (never in mitosis gene a)-related expressed kinase 1
325	Nfyc	NM_008692|NM	chr12	7866560	7868492	+	BC085261	nuclear transcription factor-Y gamma
326	Nln	NM_029447	chr13	104813277	104899655	-	BC016224	neurolysin (metallopeptidase M3 family)
327	Nol10	NM_001008421	chr12	17355299	17436901	+	BC086676	nucleolar protein 10
328	Npc2	NM_023409	chr12	86095507	86114062	-	BC007190	Niemann Pick type C2
329	Nr6a1	NM_010264	chr2	38578890	38783208	-	AF390896	nuclear receptor subfamily 6, group A, member 1
330	Nt5dc3	NM_175331	chr10	86241750	86301134	+		5'-nucleotidase domain containing 3 | cDNA sequence BC030307
331	Nudcd1	NM_026149|NM	chr15	44206775	44259853	-	BC031583	NudC domain containing 1
332	Nupl1	NM_170591	chr14	60838305	60870246	-	BC026743	nucleoporin like 1
333	Osbpl8	NM_175489|NM	chr10	110601858	110734303	+		oxysterol binding protein-like 8
334	Pcyox1	NM_025823	chr6	86336851	86347114	-	BC028308	prenylcysteine oxidase 1
335	Pcyt1a	NM_009981	chr16	32431082	32472114	+	L28956	phosphate cytidylyltransferase 1, choline, alpha isoform
336	Pdcd6	NM_011051	chr13	74440576	74454725	-	BC040079	programmed cell death 6
337	Pde4dip	NM_001039376|	chr3	97493747	97692630	-	BC050783	phosphodiesterase 4D interacting protein (myomegalin)
338	Pde6d	NM_008801	chr1	88439590	88479076	-	BC005636	phosphodiesterase 6D, cGMP-specific, rod, delta
339	Pfkfb2	NM_008825	chr1	132585759	132612391	-	BC018418	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2
340	Phc3		chr3	30798934	30799236	-	BC050266	polyhomeotic-like 3 (Drosophila)
341	Phldb2	NM_153412	chr16	45746356	45844491	-	BC050915|AF	pleckstrin homology-like domain, family B, member 2
342	Phr1							
343	Picalm	NM_146194	chr7	97278742	97357442	+	BC025566	phosphatidylinositol binding clathrin assembly protein
344	Pik3c2a	NM_011083	chr7	123483075	123586962	-	U55772	phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide
345	Pik3r1	NM_001077495|	chr13	102450716	102538172	-	BC026146	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)
346	Pik3r3	NM_181585	chr4	115894519	115975661	+	BC053102	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)
347	Pitpnc1	NM_145823	chr11	107069206	107332034	-	AB077281	phosphatidylinositol transfer protein, cytoplasmic 1
348	Pkp4	NM_026361|NM	chr2	58999077	59193265	+	BC079848	plakophilin 4
349	Plaa	NM_172695	chr4	94231830	94269942	-	BC139773	phospholipase A2, activating protein
350	Ppa1	NM_026438	chr10	61111369	61136916	+	BC010468	pyrophosphatase (inorganic) 1
351	Ppara	NM_011144|NM	chr15	85566206	85633249	+	BC016892	peroxisome proliferator activated receptor alpha
352	Ppil3	NM_027351|NM	chr1	58487838	58502330	-	BC061645	peptidylprolyl isomerase (cyclophilin)-like 3
353	Ppm1l	NM_178726	chr3	69120840	69359333	+	BC096031	protein phosphatase 1 (formerly 2C)-like
354	Ppp2r5c		chr12	111685517	111685595	+	AK129042	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
355	Ppp3ca	NM_008913	chr3	136333734	136600350	+	J05479	protein phosphatase 3, catalytic subunit, alpha isoform
356	Prdx1	NM_011034	chr16	48218718	48219317	+	D16142	peroxiredoxin 1
357	Prdx6	NM_007453	chr1	163170243	163181297	-	AF093852	peroxiredoxin 6
358	Prei4	NM_028802|NM	chr2	132354819	132403986	-	BC033408	preimplantation protein 4
359	Prkca	NM_011101	chr11	107799481	108205242	-	BC096493	protein kinase C, alpha
360	Prox1	NM_008937	chr1	191945648	191994559	-	BC051411	prospero-related homeobox 1
361	Psen1	NM_008943		85029122	85076149	+	BC071233	presenilin 1
362	Ptprg	NM_008981	chr14	12386526	13070443	+	L09562	protein tyrosine phosphatase, receptor type, G
363	Pvrl1	NM_021424	chr9	43552659	43615544	+	BC060694	poliovirus receptor-related 1
364	Pygb	NM_153781	chr2	150612524	150657486	+	BC035283	brain glycogen phosphorylase
365	Rab5a	NM_025887	chr17	53618559	53647005	+	BC096481	RAB5A, member RAS oncogene family
366	Rab5c	NM_024456	chr11	100576325	100599504	-	BC029678	RAB5C, member RAS oncogene family
367	Raph1	NM_001045513	chr1	60545154	60623613	-		Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
368	Rara	NM_009024	chr11	98799010	98836256	+	BC040383	retinoic acid receptor, alpha
369	Rb1cc1	NM_009826	chr1	6204743	6265656	+	AB070619	RB1-inducible coiled-coil 1
370	Rbed1	NM_144917	chr6	72515919	72548337	-	BC016193	RNA binding motif and ELMO domain 1
371	Rbm43	NM_030243	chr2	51779968	51790683	-	BC003333	RNA binding motif protein 43
372	Rbm47	NM_178446|NM	chr5	66409841	66542168	-	BC112902	RNA binding motif protein 47
373	Rbpj		chr5	53946945	53948438	+	AY512934	recombination signal binding protein for immunoglobulin kappa J region
374	Rcl1	NM_021525	chr19	29175865	29218419	+	BC004574	RNA terminal phosphate cyclase-like 1
375	Rel	NM_009044	chr11	23641729	23670970	-	BC139770	reticuloendotheliosis oncogene
376	Rell1	NM_145923	chr5	64300315	64360115	-	BC031198	RELT-like 1
377	Rer1	NM_026395	chr4	154448221	154460406	-	BC029189	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)
378	Rere	NM_001085492	chr4	149780449	149993598	+	BC110693	arginine glutamic acid dipeptide (RE) repeats
379	Rnd3	NM_028810	chr2	50985959	51004631	-	BC009002	Rho family GTPase 3
380	Rps6ka5	NM_153587	chr12	101787988	101963238	-	AY341873	ribosomal protein S6 kinase, polypeptide 5
381	Rsu1	NM_009105	chr2	12998595	13192935	-	BC003827	Ras suppressor protein 1
382	Safb2		chr17	56701848	56702273	-		scaffold attachment factor B2
383	Sart3	NM_016926	chr5	114192453	114221658	-	BC057156	squamous cell carcinoma antigen recognized by T-cells 3
384	Scaper	NM_001081341	chr9	55398057	55767412	-		S phase cyclin A-associated protein in the ER
385	Sec16a	NM_153125	chr2	26264953	26296942	-	BC034649	SEC16 homolog A (S. cerevisiae)
386	Sel1l	NM_001039089|	chr12	93044483	93087597	-	AF063095	sel-1 suppressor of lin-12-like (C. elegans)
387	Senp5	NM_177103	chr16	31962592	32003257	-	BC080830	SUMO/sentrin specific peptidase 5
388	Serinc1	NM_019760	chr10	57235580	57252310	-	AF181685	serine incorporator 1
389	Sertad2	NM_021372|NM	chr11	20443256	20553026	+	BC014726	SERTA domain containing 2
390	Sf3b2	NM_030109	chr19	5273932	5295448	-	BC049118	splicing factor 3b, subunit 2
391	Shf	NM_001013829	chr2	122174628	122201643	-	BC042839	Src homology 2 domain containing F
392	Shoc2	NM_019658	chr19	54018796	54107621	+	BC083060	soc-2 (suppressor of clear) homolog (C. elegans)
393	Slc25a37	NM_026331	chr14	69859903	69903160	-	AF361699	solute carrier family 25, member 37
394	Smad1	NM_008539	chr8	81862294	81923367	-	BC058693	MAD homolog 1 (Drosophila)
395	Smarca2	NM_011416|NM	chr19	26679650	26852811	+	BC075641	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
396	Smchd1	NM_028887	chr17	71693836	71797867	-	BC062946	SMC hinge domain containing 1
397	Smurf2		chr11	106683070	106683258	-		SMAD specific E3 ubiquitin protein ligase 2
398	Snrp70	NM_009224	chr7	52631824	52651063	-	BC049128	U1 small nuclear ribonucleoprotein polypeptide A
399	Sp3	NM_001018042|	chr2	72774487	72819076	-	BC079874	trans-acting transcription factor 3 | RIKEN cDNA D130067C23 gene
400	Spag9	NM_027569|NM	chr11	93857405	93987694	+	BC094670	sperm associated antigen 9
401	Srp54b							
402	Stam	NM_011484	chr2	13995739	14069965	+	BC044666	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1
403	Stard4	NM_133774	chr18	33361075	33373470	-	BC005642	StAR-related lipid transfer (START) domain containing 4
404	Stk25	NM_021537	chr1	95517328	95532304	-	BC071218	serine/threonine kinase 25 (yeast)
405	Stk39	NM_016866	chr2	68048502	68310325	-	BC051964	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)
406	Stxbp5	NM_001081344	chr10	9480711	9620481	-	AF516607	syntaxin binding protein 5 (tomosyn)
407	Suclg2	NM_011507	chr6	95423006	95668792	-	BC080781	succinate-Coenzyme A ligase, GDP-forming, beta subunit
408	Surf1	NM_013677	chr2	26768903	26772050	-	BC052500	surfeit gene 1
409	Taf2	NM_001081288	chr15	54853758	54903484	-		TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor
410	Taf3	NM_027748	chr2	9837223	9970243	-	BC094546	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor
411	Tars	NM_033074	chr15	11313418	11329413	-	BC055371	threonyl-tRNA synthetase
412	Tbc1d22a	NM_145476	chr15	86044889	86328933	+	BC066009	TBC1 domain family, member 22a
413	Tbc1d5	NM_028162	chr17	50751039	51318660	-	AK220251	TBC1 domain family, member 5
414	Timm23	NM_016897	chr1	174074403	174075032	-	AB021122	translocase of inner mitochondrial membrane 23 homolog (yeast) | similar to Translocase of inner mitochondrial
415	Tle1	NM_011599	chr4	71778176	71861896	-	BC057573	transducin-like enhancer of split 1, homolog of Drosophila E(spl)
416	Tlk2	NM_001112705|	chr11	105040121	105143490	+	AF045252	tousled-like kinase 2 (Arabidopsis)
417	Tmco4	NM_029857	chr4	138528807	138615082	+	BC013471	transmembrane and coiled-coil domains 4
418	Tnrc6b	NM_144812|NM	chr15	80541743	80771516	+	BC068158	trinucleotide repeat containing 6b
419	Tob2	NM_020507	chr15	81678700	81689226	-	AK122537	transducer of ERBB2, 2
420	Tpd52	NM_001025261|	chr3	8929436	9004515	-	AY048852	tumor protein D52
421	Tpi1	NM_009415	chr6	124760733	124764430	-	BC046761	triosephosphate isomerase 1
422	Tpp2	NM_009418	chr1	43990847	44059844	+	X81323	tripeptidyl peptidase II
423	Tram2	NM_177409|NM	chr1	20991459	21069306	-	BC018212	translocating chain-associating membrane protein 2
424	Trib1	NM_144549	chr15	59480209	59488654	+	BC006800	tribbles homolog 1 (Drosophila)
425	Trim39	NM_024468	chr17	36395817	36408949	-	AB046382	tripartite motif-containing 39
426	Trim41	NM_145377	chr11	48619906	48630855	-	BC020156	tripartite motif-containing 41 | similar to tripartite motif-containing 41
427	Trp53bp2	NM_173378	chr1	184339298	184392567	+	BC042874	transformation related protein 53 binding protein 2
428	Trp53inp1	NM_021897	chr4	11083588	11101526	+	AY034611	transformation related protein 53 inducible nuclear protein 1
429	Trpc4ap	NM_019828	chr2	155460013	155518096	-	AF509881	transient receptor potential cation channel, subfamily C, member 4 associated protein
430	Tspan9	NM_175414	chr6	127911418	128093596	-	BC052503	tetraspanin 9
431	Ttc7	NM_028639	chr17	87682226	87781099	+	BC042512	tetratricopeptide repeat domain 7
432	Tubgcp2	NM_133755	chr7	147181895	147222165	-	BC012519	tubulin, gamma complex associated protein 2
433	Tyk2	NM_018793	chr9	20908518	20935654	-	BC094240	tyrosine kinase 2
434	Ube2n	NM_080560	chr10	94977796	95008292	+	BC067069	ubiquitin-conjugating enzyme E2N
435	Ufm1	NM_026435	chr3	53659134	53667728	-	BC061065	ubiquitin-fold modifier 1
436	Usp53	NM_133857	chr3	122636519	122687365	-	BC132339	ubiquitin specific peptidase 53
437	Vdac1	NM_011694	chr11	52174617	52202899	+	U30840	voltage-dependent anion channel 1
438	Vps4b	NM_009190	chr1	108666015	108693253	-	U10119	vacuolar protein sorting 4b (yeast)
439	Vps53	NM_026664	chr11	75859728	75993132	-	BC034371	vacuolar protein sorting 53 (yeast)
440	Wasf2	NM_153423	chr4	132686493	132755644	+	AY135643	WAS protein family, member 2
441	Wdfy3		chr5	102261975	102263755	-	AB093277	WD repeat and FYVE domain containing 3
442	Wdr5	NM_080848	chr2	27249699	27392055	+	BC025801	WD repeat domain 5
443	Whsc1l1	NM_001081269|	chr8	26712778	26824872	+	BC064447	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)
444	Wnk1	NM_198703	chr6	119873989	119988625	-	AY309076	WNK lysine deficient protein kinase 1
445	Wrn	NM_011721|NM	chr8	34344845	34496352	-	BC050921	Werner syndrome homolog (human)
446	Wwtr1	NM_133784	chr3	57259571	57379802	-	BC014727	WW domain containing transcription regulator 1
447	Zbtb6	NM_146253	chr2	37282365	37286499	-	BC032933	zinc finger and BTB domain containing 6 | predicted gene, ENSMUSG00000066798
448	Zdhhc20		chr14	58449906	58450046	-	AK047968	zinc finger, DHHC domain containing 20
449	Zeb2	NM_015753	chr2	44839252	44968744	-	BC060699	zinc finger E-box binding homeobox 2
450	Zfand3	NM_148926	chr17	30142032	30346967	+	BC083124	zinc finger, AN1-type domain 3
451	Zfat1							
452	Zfp1	NM_001037665|	chr8	114167343	114194911	+	BC055796	zinc finger protein 1
453	Zfp458	NM_001001152	chr13	67355854	67370004	-	BC062958	zinc finger protein 458
454	Zfp687	NM_030074	chr3	94810486	94819359	-	AK129360	zinc finger protein 687
455	Zfp697	NM_172863	chr3	98186415	98235632	+	BC092534	zinc finger protein 697
456	Zfp707	NM_001081065	chr15	75799649	75806176	+	BC026404	zinc finger protein 707
457	Zfp780b	NM_001081021	chr7	28744154	28764158	-	BC094325	zinc finger protein 780B
458	Zfp85-rs1	NM_001001130	chr13	67848737	67856071	-	BC055337	zinc finger protein 85, related sequence 1
459	Zfyve16	NM_173392	chr13	93257704	93300765	-	BC042669	zinc finger, FYVE domain containing 16
460	Zh2c2	NM_026250	chr1	99666772	99690285	+	BC033572	zinc finger, H2C2 domain containing

Table S4	Gene symbol	Refseq ID	Chromosome	Start Position	End Position	Strand	Genbank ID	Gene Description
1	2310047O13Rik	NM_024185	chr2	12268891	12341087	-	BC027202	RIKEN cDNA 2310047O13 gene
2	2610101N10Rik	NM_0011149	chr9	95360821	95412415	-	BC068265	RIKEN cDNA 2610101N10 gene
3	9030612M13Rik	NM_172458	chr17	32908181	32924492	-	BC043671	RIKEN cDNA 9030612M13 gene
4	A230067G21Rik	NM_0010333	chr2	146086112	146337742	-	BC053994	RIKEN cDNA A230067G21 gene
5	A530082C11Rik	NM_177186	chr4	154975525	154997449	+	BC058728	RIKEN cDNA A530082C11 gene
6	Abi1	NM_0010771	chr2	22805705	22895585	-	AF420251	abl-interactor 1
7	Acly	NM_134037	chr11	100337670	100389215	-	BC056378	ATP citrate lyase
8	Actn1	NM_134156	chr12	81268532	81361303	-	BC054830	actinin, alpha 1
9	Adfp	NM_007408	chr4	86302469	86315963	-	M93275	adipose differentiation related protein
10	Agl	NM_0010813	chr3	116445969	116510327	-	BC044780	amylo-1,6-glucosidase, 4-alpha-glucanotransferase
11	Ahcy	NM_016661	chr2	154885046	154900169	-	BC086781	S-adenosylhomocysteine hydrolase
12	Ak3	NM_021299	chr19	29095322	29122445	-	BC058191	adenylate kinase 3
13	Alas1	NM_020559	chr9	106136258	106150187	-	BC022110	aminolevulinic acid synthase 1
14	Alcam	NM_009655	chr16	52251003	52454187	-	BC027280	activated leukocyte cell adhesion molecule
15	Ankrd17	NM_030886|	chr5	90656191	90795590	-	AF130371	ankyrin repeat domain 17
16	Arhgap12	NM_0010396	chr18	6024446	6136096	-	BC024633	Rho GTPase activating protein 12
17	Atp6v1e1	NM_007510	chr6	120745262	120772719	-	BC003421	VATPase, H+ transporting, lysosomal V1 subunit E1
18	Atxn2l	NM_183020	chr7	133635222	133646816	-	BC054483	ataxin 2-like
19	Bag4	NM_026121	chr8	26875008	26895681	-	AF332863	BCL2-associated athanogene 4
20	Bst2	NM_198095	chr8	74057851	74061336	-	BC087949	bone marrow stromal cell antigen 2
21	Cdc37l1	NM_025950	chr19	29064857	29092061	+	BC031761	cell division cycle 37 homolog (S. cerevisiae)-like 1
22	Chchd4	NM_133928	chr6	91414270	91423417	-	BC019405	coiled-coil-helix-coiled-coil-helix domain containing 4
23	Chmp7	NM_134078	chr14	70116807	70132348	-	BC033365	CHMP family, member 7
24	Cltc	NM_0010039	chr11	86508153	86570994	-	BC079897	clathrin, heavy polypeptide (Hc)
25	Cmtm8	NM_027294	chr9	114698463	114753270	-	AY243513	CKLF-like MARVEL transmembrane domain containing 8
26	Cnot4	NM_016877	chr6	34972065	35083715	-	BC058778	CCR4-NOT transcription complex, subunit 4
27	Cobll1	NM_177025	chr2	64926408	65077460	-	AY308746	Cobl-like 1
28	Cs	NM_026444	chr10	127774873	127799535	+	BC029754	citrate synthase
29	Csnk1a1	NM_146087	chr18	61714987	61748428	+	BC019740	casein kinase 1, alpha 1
30	Ctage5	NM_146034	chr12	60230733	60291163	+	BC026864	CTAGE family, member 5
31	Cttn	NM_007803	chr7	151621629	151656642	-	U03184	cortactin
32	Dad1|LOC100044173	NM_010015|	chr14	54855160	54873589	-	BC058116	defender against cell death 1 | hypothetical protein LOC100044173
33	Dhdh	NM_027903	chr7	52728933	52744166	-	BC116414	dihydrodiol dehydrogenase (dimeric)
34	Dhfr	NM_010049	chr13	93124738	93159008	+	BC005796	dihydrofolate reductase
35	Dhrs3	NM_011303	chr4	144482730	144518112	+	BC010972	dehydrogenase/reductase (SDR family) member 3
36	Dhx36	NM_028136	chr3	62274005	62310910	-	AF448804	DEAH (Asp-Glu-Ala-His) box polypeptide 36
37	Dnaja1	NM_008298	chr4	40669566	40681997	+	AF055664	DnaJ (Hsp40) homolog, subfamily A, member 1
38	Dpp9	NM_172624	chr17	56326105	56358311	-	BC057631	dipeptidylpeptidase 9
39	Dynll2	NM_026556	chr11	87793027	87801007	-	BC040822	dynein light chain LC8-type 2
40	Egln2	NM_053208	chr7	27943677	27951792	-	AF453879	EGL nine homolog 2 (C. elegans)
41	Eif1a	NM_010120	chr18	46757358	46769862	+	AF026481	eukaryotic translation initiation factor 1A
42	Etfdh	NM_025794	chr3	79407723	79432642	-	BC057670	electron transferring flavoprotein, dehydrogenase
43	F2r	NM_010169	chr13	96371744	96388429	-	BC031516	coagulation factor II (thrombin) receptor
44	Fbxl20	NM_028149	chr11	97943868	98010930	-	EF649694	F-box and leucine-rich repeat protein 20
45	Fbxl3	NM_015822	chr14	103479456	103498735	-	BC067203	F-box and leucine-rich repeat protein 3
46	Fech	NM_007998	chr18	64616202	64648720	-	BC006746	ferrochelatase
47	Gch1	NM_008102	chr14	47773570	47809081	-	BC005643	GTP cyclohydrolase 1
48	Gss	NM_008180	chr2	155388917	155418448	-	U35456	glutathione synthetase
49	Gtf2f1	NM_133801	chr17	57142825	57150841	-	BC031123	general transcription factor IIF, polypeptide 1
50	Hexim1	NM_138753	chr11	102977639	102981039	+	AY090614	hexamethylene bis-acetamide inducible 1
51	Hspa4	NM_008300	chr11	53073316	53113981	-	BC003770	heat shock protein 4
52	Igf1	NM_010512|	chr10	87321813	87394870	+	BC012409	insulin-like growth factor 1
53	Itpa	NM_025922	chr2	130493543	130507350	+	BC094466	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)
54	Klf9|2310051E17Rik	NM_010638	chr19	23215716	23241401	+	Y14296	Kruppel-like factor 9 | RIKEN cDNA 2310051E17 gene
55	Lasp1	NM_010688	chr11	97660986	97700078	+	BC010840	LIM and SH3 protein 1
56	Lyrm4	NM_201358	chr13	36070666	36209226	-	BC034664	LYR motif containing 4
57	Map3k1	NM_011945	chr13	112536641	112599191	-	AF117340	mitogen-activated protein kinase kinase kinase 1
58	Med8	NM_020000|	chr4	118081942	118088387	+	BC021870	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)
59	Mef2a	NM_0010337	chr7	74376970	74517744	-	BC096598	myocyte enhancer factor 2A
60	Mitf	NM_0011131	chr6	97757178	97968701	+	BC108976	microphthalmia-associated transcription factor
61	Morf4l1	NM_0010391	chr9	89986507	90009600	-	AF319621	mortality factor 4 like 1
62	Mrpl15	NM_025300	chr1	4763290	4775791	-	BC027233	mitochondrial ribosomal protein L15
63	Mthfd1l	NM_172308	chr10	6190430	6373423	-	BC030437	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
64	Mtmr2	NM_023858	chr9	13552854	13610925	+	BC063050	myotubularin related protein 2
65	Nab1	NM_008667	chr1	52514720	52557292	-	BC016886	Ngfi-A binding protein 1
66	Ncl	NM_010880	chr1	88255651	88256536	+		nucleolin
67	Nr6a1	NM_010264	chr2	38578890	38783208	-	AF390896	nuclear receptor subfamily 6, group A, member 1
68	Phldb2	NM_153412	chr16	45746356	45844491	-	BC050915|AF5	pleckstrin homology-like domain, family B, member 2
69	Pik3r1	NM_0010774	chr13	102450716	102538172	-	BC026146	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)
70	Pitpnc1	NM_145823	chr11	107069206	107332034	-	AB077281	phosphatidylinositol transfer protein, cytoplasmic 1
71	Ppa1	NM_026438	chr10	61111369	61136916	+	BC010468	pyrophosphatase (inorganic) 1
72	Ppara	NM_011144|	chr15	85566206	85633249	+	BC016892	peroxisome proliferator activated receptor alpha
73	Ppp3ca	NM_008913	chr3	136333734	136600350	+	J05479	protein phosphatase 3, catalytic subunit, alpha isoform
74	Pqlc2	NM_145384	chr4	138849945	138866600	-	BC019216	PQ loop repeat containing 2
75	Prdx6	NM_007453	chr1	163170243	163181297	-	AF093852	peroxiredoxin 6
76	Prei4	NM_028802|	chr2	132354819	132403986	-	BC033408	preimplantation protein 4
77	Psmd8	NM_026545	chr7	29959271	29965550	-	BC004075	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
78	Rab5a	NM_025887	chr17	53618559	53647005	+	BC096481	RAB5A, member RAS oncogene family
79	Rb1cc1	NM_009826	chr1	6204743	6265656	+	AB070619	RB1-inducible coiled-coil 1
80	Rbm43	NM_030243	chr2	51779968	51790683	-	BC003333	RNA binding motif protein 43
81	Rbpj	NM_009035|	chr5	53980824	54047374	+	BC051387	recombination signal binding protein for immunoglobulin kappa J region
82	Rbpms	NM_019733|	chr8	34893116	35040313	-	BC030397	RNA binding protein gene with multiple splicing
83	Rcl1	NM_021525	chr19	29175865	29218419	+	BC004574	RNA terminal phosphate cyclase-like 1
84	Rell1	NM_145923	chr5	64300315	64360115	-	BC031198	RELT-like 1
85	Rfxank	NM_011266|	chr8	72654705	72663096	-	BC010971	regulatory factor X-associated ankyrin-containing protein
86	Rpia	NM_009075	chr6	70715695	70742169	-	L35034	ribose 5-phosphate isomerase A
87	Rpl22|mCG_130059	NM_009079	chr4	151699835	151708180	+	BC021344	ribosomal protein L22 | ribosomal protein L22 pseudogene
88	Scaper	NM_0010813	chr9	55398057	55767412	-		S phase cyclin A-associated protein in the ER
89	Sdc4	NM_011521	chr2	164249747	164268688	-	D89571	syndecan 4
90	Senp5	NM_177103	chr16	31962592	32003257	-	BC080830	SUMO/sentrin specific peptidase 5
91	Smarca2	NM_011416|	chr19	26679650	26852811	+	BC075641	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
92	Spag9	NM_027569|	chr11	93857405	93987694	+	BC094670	sperm associated antigen 9
93	St13	NM_133726	chr15	81195470	81230124	-	BC003843	suppression of tumorigenicity 13
94	Stam	NM_011484	chr2	13995739	14069965	+	BC044666	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1
95	Stard4	NM_133774	chr18	33361075	33373470	-	BC005642	StAR-related lipid transfer (START) domain containing 4
96	Stk24	NM_145465	chr14	121685563	121778455	-	AY188357	serine/threonine kinase 24 (STE20 homolog, yeast)
97	Tars	NM_033074	chr15	11313418	11329413	-	BC055371	threonyl-tRNA synthetase
98	Tex2	NM_198292	chr11	106363448	106474244	-	BC057406	testis expressed gene 2
99	Tle1	NM_011599	chr4	71778176	71861896	-	BC057573	transducin-like enhancer of split 1, homolog of Drosophila E(spl)
100	Tm7sf3	NM_026281	chr6	146552011	146583062	-	DQ104329	transmembrane 7 superfamily member 3
101	Tmem33	NM_028975|	chr5	67651891	67682700	+	BC016570	transmembrane protein 33
102	Tnrc6b	NM_144812|	chr15	80541743	80771516	+	BC068158	trinucleotide repeat containing 6b
103	Tob2	NM_020507	chr15	81678700	81689226	-	AK122537	transducer of ERBB2, 2
104	Tpd52	NM_0010252	chr3	8929436	9004515	-	AY048852	tumor protein D52
105	Tpi1	NM_009415	chr6	124760733	124764430	-	BC046761	triosephosphate isomerase 1
106	Tspan9	NM_175414	chr6	127911418	128093596	-	BC052503	tetraspanin 9
107	Tubb6	NM_026473	chr18	67550373	67562403	+	BC008225	tubulin, beta 6
108	Tubgcp2	NM_133755	chr7	147181895	147222165	-	BC012519	tubulin, gamma complex associated protein 2
109	Ube2b	NM_009458	chr11	51799064	51813889	-	U57690	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)
110	Ube2e2	NM_144839	chr14	19406091	19726141	-	BC016265	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)
111	Ube2n	NM_080560	chr10	94977796	95008292	+	BC067069	ubiquitin-conjugating enzyme E2N
112	Usp32	NM_0010299	chr11	84797992	84917463	-		ubiquitin specific peptidase 32
113	Vps4b	NM_009190	chr1	108666015	108693253	-	U10119	vacuolar protein sorting 4b (yeast)
114	Wwtr1	NM_133784	chr3	57259571	57379802	-	BC014727	WW domain containing transcription regulator 1
115	Ypel5	NM_027166	chr17	73186044	73200535	+	BC085109	yippee-like 5 (Drosophila)
116	Zdhhc20	NM_029492	chr14	58451539	58509116	-	BC019536	zinc finger, DHHC domain containing 20
117	Zfand3	NM_148926	chr17	30142032	30346967	+	BC083124	zinc finger, AN1-type domain 3
118	Zfp707	NM_0010810	chr15	75799649	75806176	+	BC026404	zinc finger protein 707
119	Zh2c2	NM_026250	chr1	99666772	99690285	+	BC033572	zinc finger, H2C2 domain containing

Table S5

Functional Categories

Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
acetylation	39	34.8214286	2.42E-09	MORF4L1, MEF2A, 2610101N10RIK, AHCY, ABI1, CLTC, MTHFD1L, GSS, CTTN, TPI1, ATXN2L, DYNLL2, HEXIM1, MAP3K1, DNAJA1, DAD1, ETFDH, HSPA4, DHX36, DPP9, PIK3R1, CSNK1A1, CS, AK3, ACTN1, ACLY, TUBGCP2, NCL, PPA1, UBE2N, SPAG9, TARS, ITPA, PRDX6, LASP1, ATP6V1E1, GTF2F1, RAB5A, SMARCA2	108	2325	17854	2.7730227	4.36E-07	4.36E-07	2.98E-06
cytoplasm	39	34.8214286	2.79E-06	AHCY, CHMP7, EGLN2, ABI1, RFXANK, CNOT4, GCH1, MTMR2, ANKRD17, BAG4, CTTN, DYNLL2, HEXIM1, RB1CC1, PITPNC1, HSPA4, STAM, DPP9, TNRC6B, CDC37L1, CSNK1A1, FBXL20, STK24, ACTN1, ACLY, TLE1, WWTR1, TUBGCP2, NCL, PPA1, ST13, SPAG9, TARS, RBPMS, ITPA, PRDX6, LASP1, PHLDB2, FBXL3	108	3029	17854	2.12851693	5.02E-04	2.51E-04	0.00343407
phosphoprotein	59	52.6785714	4.88E-05	2610101N10RIK, MEF2A, MITF, CHMP7, CLTC, SDC4, TPD52, RFXANK, RELL1, ARHGAP12, CNOT4, ANKRD17, CTAGE5, CTTN, VPS4B, TUBB6, PITPNC1, STAM, FBXL20, STK24, ACTN1, TLE1, NCL, ST13, TARS, SPAG9, RBPMS, PRDX6, MED8, NAB1, RAB5A, SMARCA2, ABI1, GCH1, MTMR2, TPI1, ATXN2L, HEXIM1, MAP3K1, RB1CC1, DNAJA1, HSPA4, PPP3CA, TNRC6B, ZDHHC20, CDC37L1, PIK3R1, COBLL1, CSNK1A1, ACLY, WWTR1, TUBGCP2, TEX2, LASP1, ATP6V1E1, GTF2F1, PHLDB2, UBE2E2, TOB2	108	6311	17854	1.54548789	0.00874265	0.00292275	0.06007137
one-carbon metabolism	3	2.67857143	0.00355068	AHCY, DHFR, MTHFD1L	108	15	17854	33.062963	0.47284405	0.14791136	4.28672761
transcription regulation	19	16.9642857	0.00465837	MORF4L1, PPARA, MEF2A, KLF9, NR6A1, MITF, TLE1, WWTR1, NCL, RFXANK, CNOT4, RBPMS, HEXIM1, MED8, RB1CC1, GTF2F1, NAB1, RBPJ, SMARCA2	108	1546	17854	2.03168272	0.56849056	0.15472493	5.58908267
sh3 domain	6	5.35714286	0.0076979	CTTN, LASP1, ABI1, STAM, PIK3R1, ARHGAP12	108	204	17854	4.86220044	0.75116952	0.20691951	9.07958635
ligase	7	6.25	0.00802582	UBE2N, GSS, TARS, UBE2B, UBE2E2, MTHFD1L, CNOT4	108	290	17854	3.9903576	0.76554134	0.18715176	9.44898049
coiled coil	19	16.9642857	0.01439681	2610101N10RIK, BST2, CHMP7, ABI1, WWTR1, TPD52, RELL1, CNOT4, ANKRD17, SPAG9, CTAGE5, HEXIM1, MED8, RB1CC1, VPS4B, DHX36, TNRC6B, PHLDB2, CDC37L1	108	1732	17854	1.8134997	0.92648468	0.27839883	16.3577492
nucleotide-binding	18	16.0714286	0.01690622	CSNK1A1, STK24, AK3, ACLY, UBE2B, MTHFD1L, GCH1, GSS, UBE2N, TARS, MAP3K1, RAB5A, VPS4B, TUBB6, DHX36, HSPA4, SMARCA2, UBE2E2	108	1631	17854	1.82444308	0.95353878	0.28895193	18.9433975
Transcription	19	16.9642857	0.01754176	MORF4L1, PPARA, MEF2A, KLF9, NR6A1, MITF, TLE1, ZFP707, WWTR1, RFXANK, CNOT4, RBPMS, HEXIM1, GTF2F1, MED8, RB1CC1, NAB1, RBPJ, SMARCA2	108	1769	17854	1.77556896	0.95864403	0.27280009	19.5864809
ubl conjugation pathway	8	7.14285714	0.02642268	UBE2N, FBXL20, MED8, SENP5, UBE2B, UBE2E2, FBXL3, CNOT4	108	484	17854	2.73247628	0.99193359	0.35479426	28.0959795
activator	8	7.14285714	0.02642268	PPARA, MEF2A, RBPMS, MED8, MITF, RBPJ, SMARCA2, RFXANK	108	484	17854	2.73247628	0.99193359	0.35479426	28.0959795
rna-binding	8	7.14285714	0.02668144	ANKRD17, RBPMS, 2610101N10RIK, RBM43, RPL22, TNRC6B, NCL, CNOT4	108	485	17854	2.72684231	0.99231045	0.33346176	28.3310215
atp-binding	14	12.5	0.04395846	CSNK1A1, STK24, ACLY, UBE2B, MTHFD1L, UBE2N, GSS, TARS, MAP3K1, VPS4B, DHX36, HSPA4, SMARCA2, UBE2E2	108	1287	17854	1.79829635	0.99969393	0.46336588	42.5191905
nucleus	31	27.6785714	0.06026178	MORF4L1, PPARA, MEF2A, MITF, NR6A1, EGLN2, ABI1, SENP5, RFXANK, CNOT4, GCH1, ANKRD17, HEXIM1, RB1CC1, DHX36, PITPNC1, PPP3CA, KLF9, TLE1, ZFP707, WWTR1, UBE2B, NCL, RCL1, RBPMS, GTF2F1, MED8, NAB1, RBPJ, SMARCA2, FBXL3	108	3808	17854	1.34578762	0.99998616	0.55027632	53.4935863
Chaperone	4	3.57142857	0.06137366	ST13, BAG4, DNAJA1, CDC37L1	108	150	17854	4.40839506	0.99998881	0.53235869	54.1668429
DNA binding	5	4.46428571	0.06960806	PPARA, MITF, NR6A1, RBPJ, NCL	108	258	17854	3.20377548	0.99999771	0.55588868	58.8809321
heme biosynthesis	2	1.78571429	0.07519323	ALAS1, FECH	108	13	17854	25.4330484	0.99999923	0.56294106	61.8201896
domain:RRM	5	4.46428571	0.00435452	RBPMS, 2610101N10RIK, RBM43, TNRC6B, CNOT4	108	99	16021	7.49205013	0.81767622	0.81767622	5.88431099
domain:SH3	6	5.35714286	0.00473644	CTTN, LASP1, ABI1, STAM, PIK3R1, ARHGAP12	108	163	16021	5.46046353	0.84301412	0.60378556	6.38476508
compositionally biased region:Asp/Glu-rich (acidic)	4	3.57142857	0.03244989	KLF9, CHCHD4, NCL, F2R	108	104	16021	5.70548433	0.99999741	0.98627379	36.7720606
compositionally biased region:Poly-Thr	3	2.67857143	0.03931324	ANKRD17, RB1CC1, EGLN2	108	47	16021	9.46867612	0.99999984	0.97996792	42.7276153
mutagenesis site	10	8.92857143	0.0526155	MTMR2, PPARA, BAG4, TPI1, MAP3K1, NAB1, NR6A1, VPS4B, PPP3CA, WWTR1	108	723	16021	2.05176477	1	0.98524125	52.8161224
active site:Glycyl thioester intermediate	3	2.67857143	0.06269706	UBE2N, UBE2B, UBE2E2	108	61	16021	7.29553734	1	0.98513385	59.3345493
subunit	71	63.3928571	4.49E-07	MORF4L1, PPARA, MEF2A, CHMP7, NR6A1, MITF, TSPAN9, CLTC, SDC4, TPD52, RFXANK, MTHFD1L, RELL1, CNOT4, GSS, BAG4, ALAS1, CTTN, DYNLL2, VPS4B, TUBB6, DHX36, STAM, FECH, BST2, FBXL20, LYRM4, ACTN1, TLE1, NCL, UBE2B, DHDH, UBE2N, ST13, SPAG9, TARS, PRDX6, MED8, NAB1, RAB5A, FBXL3, AHCY, ABI1, CHCHD4, GCH1, MTMR2, TPI1, ATXN2L, HEXIM1, MAP3K1, ETFDH, DAD1, HSPA4, PPP3CA, TNRC6B, CDC37L1, PIK3R1, CSNK1A1, CS, AK3, ACLY, WWTR1, TUBGCP2, PPA1, ITPA, LASP1, ATP6V1E1, GTF2F1, RBPJ, PHLDB2, TOB2	109	7035	17178	1.59052444	8.98E-06	8.98E-06	3.42E-04
pathway	15	13.3928571	0.00140162	FECH, AHCY, LYRM4, CS, UBE2B, MTHFD1L, GCH1, UBE2N, GSS, ALAS1, TPI1, DHFR, MED8, RPIA, UBE2E2	109	893	17178	2.6471948	0.02766229	0.01392814	1.06183333
catalytic activity	29	25.8928571	0.00185456	AHCY, EGLN2, MTHFD1L, GCH1, GSS, ALAS1, TPI1, MAP3K1, ETFDH, DAD1, DPP9, PPP3CA, RPIA, ZDHHC20, CSNK1A1, FECH, STK24, CS, AK3, ACLY, UBE2B, DHDH, PPA1, UBE2N, TARS, ITPA, DHFR, PRDX6, UBE2E2	109	2553	17178	1.79016591	0.03644485	0.01229893	1.4028648
interaction	14	12.5	0.0019777	AHCY, FBXL20, ABI1, TLE1, ACLY, WWTR1, TPD52, NCL, CTTN, MAP3K1, RBPJ, SMARCA2, PIK3R1, FBXL3	109	824	17178	2.67760755	0.03881963	0.00984947	1.49540922
PTM	24	21.4285714	0.05898576	MEF2A, MITF, ABI1, TLE1, TSPAN9, CHCHD4, WWTR1, RFXANK, CNOT4, GCH1, UBE2N, SPAG9, ATXN2L, LASP1, GTF2F1, MAP3K1, ETFDH, VPS4B, TUBB6, STAM, HSPA4, ZDHHC20, PIK3R1, F2R	109	2628	17178	1.43923589	0.70356878	0.21587593	37.043177
subcellular location	83	74.1071429	0.06217433	MORF4L1, PPARA, MEF2A, TM7SF3, CHMP7, NR6A1, MITF, TSPAN9, CLTC, SENP5, SDC4, RFXANK, MTHFD1L, RELL1, CNOT4, ANKRD17, BAG4, CTAGE5, ALAS1, CTTN, DYNLL2, VPS4B, PITPNC1, DHX36, STAM, DPP9, PQLC2, FECH, BST2, STK24, FBXL20, LYRM4, ACTN1, TLE1, NCL, UBE2B, ST13, SPAG9, RCL1, TARS, DHRS3, PRDX6, MED8, NAB1, RAB5A, FBXL3, AHCY, EGLN2, ABI1, CHCHD4, GCH1, MTMR2, ALCAM, ATXN2L, MRPL15, TMEM33, HEXIM1, RB1CC1, DNAJA1, ETFDH, DAD1, HSPA4, PPP3CA, ZDHHC20, TNRC6B, CDC37L1, CSNK1A1, KLF9, CS, AK3, IGF1, ACLY, WWTR1, TUBGCP2, PPA1, ITPA, TEX2, LASP1, GTF2F1, CMTM8, RBPJ, PHLDB2, F2R	109	11804	17178	1.10814092	0.72302386	0.19262792	38.648709

Pathways

Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichr	Bonferroni	Benjamini	FDR
m_hdacPathway:Control of skeletal myogenesis by HI	4	3.57142857	0.00253713	MEF2A, IGF1, PPP3CA, PIK3R1	19	19	1171	12.9750693	0.21242255	0.21242255	2.7482719
m_pgc1aPathway:Regulation of PGC-1a	3	2.67857143	0.01345264	PPARA, MEF2A, PPP3CA	19	12	1171	15.4078947	0.72004624	0.47089343	13.8065129
m_nfatPathway:NFAT and Hypertrophy of the heart (T	4	3.57142857	0.01837776	CSNK1A1, IGF1, PPP3CA, PIK3R1	19	38	1171	6.48753463	0.825107	0.44076955	18.411147
m_fcer1Pathway:Fc Epsilon Receptor I Signaling in M	3	2.67857143	0.08433366	MAP3K1, PPP3CA, PIK3R1	19	32	1171	5.77796053	0.99974689	0.87386796	61.9581255
mmu00790:Folate biosynthesis	2	1.78571429	0.09185992	DHFR, GCH1	51	11	5738	20.456328	0.99992075	0.99992075	65.5418858
mmu04144:Endocytosis	5	4.46428571	0.0980211	RAB5A, VPS4B, STAM, CLTC, F2R	51	202	5738	2.78489614	0.99995933	0.99362291	68.0403837
P00060:Ubiquitin proteasome pathway	4	3.57142857	0.05961728	UBE2N, UBE2B, PSMD8, UBE2E2	30	91	2921	4.27985348	0.92886236	0.73328359	43.5617618
P02743:Formyltetrahydroformate biosynthesis	2	1.78571429	0.07680799	DHFR, MTHFD1L	30	8	2921	24.3416667	0.96782211	0.68193259	52.4655682

Table S6

Gene symbol	Refseq ID	Chromosome	Start Position	End Position	Strand	Genbank ID	Gene Description
1200016E24Rik							
1300002F13Rik							
1300007C21Rik							
1700018018Rik							
1810009B06Rik							
1810055002Rik							
4833417J20Rik							
A1132487							
Ass1	NR_002687|N	chr10	61533770	61535370	+	M31690	predicted gene, EG432466 | argininosuccinate synthetase 1
Camk2b	NM_007595	chr11	5869654	5965751	-	BC080273	calcium/calmodulin-dependent protein kinase II, beta
Ccrn4l	NM_009834	chr3	51028369	51055566	+	AF183960	CCR4 carbon catabolite repression 4-like (S. cerevisiae) | similar to carbon catabolite repression 4 protein homolog
Chordc1	NM_025844	chr9	18096711	18118445	+	BC018374	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1
Cirbp	NM_007705	chr10	79630586	79634400	+	BC075699	cold inducible RNA binding protein
E430026E19Rik							
Erbb3	NM_010153	chr10	128005702	128026708	-	BC106091	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
Fbxl20	**NM_028149**	**chr11**	**97943868**	**98010930**	**-**	**EF649694**	**F-box and leucine-rich repeat protein 20**
Fbxo21	NM_145564	chr5	118426742	118460200	+	BC021871	F-box protein 21
Fus	NM_139149	chr7	135110993	135125546	+	BC040827	fusion, derived from t(12;16) malignant liposarcoma (human)
Heca	NM_028440|	chr10	17618855	17738777	-	BC098509|B	RIKEN cDNA 3110003A17 gene | headcase homolog (Drosophila)
Hsp105							
Hspa1b	NM_010478	chr17	35094024	35095952	-		heat shock protein 1B | heat shock protein 1A
Hspa8	NM_031165	chr9	40609356	40613282	+	BC089322	heat shock protein 8
Hspca							
Ifit1	NM_008331	chr19	34715379	34724499	+	BC003768	interferon-induced protein with tetratricopeptide repeats 1
Ldb1	NM_010697|	chr19	46107083	46119404	-	U69270	LIM domain binding 1
Per2	NM_011066	chr1	93312559	93355873	-	AF036893|B	period homolog 2 (Drosophila) | RIKEN cDNA 9830107B12 gene
Slc25a25	NM_146118	chr2	32270004	32306942	-	BC037109	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25
Stip1	NM_016737	chr19	7095192	7114801	-	BC003794	stress-induced phosphoprotein 1
Tgoln1	NM_009443|	chr6	72558414	72566994	-	D50032|BC0	trans-golgi network protein | trans-golgi network protein 2 | hypothetical protein LOC100038890
Tuba4							

Table S7

Gene symbol	Refseq ID	Chromosome	Start Position	End Position	Strand	Genbank ID	Gene Description
0610007L01Rik	NM_0010813	chr5	130698295	130719535	+	BC033455	RIKEN cDNA 0610007L01 gene
0610009E20Rik							
0610009H04Rik							
0610038F07Rik	NM_025333	chr19	10576130	10599699	-	BC085277	RIKEN cDNA 0610038F07 gene
1110007M04Rik	NM_026742	chr4	24825248	24832148	+	BC028764	RIKEN cDNA 1110007M04 gene
1110017O22Rik							
1110038B12Rik							
1110039B18Rik		chr5	31172006	31180737	+	BC029150|BC	RIKEN cDNA 1110039B18 gene
1110059G02Rik							
1110064P04Rik							
1190002C06Rik							
1200013P24Rik	NM_029090	chr16	3884683	3904766	+	BC004837	RIKEN cDNA 1200013P24 gene
1300001I01Rik		chr11	74463042	74484349	+	BC072573	RIKEN cDNA 1300001I01 gene
1300002K09Rik	NM_028788	chr4	45803794	45899876	+	BC111889	RIKEN cDNA 1300002K09 gene
1300006C19Rik							
1300006N24Rik							
1300013F15Rik							
1300018J18Rik	NM_027905	chr15	88919537	88930770	+		RIKEN cDNA 1300018J18 gene
1500003O03Rik	NM_019769	chr2	119373443	119412760	+	BC054733	RIKEN cDNA 1500003O03 gene | similar to EF-hand Ca2+ binding protein p22
1500010M16Rik							
1500035H01Rik	NM_023831	chr9	44581092	44600797	+	BC080764|AJ	RIKEN cDNA 1500035H01 gene
1600014C10Rik	NM_0010853	chr7	38968305	38982587	+	BC085480	RIKEN cDNA 1600014C10 gene
1700012G19Rik		chr17	24607380	24608553	+	BC083113|BC	RIKEN cDNA 1700012G19 gene | jagged 2
1700021I09Rik							
1700052N19Rik	NM_024261	chr10	5891401	5914028	-	BC099894	RIKEN cDNA 1700052N19 gene
1810003N24Rik							
1810009A15Rik		chr19	8958430	8965231	+	BC047099	RIKEN cDNA 1810009A15 gene | hypothetical protein LOC100048454
1810034M08Rik							
1810044O22Rik							
1810048P08Rik							
2010013E14Rik							
2310005N03Rik	NM_025511	chr1	180249284	180252824	+	BC055277	RIKEN cDNA 2310005N03 gene
2310008M10Rik	NM_025509	chr3	130398837	130412336	-	BC021935	RIKEN cDNA 2310008M10 gene
2310042G06Rik							
2400002F11Rik							
2410002O22Rik	NM_025879|	chr13	104932234	104968519	-	BC021756	RIKEN cDNA 2410002O22 gene | hypothetical protein LOC100040518 | hypothetical protein LOC100044479
2410003B16Rik							
2410006H16Rik							
2410016F19Rik							
2510048O06Rik							
2610024B07Rik		chr7	120047773	120050298	+	BC049153	RIKEN cDNA 2610024B07 gene
2610529C04Rik							
2700060E02Rik	NM_026528	chr14	20630624	20643045	-	BC096571	RIKEN cDNA 2700060E02 gene
2700094F01Rik							
2810012H18Rik							
2810405J04Rik	NM_133747	chr17	75936431	75951183	-	BC004626	RIKEN cDNA 2810405J04 gene
2810409H07Rik							
2900045N06Rik							
2900084M01Rik							
3300001H21Rik							
4833439L19Rik		chr13	54652584	54666722	-	BC033445	RIKEN cDNA 4833439L19 gene
4921513D23Rik	NM_0010811	chr16	14111626	14163444	-	AK220341	RIKEN cDNA 4921513D23 gene
4930405M20Rik	XM_127489	chr13	93219788	93253968	-	AK162422	RIKEN cDNA 4930405M20 gene
4930542G03Rik							
4932442E05Rik		chr10	118297882	118300598	+		RIKEN cDNA 4932442E05 gene
4933407N01Rik	NM_025745	chr11	30829784	30854141	-	BC018468	RIKEN cDNA 4933407N01 gene
4933426M11Rik		chr12	81891546	81981822	+	BC040401	RIKEN cDNA 4933426M11 gene
5033425B17Rik							
5730592L21Rik							
5830458K16Rik							
5830472M02Rik	NM_029512|	chr2	163428050	163444749	+	BC052389	RIKEN cDNA 5830472M02 gene
6330407G11Rik	NM_023423	chr4	123407396	123427588	-	BC003291	RIKEN cDNA 6330407G11 gene
9030625A04Rik	NM_172488	chr14	77424008	77436424	-	BC116748	RIKEN cDNA 9030625A04 gene
9130229H14Rik							
A030012M09Rik							
AA959742							
Aars	NM_146217|	chr8	113557802	113581501	+	BC033273|BC	alanyl-tRNA synthetase | exosome component 6
Abce1	NM_015751	chr8	82207341	82235639	-	BC005422	ATP-binding cassette, sub-family E (OABP), member 1
Abtb1	NM_030251	chr6	88785910	88791894	-	AB053477	ankyrin repeat and BTB (POZ) domain containing 1
Acaa1							
Acadvl	NM_017366	chr11	69823685	69828909	-	BC026559	acyl-Coenzyme A dehydrogenase, very long chain
Acly	**NM_134037**	**chr11**	**100337670**	**100389215**	**-**	**BC056378**	**ATP citrate lyase**
Acot12	NM_028790	chr13	91881123	91925755	+	BC132050	acyl-CoA thioesterase 12
Acp2	NM_007387	chr2	91043076	91052931	+	AK128963	acid phosphatase 2, lysosomal
Acsl4	NM_207625|	chrX	138752536	138825078	-	BC058663	acyl-CoA synthetase long-chain family member 4
Acta2	NM_007392	chr19	34315581	34329826	-	BC064800	actin, alpha 2, smooth muscle, aorta
Actb	NM_007393	chr5	143664795	143668403	-	J04181	actin, beta, cytoplasmic
Actg1	NM_009609	chr11	120207003	120209806	-	AF195094	actin, gamma, cytoplasmic 1
Adrm1	NM_019822	chr2	179906293	179910988	+	BC031517	adhesion regulating molecule 1
Agpat2	NM_026212	chr2	26448610	26459811	-	BC125530	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
Agpat3	NM_053014	chr10	77734299	77814445	-	BC052382	1-acylglycerol-3-phosphate O-acyltransferase 3
Ahsa1	NM_146036	chr12	88607658	88614930	+	BC025552	AHA1, activator of heat shock protein ATPase homolog 1 (yeast)
AI132487	NM_0010123	chr12	110089339	110095025	+	BC089616	
AI195470							
Akr1c12	NM_013777	chr13	4267418	4278645	-	BC012643	aldo-keto reductase family 1, member C12
Aldh1l1	NM_027406	chr6	90500812	90549165	+	BC030722	aldehyde dehydrogenase 1 family, member L1
Aldh2	NM_009656	chr5	122017696	122043833	-	U07235	aldehyde dehydrogenase 2, mitochondrial
Aldoa	NM_007438	chr7	133938748	133942697	-	BC089495	aldolase 1, A isoform
Alg12	NM_145477	chr15	88635673	88649715	-	BC021379	asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase)
Als2	NM_028717	chr1	59219774	59294063	-	BC046828	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)
Amd1	NM_009665|	chr10	40008969	40021992	-	BC092072	S-adenosylmethionine decarboxylase 1 | S-adenosylmethionine decarboxylase 2 | S-adenosylmethionine decarboxylase, pseudogene 3
Anapc5	NM_021505|	chr5	123237468	123271348	-	BC010339	anaphase-promoting complex subunit 5
Angptl4	NM_020581	chr17	33910695	33918520	-	BC006611	angiopoietin-like 4
Ap2b1	NM_0010358	chr11	83116199	83218541	+	BC046772	adaptor-related protein complex 2, beta 1 subunit
Arcn1	NM_145985	chr9	44549651	44575899	-	BC083152	archain 1
Arf4	NM_007479	chr14	27457683	27476744	+	BC115650	ADP-ribosylation factor 4
Armet	NM_029103	chr9	106789746	106794361	-	BC038901	arginine-rich, mutated in early stage tumors
Arpc2	NM_029711	chr1	74283124	74314787	+	BC115750	actin related protein 2/3 complex, subunit 2
Arpc5l	NM_028809	chr2	38863636	38871397	+	BC024482|AK	actin related protein 2/3 complex, subunit 5-like
Arpp19	NM_021548	chr9	74885539	74908122	+	BC040206	cAMP-regulated phosphoprotein 19
Asb13	NM_080857|	chr13	3633278	3651025	+	BC018240	ankyrin repeat and SOCS box-containing protein 13
Atf4	NM_009716	chr15	80085614	80087971	+	BC085169	activating transcription factor 4
Atoh8	NM_153778	chr6	72156171	72185571	-	AB046527	atonal homolog 8 (Drosophila)
Atp2a2	NM_0011101	chr5	122892711	122952183	-	BC054531	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
Aven	NM_028844	chr2	112333121	112471227	+	BC100725	apoptosis, caspase activation inhibitor
Avpi1	NM_027106	chr19	42197765	42203517	-	BC027646	arginine vasopressin-induced 1
AW209491	NM_134067|	chr13	14722544	14731363	+	BC016098	
AW491445							
BC002216							
BC004004		chr17	29405896	29439826	+	BC058575|BC	
BC006705							
BC024806							
BC037006							
Bccip	NM_025392	chr7	140901020	140926578	+	BC048465	BRCA2 and CDKN1A interacting protein
Bop1	NM_013481	chr15	76283425	76307699	-	U77415	block of proliferation 1
Bpnt1	NM_011794	chr1	187156038	187181648	+	BC011036	bisphosphate 3'-nucleotidase 1
Brap	NM_028227	chr5	122110595	122137259	+	AF321921	BRCA1 associated protein
Bre	NM_181279|	chr5	32000347	32387320	+	BC061000	brain and reproductive organ-expressed protein
Bri3	NM_018772	chr5	145016105	145025442	+	BC095955	brain protein I3
Bsdc1	NM_133889	chr4	129138923	129165685	+	BC049111	BSD domain containing 1
Bysl	NM_016859	chr17	47737029	47748433	-	BC017530	bystin-like
Bzw1	NM_025824	chr1	58449971	58463397	+	BC028865	basic leucine zipper and W2 domains 1
C130052I12Rik							
C1ql3	NM_153155	chr2	12923514	12933374	-	AB044560	C1q-like 3
C730036D15Rik	NM_145368	chr4	49392717	49421023	-	BC010829	RIKEN cDNA C730036D15 gene
C730043O17							
Cacybp	NM_009786	chr1	162132500	162142908	-	BC025948	calcyclin binding protein
Cad	NM_023525	chr5	31357184	31380852	+	BC053097	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
Cald1	NM_145575	chr6	34548545	34724100	+	BC019435	caldesmon 1
Calm1	NM_009790	chr12	101437738	101448016	+	BC054805	calmodulin 1 | calmodulin 2 | calmodulin 3
Calr	NM_007591	chr8	87365749	87370830	-	M92988	calreticulin
Canx	NM_007597|	chr11	50107965	50139094	-	BC040244	calnexin
Car3	NM_007606	chr3	14863509	14872532	+	BC011129	carbonic anhydrase 3
Casp7	NM_007611	chr19	56471619	56516837	+	Y13088	caspase 7
Cct2	NM_007636	chr10	116488055	116500836	-	BC026918	chaperonin subunit 2 (beta)
Cct3	NM_009836	chr3	88101057	88125688	+	L20509	chaperonin subunit 3 (gamma)
Cct4	NM_009837	chr11	22890593	22903337	+	BC054773	chaperonin subunit 4 (delta)
Cct5	NM_007637	chr15	31520570	31531559	-	BC094427	chaperonin subunit 5 (epsilon)
Cct6a	NM_009838	chr5	130293261	130322247	+	BC094352	chaperonin subunit 6a (zeta)
Cct7	NM_007638	chr6	85402067	85418466	+	BC008255	chaperonin subunit 7 (eta)
Cd8b1	NM_009858	chr6	71272248	71305814	+	M17534	CD8 antigen, beta chain 1
Cdc37l1	**NM_025950**	**chr19**	**29064857**	**29092061**	**+**	**BC031761**	**cell division cycle 37 homolog (S. cerevisiae)-like 1**
Cdc42	NM_009861	chr4	136875617	136913594	-	U37720	cell division cycle 42 homolog (S. cerevisiae)
Cdk2ap1	NM_013812	chr11	48638845	48640114	-	BC083075	CDK2 (cyclin-dependent kinase 2)-associated protein 1
Chchd4	**NM_133928**	**chr6**	**91414270**	**91423417**	**-**	**BC019405**	**coiled-coil-helix-coiled-coil-helix domain containing 4**

Chka	NM_013490|N	chr19	3851773	3894369	+	BC060218	choline kinase alpha
Chordc1	NM_025844	chr9	18096711	18118445	+	BC018374	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1
Ckap1							
Cldn1	NM_016674	chr16	26356737	26371925	-	BC002003	claudin 1
Cldn2	NM_016675	chrX	136335367	136345925	+	BC085494	claudin 2
Clock	NM_007715	chr5	76639992	76733817	-	AF000998	circadian locomoter output cycles kaput
Cltb	NM_028870	chr13	54694300	54712635	-	BC070404	clathrin, light polypeptide (Lcb)
Cml2	NM_053096	chr6	85815416	85819152	-	BC039773|BC	camello-like 2
Cndp2	NM_023149	chr18	84836857	84855025	-	BC005532	CNDP dipeptidase 2 (metallopeptidase M20 family)
Cnih	NM_009919	chr14	47395257	47408013	-	AF022811	cornichon homolog (Drosophila)
Copg	NM_017477|N	chr6	87837934	87863589	+	BC024896	coatomer protein complex, subunit gamma
Copz1	NM_019817	chr15	103103330	103130300	+	BC025041	coatomer protein complex, subunit zeta 1
Cpt1a	NM_013495	chr19	3323320	3385733	+	BC046383	carnitine palmitoyltransferase 1a, liver
Crebbp	NM_0010254	chr16	4084048	4213404	-		CREB binding protein
Crebl1	NM_017406	chr17	34784091	34792019	+	BC013534	cAMP responsive element binding protein-like 1
Crp	NM_007768	chr1	174628187	174630093	+	BC011124	C-reactive protein, pentraxin-related
Csnk2b	NM_009975	chr17	35253140	35258392	-	BC003775	casein kinase 2, beta polypeptide
Csrp3	NM_013808	chr7	56085768	56103403	-	BC061131	cysteine and glycine-rich protein 3
Cxadr	NM_009988|N	chr16	78301936	78360030	+	BC016457	coxsackievirus and adenovirus receptor
Cyp2d22	NM_019823	chr15	82201902	82210592	-	BC016256	cytochrome P450, family 2, subfamily d, polypeptide 22
Cyp4f13	NM_130882	chr17	33061614	33084315	-	AF233643	cytochrome P450, family 4, subfamily f, polypeptide 13
Cyp51	NM_020010	chr5	4080674	4104697	-	BC031813	cytochrome P450, family 51
Cyp8b1	NM_010012	chr9	121823474	121825415	-	BC010973	cytochrome P450, family 8, subfamily b, polypeptide 1
D10Ertd214e							
D10Ertd438e							
D11Ertd498e							
D11Ertd636e							
D11Ertd99e							
D11Lgp2e							
D17Ertd441e							
D19Wsu162e		chr19	46673604	46731879	+	BC058949|BC	DNA segment, Chr 19, Wayne State University 162, expressed
D3Ucla1	NM_030685	chr3	58325891	58329676	-	AB041655	DNA segment, Chr 3, University of California at Los Angeles 1
D630048P19Rik							
D7Wsu128e							
D8Ertd325e							
D930001I22Rik	NM_173397	chr2	163292124	163298364	-	BC090994	RIKEN cDNA D930001I22 gene
Dctn2	NM_027151	chr10	126703455	126718863	+	BC004613	dynactin 2
Ddc	NM_016672	chr11	11714106	11798103	-	AF071068	dopa decarboxylase
Ddost	NM_007838	chr4	137860651	137868526	+	BC068132	dolichyl-di-phosphooligosaccharide-protein glycotransferase
Ddx39	NM_197982	chr8	86239098	86247247	+	BC020134	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
Ddx58	NM_172689	chr4	40151892	40186793	-	AY553221	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
Derl2	NM_033562	chr11	70820947	70832765	-	AF208064	Der1-like domain family, member 2
Dhcr7	NM_007856	chr7	151009072	151034315	+	AF057368	7-dehydrocholesterol reductase
Dhx29	NM_172594	chr13	113717928	113759640	+	BC057112	DEAH (Asp-Glu-Ala-His) box polypeptide 29
Dirc2	NM_153550	chr16	35694989	35769442	-	BC037460	disrupted in renal carcinoma 2 (human)
Dnaja1	**NM_008298**	**chr4**	**40669566**	**40681997**	**+**	**AF055664**	**DnaJ (Hsp40) homolog, subfamily A, member 1**
Dnajb11	NM_026400	chr16	22857937	22879707	+	BC018282	DnaJ (Hsp40) homolog, subfamily B, member 11
Dnajc1	NM_007869	chr2	18127960	18314438	-	BC080300	DnaJ (Hsp40) homolog, subfamily C, member 1
Dnajc3							
Dnajc5	NM_016775	chr2	181255210	181286954	+	BC012268	DnaJ (Hsp40) homolog, subfamily C, member 5
Dnclc1							
Dtx1	NM_008052	chr5	121130212	121161678	-	AB015422	deltex 1 homolog (Drosophila)
Dtymk	NM_0011056	chr1	95689160	95698482	-	BC030178	deoxythymidylate kinase
E430028B21Rik	NM_178668	chr14	27483601	27489332	-	BC064450	RIKEN cDNA E430028B21 gene
E430034L04Rik							
Ecgf1							
Eef1g	NM_026007	chr19	9041531	9052965	+		eukaryotic translation elongation factor 1 gamma
Efha1	NM_028643	chr14	58535115	58618099	-	BC031172	EF hand domain family A1
Ehd1	NM_010119	chr19	6276734	6300096	+	BC043332	EH-domain containing 1
Eif3s1							
Eif3s5							
Eif3s6ip							
Eif4a1	NM_144958	chr1	60760761	60762537	+	X03040|AK18	eukaryotic translation initiation factor 4A1
Eif4e	NM_007917	chr3	138189155	138220563	+	BC085087	eukaryotic translation initiation factor 4E
Eif4ebp1	NM_007918	chr8	28370831	28387140	+	U28656	eukaryotic translation initiation factor 4E binding protein 1
Elovl1	NM_019422|N	chr4	118100698	118105521	+	AF170907	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1
Elovl6	NM_130450	chr3	129235304	129341413	+	AY053453	ELOVL family member 6, elongation of long chain fatty acids (yeast)
Erbb3	NM_010153	chr10	128005702	128026708	-	BC106091	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
Esd	NM_016903	chr14	75132125	75150250	+	AB025408	esterase D/formylglutathione hydrolase
Ethe1	NM_023154	chr7	25372562	25393944	+	BC094044	ethylmalonic encephalopathy 1
Fah	NM_010176	chr7	91733669	91754278	-	M84145	fumarylacetoacetate hydrolase
Fahd1	NM_023480	chr17	24972079	24987247	-	BC026949	fumarylacetoacetate hydrolase domain containing 1
Fbxo22	NM_028049	chr9	55056802	55072240	+	BC018273	F-box protein 22
Fbxo31	NM_133765	chr8	124075914	124102691	-	BC026929	F-box protein 31
Fdps	NM_134469	chr3	88897510	88905867	-	BC048497	farnesyl diphosphate synthetase
Fech	**NM_007998**	**chr18**	**64616202**	**64648720**	**-**	**BC006746**	**ferrochelatase**
Fkbp1a	NM_008019	chr2	151368235	151387427	+	AB241120	FK506 binding protein 1a
Fkbp4	NM_010219	chr6	128379556	128388674	-	BC003447	FK506 binding protein 4
Gabarapl1	NM_020590	chr6	129483183	129492349	+	AF180518	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1
Gabarapl2	NM_026693	chr5	23623594	23624545	-	AF190644	gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2
Gale	NM_178389	chr4	135519667	135524093	+	BC027438	galactose-4-epimerase, UDP
Gatad1	NM_026033	chr5	3639969	3647917	-	AB047921	GATA zinc finger domain containing 1
Gch1	**NM_008102**	**chr14**	**47773570**	**47809081**	**-**	**BC005643**	**GTP cyclohydrolase 1**
Gjb2	NM_008125	chr14	57717448	57723502	-	BC013634	gap junction protein, beta 2
Gltscr2	NM_133831	chr7	16523184	16531407	-	BC017637	glioma tumor suppressor candidate region gene 2
Gm672	NM_201354	chr18	75590859	75857208	-	BC058104	gene model 672, (NCBI)
Gna11	NM_010301	chr10	80991477	81007791	-	BC011169	guanine nucleotide binding protein, alpha 11
Gne	NM_015828	chr4	44049698	44097038	-	BC015277	glucosamine
Gorasp2	NM_027352	chr2	70499633	70529800	+	BC005600	golgi reassembly stacking protein 2
Gosr2	NM_019650	chr11	103538163	103559008	-	BC051253	golgi SNAP receptor complex member 2
Gpd1	NM_010271	chr15	99548018	99555439	+	BC019391	glycerol-3-phosphate dehydrogenase 1 (soluble)
Gps1	NM_145370	chr11	120645589	120650416	+	BC103782	G protein pathway suppressor 1
Gsta3	NM_0010773	chr1	21230670	21255640	+	M73483	glutathione S-transferase, alpha 3
Gtf2f1	**NM_133801**	**chr17**	**57142825**	**57150841**	**-**	**BC031123**	**general transcription factor IIF, polypeptide 1**
H2afv	NM_130737	chr11	6328141	6339462	-	BC028539	H2A histone family, member V
H2afx	NM_010436	chr9	44142777	44144160	+	BC010336	H2A histone family, member X
H6pd	NM_173371	chr4	149353584	149383132	-	BC042677	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
Hagh	NM_024284	chr17	24987492	25001395	+	BC019817	hydroxyacyl glutathione hydrolase
Hapln1	NM_013500	chr13	89679401	89751257	+	BC066853	hyaluronan and proteoglycan link protein 1
Hbp1	NM_153198|N	chr12	32611325	32635088	-	BC026853	high mobility group box transcription factor 1
Hdhd3	NM_024257	chr4	62160046	62163248	-	BC003491	haloacid dehalogenase-like hydrolase domain containing 3
Hectd1	NM_019024	chr12	52845511	52930295	-	AK173106|BC	HECT domain containing 1
Herpud1	NM_022331	chr8	96910400	96919259	+	BC013523	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
Higd1a	NM_0011126	chr3	85719644	85720101	+	BC021594	HIG1 domain family, member 1A | similar to hypoxia induced gene 1
Hint2	NM_026871	chr4	43667099	43669322	-	BC086940	histidine triad nucleotide binding protein 2
Hip2							
Hist1h2bc	NM_023422	chr13	23776068	23784357	+	BC019673	histone cluster 1, H2bc | histone cluster 1, H2bb | histone cluster 1, H2be | histone cluster 1, H2bg | H2b histone family, member A | H2b histone
Hist2h3c1	NM_178216|N	chr3	96050608	96052427	+	BC132488|BC	histone cluster 2, H3c1 | histone cluster 2, H3b | histone cluster 2, H3c2 | histone cluster 1, H3b | histone cluster 1, H3d | histone cluster 1, H3e |
Hist2h3c1	NM_178216|N	chr3	96050608	96052427	+	BC132488|BC	histone cluster 2, H3c1 | histone cluster 2, H3b | histone cluster 2, H3c2 | histone cluster 1, H3b | histone cluster 1, H3d | histone cluster 1, H3e |
Hmgcs1	NM_145942	chr13_random	114527	132341	-	BC029693	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 | similar to Hmgcs1 protein
Hmox2	NM_010443	chr16	4726389	4766249	+	BC002011	heme oxygenase (decycling) 2
Hnrpa3	NM_146130|N	chr2	75497334	75507464	+	BC023908	heterogeneous nuclear ribonucleoprotein A3
Hnrpab	NM_0010480	chr11	51413602	51420383	-	BC043069	heterogeneous nuclear ribonucleoprotein A/B
Hnrpc							
Hnrpdl	NM_016690	chr5	100463740	100468181	-	BC021374	heterogeneous nuclear ribonucleoprotein D-like
Hnrpl							
Hook2	NM_133255	chr8	87514502	87527256	+	BC080744	hook homolog 2 (Drosophila)
Hpgd	NM_008278	chr8	58773390	58799841	+	BC021157	hydroxyprostaglandin dehydrogenase 15 (NAD)
Hsd17b12	NM_019657	chr2	93872854	93998066	-	BC090659	hydroxysteroid (17-beta) dehydrogenase 12
Hsd17b7	NM_010476	chr1	171879668	171899336	-	BC011464	hydroxysteroid (17-beta) dehydrogenase 7
Hspa4	**NM_008300**	**chr11**	**53073316**	**53113981**	**-**	**BC003770**	**heat shock protein 4**
Hspa4l	NM_011020	chr3	40549418	40594373	+	BC110662	heat shock protein 4 like
Hspa5	NM_022310	chr2	34627610	34632049	+	BC050927	heat shock protein 5
Hspb8	NM_030704	chr5	116858500	116872873	-	BC011219	heat shock protein 8
Hspca							
Hspca							
Hspcb							
Hyou1	NM_021395	chr9	44187626	44200452	+	AF228709	hypoxia up-regulated 1
Idh1	NM_010497|N	chr1	65205202	65225688	-	BC088986	isocitrate dehydrogenase 1 (NADP+), soluble
Idi1	NM_145360|N	chr2	53553379	53555893	-	BC110313	isopentenyl-diphosphate delta isomerase
Ifit1	NM_008331	chr19	34715379	34724499	+	BC003768	interferon-induced protein with tetratricopeptide repeats 1
Igfals	NM_008340	chr17	25015715	25018953	+	AK220290	insulin-like growth factor binding protein, acid labile subunit
Igtp	NM_018738|N	chr11	58013058	58036285	+	U53219|BC09	interferon gamma induced GTPase | interferon inducible GTPase 2
Ikbkg	NM_178590|N	chrX	71669951	71696859	+	AY112937	inhibitor of kappaB kinase gamma
Impdh2	NM_011830	chr8	102554392	102556074	+	M33934	inosine 5'-phosphate dehydrogenase 2
Inhbc	NM_010565	chr10	126793376	126807600	-	U95962	inhibin beta-C
Irak1	NM_008363	chrX	71259257	71269275	-	AY184362	interleukin-1 receptor-associated kinase 1
Irak2	NM_172161|N	chr6	113588482	113645005	+	BC085324	interleukin-1 receptor-associated kinase 2
Irgm	NM_008326	chr11	48678749	48684869	-	U19119	immunity-related GTPase family, M
Isg20	NM_020583|N	chr7	86058344	86065250	+	AF217484	interferon-stimulated protein
Itm1							
Itpk1	NM_172584	chr12	103806198	103943079	-	BC056464	inositol 1,3,4-triphosphate 5/6 kinase
Jagn1	NM_026365	chr6	113392597	113398221	+	BC011296	jagunal homolog 1 (Drosophila)
Kif1b	NM_207682|N	chr4	148550428	148681807	-	AF131865	kinesin family member 1B
Klhl21	NM_0010333	chr4	151383000	151391786	+		kelch-like 21 (Drosophila)
Klkb1							
Kpna1	NM_008465	chr16	35983449	36036248	+	BC006771	karyopherin (importin) alpha 1

Kpna2	NM_010655	chr11	106849943	106860839	-	D55720	karyopherin (importin) alpha 2 | similar to nuclear pore-targeting complex component of 58 kDa
Kpnb1	NM_008379	chr11	97021024	97049206	-	BC055115	karyopherin (importin) beta 1
Kras	NM_021284	chr6	145165227	145198751	-	BC004642	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog | neuroblastoma ras oncogene
Krt1-18							
Krt2-8							
Krt2-8							
Lap3	NM_024434	chr5	45884613	45903912	+	AF334160	leucine aminopeptidase 3
Ldlr	NM_010700	chr9	21528038	21554363	+	BC053041	low density lipoprotein receptor
Lgals3bp	NM_011150	chr11	118254063	118263273	-	BC090658	lectin, galactoside-binding, soluble, 3 binding protein
Lgals9	NM_010708	chr11	78776481	78798353	-	U55061	lectin, galactose binding, soluble 9
Lims2	NM_144862	chr18	32091161	32118273	+	BC010816	LIM and senescent cell antigen like domains 2
Lman1	NM_027400	chr18	66140408	66162266	-	BC057165	lectin, mannose-binding, 1
Lman2	NM_025828	chr13	55445194	55464144	-	BC055327	lectin, mannose-binding 2
LOC434401							
LOC544800							
Lrp4	NM_172668	chr2	91297858	91353936	+	AF247637	low density lipoprotein receptor-related protein 4
Lrrc3	NM_145152	chr10	77362592	77365255	-	AY061858	leucine rich repeat containing 3
Lrrc54							
Lss	NM_146006	chr10	75994363	76018226	+	BC029082	lanosterol synthase
Malat1	NR_002847	chr19	5800397	5800542	-	BC004722	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
Man2a1	NM_008549	chr17	64950989	65104450	+		mannosidase 2, alpha 1
Map1lc3b	NM_026160	chr8	124114350	124121947	+	BC086774	microtubule-associated protein 1 light chain 3 beta
Mbnl2	NM_175341|N	chr14	120674883	120830919	+	BC075665	muscleblind-like 2
Mdm2	NM_010786	chr10	117125944	117147772	-	BC092270	transformed mouse 3T3 cell double minute 2
Metap1	NM_175224	chr3	138121920	138152346	-	BC096469	methionyl aminopeptidase 1
Mid1ip1	NM_026524	chrX	10294608	10297200	+	BC052899	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))
Mknk2	NM_021462	chr10	80128072	80138619	-	AB164081	MAP kinase-interacting serine/threonine kinase 2
Mlx	NM_011550	chr11	100948624	100953521	+	BC038004	MAX-like protein X
Mmab	NM_029956	chr5	114881043	114894036	-	BC057558	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)
Morf4l2	NM_019768	chrX	133267481	133276148	-	BC075653	mortality factor 4 like 2
Morf4l2	NM_019768	chrX	133267481	133276148	-	BC075653	mortality factor 4 like 2
Mpi1							
Mrap	NM_029844	chr16	90738569	90750030	+	BC027543	melanocortin 2 receptor accessory protein
Mrpl19	NM_026490	chr6	81907820	81915943	-	BC043921	mitochondrial ribosomal protein L19
Mrps22	NM_025485	chr9	98489149	98502078	-	BC051198	mitochondrial ribosomal protein S22
Mrps23	NM_024174	chr11	88017920	88025009	+	BC019980	mitochondrial ribosomal protein S23
Mrps31	NM_020560	chr8	23521854	23540137	+	BC027430	mitochondrial ribosomal protein S31
Mrps6							
Mrps7	NM_025305	chr11	115465465	115468940	+	BC049636	mitchondrial ribosomal protein S7
Mut	NM_008650	chr17	41071656	41098598	+	X51941	methylmalonyl-Coenzyme A mutase
Mycbp	NM_019660	chr4	123582075	123589512	+	BC028344	c-myc binding protein
Myl9	NM_021019	chr2	156601165	156607394	+	BC049974	myosin, light polypeptide 9, regulatory
Naca	NM_0011131!	chr10	127472629	127485693	+	U48364	nascent polypeptide-associated complex alpha polypeptide
Nadsyn1	NM_030221	chr7	150981499	151008746	-	AJ305343	NAD synthetase 1
Nars	NM_027350	chr18	64659309	64676191	-	BC052849	asparaginyl-tRNA synthetase
Ncbp2	NM_026554	chr16	31948701	31958433	+	BC118926	nuclear cap binding protein subunit 2
Nek6	NM_021606	chr2	38367217	38443561	+	AF218847	NIMA (never in mitosis gene a)-related expressed kinase 6
Nelf	NM_0010393	chr2	24909899	24918401	+	BC006642	nasal embryonic LHRH factor
Nfkbia	NM_010907	chr12	56590588	56593582	-	BC046754	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
Nola2	NM_026631	chr11	51433275	51437216	+	BC024944	nucleolar protein family A, member 2
Nsdhl	NM_010941	chrX	70163860	70203867	+	AF100198	NAD(P) dependent steroid dehydrogenase-like
Nubp2	NM_011956	chr17	25019562	25023293	-	BC012635	nucleotide binding protein 2
Nudt18	NM_153136	chr14	70977196	70982378	+	BC036718	nudix (nucleoside diphosphate linked moiety X)-type motif 18
Odc1	NM_013614	chr12	17551778	17557890	+	BC083122	ornithine decarboxylase, structural 1
Ogt	NM_139144	chrX	98835403	98879690	+	BC057319	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
Opa3	NM_207525	chr7	19813702	19841178	+	BC094601	optic atrophy 3 (human)
Oprs1	NM_011014	chr4	41685369	41688186	-	BC002000	opioid receptor, sigma 1
ORF61	NM_0010039	chr10	79438635	79447075	-	BC080302	open reading frame 61
P2rx4	NM_011026	chr5	123157566	123179053	+	AF089751	purinergic receptor P2X, ligand-gated ion channel 4
Pcmtd2	NM_153594	chr2	181572608	181592157	+	BC040385	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2
Pcnp	NM_0010246	chr16	56015621	56029830	-	BC132588	PEST proteolytic signal containing nuclear protein
Pcsk9	NM_153565	chr4	106114947	106136934	-	BC038085	proprotein convertase subtilisin/kexin type 9
Pdcd6	NM_011051	chr13	74440576	74454725	-	BC040079	programmed cell death 6
Pdia3	NM_007952	chr2	121239638	121264423	+	BC033439	protein disulfide isomerase associated 3
Pdia4	NM_009787	chr6	47746140	47763511	-	J05186	protein disulfide isomerase associated 4
Pdia6	NM_027959	chr12	17273401	17291576	+	BC006865	protein disulfide isomerase associated 6
Pdlim1	NM_016861	chr19	40295663	40346023	-	AF053367	PDZ and LIM domain 1 (elfin)
Peci	NM_011868|N	chr13	35069617	35085985	-	AF153613	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase
Pex11a	NM_011068	chr7	86882135	86887911	-	AF093669	peroxisomal biogenesis factor 11a
Pgd	NM_0010812	chr4	148524102	148540784	-	BC008646	phosphogluconate dehydrogenase
Pin1	NM_023371	chr9	20456574	20471028	+	BC038254	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1
Plod3	NM_011962	chr5	137462889	137472409	+	BC043047	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
Pmm2	NM_016881	chr16	8637800	8657642	+	BC094448	phosphomannomutase 2
Pmvk	NM_026784	chr3	89258463	89272931	+	BC028659	phosphomevalonate kinase
Pnpla2	NM_025802	chr7	148641105	148646642	+	BC019188	patatin-like phospholipase domain containing 2
Polb	NM_011130	chr8	23738598	23763907	-	BC060998	polymerase (DNA directed), beta
Pole4	NM_025882	chr6	82596704	82602857	-	BC023189|AK	polymerase (DNA-directed), epsilon 4 (p12 subunit)
Polr2i	NM_027259	chr7	31017093	31018406	+	BC062812	polymerase (RNA) II (DNA directed) polypeptide I | similar to RNA Polymerase II subunit 14.5 kD
Pomt1	NM_145145	chr2	32092143	32110525	+	BC027325	protein-O-mannosyltransferase 1
Por	NM_008898	chr5	136165028	136211196	+	BC003240	P450 (cytochrome) oxidoreductase
Ppa1	**NM_026438**	**chr10**	**61111369**	**61136916**	**+**	**BC010468**	**pyrophosphatase (inorganic) 1**
Ppil1	NM_026845	chr17	29387773	29400916	-	BC058369	peptidylprolyl isomerase (cyclophilin)-like 1 | similar to peptidylprolyl isomerase-like 1
Ppp1r12a	NM_027892	chr10	107599249	107714631	+	BC125381	protein phosphatase 1, regulatory (inhibitor) subunit 12A
Ppp1r14b	NM_008889	chr19	7049538	7051814	+	BC082545	protein phosphatase 1, regulatory (inhibitor) subunit 14B
Ppp3ca	**NM_008913**	**chr3**	**136333734**	**136600350**	**+**	**J05479**	**protein phosphatase 3, catalytic subunit, alpha isoform**
Psmc4	NM_011874	chr7	28826731	28835088	-	BC092265	proteasome (prosome, macropain) 26S subunit, ATPase, 4
Psmc5	NM_008950	chr11	106117468	106124434	+	BC030840	protease (prosome, macropain) 26S subunit, ATPase 5
Psmd1	NM_027357	chr1	87961194	88035870	+		proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
Psmd6	NM_025550	chr14	14944698	14953725	-	BC006869	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6
Psme3	NM_011192	chr11	101177565	101184850	+	D87911	proteaseome (prosome, macropain) 28 subunit, 3
Ptcd2	NM_026873	chr13	100089604	100114642	-	BC025110	pentatricopeptide repeat domain 2
Ptdsr							
Ptges3	NM_019766	chr10	127496011	127514328	+	BC085264	prostaglandin E synthase 3 (cytosolic) | similar to Sid3177p
Ptma	NM_008972	chr1	88423300	88427273	+	BC085171	prothymosin alpha
Ptpmt1	NM_025576	chr2	90750870	90758197	-	BC026750	protein tyrosine phosphatase, mitochondrial 1
Ptpn11	NM_011202|N	chr5	121580550	121641384	-	BC057398	protein tyrosine phosphatase, non-receptor type 11
Ptprd	NM_011211|N	chr4	75587143	76240203	-	AF326559	protein tyrosine phosphatase, receptor type, D
Ptprf	NM_011213	chr4	117880818	117964002	-	AF300943	protein tyrosine phosphatase, receptor type, F
Rabggta	NM_019519	chr14	56334714	56341018	-	AF127658	Rab geranylgeranyl transferase, a subunit
Rai12	NM_018740	chr11	69781726	69794012	-	AF004107	retinoic acid induced 12
Ran	NM_009391	chr5	129526031	129530196	+	BC083356	RAN, member RAS oncogene family | similar to RAN, member RAS oncogene family
Ranbp1	NM_011239	chr16	18239880	18248806	-	BC061140	RAN binding protein 1
Rangap1	NM_011241	chr15	81534683	81560331	-	U08110	RAN GTPase activating protein 1
Rbed1	NM_144917	chr6	72515919	72548337	-	BC016193	RNA binding motif and ELMO domain 1
Rbm14	NM_019869	chr19	4800569	4811634	-	BC010294	RNA binding motif protein 14
Rbm4	NM_009032	chr19	4784293	4793877	-	BC130256	RNA binding motif protein 4
Rcl1	**NM_021525**	**chr19**	**29175865**	**29218419**	**+**	**BC004574**	**RNA terminal phosphate cyclase-like 1**
Rdh11	NM_021557	chr12	80275262	80293280	-	AF474027	retinol dehydrogenase 11
Rpl7l1	NM_025433	chr17	46910856	46919605	-	BC030165	ribosomal protein L7-like 1
Rpn1	NM_133933	chr6	88034505	88055298	+	BC016080	ribophorin I
Rwdd4a	NM_203507	chr8	48619046	48638179	+	BC016198	RWD domain containing 4A
S100a10	NM_009112	chr3	93359039	93368567	+	BC025044	S100 calcium binding protein A10 (calpactin)
Sara1							
Sc4mol	NM_025436	chr8	67196936	67212375	-	BC006802	sterol-C4-methyl oxidase-like
Sc5d	NM_172769	chr9	42062260	42072339	-	BC024132	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)
Sdc1	NM_011519	chr12	8778197	8800494	+	BC010560	syndecan 1
Sdccag3	NM_026563|N	chr2	26238322	26244826	-	BC031199	serologically defined colon cancer antigen 3
Sdf2l1	NM_022324	chr16	17130231	17132458	-	BC053425	stromal cell-derived factor 2-like 1
Sec13l1							
Sec23b	NM_019787	chr2	144382013	144416480	+	BC011160	SEC23B (S. cerevisiae)
Sec61a1	NM_016906	chr6	88453597	88468806	-	BC003707	Sec61 alpha 1 subunit (S. cerevisiae)
Senp3	NM_030702	chr11	69486612	69495586	-	AY008764	SUMO/sentrin specific peptidase 3
Serpind1	NM_008223	chr16	17331508	17343667	+	BC089610	serine (or cysteine) peptidase inhibitor, clade D, member 1
Set	NM_023871	chr2	29917563	29927315	+	BC018255	SET translocation | similar to protein phosphatase 2A inhibitor-2 I-2PP2A
Sfpq	NM_023603	chr4	126698579	126708040	+	BC089305	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
Sfrs1	NM_173374|N	chr11	87861173	87867259	+	BC046773	splicing factor, arginine/serine-rich 1 (ASF/SF2) | similar to splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
Sfrs2	NM_011358	chr11	116711215	116714405	-	AF077858	splicing factor, arginine/serine-rich 2 (SC-35)
Sfrs3	NM_013663	chr17	29169618	29180311	+	BC071196	splicing factor, arginine/serine-rich 3 (SRp20)
Shb	NM_198482	chr4	45436151	45543202	-	BC058986|BC	src homology 2 domain-containing transforming protein B
Slc17a3	NM_134069	chr13	23931329	23951623	+	BC034183	solute carrier family 17 (sodium phosphate), member 3
Slc25a15	NM_181325|N	chr8	23486479	23509025	-	AF133914	solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15
Slc25a17	NM_011399	chr15	81149345	81191204	-	AJ006341	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17
Slc25a5	NM_007451|N	chr1	79919111	79920082	-	X70847	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 | predicted gene, EG433923
Slc27a2	NM_011978	chr2	126378760	126413979	+	BC022170	solute carrier family 27 (fatty acid transporter), member 2
Slc30a10	NM_0010332	chr1	187278727	187292641	+	BC054548	solute carrier family 30, member 10
Slc35b1	NM_016752	chr11	95246236	95252983	+	D87990	solute carrier family 35, member B1
Smarcb1	NM_011418	chr10	75359518	75384341	-	AB041578	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1
Snrpd3	NM_026095	chr10	74980766	74998210	+	BC011510	small nuclear ribonucleoprotein D3
Sntb1	NM_016667	chr15	55470709	55738504	-	U89997	syntrophin, basic 1
Sntg2	NM_172951	chr12	30859858	31058193	-	AF367760	syntrophin, gamma 2
Snx3	NM_017472	chr10	42221835	42255173	+	BC116885	sorting nexin 3
Spcs2	NM_025668	chr7	106986079	107007403	-	BC050150	signal peptidase complex subunit 2 homolog (S. cerevisiae)
Spcs3	NM_029701	chr8	55605787	55615336	-	BC054817	signal peptidase complex subunit 3 homolog (S. cerevisiae)
Spnb3	NM_021287	chr19	4711223	4752352	+	BC079860	spectrin beta 3
Sqle	NM_009270	chr15	59146647	59162748	+	BC056361	squalene epoxidase
Srebf1	NM_011480	chr11	60012586	60034106	-	BC056922	sterol regulatory element binding transcription factor 1
Srm	NM_009272	chr4	147965628	147968728	+	BC005566	spermidine synthase

Srprb	NM_009275	chr9	103090363	103104416	-	BC003798	signal recognition particle receptor, B subunit
Ssh2	NM_177710	chr11	77029927	77269050	+	AB099288	slingshot homolog 2 (Drosophila)
Ssr1	NM_025965	chr13	38058474	38086026	-	AF326229	signal sequence receptor, alpha
Ssr2	NM_025448	chr3	88383593	88392338	+	BC010214	signal sequence receptor, beta
St13	**NM_133726**	**chr15**	**81195470**	**81230124**	**-**	**BC003843**	**suppression of tumorigenicity 13**
St3gal1	NM_009177	chr15	66934437	67008444	-	BC099693	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
St3gal5	NM_011375|N	chr6	72047607	72104564	+	AF119416	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
Stard5	NM_023377	chr7	90780510	90790838	+	BC058226	StAR-related lipid transfer (START) domain containing 5
Stat1	NM_009283	chr1	52176282	52218707	+	BC004808	signal transducer and activator of transcription 1
Stat2	NM_019963	chr10	127707629	127729905	+	AF206162	signal transducer and activator of transcription 2
Stch	NM_030201	chr16	75755433	75767023	-	BC085181	stress 70 protein chaperone, microsome-associated, human homolog
Stip1	NM_016737	chr19	7095192	7114801	-	BC003794	stress-induced phosphoprotein 1
Supt4h1	NM_009296|N	chr11	87551055	87557119	+	BC087923	suppressor of Ty 4 homolog 1 (S. cerevisiae) | suppressor of Ty 4 homolog 2 (S. cerevisiae)
Surf4	NM_011512	chr2	26775559	26789448	-	M63114	surfeit gene 4
Syncrip	NM_019796|N	chr9	88344576	88377235	-	AF093821	synaptotagmin binding, cytoplasmic RNA interacting protein
Syngr2	NM_009304	chr11	117670991	117675597	+	AF151985	synaptogyrin 2
Tacc1	NM_177089|N	chr8	26265024	26311921	-	AY177413	transforming, acidic coiled-coil containing protein 1
Taf12	NM_025579	chr4	131830328	131849242	+	BC019668	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor
Tardbp	NM_145556|N	chr4	147986491	148001105	-	BC025544	TAR DNA binding protein
Tbc1d17	NM_0010426	chr7	52096146	52104449	-	BC017607	TBC1 domain family, member 17
Tegt	NM_026669	chr15	99223417	99240474	+	BC005588	testis enhanced gene transcript
Tfrc	NM_011638	chr16	32609103	32632876	+	BC054522	transferrin receptor
Tgm2	NM_009373	chr2	157942138	157972128	-	BC016492	transglutaminase 2, C polypeptide
Thoc1	NM_153552	chr18	9958006	9995482	+	BC024951	THO complex 1
Thrap6							
Thrsp	NM_009381	chr7	104561454	104566020	-	BC009165	thyroid hormone responsive SPOT14 homolog (Rattus)
Timm22	NM_019818	chr11	76220681	76229794	+	AF223950	translocase of inner mitochondrial membrane 22 homolog (yeast)
Timp3	NM_011595	chr10	85763282	85812253	+	BC014713	tissue inhibitor of metalloproteinase 3
Tmed3	NM_025360	chr9	89594043	89599829	-	BC023338	transmembrane emp24 domain containing 3
Tmem41b	NM_153525	chr7	117115701	117129768	-	BC086759	transmembrane protein 41B
Tmem7							
Tnnc1	NM_009393	chr14	32021498	32024898	+	BC061172	troponin C, cardiac/slow skeletal
Tnrc15							
Tor1a	NM_144884	chr2	30816147	30823411	-	BC017683	torsin family 1, member A (torsin A)
Tpi1	**NM_009415**	**chr6**	**124760733**	**124764430**	**-**	**BC046761**	**triosephosphate isomerase 1**
Tra1							
Tram2	NM_177409|N	chr1	20991459	21069306	-	BC018212	translocating chain-associating membrane protein 2
Tsc22d3	NM_0010773	chrX	137074067	137135061	-	BC028813	TSC22 domain family 3
Tst	NM_009437	chr15	78229695	78236295	-	BC005644	thiosulfate sulfurtransferase, mitochondrial
Ttc9c	NM_027412	chr19	8883565	8893784	-	BC043061	tetratricopeptide repeat domain 9C
Tuba4							
Tuba6							
Tubb2							
Tubg1	NM_134024	chr11	100981445	100987733	+	AB158480	tubulin, gamma 1
Txndc14	NM_025868	chr17	87477611	87478498	+	BC110994	thioredoxin domain containing 14
Txndc4	NM_029572	chr4	48203584	48292461	-	AK172973	thioredoxin domain containing 4 (endoplasmic reticulum)
Txndc5	NM_145367	chr13	38592135	38620329	-	AY243534	thioredoxin domain containing 5
Ube1c							
Ube1dc1							
Ube2n	**NM_080560**	**chr10**	**94977796**	**95008292**	**+**	**BC067069**	**ubiquitin-conjugating enzyme E2N**
Ube2v1	NM_023230	chr2	167433139	167459299	-		ubiquitin-conjugating enzyme E2 variant 1
Ubqln1	NM_152234|N	chr13	58277523	58316997	-	BC026847	ubiquilin 1
Ubxd2	NM_026390	chr1	130140739	130175954	+	BC019795	UBX domain containing 2
Ugt2b34	NM_153598	chr5	87318792	87335962	-	BC028826	UDP glucuronosyltransferase 2 family, polypeptide B34
Unc50	NM_026123	chr1	37487017	37495969	+	AY017214	unc-50 homolog (C. elegans)
Upp2	NM_029692	chr2	58419798	58645381	+	BC027189	uridine phosphorylase 2
Usp2	NM_198092|N	chr9	43875104	43903710	+	AY255637	ubiquitin specific peptidase 2
Usp39	NM_138592	chr6	72268670	72295169	-	BC026983	ubiquitin specific peptidase 39
Uxs1	NM_026430	chr1	43806132	43884593	-	BC037049	UDP-glucuronate decarboxylase 1
Wbp4	NM_018765	chr14	79859744	79881354	-	AF071184	WW domain binding protein 4
Wdr45	NM_172372	chrX	7299350	7305327	+	BC011479	WD repeat domain 45
Xpo1	NM_134014|N	chr11	23156041	23197597	+	BC062912	exportin 1, CRM1 homolog (yeast)
Xrn2	NM_011917	chr2	146838755	146903736	+	BC054743	5'-3' exoribonuclease 2
Ypel3	NM_026875|N	chr7	133920489	133924024	+	AF523353	yippee-like 3 (Drosophila)
Ythdf2	NM_145393	chr4	131741972	131768171	-	BC014797	YTH domain family 2
Za20d3							
Zfp532	NM_207255	chr18	65739884	65848595	+	BC094671	zinc finger protein 532
Zfp574	NM_175477	chr7	25862284	25867500	+	BC059044	zinc finger protein 574
Zhx3	NM_177263	chr2	160596183	160698726	-	BC058111	zinc fingers and homeoboxes 3
Zranb1	NM_207302	chr7	140141305	140175634	+		zinc finger, RAN-binding domain containing 1