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MDMA's Effect on Myocardial DNA Methylation and its Association with Dilated Cardiomyopathy

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B.S.
Emory University
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Thesis Committee Chair: William Michael Caudle, Ph.D.

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Abstract

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By Ivan Ludlow

MDMA ("Ecstasy") is an illicit psychoactive drug that has increased in popularity in the past two decades. However, the cardiovascular toxicological mechanism of MDMA has not been fully characterized. The present study utilized microarray analysis to determine gene expression and DNA methylation modifications after MDMA exposure in the murine heart. Alterations in gene expression and epigenetics may serve a critical function in the development of dilated cardiomyopathy (DCM) and heart failure. Three different drug administration timeframes were used to determine the permanence of MDMA-associated DNA methylation and gene expression changes. MDMA decreased the transcription of genes found in the circadian rhythm pathway, which was verified via quantitative RT-PCR. This pathway has been shown to have an important role in regulating mitochondrial metabolism and maintaining cardiac function. Differential expression of the myosin heavy chain (Myh7) gene was identified across all treatment groups, which has been associated with cardiac dysfunction and cardiomyopathy. Furthermore, MDMA treated mice displayed genome-wide hypermethylation compared to controls. Similar genome-wide DNA methylation changes have been reported in DCM patients. Collectively, these results suggest that MDMA may be toxic to the heart through its ability to change DNA methylation patterns and alter gene transcription leading to disease onset.

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Introduction

MDMA (3,4-methylenedioxymethamphetamine, “ecstasy”) is an amphetamine derivative, with hallucinogenic and stimulant properties. (1) The popularity of MDMA has increased since the late 1980s, as its use became a feature of the underground dance scene. (2) According to the 2004 National Survey on Drug Use and Health (3), more than 17 million people 12 or older have tried MDMA at least once in their lifetime.

MDMA’s Short Term Effects

The onset of MDMA’s effects takes 20 to 60 minutes to occur, with peak effect 60 to 90 minutes after ingestion. (4) Effects can last for 3 to 5 hours. (4) MDMA produces a relaxed, euphoric state, including emotional openness, empathy, reduction of negative thoughts, and a decrease in inhibitions. (5-9) Pathophysiologically, acute administration of MDMA has been shown to increase heart rate, blood pressure and myocardial oxygen consumption in humans. (10, 11) Furthermore, a single administration of MDMA could produce significant cardiovascular toxicity in vivo. (12) Yet the immediate health risk of MDMA is minor. Emergency department and mortality data suggests that serious complications of MDMA use are less common than those associated with opioids, cocaine, or methamphetamine. (13-15)

MDMA’s Long Term Effects

The long-term health effects of MDMA pose a far greater risk than short-term outcomes. The cardiotoxicity of MDMA has been well documented. (1) MDMA increases the risk of tachycardia, arrhythmia, cardiac ischemia, myocardial infarction, and cardiomyopathy. (11, 16-18) Of particular interest, dilated cardiomyopathy (DCM) is characterized by a ventricular chamber enlargement and systolic dysfunction. ((19) Animal studies show repeated administration of MDMA or its metabolites causes eccentric left ventricular dilation, diastolic dysfunction, and contractile dysfunction in cardiomyocytes. (18) Yet, the underlying mechanisms causing cardiotoxicity of MDMA abuse are currently unclear. (20) This study proposes that MDMA reduces physiological function of the heart by altering gene expression through modifications in DNA methylation patterns.

Gene Expression Association with Cardiac Function

Alterations in gene expression can negatively affect heart function. (21, 22) Epigenetics, specifically DNA methylation, is a key factor in development of cardiomyopathy. (23, 24) DNA methylation involves the addition of a methyl group to cytosine bases in CpG nucleotides catalyzed by DNA methyltransferases (DNMT). (25) DNA methylation promotes gene silencing either by directly blocking the binding of transcription factors to DNA or by the binding of methyl-binding proteins, which can mediate gene repression through interaction with a co-repressor complex. (24) Furthermore, significant changes in DNA methylation have been identified in human dilated cardiomyopathy patients. (22, 26)

Human heart failure patients with end-stage dilated cardiomyopathy (DCM) differentially expressed (1.5- fold change) more than 100 transcripts. (27) These included the up-regulation of atrial natriuretic peptide, sarcomeric and cytoskeletal proteins (cardiac troponin and tropomyosin), stress response proteins (HSP 40 and HSP 70), and transcription/translation regulators (CCAAT box binding factor and eIF-1AY). (27) Down-regulation of cell-signaling channels and mediators, specifically for Ca^{2+} pathways (Ca^{2+}/calmodulin-dependent kinase, inositol 1,4,5- trisphosphate receptor, and SERCA), were identified. (27) In conjunction, animal studies were investigated as they transitioned from stable hypertrophy to heart failure. (28) An up-regulation of fibronectin and collagen mRNA was observed, suggesting that interstitial fibrosis found in cardiac muscles of failing hearts is regulated at the gene expression level. (28) Furthermore, an increase in abundance of TGF-β_1 mRNA, which influences fibroblast activity and is associated with pressure-overload cardiac hypertrophy, may initiate interstitial fibrosis during heart failure. (28) Therefore, studies indicate how gene expression changes correlate with cardiac function.

DNA Methylation Association with Cardiac Function

As discussed previously, DNA methylation represents one of the most common epigenetic mechanisms for controlling gene expression. Human studies have identified 5,346 disease-associated differentially methylated regions (DMR's) in cardiomyocytes from failing murine hearts after chronic left ventricular pressure overload. (29) While most DMR's were intergenic (DNA regions between genes), 5.9% of DMR's overlapped with enhancer or promoter regions marked by H3K27ac, H3K4me1 and H3K4me3 (histone modifiers) in adult cardiomyocytes. (29, 30) These differentially methylated regions were adjacent to genes involved in cardiac muscle cell development, cardiac morphogenesis and energy metabolism. (29) In conjunction, genes encoding α- and β-myosin heavy chains (Myh6 and Myh7) show progressive CpG demethylation in cardiomyocytes from failing hearts. (29) Modifications in thick filament protein content and performance are thought to underlie contraction-relaxation dysfunction in human heart failure. (31) Furthermore, adult failing cardiomyocytes expressed lower levels of Atp2a2 (a gene encoding sarcoplasmic reticulum Ca^{2+} ATPase) than adult control myocytes. (29)

A further study in human patients with DCM has detected methylation differences in genes with unknown function in heart failure, including lymphocyte antigen 75 (LY75), tyrosine kinase-type cell surface receptor HER3 (ERBB3), homeobox B13 (HOXB13), and adenosine receptor A2A (ADORA2A). (32) Significantly increased methylation changes were associated with significantly decreased changes in LY75 and ADORA2A mRNA expression, but not ERBB3 and HOXB13 expression. (32) The adenosine receptor A2A (ADORA2A) is a member of the G protein-coupled receptor family and enhances cAMP production through αGs proteins. (33) LY75, a collagen-binding mannose family receptor, mediates antigen uptake and is transcriptionally controlled by the interleukin-6 receptor (IL6Ra). (34, 35) In vivo zebrafish experiments indicated that reduced expression of LY75 and ADORA2A in cardiomyocytes leads to heart failure. (32)

MDMA’s Effect on DNA Methylation and Gene Expression

DNA methylation, oxidative stress, and cardiomyopathy are connected through the sarcoplasmic reticulum Ca-ATPase (SERCA2a), which plays an essential role in Ca^{2+} homeostasis and cardiac function. (36) SERCA2a is regulated by tumor necrosis factor-alpha (TNF-α), which when administered to cardiomyocytes increased expression of

DNA methyltransferases, enhanced methylation in the SERCA2a promoter region, and reduced SERCA2a expression. (36) These actions lead to decreased cardiac function and eventual cardiomyopathy. (36) MDMA has previously been shown to alter expression of TNF-α in cardiomyocytes. (37)

The mechanism of MDMA-induced cardiotoxicity is unknown, but alterations in gene expression and epigenetics may serve a critical function. This study identifies gene expression and DNA methylation changes mediated by MDMA use in the murine heart. C57Bl/6 mice were treated with MDMA (40mg/kg/day) once daily by intraperitoneal (IP) injection. Three different timeframes were used to ascertain the permanence of MDMA-associated DNA methylation and gene expression changes: 10 day short-term MDMA use, 35 day long-term MDMA use, and a 10+25D protocol with 10 day short-term MDMA use followed by a 25 day saline injection period (Figure 1). Microarray analysis of gene expression and epigenetic changes were analyzed for significant pathway enrichment utilizing quantitative PCR as validation.

Methods

Reagents

All reagents were analytical grade and purchased from Sigma Aldrich (St. Louis, MO) unless otherwise indicated.

Mouse Protocols

Wild-type C57Bl/6 mice were obtained from Jackson Labs (Bar Harbor, ME) and were bred to establish a colony. All mice were housed at Emory Universities AAALAC certified Vivarium, and followed IACUC protocols. Experiments used mice 8-12 weeks old of both genders. Mice were administered 40mg/kg of MDMA or saline once daily by IP for 10 or 35 days. The MDMA dose administered for these experiments was in agreement with previous studies. (38, 39) For the 10 + 25 group, mice received 10 days of 40mg/kg/day MDMA followed by 25 days of saline solution. Following MDMA or saline administration, mice were terminated by cervical dislocation under avertin anesthesia. The hearts were removed and sectioned rapidly with a razor blade (2 mm sections). Sections were fixed in 10% neutral buffered formalin and embedded in paraffin.

Gene expression analysis

Total RNA was extracted from at least 3 mouse hearts from each group using the Fibrous Tissue RNeasy kit (Qiagen, Germantown, MD). Up to 10 µg of total RNA were used to synthesize double-stranded cDNA with the SuperScript Double-Stranded cDNA Synthesis Kit (Invitrogen/Life Technologies, Grand Island, NY). Once synthesized, cDNA was labeled with Cy3 and hybridized overnight to a 12 x 135kb human expression array (Roche Nimblegen). Expression arrays were washed and scanned using a Roche Nimblegen MS200 scanner. Images were analyzed using Nimblescan software as directed by the manufacturer, including RMA normalization and generation of expression data. T-tests were conducted on expression results utilizing Bioconductor for R, with each set being compared to saline controls. Differentially expressed genes were identified as those with a $p<0.05$ and 1.5-fold change in gene expression compared to saline controls. From this data, heatmaps were generated using R. Gene ontology was performed using DAVID bioinformatics database. (40)

Quantitative RT-PCR

RNA was isolated using the same procedure as the gene expression analysis. Single-stranded cDNA was synthesized using SuperScript III (Life Technologies). Quantitative PCR was performed using SYBR green dye and a LightCycler 480 system (Roche) using manufacturer protocols. Primers were manufactured by Integrated DNA Technologies (Coralville, IA) and are shown in Supplemental Table 1. Individual sample results were normalized to controls ACTB and RN18S (Qiagen), and expressed as a fold change from saline controls.

DNA Methylation Analysis

Total cellular DNA was extracted using a MagNAPure DNA Extraction System (Roche). Total cellular DNA from 4 samples in each group were diluted in 10mM Tris-HCl, pH 8.5. The DNA was sonicated to obtain an average DNA fragment size of 200-

500bp long. A sample of DNA was set aside for normalization, and a secondary sample of sonicated DNA was enriched using the MethylCollector Ultra kit (Active Motif, Carlsbad, CA), utilizing a magnetic bead binding reaction. Enriched DNA was cleaned using MinElute Reaction Cleanup Kit (Qiagen, Valencia, CA) prior to whole genome amplification. Both methylated and input DNA was amplified using whole genome amplification (Sigma-Aldrich, St. Louis, MO) according to manufacturer protocols. The amplified DNA was cleaned using QIAquick PCR Purification Kit (Qiagen, Valencia, CA) and verified for enrichment of methylated DNA with specific PCR primers (GAPDH and HIST1 H2BH).

For DNA methylation analysis, Roche Nimblegen 2.1M Deluxe Promoter Arrays were utilized (Roche). Following the manufacturer's instructions, the DNA was fluorescently labeled and hybridized to arrays overnight at 42°C. Arrays were washed and then scanned on a Roche Nimblegen MS200 scanner. Images were analyzed by Nimblescan software as directed by the manufacturer (which included normalizing to the input DNA), resulting in a both log2 ratio values of methylated DNA compared with input for each probe and a final analysis utilizing a nonparametric, one-sided Kolmogorov-Smirnov (KS) test to determine a _log10 peak P value of the detected methylated DNA peaks. Results were annotated to the gene locations.

Statistical Analysis

Probe intensity values collected for treated and wild type mice. Student t-test ($p<0.05$) was used to compare vales for each gene sequence. Probe intensity averages were created for each treatment type per gene sequence. Results were then analyzed for gene ontology and cardiac toxicological relevance using DAVID Bioinformatics Resources. Analyses were performed for each treatment group: 10 day MDMA, 10 day MDMA and 25 day rest, and 35 day MDMA. Significant gene sequences were then compared between treatment groups.

All statistical analyses (other than those performed for microarray analyses) were performed using GraphPad Prism 5.0 (Graphpad, La Jolla, CA). Each experiment was analyzed using a one-way ANOVA or t-test were appropriate, with a $p<0.05$ deemed statistically significant. The experiments are displayed as a mean ± SEM, with all experiments performed at least 3 times each.

Results

Cardiac Physiology

No change in wet heart weight was observed between mice after 10d or 35d MDMA use compared to saline controls. Echocardiographic (ECG) measurements showed MDMA did not change left ventricular end diastolic dimension (LVEDD), fractional shortening, or ejection fraction in any of the treatment groups. Cardiac function of the mice was retained in all experimental timelines tested.

Gene Expression

Utilizing microarray technology, 17,869 genes were analyzed for changes in expression due to MDMA use. Statistically significant changes in gene expression ($p<0.05$, fold change>1.5) for 10d MDMA, 35d MDMA and 10+25d groups are identified in Supplemental Table 2. For the 10d MDMA treatment group 752 genes were differentially expressed, of which 77% were downregulated (Figure 2A). For the 10+25d treatment group 113 genes were differentially expressed, with 12% being downregulated (Figure 2B). For the 35d MDMA group 558 genes were differentially expressed, with 76% downregulated (Figure 2C). KEGG pathway mapping identified enrichment in treatment groups for MAPK pathways, Wnt signaling, and circadian rhythms (Supplemental Table 2). However, the circadian rhythm pathway was enriched in both the 10d MDMA and 35d MDMA groups but not in the 10+25d group.

Multi-set analysis of the three treatment timelines was used to identify sustained gene expression changes related pathophysiologically to cardiac function (Figure 3). Figure 3A classifies genes by treatment group and their expression results. Genes present in each section of Figure 3B are listed in Supplemental Table 3. A total of 1,314 genes were differentially expressed in all groups (Figure 3B). Only 116 were shared between at least 2 groups (Sections D, E, F and G, Figure 3B). Between the 10d and 10+25d groups one gene (Ubxn10) was significantly expressed. This suggests that genes revert back to normal expression levels after 10d MDMA administration following 25d of saline (Section D). Analysis of 10/25d and 35d MDMA groups identified 31-shared differentially expressed genes (Section E). All genes showed the same directionality in regards to expression changes (both groups display either downregulation or upregulation of the gene of interest), with 3 genes downregulated and 28 upregulated compared to controls (Section E, Figure 3B). In addition, comparison of 10d and 35d MDMA treatment groups identified 83 shared differentially expressed genes. Of this group, 82 genes showed the same directionality with 69 downregulated and 13 upregulated (Section F, Figure 3B). Pathway analysis of these 82 genes found significant enrichment in the circadian rhythm pathway. Four genes were downregulated within this pathway (ARNTL, CLOCK, NPAS2, and Per3). Lastly, one gene (Myh7) was differentially expressed in all 3-treatment groups (Section G). Myh7 was upregulated in the 10d and 35d MDMA groups, but was downregulated in the 10/25d group.

Quantitative RT-PCR

Gene expression microarray results were validated utilizing quantitative RT-PCR. Analysis was performed on members of the circadian rhythm and MAPK signaling pathways, which were identified during pathway analysis (Supplemental Table 2). Decreased mRNA abundance was expressed for NPAS2, PER3, CLOCK, and ARNTL following 10d MDMA administration (Figure 4). With the exception of PER3, these results are in agreement with the microarray analysis. Following 35d MDMA treatment NPAS2, PER3, and CLOCK expression levels returned to normal, while ARNTL exhibited decreased mRNA abundance.

DNA Methylation

DNA microarrays were used to assess gene promoter DNA methylation changes independently of gene expression changes. DNA methylation changes were identified using approximately 50bp long regions, called peaks. Analysis of the 10d MDMA group identified 57,315 significant differentially methylated peaks across 10,243 genes (Figure 5A). Of these, 71% of the peaks were hypermethylated while 29% were hypomethylated (Figure 5B). For the 10+25d group 136,604 significant differentially methylated peaks were identified across 13,919 genes, with 68% of peaks being hypermethylated and 32% being hypomethylated. In the 35d MDMA group 25,943 significant differentially methylated peaks were found across 6,466 genes, with 91% being hypermethylated and 9% being hypomethylated. While MDMA was shown to cause both hyper- and hypomethylation in cardiomyocyte DNA, hypermethylation changes were dominant across treatment groups (Figure 5B). Figure 6 provides a graphical representation of differentially methylated peak scores between treated and control groups by using a scatter plot.

A second analysis was performed to identify DNA methylation changes that correlated with gene expression changes in MDMA-treated hearts (Figure 7), with the results provided in Supplemental Table 4. In the 10d MDMA group 169 genes (22% of significantly differentially expressed genes) displayed 514 differentially methylated peaks. Of these, 82% were hypermethylated and 18% were hypomethylated (Figure 7B). In addition, the 10/25d treatment group had 54 genes (48% of significant differentially expressed genes) that exhibited 359 differentially methylated peaks. Of these, 91% were hypermethylated and 9% were hypomethylated (Figure 7B). Furthermore, the 35d MDMA treatment group contained 93 genes (17% of significant differentially expressed genes) that displayed 371 differentially methylated peaks. Of these, 100% were hypermethylated (Figure 7C). When comparing 10+25d and 35d MDMA methylated peaks, 40 peaks were differentially methylated in both groups. All peaks were hypermethylated and localized to 16 genes.

Of the four differentially expressed circadian rhythm genes identified previously (ARNTL, CLOCK, NPAS2, and Per3), only Per3 had one differentially methylated peak (which was hypermethylated). For the gene Myh7, 2 differentially methylated peaks were identified in the 10d group, 3 peaks were identified in the 10+25d group, and 1 peak was identified in the 35d group. All peaks were hypermethylated, however, none correlated between groups. Additionally, only 2 genes displayed significant DNA methylation peaks across all three MDMA treatment groups. Fam46b (a pseudogene for COX20) displayed the same hypermethylated peak across groups, while SLC25A36 (a mitochondrial pyrimidine nucleotide carrier) demonstrated 3 reproducible hypermethylated peaks.

Discussion

MDMA is a popular illicit drug with chronic abuse potential. The long-term effects of MDMA on cardiomyocytes have not been fully characterized. Alterations in gene expression and DNA methylation may be critical factors in determining the cardiotoxicity of MDMA. This study has combined the use of DNA methylation and gene expression analysis in order to understand the association between these factors and MDMA use. The results identified novel genes associated with MDMA use, specifically those within the circadian rhythm pathway (ARNTL, CLOCK, NPAS2, and Per3).

MDMA reduced transcription of the Arntl gene, which codes its analogous protein (ARNTL), also known as MOP3 or BMAL1. This protein forms a heterodimer with a bHLH-PAS protein (CLOCK) or a paralog (NPAS2). (41, 42) The CLOCK-ARNTL heterodimer activates transcription from E-box response elements, which drives genes encoding the Period (Per1, Per2, and Per3) proteins. (41) However, ARNTL is the only clock gene that by itself is necessary for circadian rhythm generation. (42) Knockout mice for the ARNTL gene displayed complete loss of circadian rhythms in locomotion and other behaviors. (42) ARNTL deficient mice developed a cardiac pathology that started with a transitory increase in myocardial mass, progressed to dilated cardiomyopathy (characterized by thinning of the myocardial walls, dilation of the left ventricle, and decreased cardiac performance), and lead to heart failure until time of death. (43) In conjunction, these mice lacked the standard diurnal variation in heart rate and blood pressure. (43, 44) Analysis of single nucleotide polymorphisms (SNPs) in rats identified two polymorphisms that occurred in the sequence encoding for ARNTL, which were associated with type II diabetes and hypertension. (45) This study suggests a causative relationship between ARNTL gene variation and type II diabetes or hypertension pathology. (45) The comparison between 10d and 35d MDMA treatment groups found a decreased expression of the Arntl gene, which could result in the changes observed in other downstream circadian rhythm genes (CLOCK, NPAS2, and Per3) and could in part account for MDMAs cardiotoxicity.

Further analysis of the ARNTL deficient mice revealed down regulation of both myosin heavy chain isoform mRNAs preceding cardiac dysfunction. (43) Reduction in myocardial contractility has been associated with changes in myosin heavy chain (MHC) isoform composition. (43) Systolic dysfunction was connected to early down regulation of both MHC isoform transcripts, but not with protein expression, suggesting both transcriptional and post-transcriptional changes in myosin gene expression. (43) MDMAs accepted association with cardiac dysfunction, cardiomyopathy, and heart failure could justify the differential expression of Myh7 across all treatment groups.

Period 3 (Per3) is one of the key components of the cardiac human clock system, and has been associated with metabolic dysfunctions. (46) Deletion of Per3 in mice had a mild influence on circadian activity. (47) However, Per3 mutations in humans have been known to affect sleep homeostasis and mood disorders. (48, 49) A significant Per3 variable number tandem repeat (VNTR) polymorphism has been linked directly to control of autonomic balance during sleep/wake cycles, and indirectly to cardiac autonomic control. (50, 51) However, a recent case-control study investigated the relationship between the VNTR polymorphism in the Per3 gene and chronic heart failure in a Caucasian population. (46) No association was found between the presence of the polymorphism and chronic heart failure. (46) Therefore, our result of Per3 gene expression downregulation may induce minimal, if any, physiological changes in heart function.

One mechanism by which the circadian rhythm pathway may affect cardiac function is through mitochondrial oxidative processes. Energy demand in the heart varies across the sleep/wake cycle to optimize its function. (52) In conjunction, time-dependent energy metabolism is subject to control by the circadian clock system, in which core clock genes play a major role. (52) Therefore without core clock genes functioning optimally, the daily rhythms in heart energy metabolism are impaired. (53, 54) Subsequently, mitochondrial dysfunction has been associated with both structural and functional abnormalities in the heart. (52) However, little is known about how the circadian clock system coordinates the heart energy balance. (52) ARNTL deficient mice displayed significant decrease in the expression of genes associated with the fatty acid oxidative pathway, the tricarboxylic acid cycle, and the mitochondrial respiratory chain in the heart. (52) These findings suggest that the circadian clock system plays an important role in regulating mitochondrial metabolism and maintaining cardiac function. (52) MDMA has been shown to decrease ARNTL expression and disrupt the circadian rhythm pathway, which could inhibit mitochondrial oxidative processes and cause cardiac dysfunction, cardiomyopathy, and heart failure.

Across all MDMA treatment groups differentially methylated peaks exhibited greater hypermethylation than hypomethylation compared to controls. Analysis of the 10d group found 71% of the peaks were hypermethylated, 68% being hypermethylated in the 10+25d group, and 91% being hypermethylated in the 35d group. Hypermethylation of CpG islands (CGI's) within the promoter region or gene body is typically linked to decreased gene expression (55), while hypomethylation of the promoter correlates with increased expression of the gene. (56, 57) This general principle is explained by DNA methylations capacity to alter accessibility of transcription factor complexes to the DNA strand. (57)

A preliminary study observed DNA methylation alterations in a number of CpG islands within human idiopathic DCM patients. Of the 90 genes deemed statistically significant, one third showed increased methylation in DCM patients, while two-thirds were significantly less methylated. (32) However, the controls of this study were patients who had previously received heart transplantation and received immunosuppressive medications, which may have an influenced genome-wide DNA methylation patterns. (32) In addition, a study that compared clinical human DCM patients and non-failing controls found that hypermethylation was the predominant DNA methylation change between groups. (22) Of the 158 genes that displayed significant alterations in DNA methylation, 90% of these genes exhibited hypermethylation. (22) Since MDMA treatment groups exhibited similar genome-wide hypermethylation changes (Figure 7) as DCM patients, it suggests that MDMA use could lead to future disease onset.

Comparisons of the DNA methylation to gene expression data found that the location of the majority of significantly differentially methylated peaks aren’t present in differentially expressed gene regions. In the 10d MDMA group, 22% of significantly differentially expressed genes (169) displayed 514 differentially methylated peaks. In addition, the 10+25d group had 54 genes (48% of significant differentially expressed genes) that exhibited 359 differentially methylated peaks. The 35d MDMA group had 17% of significant differentially expressed genes (93) that displayed 371 differentially methylated peaks. Therefore, while DNA methylation can account for a significant proportion of gene expression changes in MDMA treated groups, other epigenetic modification changes must be present.

There are several other epigenetic mechanisms that have been linked to DCM or heart failure. First, chromatin modification enables cells to regulate expression of distinct gene sequences in development and adaptation. (32, 58) Second, histone modification utilizing histone acetyltransferases (HAT's) or histone deacetylases (HDAC's) play an important role in maintaining cardiac function. (32, 59-61) Loss of HDAC1 and HDAC2 in cardiomyocytes has been shown to cause cardiac arrhythmia and heart failure. (32, 62) Third, short non-coding microRNAs (miRNA's) have been associated with gene expression changes and DCM in animal models. (32, 63-65)

DNA methylation may not be the predominant mechanism regulating heart function and DCM pathogenesis. However, this study observed differentially expressed DNA methylation peaks in gene regions with no known current function or connection to DCM. Therefore, these DNA methylation changes cannot be precluded from altering gene expression in DCM. Further analysis is required to identify pathophysiological pathways that contribute to DCM, and the epigenetic mechanisms that influence these genes. This study suggests that early-life choices, such as MDMA use, can cause measurable and stable changes in the epigenome that may contribute to subsequent disease susceptibility. The normal aging process has been shown to alter epigenetic function, including DNA methylation. (66) Aging has produced hypomethylation across multiple cell types, and appears to be a risk factor contributing to the development of human pathological states. (66) A significant loss of genomic methylation has been found in cardiomyocytes of older specimens utilizing rat and pig models. (66, 67) Coupled with MDMA use, these epigenetic changes may lead to future DCM and heart failure.

Conclusion

This study identified gene expression and DNA methylation changes facilitated by MDMA use in the murine heart. Microarray analysis identified alterations in gene expression and DNA methylation with significant pathway enrichment, which was validated through the use of quantitative PCR. Results found the circadian rhythm pathway was enriched in both the 10d MDMA and 35d MDMA treatment groups. The circadian clock system plays an important role in regulating mitochondrial metabolism and maintaining cardiac function. (52) MDMA has been shown to disrupt the circadian rhythm pathway, which could inhibit mitochondrial oxidative processes and cause cardiac dysfunction, cardiomyopathy, and heart failure. Additionally, MDMA treatment groups exhibited genome-wide hypermethylation (Figure 7) similar to those found in DCM patients, suggesting that MDMA use could lead to future disease onset. When correlating genome-wide DNA methylation and gene expression changes, this epigenetic control mechanism plays a significant role in altering heart function. Our results identified many differentially expressed genes that currently have no known link to pathophysiological changes in the heart, but therefore cannot be ruled out. In addition, other epigenetic control mechanisms can be modifying transcriptional or translational processes affecting heart function. Further study of both epigenetic mechanisms and gene expression that dictates heart function is required to better understand MDMA's true effect on the system.

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Tables and Figures

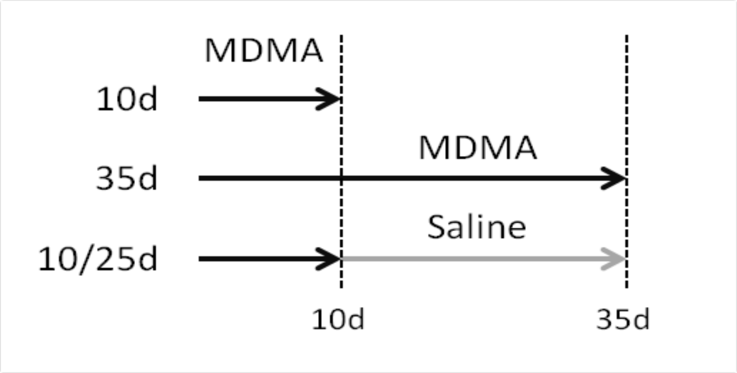


Figure 1: Treatment Methods
Diagram of the three separate timeframes utilized in this study: 10 day short-term MDMA administration, 35 day long-term MDMA administration, and a 10/25 day administration regime (protocol using 10 day short-term MDMA use followed by a 25 day saline injection period).

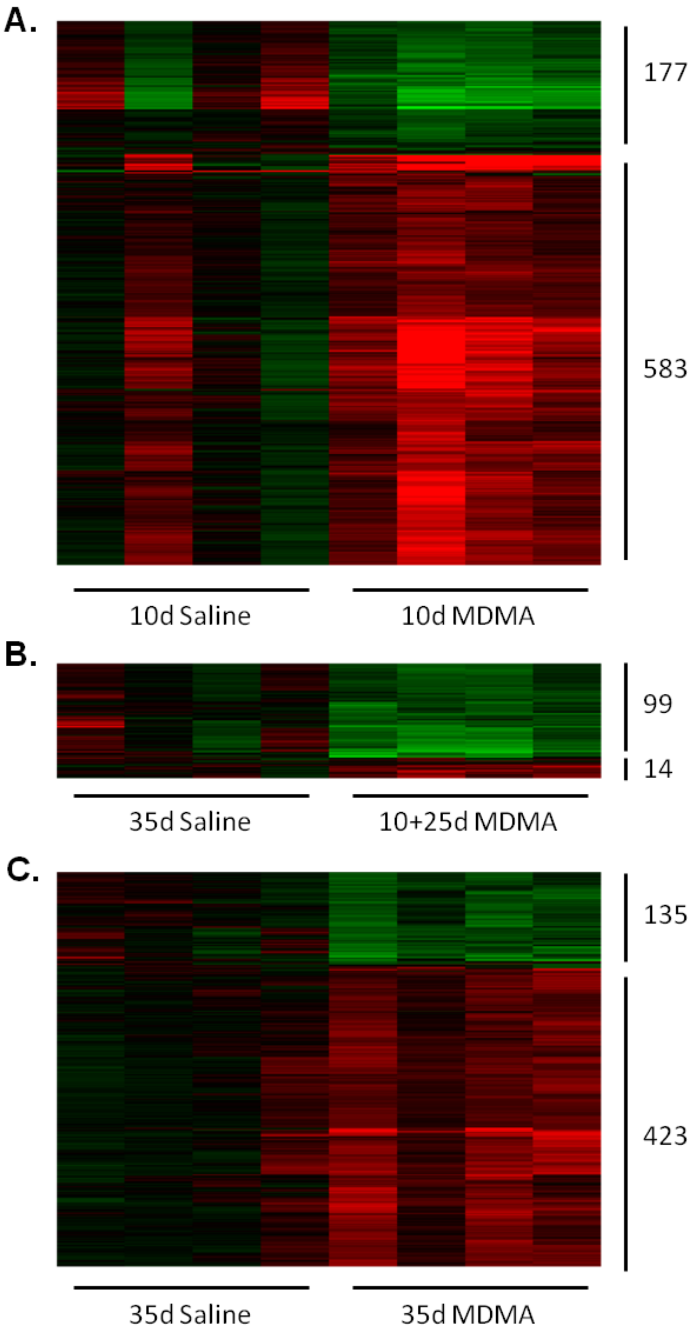


Figure 2: MDMA Induced Differential Gene Expression
Heatmap comparing gene expression levels between: (A) 10d MDMA treatment and control groups (B) 10/25d MDMA treatment and control groups (C) 35d MDMA treatment and control group. Green cells indicate down regulation of genes after MDMA administration, while red indicates up regulation compared to controls. 10d and 35d treatment groups experienced greater down regulation, while the 25d group experienced greater up regulation of genes compared to controls.

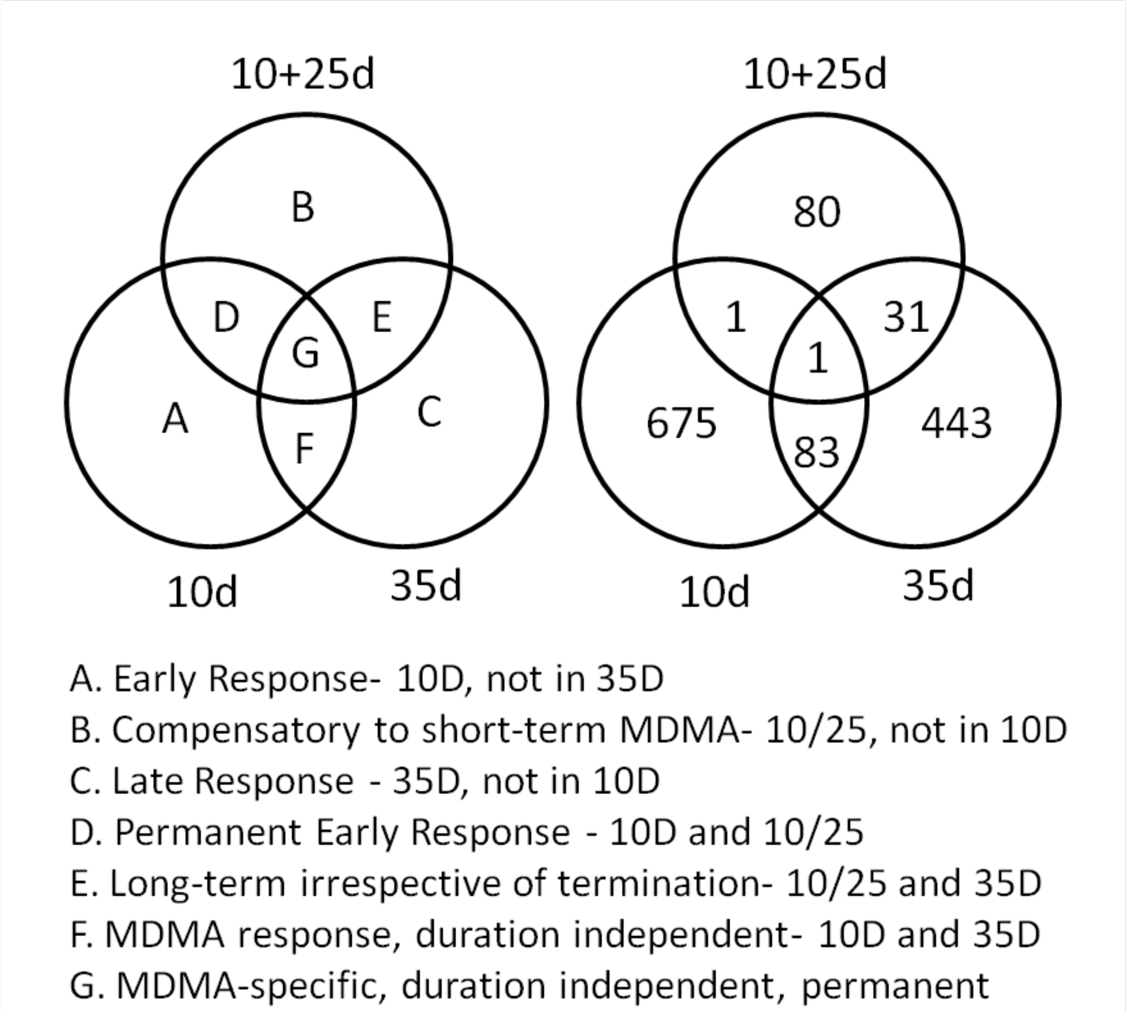


Figure 3: Gene Expression Changes between Treatment Groups.
Venn diagram identifies significant gene expression changes of each treatment group (A, B, and C), with overlap shown between gene sets (D, E, F and G). One gene was significantly expressed between 10d and 10+25d group (D), suggesting that genes revert back to normal expression levels. Comparison of 10+25d and 35d MDMA groups (E) found 31 shared differentially expressed genes. All genes showed the same directionality in regards to expression changes. Between 10d and 35d groups (F) 83 shared differentially expressed genes. Within this group 82 genes showed the same directionality.

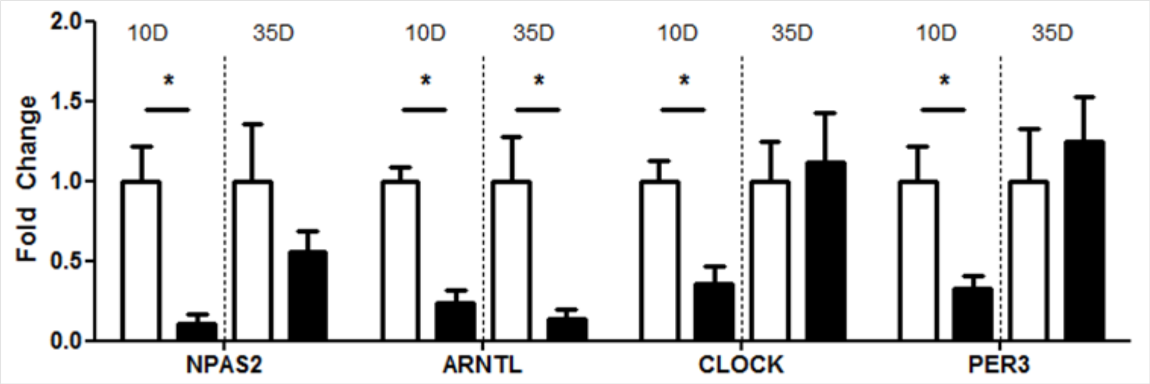


Figure 4: Differential mRNA Abundance after MDMA Treatment.
Bar graph showing mRNA abundance for NPAS2, PER3, CLOCK, and ARNTL genes indicated by fold change. White bars correspond to saline controls, and black bars correspond to MDMA treatment groups. A significant decreased in mRNA abundance was observed across all genes following 10d MDMA administration. Only ARNTL exhibited decreased mRNA abundance after 35d MDMA administration.

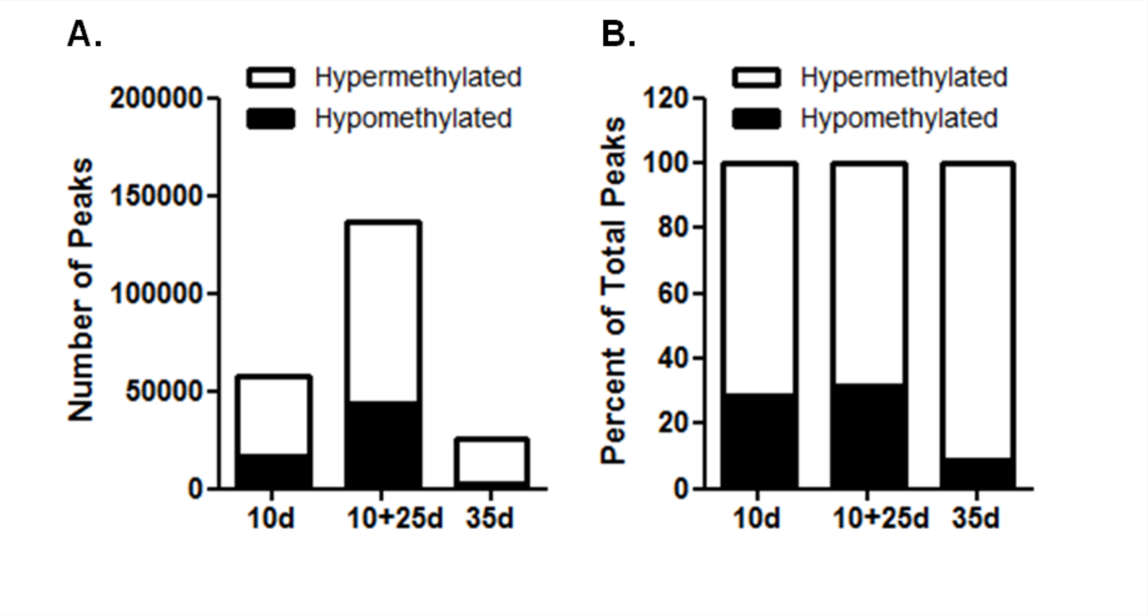
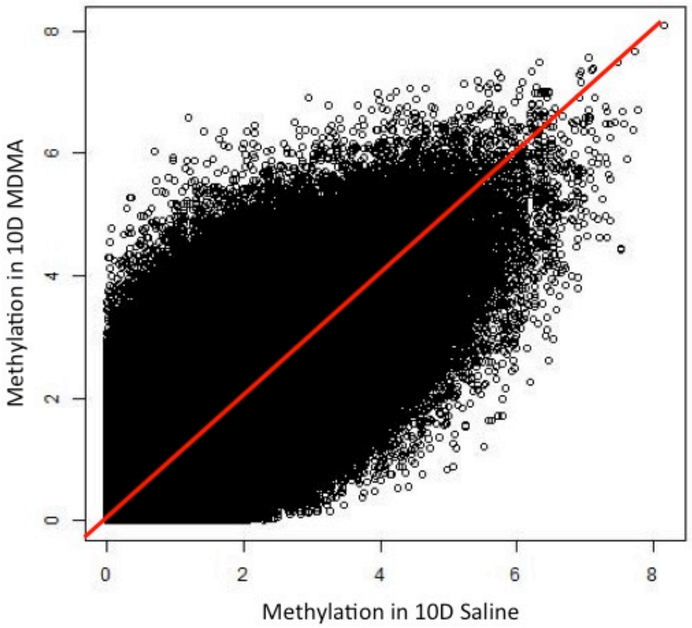
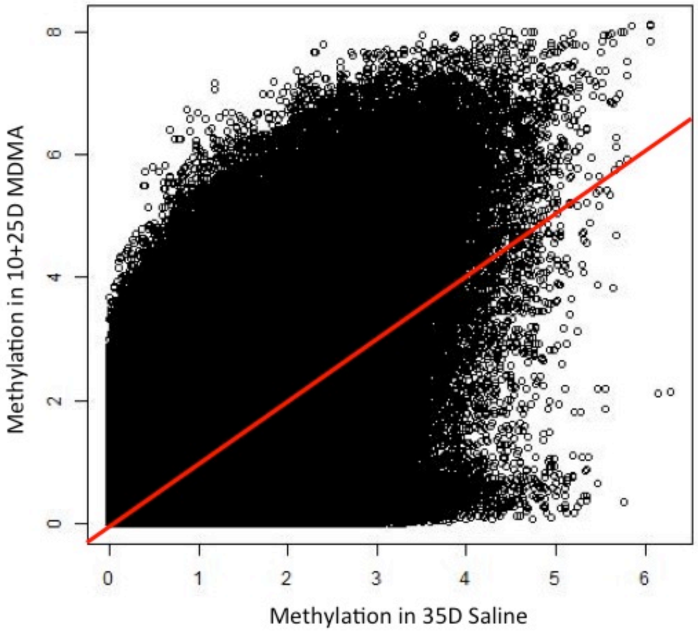


Figure 5: Change in DNA Methylation Peak Scores after MDMA Administration
Bar graph showing (A) DNA methylation changes utilizing peak scores for each treatment group. (B) Hypomethylation or hypermethylation changes associated with each corresponding peak score. MDMA use caused both hypermethylation and hypomethylation changes in cardiomyocyte DNA, however hypermethylation changes were dominant across all treatment groups.

A.


Methylation in 10D MDMA
Methylation in 10D Saline
0
2
4
6
8

B.


Methylation in 10+25D MDMA
Methylation in 35D Saline
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2
4
6
8
0
1
2
3
4
5
6

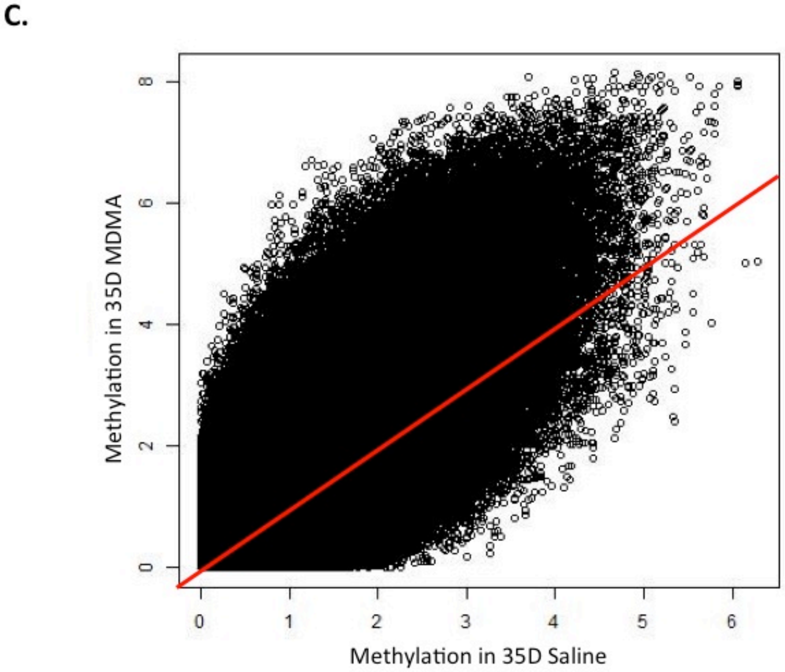

Figure 6: MDMA Induced DNA Methylation Changes
Scatter plot showing the DNA methylation peak score values between controls and MDMA treatment groups. The red line displays a 1:1 peak score ratio. Left of this line indicates hypermethylation after MDMA administration, while right of the line indicates hypomethylation after administration. Hypermethylation changes were dominant across all treatment groups after MDMA use.

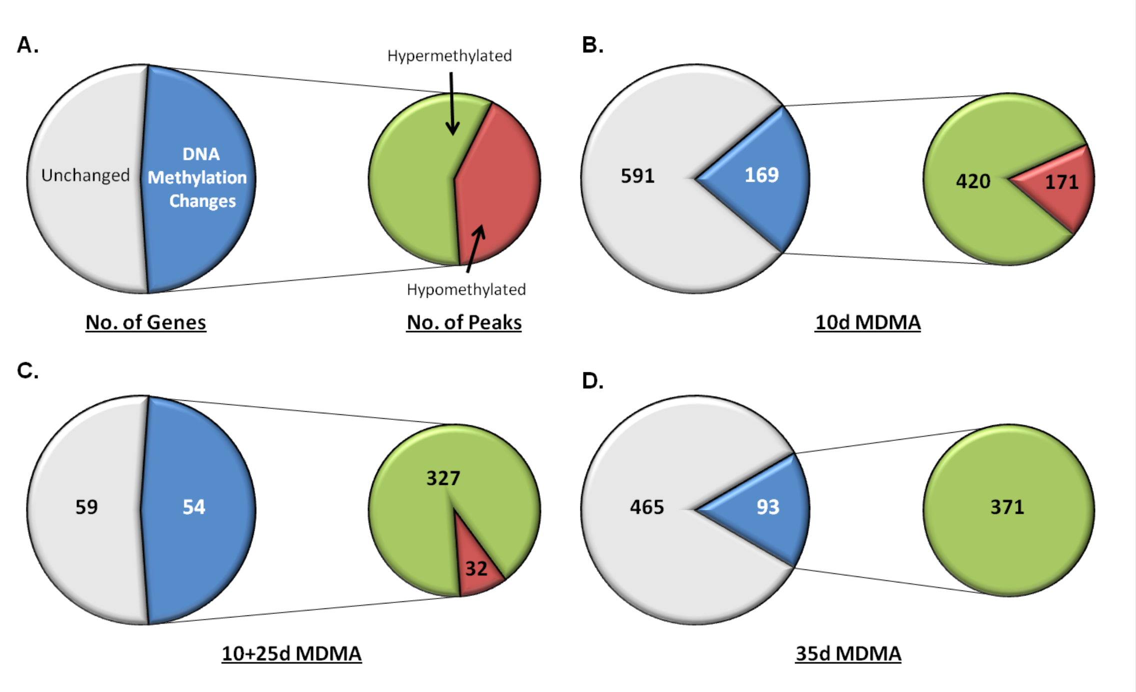

Figure 7: Correlating DNA Methylation and Gene Expression Changes.
Pie chart of differentially expressed genes that contained at least one change in methylated peaks. Charts separated by treatment groups: (B) 10d MDMA (C) 10/25d MDMA (D) 35d MDMA.

Appendices

Supplemental Table 1: MDMA Quantitative RT-PCR Primers

CLOCK
Forward: CTACCGGCTGGAGAGAGGAAA
Reverse: TTCTTGTGCTTTTCTTTCACGGGAG

NPAS2
Forward: CCCTATTTGCAGGCACCAAC
Reverse: CGGAGGTGTAGACTGTGTGG

ARNTL
Forward: ACTGACTACCAGTTAGAATATGCAG
Reverse: ATTTTGTCCCGACGCCTCTT

PER3
Forward: AGAACACAGATACCTTCGCGG
Reverse: AAAGTGCACGCTCTTGAGGA

Supplemental Table 2: MDMA-associated Differentially Expressed Genes

10d MDMA-752		
Gene Symbol	**Gene Name**	**Fold Change**
Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5	-2.577
GPR137C	G protein-coupled receptor 137C	-2.515
Gnl3l	guanine nucleotide binding protein-like 3 (nucleolar)-like	-2.430
ABCC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	-2.416
casq1	calsequestrin 1	-2.396
Ibtk	inhibitor of Bruton agammaglobulinemia tyrosine kinase	-2.268
ECE1	endothelin converting enzyme 1	-2.250
Mboat2	membrane bound O-acyltransferase domain containing 2	-2.218
SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	-2.171
Prpf8	pre-mRNA processing factor 8	-2.163
Ltbp1	latent transforming growth factor beta binding protein 1	-2.120
SLC38A1	solute carrier family 38, member 1	-2.116
MMRN1	multimerin 1	-2.097
arntl	aryl hydrocarbon receptor nuclear translocator-like	-2.089
RNF123	ring finger protein 123	-2.050
zbtb11	zinc finger and BTB domain containing 11	-2.031
RHOU	ras homolog gene family, member U	-2.024
kbtbd5	kelch repeat and BTB (POZ) domain containing 5	-2.021
PGM5	phosphoglucomutase 5	-1.993
CAMSAP1	calmodulin regulated spectrin-associated protein 1; similar to calmodulin regulated spectrin-associated protein 1	-1.945
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-1.943
ISOC1	isochorismatase domain containing 1	-1.938
hyou1	hypoxia up-regulated 1	-1.936
STAT5A	signal transducer and activator of transcription 5A	-1.935
NLRX1	NLR family member X1	-1.933
OSBP2	oxysterol binding protein 2; similar to oxysterol binding protein 2	-1.923
scaper	S phase cyclin A-associated protein in the ER	-1.919
FGL2	fibrinogen-like protein 2	-1.893
pdgfra	platelet derived growth factor receptor, alpha polypeptide	-1.891
esrrb	estrogen related receptor, beta	-1.890
slc35e3	solute carrier family 35, member E3; predicted gene 7341	-1.862
DSG2	desmoglein 2; similar to Dsg2 protein	-1.861
rdx	radixin	-1.860
KANK1	KN motif and ankyrin repeat domains 1	-1.860
SLTM	SAFB-like, transcription modulator	-1.834
lpin1	lipin 1	-1.822
IGDCC4	immunoglobulin superfamily, DCC subclass, member 4	-1.820

Gene Symbol	**Gene Name**	**Fold Change**
ZDHHC17	zinc finger, DHHC domain containing 17	-1.811
PDZRN3	PDZ domain containing RING finger 3	-1.800
CLOCK	circadian locomoter output cycles kaput	-1.798
CHRM2	cholinergic receptor, muscarinic 2, cardiac	-1.792
ITSN1	intersectin 1 (SH3 domain protein 1A)	-1.785
TMTC3	transmembrane and tetratricopeptide repeat containing 3	-1.767
NUDT12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	-1.743
Eps8	epidermal growth factor receptor pathway substrate 8	-1.729
NR3C1	nuclear receptor subfamily 3, group C, member 1	-1.727
DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	-1.722
Twsg1	twisted gastrulation homolog 1 (Drosophila)	-1.721
CCDC109A	coiled-coil domain containing 109A	-1.715
Mfsd4	major facilitator superfamily domain containing 4	-1.709
COL6A6	RIKEN cDNA E330026B02 gene	-1.706
Itgav	integrin alpha V	-1.701
JMY	junction-mediating and regulatory protein	-1.673
FRMD6	predicted gene 5780; FERM domain containing 6	-1.670
Usp7	ubiquitin specific peptidase 7	-1.667
dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	-1.664
CDC42BPA	CDC42 binding protein kinase alpha	-1.660
RPS6KC1	ribosomal protein S6 kinase polypeptide 1	-1.658
SF3B2	splicing factor 3b, subunit 2	-1.655
Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.651
sspN	sarcospan	-1.651
Zfml	zinc finger, matrin-like	-1.645
usp48	ubiquitin specific peptidase 48	-1.626
ANAPC1	anaphase promoting complex subunit 1	-1.613
KIF1B	kinesin family member 1B	-1.600
F630110N24Rik	RIKEN cDNA F630110N24 gene	-1.599
SNX9	similar to Sorting nexin 9; sorting nexin 9	-1.586
TTC38	tetratricopeptide repeat domain 38	-1.585
ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-1.584
phf17	PHD finger protein 17	-1.581
entpd4	ectonucleoside triphosphate diphosphohydrolase 4	-1.569
MIS12	MIS12 homolog (yeast)	-1.566
SLC19A2	solute carrier family 19 (thiamine transporter), member 2	-1.556
Slc9a6	solute carrier family 9 (sodium/hydrogen exchanger), member 6	-1.546
ACIN1	apoptotic chromatin condensation inducer 1	-1.545

Gene Symbol	**Gene Name**	**Fold Change**
tsr1	similar to CG7338-PA; TSR1, 20S rRNA accumulation, homolog (yeast)	-1.538
SEC31A	Sec31 homolog A (S. cerevisiae)	-1.533
DST	dystonin; hypothetical protein LOC100047109	-1.503
ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	-1.494
UBR4	ubiquitin protein ligase E3 component n-recognin 4	-1.492
CDK5RAP3	CDK5 regulatory subunit associated protein 3	-1.492
arhgef10	Rho guanine nucleotide exchange factor (GEF) 10	-1.491
RBM26	RNA binding motif protein 26	-1.487
Pms1	postmeiotic segregation increased 1 (S. cerevisiae)	-1.483
CALCRL	calcitonin receptor-like	-1.480
baz1b	bromodomain adjacent to zinc finger domain, 1B	-1.477
GJA3	gap junction protein, alpha 3	-1.473
Ptprd	protein tyrosine phosphatase, receptor type, D	-1.471
RNASEL	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)	-1.468
Gm14446	predicted gene 14446	-1.466
A630007B06Rik	RIKEN cDNA A630007B06 gene	-1.465
RBBP5	retinoblastoma binding protein 5	-1.464
PPAT	phosphoribosyl pyrophosphate amidotransferase	-1.464
NTN4	netrin 4	-1.459
eif3a	eukaryotic translation initiation factor 3, subunit A	-1.458
MYH11	myosin, heavy polypeptide 11, smooth muscle	-1.454
Nf2	neurofibromatosis 2	-1.453
MITF	microphthalmia-associated transcription factor	-1.446
CFLAR	CASP8 and FADD-like apoptosis regulator pseudogene; CASP8 and FADD-like apoptosis regulator	-1.443
LEO1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	-1.442
OTUD7B	OTU domain containing 7B	-1.438
AFAP1	actin filament associated protein 1	-1.437
LIMA1	LIM domain and actin binding 1	-1.435
Wif1	Wnt inhibitory factor 1	-1.435
OSBPL1A	oxysterol binding protein-like 1A	-1.429
TNS3	tensin 3	-1.424
Rprd2	regulation of nuclear pre-mRNA domain containing 2	-1.423
CYTSA	cytospin A	-1.422
TFPI	tissue factor pathway inhibitor	-1.417
Il1r1	interleukin 1 receptor, type I	-1.412
Mlec	malectin	-1.410
adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta); similar to metalloprotease-disintegrin meltrin beta	-1.409
dusp5	dual specificity phosphatase 5	-1.396

Gene Symbol	Gene Name	Fold Change
RAB8B	RAB8B, member RAS oncogene family	-1.393
spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	-1.391
MXD1	MAX dimerization protein 1	-1.389
mks1	Meckel syndrome, type 1	-1.387
WFIKKN2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	-1.387
SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1; predicted gene 7004	-1.379
PPP2R5C	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	-1.374
RNF141	predicted gene 10179; ring finger protein 141	-1.373
SIDT2	SID1 transmembrane family, member 2	-1.373
CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	-1.373
BOD1L	biorientation of chromosomes in cell division 1-like	-1.371
CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	-1.369
itih5	inter-alpha (globulin) inhibitor H5	-1.367
FBXW8	F-box and WD-40 domain protein 8	-1.361
ARID4B	AT rich interactive domain 4B (RBP1-like)	-1.360
PHKA2	phosphorylase kinase alpha 2	-1.356
D17Wsu92e	DNA segment, Chr 17, Wayne State University 92, expressed	-1.354
HSPA12A	heat shock protein 12A	-1.354
dhdh	dihydrodiol dehydrogenase (dimeric)	-1.352
MAPK10	mitogen-activated protein kinase 10	-1.349
ATF7IP	activating transcription factor 7 interacting protein	-1.345
Zfp839	zinc finger protein 839	-1.343
CLASP2	CLIP associating protein 2	-1.338
RORA	RAR-related orphan receptor alpha	-1.331
adra1b	adrenergic receptor, alpha 1b	-1.330
SCML4	sex comb on midleg-like 4 (Drosophila)	-1.330
MKLN1	muskelin 1, intracellular mediator containing kelch motifs	-1.321
MIER1	mesoderm induction early response 1 homolog (Xenopus laevis	-1.318
Slfn5	schlafen 5; hypothetical protein LOC100047131	-1.316
PELI1	pellino 1	-1.314
BC068281	cDNA sequence BC068281	-1.311
bpnt1	bisphosphate 3'-nucleotidase 1; similar to bisphosphate 3-nucleotidase 1	-1.305
slc39a9	solute carrier family 39 (zinc transporter), member 9	-1.299
4930430F08Rik	RIKEN cDNA 4930430F08 gene	-1.298
SDCCAG1	serologically defined colon cancer antigen 1	-1.297
NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	-1.293
Ino80	INO80 homolog (S. cerevisiae); similar to yeast INO80-like protein	-1.283
Fam122b	family with sequence similarity 122, member B	-1.276

Gene Symbol	Gene Name	Fold Change
P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide	-1.276
DSTYK	dual serine/threonine and tyrosine protein kinase	-1.272
Tnpo2	transportin 2 (importin 3, karyopherin beta 2b)	-1.269
TMEM35	transmembrane protein 35	-1.263
Ubap2l	ubiquitin associated protein 2-like	-1.259
SNN	stannin	-1.256
Dhrs3	dehydrogenase/reductase (SDR family) member 3	-1.255
MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like; hypothetical protein LOC100044924	-1.254
3632451O06Rik	RIKEN cDNA 3632451O06 gene	-1.253
AHCYL1	S-adenosylhomocysteine hydrolase-like 1	-1.252
BRWD1	bromodomain and WD repeat domain containing 1	-1.250
CC2D2A	coiled-coil and C2 domain containing 2A	-1.250
AHDC1	AT hook, DNA binding motif, containing 1	-1.248
MON2	MON2 homolog (yeast)	-1.247
IRF2BP2	interferon regulatory factor 2 binding protein 2	-1.245
ART3	ADP-ribosyltransferase 3	-1.245
Bach1	BTB and CNC homology 1	-1.242
Cep57	centrosomal protein 57	-1.242
NEO1	neogenin	-1.241
SLC41A1	solute carrier family 41, member 1	-1.236
lpar1	lysophosphatidic acid receptor 1	-1.235
Erbb2ip	Erbb2 interacting protein	-1.234
GUCY1A3	guanylate cyclase 1, soluble, alpha 3	-1.234
Hspa4l	heat shock protein 4 like	-1.230
WDTC1	WD and tetratricopeptide repeats 1; similar to WD and tetratricopeptide repeats 1	-1.229
CNNM3	cyclin M3	-1.228
CREBL2	cAMP responsive element binding protein-like 2	-1.227
FBXL16	F-box and leucine-rich repeat protein 16	-1.226
PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	-1.226
STARD13	StAR-related lipid transfer (START) domain containing 13; similar to serologically defined colon cancer antigen 13	-1.224

Gene Symbol	Gene Name	Fold Change
RPS27A	predicted gene 5928; predicted gene 12617; predicted gene 4802; similar to ribosomal protein S27a; predicted gene 13215; predicted gene 6111; predicted gene 7808; predicted gene 6014; predicted gene 8317; ubiquitin C; ubiquitin B; similar to fusion protein: ubiquitin (bases 43_513); ribosomal protein S27a (bases 217_532); similar to ubiquitin B; predicted gene 8649; ribosomal protein S27A; predicted gene 11517; predicted gene 11808; predicted gene 8430; RIKEN cDNA 2810422J05 gene; similar to Ubc protein; predicted gene 13815; ubiquitin A-52 residue ribosomal protein fusion product 1; predicted gene 8797; predicted gene 1821; predicted gene 11759; predicted gene 5239; predicted gene 6438	-1.224
Epb4.1l2	erythrocyte protein band 4.1-like 2	-1.223
PTPRK	protein tyrosine phosphatase, receptor type, K	-1.221
Golph3l	golgi phosphoprotein 3-like	-1.218
USP20	ubiquitin specific peptidase 20	-1.217
Ccdc47	coiled-coil domain containing 47	-1.214
DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	-1.213
CLIP4	CAP-GLY domain containing linker protein family, member 4; similar to CAP-GLY domain containing linker protein family, member 4	-1.207
9030420J04Rik	RIKEN cDNA 9030420J04 gene	-1.205
MR1	major histocompatibility complex, class I-related	-1.204
NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	-1.201
WDSUB1	WD repeat, SAM and U-box domain containing 1	-1.199
nhsl1	NHS-like 1	-1.197
TNRC6A	trinucleotide repeat containing 6a	-1.196
HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	-1.193
SIAE	sialic acid acetylesterase	-1.192
D14Abb1e	DNA segment, Chr 14, Abbott 1 expressed	-1.184
CD99L2	CD99 antigen-like 2	-1.175
ikbip	RIKEN cDNA 1200009F10 gene	-1.174
GPATCH1	G patch domain containing 1	-1.171
anxa11	annexin A11; predicted gene 2260; predicted gene 2274	-1.169
Smc1a	structural maintenance of chromosomes 1A	-1.168
secisbp2	SECIS binding protein 2	-1.167
ZADH2	zinc binding alcohol dehydrogenase, domain containing 2	-1.165
atg16l1	autophagy-related 16-like 1 (yeast)	-1.164
PAQR3	progestin and adipoQ receptor family member III	-1.157
RUFY3	RUN and FYVE domain containing 3	-1.148
maeA	macrophage erythroblast attacher	-1.147
SASH1	SAM and SH3 domain containing 1; predicted gene 2082	-1.146
MYLIP	myosin regulatory light chain interacting protein	-1.145

Gene Symbol	**Gene Name**	**Fold Change**
Ube4b	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	-1.145
MICAL3	microtubule associated monoxygenase, calponin and LIM domain containing 3	-1.145
NUMA1	nuclear mitotic apparatus protein 1	-1.143
MAOB	monoamine oxidase B	-1.142
mtr	5-methyltetrahydrofolate-homocysteine methyltransferase	-1.140
ERN1	endoplasmic reticulum (ER) to nucleus signalling 1	-1.139
TOP3B	topoisomerase (DNA) III beta	-1.138
NPAS2	neuronal PAS domain protein 2	-1.138
bat3	HLA-B-associated transcript 3	-1.138
Zfp507	zinc finger protein 507	-1.136
Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	-1.136
ZMAT1	zinc finger, matrin type 1	-1.135
PPM1B	similar to serine/threonine phosphatase; protein phosphatase 1B, magnesium dependent, beta isoform	-1.132
NBEA	neurobeachin	-1.130
GFPT1	glutamine fructose-6-phosphate transaminase 1	-1.128
9630028I04Rik	RIKEN cDNA 9630028I04 gene	-1.128
Gm13767	protein tyrosine phosphatase, receptor type, J; predicted gene 13768; predicted gene 13767	-1.126
Gm13768	protein tyrosine phosphatase, receptor type, J; predicted gene 13768; predicted gene 13767	-1.126
PTPRJ	protein tyrosine phosphatase, receptor type, J; predicted gene 13768; predicted gene 13767	-1.126
MTDH	metadherin	-1.121
hdac9	histone deacetylase 9	-1.120
ACVR1B	activin A receptor, type 1B	-1.118
Sin3b	transcriptional regulator, SIN3B (yeast)	-1.116
Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	-1.114
HUS1	Hus1 homolog (S. pombe)	-1.112
MEF2A	similar to Myocyte enhancer factor 2A; myocyte enhancer factor 2A	-1.111
ZC3H12C	zinc finger CCCH type containing 12C	-1.111
pbrm1	polybromo 1	-1.109
CHD6	chromodomain helicase DNA binding protein 6; predicted gene 8291	-1.108
CRHR2	corticotropin releasing hormone receptor 2	-1.108
4732416N19Rik	RIKEN cDNA 4732416N19 gene	-1.102
HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	-1.101
Znfx1	zinc finger, NFX1-type containing 1	-1.100
CYB5D1	cytochrome b5 domain containing 1; predicted gene 6685	-1.098

Gene Symbol	Gene Name	Fold Change
TTC9C	tetratricopeptide repeat domain 9C	-1.095
ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	-1.094
5930434B04Rik	RIKEN cDNA 5930434B04 gene; hypothetical protein LOC100047034	-1.094
STAU1	staufen (RNA binding protein) homolog 1 (Drosophila)	-1.094
AKAP13	A kinase (PRKA) anchor protein 13	-1.092
RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	-1.088
SCLY	selenocysteine lyase	-1.088
AI597468	expressed sequence AI597468	-1.086
PKP4	plakophilin 4	-1.083
DLG1	discs, large homolog 1 (Drosophila); similar to Discs, large homolog 1 (Drosophila)	-1.081
NBR1	neighbor of Brca1 gene 1	-1.079
BC032203	cDNA sequence BC032203	-1.079
ANKRD17	ankyrin repeat domain 17	-1.078
Eif4g3	eukaryotic translation initiation factor 4 gamma, 3; similar to Eukaryotic translation initiation factor 4 gamma 3 (eIF-4-gamma 3) (eIF-4G 3) (eIF4G 3) (eIF-4-gamma II) (eIF4GII)	-1.076
Slc29a3	solute carrier family 29 (nucleoside transporters), member 3	-1.075
ZBTB7A	zinc finger and BTB domain containing 7a	-1.069
PTPN21	protein tyrosine phosphatase, non-receptor type 21	-1.068
ficd	FIC domain containing	-1.067
Wasf2	WAS protein family, member 2	-1.065
CREBBP	CREB binding protein	-1.065
Zfp316	zinc finger protein 316	-1.061
CDK12	CDC2-related kinase, arginine/serine-rich	-1.059
suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	-1.058
CHAC1	ChaC, cation transport regulator-like 1 (E. coli)	-1.057
UBD	ubiquitin D	-1.056
usp53	ubiquitin specific peptidase 53	-1.056
YIPF6	similar to Yip1 domain family, member 6; Yip1 domain family, member 6	-1.056
Trim35	tripartite motif-containing 35	-1.055
Zfp629	zinc finger protein 629	-1.054
UBAC2	ubiquitin associated domain containing 2	-1.053
Cdk6	cyclin-dependent kinase 6	-1.050
ZSCAN2	zinc finger and SCAN domain containing 2	-1.049
GAB2	growth factor receptor bound protein 2-associated protein 2	-1.046
lats1	large tumor suppressor	-1.046
dagla	diacylglycerol lipase, alpha	-1.046
Add1	adducin 1 (alpha)	-1.045
UNC119B	unc-119 homolog B (C. elegans)	-1.045
slu7	SLU7 splicing factor homolog (S. cerevisiae)	-1.043

Gene Symbol	Gene Name	Fold Change
NAAA	N-acylethanolamine acid amidase	-1.042
4930402H24Rik	RIKEN cDNA 4930402H24 gene	-1.041
sec22c	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	-1.039
TRPC4AP	transient receptor potential cation channel, subfamily C, member 4 associated protein	-1.038
SEMA4B	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	-1.038
Pde7b	phosphodiesterase 7B	-1.036
1500011H22Rik	RIKEN cDNA 1500011H22 gene	-1.032
MAP2K7	predicted gene 14378; similar to transforming growth factor, beta receptor III (betaglycan, 300kDa); mitogen-activated protein kinase kinase 7	-1.028
CD93	CD93 antigen	-1.027
TRIM55	tripartite motif-containing 55	-1.024
slc39a1	solute carrier family 39 (zinc transporter), member 1; similar to Zinc transporter ZIP1 (Zinc-iron regulated transporter-like) (Solute carrier family 39 member 1)	-1.020
ARID5B	similar to modulator recognition factor 2; AT rich interactive domain 5B (MRF1-like)	-1.020
DSC2	desmocollin 2	-1.019
SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1; similar to solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	-1.018
npepps	aminopeptidase puromycin sensitive	-1.018
RPS6KA5	ribosomal protein S6 kinase, polypeptide 5	-1.016
SUN1	unc-84 homolog A (C. elegans)	-1.016
SH3PXD2A	SH3 and PX domains 2A; similar to Fish protein	-1.014
UBXN7	UBX domain protein 7	-1.013
SLC4A4	solute carrier family 4 (anion exchanger), member 4	-1.012
keap1	kelch-like ECH-associated protein 1	-1.011
RBBP6	retinoblastoma binding protein 6	-1.010
mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	-1.009
TBC1D4	TBC1 domain family, member 4	-1.004
taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.002
CASZ1	castor homolog 1, zinc finger (Drosophila); similar to castor homolog 1, zinc finger	-1.001
ATP5G1	predicted gene 12337; predicted gene 10039; predicted gene 4479; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	-0.998
RCN2	reticulocalbin 2	-0.994
Whrn	whirlin	-0.993

Gene Symbol	Gene Name	Fold Change
NUP160	nucleoporin 160	-0.991
EHMT1	similar to euchromatic histone methyltransferase 1; euchromatic histone methyltransferase 1	-0.990
BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	-0.990
ULK1	Unc-51 like kinase 1 (C. elegans)	-0.987
Stxbp4	syntaxin binding protein 4	-0.986
tmem129	transmembrane protein 129	-0.986
Myst2	MYST histone acetyltransferase 2	-0.985
SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	-0.981
Pdzd2	PDZ domain containing 2	-0.981
TUBGCP5	tubulin, gamma complex associated protein 5	-0.977
RBM45	similar to developmentally regulated RNA-binding protein 1; RNA binding motif protein 45	-0.972
Adrbk2	adrenergic receptor kinase, beta 2	-0.966
ABR	active BCR-related gene	-0.966
Pcf11	cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	-0.966
ARID4A	AT rich interactive domain 4A (RBP1-like)	-0.965
ednrb	endothelin receptor type B	-0.965
H13	histocompatibility 13	-0.961
AFTPH	aftiphilin	-0.961
PREPL	prolyl endopeptidase-like	-0.959
TTC3	tetratricopeptide repeat domain 3	-0.956
SMARCAL1	SWI/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	-0.952
ARNT	aryl hydrocarbon receptor nuclear translocator	-0.951
ROCK2	Rho-associated coiled-coil containing protein kinase 2	-0.949
0610007P08Rik	RIKEN cDNA 0610007P08 gene	-0.948
smek2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	-0.947
Lpcat3	lysophosphatidylcholine acyltransferase 3	-0.945
AI848100	expressed sequence AI848100	-0.944
FKBP15	FK506 binding protein 15	-0.943
BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	-0.942
Fam150b	family with sequence similarity 150, member B	-0.938
MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	-0.935
Zfp346	zinc finger protein 346	-0.933
Acad10	acyl-Coenzyme A dehydrogenase family, member 10	-0.932
TET3	tet oncogene family member 3	-0.932
Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2	-0.929
ITPR1	inositol 1,4,5-triphosphate receptor 1	-0.923
WDR33	WD repeat domain 33	-0.923

Gene Symbol	Gene Name	Fold Change
SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	-0.918
dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	-0.918
IPO8	importin 8	-0.917
glyr1	RIKEN cDNA 3930401K13 gene	-0.916
Klhl38	kelch-like 38 (Drosophila)	-0.916
EVI5	ecotropic viral integration site 5	-0.915
Myo18a	myosin XVIIIA	-0.915
D19Wsu162e	DNA segment, Chr 19, Wayne State University 162, expressed	-0.908
Nup88	nucleoporin 88	-0.907
Atf2	activating transcription factor 2; similar to Cyclic AMP-dependent transcription factor ATF-2 (Activating transcription factor 2) (cAMP response element-binding protein CRE-BP1) (MXBP protein)	-0.907
Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)	-0.906
LMBRD1	LMBR1 domain containing 1	-0.906
SFRS11	splicing factor, arginine/serine-rich 11	-0.900
Zfp608	zinc finger protein 608	-0.900
CEP76	centrosomal protein 76	-0.899
Ap1g1	adaptor protein complex AP-1, gamma 1 subunit	-0.895
Zfp516	zinc finger protein 516	-0.893
4930471M23Rik	RIKEN cDNA 4930471M23 gene	-0.892
cul4a	cullin 4A	-0.890
Pim1	proviral integration site 1	-0.888
Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha isoform	-0.888
Sik1	salt inducible kinase 1	-0.887
D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed	-0.887
Bat2l	HLA-B associated transcript 2-like	-0.886
CCDC66	coiled-coil domain containing 66	-0.884
fam192a	RIKEN cDNA 2310065K24 gene	-0.883
HOMER1	homer homolog 1 (Drosophila)	-0.881
GGA3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	-0.878
adcy5	adenylate cyclase 5; similar to adenylate cyclase 5	-0.878
FBXO9	f-box protein 9	-0.877
ADD3	adducin 3 (gamma)	-0.875
tmem57	transmembrane protein 57	-0.874
KPNA6	karyopherin (importin) alpha 6	-0.870
Zfp251	zinc finger protein 251	-0.869
Tpcn1	two pore channel 1	-0.866
Txnl4b	thioredoxin-like 4B	-0.865
phkg1	phosphorylase kinase gamma 1	-0.864

Gene Symbol	Gene Name	Fold Change
EIF5	similar to Eukaryotic translation initiation factor 5; eukaryotic translation initiation factor 5	-0.864
cbx4	chromobox homolog 4 (Drosophila Pc class)	-0.862
Tet1	tet oncogene 1	-0.862
CLEC16A	C-type lectin domain family 16, member A	-0.861
ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	-0.860
Fnbp1	formin binding protein 1	-0.859
Zfp828	zinc finger protein 828	-0.857
ANKHD1	ankyrin repeat and KH domain containing 1; eukaryotic translation initiation factor 4E binding protein 3	-0.856
GIGYF2	GRB10 interacting GYF protein 2	-0.854
FAM13B	family with sequence similarity 13, member B	-0.853
ANK3	ankyrin 3, epithelial	-0.853
MKL2	MKL/myocardin-like 2	-0.852
SNAP91	synaptosomal-associated protein 91	-0.852
Med13l	mediator complex subunit 13-like	-0.851
ELP3	elongation protein 3 homolog (S. cerevisiae)	-0.850
MIB1	mindbomb homolog 1 (Drosophila)	-0.839
C130039O16Rik	RIKEN cDNA C130039O16 gene	-0.838
Polr3f	polymerase (RNA) III (DNA directed) polypeptide F	-0.836
Rabgap1l	RAB GTPase activating protein 1-like	-0.832
Zfp609	zinc finger protein 609	-0.831
rgp1	RGP1 retrograde golgi transport homolog (S. cerevisiae)	-0.831
SMURF2	SMAD specific E3 ubiquitin protein ligase 2; similar to SMAD specific E3 ubiquitin protein ligase 2	-0.830
Zfp426	zinc finger protein 426	-0.830
Zfp532	zinc finger protein 532	-0.826
PTPN11	protein tyrosine phosphatase, non-receptor type 11	-0.823
Ubxn10	UBX domain protein 10	-0.819
Gpn3	GPN-loop GTPase 3	-0.816
rufy1	RUN and FYVE domain containing 1	-0.814
maf	similar to c-Maf long form; avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	-0.813
ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	-0.813
tpr	similar to nuclear pore complex-associated intranuclear coiled-coil protein TPR; translocated promoter region	-0.812
PLD1	phospholipase D1	-0.811
HUWE1	HECT, UBA and WWE domain containing 1	-0.809
9330129D05Rik	RIKEN cDNA 9330129D05 gene	-0.808
Golim4	golgi integral membrane protein 4	-0.806

Gene Symbol	Gene Name	Fold Change
B230208H17Rik	RIKEN cDNA B230208H17 gene	-0.802
NFE2L1	nuclear factor, erythroid derived 2,-like 1	-0.802
FNDC3A	fibronectin type III domain containing 3A	-0.802
Rab3gap1	RAB3 GTPase activating protein subunit 1	-0.800
celsr1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	-0.796
rrs1	predicted gene 5067; RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	-0.793
ITGA7	integrin alpha 7	-0.791
ASAH2	N-acylsphingosine amidohydrolase 2	-0.791
Rnf38	ring finger protein 38	-0.790
C7	complement component 7	-0.790
Pgcp	plasma glutamate carboxypeptidase	-0.790
BAT4	predicted gene 5628; HLA-B associated transcript 4	-0.788
D6Wsu116e	DNA segment, Chr 6, Wayne State University 116, expressed	-0.787
TNFAIP3	tumor necrosis factor, alpha-induced protein 3	-0.787
stk24	serine/threonine kinase 24 (STE20 homolog, yeast)	-0.785
Top3a	similar to topoisomerase III; topoisomerase (DNA) III alpha	-0.785
CEACAM	carcinoembryonic antigen-related cell adhesion molecule 1; carcinoembryonic antigen-related cell adhesion molecule 2	-0.782
slc39a14	solute carrier family 39 (zinc transporter), member 14	-0.778
elk1	ELK1, member of ETS oncogene family	-0.777
PHLDB2	pleckstrin homology-like domain, family B, member 2	-0.777
CNOT2	CCR4-NOT transcription complex, subunit 2	-0.776
TOR1AIP1	torsin A interacting protein 1	-0.775
1110038D17Rik	RIKEN cDNA 1110038D17 gene	-0.775
1110021J02Rik	RIKEN cDNA 1110021J02 gene	-0.773
TOP1	topoisomerase (DNA) I	-0.770
ABLIM2	actin-binding LIM protein 2	-0.770
ZC3H6	zinc finger CCCH type containing 6	-0.769
Clasp1	CLIP associating protein 1	-0.769
ELF2	E74-like factor 2	-0.768
ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit A2	-0.768
srr	serine racemase	-0.767
ARL15	ADP-ribosylation factor-like 15	-0.765
TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-0.763
Zeb2	zinc finger E-box binding homeobox 2	-0.763
Laptm4b	predicted gene 6705; lysosomal-associated protein transmembrane 4B	-0.762
LRP6	similar to LDL receptor-related protein 6; low density lipoprotein receptor-related protein 6	-0.756

Gene Symbol	Gene Name	Fold Change
DGKE	diacylglycerol kinase, epsilon	-0.756
pja2	praja 2, RING-H2 motif containing	-0.755
Papola	poly (A) polymerase alpha	-0.753
AMBRA1	autophagy/beclin 1 regulator 1	-0.752
cdk8	predicted gene 7107; cyclin-dependent kinase 8	-0.752
dyrk2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-0.751
Rab2b	RAB2B, member RAS oncogene family	-0.741
Sbno1	sno, strawberry notch homolog 1 (Drosophila)	-0.741
Ubqln1	ubiquilin 1	-0.740
tab2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	-0.738
WDR35	WD repeat domain 35	-0.737
ncf1	neutrophil cytosolic factor 1	-0.735
SEC23A	SEC23A (S. cerevisiae)	-0.735
Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	-0.735
ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit A1	-0.729
RUNDC1	RUN domain containing 1	-0.729
LOC100046125	RAB5A, member RAS oncogene family; similar to small GTP-binding protein rab5	-0.728
rab5a	RAB5A, member RAS oncogene family; similar to small GTP-binding protein rab5	-0.728
Trp53bp2	transformation related protein 53 binding protein 2	-0.727
TAOK3	TAO kinase 3	-0.725
CBX5	chromobox homolog 5 (Drosophila HP1a)	-0.725
SMURF1	SMAD specific E3 ubiquitin protein ligase 1	-0.723
ZEB1	zinc finger E-box binding homeobox 1	-0.722
MAMLD1	mastermind-like domain containing 1	-0.720
PEX12	peroxisomal biogenesis factor 12	-0.719
Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	-0.717
EPC2	enhancer of polycomb homolog 2 (Drosophila); similar to Enhancer of polycomb homolog 2	-0.717
PABPC4	similar to Poly A binding protein, cytoplasmic 4; poly(A) binding protein, cytoplasmic 4; predicted gene 12623; predicted gene 5088; hypothetical protein LOC100044219	-0.714
NCKAP5	RIKEN cDNA E030049G20 gene	-0.712
CSNK1G1	casein kinase 1, gamma 1	-0.710
DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	-0.709
Slc38a4	solute carrier family 38, member 4	-0.709
D18Ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed	-0.708
RBM27	RNA binding motif protein 27	-0.708
ASB4	ankyrin repeat and SOCS box-containing 4	-0.706
agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	-0.704
STX18	syntaxin 18	-0.702

Gene Symbol	Gene Name	Fold Change
SEC23IP	Sec23 interacting protein	-0.702
IGHMBP2	immunoglobulin mu binding protein 2	-0.702
Foxk2	forkhead box K2	-0.699
EXOSC9	exosome component 9; similar to Exosome complex exonuclease RRP45 (Exosome component 9) (Polymyositis/scleroderma autoantigen 1) (Autoantigen PM/Scl 1) (Polymyositis/scleroderma autoantigen 75 kDa) (PM/Scl-75) (P75 polymyositis-scleroderma overlap syndrome-associated a...	-0.697
PDIA3	protein disulfide isomerase associated 3	-0.697
eprs	similar to Bifunctional aminoacyl-tRNA synthetase; glutamyl-prolyl-tRNA synthetase	-0.696
SAPS2	SAPS domain family, member 2	-0.687
PPIG	peptidyl-prolyl isomerase G (cyclophilin G)	-0.684
SMG7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	-0.684
2810407C02Rik	RIKEN cDNA 2810407C02 gene	-0.683
Mapk9	mitogen-activated protein kinase 9	-0.681
FAM179B	family with sequence similarity 179, member B	-0.681
RNF130	ring finger protein 130; similar to Ring finger protein 130	-0.676
Ccndbp1	cyclin D-type binding-protein 1	-0.676
CPSF3	cleavage and polyadenylation specificity factor 3	-0.674
WAC	similar to WW domain-containing adapter protein with coiled-coil; WW domain containing adaptor with coiled-coil	-0.673
Dnaja4	similar to DnaJ (Hsp40) homolog, subfamily A, member 4; DnaJ (Hsp40) homolog, subfamily A, member 4	-0.673
cast	calpastatin	-0.669
Trim63	similar to tripartite motif-containing 63; tripartite motif-containing 63	-0.667
lpp	LIM domain containing preferred translocation partner in lipoma	-0.666
TXNDC5	thioredoxin domain containing 5	-0.665
khnyn	RIKEN cDNA 9130227C08Rik gene	-0.664
PEX11A	peroxisomal biogenesis factor 11 alpha	-0.663
Hsp90b1	heat shock protein 90, beta (Grp94), member 1	-0.662
METT11D1	methyltransferase 11 domain containing 1	-0.661
H2-T23	histocompatibility 2, T region locus 23; similar to RT1 class Ib, locus H2-Q-like, grc region	-0.658
GAA	glucosidase, alpha, acid	-0.656
GTF3C1	general transcription factor III C 1	-0.653
ROCK1	Rho-associated coiled-coil containing protein kinase 1	-0.649
CHD1	chromodomain helicase DNA binding protein 1	-0.647
Mtus2	RIKEN cDNA C130038G02 gene	-0.647
glcci1	similar to glucocorticoid induced transcript 1; predicted gene 5815; glucocorticoid induced transcript 1	-0.647

Gene Symbol	**Gene Name**	**Fold Change**
SLC36A1	solute carrier family 36 (proton/amino acid symporter), member 1	-0.645
ACAD9	acyl-Coenzyme A dehydrogenase family, member 9	-0.642
Ik	IK cytokine	-0.638
ngly1	N-glycanase 1	-0.637
Thap2	THAP domain containing, apoptosis associated protein 2	-0.636
B3GNTL1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	-0.635
FLYWCH1	FLYWCH-type zinc finger 1	-0.635
CALD1	caldesmon 1	-0.634
ASB7	ankyrin repeat and SOCS box-containing 7	-0.634
2210018M11Rik	RIKEN cDNA 2210018M11 gene	-0.634
PSIP1	PC4 and SFRS1 interacting protein 1	-0.633
Iqsec1	IQ motif and Sec7 domain 1	-0.631
thrA	thyroid hormone receptor alpha; similar to thyroid hormone receptor	-0.631
Canx	calnexin	-0.631
nin	ninein	-0.625
Pcp4l1	Purkinje cell protein 4-like 1	-0.622
NUP107	nucleoporin 107	-0.620
PRPF31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	-0.618
DAG1	dystroglycan 1	-0.614
NFYB	nuclear transcription factor-Y beta	-0.614
SLK	STE20-like kinase (yeast)	-0.614
Obsl1	obscurin-like 1	-0.613
NFIC	nuclear factor I/C	-0.609
WNT5A	wingless-related MMTV integration site 5A	-0.608
Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	-0.607
Tmtc4	transmembrane and tetratricopeptide repeat containing 4	-0.604
sf3a3	splicing factor 3a, subunit 3	-0.604
E430018J23Rik	RIKEN cDNA E430018J23 gene; RIKEN cDNA 9130019O22 gene	-0.598
Cnot10	CCR4-NOT transcription complex, subunit 10	-0.597
copb2	coatomer protein complex, subunit beta 2 (beta prime)	-0.594
Senp5	SUMO/sentrin specific peptidase 5	-0.588
ADSL	adenylosuccinate lyase	-0.587
TUBB2C	tubulin, beta 2c, psuedogene 1; tubulin, beta 2C; tubulin, beta 2c, pseudogene 2	-0.585
PLEKHG5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	0.588
FAM189B	RIKEN cDNA 1110013L07 gene	0.588

Gene Symbol	**Gene Name**	**Fold Change**
Ggnbp1	gametogenetin binding protein 1; RIKEN cDNA 0610031G08 gene	0.589
ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	0.595
NLN	neurolysin (metallopeptidase M3 family)	0.599
cry2	similar to mKIAA0658 protein; cryptochrome 2 (photolyase-like)	0.599
Inpp5d	inositol polyphosphate-5-phosphatase D	0.601
1110034B05Rik	RIKEN cDNA 1110034B05 gene	0.602
D430042O09Rik	RIKEN cDNA D430042O09 gene	0.608
FGD5	FYVE, RhoGEF and PH domain containing 5	0.610
EPOR	erythropoietin receptor	0.612
ppp1r14b	predicted gene 9103; predicted gene 8503; similar to protein phosphatase 1, regulatory (inhibitor) subunit 14B; protein phosphatase 1, regulatory (inhibitor) subunit 14B	0.613
BANP	BTG3 associated nuclear protein	0.614
PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	0.614
E4F1	E4F transcription factor 1	0.618
Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	0.619
ARHGAP9	Rho GTPase activating protein 9	0.619
PARP8	poly (ADP-ribose) polymerase family, member 8	0.621
PGM2L1	phosphoglucomutase 2-like 1	0.623
BC028528	cDNA sequence BC028528	0.625
NRM	nurim (nuclear envelope membrane protein)	0.625
ALOX12	arachidonate 12-lipoxygenase	0.628
2700081O15Rik	RIKEN cDNA 2700081O15 gene	0.634
8430427H17Rik	RIKEN cDNA 8430427H17 gene	0.635
B230354K17Rik	RIKEN cDNA B230354K17 gene	0.636
Endou	placental protein 11 related	0.637
KIF26A	kinesin family member 26A	0.639
ACSF3	acyl-CoA synthetase family member 3	0.640
LRRC27	leucine rich repeat containing 27	0.643
1300003B13Rik	RIKEN cDNA 1300003B13 gene; hypothetical protein LOC100044281	0.644
RASD2	RASD family, member 2	0.648
LRRN4CL	LRRN4 C-terminal like	0.648
MYO5A	myosin VA	0.652
6230427J02Rik	RIKEN cDNA 6230427J02 gene	0.657
fam48a	family with sequence similarity 48, member A	0.667
INCENP	inner centromere protein	0.667

Gene Symbol	Gene Name	Fold Change
limk1	LIM-domain containing, protein kinase	0.669
Cdc25b	cell division cycle 25 homolog B (S. pombe)	0.670
STK10	serine/threonine kinase 10	0.673
Fam109a	family with sequence similarity 109, member A	0.673
SCARF2	scavenger receptor class F, member 2	0.677
BC016495	cDNA sequence BC016495	0.679
Dgcr14	DiGeorge syndrome critical region gene 14	0.681
GPR137B	similar to Gpr137b protein; G protein-coupled receptor 137B	0.682
Car14	carbonic anhydrase 14	0.682
2300009A05Rik	RIKEN cDNA 2300009A05 gene	0.684
LXN	latexin	0.687
grk6	G protein-coupled receptor kinase 6	0.690
2310046K01Rik	RIKEN cDNA 2310046K01 gene	0.690
Pole	polymerase (DNA directed), epsilon	0.691
Odf2	outer dense fiber of sperm tails 2; similar to outer dense fiber of sperm tails 2	0.692
NRIP2	nuclear receptor interacting protein 2	0.696
Tspan17	tetraspanin 17	0.699
Rap1gap	Rap1 GTPase-activating protein	0.701
1700029G01Rik	RIKEN cDNA 1700029G01 gene	0.701
Pisd-ps3	phosphatidylserine decarboxylase, pseudogene 3	0.702
TTBK2	tau tubulin kinase 2; congenital dyserythropoietic anemia, type I (human)	0.703
CD86	CD86 antigen	0.708
3110062M04Rik	RIKEN cDNA 3110062M04 gene	0.709
TMEM120B	transmembrane protein 120B	0.711
TRPV4	transient receptor potential cation channel, subfamily V, member 4	0.711
BTBD19	RIKEN cDNA 9530048O09 gene	0.715
PRKCB	protein kinase C, beta	0.719
tef	thyrotroph embryonic factor	0.724
Hmcn2	hemicentin 2	0.731
LRMP	lymphoid-restricted membrane protein	0.732
Rgs10	regulator of G-protein signalling 10	0.734
Pcdh19	protocadherin 19	0.738
PHF21A	PHD finger protein 21A	0.741
MERTK	c-mer proto-oncogene tyrosine kinase	0.742
PI16	peptidase inhibitor 16	0.743
lhx6	LIM homeobox protein 6	0.744

Gene Symbol	Gene Name	Fold Change
MATR3	matrin 3; similar to Matrin 3	0.754
IL10RA	interleukin 10 receptor, alpha	0.757
DNM1	dynamin 1	0.763
SLC35E2	RIKEN cDNA A530082C11 gene	0.764
NMB	neuromedin B	0.768
DNMT3B	DNA methyltransferase 3B	0.768
4930503L19Rik	RIKEN cDNA 4930503L19 gene	0.776
GstT2	glutathione S-transferase, theta 2	0.781
THSD1	thrombospondin, type I, domain 1	0.782
Zfp710	zinc finger protein 710	0.791
LTC4S	leukotriene C4 synthase	0.792
6330503K22Rik	RIKEN cDNA 6330503K22 gene	0.795
Zfp280c	zinc finger protein 280C	0.797
IFFO1	intermediate filament family orphan 1	0.798
DNM3	dynamin 3	0.800
SFRS16	splicing factor, arginine/serine-rich 16	0.802
CCDC88C	coiled-coil domain containing 88C	0.803
2700046G09Rik	RIKEN cDNA 2700046G09 gene	0.806
fbxl12	F-box and leucine-rich repeat protein 12	0.807
CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	0.813
FAM102A	family with sequence similarity 102, member A	0.817
dbp	D site albumin promoter binding protein	0.818
TACC2	transforming, acidic coiled-coil containing protein 2	0.820
Wdr62	similar to WD repeat domain 62; WD repeat domain 62	0.827
EMID1	EMI domain containing 1	0.846
arrb2	arrestin, beta 2	0.865
GMIP	Gem-interacting protein	0.873
CEP152	centrosomal protein 152	0.879
Adora2a	adenosine A2a receptor	0.881
Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	0.887
STARD9	START domain containing 9	0.892
Gm4983	predicted gene 4983	0.901
Hjurp	RIKEN cDNA 6430706D22 gene; similar to RIKEN cDNA 6430706D22 gene; RIKEN cDNA A730008H23 gene	0.903
RAB4B	RAB4B, member RAS oncogene family	0.904
1110038B12Rik	RIKEN cDNA 1110038B12 gene	0.907
PACS1	phosphofurin acidic cluster sorting protein 1	0.908
TLE2	transducin-like enhancer of split 2, homolog of Drosophila E(spl)	0.911
9330188P03Rik	RIKEN cDNA 9330188P03 gene	0.928

Gene Symbol	Gene Name	Fold Change
camk1	calcium/calmodulin-dependent protein kinase I	0.929
GRB10	growth factor receptor bound protein 10	0.977
NAV3	neuron navigator 3	0.998
KIFC2	kinesin family member C2	1.007
Rasgrp2	RAS, guanyl releasing protein 2	1.010
Mapk11	mitogen-activated protein kinase 11	1.017
pola2	polymerase (DNA directed), alpha 2	1.024
Gp49a	glycoprotein 49 A; leukocyte immunoglobulin-like receptor, subfamily B, member 4	1.030
LRRC45	leucine rich repeat containing 45	1.037
camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	1.040
Rps6kl1	ribosomal protein S6 kinase-like 1	1.041
CIT	citron	1.050
myl6	predicted gene 5915; predicted gene 8894; myosin, light polypeptide 6, alkali, smooth muscle and non-muscle; predicted gene 10080	1.054
DPEP2	dipeptidase 2	1.055
DARC	Duffy blood group, chemokine receptor	1.068
BARD1	BRCA1 associated RING domain 1	1.069
2010111I01Rik	RIKEN cDNA 2010111I01 gene	1.080
SIGIRR	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	1.086
Frmd4a	FERM domain containing 4A	1.096
STX1A	syntaxin 1A (brain)	1.136
1600020E01Rik	RIKEN cDNA 1600020E01 gene	1.141
2700023E23Rik	RIKEN cDNA 2700023E23 gene	1.146
GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	1.153
DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	1.153
Snora68	small nucleolar RNA, H/ACA box 68	1.156
SAPS3	SAPS domain family, member 3	1.159
ARHGAP33	sorting nexin 26	1.202
HMGN3	high mobility group nucleosomal binding domain 3	1.209
CPNE7	copine VII	1.213
MEG3	maternally expressed 3	1.229
KIF23	kinesin family member 23	1.239
PRDM5	PR domain containing 5	1.252
Brms1	breast cancer metastasis-suppressor 1	1.279
cdkal1	CDK5 regulatory subunit associated protein 1-like 1	1.285
SORBS2	sorbin and SH3 domain containing 2	1.302
ankrd11	ankyrin repeat domain 11	1.312
ELMO1	engulfment and cell motility 1, ced-12 homolog (C. elegans)	1.375

Gene Symbol	**Gene Name**	**Fold Change**
cyp4b1	predicted gene 12839; cytochrome P450, family 4, subfamily b, polypeptide 1	1.398
Fyco1	FYVE and coiled-coil domain containing 1	1.400
Snhg12	hypothetical protein LOC100039864	1.423
1110017F19Rik	RIKEN cDNA 1110017F19 gene	1.450
E130306D19Rik	RIKEN cDNA E130306D19 gene	1.462
SEPT14	septin 14; RIKEN cDNA 1700017B05 gene	1.487
Ubn1	ubinuclein 1	1.494
LIMS1	LIM and senescent cell antigen-like domains 1	1.503
AFG3L2	similar to AFG3(ATPase family gene 3)-like 2 (yeast); AFG3(ATPase family gene 3)-like 2 (yeast)	1.524
CUL5	cullin 5	1.548
Man1a	mannosidase 1, alpha	1.550
Qsox1	quiescin Q6 sulfhydryl oxidase 1	1.562
atp6v1b2	ATPase, H+ transporting, lysosomal V1 subunit B2	1.566
AATF	apoptosis antagonizing transcription factor	1.569
chd7	chromodomain helicase DNA binding protein 7	1.572
rnmt	RNA (guanine-7-) methyltransferase	1.618
ZCCHC4	zinc finger, CCHC domain containing 4	1.641
Sap25	sin3A-binding protein, SAP25	1.642
OSBPL3	oxysterol binding protein-like 3	1.643
LRRK1	leucine-rich repeat kinase 1	1.647
MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	1.658
SRP72	signal recognition particle 72	1.684
F13A1	coagulation factor XIII, A1 subunit	1.697
SSBP2	single-stranded DNA binding protein 2; predicted gene 12470	1.713
BICC1	bicaudal C homolog 1 (Drosophila)	1.908
PDK1	pyruvate dehydrogenase kinase, isoenzyme 1	1.949
SIPA1L1	signal-induced proliferation-associated 1 like 1	2.108
per3	period homolog 3 (Drosophila)	2.108
NAV1	neuron navigator 1	2.180

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Gene Symbol	**Gene Name**	**Fold Change**
TMEM117	transmembrane protein 117	-1.214
timp4	tissue inhibitor of metalloproteinase 4	-1.187
ABLIM1	actin-binding LIM protein 1	-1.145
TTN	titin	-0.949
CLIP1	CAP-GLY domain containing linker protein 1	-0.936
FSD1L	fibronectin type III and SPRY domain containing 1-like	-0.864
Ppip5k1	histidine acid phosphatase domain containing 2A	-0.811
RNF44	ring finger protein 44	-0.806
LAMA4	laminin, alpha 4	-0.805
HS3ST5	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	-0.799
Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	-0.794
IFI44	interferon-induced protein 44	-0.735
Prnd	prion protein dublet	-0.698
MTCP1	mature T-cell proliferation 1	-0.635
tm9sf1	transmembrane 9 superfamily member 1	0.594
TNNT3	troponin T3, skeletal, fast	0.597
ODC1	predicted gene 6742; ornithine decarboxylase, structural 1; similar to Ornithine decarboxylase (ODC); predicted gene 7993; predicted gene 15645; predicted gene 9115; predicted gene 7278	0.601
MARCH8	membrane-associated ring finger (C3HC4) 8	0.607
A130040M12Rik	RIKEN cDNA A130040M12 gene	0.626
MBP	myelin basic protein	0.627
Gm13212	predicted gene 13212	0.628
USP4	ubiquitin specific peptidase 4 (proto-oncogene)	0.632
H2-Bl	histocompatibility 2, blastocyst; predicted gene 8810	0.632
CAR3	carbonic anhydrase 3	0.634
sh3glb1	SH3-domain GRB2-like B1 (endophilin)	0.638
KCNN4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	0.651
CDSN	corneodesmosin; hypothetical protein LOC100043961	0.652
Ubxn10	UBX domain protein 10	0.652
lipA	lysosomal acid lipase A	0.659
KIF1A	kinesin family member 1A	0.668
zfand6	zinc finger, AN1-type domain 6	0.669
PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1); similar to mKIAA1230 protein	0.677
Psg16	pregnancy specific glycoprotein 16	0.682
Rmnd1	required for meiotic nuclear division 1 homolog (S. cerevisiae); predicted gene 5512	0.682
bmp2	bone morphogenetic protein 2	0.684

Gene Symbol	Gene Name	Fold Change
C4a	similar to Complement C4 precursor; complement component 4A (Rodgers blood group); similar to complement C4; complement component 4B (Childo blood group)	0.690
TRIM11	tripartite motif-containing 11	0.690
MORF4L1	predicted gene 6747; RIKEN cDNA A730098P11 gene; mortality factor 4 like 1; predicted gene 8663; predicted gene 4835	0.691
6720457D02Rik	RIKEN cDNA 6720457D02 gene	0.702
galE	galactose-4-epimerase, UDP	0.703
Prf1	perforin 1 (pore forming protein)	0.707
Gm6607	predicted gene 6607	0.710
ARHGEF12	predicted gene 7281; predicted gene 5831; similar to SP140 nuclear body protein (predicted); Rho guanine nucleotide exchange factor (GEF) 12	0.710
H2-K1	histocompatibility 2, K1, K region; similar to H-2K(d) antigen	0.713
Cd59b	CD59b antigen	0.714
Zfp808	predicted gene 3325; predicted gene 7036	0.721
Hspg2	perlecan (heparan sulfate proteoglycan 2)	0.721
Cd1d1	CD1d1 antigen; CD1d2 antigen	0.724
Ecsit	ECSIT homolog (Drosophila)	0.730
2410017P09Rik	RIKEN cDNA 2410017P09 gene	0.735
TRAF5	TNF receptor-associated factor 5	0.737
NIPSNAP1	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	0.749
Gm8113	predicted gene 8113	0.753
SALL2	sal-like 2 (Drosophila)	0.755
EEF1A1	predicted gene 5869; predicted gene 7161; predicted gene 7105; predicted gene 5822; similar to eukaryotic translation elongation factor 1 alpha 1; predicted gene 6192; predicted gene 6392; predicted gene 6767; predicted gene 6170; predicted gene 6548; predicted gene 6789; eukaryotic translation elongation factor 1 alpha 1	0.760
CCBL1	cysteine conjugate-beta lyase 1	0.762
CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	0.765
CFB	complement factor B	0.791
PARL	presenilin associated, rhomboid-like	0.796
Gm13152	predicted gene 13152	0.817
2410018L13Rik	RIKEN cDNA 2410018L13 gene	0.821
MSLN	mesothelin	0.827
tubb3	tubulin, beta 3; tubulin, beta 3, pseudogene 1	0.836
RBP4	retinol binding protein 4, plasma	0.854
CNTN2	contactin 2	0.862

Gene Symbol	Gene Name	Fold Change
Ifi27l2a	interferon, alpha-inducible protein 27 like 2A	0.865
Eif1	predicted gene 5265; similar to suppressor of initiator codon mutations, related sequence 1; predicted gene 4017; predicted gene 6913; predicted gene 7688; predicted gene 6535; predicted gene 6900; predicted gene 5471; predicted gene 7845; predicted gene 5450; predicted gene 6155; predicted gene 7253; predicted gene 10713; similar to translation initiation factor SUI1; predicted gene 6428; similar to Eukaryotic translation initiation factor 1 (eIF1) (Protein translation factor SUI1 homolog); predicted gene, EG434356; similar to isolog of yeast sui1 and rice gos2; putative; eukaryotic translation initiation factor 1	0.868
EG634650	predicted gene, EG634650; guanylate-binding protein 10; RIKEN cDNA 5830443L24 gene	0.871
Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	0.886
2810408B13Rik	RIKEN cDNA 2810408B13 gene	0.906
TLE1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	0.913
PCK1	phosphoenolpyruvate carboxykinase 1, cytosolic	0.916
Fam58b	predicted gene 9731; RIKEN cDNA 1810009O10 gene	0.937
CFH	complement component factor h; similar to complement component factor H	0.947
ANG2	angiogenin, ribonuclease A family, member 2	0.967
Acat3	acetyl-Coenzyme A acetyltransferase 3	0.973
CYP2E1	cytochrome P450, family 2, subfamily e, polypeptide 1	0.986
Gm5069	predicted gene 5069	1.027
Scd1	stearoyl-Coenzyme A desaturase 1	1.027
Hmgb1-rs17	high mobility group box 1, related sequence 17	1.030
ACOT7	acyl-CoA thioesterase 7	1.071
Gm4987	predicted gene 4987	1.075
ATP6	Cytochrome c oxidase subunit 3; ATP synthase subunit a; ATP synthase protein 8	1.096
ATP8	Cytochrome c oxidase subunit 3; ATP synthase subunit a; ATP synthase protein 8	1.096
COX3	Cytochrome c oxidase subunit 3; ATP synthase subunit a; ATP synthase protein 8	1.096

Gene Symbol	**Gene Name**	**Fold Change**
rps2	predicted gene 9168; predicted gene 7561; predicted gene 12091; predicted gene 5921; predicted gene 8841; predicted gene 8842; predicted gene 7143; predicted gene 4968; predicted gene 6576; predicted gene 8520; predicted gene 7520; similar to 40S ribosomal protein S2; ribosomal protein S2 pseudogene; predicted gene 11687; predicted gene 7502; similar to MGC27348 protein; predicted gene 6456; predicted gene 5786; predicted gene 6549; predicted gene 6359; predicted gene 7432; predicted gene 9013; predicted gene 6311; predicted gene 6139; predicted gene 12366; predicted gene 7428; predicted gene 14583; predicted gene 8553; predicted gene 5070; predicted gene 4974; predicted gene 6412; ribosomal protein S2	1.119
MFF	mitochondrial fission factor; hypothetical protein LOC637796	1.129
CYB5R4	cytochrome b5 reductase 4	1.138
Ogdh	oxoglutarate dehydrogenase (lipoamide)	1.146
Mrps5	predicted gene 13328; mitochondrial ribosomal protein S5	1.158
AU040829	expressed sequence AU040829	1.215
h2-aa	histocompatibility 2, class II antigen A, alpha; histocompatibility 2, class II antigen E alpha	1.227
FCGR3	Fc receptor, IgG, low affinity III	1.233
DCUN1D1	similar to RP42; DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	1.238
FGD4	FYVE, RhoGEF and PH domain containing 4	1.247
CIDEC	cell death-inducing DFFA-like effector c	1.271
Alox8	arachidonate 8-lipoxygenase	1.272
Tuba3a	predicted gene 5366; tubulin, alpha 3B; tubulin, alpha 3A	1.277
2610036A22Rik	RIKEN cDNA 2610036A22 gene	1.342
shox2	short stature homeobox 2	1.370
Aldoart1	predicted gene 8659; aldolase 1, A isoform, retrogene 1	1.393
Gm6316	predicted gene 6316	1.397
acp5	acid phosphatase 5, tartrate resistant	1.405
HMMR	hyaluronan mediated motility receptor (RHAMM)	1.440
LOC547349	similar to MHC class I antigen precursor; predicted gene 10499	1.458
ADIPOQ	adiponectin, C1Q and collagen domain containing	1.481
Cd300c	CD300C antigen; hypothetical protein LOC100044158	1.533
Csl	citrate synthase like	1.626
Gm6498	predicted gene 6498	1.731
RETN	resistin	1.736
Apoc1	apolipoprotein C-I	1.902
H2-Q10	histocompatibility 2, Q region locus 10	1.933
SQRDL	sulfide quinone reductase-like (yeast)	2.098

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Gene Symbol	**Gene Name**	**Fold Change**
arntl	aryl hydrocarbon receptor nuclear translocator-like	-2.000
4933401F05Rik	RIKEN cDNA 4933401F05 gene	-1.507
SAMD9L	sterile alpha motif domain containing 9-like	-1.398
DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	-1.374
Prrg1	proline rich Gla (G-carboxyglutamic acid) 1	-1.365
Lmbrd2	LMBR1 domain containing 2	-1.303
cnot1	predicted gene 6158; CCR4-NOT transcription complex, subunit 1	-1.297
tmem45b	transmembrane protein 45b	-1.291
CYP1B1	cytochrome P450, family 1, subfamily b, polypeptide 1	-1.290
ST8SIA6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	-1.264
Fam150b	family with sequence similarity 150, member B	-1.263
SLC39A10	solute carrier family 39 (zinc transporter), member 10	-1.210
TOP2B	topoisomerase (DNA) II beta	-1.191
ermp1	endoplasmic reticulum metallopeptidase 1	-1.187
Rnf144b	ring finger protein 144B	-1.186
Btbd3	BTB (POZ) domain containing 3; predicted gene 7712; similar to BTB/POZ domain containing protein 3	-1.163
Zfp317	zinc finger protein 317	-1.157
MIER1	mesoderm induction early response 1 homolog (Xenopus laevis	-1.157
Aldob	aldolase B, fructose-bisphosphate	-1.157
CDC42BPA	CDC42 binding protein kinase alpha	-1.154
FSD1L	fibronectin type III and SPRY domain containing 1-like	-1.152
4933411K20Rik	RIKEN cDNA 4933411K20 gene	-1.150
NR3C1	nuclear receptor subfamily 3, group C, member 1	-1.149
NCOR1	nuclear receptor co-repressor 1	-1.140
Zfp449	zinc finger protein 449	-1.139
Zfhx2	zinc finger homeobox 2; similar to Zinc finger protein 409	-1.132
EXOC6B	exocyst complex component 6B	-1.124
GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	-1.121
Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.119
RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	-1.119
SLC25A36	solute carrier family 25, member 36	-1.107
FLNB	filamin, beta	-1.102
Tgtp1	T-cell specific GTPase 2; T-cell specific GTPase	-1.096
Cxcl9	chemokine (C-X-C motif) ligand 9	-1.095
prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	-1.085
SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	-1.083
Zfml	zinc finger, matrin-like	-1.082

Gene Symbol	Gene Name	Fold Change
BRWD1	bromodomain and WD repeat domain containing 1	-1.070
Sbf2	SET binding factor 2	-1.051
Necap1	NECAP endocytosis associated 1	-1.048
LNPEP	leucyl/cystinyl aminopeptidase	-1.043
ITCH	itchy, E3 ubiquitin protein ligase	-1.041
SACM1L	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	-1.036
bchE	butyrylcholinesterase	-1.031
DENND4C	DENN/MADD domain containing 4C	-1.023
YES1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	-1.020
D14Abb1e	DNA segment, Chr 14, Abbott 1 expressed	-1.017
FAM179B	family with sequence similarity 179, member B	-1.017
FAM126B	family with sequence similarity 126, member B	-1.015
NBEAL1	neurobeachin like 1	-1.009
agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	-1.007
STON1	stonin 1	-1.006
CDKN1A	cyclin-dependent kinase inhibitor 1A (P21)	-1.000
Cpsf6	cleavage and polyadenylation specific factor 6	-0.994
Lifr	leukemia inhibitory factor receptor	-0.992
DNAJC28	DnaJ (Hsp40) homolog, subfamily C, member 28	-0.988
Thap2	THAP domain containing, apoptosis associated protein 2	-0.984
Nnat	neuronatin	-0.984
FPGT	fucose-1-phosphate guanylyltransferase	-0.981
IKZF5	IKAROS family zinc finger 5	-0.979
Pknox1	Pbx/knotted 1 homeobox	-0.974
CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1; carcinoembryonic antigen-related cell adhesion molecule 2	-0.974
NUDT12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	-0.972
MEX3C	mex3 homolog C (C. elegans)	-0.971
lats1	large tumor suppressor	-0.969
YY2	membrane-bound transcription factor peptidase, site 2; similar to zinc finger, X-linked, duplicated B; Yy2 transcription factor	-0.959
IFI44	interferon-induced protein 44	-0.958
ARL5B	ADP-ribosylation factor-like 5B	-0.958
JMJD1C	jumonji domain containing 1C	-0.951
Zfp568	zinc finger protein 568	-0.951
lpgat1	lysophosphatidylglycerol acyltransferase 1	-0.951
USP34	ubiquitin specific peptidase 34	-0.946
IRS1	insulin receptor substrate 1	-0.944
Zfp800	zinc finger protein 800	-0.937
Vprbp	Vpr (HIV-1) binding protein	-0.931
PCDH12	protocadherin 12	-0.923
Ankrd13c	ankyrin repeat domain 13c	-0.922

Gene Symbol	Gene Name	Fold Change
abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	-0.919
9030420J04Rik	RIKEN cDNA 9030420J04 gene	-0.919
1200011I18Rik	RIKEN cDNA 1200011I18 gene	-0.919
DCUN1D2	DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)	-0.918
TMC7	transmembrane channel-like gene family 7; similar to Tmc7 protein	-0.918
NPAS2	neuronal PAS domain protein 2	-0.916
SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	-0.916
1110037F02Rik	RIKEN cDNA 1110037F02 gene	-0.914
Kitl	kit ligand	-0.913
DPY19L4	dpy-19-like 4 (C. elegans)	-0.911
NFYA	nuclear transcription factor-Y alpha	-0.911
B630005N14Rik	RIKEN cDNA B630005N14 gene	-0.911
ELL2	elongation factor RNA polymerase II 2	-0.910
4930523C07Rik	RIKEN cDNA 4930523C07 gene	-0.910
ARHGAP5	Rho GTPase activating protein 5	-0.910
ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	-0.909
Gm14446	predicted gene 14446	-0.908
2610305D13Rik	RIKEN cDNA 2610305D13 gene	-0.907
Skil	SKI-like	-0.901
smek1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	-0.899
thrB	thyroid hormone receptor beta	-0.898
RGS4	regulator of G-protein signaling 4	-0.897
PDIK1L	PDLIM1 interacting kinase 1 like	-0.892
Zc3h11a	zinc finger CCCH type containing 11A	-0.892
CD83	CD83 antigen	-0.890
CYLD	cylindromatosis (turban tumor syndrome)	-0.890
1700081L11Rik	hypothetical protein LOC100043982; RIKEN cDNA 1700081L11 gene	-0.888
ABLIM1	actin-binding LIM protein 1	-0.885
Tsga10	testis specific 10	-0.883
lysmd3	LysM, putative peptidoglycan-binding, domain containing 3	-0.881
Slfn5	schlafen 5; hypothetical protein LOC100047131	-0.881
ZMYM1	zinc finger, MYM domain containing 1	-0.879
Sox7	SRY-box containing gene 7	-0.879
PTPN4	protein tyrosine phosphatase, non-receptor type 4	-0.879
rgs3	regulator of G-protein signaling 3	-0.878
RBM26	RNA binding motif protein 26	-0.878
Med14	mediator complex subunit 14	-0.877
suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	-0.874
VPS13A	vacuolar protein sorting 13A (yeast)	-0.873
Klhdc1	kelch domain containing 1	-0.870

Gene Symbol	Gene Name	Fold Change
Zfp420	zinc finger protein 420	-0.869
eml4	echinoderm microtubule associated protein like 4	-0.868
DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1c	-0.864
AGTPBP1	ATP/GTP binding protein 1	-0.864
CLOCK	circadian locomoter output cycles kaput	-0.863
Enpp4	ectonucleotide pyrophosphatase/phosphodiesterase 4	-0.863
ZBTB1	similar to Zinc finger and BTB domain containing 1; zinc finger and BTB domain containing 1	-0.862
TMX3	thioredoxin-related transmembrane protein 3	-0.861
PHKA1	phosphorylase kinase alpha 1	-0.859
cstf2	cleavage stimulation factor, 3' pre-RNA subunit 2	-0.858
MME	membrane metallo endopeptidase	-0.857
ARHGAP29	Rho GTPase activating protein 29	-0.856
camsap1l1	calmodulin regulated spectrin-associated protein 1-like 1	-0.856
Abca6	ATP-binding cassette, sub-family A (ABC1), member 6	-0.855
3110057O12Rik	RIKEN cDNA 3110057O12 gene; predicted gene 2011	-0.854
Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	-0.853
ZZZ3	zinc finger, ZZ domain containing 3; predicted gene 8261	-0.852
ITGB6	integrin beta 6	-0.851
NUP160	nucleoporin 160	-0.851
BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	-0.849
ubr7	ubiquitin protein ligase E3 component n-recognin 7 (putative)	-0.847
Trp53inp1	transformation related protein 53 inducible nuclear protein 1	-0.844
6530418L21Rik	RIKEN cDNA 6530418L21 gene	-0.840
DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27	-0.838
Ccdc141	RIKEN cDNA 2610301F02 gene	-0.837
2310014F06Rik	RIKEN cDNA 2310014F06 gene	-0.836
TBC1D14	similar to mKIAA1322 protein; TBC1 domain family, member 14	-0.836
4932441K18Rik	predicted gene 8258; similar to factor inhibiting activating transcription factor 4 (ATF4)-mediated transcription; RIKEN cDNA 4932441K18 gene	-0.833
NOL9	nucleolar protein 9	-0.833
SCGB1C1	secretoglobin, family 1C, member 1	-0.833
PHF6	PHD finger protein 6	-0.832
MFSD8	major facilitator superfamily domain containing 8	-0.829
FNDC3A	fibronectin type III domain containing 3A	-0.828
TLR4	toll-like receptor 4	-0.828
GTF2H1	general transcription factor II H, polypeptide 1; similar to 62 kDa subunit of TFIIH	-0.827
uckl1	uridine-cytidine kinase 1-like 1	-0.827

Gene Symbol	Gene Name	Fold Change
RASA2	RAS p21 protein activator 2	-0.825
zbtb11	zinc finger and BTB domain containing 11	-0.823
SLC31A2	solute carrier family 31, member 2	-0.820
SASH1	SAM and SH3 domain containing 1; predicted gene 2082	-0.820
Atf2	activating transcription factor 2; similar to Cyclic AMP-dependent transcription factor ATF-2 (Activating transcription factor 2) (cAMP response element-binding protein CRE-BP1) (MXBP protein)	-0.816
BEND7	BEN domain containing 7	-0.809
MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	-0.804
slc39a9	solute carrier family 39 (zinc transporter), member 9	-0.800
clpB	ClpB caseinolytic peptidase B homolog (E. coli)	-0.799
MON2	MON2 homolog (yeast)	-0.797
Zfp191	zinc finger protein 191	-0.796
FCHO2	FCH domain only 2	-0.794
Pla2g16	phospholipase A2, group XVI	-0.792
PPP1R15B	protein phosphatase 1, regulatory (inhibitor) subunit 15b	-0.791
Olfr558	olfactory receptor 558	-0.787
ZMAT1	zinc finger, matrin type 1	-0.786
SMURF2	SMAD specific E3 ubiquitin protein ligase 2; similar to SMAD specific E3 ubiquitin protein ligase 2	-0.784
Fam116a	family with sequence similarity 116, member A	-0.783
RABEP1	rabaptin, RAB GTPase binding effector protein 1	-0.782
DLG1	discs, large homolog 1 (Drosophila); similar to Discs, large homolog 1 (Drosophila)	-0.782
ralgapa1	GTPase activating RANGAP domain-like 1	-0.782
prps2	phosphoribosyl pyrophosphate synthetase 2	-0.782
ATP7A	ATPase, Cu++ transporting, alpha polypeptide	-0.780
SLC19A2	solute carrier family 19 (thiamine transporter), member 2	-0.780
Hist2h2aa1	histone cluster 2, H3b; histone cluster 1, H3f; histone cluster 1, H3e; histone cluster 2, H3c1; histone cluster 1, H3d; histone cluster 1, H3c; histone cluster 1, H3b; histone cluster 2, H3c2; histone cluster 2, H2aa1; histone cluster 2, H2aa2	-0.779
DGKH	diacylglycerol kinase, eta	-0.778
Tial1	Tia1 cytotoxic granule-associated RNA binding protein-like 1	-0.778
DPYD	dihydropyrimidine dehydrogenase	-0.778
Crem	cAMP responsive element modulator	-0.778
CEPT1	choline/ethanolaminephosphotransferase 1	-0.778
rnf26	hypothetical protein LOC100048200; ring finger protein 26; predicted gene 9008	-0.776
fgf13	fibroblast growth factor 13	-0.776
D930016D06Rik	RIKEN cDNA D930016D06 gene	-0.775
EEA1	early endosome antigen 1	-0.774

Gene Symbol	Gene Name	Fold Change
AK129341	similar to CDNA sequence AK129341; cDNA sequence AK129341	-0.773
NF1	neurofibromatosis 1	-0.773
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	-0.773
pex1	peroxisomal biogenesis factor 1	-0.772
Atp8b1	ATPase, class I, type 8B, member 1	-0.770
Olfr1036	olfactory receptor 1036	-0.770
ZDHHC17	zinc finger, DHHC domain containing 17	-0.770
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	-0.769
6720456H20Rik	RIKEN cDNA 6720456H20 gene	-0.768
MITF	microphthalmia-associated transcription factor	-0.764
EVI5	ecotropic viral integration site 5	-0.763
CCDC109A	coiled-coil domain containing 109A	-0.762
GTF3C4	general transcription factor IIIC, polypeptide 4	-0.762
mudeng	MU-2/AP1M2 domain containing, death-inducing	-0.762
tmem33	transmembrane protein 33	-0.762
sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated); similar to PTB-associated splicing factor	-0.760
Twsg1	twisted gastrulation homolog 1 (Drosophila)	-0.760
Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)	-0.759
H13	histocompatibility 13	-0.756
Gpld1	glycosylphosphatidylinositol specific phospholipase D1	-0.755
Acot1	acyl-CoA thioesterase 1	-0.755
Ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha; RIKEN cDNA 3222402P14 gene	-0.753
QTRTD1	queuine tRNA-ribosyltransferase domain containing 1	-0.753
C430048L16Rik	RIKEN cDNA C430048L16 gene	-0.751
ZC3H12C	zinc finger CCCH type containing 12C	-0.750
SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12	-0.750
HSPH1	heat shock 105kDa/110kDa protein 1	-0.749
IPO11	importin 11	-0.747
NCK1	non-catalytic region of tyrosine kinase adaptor protein 1	-0.747
KDM3A	lysine (K)-specific demethylase 3A	-0.746
ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	-0.741
MAP3K8	mitogen-activated protein kinase kinase kinase 8	-0.739
SHPRH	SNF2 histone linker PHD RING helicase	-0.738

Gene Symbol	**Gene Name**	**Fold Change**
RPS27A	predicted gene 5928; predicted gene 12617; predicted gene 4802; similar to ribosomal protein S27a; predicted gene 13215; predicted gene 6111; predicted gene 7808; predicted gene 6014; predicted gene 8317; ubiquitin C; ubiquitin B; similar to fusion protein: ubiquitin (bases 43_513); ribosomal protein S27a (bases 217_532); similar to ubiquitin B; predicted gene 8649; ribosomal protein S27A; predicted gene 11517; predicted gene 11808; predicted gene 8430; RIKEN cDNA 2810422J05 gene; similar to Ubc protein; predicted gene 13815; ubiquitin A-52 residue ribosomal protein fusion product 1; predicted gene 8797; predicted gene 1821; predicted gene 11759; predicted gene 5239; predicted gene 6438	-0.737
RSBN1L	round spermatid basic protein 1-like	-0.736
Golga1	golgi autoantigen, golgin subfamily a, 1	-0.735
NUP98	nucleoporin 98	-0.735
ASB15	ankyrin repeat and SOCS box-containing 15	-0.734
MTPAP	mitochondrial poly(A) polymerase	-0.733
SLC20A1	solute carrier family 20, member 1	-0.732
RB1CC1	RB1-inducible coiled-coil 1	-0.732
FMR1	fragile X mental retardation syndrome 1 homolog	-0.731
NAA30	N-acetyltransferase 12	-0.731
BMI1	Bmi1 polycomb ring finger oncogene	-0.729
ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	-0.728
pkn2	protein kinase N2	-0.728
Ctage5	CTAGE family, member 5	-0.727
SFMBT1	Scm-like with four mbt domains 1	-0.727
AFF4	AF4/FMR2 family, member 4	-0.726
Taf5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-0.725
pstpip2	proline-serine-threonine phosphatase-interacting protein 2	-0.724
Bcl3	B-cell leukemia/lymphoma 3	-0.724
ARID4B	AT rich interactive domain 4B (RBP1-like)	-0.723
Papola	poly (A) polymerase alpha	-0.722
etnk1	ethanolamine kinase 1	-0.722
KLHL9	kelch-like 9 (Drosophila)	-0.718
gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	-0.717
Erbb2ip	Erbb2 interacting protein	-0.716
PDS5A	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	-0.715
Zfp354a	zinc finger protein 354A	-0.714
senp8	SUMO/sentrin specific peptidase 8	-0.710
2010321M09Rik	RIKEN cDNA 2010321M09 gene	-0.709
gtf2h2	general transcription factor II H, polypeptide 2	-0.705
TANK	TRAF family member-associated Nf-kappa B activator	-0.705

Gene Symbol	Gene Name	Fold Change
MYO1D	myosin ID	-0.705
1810074P20Rik	RIKEN cDNA 1810074P20 gene	-0.704
Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	-0.703
Gimap9	GTPase, IMAP family member 9	-0.702
dhdh	dihydrodiol dehydrogenase (dimeric)	-0.701
RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	-0.700
PRDM10	PR domain containing 10	-0.700
CUL5	cullin 5	-0.700
IFIH1	interferon induced with helicase C domain 1	-0.700
Foxk2	forkhead box K2	-0.699
BC016423	cDNA sequence BC016423	-0.696
DNM1L	dynamin 1-like	-0.695
5730601F06Rik	RIKEN cDNA 5730601F06 gene	-0.695
TNNI3K	TNNI3 interacting kinase	-0.694
ELAC1	elaC homolog 1 (E. coli)	-0.693
CDKN2AIP	CDKN2A interacting protein	-0.692
Zfp128	zinc finger protein 128	-0.691
AV039307	expressed sequence AV039307	-0.690
Trpc3	transient receptor potential cation channel, subfamily C, member 3	-0.689
FAM89A	hypothetical protein LOC100047808; family with sequence similarity 89, member A; similar to mammary tumor virus receptor 2 isoform-like	-0.689
Pcf11	cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	-0.689
TXNDC11	thioredoxin domain containing 11	-0.687
JMY	junction-mediating and regulatory protein	-0.687
Mospd2	motile sperm domain containing 2	-0.687
INPP4B	inositol polyphosphate-4-phosphatase, type II	-0.684
SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	-0.683
SYNJ1	synaptojanin 1	-0.683
Zfp386	zinc finger protein 386 (Kruppel-like)	-0.683
prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-0.682
COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	-0.682
Sptlc2	serine palmitoyltransferase, long chain base subunit 2	-0.682
WARS2	tryptophanyl tRNA synthetase 2 (mitochondrial)	-0.681
ACTR6	ARP6 actin-related protein 6 homolog (yeast)	-0.681
ST7L	suppression of tumorigenicity 7-like	-0.681
nsun6	NOL1/NOP2/Sun domain family member 6	-0.675
Ube2ql1	RIKEN cDNA 3110006E14 gene	-0.675
HAUS2	HAUS augmin-like complex, subunit 2	-0.673
CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	-0.672

Gene Symbol	Gene Name	Fold Change
ZFP62	zinc finger protein 62	-0.671
1110020G09Rik	RIKEN cDNA 1110020G09 gene	-0.671
CCNG2	cyclin G2	-0.669
BC049349	cDNA sequence BC049349	-0.668
SIAE	sialic acid acetylesterase	-0.668
Zfp799	zinc finger protein 799	-0.665
Fam108b	family with sequence similarity 108, member B	-0.665
TTC9C	tetratricopeptide repeat domain 9C	-0.664
IMPAD1	inositol monophosphatase domain containing 1	-0.663
ASAH2	N-acylsphingosine amidohydrolase 2	-0.663
FUBP1	far upstream element (FUSE) binding protein 1	-0.662
NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	-0.661
LANCL2	LanC (bacterial lantibiotic synthetase component C)-like 2	-0.661
CPEB4	cytoplasmic polyadenylation element binding protein 4	-0.659
CHD9	chromodomain helicase DNA binding protein 9	-0.659
AI607873	expressed sequence AI607873	-0.659
COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	-0.658
smug1	single-strand selective monofunctional uracil DNA glycosylase	-0.658
FMNL2	formin-like 2	-0.657
SLC30A9	solute carrier family 30 (zinc transporter), member 9	-0.655
crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	-0.653
tbc1d23	TBC1 domain family, member 23	-0.653
PYGO2	pygopus 2	-0.651
KDM1B	amine oxidase, flavin containing 1	-0.651
TOM1L1	target of myb1-like 1 (chicken)	-0.650
Phf10	PHD finger protein 10	-0.649
ATP5G1	predicted gene 12337; predicted gene 10039; predicted gene 4479; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	-0.648
Gm12337	predicted gene 12337; predicted gene 10039; predicted gene 4479; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	-0.648
Ncoa2	nuclear receptor coactivator 2	-0.646
Snx13	sorting nexin 13	-0.646
ALG10B	asparagine-linked glycosylation 10 homolog B (yeast, alpha-1,2-glucosyltransferase)	-0.646
E430024P14Rik	RIKEN cDNA E430024P14 gene	-0.645
MTMR10	myotubularin related protein 10	-0.644
Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	-0.644
CNOT4	CCR4-NOT transcription complex, subunit 4	-0.644
AFF1	AF4/FMR2 family, member 1	-0.644
Zfp644	zinc finger protein 644	-0.644

Gene Symbol	Gene Name	Fold Change
Shq1	SHQ1 homolog (S. cerevisiae)	-0.643
UNC119B	unc-119 homolog B (C. elegans)	-0.643
ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	-0.642
CNOT2	CCR4-NOT transcription complex, subunit 2	-0.642
1110018J18Rik	hypothetical protein LOC100044674; RIKEN cDNA 1110018J18 gene	-0.641
vps37a	vacuolar protein sorting 37A (yeast); similar to Vps37a protein	-0.640
B3GALNT2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2	-0.639
ociad1	OCIA domain containing 1	-0.639
Exoc2	exocyst complex component 2	-0.638
MAPK1	mitogen-activated protein kinase 1	-0.637
Cep57	centrosomal protein 57	-0.636
Zfp281	zinc finger protein 281	-0.636
Ccdc137	coiled-coil domain containing 137	-0.635
Pde1c	phosphodiesterase 1C	-0.634
INTU	inturned planar cell polarity effector homolog (Drosophila)	-0.634
KIT	kit oncogene	-0.634
Zfp715	zinc finger protein 715	-0.633
Kcnip2	Kv channel-interacting protein 2	-0.632
KPNA1	karyopherin (importin) alpha 1	-0.632
PDGFD	platelet-derived growth factor, D polypeptide	-0.632
1110028C15Rik	RIKEN cDNA 1110028C15 gene	-0.631
TSC22D2	TSC22 domain family, member 2	-0.631
BPTF	bromodomain PHD finger transcription factor	-0.631
AFTPH	aftiphilin	-0.631
AMBRA1	autophagy/beclin 1 regulator 1	-0.630
Eif3e	eukaryotic translation initiation factor 3, subunit E	-0.630
Slc29a1	solute carrier family 29 (nucleoside transporters), member 1	-0.628
TRMT61B	tRNA methyltransferase 61 homolog B (S. cerevisiae)	-0.625
sirt1	sirtuin 1 (silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	-0.625
KDM3B	KDM3B lysine (K)-specific demethylase 3B	-0.624
NUBPL	predicted gene 7514; nucleotide binding protein-like	-0.624
CWF19L2	hypothetical protein LOC100044213; CWF19-like 2, cell cycle control (S. pombe)	-0.623
Gpr116	G protein-coupled receptor 116	-0.623
Nipa2	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	-0.622
LNX2	ligand of numb-protein X 2	-0.621
Larp4	La ribonucleoprotein domain family, member 4; predicted gene 14373; predicted gene 8177	-0.620
SOX18	SRY-box containing gene 18	-0.619
Tmod4	tropomodulin 4	-0.618

Gene Symbol	Gene Name	Fold Change
tpp2	tripeptidyl peptidase II	-0.618
MTFR1	mitochondrial fission regulator 1	-0.616
WDR13	WD repeat domain 13	-0.615
TMTC1	transmembrane and tetratricopeptide repeat containing 1	-0.615
tmed7	transmembrane emp24 protein transport domain containing 7	-0.614
Ulk2	Unc-51 like kinase 2 (C. elegans)	-0.612
4930486L24Rik	RIKEN cDNA 4930486L24 gene	-0.612
Spnb1	spectrin beta 1	-0.611
IMMT	inner membrane protein, mitochondrial	-0.611
MTMR1	myotubularin related protein 1	-0.610
PTPRG	protein tyrosine phosphatase, receptor type, G; similar to protein tyrosine phosphatase, receptor type, G	-0.610
ISOC1	isochorismatase domain containing 1	-0.610
Tmed5	transmembrane emp24 protein transport domain containing 5; similar to Transmembrane emp24 protein transport domain containing 5	-0.610
Gm13111	predicted gene 13111	-0.609
NCOA6	nuclear receptor coactivator 6	-0.609
CTNNA3	catenin (cadherin associated protein), alpha 3	-0.608
ERAP1	endoplasmic reticulum aminopeptidase 1	-0.608
Rnf170	ring finger protein 170	-0.608
DPEP1	dipeptidase 1 (renal)	-0.608
Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	-0.608
HEY2	hairy/enhancer-of-split related with YRPW motif 2	-0.605
Plxna2	plexin A2	-0.604
1110018G07Rik	RIKEN cDNA 1110018G07 gene	-0.604
CCDC25	coiled-coil domain containing 25	-0.604
TUBGCP5	tubulin, gamma complex associated protein 5	-0.604
SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	-0.603
Tbk1	TANK-binding kinase 1	-0.602
MLH3	mutL homolog 3 (E coli)	-0.602
irak3	interleukin-1 receptor-associated kinase 3	-0.602
ARMC1	armadillo repeat containing 1	-0.602
RNF214	ring finger protein 214	-0.601
bmpr2	bone morphogenic protein receptor, type II (serine/threonine kinase)	-0.601
TIAM2	T-cell lymphoma invasion and metastasis 2	-0.601
Cdk6	cyclin-dependent kinase 6	-0.599
ORC4L	origin recognition complex, subunit 4-like (S. cerevisiae)	-0.599
1190005F20Rik	RIKEN cDNA 1190005F20 gene	-0.599
AP3M1	adaptor-related protein complex 3, mu 1 subunit; similar to Adapter-related protein complex 3 mu 1 subunit (Mu-adaptin 3A) (AP-3 adapter complex mu3A subunit)	-0.599

Gene Symbol	Gene Name	Fold Change
A130022J15Rik	RIKEN cDNA A130022J15 gene	-0.599
Serpinb6b	serine (or cysteine) peptidase inhibitor, clade B, member 6b	-0.597
PAQR3	progestin and adipoQ receptor family member III	-0.597
HUS1	Hus1 homolog (S. pombe)	-0.596
2410042D21Rik	RIKEN cDNA 2410042D21 gene	-0.595
Zfp131	zinc finger protein 131; similar to putative transcription factor ZNF131	-0.595
UBOX5	U box domain containing 5	-0.594
taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-0.594
0610007P08Rik	RIKEN cDNA 0610007P08 gene	-0.593
NT5E	5' nucleotidase, ecto	-0.593
atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	-0.593
UBA6	ubiquitin-like modifier activating enzyme 6	-0.593
DENND5B	DENN/MADD domain containing 5B	-0.591
SH3TC2	SH3 domain and tetratricopeptide repeats 2	-0.591
TRIM34	similar to tripartite motif protein TRIM34 alpha; tripartite motif-containing 34; similar to Tripartite motif protein 34	-0.590
9930021J03Rik	RIKEN cDNA 9930021J03 gene	-0.590
Rrm2b	ribonucleotide reductase M2 B (TP53 inducible); predicted gene 8616; hypothetical protein LOC674236	-0.589
TMEM168	transmembrane protein 168	-0.587
NUP35	predicted gene 4353; nucleoporin 35	-0.587
Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	-0.586
CHD1	chromodomain helicase DNA binding protein 1	-0.586
Trpc1	transient receptor potential cation channel, subfamily C, member 1	-0.586
Lsp1	lymphocyte specific 1	0.588
ZDHHC4	zinc finger, DHHC domain containing 4	0.593
OLFML3	olfactomedin-like 3	0.598
LOC100134990	selenoprotein K pseudogene	0.599
FAM189B	RIKEN cDNA 1110013L07 gene	0.601
EXTL1	exostoses (multiple)-like 1	0.605
SUV420H2	suppressor of variegation 4-20 homolog 2 (Drosophila)	0.608
bolA2	bolA-like 2 (E. coli)	0.609
EXOC3L	exocyst complex component 3-like	0.609
pemt	phosphatidylethanolamine N-methyltransferase	0.614
Myg1	melanocyte proliferating gene 1	0.615
Naglu	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	0.616
SLC39A13	solute carrier family 39 (metal ion transporter), member 13	0.617
LTC4S	leukotriene C4 synthase	0.619
IFFO1	intermediate filament family orphan 1	0.619

Gene Symbol	Gene Name	Fold Change
FAM18A	family with sequence similarity 18, member A	0.619
2610002J02Rik	RIKEN cDNA 2610002J02 gene	0.620
RHOD	ras homolog gene family, member D	0.620
TMEM97	transmembrane protein 97; predicted gene 5809	0.624
DNM1	dynamin 1	0.625
Susd2	sushi domain containing 2	0.626
rpap1	RNA polymerase II associated protein 1	0.627
PLA2G15	phospholipase A2, group XV	0.627
1010001B22Rik	RIKEN cDNA 1010001B22 gene	0.632
Gm5069	predicted gene 5069	0.635
CTSZ	cathepsin Z	0.639
Flt3l	FMS-like tyrosine kinase 3 ligand	0.639
pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	0.643
2310057J16Rik	RIKEN cDNA 2310057J16 gene	0.644
6720463M24Rik	RIKEN cDNA 6720463M24 gene	0.644
FOXO3	forkhead box O3	0.654
Tspan17	tetraspanin 17	0.658
Hjurp	RIKEN cDNA 6430706D22 gene; similar to RIKEN cDNA 6430706D22 gene; RIKEN cDNA A730008H23 gene	0.660
map2k6	mitogen-activated protein kinase kinase 6	0.661
2410018L13Rik	RIKEN cDNA 2410018L13 gene	0.661
1810024B03Rik	RIKEN cDNA 1810024B03 gene	0.662
GLI1	GLI-Kruppel family member GLI1	0.667
STXBP2	syntaxin binding protein 2	0.671
SH3BP1	similar to SH3-domain binding protein 1; SH3-domain binding protein 1; similar to SH3 domain-binding protein 1 (3BP-1)	0.672
MYL6B	myosin, light polypeptide 6B	0.675
lipA	lysosomal acid lipase A	0.678
nfix	nuclear factor I/X	0.680
Mfsd7a	major facilitator superfamily domain containing 7A	0.680
Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	0.681
MRGPRE	MAS-related GPR, member E	0.682
capG	capping protein (actin filament), gelsolin-like	0.686
Zfp688	zinc finger protein 688	0.687
SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	0.690
Ccl21a	chemokine (C-C motif) ligand 21A; predicted gene 1987	0.692
ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand; predicted gene 8539	0.695
Pak6	p21 protein (Cdc42/Rac)-activated kinase 6	0.697
Il1rl2	interleukin 1 receptor-like 2	0.700
PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	0.706
1110038F14Rik	RIKEN cDNA 1110038F14 gene	0.706

Gene Symbol	Gene Name	Fold Change
2610036A22Rik	RIKEN cDNA 2610036A22 gene	0.707
NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	0.709
FIGF	c-fos induced growth factor	0.711
Scd2	stearoyl-Coenzyme A desaturase 2	0.714
Gm4987	predicted gene 4987	0.714
TMEM219	transmembrane protein 219	0.719
FAM109B	family with sequence similarity 109, member B	0.719
galT	galactose-1-phosphate uridyl transferase	0.725
PARL	presenilin associated, rhomboid-like	0.732
dbp	D site albumin promoter binding protein	0.737
Fam58b	predicted gene 9731; RIKEN cDNA 1810009O10 gene	0.738
1700120C14Rik	RIKEN cDNA 1700120C14 gene	0.742
Gm129	predicted gene 129	0.743
PLD4	phospholipase D family, member 4	0.745
RCOR2	REST corepressor 2	0.750
AI413582	expressed sequence AI413582; hypothetical protein LOC100044974	0.752
Fam46b	family with sequence similarity 46, member B	0.753
Hspg2	perlecan (heparan sulfate proteoglycan 2)	0.754
Cpt1c	carnitine palmitoyltransferase 1c	0.759
Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	0.765
C1RL	complement component 1, r subcomponent-like	0.769
SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	0.769
haus4	HAUS augmin-like complex, subunit 4	0.772
1110038B12Rik	RIKEN cDNA 1110038B12 gene	0.774
CEND1	cell cycle exit and neuronal differentiation 1	0.780
MFF	mitochondrial fission factor; hypothetical protein LOC637796	0.783
Mtap6	microtubule-associated protein 6	0.784
Ifi27l2a	interferon, alpha-inducible protein 27 like 2A	0.787
PNPLA2	patatin-like phospholipase domain containing 2	0.790
LAPTM5	lysosomal-associated protein transmembrane 5	0.793
camk1	calcium/calmodulin-dependent protein kinase I	0.797
phf19	PHD finger protein 19	0.803
TMPRSS13	transmembrane protease, serine 13	0.813
Ppfia4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	0.814
Rgs10	regulator of G-protein signalling 10	0.819
tspan4	tetraspanin 4	0.822
TRIM11	tripartite motif-containing 11	0.825
CEP164	centrosomal protein 164	0.827
Per1	period homolog 1 (Drosophila)	0.832
Ccdc136	coiled-coil domain containing 136	0.834

Gene Symbol	Gene Name	Fold Change
TRAF5	TNF receptor-associated factor 5	0.834
ANG2	angiogenin, ribonuclease A family, member 2	0.839
Wdr62	similar to WD repeat domain 62; WD repeat domain 62	0.841
Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.845
CD37	CD37 antigen	0.849
DPF3	D4, zinc and double PHD fingers, family 3	0.850
Hmgb1-rs17	high mobility group box 1, related sequence 17	0.859
calml4	calmodulin-like 4	0.859
Tuba3a	predicted gene 5366; tubulin, alpha 3B; tubulin, alpha 3A	0.859
MAMSTR	MEF2 activating motif and SAP domain containing transcriptional regulator	0.866
Pacsin1	protein kinase C and casein kinase substrate in neurons 1	0.879
SALL2	sal-like 2 (Drosophila)	0.883
Atxn7l1	ataxin 7-like 1	0.885
F10	coagulation factor X	0.899
per3	period homolog 3 (Drosophila)	0.903
Cd247	CD247 antigen	0.915
AU040829	expressed sequence AU040829	0.918
Cyp4f16	cytochrome P450, family 4, subfamily f, polypeptide 16	0.934
H2-Q10	histocompatibility 2, Q region locus 10	0.937
LOC547349	similar to MHC class I antigen precursor; predicted gene 10499	0.940
Aldoart1	predicted gene 8659; aldolase 1, A isoform, retrogene 1	0.942
fbxl19	F-box and leucine-rich repeat protein 19	0.947
2300009N04Rik	RIKEN cDNA 2300009N04 gene	0.975
Gm6316	predicted gene 6316	0.976
2200002D01Rik	RIKEN cDNA 2200002D01 gene	0.982
FCGR3	Fc receptor, IgG, low affinity III	0.988
5930430L01Rik	RIKEN cDNA 5930430L01 gene	0.989
Dnase2a	deoxyribonuclease II alpha	1.007
Csl	citrate synthase like	1.011
Gm6498	predicted gene 6498	1.030
CYB5R4	cytochrome b5 reductase 4	1.032
EMID1	EMI domain containing 1	1.080
PRRT2	proline-rich transmembrane protein 2	1.092
FGD4	FYVE, RhoGEF and PH domain containing 4	1.096
SV2A	synaptic vesicle glycoprotein 2 a	1.139
Iqgap3	IQ motif containing GTPase activating protein 3	1.147
AGER	advanced glycosylation end product-specific receptor	1.185
Aldh3b1	aldehyde dehydrogenase 3 family, member B1	1.232
HMMR	hyaluronan mediated motility receptor (RHAMM)	1.386
Ptprs	protein tyrosine phosphatase, receptor type, S	1.464
Cd300c	CD300C antigen; hypothetical protein LOC100044158	1.554

Supplemental Table 3: Differentially Expressed Genes Between Treatment Groups

Section A - 667 genes		
Gene Symbol	**Gene Name**	**10d Fold Change**
Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5	-2.577
GPR137C	G protein-coupled receptor 137C	-2.515
Gnl3l	guanine nucleotide binding protein-like 3 (nucleolar)-like	-2.430
ABCC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	-2.416
casq1	calsequestrin 1	-2.396
Ibtk	inhibitor of Bruton agammaglobulinemia tyrosine kinase	-2.268
ECE1	endothelin converting enzyme 1	-2.250
Mboat2	membrane bound O-acyltransferase domain containing 2	-2.218
SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	-2.171
Prpf8	pre-mRNA processing factor 8	-2.163
Ltbp1	latent transforming growth factor beta binding protein 1	-2.120
SLC38A1	solute carrier family 38, member 1	-2.116
MMRN1	multimerin 1	-2.097
RNF123	ring finger protein 123	-2.050
RHOU	ras homolog gene family, member U	-2.024
kbtbd5	kelch repeat and BTB (POZ) domain containing 5	-2.021
PGM5	phosphoglucomutase 5	-1.993
CAMSAP1	calmodulin regulated spectrin-associated protein 1; similar to calmodulin regulated spectrin-associated protein 1	-1.945
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-1.943
hyou1	hypoxia up-regulated 1	-1.936
STAT5A	signal transducer and activator of transcription 5A	-1.935
NLRX1	NLR family member X1	-1.933
OSBP2	oxysterol binding protein 2; similar to oxysterol binding protein 2	-1.923
scaper	S phase cyclin A-associated protein in the ER	-1.919
FGL2	fibrinogen-like protein 2	-1.893
pdgfra	platelet derived growth factor receptor, alpha polypeptide	-1.891
esrrb	estrogen related receptor, beta	-1.890
slc35e3	solute carrier family 35, member E3; predicted gene 7341	-1.862
DSG2	desmoglein 2; similar to Dsg2 protein	-1.861
rdx	radixin	-1.860
KANK1	KN motif and ankyrin repeat domains 1	-1.860
SLTM	SAFB-like, transcription modulator	-1.834
lpin1	lipin 1	-1.822
IGDCC4	immunoglobulin superfamily, DCC subclass, member 4	-1.820
ABI3BP	ABI gene family, member 3 (NESH) binding protein	-1.819
HEATR5B	HEAT repeat containing 5B; similar to CG2747-PB, isoform B	-1.805
PDZRN3	PDZ domain containing RING finger 3	-1.800
CHRM2	cholinergic receptor, muscarinic 2, cardiac	-1.792

Gene Symbol	Gene Name	10d Fold Change
ITSN1	intersectin 1 (SH3 domain protein 1A)	-1.785
TMTC3	transmembrane and tetratricopeptide repeat containing 3	-1.767
Eps8	epidermal growth factor receptor pathway substrate 8	-1.729
Mfsd4	major facilitator superfamily domain containing 4	-1.709
COL6A6	RIKEN cDNA E330026B02 gene	-1.706
Itgav	integrin alpha V	-1.701
FRMD6	predicted gene 5780; FERM domain containing 6	-1.670
Usp7	ubiquitin specific peptidase 7	-1.667
dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	-1.664
RPS6KC1	ribosomal protein S6 kinase polypeptide 1	-1.658
SF3B2	splicing factor 3b, subunit 2	-1.655
sspN	sarcospan	-1.651
usp48	ubiquitin specific peptidase 48	-1.626
ANAPC1	anaphase promoting complex subunit 1	-1.613
KIF1B	kinesin family member 1B	-1.600
F630110N24Rik	RIKEN cDNA F630110N24 gene	-1.599
SNX9	similar to Sorting nexin 9; sorting nexin 9	-1.586
TTC38	tetratricopeptide repeat domain 38	-1.585
ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-1.584
phf17	PHD finger protein 17	-1.581
entpd4	ectonucleoside triphosphate diphosphohydrolase 4	-1.569
MIS12	MIS12 homolog (yeast)	-1.566
Slc9a6	solute carrier family 9 (sodium/hydrogen exchanger), member 6	-1.546
ACIN1	apoptotic chromatin condensation inducer 1	-1.545
tsr1	similar to CG7338-PA; TSR1, 20S rRNA accumulation, homolog (yeast)	-1.538
PDE4D	phosphodiesterase 4D, cAMP specific	-1.534
SEC31A	Sec31 homolog A (S. cerevisiae)	-1.533
DST	dystonin; hypothetical protein LOC100047109	-1.503
EPHA4	Eph receptor A4	-1.495
UBR4	ubiquitin protein ligase E3 component n-recognin 4	-1.492
CDK5RAP3	CDK5 regulatory subunit associated protein 3	-1.492
arhgef10	Rho guanine nucleotide exchange factor (GEF) 10	-1.491
Pms1	postmeiotic segregation increased 1 (S. cerevisiae)	-1.483
CALCRL	calcitonin receptor-like	-1.480
baz1b	bromodomain adjacent to zinc finger domain, 1B	-1.477
GJA3	gap junction protein, alpha 3	-1.473
Ptprd	protein tyrosine phosphatase, receptor type, D	-1.471
RNASEL	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)	-1.468
A630007B06Rik	RIKEN cDNA A630007B06 gene	-1.465

Gene Symbol	Gene Name	10d Fold Change
RBBP5	retinoblastoma binding protein 5	-1.464
PPAT	phosphoribosyl pyrophosphate amidotransferase	-1.464
NTN4	netrin 4	-1.459
eif3a	eukaryotic translation initiation factor 3, subunit A	-1.458
MYH11	myosin, heavy polypeptide 11, smooth muscle	-1.454
Nf2	neurofibromatosis 2	-1.453
CFLAR	CASP8 and FADD-like apoptosis regulator pseudogene; CASP8 and FADD-like apoptosis regulator	-1.443
LEO1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	-1.442
OTUD7B	OTU domain containing 7B	-1.438
AFAP1	actin filament associated protein 1	-1.437
LIMA1	LIM domain and actin binding 1	-1.435
Wif1	Wnt inhibitory factor 1	-1.435
OSBPL1A	oxysterol binding protein-like 1A	-1.429
TNS3	tensin 3	-1.424
Rprd2	regulation of nuclear pre-mRNA domain containing 2	-1.423
CYTSA	cytospin A	-1.422
TFPI	tissue factor pathway inhibitor	-1.417
Il1r1	interleukin 1 receptor, type I	-1.412
Mlec	malectin	-1.410
adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta); similar to metalloprotease-disintegrin meltrin beta	-1.409
dusp5	dual specificity phosphatase 5	-1.396
RAB8B	RAB8B, member RAS oncogene family	-1.393
spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	-1.391
POLH	polymerase (DNA directed), eta (RAD 30 related)	-1.390
MXD1	MAX dimerization protein 1	-1.389
mks1	Meckel syndrome, type 1	-1.387
WFIKKN2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	-1.387
SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1; predicted gene 7004	-1.379
PPP2R5C	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	-1.374
RNF141	predicted gene 10179; ring finger protein 141	-1.373
SIDT2	SID1 transmembrane family, member 2	-1.373
CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	-1.373
BOD1L	biorientation of chromosomes in cell division 1-like	-1.371
CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	-1.369
itih5	inter-alpha (globulin) inhibitor H5	-1.367
FBXW8	F-box and WD-40 domain protein 8	-1.361
PHKA2	phosphorylase kinase alpha 2	-1.356

Gene Symbol	Gene Name	10d Fold Change
D17Wsu92e	DNA segment, Chr 17, Wayne State University 92, expressed	-1.354
HSPA12A	heat shock protein 12A	-1.354
MAPK10	mitogen-activated protein kinase 10	-1.349
ATF7IP	activating transcription factor 7 interacting protein	-1.345
Zfp839	zinc finger protein 839	-1.343
CLASP2	CLIP associating protein 2	-1.338
RORA	RAR-related orphan receptor alpha	-1.331
adra1b	adrenergic receptor, alpha 1b	-1.330
SCML4	sex comb on midleg-like 4 (Drosophila)	-1.330
MKLN1	muskelin 1, intracellular mediator containing kelch motifs	-1.321
PELI1	pellino 1	-1.314
BC068281	cDNA sequence BC068281	-1.311
bpnt1	bisphosphate 3'-nucleotidase 1; similar to bisphosphate 3-nucleotidase 1	-1.305
4930430F08Rik	RIKEN cDNA 4930430F08 gene	-1.298
SDCCAG1	serologically defined colon cancer antigen 1	-1.297
NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	-1.293
Ino80	INO80 homolog (S. cerevisiae); similar to yeast INO80-like protein	-1.283
Fam122b	family with sequence similarity 122, member B	-1.276
P4HA2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide	-1.276
DSTYK	dual serine/threonine and tyrosine protein kinase	-1.272
Tnpo2	transportin 2 (importin 3, karyopherin beta 2b)	-1.269
Arl13a	ADP-ribosylation factor-like 13A	-1.263
TMEM35	transmembrane protein 35	-1.263
Ubap2l	ubiquitin associated protein 2-like	-1.259
SNN	stannin	-1.256
Dhrs3	dehydrogenase/reductase (SDR family) member 3	-1.255
MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like; hypothetical protein LOC100044924	-1.254
3632451O06Rik	RIKEN cDNA 3632451O06 gene	-1.253
AHCYL1	S-adenosylhomocysteine hydrolase-like 1	-1.252
CC2D2A	coiled-coil and C2 domain containing 2A	-1.250
AHDC1	AT hook, DNA binding motif, containing 1	-1.248
IRF2BP2	interferon regulatory factor 2 binding protein 2	-1.245
ART3	ADP-ribosyltransferase 3	-1.245
Bach1	BTB and CNC homology 1	-1.242
NEO1	neogenin	-1.241
SLC41A1	solute carrier family 41, member 1	-1.236
lpar1	lysophosphatidic acid receptor 1	-1.235
GUCY1A3	guanylate cyclase 1, soluble, alpha 3	-1.234

Gene Symbol	Gene Name	10d Fold Change
Hspa4l	heat shock protein 4 like	-1.230
WDTC1	WD and tetratricopeptide repeats 1; similar to WD and tetratricopeptide repeats 1	-1.229
CNNM3	cyclin M3	-1.228
CREBL2	cAMP responsive element binding protein-like 2	-1.227
FBXL16	F-box and leucine-rich repeat protein 16	-1.226
PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	-1.226
STARD13	StAR-related lipid transfer (START) domain containing 13; similar to serologically defined colon cancer antigen 13	-1.224
Epb4.1l2	erythrocyte protein band 4.1-like 2	-1.223
PTPRK	protein tyrosine phosphatase, receptor type, K	-1.221
Golph3l	golgi phosphoprotein 3-like	-1.218
USP20	ubiquitin specific peptidase 20	-1.217
Ccdc47	coiled-coil domain containing 47	-1.214
DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	-1.213
CLIP4	CAP-GLY domain containing linker protein family, member 4; similar to CAP-GLY domain containing linker protein family, member 4	-1.207
MR1	major histocompatibility complex, class I-related	-1.204
NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	-1.201
WDSUB1	WD repeat, SAM and U-box domain containing 1	-1.199
nhsl1	NHS-like 1	-1.197
TNRC6A	trinucleotide repeat containing 6a	-1.196
HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	-1.193
CD99L2	CD99 antigen-like 2	-1.175
ikbip	RIKEN cDNA 1200009F10 gene	-1.174
GPATCH1	G patch domain containing 1	-1.171
anxa11	annexin A11; predicted gene 2260; predicted gene 2274	-1.169
Smc1a	structural maintenance of chromosomes 1A	-1.168
secisbp2	SECIS binding protein 2	-1.167
ZADH2	zinc binding alcohol dehydrogenase, domain containing 2	-1.165
atg16l1	autophagy-related 16-like 1 (yeast)	-1.164
RUFY3	RUN and FYVE domain containing 3	-1.148
maeA	macrophage erythroblast attacher	-1.147
MYLIP	myosin regulatory light chain interacting protein	-1.145
Ube4b	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	-1.145
MICAL3	microtubule associated monoxygenase, calponin and LIM domain containing 3	-1.145
NUMA1	nuclear mitotic apparatus protein 1	-1.143
MAOB	monoamine oxidase B	-1.142
mtr	5-methyltetrahydrofolate-homocysteine methyltransferase	-1.140
ERN1	endoplasmic reticulum (ER) to nucleus signalling 1	-1.139
TOP3B	topoisomerase (DNA) III beta	-1.138

Gene Symbol	Gene Name	10d Fold Change
bat3	HLA-B-associated transcript 3	-1.138
Zfp507	zinc finger protein 507	-1.136
Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	-1.136
PLEKHA2	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2	-1.132
PPM1B	similar to serine/threonine phosphatase; protein phosphatase 1B, magnesium dependent, beta isoform	-1.132
NBEA	neurobeachin	-1.130
GFPT1	glutamine fructose-6-phosphate transaminase 1	-1.128
9630028I04Rik	RIKEN cDNA 9630028I04 gene	-1.128
PTPRJ	protein tyrosine phosphatase, receptor type, J; predicted gene 13768; predicted gene 13767	-1.126
Gm13767	protein tyrosine phosphatase, receptor type, J; predicted gene 13768; predicted gene 13767	-1.126
Gm13768	protein tyrosine phosphatase, receptor type, J; predicted gene 13768; predicted gene 13767	-1.126
MTDH	metadherin	-1.121
hdac9	histone deacetylase 9	-1.120
ACVR1B	activin A receptor, type 1B	-1.118
Sin3b	transcriptional regulator, SIN3B (yeast)	-1.116
Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	-1.114
MEF2A	similar to Myocyte enhancer factor 2A; myocyte enhancer factor 2A	-1.111
pbrm1	polybromo 1	-1.109
CHD6	chromodomain helicase DNA binding protein 6; predicted gene 8291	-1.108
CRHR2	corticotropin releasing hormone receptor 2	-1.108
4732416N19Rik	RIKEN cDNA 4732416N19 gene	-1.102
HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	-1.101
Znfx1	zinc finger, NFX1-type containing 1	-1.100
CYB5D1	cytochrome b5 domain containing 1; predicted gene 6685	-1.098
ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	-1.094
5930434B04Rik	RIKEN cDNA 5930434B04 gene; hypothetical protein LOC100047034	-1.094
STAU1	staufen (RNA binding protein) homolog 1 (Drosophila)	-1.094
AKAP13	A kinase (PRKA) anchor protein 13	-1.092
SCLY	selenocysteine lyase	-1.088
AI597468	expressed sequence AI597468	-1.086
PKP4	plakophilin 4	-1.083
NBR1	neighbor of Brca1 gene 1	-1.079

Gene Symbol	Gene Name	10d Fold Change
BC032203	cDNA sequence BC032203	-1.079
ANKRD17	ankyrin repeat domain 17	-1.078
Pigw	phosphatidylinositol glycan anchor biosynthesis, class W	-1.077
Eif4g3	eukaryotic translation initiation factor 4 gamma, 3; similar to Eukaryotic translation initiation factor 4 gamma 3 (eIF-4-gamma 3) (eIF-4G 3) (eIF4G 3) (eIF-4-gamma II) (eIF4GII)	-1.076
Slc29a3	solute carrier family 29 (nucleoside transporters), member 3	-1.075
ZBTB7A	zinc finger and BTB domain containing 7a	-1.069
PTPN21	protein tyrosine phosphatase, non-receptor type 21	-1.068
ficd	FIC domain containing	-1.067
Wasf2	WAS protein family, member 2	-1.065
CREBBP	CREB binding protein	-1.065
Zfp316	zinc finger protein 316	-1.061
CDK12	CDC2-related kinase, arginine/serine-rich	-1.059
CHAC1	ChaC, cation transport regulator-like 1 (E. coli)	-1.057
UBD	ubiquitin D	-1.056
usp53	ubiquitin specific peptidase 53	-1.056
YIPF6	similar to Yip1 domain family, member 6; Yip1 domain family, member 6	-1.056
Trim35	tripartite motif-containing 35	-1.055
Zfp629	zinc finger protein 629	-1.054
UBAC2	ubiquitin associated domain containing 2	-1.053
ZSCAN2	zinc finger and SCAN domain containing 2	-1.049
GAB2	growth factor receptor bound protein 2-associated protein 2	-1.046
dagla	diacylglycerol lipase, alpha	-1.046
Add1	adducin 1 (alpha)	-1.045
slu7	SLU7 splicing factor homolog (S. cerevisiae)	-1.043
NAAA	N-acylethanolamine acid amidase	-1.042
4930402H24Rik	RIKEN cDNA 4930402H24 gene	-1.041
sec22c	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	-1.039
TRPC4AP	transient receptor potential cation channel, subfamily C, member 4 associated protein	-1.038
SEMA4B	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	-1.038
Pde7b	phosphodiesterase 7B	-1.036
1500011H22Rik	RIKEN cDNA 1500011H22 gene	-1.032
MAP2K7	predicted gene 14378; similar to transforming growth factor, beta receptor III (betaglycan, 300kDa); mitogen-activated protein kinase kinase 7	-1.028
CD93	CD93 antigen	-1.027
TRIM55	tripartite motif-containing 55	-1.024
Gm505	predicted gene 505	-1.023

Gene Symbol	Gene Name	10d Fold Change
slc39a1	solute carrier family 39 (zinc transporter), member 1; similar to Zinc transporter ZIP1 (Zinc-iron regulated transporter-like) (Solute carrier family 39 member 1)	-1.020
ARID5B	similar to modulator recognition factor 2; AT rich interactive domain 5B (MRF1-like)	-1.020
DSC2	desmocollin 2	-1.019
SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1; similar to solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	-1.018
npepps	aminopeptidase puromycin sensitive	-1.018
RPS6KA5	ribosomal protein S6 kinase, polypeptide 5	-1.016
SUN1	unc-84 homolog A (C. elegans)	-1.016
SH3PXD2A	SH3 and PX domains 2A; similar to Fish protein	-1.014
UBXN7	UBX domain protein 7	-1.013
SLC4A4	solute carrier family 4 (anion exchanger), member 4	-1.012
keap1	kelch-like ECH-associated protein 1	-1.011
RBBP6	retinoblastoma binding protein 6	-1.010
mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	-1.009
TBC1D4	TBC1 domain family, member 4	-1.004
taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.002
CASZ1	castor homolog 1, zinc finger (Drosophila); similar to castor homolog 1, zinc finger	-1.001
RCN2	reticulocalbin 2	-0.994
Whrn	whirlin	-0.993
EHMT1	similar to euchromatic histone methyltransferase 1; euchromatic histone methyltransferase 1	-0.990
ULK1	Unc-51 like kinase 1 (C. elegans)	-0.987
Stxbp4	syntaxin binding protein 4	-0.986
tmem129	transmembrane protein 129	-0.986
Myst2	MYST histone acetyltransferase 2	-0.985
SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	-0.981
Pdzd2	PDZ domain containing 2	-0.981
RBM45	similar to developmentally regulated RNA-binding protein 1; RNA binding motif protein 45	-0.972
Extl2	exostoses (multiple)-like 2	-0.967
Adrbk2	adrenergic receptor kinase, beta 2	-0.966
ABR	active BCR-related gene	-0.966
ARID4A	AT rich interactive domain 4A (RBP1-like)	-0.965
ednrb	endothelin receptor type B	-0.965
PREPL	prolyl endopeptidase-like	-0.959
TTC3	tetratricopeptide repeat domain 3	-0.956

Gene Symbol	Gene Name	10d Fold Change
SMARCAL1	SWI/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	-0.952
ARNT	aryl hydrocarbon receptor nuclear translocator	-0.951
ROCK2	Rho-associated coiled-coil containing protein kinase 2	-0.949
smek2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	-0.947
Lpcat3	lysophosphatidylcholine acyltransferase 3	-0.945
AI848100	expressed sequence AI848100	-0.944
FKBP15	FK506 binding protein 15	-0.943
BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	-0.942
MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	-0.935
Zfp346	zinc finger protein 346	-0.933
Acad10	acyl-Coenzyme A dehydrogenase family, member 10	-0.932
TET3	tet oncogene family member 3	-0.932
Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2	-0.929
ITPR1	inositol 1,4,5-triphosphate receptor 1	-0.923
WDR33	WD repeat domain 33	-0.923
SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	-0.918
dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	-0.918
IPO8	importin 8	-0.917
glyr1	RIKEN cDNA 3930401K13 gene	-0.916
Klhl38	kelch-like 38 (Drosophila)	-0.916
Myo18a	myosin XVIIIA	-0.915
D19Wsu162e	DNA segment, Chr 19, Wayne State University 162, expressed	-0.908
Nup88	nucleoporin 88	-0.907
LMBRD1	LMBR1 domain containing 1	-0.906
RRBP1	ribosome binding protein 1	-0.903
SFRS11	splicing factor, arginine/serine-rich 11	-0.900
Zfp608	zinc finger protein 608	-0.900
CEP76	centrosomal protein 76	-0.899
Ap1g1	adaptor protein complex AP-1, gamma 1 subunit	-0.895
Zfp516	zinc finger protein 516	-0.893
4930471M23 Rik	RIKEN cDNA 4930471M23 gene	-0.892
cul4a	cullin 4A	-0.890
Pim1	proviral integration site 1	-0.888
Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha isoform	-0.888
Sik1	salt inducible kinase 1	-0.887
D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed	-0.887
Bat2l	HLA-B associated transcript 2-like	-0.886
CCDC66	coiled-coil domain containing 66	-0.884
fam192a	RIKEN cDNA 2310065K24 gene	-0.883
HOMER1	homer homolog 1 (Drosophila)	-0.881

Gene Symbol	**Gene Name**	**10d Fold Change**
GGA3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	-0.878
adcy5	adenylate cyclase 5; similar to adenylate cyclase 5	-0.878
FBXO9	f-box protein 9	-0.877
ADD3	adducin 3 (gamma)	-0.875
tmem57	transmembrane protein 57	-0.874
KPNA6	karyopherin (importin) alpha 6	-0.870
Zfp251	zinc finger protein 251	-0.869
Tpcn1	two pore channel 1	-0.866
Txnl4b	thioredoxin-like 4B	-0.865
phkg1	phosphorylase kinase gamma 1	-0.864
EIF5	similar to Eukaryotic translation initiation factor 5; eukaryotic translation initiation factor 5	-0.864
cbx4	chromobox homolog 4 (Drosophila Pc class)	-0.862
Tet1	tet oncogene 1	-0.862
CLEC16A	C-type lectin domain family 16, member A	-0.861
ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	-0.860
Fnbp1	formin binding protein 1	-0.859
Zfp828	zinc finger protein 828	-0.857
ANKHD1	ankyrin repeat and KH domain containing 1; eukaryotic translation initiation factor 4E binding protein 3	-0.856
GIGYF2	GRB10 interacting GYF protein 2	-0.854
FAM13B	family with sequence similarity 13, member B	-0.853
ANK3	ankyrin 3, epithelial	-0.853
MKL2	MKL/myocardin-like 2	-0.852
SNAP91	synaptosomal-associated protein 91	-0.852
NAP1L1	similar to nucleosome assembly protein 1-like 1; nucleosome assembly protein 1-like 1	-0.851
Med13l	mediator complex subunit 13-like	-0.851
ELP3	elongation protein 3 homolog (S. cerevisiae)	-0.850
MIB1	mindbomb homolog 1 (Drosophila)	-0.839
C130039O16 Rik	RIKEN cDNA C130039O16 gene	-0.838
Polr3f	polymerase (RNA) III (DNA directed) polypeptide F	-0.836
Rabgap1l	RAB GTPase activating protein 1-like	-0.832
Zfp609	zinc finger protein 609	-0.831
rgp1	RGP1 retrograde golgi transport homolog (S. cerevisiae)	-0.831
Zfp426	zinc finger protein 426	-0.830
Zfp532	zinc finger protein 532	-0.826
PTPN11	protein tyrosine phosphatase, non-receptor type 11	-0.823
Gpn3	GPN-loop GTPase 3	-0.816
rufy1	RUN and FYVE domain containing 1	-0.814
maf	similar to c-Maf long form; avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	-0.813

Gene Symbol	Gene Name	10d Fold Change
ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	-0.813
tpr	similar to nuclear pore complex-associated intranuclear coiled-coil protein TPR; translocated promoter region	-0.812
PLD1	phospholipase D1	-0.811
HUWE1	HECT, UBA and WWE domain containing 1	-0.809
9330129D05Rik	RIKEN cDNA 9330129D05 gene	-0.808
Golim4	golgi integral membrane protein 4	-0.806
B230208H17 Rik	RIKEN cDNA B230208H17 gene	-0.802
NFE2L1	nuclear factor, erythroid derived 2,-like 1	-0.802
Rab3gap1	RAB3 GTPase activating protein subunit 1	-0.800
celsr1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	-0.796
rrs1	predicted gene 5067; RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	-0.793
ITGA7	integrin alpha 7	-0.791
Rnf38	ring finger protein 38	-0.790
C7	complement component 7	-0.790
Pgcp	plasma glutamate carboxypeptidase	-0.790
BAT4	predicted gene 5628; HLA-B associated transcript 4	-0.788
D6Wsu116e	DNA segment, Chr 6, Wayne State University 116, expressed	-0.787
LPHN1	latrophilin 1	-0.787
TNFAIP3	tumor necrosis factor, alpha-induced protein 3	-0.787
stk24	serine/threonine kinase 24 (STE20 homolog, yeast)	-0.785
Top3a	similar to topoisomerase III; topoisomerase (DNA) III alpha	-0.785
CEACAM	carcinoembryonic antigen-related cell adhesion molecule 1; carcinoembryonic antigen-related cell adhesion molecule 2	-0.782
slc39a14	solute carrier family 39 (zinc transporter), member 14	-0.778
elk1	ELK1, member of ETS oncogene family	-0.777
PHLDB2	pleckstrin homology-like domain, family B, member 2	-0.777
TOR1AIP1	torsin A interacting protein 1	-0.775
1110038D17Rik	RIKEN cDNA 1110038D17 gene	-0.775
1110021J02Rik	RIKEN cDNA 1110021J02 gene	-0.773
TOP1	topoisomerase (DNA) I	-0.770
ABLIM2	actin-binding LIM protein 2	-0.770
ZC3H6	zinc finger CCCH type containing 6	-0.769
Clasp1	CLIP associating protein 1	-0.769
ELF2	E74-like factor 2	-0.768
ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit A2	-0.768

Gene Symbol	Gene Name	10d Fold Change
srr	serine racemase	-0.767
ARL15	ADP-ribosylation factor-like 15	-0.765
TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-0.763
Zeb2	zinc finger E-box binding homeobox 2	-0.763
Laptm4b	predicted gene 6705; lysosomal-associated protein transmembrane 4B	-0.762
LRP6	similar to LDL receptor-related protein 6; low density lipoprotein receptor-related protein 6	-0.756
DGKE	diacylglycerol kinase, epsilon	-0.756
pja2	praja 2, RING-H2 motif containing	-0.755
cdk8	predicted gene 7107; cyclin-dependent kinase 8	-0.752
dyrk2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-0.751
Rab2b	RAB2B, member RAS oncogene family	-0.741
Sbno1	sno, strawberry notch homolog 1 (Drosophila)	-0.741
Ubqln1	ubiquilin 1	-0.740
tab2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	-0.738
WDR35	WD repeat domain 35	-0.737
ncf1	neutrophil cytosolic factor 1	-0.735
SEC23A	SEC23A (S. cerevisiae)	-0.735
Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	-0.735
TLK2	predicted gene 13161; tousled-like kinase 2 (Arabidopsis)	-0.729
ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit A1	-0.729
RUNDC1	RUN domain containing 1	-0.729
LOC100046125	RAB5A, member RAS oncogene family; similar to small GTP-binding protein rab5	-0.728
rab5a	RAB5A, member RAS oncogene family; similar to small GTP-binding protein rab5	-0.728
Trp53bp2	transformation related protein 53 binding protein 2	-0.727
TAOK3	TAO kinase 3	-0.725
CBX5	chromobox homolog 5 (Drosophila HP1a)	-0.725
SMURF1	SMAD specific E3 ubiquitin protein ligase 1	-0.723
ZEB1	zinc finger E-box binding homeobox 1	-0.722
MAMLD1	mastermind-like domain containing 1	-0.720
PEX12	peroxisomal biogenesis factor 12	-0.719
Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	-0.717
EPC2	enhancer of polycomb homolog 2 (Drosophila); similar to Enhancer of polycomb homolog 2	-0.717
PABPC4	similar to Poly A binding protein, cytoplasmic 4; poly(A) binding protein, cytoplasmic 4; predicted gene 12623; predicted gene 5088; hypothetical protein LOC100044219	-0.714
NCKAP5	RIKEN cDNA E030049G20 gene	-0.712

Gene Symbol	Gene Name	10d Fold Change
CSNK1G1	casein kinase 1, gamma 1	-0.710
DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	-0.709
Slc38a4	solute carrier family 38, member 4	-0.709
D18Ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed	-0.708
RBM27	RNA binding motif protein 27	-0.708
ASB4	ankyrin repeat and SOCS box-containing 4	-0.706
agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	-0.704
STX18	syntaxin 18	-0.702
SEC23IP	Sec23 interacting protein	-0.702
IGHMBP2	immunoglobulin mu binding protein 2	-0.702
EXOSC9	exosome component 9; similar to Exosome complex exonuclease RRP45 (Exosome component 9) (Polymyositis/scleroderma autoantigen 1) (Autoantigen PM/Scl 1) (Polymyositis/scleroderma autoantigen 75 kDa) (PM/Scl-75) (P75 polymyositis-scleroderma overlap syndrome-associated a...	-0.697
PDIA3	protein disulfide isomerase associated 3	-0.697
eprs	similar to Bifunctional aminoacyl-tRNA synthetase; glutamyl-prolyl-tRNA synthetase	-0.696
SAPS2	SAPS domain family, member 2	-0.687
PPIG	peptidyl-prolyl isomerase G (cyclophilin G)	-0.684
SMG7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	-0.684
2810407C02Rik	RIKEN cDNA 2810407C02 gene	-0.683
ddx10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	-0.682
Mapk9	mitogen-activated protein kinase 9	-0.681
RNF130	ring finger protein 130; similar to Ring finger protein 130	-0.676
Ccndbp1	cyclin D-type binding-protein 1	-0.676
CPSF3	cleavage and polyadenylation specificity factor 3	-0.674
WAC	similar to WW domain-containing adapter protein with coiled-coil; WW domain containing adaptor with coiled-coil	-0.673
Dnaja4	similar to DnaJ (Hsp40) homolog, subfamily A, member 4; DnaJ (Hsp40) homolog, subfamily A, member 4	-0.673
cast	calpastatin	-0.669
Trim63	similar to tripartite motif-containing 63; tripartite motif-containing 63	-0.667
lpp	LIM domain containing preferred translocation partner in lipoma	-0.666
TXNDC5	thioredoxin domain containing 5	-0.665
khnyn	RIKEN cDNA 9130227C08Rik gene	-0.664
PEX11A	peroxisomal biogenesis factor 11 alpha	-0.663
Hsp90b1	heat shock protein 90, beta (Grp94), member 1	-0.662
METT11D1	methyltransferase 11 domain containing 1	-0.661
H2-T23	histocompatibility 2, T region locus 23; similar to RT1 class Ib, locus H2-Q-like, grc region	-0.658

Gene Symbol	Gene Name	10d Fold Change
GAA	glucosidase, alpha, acid	-0.656
GTF3C1	general transcription factor III C 1	-0.653
ROCK1	Rho-associated coiled-coil containing protein kinase 1	-0.649
Mtus2	RIKEN cDNA C130038G02 gene	-0.647
glcci1	similar to glucocorticoid induced transcript 1; predicted gene 5815; glucocorticoid induced transcript 1	-0.647
SLC36A1	solute carrier family 36 (proton/amino acid symporter), member 1	-0.645
ACAD9	acyl-Coenzyme A dehydrogenase family, member 9	-0.642
Ik	IK cytokine	-0.638
ngly1	N-glycanase 1	-0.637
B3GNTL1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	-0.635
FLYWCH1	FLYWCH-type zinc finger 1	-0.635
CALD1	caldesmon 1	-0.634
ASB7	ankyrin repeat and SOCS box-containing 7	-0.634
2210018M11 Rik	RIKEN cDNA 2210018M11 gene	-0.634
PSIP1	PC4 and SFRS1 interacting protein 1	-0.633
Iqsec1	IQ motif and Sec7 domain 1	-0.631
thrA	thyroid hormone receptor alpha; similar to thyroid hormone receptor	-0.631
Canx	calnexin	-0.631
nin	ninein	-0.625
Pcp4l1	Purkinje cell protein 4-like 1	-0.622
NUP107	nucleoporin 107	-0.620
PRPF31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	-0.618
DAG1	dystroglycan 1	-0.614
NFYB	nuclear transcription factor-Y beta	-0.614
SLK	STE20-like kinase (yeast)	-0.614
Obsl1	obscurin-like 1	-0.613
NFIC	nuclear factor I/C	-0.609
WNT5A	wingless-related MMTV integration site 5A	-0.608
Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	-0.607
Tmtc4	transmembrane and tetratricopeptide repeat containing 4	-0.604
sf3a3	splicing factor 3a, subunit 3	-0.604
E430018J23Rik	RIKEN cDNA E430018J23 gene; RIKEN cDNA 9130019O22 gene	-0.598
Cnot10	CCR4-NOT transcription complex, subunit 10	-0.597
copb2	coatomer protein complex, subunit beta 2 (beta prime)	-0.594
Senp5	SUMO/sentrin specific peptidase 5	-0.588
ADSL	adenylosuccinate lyase	-0.587
TUBB2C	tubulin, beta 2c, psuedogene 1; tubulin, beta 2C; tubulin, beta 2c, pseudogene 2	-0.585

Gene Symbol		10d Fold
PLEKHG5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	0.588
Ggnbp1	gametogenetin binding protein 1; RIKEN cDNA 0610031G08 gene	0.589
ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	0.595
NLN	neurolysin (metallopeptidase M3 family)	0.599
cry2	similar to mKIAA0658 protein; cryptochrome 2 (photolyase-like)	0.599
Inpp5d	inositol polyphosphate-5-phosphatase D	0.601
1110034B05Rik	RIKEN cDNA 1110034B05 gene	0.602
D430042O09Rik	RIKEN cDNA D430042O09 gene	0.608
FGD5	FYVE, RhoGEF and PH domain containing 5	0.610
EPOR	erythropoietin receptor	0.612
ppp1r14b	predicted gene 9103; predicted gene 8503; similar to protein phosphatase 1, regulatory (inhibitor) subunit 14B; protein phosphatase 1, regulatory (inhibitor) subunit 14B	0.613
BANP	BTG3 associated nuclear protein	0.614
PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	0.614
E4F1	E4F transcription factor 1	0.618
Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	0.619
ARHGAP9	Rho GTPase activating protein 9	0.619
PARP8	poly (ADP-ribose) polymerase family, member 8	0.621
PGM2L1	phosphoglucomutase 2-like 1	0.623
BC028528	cDNA sequence BC028528	0.625
NRM	nurim (nuclear envelope membrane protein)	0.625
ALOX12	arachidonate 12-lipoxygenase	0.628
2700081O15Rik	RIKEN cDNA 2700081O15 gene	0.634
8430427H17Rik	RIKEN cDNA 8430427H17 gene	0.635
B230354K17Rik	RIKEN cDNA B230354K17 gene	0.636
Endou	placental protein 11 related	0.637
KIF26A	kinesin family member 26A	0.639
ACSF3	acyl-CoA synthetase family member 3	0.640
LRRC27	leucine rich repeat containing 27	0.643
1300003B13Rik	RIKEN cDNA 1300003B13 gene; hypothetical protein LOC100044281	0.644
RASD2	RASD family, member 2	0.648
LRRN4CL	LRRN4 C-terminal like	0.648
MYO5A	myosin VA	0.652
6230427J02Rik	RIKEN cDNA 6230427J02 gene	0.657

Gene Symbol	Gene Name	10d Fold Change
fam48a	family with sequence similarity 48, member A	0.667
INCENP	inner centromere protein	0.667
limk1	LIM-domain containing, protein kinase	0.669
Cdc25b	cell division cycle 25 homolog B (S. pombe)	0.670
STK10	serine/threonine kinase 10	0.673
Fam109a	family with sequence similarity 109, member A	0.673
SCARF2	scavenger receptor class F, member 2	0.677
BC016495	cDNA sequence BC016495	0.679
Dgcr14	DiGeorge syndrome critical region gene 14	0.681
GPR137B	similar to Gpr137b protein; G protein-coupled receptor 137B	0.682
Car14	carbonic anhydrase 14	0.682
2300009A05Rik	RIKEN cDNA 2300009A05 gene	0.684
LXN	latexin	0.687
grk6	G protein-coupled receptor kinase 6	0.690
2310046K01Rik	RIKEN cDNA 2310046K01 gene	0.690
Pole	polymerase (DNA directed), epsilon	0.691
Odf2	outer dense fiber of sperm tails 2; similar to outer dense fiber of sperm tails 2	0.692
NRIP2	nuclear receptor interacting protein 2	0.696
Rap1gap	Rap1 GTPase-activating protein	0.701
1700029G01Rik	RIKEN cDNA 1700029G01 gene	0.701
Pisd-ps3	phosphatidylserine decarboxylase, pseudogene 3	0.702
TTBK2	tau tubulin kinase 2; congenital dyserythropoietic anemia, type I (human)	0.703
CD86	CD86 antigen	0.708
3110062M04Rik	RIKEN cDNA 3110062M04 gene	0.709
TMEM120B	transmembrane protein 120B	0.711
TRPV4	transient receptor potential cation channel, subfamily V, member 4	0.711
BTBD19	RIKEN cDNA 9530048O09 gene	0.715
PRKCB	protein kinase C, beta	0.719
tef	thyrotroph embryonic factor	0.724
Hmcn2	hemicentin 2	0.731
LRMP	lymphoid-restricted membrane protein	0.732
Pcdh19	protocadherin 19	0.738
PHF21A	PHD finger protein 21A	0.741
MERTK	c-mer proto-oncogene tyrosine kinase	0.742
PI16	peptidase inhibitor 16	0.743
lhx6	LIM homeobox protein 6	0.744
MATR3	matrin 3; similar to Matrin 3	0.754

Gene Symbol	Gene Name	10d Fold Change
IL10RA	interleukin 10 receptor, alpha	0.757
SLC35E2	RIKEN cDNA A530082C11 gene	0.764
NMB	neuromedin B	0.768
DNMT3B	DNA methyltransferase 3B	0.768
4930503L19Rik	RIKEN cDNA 4930503L19 gene	0.776
GstT2	glutathione S-transferase, theta 2	0.781
THSD1	thrombospondin, type I, domain 1	0.782
Zfp710	zinc finger protein 710	0.791
6330503K22Rik	RIKEN cDNA 6330503K22 gene	0.795
Zfp280c	zinc finger protein 280C	0.797
DNM3	dynamin 3	0.800
SFRS16	splicing factor, arginine/serine-rich 16	0.802
CCDC88C	coiled-coil domain containing 88C	0.803
2700046G09Rik	RIKEN cDNA 2700046G09 gene	0.806
fbxl12	F-box and leucine-rich repeat protein 12	0.807
CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	0.813
FAM102A	family with sequence similarity 102, member A	0.817
TACC2	transforming, acidic coiled-coil containing protein 2	0.820
arrb2	arrestin, beta 2	0.865
GMIP	Gem-interacting protein	0.873
CEP152	centrosomal protein 152	0.879
Adora2a	adenosine A2a receptor	0.881
STARD9	START domain containing 9	0.892
Gm4983	predicted gene 4983	0.901
RAB4B	RAB4B, member RAS oncogene family	0.904
PACS1	phosphofurin acidic cluster sorting protein 1	0.908
TLE2	transducin-like enhancer of split 2, homolog of Drosophila E(spl)	0.911
9330188P03Rik	RIKEN cDNA 9330188P03 gene	0.928
GRB10	growth factor receptor bound protein 10	0.977
NAV3	neuron navigator 3	0.998
KIFC2	kinesin family member C2	1.007
Rasgrp2	RAS, guanyl releasing protein 2	1.010
Mapk11	mitogen-activated protein kinase 11	1.017
pola2	polymerase (DNA directed), alpha 2	1.024
Gp49a	glycoprotein 49 A; leukocyte immunoglobulin-like receptor, subfamily B, member 4	1.030
LRRC45	leucine rich repeat containing 45	1.037
camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	1.040
Rps6kl1	ribosomal protein S6 kinase-like 1	1.041

Gene Symbol	Gene Name	10d Fold Change
CIT	citron	1.050
myl6	predicted gene 5915; predicted gene 8894; myosin, light polypeptide 6, alkali, smooth muscle and non-muscle; predicted gene 10080	1.054
DPEP2	dipeptidase 2	1.055
DARC	Duffy blood group, chemokine receptor	1.068
BARD1	BRCA1 associated RING domain 1	1.069
2010111I01Rik	RIKEN cDNA 2010111I01 gene	1.080
SIGIRR	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	1.086
Frmd4a	FERM domain containing 4A	1.096
STX1A	syntaxin 1A (brain)	1.136
1600020E01Rik	RIKEN cDNA 1600020E01 gene	1.141
2700023E23Rik	RIKEN cDNA 2700023E23 gene	1.146
GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	1.153
DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	1.153
Snora68	small nucleolar RNA, H/ACA box 68	1.156
SAPS3	SAPS domain family, member 3	1.159
ARHGAP33	sorting nexin 26	1.202
HMGN3	high mobility group nucleosomal binding domain 3	1.209
CPNE7	copine VII	1.213
MEG3	maternally expressed 3	1.229
KIF23	kinesin family member 23	1.239
PRDM5	PR domain containing 5	1.252
Brms1	breast cancer metastasis-suppressor 1	1.279
cdkal1	CDK5 regulatory subunit associated protein 1-like 1	1.285
SORBS2	sorbin and SH3 domain containing 2	1.302
ankrd11	ankyrin repeat domain 11	1.312
ELMO1	engulfment and cell motility 1, ced-12 homolog (C. elegans)	1.375
cyp4b1	predicted gene 12839; cytochrome P450, family 4, subfamily b, polypeptide 1	1.398
Fyco1	FYVE and coiled-coil domain containing 1	1.400
Snhg12	hypothetical protein LOC100039864	1.423
1110017F19Rik	RIKEN cDNA 1110017F19 gene	1.450
E130306D19Rik	RIKEN cDNA E130306D19 gene	1.462
SEPT14	septin 14; RIKEN cDNA 1700017B05 gene	1.487
Ubn1	ubinuclein 1	1.494
LIMS1	LIM and senescent cell antigen-like domains 1	1.503

Gene Symbol	Gene Name	10d Fold Change
AFG3L2	similar to AFG3(ATPase family gene 3)-like 2 (yeast); AFG3(ATPase family gene 3)-like 2 (yeast)	1.524
Man1a	mannosidase 1, alpha	1.550
Qsox1	quiescin Q6 sulfhydryl oxidase 1	1.562
atp6v1b2	ATPase, H+ transporting, lysosomal V1 subunit B2	1.566
AATF	apoptosis antagonizing transcription factor	1.569
chd7	chromodomain helicase DNA binding protein 7	1.572
rnmt	RNA (guanine-7-) methyltransferase	1.618
ZCCHC4	zinc finger, CCHC domain containing 4	1.641
Sap25	sin3A-binding protein, SAP25	1.642
OSBPL3	oxysterol binding protein-like 3	1.643
LRRK1	leucine-rich repeat kinase 1	1.647
MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	1.658
SRP72	signal recognition particle 72	1.684
F13A1	coagulation factor XIII, A1 subunit	1.697
SSBP2	single-stranded DNA binding protein 2; predicted gene 12470	1.713
BICC1	bicaudal C homolog 1 (Drosophila)	1.908
PDK1	pyruvate dehydrogenase kinase, isoenzyme 1	1.949
SIPA1L1	signal-induced proliferation-associated 1 like 1	2.108
NAV1	neuron navigator 1	2.180

Section B - 80 genes		
Gene Symbol	**Gene Name**	**10+25d Fold Change**
TMEM117	transmembrane protein 117	-1.214
timp4	tissue inhibitor of metalloproteinase 4	-1.187
TTN	titin	-0.949
CLIP1	CAP-GLY domain containing linker protein 1	-0.936
Ppip5k1	histidine acid phosphatase domain containing 2A	-0.811
RNF44	ring finger protein 44	-0.806
LAMA4	laminin, alpha 4	-0.805
HS3ST5	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	-0.799
Prnd	prion protein dublet	-0.698
MTCP1	mature T-cell proliferation 1	-0.635
tm9sf1	transmembrane 9 superfamily member 1	0.594
TNNT3	troponin T3, skeletal, fast	0.597
ODC1	predicted gene 6742; ornithine decarboxylase, structural 1; similar to Ornithine decarboxylase (ODC); predicted gene 7993; predicted gene 15645; predicted gene 9115; predicted gene 7278	0.601
MARCH8	membrane-associated ring finger (C3HC4) 8	0.607
A130040M12Rik	RIKEN cDNA A130040M12 gene	0.626
MBP	myelin basic protein	0.627
Gm13212	predicted gene 13212	0.628
USP4	ubiquitin specific peptidase 4 (proto-oncogene)	0.632
H2-Bl	histocompatibility 2, blastocyst; predicted gene 8810	0.632
CAR3	carbonic anhydrase 3	0.634
sh3glb1	SH3-domain GRB2-like B1 (endophilin)	0.638
KCNN4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	0.651
CDSN	corneodesmosin; hypothetical protein LOC100043961	0.652
KIF1A	kinesin family member 1A	0.668
zfand6	zinc finger, AN1-type domain 6	0.669
PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1); similar to mKIAA1230 protein	0.677
Psg16	pregnancy specific glycoprotein 16	0.682
Rmnd1	required for meiotic nuclear division 1 homolog (S. cerevisiae); predicted gene 5512	0.682
bmp2	bone morphogenetic protein 2	0.684
C4a	similar to Complement C4 precursor; complement component 4A (Rodgers blood group); similar to complement C4; complement component 4B (Childo blood group)	0.690
MORF4L1	predicted gene 6747; RIKEN cDNA A730098P11 gene; mortality factor 4 like 1; predicted gene 8663; predicted gene 4835	0.691
6720457D02Rik	RIKEN cDNA 6720457D02 gene	0.702

Gene Symbol	Gene Name	10+25d Fold Change
galE	galactose-4-epimerase, UDP	0.703
Prf1	perforin 1 (pore forming protein)	0.707
Gm6607	predicted gene 6607	0.710
ARHGEF12	predicted gene 7281; predicted gene 5831; similar to SP140 nuclear body protein (predicted); Rho guanine nucleotide exchange factor (GEF) 12	0.710
H2-K1	histocompatibility 2, K1, K region; similar to H-2K(d) antigen	0.713
Cd59b	CD59b antigen	0.714
Zfp808	predicted gene 3325; predicted gene 7036	0.721
Cd1d1	CD1d1 antigen; CD1d2 antigen	0.724
Ecsit	ECSIT homolog (Drosophila)	0.730
2410017P09Rik	RIKEN cDNA 2410017P09 gene	0.735
NIPSNAP1	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	0.749
Gm8113	predicted gene 8113	0.753
EEF1A1	predicted gene 5869; predicted gene 7161; predicted gene 7105; predicted gene 5822; similar to eukaryotic translation elongation factor 1 alpha 1; predicted gene 6192; predicted gene 6392; predicted gene 6767; predicted gene 6170; predicted gene 6548; predicted gene 6789; eukaryotic translation elongation factor 1 alpha 1	0.760
CCBL1	cysteine conjugate-beta lyase 1	0.762
CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	0.765
CFB	complement factor B	0.791
Gm13152	predicted gene 13152	0.817
MSLN	mesothelin	0.827
tubb3	tubulin, beta 3; tubulin, beta 3, pseudogene 1	0.836
RBP4	retinol binding protein 4, plasma	0.854
CNTN2	contactin 2	0.862
Eif1	predicted gene 5265; similar to suppressor of initiator codon mutations, related sequence 1; predicted gene 4017; predicted gene 6913; predicted gene 7688; predicted gene 6535; predicted gene 6900; predicted gene 5471; predicted gene 7845; predicted gene 5450; predicted gene 6155; predicted gene 7253; predicted gene 10713; similar to translation initiation factor SUI1; predicted gene 6428; similar to Eukaryotic translation initiation factor 1 (eIF1) (Protein translation factor SUI1 homolog); predicted gene, EG434356; similar to isolog of yeast sui1 and rice gos2; putative; eukaryotic translation initiation factor 1	0.868
EG634650	predicted gene, EG634650; guanylate-binding protein 10; RIKEN cDNA 5830443L24 gene	0.871
Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	0.886
2810408B13Rik	RIKEN cDNA 2810408B13 gene	0.906

Gene Symbol	Gene Name	10+25d Fold Change
TLE1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	0.913
PCK1	phosphoenolpyruvate carboxykinase 1, cytosolic	0.916
CFH	complement component factor h; similar to complement component factor H	0.947
Acat3	acetyl-Coenzyme A acetyltransferase 3	0.973
CYP2E1	cytochrome P450, family 2, subfamily e, polypeptide 1	0.986
Scd1	stearoyl-Coenzyme A desaturase 1	1.027
ACOT7	acyl-CoA thioesterase 7	1.071
ATP6	Cytochrome c oxidase subunit 3; ATP synthase subunit a; ATP synthase protein 8	1.096
ATP8	Cytochrome c oxidase subunit 3; ATP synthase subunit a; ATP synthase protein 8	1.096
COX3	Cytochrome c oxidase subunit 3; ATP synthase subunit a; ATP synthase protein 8	1.096
rps2	predicted gene 9168; predicted gene 7561; predicted gene 12091; predicted gene 5921; predicted gene 8841; predicted gene 8842; predicted gene 7143; predicted gene 4968; predicted gene 6576; predicted gene 8520; predicted gene 7520; similar to 40S ribosomal protein S2; ribosomal protein S2 pseudogene; predicted gene 11687; predicted gene 7502; similar to MGC27348 protein; predicted gene 6456; predicted gene 5786; predicted gene 6549; predicted gene 6359; predicted gene 7432; predicted gene 9013; predicted gene 6311; predicted gene 6139; predicted gene 12366; predicted gene 7428; predicted gene 14583; predicted gene 8553; predicted gene 5070; predicted gene 4974; predicted gene 6412; ribosomal protein S2	1.119
Ogdh	oxoglutarate dehydrogenase (lipoamide)	1.146
Mrps5	predicted gene 13328; mitochondrial ribosomal protein S5	1.158
h2-aa	histocompatibility 2, class II antigen A, alpha; histocompatibility 2, class II antigen E alpha	1.227
DCUN1D1	similar to RP42; DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	1.238
CIDEC	cell death-inducing DFFA-like effector c	1.271
Alox8	arachidonate 8-lipoxygenase	1.272
shox2	short stature homeobox 2	1.370
acp5	acid phosphatase 5, tartrate resistant	1.405
ADIPOQ	adiponectin, C1Q and collagen domain containing	1.481
RETN	resistin	1.736
Apoc1	apolipoprotein C-I	1.902
SQRDL	sulfide quinone reductase-like (yeast)	2.098

Section C - 443 genes		
Gene Symbol	Gene Name	35d Fold Change
4933401F05Rik	RIKEN cDNA 4933401F05 gene	-1.507
SAMD9L	sterile alpha motif domain containing 9-like	-1.398
Prrg1	proline rich Gla (G-carboxyglutamic acid) 1	-1.365
Lmbrd2	LMBR1 domain containing 2	-1.303
cnot1	predicted gene 6158; CCR4-NOT transcription complex, subunit 1	-1.297
tmem45b	transmembrane protein 45b	-1.291
CYP1B1	cytochrome P450, family 1, subfamily b, polypeptide 1	-1.290
ST8SIA6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	-1.264
SLC39A10	solute carrier family 39 (zinc transporter), member 10	-1.210
TOP2B	topoisomerase (DNA) II beta	-1.191
ermp1	endoplasmic reticulum metallopeptidase 1	-1.187
Rnf144b	ring finger protein 144B	-1.186
Btbd3	BTB (POZ) domain containing 3; predicted gene 7712; similar to BTB/POZ domain containing protein 3	-1.163
Zfp317	zinc finger protein 317	-1.157
Aldob	aldolase B, fructose-bisphosphate	-1.157
4933411K20Rik	RIKEN cDNA 4933411K20 gene	-1.150
NCOR1	nuclear receptor co-repressor 1	-1.140
Zfp449	zinc finger protein 449	-1.139
Zfhx2	zinc finger homeobox 2; similar to Zinc finger protein 409	-1.132
EXOC6B	exocyst complex component 6B	-1.124
GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	-1.121
SLC25A36	solute carrier family 25, member 36	-1.107
FLNB	filamin, beta	-1.102
Tgtp1	T-cell specific GTPase 2; T-cell specific GTPase	-1.096
Cxcl9	chemokine (C-X-C motif) ligand 9	-1.095
prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	-1.085
SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	-1.083
Sbf2	SET binding factor 2	-1.051
Necap1	NECAP endocytosis associated 1	-1.048
LNPEP	leucyl/cystinyl aminopeptidase	-1.043
ITCH	itchy, E3 ubiquitin protein ligase	-1.041
SACM1L	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	-1.036
bchE	butyrylcholinesterase	-1.031
DENND4C	DENN/MADD domain containing 4C	-1.023
YES1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	-1.020

Gene Symbol	Gene Name	35d Fold Change
FAM126B	family with sequence similarity 126, member B	-1.015
NBEAL1	neurobeachin like 1	-1.009
agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	-1.007
STON1	stonin 1	-1.006
CDKN1A	cyclin-dependent kinase inhibitor 1A (P21)	-1.000
Cpsf6	cleavage and polyadenylation specific factor 6	-0.994
Lifr	leukemia inhibitory factor receptor	-0.992
DNAJC28	DnaJ (Hsp40) homolog, subfamily C, member 28	-0.988
Nnat	neuronatin	-0.984
FPGT	fucose-1-phosphate guanylyltransferase	-0.981
IKZF5	IKAROS family zinc finger 5	-0.979
Pknox1	Pbx/knotted 1 homeobox	-0.974
CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1; carcinoembryonic antigen-related cell adhesion molecule 2	-0.974
MEX3C	mex3 homolog C (C. elegans)	-0.971
YY2	membrane-bound transcription factor peptidase, site 2; similar to zinc finger, X-linked, duplicated B; Yy2 transcription factor	-0.959
ARL5B	ADP-ribosylation factor-like 5B	-0.958
JMJD1C	jumonji domain containing 1C	-0.951
Zfp568	zinc finger protein 568	-0.951
lpgat1	lysophosphatidylglycerol acyltransferase 1	-0.951
USP34	ubiquitin specific peptidase 34	-0.946
IRS1	insulin receptor substrate 1	-0.944
Zfp800	zinc finger protein 800	-0.937
PCDH12	protocadherin 12	-0.923
Ankrd13c	ankyrin repeat domain 13c	-0.922
abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	-0.919
1200011I18Rik	RIKEN cDNA 1200011I18 gene	-0.919
DCUN1D2	DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)	-0.918
TMC7	transmembrane channel-like gene family 7; similar to Tmc7 protein	-0.918
SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	-0.916
1110037F02Rik	RIKEN cDNA 1110037F02 gene	-0.914
Kitl	kit ligand	-0.913
DPY19L4	dpy-19-like 4 (C. elegans)	-0.911
NFYA	nuclear transcription factor-Y alpha	-0.911
B630005N14Rik	RIKEN cDNA B630005N14 gene	-0.911
ELL2	elongation factor RNA polymerase II 2	-0.910
4930523C07Rik	RIKEN cDNA 4930523C07 gene	-0.910

Gene Symbol	Gene Name	35d Fold Change
ARHGAP5	Rho GTPase activating protein 5	-0.910
ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	-0.909
2610305D13Rik	RIKEN cDNA 2610305D13 gene	-0.907
Skil	SKI-like	-0.901
smek1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	-0.899
thrB	thyroid hormone receptor beta	-0.898
RGS4	regulator of G-protein signaling 4	-0.897
PDIK1L	PDLIM1 interacting kinase 1 like	-0.892
Zc3h11a	zinc finger CCCH type containing 11A	-0.892
CD83	CD83 antigen	-0.890
CYLD	cylindromatosis (turban tumor syndrome)	-0.890
1700081L11Rik	hypothetical protein LOC100043982; RIKEN cDNA 1700081L11 gene	-0.888
Tsga10	testis specific 10	-0.883
lysmd3	LysM, putative peptidoglycan-binding, domain containing 3	-0.881
ZMYM1	zinc finger, MYM domain containing 1	-0.879
Sox7	SRY-box containing gene 7	-0.879
PTPN4	protein tyrosine phosphatase, non-receptor type 4	-0.879
rgs3	regulator of G-protein signaling 3	-0.878
Med14	mediator complex subunit 14	-0.877
VPS13A	vacuolar protein sorting 13A (yeast)	-0.873
Klhdc1	kelch domain containing 1	-0.870
Zfp420	zinc finger protein 420	-0.869
eml4	echinoderm microtubule associated protein like 4	-0.868
DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1c	-0.864
AGTPBP1	ATP/GTP binding protein 1	-0.864
Enpp4	ectonucleotide pyrophosphatase/phosphodiesterase 4	-0.863
ZBTB1	similar to Zinc finger and BTB domain containing 1; zinc finger and BTB domain containing 1	-0.862
TMX3	thioredoxin-related transmembrane protein 3	-0.861
PHKA1	phosphorylase kinase alpha 1	-0.859
cstf2	cleavage stimulation factor, 3' pre-RNA subunit 2	-0.858
MME	membrane metallo endopeptidase	-0.857
ARHGAP29	Rho GTPase activating protein 29	-0.856
camsap1l1	calmodulin regulated spectrin-associated protein 1-like 1	-0.856
Abca6	ATP-binding cassette, sub-family A (ABC1), member 6	-0.855
3110057O12Rik	RIKEN cDNA 3110057O12 gene; predicted gene 2011	-0.854
Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	-0.853
ZZZ3	zinc finger, ZZ domain containing 3; predicted gene 8261	-0.852
ITGB6	integrin beta 6	-0.851

Gene Symbol	Gene Name	35d Fold Change
ubr7	ubiquitin protein ligase E3 component n-recognin 7 (putative)	-0.847
Trp53inp1	transformation related protein 53 inducible nuclear protein 1	-0.844
6530418L21Rik	RIKEN cDNA 6530418L21 gene	-0.840
DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27	-0.838
Ccdc141	RIKEN cDNA 2610301F02 gene	-0.837
2310014F06Rik	RIKEN cDNA 2310014F06 gene	-0.836
TBC1D14	similar to mKIAA1322 protein; TBC1 domain family, member 14	-0.836
4932441K18Rik	predicted gene 8258; similar to factor inhibiting activating transcription factor 4 (ATF4)-mediated transcription; RIKEN cDNA 4932441K18 gene	-0.833
NOL9	nucleolar protein 9	-0.833
SCGB1C1	secretoglobin, family 1C, member 1	-0.833
PHF6	PHD finger protein 6	-0.832
MFSD8	major facilitator superfamily domain containing 8	-0.829
TLR4	toll-like receptor 4	-0.828
GTF2H1	general transcription factor II H, polypeptide 1; similar to 62 kDa subunit of TFIIH	-0.827
uckl1	uridine-cytidine kinase 1-like 1	-0.827
RASA2	RAS p21 protein activator 2	-0.825
SLC31A2	solute carrier family 31, member 2	-0.820
BEND7	BEN domain containing 7	-0.809
MOBKL1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	-0.804
clpB	ClpB caseinolytic peptidase B homolog (E. coli)	-0.799
Zfp191	zinc finger protein 191	-0.796
FCHO2	FCH domain only 2	-0.794
Pla2g16	phospholipase A2, group XVI	-0.792
PPP1R15B	protein phosphatase 1, regulatory (inhibitor) subunit 15b	-0.791
Olfr558	olfactory receptor 558	-0.787
Fam116a	family with sequence similarity 116, member A	-0.783
RABEP1	rabaptin, RAB GTPase binding effector protein 1	-0.782
ralgapa1	GTPase activating RANGAP domain-like 1	-0.782
prps2	phosphoribosyl pyrophosphate synthetase 2	-0.782
ATP7A	ATPase, Cu++ transporting, alpha polypeptide	-0.780
Hist2h2aa1	histone cluster 2, H3b; histone cluster 1, H3f; histone cluster 1, H3e; histone cluster 2, H3c1; histone cluster 1, H3d; histone cluster 1, H3c; histone cluster 1, H3b; histone cluster 2, H3c2; histone cluster 2, H2aa1; histone cluster 2, H2aa2	-0.779
DGKH	diacylglycerol kinase, eta	-0.778
Tial1	Tia1 cytotoxic granule-associated RNA binding protein-like 1	-0.778
DPYD	dihydropyrimidine dehydrogenase	-0.778
Crem	cAMP responsive element modulator	-0.778

Gene Symbol	Gene Name	35d Fold Change
CEPT1	choline/ethanolaminephosphotransferase 1	-0.778
rnf26	hypothetical protein LOC100048200; ring finger protein 26; predicted gene 9008	-0.776
fgf13	fibroblast growth factor 13	-0.776
D930016D06 Rik	RIKEN cDNA D930016D06 gene	-0.775
EEA1	early endosome antigen 1	-0.774
AK129341	similar to CDNA sequence AK129341; cDNA sequence AK129341	-0.773
NF1	neurofibromatosis 1	-0.773
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	-0.773
pex1	peroxisomal biogenesis factor 1	-0.772
Atp8b1	ATPase, class I, type 8B, member 1	-0.770
Olfr1036	olfactory receptor 1036	-0.770
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	-0.769
6720456H20Rik	RIKEN cDNA 6720456H20 gene	-0.768
GTF3C4	general transcription factor IIIC, polypeptide 4	-0.762
mudeng	MU-2/AP1M2 domain containing, death-inducing	-0.762
tmem33	transmembrane protein 33	-0.762
sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated); similar to PTB-associated splicing factor	-0.760
Gpld1	glycosylphosphatidylinositol specific phospholipase D1	-0.755
Acot1	acyl-CoA thioesterase 1	-0.755
Ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha; RIKEN cDNA 3222402P14 gene	-0.753
QTRTD1	queuine tRNA-ribosyltransferase domain containing 1	-0.753
C430048L16Rik	RIKEN cDNA C430048L16 gene	-0.751
SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12	-0.750
HSPH1	heat shock 105kDa/110kDa protein 1	-0.749
IPO11	importin 11	-0.747
NCK1	non-catalytic region of tyrosine kinase adaptor protein 1	-0.747
KDM3A	lysine (K)-specific demethylase 3A	-0.746
ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	-0.741
MAP3K8	mitogen-activated protein kinase kinase kinase 8	-0.739
SHPRH	SNF2 histone linker PHD RING helicase	-0.738
RSBN1L	round spermatid basic protein 1-like	-0.736
Golga1	golgi autoantigen, golgin subfamily a, 1	-0.735
NUP98	nucleoporin 98	-0.735
ASB15	ankyrin repeat and SOCS box-containing 15	-0.734
MTPAP	mitochondrial poly(A) polymerase	-0.733

Gene Symbol	**Gene Name**	**35d Fold Change**
SLC20A1	solute carrier family 20, member 1	-0.732
RB1CC1	RB1-inducible coiled-coil 1	-0.732
FMR1	fragile X mental retardation syndrome 1 homolog	-0.731
NAA30	N-acetyltransferase 12	-0.731
BMI1	Bmi1 polycomb ring finger oncogene	-0.729
ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	-0.728
pkn2	protein kinase N2	-0.728
Ctage5	CTAGE family, member 5	-0.727
SFMBT1	Scm-like with four mbt domains 1	-0.727
AFF4	AF4/FMR2 family, member 4	-0.726
Taf5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-0.725
pstpip2	proline-serine-threonine phosphatase-interacting protein 2	-0.724
Bcl3	B-cell leukemia/lymphoma 3	-0.724
etnk1	ethanolamine kinase 1	-0.722
KLHL9	kelch-like 9 (Drosophila)	-0.718
gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	-0.717
PDS5A	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	-0.715
Zfp354a	zinc finger protein 354A	-0.714
senp8	SUMO/sentrin specific peptidase 8	-0.710
2010321M09 Rik	RIKEN cDNA 2010321M09 gene	-0.709
gtf2h2	general transcription factor II H, polypeptide 2	-0.705
TANK	TRAF family member-associated Nf-kappa B activator	-0.705
MYO1D	myosin ID	-0.705
1810074P20Rik	RIKEN cDNA 1810074P20 gene	-0.704
Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	-0.703
Gimap9	GTPase, IMAP family member 9	-0.702
RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	-0.700
PRDM10	PR domain containing 10	-0.700
IFIH1	interferon induced with helicase C domain 1	-0.700
BC016423	cDNA sequence BC016423	-0.696
DNM1L	dynamin 1-like	-0.695
5730601F06Rik	RIKEN cDNA 5730601F06 gene	-0.695
TNNI3K	TNNI3 interacting kinase	-0.694
ELAC1	elaC homolog 1 (E. coli)	-0.693
CDKN2AIP	CDKN2A interacting protein	-0.692
Zfp128	zinc finger protein 128	-0.691
AV039307	expressed sequence AV039307	-0.690
Trpc3	transient receptor potential cation channel, subfamily C, member 3	-0.689

Gene Symbol	Gene Name	35d Fold Change
FAM89A	hypothetical protein LOC100047808; family with sequence similarity 89, member A; similar to mammary tumor virus receptor 2 isoform-like	-0.689
TXNDC11	thioredoxin domain containing 11	-0.687
Mospd2	motile sperm domain containing 2	-0.687
INPP4B	inositol polyphosphate-4-phosphatase, type II	-0.684
SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	-0.683
SYNJ1	synaptojanin 1	-0.683
Zfp386	zinc finger protein 386 (Kruppel-like)	-0.683
prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-0.682
COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	-0.682
Sptlc2	serine palmitoyltransferase, long chain base subunit 2	-0.682
WARS2	tryptophanyl tRNA synthetase 2 (mitochondrial)	-0.681
ACTR6	ARP6 actin-related protein 6 homolog (yeast)	-0.681
ST7L	suppression of tumorigenicity 7-like	-0.681
nsun6	NOL1/NOP2/Sun domain family member 6	-0.675
Ube2ql1	RIKEN cDNA 3110006E14 gene	-0.675
HAUS2	HAUS augmin-like complex, subunit 2	-0.673
CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	-0.672
ZFP62	zinc finger protein 62	-0.671
1110020G09Rik	RIKEN cDNA 1110020G09 gene	-0.671
CCNG2	cyclin G2	-0.669
BC049349	cDNA sequence BC049349	-0.668
Zfp799	zinc finger protein 799	-0.665
Fam108b	family with sequence similarity 108, member B	-0.665
IMPAD1	inositol monophosphatase domain containing 1	-0.663
FUBP1	far upstream element (FUSE) binding protein 1	-0.662
NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	-0.661
LANCL2	LanC (bacterial lantibiotic synthetase component C)-like 2	-0.661
CPEB4	cytoplasmic polyadenylation element binding protein 4	-0.659
CHD9	chromodomain helicase DNA binding protein 9	-0.659
AI607873	expressed sequence AI607873	-0.659
COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	-0.658
smug1	single-strand selective monofunctional uracil DNA glycosylase	-0.658
SLC30A9	solute carrier family 30 (zinc transporter), member 9	-0.655
crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	-0.653
tbc1d23	TBC1 domain family, member 23	-0.653
PYGO2	pygopus 2	-0.651
KDM1B	amine oxidase, flavin containing 1	-0.651
TOM1L1	target of myb1-like 1 (chicken)	-0.650

Gene Symbol	Gene Name	35d Fold Change
Phf10	PHD finger protein 10	-0.649
Gm12337	predicted gene 12337; predicted gene 10039; predicted gene 4479; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	-0.648
Ncoa2	nuclear receptor coactivator 2	-0.646
Snx13	sorting nexin 13	-0.646
ALG10B	asparagine-linked glycosylation 10 homolog B (yeast, alpha-1,2-glucosyltransferase)	-0.646
E430024P14Rik	RIKEN cDNA E430024P14 gene	-0.645
MTMR10	myotubularin related protein 10	-0.644
Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	-0.644
CNOT4	CCR4-NOT transcription complex, subunit 4	-0.644
AFF1	AF4/FMR2 family, member 1	-0.644
Zfp644	zinc finger protein 644	-0.644
Shq1	SHQ1 homolog (S. cerevisiae)	-0.643
1110018J18Rik	hypothetical protein LOC100044674; RIKEN cDNA 1110018J18 gene	-0.641
vps37a	vacuolar protein sorting 37A (yeast); similar to Vps37a protein	-0.640
B3GALNT2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2	-0.639
ociad1	OCIA domain containing 1	-0.639
Exoc2	exocyst complex component 2	-0.638
MAPK1	mitogen-activated protein kinase 1	-0.637
Zfp281	zinc finger protein 281	-0.636
Ccdc137	coiled-coil domain containing 137	-0.635
Pde1c	phosphodiesterase 1C	-0.634
INTU	inturned planar cell polarity effector homolog (Drosophila)	-0.634
KIT	kit oncogene	-0.634
Zfp715	zinc finger protein 715	-0.633
Kcnip2	Kv channel-interacting protein 2	-0.632
KPNA1	karyopherin (importin) alpha 1	-0.632
PDGFD	platelet-derived growth factor, D polypeptide	-0.632
1110028C15Rik	RIKEN cDNA 1110028C15 gene	-0.631
TSC22D2	TSC22 domain family, member 2	-0.631
BPTF	bromodomain PHD finger transcription factor	-0.631
Eif3e	eukaryotic translation initiation factor 3, subunit E	-0.630
Slc29a1	solute carrier family 29 (nucleoside transporters), member 1	-0.628
TRMT61B	tRNA methyltransferase 61 homolog B (S. cerevisiae)	-0.625
sirt1	sirtuin 1 (silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	-0.625
KDM3B	KDM3B lysine (K)-specific demethylase 3B	-0.624

Gene Symbol	Gene Name	35d Fold Change
NUBPL	predicted gene 7514; nucleotide binding protein-like	-0.624
CWF19L2	hypothetical protein LOC100044213; CWF19-like 2, cell cycle control (S. pombe)	-0.623
Gpr116	G protein-coupled receptor 116	-0.623
Nipa2	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	-0.622
LNX2	ligand of numb-protein X 2	-0.621
Larp4	La ribonucleoprotein domain family, member 4; predicted gene 14373; predicted gene 8177	-0.620
SOX18	SRY-box containing gene 18	-0.619
Tmod4	tropomodulin 4	-0.618
tpp2	tripeptidyl peptidase II	-0.618
MTFR1	mitochondrial fission regulator 1	-0.616
WDR13	WD repeat domain 13	-0.615
TMTC1	transmembrane and tetratricopeptide repeat containing 1	-0.615
tmed7	transmembrane emp24 protein transport domain containing 7	-0.614
Ulk2	Unc-51 like kinase 2 (C. elegans)	-0.612
4930486L24Rik	RIKEN cDNA 4930486L24 gene	-0.612
Spnb1	spectrin beta 1	-0.611
IMMT	inner membrane protein, mitochondrial	-0.611
MTMR1	myotubularin related protein 1	-0.610
PTPRG	protein tyrosine phosphatase, receptor type, G; similar to protein tyrosine phosphatase, receptor type, G	-0.610
Tmed5	transmembrane emp24 protein transport domain containing 5; similar to Transmembrane emp24 protein transport domain containing 5	-0.610
Gm13111	predicted gene 13111	-0.609
NCOA6	nuclear receptor coactivator 6	-0.609
CTNNA3	catenin (cadherin associated protein), alpha 3	-0.608
ERAP1	endoplasmic reticulum aminopeptidase 1	-0.608
Rnf170	ring finger protein 170	-0.608
DPEP1	dipeptidase 1 (renal)	-0.608
Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	-0.608
HEY2	hairy/enhancer-of-split related with YRPW motif 2	-0.605
Plxna2	plexin A2	-0.604
1110018G07Rik	RIKEN cDNA 1110018G07 gene	-0.604
CCDC25	coiled-coil domain containing 25	-0.604
SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	-0.603
Tbk1	TANK-binding kinase 1	-0.602
MLH3	mutL homolog 3 (E coli)	-0.602
irak3	interleukin-1 receptor-associated kinase 3	-0.602

Gene Symbol	Gene Name	35d Fold Change
ARMC1	armadillo repeat containing 1	-0.602
RNF214	ring finger protein 214	-0.601
bmpr2	bone morphogenic protein receptor, type II (serine/threonine kinase)	-0.601
TIAM2	T-cell lymphoma invasion and metastasis 2	-0.601
ORC4L	origin recognition complex, subunit 4-like (S. cerevisiae)	-0.599
1190005F20Rik	RIKEN cDNA 1190005F20 gene	-0.599
AP3M1	adaptor-related protein complex 3, mu 1 subunit; similar to Adapter-related protein complex 3 mu 1 subunit (Mu-adaptin 3A) (AP-3 adapter complex mu3A subunit)	-0.599
A130022J15Rik	RIKEN cDNA A130022J15 gene	-0.599
Serpinb6b	serine (or cysteine) peptidase inhibitor, clade B, member 6b	-0.597
2410042D21Rik	RIKEN cDNA 2410042D21 gene	-0.595
Zfp131	zinc finger protein 131; similar to putative transcription factor ZNF131	-0.595
UBOX5	U box domain containing 5	-0.594
taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-0.594
NT5E	5' nucleotidase, ecto	-0.593
atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	-0.593
UBA6	ubiquitin-like modifier activating enzyme 6	-0.593
DENND5B	DENN/MADD domain containing 5B	-0.591
SH3TC2	SH3 domain and tetratricopeptide repeats 2	-0.591
TRIM34	similar to tripartite motif protein TRIM34 alpha; tripartite motif-containing 34; similar to Tripartite motif protein 34	-0.590
9930021J03Rik	RIKEN cDNA 9930021J03 gene	-0.590
Rrm2b	ribonucleotide reductase M2 B (TP53 inducible); predicted gene 8616; hypothetical protein LOC674236	-0.589
TMEM168	transmembrane protein 168	-0.587
NUP35	predicted gene 4353; nucleoporin 35	-0.587
Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	-0.586
Trpc1	transient receptor potential cation channel, subfamily C, member 1	-0.586
Lsp1	lymphocyte specific 1	0.588
ZDHHC4	zinc finger, DHHC domain containing 4	0.593
OLFML3	olfactomedin-like 3	0.598
LOC100134990	selenoprotein K pseudogene	0.599
EXTL1	exostoses (multiple)-like 1	0.605
SUV420H2	suppressor of variegation 4-20 homolog 2 (Drosophila)	0.608

Gene Symbol	Gene Name	35d Fold Change
bolA2	bolA-like 2 (E. coli)	0.609
EXOC3L	exocyst complex component 3-like	0.609
pemt	phosphatidylethanolamine N-methyltransferase	0.614
Myg1	melanocyte proliferating gene 1	0.615
Naglu	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	0.616
SLC39A13	solute carrier family 39 (metal ion transporter), member 13	0.617
FAM18A	family with sequence similarity 18, member A	0.619
2610002J02Rik	RIKEN cDNA 2610002J02 gene	0.620
RHOD	ras homolog gene family, member D	0.620
TMEM97	transmembrane protein 97; predicted gene 5809	0.624
Susd2	sushi domain containing 2	0.626
rpap1	RNA polymerase II associated protein 1	0.627
PLA2G15	phospholipase A2, group XV	0.627
1010001B22Rik	RIKEN cDNA 1010001B22 gene	0.632
CTSZ	cathepsin Z	0.639
Flt3l	FMS-like tyrosine kinase 3 ligand	0.639
pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	0.643
2310057J16Rik	RIKEN cDNA 2310057J16 gene	0.644
6720463M24 Rik	RIKEN cDNA 6720463M24 gene	0.644
FOXO3	forkhead box O3	0.654
map2k6	mitogen-activated protein kinase kinase 6	0.661
1810024B03Rik	RIKEN cDNA 1810024B03 gene	0.662
GLI1	GLI-Kruppel family member GLI1	0.667
STXBP2	syntaxin binding protein 2	0.671
SH3BP1	similar to SH3-domain binding protein 1; SH3-domain binding protein 1; similar to SH3 domain-binding protein 1 (3BP-1)	0.672
MYL6B	myosin, light polypeptide 6B	0.675
nfix	nuclear factor I/X	0.680
Mfsd7a	major facilitator superfamily domain containing 7A	0.680
Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	0.681
MRGPRE	MAS-related GPR, member E	0.682
capG	capping protein (actin filament), gelsolin-like	0.686
Zfp688	zinc finger protein 688	0.687
SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	0.690
Ccl21a	chemokine (C-C motif) ligand 21A; predicted gene 1987	0.692
ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand; predicted gene 8539	0.695
Pak6	p21 protein (Cdc42/Rac)-activated kinase 6	0.697

Gene Symbol	Gene Name	35d Fold Change
Il1rl2	interleukin 1 receptor-like 2	0.700
PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	0.706
1110038F14Rik	RIKEN cDNA 1110038F14 gene	0.706
NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	0.709
FIGF	c-fos induced growth factor	0.711
Scd2	stearoyl-Coenzyme A desaturase 2	0.714
TMEM219	transmembrane protein 219	0.719
FAM109B	family with sequence similarity 109, member B	0.719
galT	galactose-1-phosphate uridyl transferase	0.725
1700120C14Rik	RIKEN cDNA 1700120C14 gene	0.742
Gm129	predicted gene 129	0.743
PLD4	phospholipase D family, member 4	0.745
RCOR2	REST corepressor 2	0.750
AI413582	expressed sequence AI413582; hypothetical protein LOC100044974	0.752
Fam46b	family with sequence similarity 46, member B	0.753
Cpt1c	carnitine palmitoyltransferase 1c	0.759
C1RL	complement component 1, r subcomponent-like	0.769
SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	0.769
haus4	HAUS augmin-like complex, subunit 4	0.772
CEND1	cell cycle exit and neuronal differentiation 1	0.780
Mtap6	microtubule-associated protein 6	0.784
PNPLA2	patatin-like phospholipase domain containing 2	0.790
LAPTM5	lysosomal-associated protein transmembrane 5	0.793
phf19	PHD finger protein 19	0.803
TMPRSS13	transmembrane protease, serine 13	0.813
Ppfia4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	0.814
tspan4	tetraspanin 4	0.822
CEP164	centrosomal protein 164	0.827
Per1	period homolog 1 (Drosophila)	0.832
Ccdc136	coiled-coil domain containing 136	0.834
Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.845
CD37	CD37 antigen	0.849
DPF3	D4, zinc and double PHD fingers, family 3	0.850
calml4	calmodulin-like 4	0.859
MAMSTR	MEF2 activating motif and SAP domain containing transcriptional regulator	0.866
Pacsin1	protein kinase C and casein kinase substrate in neurons 1	0.879
Atxn7l1	ataxin 7-like 1	0.885

Gene Symbol	**Gene Name**	**35d Fold Change**
F10	coagulation factor X	0.899
Cd247	CD247 antigen	0.915
Cyp4f16	cytochrome P450, family 4, subfamily f, polypeptide 16	0.934
fbxl19	F-box and leucine-rich repeat protein 19	0.947
2300009N04Rik	RIKEN cDNA 2300009N04 gene	0.975
2200002D01Rik	RIKEN cDNA 2200002D01 gene	0.982
5930430L01Rik	RIKEN cDNA 5930430L01 gene	0.989
Dnase2a	deoxyribonuclease II alpha	1.007
PRRT2	proline-rich transmembrane protein 2	1.092
SV2A	synaptic vesicle glycoprotein 2 a	1.139
Iqgap3	IQ motif containing GTPase activating protein 3	1.147
AGER	advanced glycosylation end product-specific receptor	1.185
Aldh3b1	aldehyde dehydrogenase 3 family, member B1	1.232
Ptprs	protein tyrosine phosphatase, receptor type, S	1.464

Section D - 1 Gene			
Gene Symbol	**Gene Name**	**10d Fold Change**	**10+25d Fold Change**
Ubxn10	UBX domain protein 10	-0.819	0.652

Section E - 31 genes			
Gene Symbol	**Gene Name**	**10+25d Fold Change**	**35d Fold Change**
FSD1L	fibronectin type III and SPRY domain containing 1-like	-0.864	-1.152
IFI44	interferon-induced protein 44	-0.735	-0.958
ABLIM1	actin-binding LIM protein 1	-1.145	-0.885
Gm5069	predicted gene 5069	1.027	0.635
2410018L13Rik	RIKEN cDNA 2410018L13 gene	0.821	0.661
lipA	lysosomal acid lipase A	0.659	0.678
2610036A22Rik	RIKEN cDNA 2610036A22 gene	1.342	0.707
Gm4987	predicted gene 4987	1.075	0.714
PARL	presenilin associated, rhomboid-like	0.796	0.732
Fam58b	predicted gene 9731; RIKEN cDNA 1810009O10 gene	0.937	0.738
Hspg2	perlecan (heparan sulfate proteoglycan 2)	0.721	0.754
MFF	mitochondrial fission factor; hypothetical protein LOC637796	1.129	0.783
Ifi27l2a	interferon, alpha-inducible protein 27 like 2A	0.865	0.787
TRIM11	tripartite motif-containing 11	0.690	0.825
TRAF5	TNF receptor-associated factor 5	0.737	0.834
ANG2	angiogenin, ribonuclease A family, member 2	0.967	0.839
Hmgb1-rs17	high mobility group box 1, related sequence 17	1.030	0.859
Tuba3a	predicted gene 5366; tubulin, alpha 3B; tubulin, alpha 3A	1.277	0.859
SALL2	sal-like 2 (Drosophila)	0.755	0.883
AU040829	expressed sequence AU040829	1.215	0.918
H2-Q10	histocompatibility 2, Q region locus 10	1.933	0.937
LOC547349	similar to MHC class I antigen precursor; predicted gene 10499	1.458	0.940

Gene Symbol	Gene Name	10+25d Fold Change	35d Fold Change
Aldoart1	predicted gene 8659; aldolase 1, A isoform, retrogene 1	1.393	0.942
Gm6316	predicted gene 6316	1.397	0.976
FCGR3	Fc receptor, IgG, low affinity III	1.233	0.988
Csl	citrate synthase like	1.626	1.011
Gm6498	predicted gene 6498	1.731	1.030
CYB5R4	cytochrome b5 reductase 4	1.138	1.032
FGD4	FYVE, RhoGEF and PH domain containing 4	1.247	1.096
HMMR	hyaluronan mediated motility receptor (RHAMM)	1.440	1.386
Cd300c	CD300C antigen; hypothetical protein LOC100044158	1.533	1.554

Section F - 83 genes			
Gene Symbol	**Gene Name**	**10d Fold Change**	**35d Fold Change**
arntl	aryl hydrocarbon receptor nuclear translocator-like	-2.089	-2.000
zbtb11	zinc finger and BTB domain containing 11	-2.031	-0.823
ISOC1	isochorismatase domain containing 1	-1.938	-0.610
ZDHHC17	zinc finger, DHHC domain containing 17	-1.811	-0.770
CLOCK	circadian locomoter output cycles kaput	-1.798	-0.863
NUDT12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	-1.743	-0.972
NR3C1	nuclear receptor subfamily 3, group C, member 1	-1.727	-1.149
DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	-1.722	-1.374
Twsg1	twisted gastrulation homolog 1 (Drosophila)	-1.721	-0.760
CCDC109A	coiled-coil domain containing 109A	-1.715	-0.762
JMY	junction-mediating and regulatory protein	-1.673	-0.687
CDC42BPA	CDC42 binding protein kinase alpha	-1.660	-1.154

Gene Symbol	Gene Name	10d Fold Change	35d Fold Change
Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.651	-1.119
Zfml	zinc finger, matrin-like	-1.645	-1.082
SLC19A2	solute carrier family 19 (thiamine transporter), member 2	-1.556	-0.780
ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	-1.494	-0.642
RBM26	RNA binding motif protein 26	-1.487	-0.878
Gm14446	predicted gene 14446	-1.466	-0.908
MITF	microphthalmia-associated transcription factor	-1.446	-0.764
ARID4B	AT rich interactive domain 4B (RBP1-like)	-1.360	-0.723
dhdh	dihydrodiol dehydrogenase (dimeric)	-1.352	-0.701
MIER1	mesoderm induction early response 1 homolog (Xenopus laevis	-1.318	-1.157
Slfn5	schlafen 5; hypothetical protein LOC100047131	-1.316	-0.881
slc39a9	solute carrier family 39 (zinc transporter), member 9	-1.299	-0.800
BRWD1	bromodomain and WD repeat domain containing 1	-1.250	-1.070
MON2	MON2 homolog (yeast)	-1.247	-0.797
Cep57	centrosomal protein 57	-1.242	-0.636
Erbb2ip	Erbb2 interacting protein	-1.234	-0.716

Gene Symbol	**Gene Name**	**10d Fold Change**	**35d Fold Change**
RPS27A	predicted gene 5928; predicted gene 12617; predicted gene 4802; similar to ribosomal protein S27a; predicted gene 13215; predicted gene 6111; predicted gene 7808; predicted gene 6014; predicted gene 8317; ubiquitin C; ubiquitin B; similar to fusion protein: ubiquitin (bases 43_513); ribosomal protein S27a (bases 217_532); similar to ubiquitin B; predicted gene 8649; ribosomal protein S27A; predicted gene 11517; predicted gene 11808; predicted gene 8430; RIKEN cDNA 2810422J05 gene; similar to Ubc protein; predicted gene 13815; ubiquitin A-52 residue ribosomal protein fusion product 1; predicted gene 8797; predicted gene 1821; predicted gene 11759; predicted gene 5239; predicted gene 6438	-1.224	-0.737
Vprbp	Vpr (HIV-1) binding protein	-1.218	-0.931
9030420J04Rik	RIKEN cDNA 9030420J04 gene	-1.205	-0.919
SIAE	sialic acid acetylesterase	-1.192	-0.668
D14Abb1e	DNA segment, Chr 14, Abbott 1 expressed	-1.184	-1.017
PAQR3	progestin and adipoQ receptor family member III	-1.157	-0.597
SASH1	SAM and SH3 domain containing 1; predicted gene 2082	-1.146	-0.820
NPAS2	neuronal PAS domain protein 2	-1.138	-0.916
ZMAT1	zinc finger, matrin type 1	-1.135	-0.786
HUS1	Hus1 homolog (S. pombe)	-1.112	-0.596
ZC3H12C	zinc finger CCCH type containing 12C	-1.111	-0.750
TTC9C	tetratricopeptide repeat domain 9C	-1.095	-0.664

Gene Symbol	Gene Name	10d Fold Change	35d Fold Change
RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	-1.088	-1.119
DLG1	discs, large homolog 1 (Drosophila); similar to Discs, large homolog 1 (Drosophila)	-1.081	-0.782
suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	-1.058	-0.874
Cdk6	cyclin-dependent kinase 6	-1.050	-0.599
lats1	large tumor suppressor	-1.046	-0.969
UNC119B	unc-119 homolog B (C. elegans)	-1.045	-0.643
ATP5G1	predicted gene 12337; predicted gene 10039; predicted gene 4479; ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	-0.998	-0.648
NUP160	nucleoporin 160	-0.991	-0.851
BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	-0.990	-0.849
TUBGCP5	tubulin, gamma complex associated protein 5	-0.977	-0.604
Pcf11	cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	-0.966	-0.689
H13	histocompatibility 13	-0.961	-0.756
AFTPH	aftiphilin	-0.961	-0.631
0610007P08Rik	RIKEN cDNA 0610007P08 gene	-0.948	-0.593
Fam150b	family with sequence similarity 150, member B	-0.938	-1.263
EVI5	ecotropic viral integration site 5	-0.915	-0.763
Atf2	activating transcription factor 2; similar to Cyclic AMP-dependent transcription factor ATF-2 (Activating transcription factor 2) (cAMP response element-binding protein CRE-BP1) (MXBP protein)	-0.907	-0.816

Gene Symbol	**Gene Name**	**10d Fold Change**	**35d Fold Change**
Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)	-0.906	-0.759
SMURF2	SMAD specific E3 ubiquitin protein ligase 2; similar to SMAD specific E3 ubiquitin protein ligase 2	-0.830	-0.784
FNDC3A	fibronectin type III domain containing 3A	-0.802	-0.828
ASAH2	N-acylsphingosine amidohydrolase 2	-0.791	-0.663
CNOT2	CCR4-NOT transcription complex, subunit 2	-0.776	-0.642
Papola	poly (A) polymerase alpha	-0.753	-0.722
AMBRA1	autophagy/beclin 1 regulator 1	-0.752	-0.630
Foxk2	forkhead box K2	-0.699	-0.699
FAM179B	family with sequence similarity 179, member B	-0.681	-1.017
CHD1	chromodomain helicase DNA binding protein 1	-0.647	-0.586
Thap2	THAP domain containing, apoptosis associated protein 2	-0.636	-0.984
FMNL2	formin-like 2	-0.625	-0.657
FAM189B	RIKEN cDNA 1110013L07 gene	0.588	0.601
Tspan17	tetraspanin 17	0.699	0.658
Rgs10	regulator of G-protein signalling 10	0.734	0.819
DNM1	dynamin 1	0.763	0.625
LTC4S	leukotriene C4 synthase	0.792	0.619
IFFO1	intermediate filament family orphan 1	0.798	0.619
dbp	D site albumin promoter binding protein	0.818	0.737
Wdr62	similar to WD repeat domain 62; WD repeat domain 62	0.827	0.841
EMID1	EMI domain containing 1	0.846	1.080
Hjurp	RIKEN cDNA 6430706D22 gene; similar to RIKEN cDNA 6430706D22 gene; RIKEN cDNA A730008H23 gene	0.903	0.660
1110038B12Rik	RIKEN cDNA 1110038B12 gene	0.907	0.774
camk1	calcium/calmodulin-dependent protein kinase I	0.929	0.797

Gene Symbol	**Gene Name**	**10d Fold Change**	**35d Fold Change**
CUL5	cullin 5	1.548	-0.700
per3	period homolog 3 (Drosophila)	2.108	0.903

Section G - 1 Gene				
Gene Symbol	**Gene Name**	**10d Fold Change**	**10+25d Fold Change**	**35d Fold Change**
Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	0.887	-0.794	0.765

Supplemental Table 4: Differential Promoter DNA Methylation for MDMA-associated Differentially Expressed Genes

10d MDMA			
Gene ID	**Gene Symbol**	**Hypermethylated Peaks**	**Hypomethylated Peaks**
BC004850	Twsg1	16	0
NM_001142924	Tcf7l2	14	0
NM_019883	RPS27A	11	0
NM_007964	EVI5	10	0
BC010210	GAA	8	3
NM_206958	Ltbp1	8	0
BC145775	ACVR1B	7	0
NM_001029990	METT11D1	7	5
NM_011112	Papola	7	0
NM_027052	Slc38a4	7	0
BC010445	Hsp90b1	6	0
NM_011882	RNASEL	6	2
NM_016801	STX1A	6	1
NM_026440	rnmt	6	0
NM_031397	BICC1	6	0
BC005583	DARC	5	0
BC014739	Ik	5	0
BC053104	Zfp516	5	0
BC131653	DSG2	5	0
BC132193	B3GNTL1	5	0
BC152329	ALOX12	5	0
NM_001081022	D430042O09Rik	5	0
NM_001162533	1700029G01Rik	5	0
NM_010771	MATR3	5	0
NM_010831	Sik1	5	0
NM_025691	SRP72	5	0
NM_153560	FAM102A	5	0
BC009653	npepps	4	0
BC018376	PRPF31	4	0
BC062125	Hjurp	4	0
BC115538	6230427J02Rik	4	3
BC115937	PGM5	4	0
BC132595	esrrb	4	2
BC148292	SLC4A4	4	0
NM_001033259	CCDC109A	4	0
NM_001162921	ZC3H12C	4	0
NM_001163026	DNAJC13	4	0
NM_010605	Kcnj5	4	0

Gene ID	**Gene Symbol**	**Hypermethylated Peaks**	**Hypomethylated Peaks**
NM_011068	PEX11A	4	0
NM_013791	MKLN1	4	0
NM_021504	ngly1	4	0
NM_144925	TNRC6A	4	0
NM_145358	camkk2	4	0
BC010719	NFYB	3	0
BC013766	DNAJC3	3	0
BC013807	CD86	3	0
BC014714	HMGCS2	3	0
BC021750	NRM	3	0
BC026369	D19Wsu162e	3	0
BC046459	E4F1	3	1
BC055732	keap1	3	0
BC058602	OSBP2	3	0
BC086652	HEATR5B	3	0
BC099556	CYB5D1	3	2
BC148725	DGKE	3	0
NM_001081064	Pdzd2	3	0
NM_001085472	ACIN1	3	4
NM_001159634	Bat2l	3	0
NM_001163159	Pcyt1a	3	0
NM_001163502	C130039O16Rik	3	0
NM_011067	per3	3	0
NM_023596	Slc29a3	3	0
NM_028820	1700017B05Rik	3	0
NM_153585	Cnot10	3	0
NM_198894	ABR	3	0
BC010585	BCL11A	2	0
BC012707	GstT2	2	0
BC020316	phf17	2	0
BC027099	Ubxn10	2	0
BC028528	BC028528	2	0
BC055834	ikbip	2	0
BC113144	WFIKKN2	2	0
BC148308	dagla	2	0
NM_001045528	FKBP15	2	0
NM_001081288	Taf2	2	0
NM_001113248	Sin3b	2	0
NM_001143755	LRRC27	2	0
NM_001159636	WDSUB1	2	0
NM_001161775	MYH11	2	0
NM_007823	cyp4b1	2	0

Gene ID	Gene Symbol	Hypermethylated Peaks	Hypomethylated Peaks
NM_009670	ANK3	2	0
NM_010398	H2-T23	2	0
NM_010860	myl6	2	0
NM_016680	SFRS16	2	0
NM_016920	ATP6V0A1	2	0
NM_025481	SMURF2	2	0
NM_028826	SEPT14	2	0
NM_057171	bat3	2	0
NM_146207	cul4a	2	0
NM_177226	Zfp629	2	0
NM_178884	Obsl1	2	0
BC004612	PREPL	1	0
BC004650	stk24	1	0
BC004833	KPNA6	1	0
BC005547	TUBB2C	1	1
BC010346	Tspan17	1	0
BC011036	bpnt1	1	0
BC018425	WNT5A	1	1
BC025557	EIF5	1	0
BC043314	itih5	1	0
BC052909	LRMP	1	0
BC092058	sf3a3	1	1
BC100569	CPSF3	1	0
BC106091	Erbb3	1	0
BC108991	ATP6V0A2	1	0
BC115521	LXN	1	0
BC119182	NTN4	1	0
BC119216	CEP76	1	0
BC132383	FBXL16	1	7
NM_001033285	CDC42BPA	1	0
NM_001038700	Fnbp1	1	0
NM_001077636	Pigw	1	3
NM_001081203	Sbno1	1	0
NM_001083587	TNS3	1	1
NM_001103179	BRWD1	1	0
NM_001109905	STAU1	1	0
NM_001110275	ITSN1	1	0
NM_001159551	H13	1	0
NM_001161618	CUL5	1	0
NM_001163311	srr	1	0
NM_001163741	1110021J02Rik	1	0
NM_001164099	ADD3	1	0

Gene ID	**Gene Symbol**	**Hypermethylated Peaks**	**Hypomethylated Peaks**
NM_001165983	Ubap2l	1	0
NM_008306	NDST1	1	0
NM_008441	KIF1B	1	0
NM_008983	PTPRK	1	0
NM_010898	Nf2	1	0
NM_011510	ABCC8	1	0
NM_011714	baz1b	1	0
NM_016717	SCLY	1	0
NM_021540	RNF130	1	1
NM_024281	RRBP1	1	0
NM_026361	PKP4	1	0
NM_027130	AFG3L2	1	0
NM_146186	Wdr62	1	0
NM_153599	cdk8	1	0
NM_153791	FLYWCH1	1	0
NM_172536	Zfp609	1	0
NM_172938	SCML4	1	0
NM_172967	4930503L19Rik	1	0
NM_173390	nhsl1	1	0
NM_175128	4930430F08Rik	1	0
NM_183029	Igf2bp2	1	0
NM_183201	Slfn5	1	0
BC010442	E430018J23Rik	0	1
BC132373	Txnl4b	0	1
BC157054	Fyco1	0	1
NM_010751	MXD1	0	1
NM_023734	PI16	0	1
NM_030225	DLST	0	1
NM_031999	GPR137B	0	1
BC005699	fbxl12	0	2
BC029088	tmem129	0	2
BC075648	8430427H17Rik	0	2
BC121789	Myh7	0	2
NM_001081453	nin	0	2
NM_001130450	NFE2L1	0	2
NM_001135657	PTPRJ	0	2
NM_007862	DLG1	0	2
NM_009410	Top3a	0	2
NM_153139	SLC36A1	0	2
NM_153587	RPS6KA5	0	2
NM_203491	CHRM2	0	2
BC094230	NRIP2	0	3

Gene ID	**Gene Symbol**	**Hypermethylated Peaks**	**Hypomethylated Peaks**
BC156704	ABLIM2	0	3
NM_001081061	BDP1	0	3
NM_001164159	SAPS3	0	3
BC156640	Endou	0	4
NM_001014995	FAM189B	0	4
NM_001166391	F13A1	0	5
	TOTAL	420	94

10+25d MDMA			
Gene ID	**Gene Symbol**	**Hypermethylated Peaks**	**Hypomethylated Peaks**
NM_011413	C4a	46	0
BC020072	ATP8	41	0
NM_009449	Tuba3a	24	0
NM_029963	Mrps5	21	0
NM_181858	Cd59b	16	0
NM_011508	Eif1	12	0
BC025976	Ckmt1	10	0
NM_010381	h2-aa	10	0
BC037629	PCK1	9	0
NM_025343	Rmnd1	9	0
BC051196	RETN	8	0
BC049873	Acat3	7	0
NM_013552	HMMR	7	0
NM_001126338	Prnd	7	0
BC031809	RBP4	7	0
BC028770	ADIPOQ	6	0
NM_001110009	Apoc1	5	0
NM_001142706	CFB	5	0
NM_008305	Hspg2	5	0
NM_178789	TMEM117	5	0
NM_011633	TRAF5	5	0
BC031357	tubb3	5	0
NM_027144	ARHGEF12	5	2
BC011118	CEBPA	5	3
NM_012029	Ecsit	4	0
BC027099	Ubxn10	4	0
BC156787	Gm6316	4	1
NM_011599	TLE1	4	8
NM_007639	Cd1d1	3	0
BC121789	Myh7	3	0
NM_008503	rps2	3	0
NM_177129	CNTN2	3	1
NM_011652	TTN	3	1
NM_001102404	acp5	2	0
NM_001039646	EG634650	2	0
NM_013614	ODC1	2	0
BC099676	CIDEC	1	0
BC050750	Csl	1	0
NM_139233	FGD4	1	0
BC011215	H2-Q10	1	0
BC111882	IFI44	1	0

Gene ID	Gene Symbol	Hypermethylated Peaks	Hypomethylated Peaks
BC010274	KCNN4	1	0
BC058564	lipA	1	0
BC016597	MFF	1	0
BC055453	Scd1	1	0
NM_019765	CLIP1	1	2
BC037431	DCUN1D1	0	1
BC027438	galE	0	1
NM_001085510	Gm4987	0	2
NM_001081208	HS3ST5	0	2
NM_019464	sh3glb1	0	2
NM_013665	shox2	0	2
BC011129	CAR3	0	3
	TOTAL	327	31

35d MDMA			
Gene ID	**Gene Symbol**	**Hypermethylated Peaks**	**Hypomethylated Peaks**
BC020175	DNAJC28	15	0
BC036984	Nnat	15	0
BC145856	Olfr1036	14	0
NM_001099742	SCGB1C1	13	0
BC004850	Twsg1	12	0
NM_010686	LAPTM5	10	0
NM_021713	Myg1	10	0
BC018323	dbp	9	0
BC052183	6720463M24Rik	8	0
BC061182	AGER	8	0
BC023032	CEND1	8	0
NM_009449	Tuba3a	8	0
BC096430	BEND7	7	0
BC018378	HSPH1	7	0
BC006771	KPNA1	7	0
NM_001159593	SLC20A1	7	0
BC008171	SLC25A36	7	0
BC046597	Aldh3b1	6	0
NM_001113391	Cd247	6	0
BC066155	Cpt1c	6	0
BC048814	NUP35	6	0
NM_172715	AGPAT9	5	0
NM_001033436	Atxn7l1	5	0
NM_001024504	DCUN1D2	5	0
BC075652	map2k6	5	0
NM_001081981	nfix	5	0
BC068020	Tmod4	5	0
NM_207228	Tsga10	5	0
NM_001039198	Zfhx2	5	0
NM_001033355	Zfp568	5	0
BC145708	B630005N14Rik	4	0
BC026662	Ccdc137	4	0
NM_001114879	D14Abb1e	4	0
BC038001	Fam46b	4	0
BC019201	GPAM	4	0
NM_001146703	MAMSTR	4	0
BC010318	pck2	4	0
BC109178	Rgs10	4	0
NM_001033865	RPS27A	4	0
NM_011633	TRAF5	4	0
NM_026137	WDR13	4	0

Gene ID	Gene Symbol	Hypermethylated Peaks	Hypomethylated Peaks
NM_198957	C430048L16Rik	3	0
BC058778	CNOT4	3	0
BC011215	H2-Q10	3	0
NM_013552	HMMR	3	0
NM_001159564	ITGB6	3	0
NM_001025208	LOC547349	3	0
NM_016985	MTMR1	3	0
BC005485	OLFML3	3	0
NM_016670	Pknox1	3	0
BC024911	TMEM168	3	0
NM_025970	ZBTB8OS	3	0
BC096552	Zfp799	3	0
BC003216	2410042D21Rik	2	0
NM_176850	BPTF	2	0
NM_177788	EXOC3L	2	0
NM_007972	F10	2	0
NM_008156	Gpld1	2	0
BC062125	Hjurp	2	0
NM_019424	Hps1	2	0
NM_008305	Hspg2	2	0
NM_029665	IPO11	2	0
BC120727	Lmbrd2	2	0
BC130227	MIER1	2	0
BC055074	MTMR10	2	0
BC002015	NCK1	2	0
BC003763	PIP5K1A	2	0
NM_026869	PYGO2	2	0
NM_153762	rnf26	2	0
BC046587	SV2A	2	0
NM_198630	1810024B03Rik	1	0
NM_025826	ACADSB	1	0
BC019496	agt	1	0
NM_001025093	Atf2	1	0
BC061197	bolA2	1	0
BC003480	capG	1	0
NM_001033259	CCDC109A	1	0
BC003492	DPEP1	1	0
BC046610	ERAP1	1	0
NM_001005868	Erbb2ip	1	0
NM_001081213	ermp1	1	0
NM_030257	lysmd3	1	0
BC121789	Myh7	1	0

Gene ID	**Gene Symbol**	**Hypermethylated Peaks**	**Hypomethylated Peaks**
NM_013792	Naglu	1	0
NM_027777	pex1	1	0
BC018418	Pfkfb2	1	0
BC002206	Phf10	1	0
NM_001102563	PRRT2	1	0
BC099447	SLC31A2	1	0
BC129910	Tbk1	1	0
BC063048	UBA6	1	0
BC110396	vps37a	1	0
BC117788	ZDHHC17	1	0
	TOTAL	371	0