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## Comparative Epigenomics of Human and Mouse Mammary Tumors

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### Abstract

Gene silencing by aberrant epigenetic chromatin alteration is a well-recognized event contributing to tumorigenesis. While genetically engineered tumor-prone mouse models have proven a powerful tool in understanding many aspects of carcinogenesis, to date few studies have focused on epigenetic alterations in mouse tumors. To uncover epigenetically silenced tumor suppressor genes (TSGs) in mouse mammary tumor cells, we conducted initial genome-wide screening by combining the treatment of cultured cells with the DNA demethylating drug 5-aza-2'-deoxycytidine (5-azadC) and the histone deacetylase inhibitor trichostatin A (TSA) with expression microarray. By conducting this initial screen on EMT6 cells and applying protein function and genomic structure criteria to genes identified as upregulated in response to 5-azadC/TSA, we were able to identify 2 characterized breast cancer TSGs (*Timp3* and *Rprm*) and 4 putative TSGs (*Atp1B2*, *Dusp2*, *FoxJ1* and *Smpd3*) silenced in this line. By testing a panel of ten mouse mammary tumor lines, we determined that each of these genes is commonly hypermethylated, albeit with varying frequency. Furthermore, by examining a panel of human breast tumor lines and primary tumors we observed that the human orthologs of *ATP1B2*, *FOXJ1* and *SMPD3* are aberrantly hypermethylated in the human disease while *DUSP2* was not hypermethylated in primary breast tumors. Finally, we examined hypermethylation of several genes targeted for epigenetic silencing in human breast tumors in our panel of ten mouse mammary tumor lines. We observed that the orthologs of *Cdh1*, *RarB*, *Gstp1*, *RassF1* genes were hypermethylated, while neither *Dapk1* nor *Wif1* were aberrantly methylated in this panel of mouse tumor lines. From this study, we conclude that there is significant, but not absolute, overlap in the epigenome of human and mouse mammary tumors.

### INTRODUCTION

Tumorigenesis is a multi-step process stemming from increased oncogene activity in concert with constrained tumor suppressor gene (TSG) activity (Weinberg 1996). Such disease-producing changes in cellular phenotype result from dysregulation of gene expression and/or protein function attributable to genetic and/or epigenetic changes within the genome.

Several well-studied TSGs and other growth regulatory genes undergo de novo hypermethylation and consequential transcriptional silencing in human cancer cells. Aberrant cytosine methylation leading to gene silencing occurs at discreet, clustered 5'-

CG-3' dinucleotides (referred to as CpG islands) within the genome (Bird 1992). This cancer-associated CpG methylation is part of a complex set of epigenetic events that transform chromatin from a transcriptionally-active to an inactive state (Wolffe 2001) and epigenetic gene silencing is now widely recognized as either a causative or correlative event in tumor development (Jones and Baylin 2002; Robertson 2005) and is now widely regarded as one of the 'hits' in the Knudsen hypothesis leading to TSG inactivation (Jones and Laird 1999).

In recent years, numerous laboratories have developed tumor-prone mouse models owing to engineered over-expression of oncogenes or lost TSG expression. Clearly, these models have provided a powerful tool in studying tumorigenesis and unique insight into the molecular mechanisms that give rise to cancer in humans. For example, *BRCA1*, a TSG associated with breast and ovarian tumors in humans (Bishop 1999; Struwing et al., 1997), when conditionally deleted within the mammary epithelium of p53 heterozygous mice greatly increases mammary tumor incidence (Xu et al., 1999). This observation lends strong evidence as to the role *BRCA1* plays in breast tumor suppression.

What remains less explored is the role that epigenetics plays during tumorigenesis in mice. While it seems straightforward to presume that gene silencing occurs in a parallel fashion in both human and mouse tumors, mice have not been widely utilized as a platform for either the discovery of epigenetically silenced genes or to study the role that gene silencing plays in the process of tumorigenesis. In one of the few studies to utilize a tumor-prone model system to dissect epigenetic events during disease progression, Yu et al (2005a) used Restriction Landmark Genomic Scanning (RLGS) to investigate aberrant DNA methylation events in a mouse model of T/natural killer acute lymphoblastic leukemia. These investigators observed nonrandom, aberrant DNA methylation occurring during tumorigenesis but was not present in benign preleukemic cells. Further, the inhibitor of DNA binding 4 (*Idb4*) gene was identified as a putative TSG silenced via promoter hypermethylation in mouse, and this gene was found epigenetically silenced in human leukemia as well. Similarly, Costello and colleagues found that *SLC5A8*, which encodes a sodium monocarboxylate cotransporter, was epigenetically silenced in both mouse and human brain tumors (Hong et al., 2005). These studies underscore the high potential of mice as a model system to understand the epigenetic basis of cancer and, potentially, other diseases as well.

A list of well-characterized TSG including *BRCA1*, *CDKN2A*, *SFN*, *CDH1*, and *CST6* are targets for epigenetic silencing in breast cancer (Dobrovic and Simpfordorfer 1997; Esteller et al., 2000; Ferguson et al., 2000; Nass et al., 2000; Holst et al., 2003; Ai et al., 2006). However, at present, we are unaware of any genes that have been identified as targets for epigenetic silencing in mouse mammary tumors. To initially address this question, we conducted a screen for epigenetically silenced genes in a mouse mammary tumor line using an approach termed "pharmacological unmasking" (Esteller 2007). This often used approach examines changes in gene expression in response to the global DNA demethylating drug 5-aza-2'-deoxycytidine (5-azadC) and the histone deacetylase (HDAC) inhibitor trichostatin A (TSA) via microarray. Our screen was conducted using a mouse mammary cell line and identified ~1,000 genes that were upregulated  $\geq 5$ -fold in response to 5-azadC/TSA in this line. Based on gene function and genomic architecture in mouse and man, several candidates identified in the initial screen were selected for further study.

## MATERIALS and METHODS

### Cell Culture and Drug Treatment

Mouse mammary tumor lines 410.4, 410 and 66.1 were obtained from Dr. A. Fulton (University of Maryland, Baltimore, MD), D2F2 and 4T1 from Dr. F. Miller (Karamanos Cancer Foundation, Detroit, MI), LM2 and LM3 from Dr. E. Bal de Kier Joffé (Universidad de Buenos Aires, Argentina) and D1K2 and NeuT from Dr. B. Law (University of Florida, Gainesville, FL). The mouse mammary tumor line EMT6 was purchased from American Type Culture Collection (ATCC, Manassas, VA).

LM2 and LM3 were grown in Eagle's MEM with 2 mM L-glutamine, 1.5g/L sodium bicarbonate, 0.1 mmol/L nonessential amino acids, and 1.0 mmol/L sodium pyruvate. 4T1 were cultured in RPMI 1640 with 2 mmol/L L-glutamine, 1.5 g/L sodium bicarbonate, 4.5 g/L glucose, 10 mmol/L HEPES, and 1.0 mmol/L sodium pyruvate. 410, 410.4, 66.1, NeuT, D2F2, and D1K2 were maintained in DMEM with 2mM L-glutamine, 0.1 mmol/L nonessential amino acids. EMT6 was cultured in Waymouth's MB 752/1 medium with 2mM L-glutamine. All cell lines were maintained in medium supplemented with 10% (v/v) heat-inactivated fetal bovine serum (Invitrogen, Carlsbad, CA) at 37°C in 5% CO<sub>2</sub> humidified atmosphere. Human breast tumor cell lines were cultured as previously outlined (Ai et al., 2006).

Where indicated, cell lines were treated with 5 µM 5-azadC for 5 days (fresh drug was added every 24 hours) followed by a 24-hour treatment with 100 nM TSA. All drugs were purchased from Sigma.

### Human Breast Tumor Specimens

Fifteen fresh-frozen archival breast tumors were obtained from the University of Florida Shands Cancer Center Molecular Tissue Bank. All specimens and pertinent patient information were treated in accordance with policies of the institutional review board (IRB) of the University of Florida Health Sciences Center. Tumors analyzed in this study were examined by a surgical pathologist and identified as invasive breast adenocarcinoma (stage II or III). Where indicated, matched normal breast tissue was obtained from disease-free surgical margin.

### Microarray Analysis

Total RNA was extracted from EMT6 cells either untreated or treated with the global DNA demethylating agent 5-aza-2'-deoxycytidine (5-azadC) and the histone deacetylase inhibitor (HDAC) TSA. The quantity and purity of the extracted RNA was evaluated using a Nanodrop ND-100 spectrophotometer (Nanodrop Technologies, Wilmington, DE) and its integrity measured using an Agilent Bioanalyzer. Five hundred nanograms (500 ng) of total RNA was amplified and labeled with a fluorescent dye (Cy3) using a Low RNA Input Linear Amplification Labeling kit (Agilent Technologies, Palo Alto, CA). Abundance and quality fluorescently labeled cRNA was also assessed using a Nanodrop ND-1000 spectrophotometer and an Agilent Bioanalyzer. The labeled cRNA (1.65 µg) was hybridized to an Agilent Mouse Whole Genome Oligo Microarray (Agilent Technologies, Inc., Palo Alto, CA) for 17 hrs prior to washing and scanning. Data was extracted from scanned images using Agilent's Feature Extraction Software.

### Gene Expression Analysis by RT-PCR

RT-PCR was carried out according to established protocols (Ai et al., 2006). Briefly, untreated and 5-azadC/TSA treated mouse mammary tumor cells were homogenized in Trizol (Invitrogen), and total RNA purified according to the manufacturer's instructions.

First-strand cDNA synthesis was carried out using SuperScript III reverse transcriptase (Invitrogen). Subsequently, this cDNA was used in PCR reactions using *Timp3*, *Rprm*, *Smpd3*, *Atp1B2*, *Dusp2* and *FoxJ1*-specific oligonucleotide primers as listed in Supplemental Table I. Mouse glyceraldehyde-3-phosphate dehydrogenase (*Gapdh*) served as a control to assure equivalent RNA in each reaction. Following PCR, reactions were analyzed by electrophoresis on 10% polyacrylamide gels followed by staining with ethidium bromide.

### Extraction and Sodium Bisulfite Modification of Genomic DNA

Genomic DNA (gDNA) was isolated from human breast tumor tissue samples and cultured human and mouse cell lines using a Qiagen Blood and Cell Culture DNA kit (Qiagen, Inc., Valencia, VA) and stored at  $-20^{\circ}\text{C}$  before use. DNA was modified with EZ DNA Methylation kit (ZYMO Research Co., Orange, CA) according to the manufacturer's instructions. Briefly,  $\sim 1.0$   $\mu\text{g}$  denatured gDNA was treated with sodium bisulfite at  $50^{\circ}\text{C}$  for  $\sim 16$  hours in the dark. Following this, samples were applied to supplied columns, desulfonation conducted, and DNA was subsequently eluted in a volume of 20  $\mu\text{L}$  with supplied elution buffer. One  $\mu\text{L}$  of bisulfite-converted gDNA solution was generally used in subsequent PCR reactions.

### Methylation Specific-PCR

Primers used for Methylation Specific-PCR (MSP) analyses are listed in Supplemental Table II. MSP reactions were conducted using Qiagen HotStarTaq DNA polymerase and supplied 1X PCR buffer supplemented with 0.1 mmol/L dNTPs, 2.5 mmol/L  $\text{MgCl}_2$ , and 0.5  $\mu\text{mol/L}$  each of forward and reverse primers and bisulfite-converted gDNA. Following thermocycling, PCR products were loaded 10% polyacrylamide gels and visualized using ethidium bromide.

Human placental gDNA (Biochain Institute, Hayward, CA) and mouse gDNA isolated from tail snips of wildtype C57BL/6 mice were used in primer validation experiments of human and mouse MSP, respectively and where indicated DNA was methylated *in vitro* using *SssI* methylase (NEB, Ipswich, MA) as outlined previously (Vo et al., 2004).

### Pyrosequencing

PCR reactions were conducted on bisulfite-converted gDNA as described above. Supplemental Table III summarizes pyrosequencing primers and sequence analyzed in each gene. Following PCR amplification using a biotinylated reverse primer, 5–20  $\mu\text{L}$  of PCR product was mixed with 2  $\mu\text{L}$  of streptavidin-coated sepharose beads (GE Healthcare Bio-Sciences AB, Uppsala, Sweden), 40  $\mu\text{L}$  of binding buffer (10 mM Tris-HCl, 2 M NaCl, 1mM EDTA, 0.1% Tween 20, pH 7.6), and brought up to 80  $\mu\text{L}$  total volume with  $\text{dH}_2\text{O}$ . This mixture was immobilized on streptavidin beads by shaking constantly at 1400 rpm for 10 minutes at RT. The beads were subsequently harvested using a vacuum preparation workstation and appropriate sequencing primer added to a final concentration of 330 nM. The sequencing primers were subsequently annealed to the template by incubating the samples at  $80^{\circ}\text{C}$  for 2 min and cooled at RT for 10 min prior to analysis. Pyrosequencing was conducted using a PyroMark MD system (Biotage AP, Uppsala, Sweden), and sequence analysis conducted using supplied software.

## RESULTS

The focus of this investigation was to compare mouse and human mammary cancer for potential overlap in tumor epigenotype across these two species. Our screening strategy entailed utilizing the mouse mammary tumor line EMT6 in a pharmacological unmasking

screen (Esteller 2007). Briefly, EMT6 cells were treated with the global DNA demethylating agent 5-aza-2'-deoxycytidine (5-azadC) and the histone deacetylase (HDAC) inhibitor trichostatin A (TSA) to de-repress epigenetically silenced genes. After drug treatment, which was found to have minimal toxicity in EMT6 cells by MTT assay (data not shown), total RNA was harvested from two replicate cultures of drug treated and untreated EMT6 cells and used to probe Agilent Mouse Whole Genome microarrays.

Of the ~44,000 transcripts measured on these microarrays, an average of 54% were detected as significantly above background levels in each of the hybridizations (range: 51 to 57%). The intensity values from the replicate samples for both the treated and untreated cultures had Pearson correlation values greater than 0.97, suggesting that the reproducibility of the results was very high. Reproducibility of the within-group samples, along with the differences between the two groups, were also apparent when the z-score transformed intensity values for the 2,252 transcripts found to be differentially expressed (984 upregulated, 1,268 downregulated) using an absolute fold change criterion of 5-fold and a log ratio p-value of 0.001 were compared (Fig 1).

### Identification of candidate epigenetically silenced genes in the EMT6 mouse mammary tumor cell line

Following the initial screen by expression microarray, we established a series of bioinformatic criteria to narrow our search for epigenetically silenced tumor suppressor genes (TSGs) in the EMT6 cell line. From the entire list of genes measured by the microarray, we first excluded genes that showed a moderate change in expression in response to 5-azadC/TSA. Therefore, we required that a candidate gene demonstrate at least a 5-fold increase with a log ratio *p*-value of 0.001 to be considered further. This narrowed our focus to 984 genes of interest (Fig 2). (A listing of all 984 genes identified is given in Supplemental Table IV.)

Next, we used protein function and genomic structure criteria to further define potential TSGs that are targets for epigenetic silencing in EMT6 cells. We were principally interested in studying genes that encode proteins with an established tumor suppressor activity(ies), or a function consistent with tumor suppressive activity. Specifically, we included in our study gene products where previously published studies support a gene function that either antagonizes cell growth, activates apoptosis or suppresses anti-apoptotic processes, restrains cellular invasiveness, or inhibits angiogenic processes.

We next excluded from the list of putative/characterized TSGs those genes that do not possess a canonical CpG island within 5' flanking region in both the human and mouse orthologs using the UC Santa Cruz genome browser (<http://genome.ucsc.edu>) to investigate genomic architecture of various candidate genes. We used the algorithm within the UCSC genome browser that scores the presence of CpG islands in genomic DNA using criteria originally established by Gardiner-Garden and Frommer (Gardiner-Garden and Frommer 1987). Our rationale for establishing these criteria is that genes which possess both features (*i.e.*, putative TSG activity and the presence of a CpG island that overlaps the translational start site of the gene) are likely to identify high-value candidate targets for epigenetic silencing. Of the 984 genes initially identified as being upregulated  $\geq 5$ -fold in our expression microarray screen, this bioinformatic investigation identified 37 genes meeting the outlined criteria (see Supplemental Table V). Of this, 26 genes were further investigated in this study.

Our next test was to confirm 5-azadC/TSA-induced upregulation of gene expression by RT-PCR. This revealed 12 genes where the gene upregulation detected by microarray was confirmed by RT-PCR and 14 genes whose upregulation could not be independently



confirmed using an independent set of RNA samples isolated from drug treated/untreated EMT6 cells. Methylation-Specific PCR (MSP), a common methodology to examine DNA methylation (Herman et al., 1996), was subsequently used to judge methylation within the CpG islands associated with remaining 12 candidate genes. This analysis revealed that six genes exhibited no methylation as judged by MSP. This may indicate that the 5-azadC/TSA-induced increase in expression of these genes is indirect in nature and/or that silencing of these genes is controlled by chromatin modifications other than CpG methylation (*e.g.*, transcriptionally-repressive histone modifications). The later of these possibilities is quite possible since our drug treatment regimen included the histone deacetylase inhibitor TSA. As a result of these efforts our focus narrowed to six genes: Tissue Inhibitor of Metalloproteinase 3 (*Timp3*), TP53-dependent G2 Arrest Mediator Candidate also termed Reprimo (*Rprm*), Sphingomyelin Phosphodiesterase 3 Neutral (*Smpd3*), ATPase, Na<sup>+</sup>/K<sup>+</sup> Transporting, Beta 2 Polypeptide (*Atp1B2*), Dual-Specificity Phosphatase 2 (*Dusp2*), and ForkheadboxJ1 (*FoxJ1*).

### Silencing of *Timp3* and *Rprm* in mouse mammary tumor cell lines

*Timp3* and *Rprm* are well-characterized TSGs silenced in human breast cancer (Bachman et al., 1999; Takahashi et al., 2005). To test how commonly these genes are epigenetically silenced in mouse mammary tumor lines, we acquired 9 distinct cultured mouse mammary tumor lines (designated 410.4, 410, LM3, LM2, D1K2, NeuT, D2F2, 66.1 and 4T1), in addition to the EMT6 cell line. As outlined above, RT-PCR was used to confirm increased expression in response to 5-azadC/TSA; however, due to high-levels of toxicity to this drug cocktail, we found that only four of these cell lines (EMT6, 410.4, 410, and LM3) showed sufficiently low toxicity (>75% viability 48 hrs after 5  $\mu$ M 5-azadC treatment) to be appropriate subjects for this experiment. These lines were cultured in the presence or absence of 5-azadC and TSA, total RNA harvested and subsequently cDNA synthesized. Results of this RT-PCR experiment clearly indicated that the abundance of *Timp3* and *Rprm* transcripts increased substantially following treatment of each line with 5-azadC/TSA (Fig 3A). Parallel reactions using primers specific for the mouse form of *Gapdh* confirmed equivalent RNA abundance in each PCR reaction.

We next investigated the methylation status of *Timp3* and *Rprm* in our full panel of mouse mammary tumor line by designing MSP primers using a publically available on-line primer design program ([www.mspprimer.org/cgi-mspprimer/design.cgi](http://www.mspprimer.org/cgi-mspprimer/design.cgi)). All primer sets designed for the analysis for DNA methylation status (both MSP and pyrosequencing analysis) were designed to assay DNA methylation at, or in close proximity to, the transcriptional start site (TSS) of candidate genes since this region is most likely to have undergone dense methylation during the process of epigenetic silencing (Bird 2002; Jones and Baylin 2002).

Primers were designed specific for both the mouse *Timp3* and *Rprm* genes and validated using mouse genomic DNA extracted from tail clippings of C57BL/6 mice. This mouse genomic DNA was either methylated *in vitro* with *SssI* methylase or not methylated prior to bisulfite conversion. MSP reactions conducted using this control DNA indicated that our designed primers discriminate between the *Timp3* and *Rprm* genes in either a methylated or unmethylated state (Fig 3B). Subsequently, these MSP primer sets were used to probe the methylation status of the *Timp3* and *Rprm* gene in our panel of 10 mouse mammary tumor cell lines (Fig 3C). With the exception of D2F2, a methylated-specific (M) amplicon was detected when the *Timp3* gene was analyzed using bisulfite-converted genomic DNA isolated from each cell line. While amplification of both unmethylated and methylated-specific MSP products is a common finding in MSP analysis (Herman et al., 1996), potentially attributable to heterogeneous promoter methylation within the tumor cell population, this result indicates the presence of methylated CpG within the *Timp3* gene in at

least a subset of cells of each line except D2F2 where the *Timp3* promoter appears to be unmethylated.

As an independent means of quantitatively analyzing DNA methylation, we conducted pyrosequencing on mouse *Timp3* and *Rprm* genes in the EMT6 and LM3 cell lines. Pyrosequencing, like MSP, analyzes bisulfite-converted genomic DNA as a template for PCR; however, pyrosequencing is conducted on PCR products amplified using primers that do not contain internal CpG dinucleotides. Thus, amplification occurs in a manner that is unbiased by DNA methylation status. Subsequently, methylation at distinct CpGs can be determined quantitatively in a pool of genomic DNA (Colella et al., 2003; Tost et al., 2003).

The primer design developed for the mouse *Timp3* gene allowed for analysis of 9 CpG dinucleotides within a ~45 bp portion of the CpG island associated with this gene. Pyrosequencing analysis, consistent with MSP results, indicated that *Timp3* was methylated in both EMT6 and LM3 cell lines. Moreover, all the CpG dinucleotides investigated using this approach displayed methylation suggesting a high level of methylation density, although CpG methylation was not uniform over the region interrogated. The average CpG methylation measured in this region was 79% in EMT6 and 76% in LM3 (Fig 3D). The pyrosequencing protocol developed for *Rprm* analyzed 6 CpG dinucleotides over a ~35 bp region of the CpG island within this gene. Similar to *Timp3* analysis, all CpG within this region of the *Rprm* gene exhibit significant methylation with average CpG methylation of 84% and 86% in EMT6 and LM3 cells, respectively (Fig 3E).

Pyrosequencing analysis was also conducted on control (mouse tail) DNA samples (Fig 3D,E). For both *Timp3* and *Rprm* genes, average CpG methylation measured was 7%, indicating very low levels of DNA methylation in this control DNA sample. This result indicates that methylation of the CpG islands associated with the *Timp3* and *Rprm* genes in the mouse genome is a tumor-associated event. Moreover, when our DNA methylation analysis is combined with the results of our RT-PCR experiments using the DNA demethylating agent 5-azadC, we conclude that the *Timp3* and *Rprm* genes are targeted for epigenetic silencing in mouse mammary tumor lines through aberrant gene methylation. Considering most of the 10 distinct cell lines display this feature, silencing of these genes is apparently a common event in cultured mouse mammary tumor cells. Since both *Timp3* and *Rprm* are also targets for epigenetic silencing in human breast tumor line and primary tumors, these results reinforce the validity of our expression microarray screen for epigenetically silenced genes in mouse mammary tumor lines and establish a point of epigenetic overlap between mouse and human mammary gland tumors.

### **The *Atp1B2*, *Smpd3*, *Dusp2* and *FoxJ1* genes are targets for epigenetic silencing in mouse mammary tumor cell lines**

In addition to *Timp3* and *Rprm*, our screen identified four genes (*Atp1B2*, *Smpd3*, *Dusp2* and *FoxJ1*) that were strong candidates for epigenetic silencing in the EMT6 line. RT-PCR was conducted on EMT6, 410.4, 410, and LM3 cells cultured in the presence or absence of 5-azadC/TSA using primers designed specifically for the mouse orthologs of these genes. RT-PCR analysis of the *Atp1B2* transcript in EMT6 cells showed a clear upregulation of this transcript in response to 5-azadC/TSA (Fig 4A). Conversely, 410.4 and LM3 cells displayed no detectable upregulation of *Atp1B2* expression and analysis of 410 cells showed a slight (~2-fold) increase in *Atp1B2* expression following 5-azadC/TSA treatment. RT-PCR results showed strong upregulation of *Dusp2* expression in 5-azadC/TSA treated EMT6, 410 and 410.4 cells while LM3 cells showed no increased expression of this gene in drug treated LM3 cells. *Smpd3* showed marked increases in gene expression in each cell line in response to 5-azadC/TSA. Similarly, *FoxJ1* showed clear upregulation in drug treated EMT6 and

LM3 cells while expression was more modestly increased in drug treated 410 and 410.4 cells.

Based on the positive RT-PCR results outlined above, we designed MSP primers for the mouse forms of the *Atp1B2*, *Smpd3*, *Dusp2* and *FoxJ1* genes. As shown (Fig 4B), validation experiments using *in vitro* methylated/unmethylated mouse genomic DNA confirmed that MSP primer sets were capable of determining the methylation state of each gene. In EMT6 and 410 cells, MSP analysis of the *Atp1B2* gene indicated abundant M-specific amplicon indicating that this gene is hypermethylated in these cell lines. This result is consistent with the increased expression of this gene observed in RT-PCR experiments. In 410.4 cells, slight amplification of the M-specific band was noted and no M-specific amplicon was detected when genomic DNA isolated from LM3 cells was assayed, indicating that methylation of this gene is not a prominent feature in this cell line. MSP analysis of the other lines in our panel of mouse mammary tumor cells indicated that only 66.1 cells display prominent amplification of the M-specific product from the *Atp1B2* gene. Reduced amplification of the M-specific product was observed in 4T1 and D2F2 cells while no M-specific product was obtained from the other 3 lines (LM2, D1K2 and NeuT) in our panel.

MSP analysis of the *Dusp2* gene in EMT6, 410.4 and 410 cells indicated strong amplification of the M-specific product (Fig 4C). When combined with the clear upregulation of the *Dusp2* transcript when each of these lines were treated with 5-azadC/TSA, this result indicates that this gene is epigenetically silenced in these lines. Conversely, no aberrant methylation of the *Dusp2* gene in LM3 cells was observed. In the remaining six lines in our panel, methylation of the *Dusp2* gene was observed in D1K2, NeuT and 66.1 cells and no M-specific amplicon was observed when LM2, D2F2 and 4T1 cells were assayed by MSP.

When the *Smpd3* gene was analyzed by MSP, methylation of this gene was observed in all of the cell lines in our panel with the exception of NeuT and D2F2 (Fig 4C). Since we observed upregulation of the *Smpd3* in each of the four cell lines treated with 5-azadC/TSA, MSP results are consistent with epigenetic silencing of the *Smpd3* gene in cultured mammary tumor lines. Similarly, all ten cultured mammary tumor lines displayed methylation of the *FoxJ1* gene as judged by MSP. Again, this is consistent with our observation of increased *FoxJ1* expression in 5-azadC/TSA treated cells and indicates that the *FoxJ1* is commonly targeted for epigenetic silencing in cultured mouse mammary tumor lines. In sum, these lines of experimentation indicate that the *Atp1B2*, *Dusp2*, *Smpd3* and *FoxJ1* genes are epigenetically silenced in mouse mammary tumor lines; however, the occurrence of these aberrant events is variable within this panel of cultured lines.

### **Analysis of ATP1B2, DUSP2, SMPD3 and FOXJ1 hypermethylation in human breast cancer lines and primary breast tumors**

The *ATP1B2*, *DUSP2*, *SMPD3* and *FOXJ1* genes have not previously been characterized as targets for epigenetic silencing in human breast tumors. Thus, we examined the methylation status of each of these genes in a panel of eight cultured human breast cancer cell lines by designing MSP primer sets for the human ortholog of each gene. Validation experiments using *in vitro* methylated/unmethylated human placental genomic DNA indicated that each of these primer sets can discriminate between methylated and unmethylated forms of these four genes (Fig 5A). MSP analysis of the *ATP1B2* gene in our panel of human breast tumor lines indicated robust amplification of the methylation-specific product in MCF-7, MDA-MB-435 and BT-474 cells while MDA-MB-468 cells show moderate accumulation of the M amplicon and low level amplification of the M product was observed in MDA-MB-231. Other lines in our panel (T-47D, BT-549 and SKBR3) displayed no evidence of *ATP1B2* methylation. MSP analysis of the *SMPD3* gene determined that MDA-MB-231, MDA-



MB-435 and BT-474 cells display methylation of this gene, while the other cell lines show no evidence of *SMPD3* methylation. Similarly, *DUSP2* was found to be methylated in MCF7, MDA-MB-231 and BT-549 cells but not in T-47D, MDA-MB-468, SKBR3, MDA-MB-435 and BT-474 cells. Finally, MSP analysis of the *FOXJ1* gene indicates strong amplification of the M-specific amplicon in MDA-MB-231, MDA-MB-435 and BT-474 cells. Weak amplification of the M-specific *FOXJ1* amplicon was observed in MCF-7, MDA-MB-468 and BT-549. No amplification of the *FOXJ1* M-specific product was observed in either T-47D or SKBR3 cells.

To confirm the MSP results obtained when the methylation status of the *ATP1B2*, *DUSP2*, *SMPD3* and *FOXJ1* genes was scored by MSP, we conducted pyrosequencing. The pyrosequencing assay developed for the human *ATP1B2* gene scores methylation of seven CpG dinucleotides within a ~30 nt region of the CpG island within the 5' end of the human *ATP1B2* gene. When genomic DNA harvested from MCF-7 cells was analyzed by pyrosequencing, we observed low (3%) to moderate (29%) levels of CpG methylation within this cell line in the *ATP1B2* gene (Fig 5C). Overall, average CpG methylation measured within the *ATP1B2* gene was 17% in this cell line. In BT-474 cells, we observed markedly higher methylation within the *ATP1B2* gene with average CpG methylation of 34%. Pyrosequencing of control (human placental) DNA showed a low level of CpG methylation (4.6%) in this gene.

Pyrosequencing analysis of the *SMPD3* gene showed high average levels of CpG methylation (56% and 71%) within the *SMPD3* gene in MDA-MB-231 and BT-474 cells, respectively (Fig 5D). Conversely, low levels of CpG methylation (0.8%) of the *SMPD3* gene was measured in control DNA. Consistent with MSP results, we observed methylation of the CpG island associated with the human *DUSP2* gene in MDA-MB-231 (88%) and BT-549 (44%) cells with low (5.5%) CpG methylation measured in control DNA (Fig 5E). We also observed CpG methylation within the human *FOXJ1* gene in MDA-MB-231 (40%) and BT-474 (63%) cells and control DNA displayed low (5.5%) CpG methylation within *FOXJ1* (Fig 5F). Taken together, both MSP and pyrosequencing analyses indicate that the *ATP1B2*, *DUSP2*, *SMPD3* and *FOXJ1* are aberrantly methylated, albeit at differing frequencies, in cultured human breast tumor lines.

Next, we conducted MSP analysis to examine *ATP1B2*, *DUSP2*, *SMPD3* and *FOXJ1* gene methylation in primary breast tumor/normal mammary tissue samples. Fifteen frozen human breast tumors were obtained and patient-matched disease-free breast tissue were obtained with two of these tumor samples (Tumor72 and Tumor75). Genomic DNA was isolated, bisulfite modified, and used in MSP reactions with primers specific for the *ATP1B2*, *DUSP2*, *SMPD3* and *FOXJ1* genes. In all normal breast tissue samples, we observed exclusive amplification of the unmethylated-specific (U) amplicon, indicating that these genes are not methylated in normal mammary tissue (Fig 6A). When patient-matched breast tumor samples were analyzed by MSP, we observed methylation of the *SMPD3* gene in both Tumor72 and Tumor75. Further, methylation of the *FOXJ1* gene was observed in Tumor72. No methylation of either *DUSP2* or *ATP1B2* was observed in either Tumor72 or Tumor75.

Figure 6B shows a representative subset of additional breast tumors analyzed by MSP. We observed methylation of the *SMPD3* gene in Tumor 62, 66 and 70. Overall, we observed *SMPD3* methylation in 60% of breast tumors investigated (9 out of 15). We observed methylation of the *ATP1B2* gene in Tumor 61, 68 and 70 and, overall, detected a 20% rate (3/15) of *ATP1B2* methylation in breast tumors. In contrast, *FOXJ1* was found to be commonly methylated in human breast tumors; specifically, we observed that 11 out of 15 tumors surveyed (73%) displayed aberrant *FOXJ1* methylation as scored by MSP. Taken

together, MSP analysis suggests that promoter hypermethylation the *ATP1B2*, *SMPD3* and *FOXJ1* occur in primary human breast tumors with varying occurrence.

Despite the fact that we documented hypermethylation of *DUSP2* in cultured human breast cancer lines, this gene was found to be unmethylated in all human breast tumors examined (Fig 6B). *DUSP2* encodes a phosphatase (also known as PAC1) that dephosphorylates and inactivates mitogen-activated protein (MAP) kinases (Chu et al., 1996) and is a transcriptional target of p53 in signalling apoptosis (Yin et al., 2003). These properties make this gene an excellent candidate TSG and *DUSP2* hypermethylation has been reported in prostate cancer (Yu et al., 2005b). However, we did not observe methylation of this gene in primary tumors leading us to conclude that epigenetic silencing of *DUSP2* in human breast cancer is likely a rare event.

### **Analysis of methylation status of characterized targets for epigenetic silencing in human breast tumors in cultured mouse mammary tumor lines**

Finally, we determined the methylation status of well-defined TSGs known to be targets for epigenetic silencing in human breast cancer in our panel of cultured mouse mammary tumor lines. We designed MSP primer sets to assay methylation within the CpG islands associated with the mouse orthologs of the *Cdh1*, *RarB*, *Gstp1*, *Dapk1*, *RassF1* and *Wif1* genes. Validation experiments using *in vitro* methylated/unmethylated mouse genomic DNA indicate that each of these primer sets can delineate gene methylation status (Fig 7A).

Our MSP analyses indicate that *RassF1* and *RarB* were commonly methylated in our panel of mouse mammary tumor lines with 90% and 80% showing significant methylation, respectively (Fig 7B). In contrast, methylation of *Cdh1* and *Gstp1* were far less commonly encountered in this panel of cell lines with 30% and 10%, respectively, displaying methylation of these genes. In all mouse mammary cell lines, we observed exclusive amplification of the unmethylated-specific products for *Dapk1* and *Wif1* genes indicating that neither gene is methylated in this panel of mouse cell lines.

## **DISCUSSION**

### **Comparative epigenomics of mouse and human mammary tumors**

By coupling genome-wide screening with bioinformatics analyses and inspection of publically available mouse and human genome sequence, we were able to characterize 6 candidate genes as targets for epigenetic silencing in the EMT6 line. These genes are: *Timp3*, *Rprm*, *Smpd3*, *Dusp2*, *Atp1B2*, and *FoxJ1*. Of these, *Timp3* and *Rprm* have already been characterized as TSGs and targets for epigenetic silencing in human breast and other tumor types (Esteller et al., 2001; Takahashi et al., 2005; Kim et al., 2006;). The fact that our initial screening identified these TSGs as silencing candidates in EMT6 underscores the successful nature of our initial screen. Moreover, since analysis of 10 distinct mouse mammary tumor lines shows that both *Timp3* and *Rprm* are commonly silenced in cell lines of this type, we conclude that both human and mouse mammary tumors share silencing of these tumor suppressor genes in common.

A combination of RT-PCR and MSP confirmed that *Smpd3*, *Dusp2*, *Atp1B2*, and *FoxJ1* are silenced in mouse mammary tumor lines. Our findings indicate that *Atp1B2* is a target, although likely an uncommon one, for silencing in mouse mammary cell lines. The other 3 genes identified in our screen appear to be more commonly hypermethylated in mouse mammary tumor lines. We observed significant amplification of the M-specific amplicon specific for *Dusp2* in 60% of the cell lines tested, *Smpd3* in 80%, and *FoxJ1* in 100%. When a panel of eight human breast tumor cell lines were assayed for methylation by pyrosequencing and/or MSP, we observed substantial methylation of the *ATP1B2* gene in

50% (4/8) cell lines assayed. Also, *SMPD3*, *DUSP2*, and *FOXJ1* methylation was detected in 38% (3/8) of the cell lines surveyed. Of note, methylation of each of these genes, with the exception of *DUSP2*, was observed in human primary breast tumors and MSP analysis of normal breast tissue showed methylation of these genes to be a disease-associated event. The fact that *DUSP2* methylation was observed in cultured human cell lines but not primary tumors strongly suggests that silencing of this gene is likely a rare event in human breast tumors.

As part of our study we also examined the methylation status of 6 genes known to be targets of epigenetic silencing in human breast tumors in our panel of cultured mouse mammary tumor lines. In this investigation the mouse ortholog of the *Cdh1*, *Gstp1*, *RarB*, *Wif1*, *RassF1*, and *Dapk1* genes were assayed by MSP. We observed, to various extents, that *Cdh1*, *Gstp1*, *RarB*, and *RassF1* were hypermethylated in our panel of mouse tumor lines. However, we obtained no evidence that either the *Wif1* or *Dapk1* genes are aberrantly methylated in any of these lines.

When the results of our studies on various epigenetically silenced genes in human and mouse cultured mammary tumor cell lines and human primary breast tumors are considered collectively, we conclude that there is significant overlap in the mammary tumor cell epigenome between these two species. Of the twelve genes studied, only *Wif1* and *Dapk1* were found not be silenced in both species. While *Dusp2* was found to be commonly hypermethylated in mouse cell lines, methylation of this gene was less commonly observed in cultured human lines and no evidence for hypermethylation was observed in primary human breast tumors. These results indicate that some genes targeted for epigenetic silencing in human breast tumors are also aberrantly methylated in mouse mammary tumor lines demonstrating considerable but not absolute overlap in the mammary tumor epigenome between these two species.

### **SMPD3, ATP1B2 and FOXJ1 as novel targets for epigenetic silencing in human breast cancer**

Sphingomyelinases (SMases) belong to a multigene family of phosphodiesterases. Each of the three well-characterized SMases (*SMPD1*, *SMPD2*, and *SMPD3*) hydrolyze sphingomyelin to ceramide and phosphocholine. The acid sphingomyelinase *SMPD1* is located in the endolysosomal compartment, while the neutral SMases (nSMases) *SMPD2* and *SMPD3* are located within the endoplasmic reticulum membranes and in the Golgi apparatus, respectively (Stoffel et al., 2007). nSMases are a major intracellular regulator of ceramide, a bioactive lipid.

Several lines of evidence support the view that the ability of nSMases contribute to proliferation of cancer cells and/or to their invasiveness. Of note, the *SMPD3* locus is present, as well as six members of the cadherin family, with chromosome 16q22.1, and genetic alterations in this region have been implicated in the progression of various cancers, notably breast cancer (Chalmers et al., 2001; Driouch et al., 1997). Moreover, it has recently been shown that reduction of ceramide levels due to inhibition of nSMase in Hs578T breast adenocarcinoma cells overexpressing caveolin-1 results in a significant enhancement in Akt activation a well-characterized pro-growth, pro-survival mechanism (Wu et al., 2007). Ample evidence also supports a role for ceramide in the activation of apoptosis. For example, Luberto et al (2002) showed inhibition of TNF- $\alpha$ -induced cell death in MCF7 cells using a novel inhibitor of nSMase activity. Data obtained in this study indicates that ceramide induces conformational changes in Bax and activates mitochondrial phosphatase 2A, which, in turn, dephosphorylates Bcl-2. These two events clearly link ceramide and nSMases to the activation of cell death. Similarly, studies link ceramide to the regulation of

cell cycle progression by inducing growth arrest by promoting dephosphorylation of the Rb tumor suppressor (Alesse et al., 1998).

In this report, we show that the *SMPD3* gene in both mouse and man is a target for epigenetic silencing in mammary tumors. To our knowledge, this is the first report of the *SMPD3* gene being targeted for silencing during tumorigenesis. Functionally, this aberrant event will result in decreased ceramide production in response to normal physiological cues promoting dysregulation of both cellular death and growth programs. Thus, this event has clear implications in the process of breast tumorigenesis.

The protein encoded by *ATP1B2* is a member of the Na<sup>+</sup>/K<sup>+</sup> ATPase beta chain protein family. Na<sup>+</sup>/K<sup>+</sup> ATPases, which are composed of two subunits (a large catalytic subunit (alpha) and a smaller glycoprotein subunit (beta)), are integral membrane proteins responsible for establishing and maintaining the electrochemical gradients of Na<sup>+</sup> and K<sup>+</sup> ions across the plasma membrane. This process is essential for osmoregulation, for sodium-coupled transport of a variety of organic and inorganic molecules, and for electrical excitability of nerve and muscle (Dobretsov and Stimers 2005).

The adhesion molecule on glia (AMOG) protein was originally identified as a neural cell adhesion molecule and controls neuron–astrocyte adhesion as well as neural cell migration *in vitro* (Antonicek et al., 1987), was later found to be encoded by the *ATP1B2* gene (Gloor et al., 1990). Others (van den Boom et al., 2006) recently showed that the *ATP1B2* gene was targeted for epigenetic silencing via aberrant gene methylation in malignant glioma cells. This finding, supported by the observation that reduced ATP1B2 expression is associated with increased tumor grade (Senner et al., 2003), led these investigators to propose that *ATP1B2* silencing could be a significant event in glioma development. Our results indicate that *Atp1B2* is epigenetically silenced in a subset of cell lines in our panel of mouse mammary tumor lines and its human ortholog is subject to gene hypermethylation in both human breast tumor cell lines and primary tumors. Given the role that this gene product plays in controlling glial migration, these findings suggest that silencing of *ATP1B2* may influence breast tumor cell migration as well. This compelling notion requires further investigation.

FOXJ1 is a member of the fork head gene family of transcription factors originally identified in *Drosophila*, and a large family of FOX genes are currently characterized in humans (Kato 2004). In mammalian cells, FOXJ1 has been shown to suppress NFκB transcriptional activity *in vitro* and suppress inflammation *in vivo* (Lin et al., 2004). While NFκB is a key regulator of immune response, dysregulation of NFκB often drives deregulated growth, resistance to apoptosis, and increased metastatic potential (Lu and Stark 2004). Since FOXJ1 functions as an antagonist to NFκB activity it is reasonable to suggest that this molecule functions as a TSG, and others have commented that FOXJ1 is an excellent candidate for anti-cancer therapy (Chen 2004). While the role of FOXJ1 in cancer suppression remains to be explored, our finding that this gene is a common target for aberrant hypermethylation in both cultured cells and primary tumors strongly suggests that FOXJ1 silencing is potentially an important event in breast tumorigenesis.

In conclusion, our study has documented considerable, but not absolute, overlap exists between the epigenome of mouse and human mammary tumors. This finding supports the possible utility of using mouse as a model system to understand early epigenetic events during tumorigenesis as well as the general impact of aberrant chromatin remodeling events in cancer. Moreover, our study revealed several putative TSG that are novel targets for epigenetic silencing in human breast cancer.

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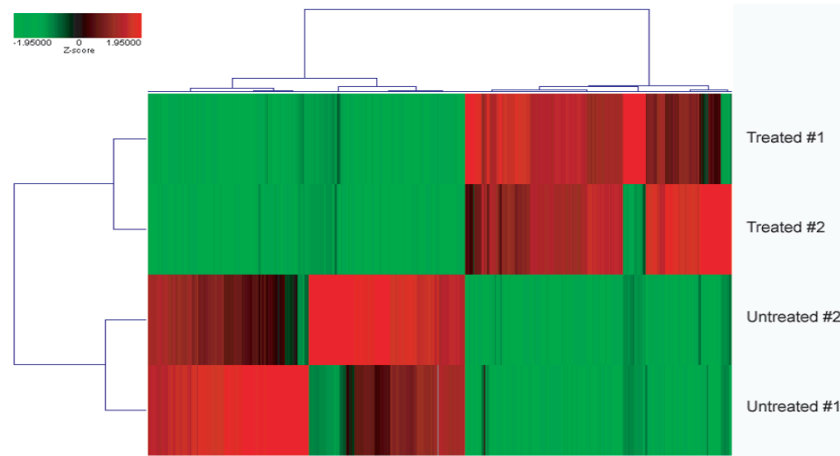
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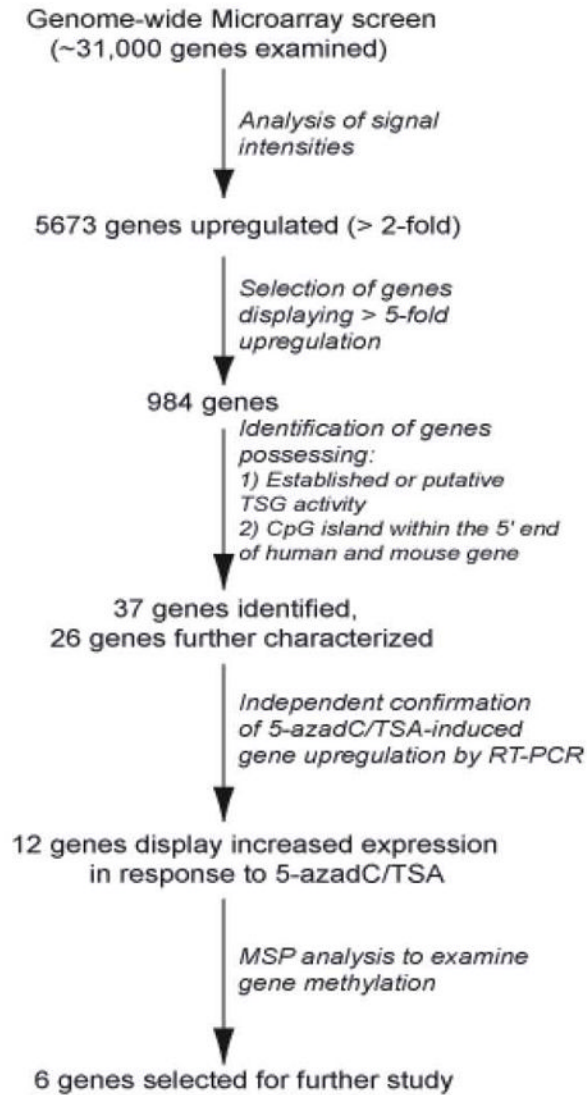
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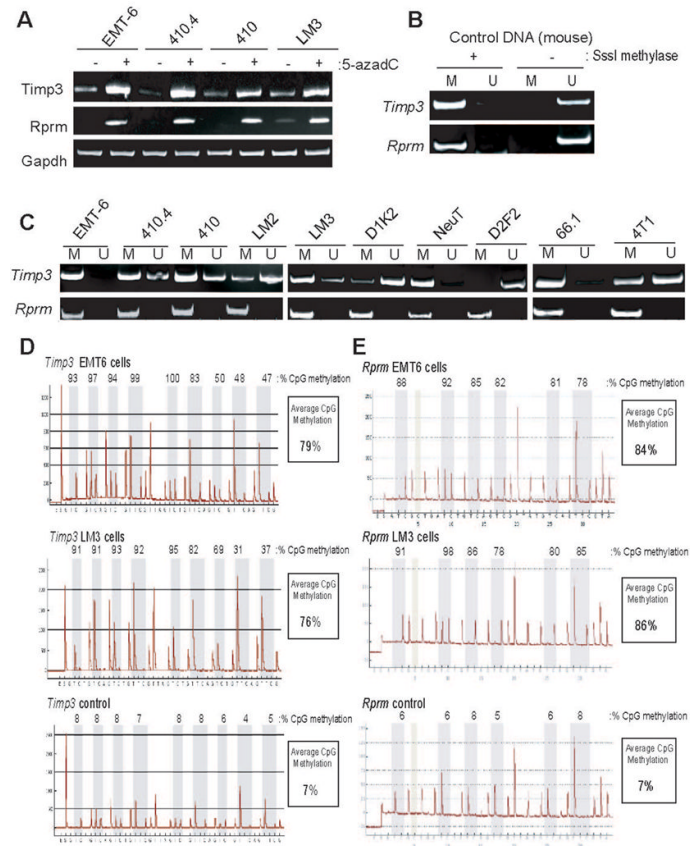


**Figure 1. Hierarchical clustering of the differentially expressed transcripts in all of the biological replicate samples**

Two-way hierarchical clustering using Ward's Minimum Variance as the heuristic criteria and Euclidean distance as the similarity metric was performed on all 4 samples using the z-score transformed expression values for the 2,339 transcripts that were identified as differentially expressed (fold-change > 5, log ratio p-value < 0.001) when the two groups were compared to each other (984 genes displayed increased expression, 1,355 displayed decreased expression in response to 5-azadC/TSA). The degree of relatedness between each sample is represented by the dendrogram (hierarchical tree) presented in this figure, wherein the height of each branch represents the distance between the 2 objects being connected. The relationship between the color intensity and the expression level is illustrated by the color bar.

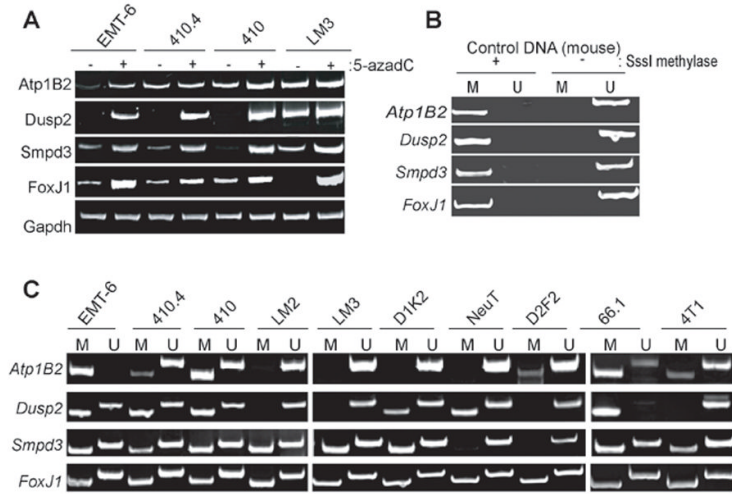


**Figure 2.** Flow chart summarizing various experimental steps used following initial microarray screen for epigenetically silenced genes in the EMT6 cell line.



**Figure 3. Analysis of *Timp3* and *Rprm* silencing in cultured mouse mammary tumor cell lines**  
**A** Indicated mouse mammary tumor lines were either treated or not with a combination of 5-azadC and TSA. Subsequently, total RNA was harvested, cDNA synthesis performed, and PCR reactions conducted using primers specific for the *Timp3* (top) or *Rprm* (middle) genes. Also, PCR reactions using primers specific for the *Gapdh* gene (bottom) were conducted to assure equivalent RNA abundance in each reaction. **B.** MSP primers were designed specific to the mouse *Timp3* (top) and *Rprm* (bottom) genes. Primers designed to amplify methylated (M) or unmethylated (U) regions of the CpG island associated with each gene were tested in PCR reactions using mouse genomic DNA either incubated in the presence or absence of *SssI* methylase prior to bisulfite conversion. **C.** Genomic DNA harvested from mouse mammary tumor lines EMT6, 410.4, 410, LM3, LM2, NeuT, D2F2, 66.1, 4T1, D1K2 were bisulfite converted and used in MSP reactions with methylated-specific (M) or unmethylated-specific (U) primers. **D.** Pyrosequencing analysis was conducted on the *Timp3* gene using bisulfite-modified genomic DNA from EMT6 and LM3 tumor lines, and mouse genomic DNA as a control. Shown are obtained pyrograms, measured methylation at CpG dinucleotides within the gene region analyzed, and the average CpG methylation within this region of the *Timp3* gene. **E.** Pyrosequencing analysis of the *Rprm* gene was conducted on EMT6 and LM3 lines and mouse genomic DNA as outlined in D.

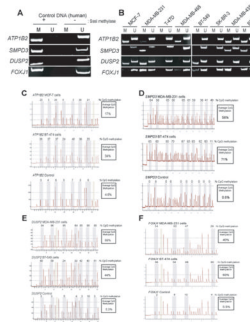




**Figure 4. Analysis of *Atp1B2*, *Dusp2*, *Smpd3* and *FoxJ1* silencing in mouse mammary tumor lines**

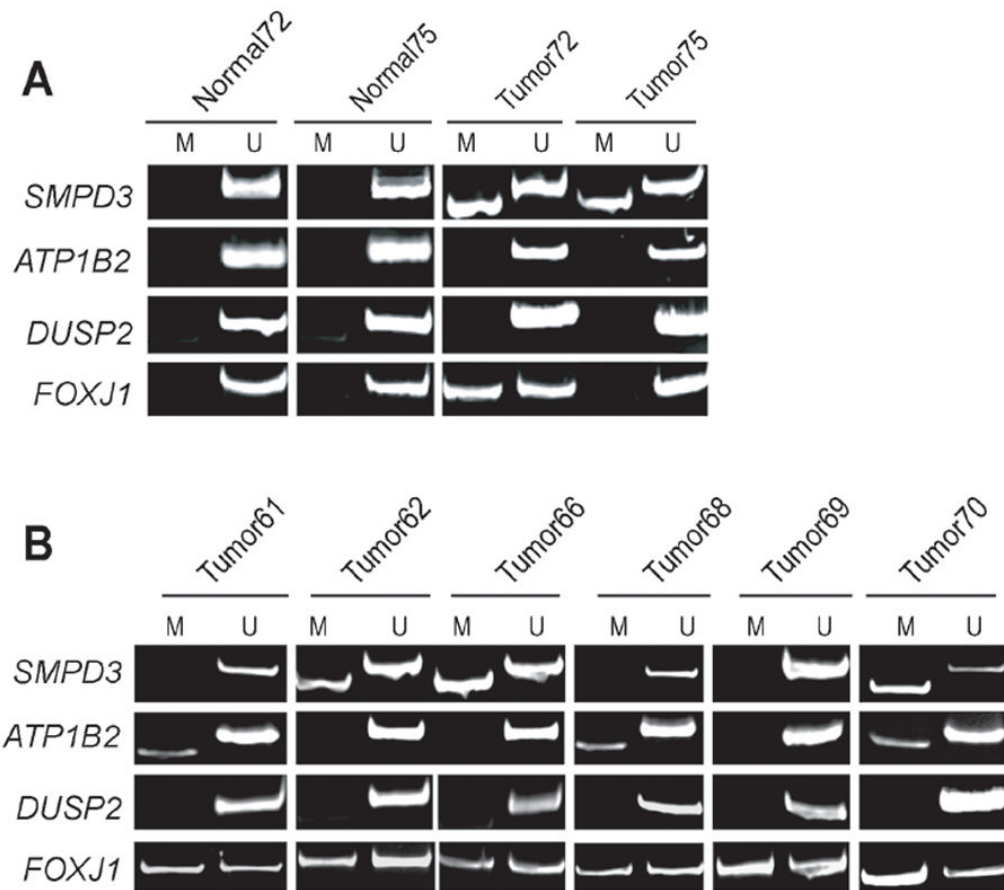
**A** RT-PCR was conducted on cDNA synthesized from indicated mouse mammary tumor lines treated and untreated with 5-azadC/TSA using primers specific for each indicated gene.

**B.** MSP primers specific for each gene were designed and subsequently validated using bisulfite-modified mouse genomic DNA either methylated or not prior to bisulfite conversion. **C.** MSP analysis of these four genes using DNA harvested from the indicated mouse mammary cell lines was conducted.



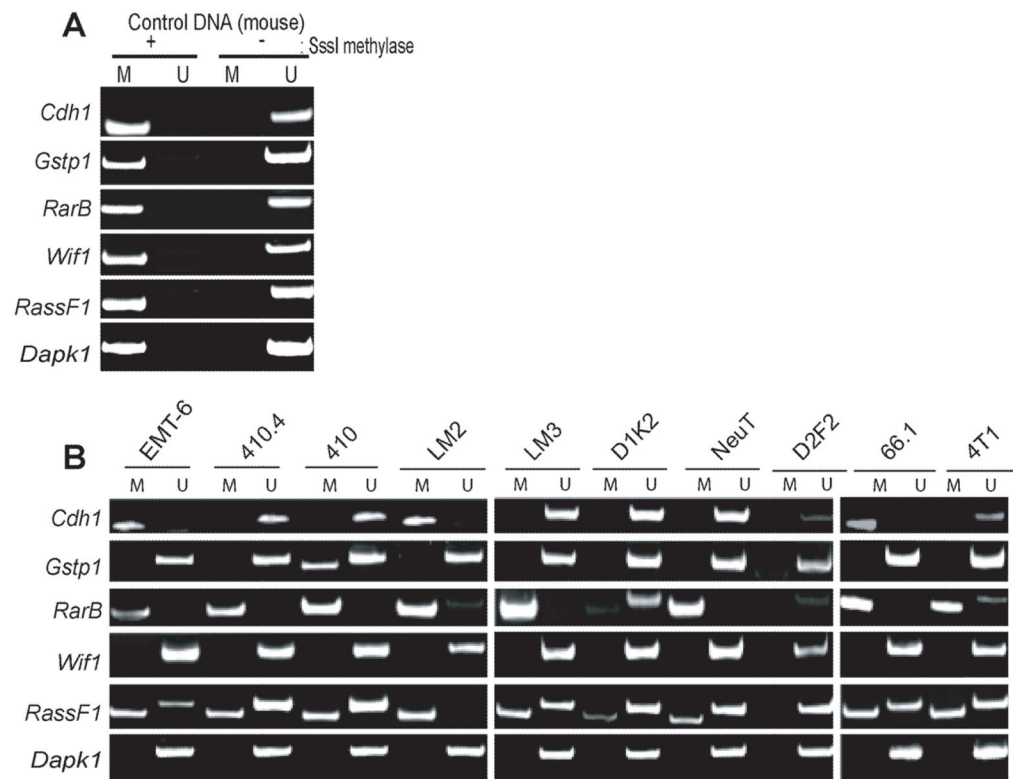
**Figure 5. Analysis of ATP1B2, DUSP2, SMPD3 and FOXJ1 methylation in human breast tumor cell lines**

**A** MSP primers were designed to the human ortholog of each indicated gene and validated using human placental DNA that was incubated in the presence or absence of *SssI* methylase prior to bisulfite conversion. **B.** MSP analysis of indicated genes was conducted on indicated human breast tumor cell lines. **C.** Pyrosequencing analysis of the *ATP1B2* gene was conducted using genomic DNA harvested from MCF-7, BT-474, and human placenta (control). **D.** Pyrosequencing analysis of the *SMPD3* gene in MDA-MB-231, BT-474 and control DNA. **E.** Pyrosequencing analysis of the *DUSP2* gene in MDA-MB-231, BT-549 and control DNA. **F.** Pyrosequencing analysis of the *FOXJ1* gene in MDA-MB-231, BT-474 and control DNA samples.



**Figure 6. Analysis of ATP1B2, DUSP2, SMPD3 and FOXJ1 methylation in primary human breast tumors**

**A** MSP analysis of the indicated genes was conducted on human primary breast tumors and patient-matched normal breast tissue. **B.** Representative MSP analysis of six additional human primary breast tumors.



**Figure 7. Analysis of genes characterized as targets for epigenetic silencing in human breast tumors in a panel of mouse mammary tumor lines**

A MSP primers were designed to the mouse orthologs of the *Cdh1*, *Gstp1*, *RarB*, *Wif1*, *RassF1* and *Dapk1* genes. Primer sets were validated using control mouse genomic DNA that was either methylated/unmethylated *in vitro* prior to bisulfite conversion. B. MSP analysis of indicated genes was conducted on bisulfite-converted DNA isolated from indicated mouse mammary tumor lines. gDNA was harvested from the cell lines and bisulfite-modified. These DNA samples were used in MSP analyses.

Table 1

## RT-PCR Primers

Primer Designation	Human/Mouse	Primer Sequence (5' → 3')	Orientation (Forw/Rev)	Annealing Temp (°C)	Thermocycles	Product Size (bp)
Gapdh-RT	M	AACGACCCCTTCAITTGAC TCCACGACATACACAGCAC	F R	57	30	191
Timp3-RT	M	AATTCTCTGCTCAGGCTCCTGTT AGCATGGTCATTTCTCCGGTTCT	F R	60	30	429
Rpm1-RT	M	TATTCGCCACGCTGCAGACCTAAT AAACCGTGCAGACAGGAGCTAAGA	F R	60	30	359
Smpd3-RT	M	ACATCGATTCTCCACCAACACCT AATTCCGACAATGCAGCTGTCTC	F R	60	30	227
Alp1b2-RT	M	TGCTTCTGGAAATGTCCTTGAACCT TGGGTGGATGAGACCATTTCTGT	F R	60	30	368
Dusp2-RT	M	TGGTCTGTGGAAATCTTGGCCCTA AATCAGGTATGCCAGGCAGATGGT	F R	60	31	307
FoxJ1-RT	M	AAGGTAACCTTTGACTGGGAGGCCA AGGATGTGCCCAAGAAAGGTCTCAT	F R	60	30	225



Table II

## Methylation-Specific PCR (MSP) Primers

Primer Designation	Human/Mouse	Primer Sequence (5' → 3')	Orientation (Forw/Rev)	Annealing Temp (°C)	Thermo- cycles	Product Size (bp)
<i>Timp3</i> -MSP-M	M	CGGAGGGGGCGGATTC	F	60	40	84
		CACGAATCCGCGAAACCAAC	R			
<i>Timp3</i> -MSP-U	M	TGGAGGGGGTGGATTTT	F	55	40	184
		ACACAAATCCACAAAAACCAAC	R			
<i>Rprm</i> -MSP-M	M	GTCGGGTATTGTTCTTCGC	F	58	40	96
		ACTAAATTCACGAAAAACAAACGAAAAACCG	R			
<i>Rprm</i> -MSP-U	M	GTTAGTGTTTTGTGGGTAATTTGTTTGTG	F	58	40	96
		ACACTAAATTCATCACAACAAAAACAAAAACCA	R			
<i>Smpd3</i> -MSP-M	M	GGGTTTTTAGAGACGGTTTTTCGC	F	59	40	90
		GCTCCAAATACTAAATCCGAAAAAACTCCG	R			
<i>Smpd3</i> -MSP-U	M	TGATTGGGGTTTTTAGAGATGGTTTTTGTG	F	58	40	90
		CCACTCCAAATACTAAATCCAAAAAACTCCA	R			
<i>Alp1b2</i> -MSP-M	M	CGTGGAGGGTTTTAGCGC	F	58	40	74
		AAACACGAAACGAAATCCCGACG	R			
<i>Acup1b2</i> -MSP-U	M	GTGTGGAGGGTTTTTAGTGTG	F	57.5	40	74
		AACCATCTTAAAAACACAAAAACAAATCCCAACA	R			
<i>Dusp2</i> -MSP-M	M	GTTCGTTTTTGGTTTTTGTGGAGTTAC	F	58.5	40	102
		AAAAACAACGACGAAAAATACCGCG	R			
<i>Dusp2</i> -MSP-U	M	TGTTGTTTTGTTTTTGGTTTTTGTGGAGTTATG	F	58	40	102
		ACAAAAACAAAAACAAAAACAAAAATACCAACA	R			
<i>Foxj1</i> -MSP-M	M	GGTTTTTTAGCGGTTAAATTCGACGC	F	59	40	86
		GCTAAATCTCACGCGAATACTCG	R			
<i>Foxj1</i> -MSP-U	M	GGTTGGGTTTTTTAGTGGTTAAATTTGATGTG	F	58	40	86
		CCCACACTAAATCTCACAACAAATACTCA	R			
<i>SMPD3</i> -MSP-M	H	TTAGATTTGCGGTCGGGAGTTC	F	58.5	40	100
		AACACTAACCTCTAACGACGAACG	R			
<i>SMPD3</i> -MSP-U	H	TTGTTGTTAGATTTGTGGTTGGGAGTTTG	F	58.5	40	100

Primer Designation	Human/Mouse	Primer Sequence (5' → 3')	Orientation (Forw/Rev)	Annealing Temp (°C)	Thermo- cycles	Product Size (bp)
<i>ATP1B2</i> -MSP-M	H	AAATTCACAACAACACTAACCCTCTAACACAAAACA GGCGATCGGGGTTTC	R F	59	40	116
<i>ATP1B2</i> -MSP-U	H	CCGATAATAACTCAACCGCGAAAATAAAAACG GTATAAAGATTGTGTTGGTGATTGTGGGTTTGG ACACCAATAATAACTCAACCAACCAAAAATAAAAACA	R F R	58.5	40	116
<i>DUSP2</i> -MSP-M	H	TTATCGTTACGAGAGTTCGGGAC CGCAACAACGTACCCCAACG	F R	58	40	119
<i>DUSP2</i> -MSP-U	H	GGTAGTATTATTGTTATGAGAGTTTGGGATG AAATCCACAACAACATACCCCAACA	F R	58.5	40	119
<i>FOXJ1</i> -MSP-M	H	TTTTAGAACGAAACGGATTATATAGC ACACTTACCCTCTCCCTAACGGAC	F R	59	40	193
<i>FOXJ1</i> -MSP-U	H	TTTAGAATGAATGGATTATATAGTGG AACACTTACCCTCTCCCTAACCAAC	F R	58	40	193
<i>Ecad</i> -MSP-M	M	GGTTAAITCGGTTTGTTCGATCGTATTC GAACTCCATAACGAACCCG	F R	58	40	75
<i>Ecad</i> -MSP-U	M	GTTTGGTTAAITGGTTTTTGTGTGATGTGATTTG ACCAAACTCCATAACAAACCCA	F R	58	40	75
<i>RassF1</i> -MSP-M	M	GGGCGGTCTGGAAATTC CCCTCCGAATAACTCGCTATAAAAAACG	F R	58.5	40	99
<i>RassF1</i> -MSP-U	M	AGGGTGGTTGTGGAAATTTG CAAAACCTCCAAAATAACTCACTATAAAAAACA	F R	57.5	40	99
<i>Gstp1</i> -MSP-M	M	GAAATTCGTAITTAGTAGGTAGTGTGAGTTCGTTTC CGATACAAAAAACGCCAATCGTAAACG	F R	58	40	106
<i>Gstp1</i> -MSP-U	M	TGAAATTTGTATTTAGTAGGTAGTGTGTTGTTTGG AACTACCAATAACAAAAACCAATCATAAACA	F R	58	40	106
<i>Rarb</i> -MSP-M	M	GATTTAAAGTTTTTTTTTTAGGGCAGCGTTC GAACAAAAAACGTCTAAACACCG	F R	56.5	40	89
<i>Rarb</i> -MSP-U	M	AITGATTTAAAGTTTTTTTTTTAGGGTGTGTTTGG CCCAACAAAAAACATCTAAACACCA	F R	56.5	40	89

Primer Designation	Human/Mouse	Primer Sequence (5' → 3')	Orientation (Forw/Rev)	Annealing Temp (°C)	Thermo- cycles	Product Size (bp)
<i>Dapk1</i> -MSP-M	M	TTCCGGTCCGGGAGTC	F	59	40	110
		CAAAITCCTCGCCGATATCGTAATAATCG	R			
<i>Dapk1</i> -MSP-U	M	GATGGTTTGGGTTGGAGTTG	F	57.5	40	110
		CTACCCAAITCCTCACCAATATCAATAATAATCA	R			
<i>Wif1</i> -MSP-M	M	GGGTATCCGGTTTCGTTTC	F	58.5	40	96
		CTACTAACAAAAACGAAACACTAAAAACGACCG	R			
<i>Wif1</i> -MSP-U	M	GGGTTTATTGGGTATTGGTTTGGTTTTGTTTTG	F	58	40	96
		ACTACTAACAAAAAACAAACACTAAAAAACAAACCA	R			

Table III

Pyrosequencing Primers (Amplification and Sequencing)

Primer Designation	Human/Mouse	Primer Sequence (5' → 3')	Orientation (Forw/Rev)	Annealing Temp (°C)	Thermo-cycles	Product Size (bp)
<i>Rprm</i> -PYRO	M	TTGTAGTTAAGGAAGAAGATGTTAAAAATTAT	F	50.5	50	344
		AACCTAAAACTTTAAAAAATAAAAACTAAAAAAC	R			
		GTTTGGGTGTAGTAG	SEQ*			
<i>Temp3</i> -PYRO	M	YGTATYGYGYGTTTATAGYGTITYGTAT	SEQ to analyze**	50	50	195
		GATGAAITTTTGTGTTTAGGTTT	F			
		AAAATCCAAAACACTACAAAAATAAT	R			
		TTTTATAAGGATTTGAA	SEQ*			
<i>ATP1B2</i> -PYRO	H	YGGTTYGGTYGGTITYGTTTGYGTYGTYGTTTTYGGTITYGTT	SEQ to analyze**	56	50	123
		GGTGGGAAGGGGTGGGTATTT	F			
		CAACCAAAAAATAAAAAACCCCAAAA	R			
		GGGGTGGGTATTTTT	SEQ*			
<i>DUSP2</i> -PYRO	H	YGYGTYGGYGATYGGGTTTTYGTATT	SEQ to analyze**	53	50	242
		GAAATTTTAGTTAGTTAGATTG	F			
		CCTCCAACCCCATAACCCACC	R			
		GTTTTTGTATGGTGTTT	SEQ*			
<i>FOXJ1</i> -PYRO	H	YGGAGGTYGGTTAYGGGTAITTAATYGGGTYGTYGGYGA	SEQ to analyze**	52	50	290
		TTTTAGTTTAGTTTTTAATTTAGGTTT	F			
		ACACTTACCCTCTCCCTAAC	R			
		GTTTTAGGAGTAGTTGA	SEQ*			
<i>SMPD3</i> -PYRO	H	YGTITTTAAAGYGTAYGGGATAGGAAGGGGTGGGGYGA	SEQ to analyze**	53.5	50	305
		GGATGIGGTTTTGAAAGGAGAGATTT	F			
		GAAATCAACAACACTAACCTCTA	R			
		GGGTTGTGAGGAG	SEQ*			
		TYGGATTYAGAGTYGAGAGTYGTYGTYGTTGTYGGTYGTYGTT	SEQ to analyze**			

\* SEQ: Sequencing primer



Table IV

## Microarray Data

Shown are the 984 genes found to be  $\geq 5$ -fold upregulated in 5-azadC treated EMT6 cells, genes subject to further study are indicated in magenta.

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
6720406K03	hypothetical protein 6720406K03	AK032705	63.47921	2.69E-07
Gcg	Glucagon, mRNA (cDNA clone MGC:14058 IMAGE:4218718)	AK050538	63.45748	2.73E-07
2900027M19Rik	Transmembrane protein 28 (Tmem28), mRNA	AK045452	63.31421	2.98E-07
D830044D21Rik	RIKEN cDNA D830044D21 gene (D830044D21Rik), mRNA	NM_177210	61.82942	2.46E-07
Pkd1l2	Polycystic kidney disease 1 like 2 (Pkd1l2), mRNA	NM_029686	60.27456	2.10E-44
<b>Tspan33</b>	<b>Tetraspanin 33 (Tspan33), mRNA</b>	<b>NM_146173</b>	<b>58.68657</b>	<b>8.71E-33</b>
4930442J19Rik	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930442J19 product: unclassifiable, full insert sequence	AK015363	56.56114	9.32E-08
2610024A01Rik	RIKEN cDNA 2610024A01 gene (2610024A01Rik), mRNA	BC059048	49.58956	4.61E-08
Fgf11	Fibroblast growth factor 11 (Fgf11), mRNA	BC066859	48.44208	8.99E-26
AF366264	CDNA sequence AF366264 (AF366264), mRNA	NM_153093	47.83025	3.85E-08
Ung2	PREDICTED: similar to uracil-DNA glycosylase 2 [Mus musculus], mRNA sequence	AK053890	47.79745	3.05E-17
6430548M08Rik	RIKEN cDNA 6430548M08 gene, mRNA (cDNA clone MGC:38801 IMAGE:5359842)	AK122299	44.75741	1.10E-15
Serpini1	Serine (or cysteine) peptidase inhibitor, clade I, member 1, mRNA (cDNA clone MGC:6413 IMAGE:3588856)	NM_009250	44.68072	1.38E-15
Dpep1	Dipeptidase 1 (renal), mRNA (cDNA clone MGC:6318 IMAGE:2812088)	NM_007876	44.65215	2.73E-29
<b>Cabel1</b>	<b>Chaperone, ABC1 activity of bc1 complex like (S. pombe), mRNA (cDNA clone MGC:31744 IMAGE:4922892)</b>	<b>NM_023341</b>	<b>41.85896</b>	<b>2.83E-24</b>
1190002H23Rik	RIKEN cDNA 1190002H23 gene (1190002H23Rik), mRNA	NM_025427	39.94254	9.82E-29
1600029D21Rik	RIKEN cDNA 1600029D21 gene (1600029D21Rik), mRNA	NM_029639	39.51588	1.83E-22
4930522H14Rik	RIKEN cDNA 4930522H14 gene (4930522H14Rik), mRNA	NM_026291	39.45048	5.43E-08
TC982356	Unknown		39.22191	3.98E-43
Xist	Xist (X inactive specific transcript) mRNA for open reading frame	X59289	37.43628	1.34E-23
<b>Dusp2</b>	<b>Dual specificity phosphatase 2 (Dusp2), mRNA</b>	<b>NM_010090</b>	<b>37.08016</b>	<b>1.15E-17</b>
BB133117	Transcribed locus	BB133117	37.05725	2.84E-13
<b>Nik</b>	<b>Nemo like kinase (Nik), mRNA</b>	<b>AK031461</b>	<b>35.36866</b>	<b>1.11E-08</b>
6430548M08Rik	RIKEN cDNA 6430548M08 gene, mRNA (cDNA clone MGC:38801 IMAGE:5359842)	NM_172286	33.78417	6.01E-14
BC011467	CDNA sequence BC011467, mRNA (cDNA clone MGC:37865 IMAGE:5100525)	BC025823	32.62732	6.73E-17
LOC545748	similar to hypothetical protein LOC280487	AK031095	32.16875	3.93E-17
9630025C22	hypothetical protein 9630025C22	NM_177597	30.76949	9.72E-12
Hspa1a	Heat shock protein (hsp68) mRNA, clone MHS213	NM_010479	30.68889	6.14E-11



Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
<b>Timp3</b>	<b>Tissue inhibitor of metalloproteinase 3, mRNA (cDNA clone MGC:25359 IMAGE:4239015)</b>	<b>NM_011595</b>	<b>30.407</b>	<b>3.63E-12</b>
H2-DMb1	Histocompatibility 2, class II, locus Mb1, mRNA (cDNA clone MGC:5741 IMAGE:3486844)	NM_010387	30.20498	1.12E-44
Artdc4	Arrestin domain containing 4 (Artdc4), mRNA	NM_025549	30.05997	1.22E-14
9330117B14	Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330117B14 product: unclassifiable, full insert sequence.	AK033923	29.13712	8.04E-09
Sema4f	Sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain (Sema4f), mRNA	NM_011350	29.0931	1.55E-14
Fzd9	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:CI30077B15 product: fizzled homolog 9 (Drosophila), full insert sequence.	AK021164	28.87872	2.71E-19
Zfpn1a4	Zinc finger protein, subfamily 1A, 4 (Eos) (Zfpn1a4), mRNA	AK041640	27.41483	4.91E-20
Osbp2	Oxysterol binding protein 2 (Osbp2), mRNA	AK049816	27.39835	3.84E-24
A930035123Rik	PREDICTED: Mus musculus RIKEN cDNA A930035123 gene (A930035123Rik), mRNA	AK041893	27.09363	3.60E-28
Tmem25	Transmembrane protein 25 (Tmem25), mRNA	NM_027865	26.96004	2.00E-25
Selenbp1	Selenium binding protein 1, mRNA (cDNA clone MGC:18519 IMAGE:4209393)	NM_009150	26.94885	3.24E-18
Tipi	Tissue factor pathway inhibitor, mRNA (cDNA clone MGC:37332 IMAGE:4975683)	NM_011576	26.6853	9.47E-30
Klk16	Kallikrein 16, mRNA (cDNA clone MGC:18522 IMAGE:4165443)	NM_008454	26.63172	8.21E-09
Cd248	CD248 antigen, endostalin (Cd248), mRNA	NM_054042	26.56997	7.43E-19
Pte2a	Phosphodiesterase 2A, cGMP-stimulated, mRNA (cDNA clone IMAGE:4949471)	BC006845	26.40924	2.97E-19
Agxt2l1	Alanine-glyoxylate aminotransferase 2-like 1 (Agxt2l1), mRNA	AK030395	25.35919	8.75E-09
Slc30a1	Solute carrier family 30 (zinc transporter), member 1 (Slc30a1), mRNA	AK048209	25.18293	7.34E-19
8030431J09Rik	Ankyrin repeat and BTB (POZ) domain containing 2, mRNA (cDNA clone MGC:62845 IMAGE:6493840)	AK033113	24.99684	1.12E-15
1700030G11Rik	PREDICTED: RIKEN cDNA 1700030G11 [Mus musculus], mRNA sequence	AK006546	24.99246	0.00001
Mifl	Myeloid leukemia factor 1, mRNA (cDNA clone MGC:41163 IMAGE:1495721)	NM_010801	24.45573	7.37E-15
A_51_P306031	Unknown		23.98088	4.47E-25
Chi3l3	Chitinase 3-like 3 (Chi3l3), mRNA	NM_009892	23.96213	1.01E-38
<b>Dbccr1</b>	<b>BRINP mRNA for BMP/retinoic acid-inducible neural-specific protein (BRINP)</b>	<b>NM_019967</b>	<b>23.93755</b>	<b>3.66E-17</b>
B230362M20Rik	RIKEN cDNA B230362M20 gene (B230362M20Rik), mRNA	NM_177273	23.77677	1.66E-08
9030221C07Rik	Aromatic-prefering amino acid transporter (Arpat)	NM_177802	23.37548	0.00001
Sipa1l2	Signal-induced proliferation-associated 1 like 2, mRNA (cDNA clone IMAGE:30360538)	AK122501	23.25885	4.47E-36
Gm364	PREDICTED: similar to hypothetical protein [Mus musculus], mRNA sequence	AV280269	23.15239	6.48E-38
Selenbp2	Selenium binding protein 2, mRNA (cDNA clone MGC:35927 IMAGE:5096831)	NM_019414	23.06403	1.19E-14
Lin7b	Lin 7 homolog b (C. elegans), mRNA (cDNA clone MGC:18338 IMAGE:4164883)	NM_011698	22.83365	6.72E-27
Tacstd1	Tumor-associated calcium signal transducer 1, mRNA (cDNA clone MGC:11680 IMAGE:3711069)	NM_008532	22.5851	4.03E-33

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Eml5	Echinoderm microtubule associated protein like 5, mRNA (cDNA clone IMAGE:4953665)	BC027154	22.21267	2.27E-28
Fank1	Fibronectin type 3 and ankyrin repeat domains 1 (Fank1), mRNA	NM_025850	22.05824	3.68E-22
1700001J03Rik	RIKEN cDNA 1700001J03 gene (1700001J03Rik), mRNA	BC048528	21.14908	3.13E-26
NAP059666-1	Unknown		21.09742	3.79E-06
<b>Klf2</b>	<b>Kruppel-like factor 2 (lung) (Klf2), mRNA</b>	<b>NM_008452</b>	<b>20.99121</b>	<b>2.75E-09</b>
AK054415	Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330023G08 product: phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide, full insert sequence.	AK054415	20.9248	0.00003
D330017J20Rik	MKIAA1170 protein	AK122459	20.91998	8.39E-35
NAP108451-1	Unknown		20.55861	0.00005
Gp2	Glycoprotein 2 (zymogen granule membrane) (Gp2), mRNA	NM_025989	20.50423	3.80E-08
Ush2a	PREDICTED: Mus musculus similar to usherin isoform B (LOC545397), mRNA	AK044721	20.08695	2.99E-08
Abca3	Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730004H09 product: ATP-binding cassette, sub-family A (ABC1), member 3, full insert sequence.	AK089316	19.91308	2.21E-08
Sned1	Secreted nidogen domain protein (Snep gene), splice form SNEP	NM_172463	19.73947	1.44E-21
4930488E11Rik	RIKEN cDNA 4930488E11 gene, mRNA (cDNA clone MGC:106799 IMAGE:3373135)	NM_207267	19.66398	1.42E-30
Ew5	Ets variant gene 5, mRNA (cDNA clone MGC:28414 IMAGE:4036564)	NM_023794	19.61583	5.13E-27
Disp2	Dispatched homolog 2 (Drosophila) (Disp2), mRNA	NM_170593	19.59815	5.48E-08
ENSMUST00000064479	Unknown		19.4577	8.91E-11
TC952297	AF302077 neprilysin-like peptidase gamma [Mus musculus], partial (4%) [TC952297]		19.41319	8.90E-30
Igpb1	Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720407F13 product: immunoglobulin (CD79A) binding protein 1, full insert sequence.	AK032709	19.30429	2.63E-08
TC1019179	Unknown		19.29024	1.03E-22
Cd248	CD248 antigen, endosialin (Cd248), mRNA	NM_054042	19.23851	4.63E-24
Arhgap29	Rho GTPase activating protein 29 (Arhgap29), mRNA	NM_172525	19.18384	3.71E-10
E430004F17Rik	RIKEN cDNA E430004F17 gene (E430004F17Rik), mRNA	NM_183199	19.05738	5.93E-16
Stard10	START domain containing 10 (Stard10), mRNA	NM_019990	18.91585	1.20E-12
Fn3k	Fructosamine 3 kinase (Fn3k), mRNA	NM_022014	18.91504	1.03E-24
Pfn2	Profilin 2, mRNA (cDNA clone MGC:35930 IMAGE:5059568)	NM_019410	18.78823	1.79E-18
Ptgfr	Prostaglandin F receptor (Ptgfr), mRNA	AK086563	18.75204	3.09E-08
Man1a	Mannosidase 1, alpha, mRNA (cDNA clone MGC:18448 IMAGE:4223319)	NM_008548	18.7403	3.14E-08
Vwf	Von Willebrand factor (Vwf) mRNA, exon 1 and 5'UTR	AK044921	18.63142	5.82E-08
Kif27	Kinesin family member 27 (Kif27), mRNA	NM_175214	18.39237	2.38E-42
Sh2d4b	SH2 domain containing 4B (Sh2d4b), mRNA	NM_177816	18.37578	5.13E-08

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Sh2d1b	SH2 domain protein 1B (Sh2d1b), mRNA	NM_012009	18.35538	3.50E-08
Arhgap29	Rho GTPase activating protein 29 (Arhgap29), mRNA	NM_172525	17.9961	1.04E-10
A1450469	Transcribed locus	A1450469	17.7114	4.97E-28
4930504O13Rik	RIKEN cDNA 4930504O13 gene (4930504O13Rik), mRNA	NM_207527	17.60137	7.87E-08
Anxa6	Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810407D22 product: annexin A6, full insert sequence.	AK013026	17.41486	1.20E-08
Mical2	MKIAA0750 protein	NM_177282	17.22894	1.87E-11
Lrrc15	Leucine rich repeat containing 15 (Lrrc15), mRNA	BC050245	17.22617	1.28E-27
NM_133237	Mus musculus cDNA sequence AB023957 (AB023957), mRNA [NM_133237]	NM_133237	17.09971	2.44E-31
Myl2	Myosin, light polypeptide 2, regulatory, cardiac, slow (Myl2), mRNA	NM_010861	17.05658	5.16E-06
Trib2	Tribbles homolog 2 (Drosophila), mRNA (cDNA clone MGC:32449 IMAGE:5043179)	NM_144551	16.9309	1.31E-20
A930037G23Rik	RIKEN cDNA A930037G23 gene, mRNA (cDNA clone MGC:67253 IMAGE:6403474)	NM_178787	16.70077	1.01E-25
Derl3	Der1-like domain family, member 3 (Derl3), mRNA	NM_024440	16.70039	2.27E-08
Rasl11b	RAS-like, family 11, member B, mRNA (cDNA clone MGC:7064 IMAGE:3156762)	AK004534	16.64886	4.78E-26
A130052D22	Mus musculus hypothetical protein A130052D22 (A130052D22), mRNA [NM_183306]	NM_183306	16.27097	3.94E-29
Soat1	Sterol O-acyltransferase 1, mRNA (cDNA clone IMAGE:4007277)	BC025091	16.22614	2.66E-44
Adam30	A disintegrin and metalloproteinase domain 30 (Adam30), mRNA	AK077058	16.15904	0.00015
Abtb2	Ankyrin repeat and BTB (POZ) domain containing 2, mRNA (cDNA clone MGC:62845 IMAGE:6493840)	NM_178890	16.12632	2.87E-27
<b>Dock4</b>	<b>MKIAA0716 protein</b>	<b>AK085106</b>	<b>15.90782</b>	<b>4.44E-37</b>
6720468P15Rik	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430057M21 product: unclassifiable, full insert sequence	AK078497	15.87182	4.79E-06
Cxcl4	Chemokine (C-X-C motif) ligand 4 (Cxcl4), mRNA	NM_019932	15.81666	7.84E-36
Otub2	OTU domain, ubiquitin aldehyde binding 2 (Otub2), mRNA	NM_026580	15.80523	1.53E-15
Thyn1	Thymocyte protein mThy28	AK037947	15.5622	1.23E-07
E130308A19Rik	RIKEN cDNA E130308A19 gene (E130308A19Rik), transcript variant 1, mRNA	AK038359	15.44643	1.28E-07
0610042C05Rik	RIKEN cDNA 0610042C05 gene, mRNA (cDNA clone MGC:37398 IMAGE:4977394)	AK076350	15.44004	4.96E-07
Chn2	Beta chimaerin (bch gene)	NM_023543	15.41819	2.69E-07
Rab3b	RAB3B, member RAS oncogene family (Rab3b), mRNA	NM_023537	15.2858	2.35E-15
Anxa6	Annexin A6, mRNA (cDNA clone MGC:6574 IMAGE:3482035)	NM_013472	15.14969	1.10E-13
Nedd9	Neural precursor cell expressed, developmentally down-regulated gene 9, mRNA (cDNA clone IMAGE:3499250)	NM_017464	15.10892	1.79E-15
Dazl	Deleted in azoospermia-like (Dazl), mRNA	NM_010021	15.03384	3.11E-43
Gleci1	Glucocorticoid induced transcript 1 (Gleci1), transcript variant 1, mRNA	AK042221	14.97325	2.00E-07

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Tfdp2	Transcription factor Dp 2, mRNA (cDNA clone IMAGE:30604420)	NM_178667	14.96471	2.55E-17
<b>Cacnalg</b>	<b>Calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacnalg), mRNA</b>	<b>NM_009783</b>	<b>14.95897</b>	<b>1.24E-16</b>
Ifna4	Interferon alpha family, gene 4 (Ifna4), mRNA	NM_010504	14.95108	1.76E-07
Notch3	Notch gene homolog 3 (Drosophila) (Notch3), mRNA	NM_008716	14.90218	1.13E-28
Paesin1	Protein kinase C and casein kinase substrate in neurons 1, mRNA (cDNA clone MGC:25285 IMAGE:4527708)	NM_011861	14.88882	1.74E-11
<b>Apl1b2</b>	<b>ATPase, Na+/K+ transporting, beta 2 polypeptide (Apl1b2), mRNA</b>	<b>NM_013415</b>	<b>14.7351</b>	<b>1.07E-22</b>
Habp2	HYALURONIC ACID BINDING PROTEIN 2; HYALURONIC ACID-BINDING PROTEIN 2. [Source:RefSeq;Acc:NM_146101] [ENSMUST00000026060]	14.65301	14.65301	2.18E-06
Fabp7	Fatty acid binding protein 7, brain (Fabp7), mRNA	NM_021272	14.34666	4.16E-06
D14Erd171e	DNA segment, Chr 14, ERATO Doi 171, expressed, mRNA (cDNA clone MGC:59433 IMAGE:6331997)	AK039674	14.3364	2.78E-07
Oas1d	2'-5'oligoadenylate synthetase 1D (Oas1d)	NM_133893	14.18881	1.11E-14
Nid1	Nidogen 1 (Nid1), mRNA	NM_010917	14.08903	5.04E-23
Mcf2l	Mcf2 transforming sequence-like (Mcf2l), mRNA	NM_178076	14.07378	6.06E-26
Hbb-b1	Hemoglobin, beta adult major chain, mRNA (cDNA clone MGC:40691 IMAGE:3988455)	NM_008220	14.02514	4.51E-07
Prg4	PREDICTED: proteoglycan 4 [Mus musculus], mRNA sequence	AB034730	14.01659	1.28E-07
4930524B15Rik	RIKEN cDNA 4930524B15 gene (4930524B15Rik), mRNA	NM_026262	13.99617	8.54E-07
4833416E15Rik	0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833416E15 product: unclassifiable, full insert sequence	AK014707	13.9541	1.99E-43
Zfp422-rs1	zinc finger protein 422, related sequence 1	AK083028	13.94195	3.70E-34
A1607043	Adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010310C07 product: unclassifiable, full insert sequence	A1607043	13.90419	1.08E-12
Dnajc5b	DnaJ (Hsp40) homolog, subfamily C, member 5 beta (Dnajc5b), mRNA	NM_025489	13.89499	0.00001
Slc2a6	Solute carrier family 2 (facilitated glucose transporter), member 6 (Slc2a6), mRNA	NM_172659	13.84051	3.99E-43
Dretmb1a	down-regulated by Ctmb1, a	NM_053090	13.83104	1.14E-34
Sdc4	Syndecan 4, mRNA (cDNA clone MGC:11456 IMAGE:3154160)	NM_011521	13.79767	7.42E-23
Eli3	Elongation factor RNA polymerase II-like 3 (Eli3), mRNA	NM_145973	13.77959	5.40E-23
Stard10	START domain containing 10 (Stard10), mRNA	NM_019990	13.74577	6.06E-19
Mapk8ip1	JNK interacting protein-1b (JIP-1b)	AK053819	13.62189	1.54E-12
1110051M20Rik	RIKEN cDNA 1110051M20 gene, transcript variant 2, mRNA (cDNA clone MGC:103036 IMAGE:6440075)	AK053282	13.62105	1.43E-18
Ppfia4	MKIAA0897 protein	XM_129443	13.46761	1.10E-27
Itga6	Integrin alpha 6 (Itga6), mRNA	BC024571	13.44888	1.15E-11
Nfatic2	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130082H17 product: nuclear factor of activated T-cells, cytoplasmic 2, full insert	AK081853	13.39808	9.81E-45
4933401N24Rik	RIKEN cDNA 4933401N24 gene (4933401N24Rik), mRNA	NM_175367	13.39483	1.76E-41

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Mpp7	Membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7), mRNA (cDNA clone IMAGE:6532780)	AK036956	13.36708	1.64E-28
Acpp	Acid phosphatase, prostate (Acpp), transcript variant 2, mRNA	NM_207668	13.35389	1.35E-17
AK038010	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130071G05 product: unclassifiable, full insert sequence	AK038010	13.30008	5.17E-07
XM_156408	Mus musculus similar to RIKEN cDNA 2610524H06 gene (LOC239727), mRNA [XM_156408]	XM_156408	13.28002	4.58E-14
Itga6	Integrin alpha 6 (Itga6), mRNA	NM_008397	13.26801	5.17E-12
1300013J15Rik	RIKEN cDNA 1300013J15 gene, mRNA (cDNA clone MGC:28678 IMAGE:4238749)	NM_026183	13.1909	1.26E-20
Hsd17b13	Hydroxysteroid (17-beta) dehydrogenase 13, mRNA (cDNA clone MGC:30360 IMAGE:5132342)	AK050378	13.159	8.50E-07
Ankrd13d	Ankyrin repeat domain 13 family, member D (Ankrd13d), mRNA	NM_026720	13.07501	1.65E-18
Sh3ic1	SH3 domain and tetratricopeptide repeats 1, mRNA (cDNA clone IMAGE:3490511)	NM_194344	13.05323	1.40E-45
Gas6	Growth arrest specific 6, mRNA (cDNA clone MGC:6124 IMAGE:3592398)	NM_019521	13.04704	3.30E-34
Fank1	Fibronectin type 3 and ankyrin repeat domains 1 (Fank1), mRNA	NM_025850	13.03388	2.66E-34
6430590A10Rik	Mus musculus RIKEN cDNA 6430590A10 gene (6430590A10Rik), mRNA [NM_177017]	NM_177017	12.97531	0.00001
Nck2	Non-catalytic region of tyrosine kinase adaptor protein 2, mRNA (cDNA clone MGC:7093 IMAGE:3157491)	AK042129	12.94784	4.72E-07
1700123K08Rik	RIKEN cDNA 1700123K08 gene (1700123K08Rik), mRNA	NM_029693	12.92483	2.79E-11
Jag1	Jagged1 (Jag1)	NM_013822	12.89675	1.67E-18
Cacnalg	Calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacnalg), mRNA	NM_009783	12.88716	9.48E-20
2410003J06Rik	RIKEN cDNA 2410003J06 gene, mRNA (cDNA clone MGC:60956 IMAGE:30007513)	AK010362	12.79956	2.82E-16
Pgbd5	PiggyBac transposable element derived 5, mRNA (cDNA clone MGC:106643 IMAGE:30606749)	AK013562	12.79654	1.93E-30
Nfe2l3	Nuclear factor, erythroid derived 2, like 3, mRNA (cDNA clone MGC:5702 IMAGE:3485182)	NM_010903	12.78367	8.28E-39
D3330012F22Rik	Mus musculus RIKEN cDNA D3330012F22 gene (D3330012F22Rik), mRNA.	NM_178752	12.76423	3.55E-12
Odz3	ODZ3 (Odz3)	NM_011857	12.75018	6.34E-06
Plat	Plasminogen activator, tissue, mRNA (cDNA clone MGC:18508 IMAGE:4038404)	NM_008872	12.73118	5.16E-23
Hist1h1e	Histone 1, H1e (Hist1h1e), mRNA	AK047852	12.71911	1.20E-35
Aip6v0e2	ATPase, H+ transporting, lysosomal, V0 subunit E isoform 2 (Aip6v0e2), mRNA	NM_133764	12.6221	7.20E-18
Capn5	Calpain 5, mRNA (cDNA clone MGC:25253 IMAGE:4458488)	NM_007602	12.51361	5.38E-23
Fzd4	Frizzled homolog 4 (Drosophila), mRNA (cDNA clone MGC:18403 IMAGE:4238940)	NM_008055	12.51026	5.20E-28
Nppb	Natriuretic peptide precursor type B (Nppb), mRNA	NM_008726	12.3018	2.94E-13
4631402N15Rik	RIKEN cDNA 4631402N15 gene	AK028622	12.293	1.87E-06
Hey1	Hairy-related transcription factor 1 (Hrt1)	NM_010423	12.27919	9.21E-35
Cldn19	Claudin 19 (Cldn19), mRNA	NM_153105	12.26932	2.86E-06
Olfir488	Olfactory receptor 488 (Olfir488), mRNA	NM_146732	12.23274	1.87E-06

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
4930402F06Rik	PREDICTED: hypothetical protein LOC74854 [Mus musculus], mRNA sequence	XM_130219	12.21738	2.16E-06
Aldh6a1	Aldehyde dehydrogenase family 6, subfamily A1, mRNA (cDNA clone MGC:28587 IMAGE:4212084)	NM_134042	12.14788	1.68E-44
Olfir512	Olfactory receptor 512 (Olfir512), mRNA	NM_146724	12.01476	1.44E-06
Baiap211	BAI1-associated protein 2-like 1 (Baiap211), mRNA	NM_025833	11.99713	2.71E-21
Gent1	Glucosaminyl (N-acetyl) transferase 1, core 2, mRNA (cDNA clone MGC:11452 IMAGE:3154671)	NM_010265	11.98347	1.35E-11
C330006F03Rik	Homer homolog 1 (Drosophila) (Homer1), transcript variant L, mRNA	AK049142	11.98031	1.54E-10
Wfde12	WAP four-disulfide core domain 12, mRNA (cDNA clone MGC:32134 IMAGE:4923469)	NM_138684	11.9789	4.85E-23
Als2cr15	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 15, mRNA (cDNA clone MGC:90771 IMAGE:30355976)	NM_027407	11.97403	2.12E-20
Phrf2	Putative homeodomain transcription factor 2, mRNA (cDNA clone MGC:60851 IMAGE:30050876)	AK035536	11.97298	4.35E-26
Itga4	Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130050E18 product: integrin alpha 4, full insert sequence.	AK037794	11.95943	1.52E-06
Col5a3	Asp6 mRNA for adipocyte-specific protein 6	NM_016919	11.95215	2.56E-07
Egr1	Early growth response 1 (Egr1), mRNA	NM_007913	11.93462	4.12E-43
Muc2	Mucin 2, mRNA (cDNA clone MGC:37529 IMAGE:4986546)	AK008250	11.89613	5.08E-08
Dctnmb1a	down-regulated by Cttnb1, a	NM_053090	11.8877	1.99E-36
Ctss	Cathepsin S, mRNA (cDNA clone MGC:6643 IMAGE:3495719)	NM_021281	11.87519	2.68E-24
D7Erd413e	Mus musculus DNA segment, Chr 7, ERATO Doi 413, expressed (D7Erd413e), mRNA [NM_177468]	NM_177468	11.87163	2.22E-07
Fcmd	Fukuyama type congenital muscular dystrophy homolog (human) (Fcmd), mRNA	NM_139309	11.84098	2.11E-06
Rab26	RAB26, member RAS oncogene family, mRNA (cDNA clone MGC:107516 IMAGE:6436242)	AK043912	11.75247	1.64E-12
Gm520	Mus musculus similar to hypothetical protein FLJ35880 (LOC245027), mRNA [XM_147082]	XM_147082	11.75046	4.73E-11
Rasgef1a	PREDICTED: RasGEF domain family, member 1A [Mus musculus], mRNA sequence	AK018120	11.73011	8.35E-29
Chma10	cholinergic receptor, nicotinic, alpha polypeptide 10	AK033068	11.71933	6.66E-15
Ptpn13	Protein tyrosine phosphatase, non-receptor type 13 (Ptpn13), mRNA	AK033818	11.71558	4.43E-33
BC039632	CDNA sequence BC039632, mRNA (cDNA clone IMAGE:5124409)	BC039632	11.63456	4.31E-15
4632419I22Rik	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632419I22, product: unclassifiable, full insert sequence.	AK014588	11.6079	3.26E-06
Rab3il1	RAB3A interacting protein (rab3)-like 1 (Rab3il1), mRNA	NM_144538	11.55758	7.46E-24
Rapgef2	Rap guanine nucleotide exchange factor (GEF) 2, mRNA (cDNA clone IMAGE:30545886)	BM247313	11.55429	3.38E-06
Cpeb4	Cytoplasmic polyadenylation element binding protein 4 (Cpeb4), mRNA	AK079421	11.54925	5.71E-19
Ctgf	Connective tissue growth factor, mRNA (cDNA clone MGC:8122 IMAGE:3589136)	NM_010217	11.54686	1.93E-08
Wnt6	Wingless-related MMTV integration site 6 (Wnt6), mRNA	NM_009526	11.37961	1.23E-17
Atp7a	ATPase, Cu++ transporting, alpha polypeptide (Atp7a), mRNA	AK033254	11.34701	1.47E-28



Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Efemp1	Epidermal growth factor-containing fibulin-like extracellular matrix protein 1 (Efemp1), mRNA	NM_146015	11.34476	3.71E-35
Cyp2s1	Cytochrome P450, family 2, subfamily s, polypeptide 1, mRNA (cDNA clone IMAGE:4986756)	NM_028775	11.3342	8.41E-25
Plat	Plasminogen activator, tissue, mRNA (cDNA clone MGC:18508 IMAGE:4038404)	NM_008872	11.28647	2.45E-19
Hmg20a	High mobility group 20A, mRNA (cDNA clone MGC:12002 IMAGE:3602239)	AK032790	11.27672	1.40E-45
NAP002592-003	Unknown	NM_008909	11.26244	2.03E-08
Ppl	Periplakin (Ppl), mRNA		11.23955	1.47E-09
TC976091	AY129963 GPI-gamma 4; GPIgamma4 [Mus musculus], partial (72%) [TC976091]		11.21971	2.49E-24
BC067047	PREDICTED: PREX1 protein [Mus musculus], mRNA sequence	AK090301	11.18218	2.25E-21
Tekt1	Tektin 1 (Tekt1), mRNA	NM_011569	11.17168	2.41E-26
Atrn1	Attractin like 1, mRNA (cDNA clone IMAGE:4221668)	AK050882	11.16275	1.82E-14
4930470F04Rik	RAB11 family interacting protein 2 (class I) (Rab11fip2), mRNA	AK015532	11.14061	0.00748
Svep1	Sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1, mRNA (cDNA clone IMAGE:3582135)	AK035533	11.11646	3.62E-06
AK052909	16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830036I24 product: weakly similar to CYTOCHROME C OXIDASE POLYPEPTIDE VA, MITOCHONDRIAL PRECURSOR (EC 1.9.3.1) [Rattus norvegicus], full insert sequence	AK052909	11.00683	1.38E-15
Lrp4	MKIAA0816 protein	AK032360	11.00157	7.64E-06
Khk	Ketohexokinase, mRNA (cDNA clone MGC:18722 IMAGE:4235560)	NM_008439	10.99577	1.01E-23
Mpp7	Membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7), mRNA (cDNA clone IMAGE:6532780)	BC049662	10.97808	2.54E-27
Muc3	Mucin 3, intestinal, mRNA (cDNA clone IMAGE:4989899)	BC058768	10.94339	2.55E-18
3-Mar	Membrane-associated ring finger (C3HC4) 3 (March3), mRNA	AK085528	10.91169	6.53E-19
Baiap211	BAI1-associated protein 2-like 1 (Baiap211), mRNA	NM_025833	10.90945	1.29E-08
Ptger2	Prostaglandin E receptor 2 (subtype EP2), mRNA (cDNA clone MGC:6041 IMAGE:3487087)	NM_008964	10.83013	1.65E-07
Tnfrap6	Tumor necrosis factor alpha induced protein 6, mRNA (cDNA clone MGC:13914 IMAGE:4208738)	AK078295	10.7698	2.30E-17
AK037893	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230098A08 product: hypothetical protein, full insert sequence	AK037893	10.7616	3.07E-15
Ppic	Peptidylprolyl isomerase C, mRNA (cDNA clone MGC:31015 IMAGE:5026674)	NM_008908	10.73102	1.49E-26
Kenj1	Potassium inwardly-rectifying channel, subfamily J, member 1, mRNA (cDNA clone MGC:18350 IMAGE:4241262)	NM_019659	10.65826	0.00005
Zfp423	Early B-cell factor-associated zinc finger protein (Ebfaz)	NM_033327	10.59541	6.09E-06
Rora	RAR-related orphan receptor alpha, mRNA (cDNA clone MGC:5892 IMAGE:3592667)	AK087905	10.59469	9.75E-10
AK050947	9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030042L12 product: unclassifiable, full insert sequence	AK050947	10.59118	5.88E-06
AK076715	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930420A11 product: unclassifiable, full insert sequence.	AK076715	10.58991	2.55E-06
Ttn	Titin, mRNA (cDNA clone IMAGE:5149168)	AK009965	10.56327	0.00001

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
AK038867	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230069K02 product: hypothetical protein, full insert sequence	AK038867	10.55157	0.00001
Ifrd1	Interferon-related developmental regulator 1 (Ifrd1), mRNA	AK078888	10.54876	2.35E-12
Bmp8a	Bone morphogenetic protein 8a (Bmp8a), mRNA	NM_007558	10.50666	1.72E-12
NP_TR6JSE50FPA	olfactory receptor NP_TR6JSE50FPA	NM_203509	10.50266	6.41E-23
TC1084975	AE003651 CG13260-PA (Drosophila melanogaster), partial (10%) [TC1084975]		10.49094	2.76E-07
Tnfrsf6	Tumor necrosis factor alpha induced protein 6, mRNA (cDNA clone MGC:13914 IMAGE:4208738)	NM_009398	10.44943	2.17E-09
LOC432449	hypothetical gene supported by AK038984	AK038984	10.44738	2.83E-07
2900041A09Rik	RIKEN cDNA 2900041A09 gene (2900041A09Rik), mRNA	NM_182839	10.44139	8.16E-28
1600015H20Rik	RIKEN cDNA 1600015H20 gene, mRNA (cDNA clone IMAGE:3592288)	NM_024237	10.43001	4.20E-45
4930412F09Rik	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930412F09 product: unclassifiable, full insert sequence.	AK015119	10.4231	6.86E-26
1700108L22Rik	RIKEN cDNA 1700108L22 gene, mRNA (cDNA clone MGC:38253 IMAGE:5324328)	AK037099	10.41494	4.96E-24
Tjp3	Tight junction protein 3, mRNA (cDNA clone MGC:11960 IMAGE:3600848)	NM_013769	10.41438	5.26E-21
NAP053018-1	Unknown		10.38831	1.26E-44
Ibrdc3	IBR domain containing 3, mRNA (cDNA clone IMAGE:5254400)	AK015966	10.37732	9.05E-35
Slco4a1	Solute carrier organic anion transporter family, member 4a1 (Slco4a1), mRNA	NM_148933	10.35873	7.30E-26
E430024C06Rik	Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430003N15 product: unclassifiable, full insert sequence.	AK088091	10.34123	3.10E-23
1500026H17Rik	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230317N08 product: unclassifiable, full insert sequence	AK005299	10.33636	4.98E-16
3110057O12Rik	RIKEN cDNA 3110057O12 gene, mRNA (cDNA clone IMAGE:4007705)	NM_026622	10.33092	1.71E-11
Pppm	Protein tyrosine phosphatase, receptor type, M (Pppm), mRNA	AK047905	10.30778	8.35E-06
Hemtl	17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:19200059J21 product:11 beta-hydroxylase homolog [Mus sp], full insert sequence	AK078619	10.30203	7.99E-06
Stau1	Staufen (RNA binding protein) homolog 1 (Drosophila), mRNA (cDNA clone MGC:13708 IMAGE:4188394)	AK030890	10.2707	2.31E-16
Hist1h1d	Histone 1, H1d (Hist1h1d), mRNA	NM_145713	10.25591	3.12E-13
D16H22S680E	DNA segment, Chr 16, human D22S680E, expressed (D16H22S680E), mRNA	AK047383	10.23081	1.29E-32
Rgl1	Ral guanine nucleotide dissociation stimulator-like 1, mRNA (cDNA clone MGC:18430 IMAGE:4241244)	AK032340	10.22274	1.40E-45
8430422M09Rik	Mus musculus RIKEN cDNA 8430422M09 gene (8430422M09Rik), mRNA [XM_148115]	XM_148115	10.21893	0.00001
Kcnab3	Potassium voltage-gated channel, shaker-related subfamily, beta member 3, mRNA (cDNA clone MGC:27635 IMAGE:4507029)	NM_010599	10.2158	1.74E-06
Slc25a21	Solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21, mRNA (cDNA clone MGC:67702 IMAGE:5042653)	NM_172577	10.21333	5.59E-14

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Col20a1	Collagen, type XX, alpha 1, mRNA (cDNA clone IMAGE:5366843)	AK006759	10.16397	3.65E-12
Hrb1	HIV-1 Rev binding protein-like (Hrb1), transcript variant 1, mRNA	AK037434	10.14872	3.47E-17
NM_029423	Mus musculus RIKEN cDNA 4833414G05 gene (4833414G05Rik), mRNA [NM_029423]	NM_029423	10.1245	3.34E-13
Kenma1	Large conductance calcium activated potassium BK channel STREX-1 variant (Slo)	AK052354	10.12088	7.76E-06
Hivep3	Clone 5'RACE1 ZAS3 (Krc) mRNA, 5' UTR	AK087330	10.11146	8.57E-37
Isl2	Insulin related protein 2 (islet 2) (Isl2), mRNA	NM_027397	10.06446	6.70E-06
A930034L06Rik	RIKEN cDNA A930034L06 gene (A930034L06Rik), mRNA	NM_175692	10.0482	3.73E-14
Rhbq	Rhesus blood group-associated B glycoprotein, mRNA (cDNA clone MGC:35874 IMAGE:4218889)	NM_021375	10.00581	2.67E-18
Grp1	GH regulated TBC protein 1, mRNA (cDNA clone MGC:27905 IMAGE:3500563)	NM_025768	9.93642	5.59E-28
Ptkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2, mRNA (cDNA clone MGC:25723 IMAGE:3979400)	AK016729	9.92957	3.07E-35
BC049806	CDNA sequence BC049806, mRNA (cDNA clone MGC:76460 IMAGE:30431671)	NM_172513	9.90803	1.62E-19
Cdc14a	CDC14 cell division cycle 14 homolog A (S. cerevisiae), mRNA (cDNA clone MGC:100044 IMAGE:30356962)	AK048250	9.87444	0.0038
Hist1h4i	Mus musculus histone 2, H4, mRNA (cDNA clone IMAGE:4205460), partial cds.	BC019757	9.86807	1.47E-19
Mcam	Melanoma cell adhesion molecule, mRNA (cDNA clone MGC:35823 IMAGE:5372497)	NM_023061	9.84222	1.58E-07
Mif2	Antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 (Mfi2), mRNA	NM_013900	9.83413	4.36E-21
Dock4	MKIAA0716 protein	BC051125	9.81909	2.29E-11
Xlr3b	X-linked lymphocyte-regulated 3B (Xlr3b), mRNA	NM_011727	9.78323	6.44E-14
NAP069339-1	Unknown	9.77056	2.40E-32	
2610018105Rik	Mus musculus RIKEN cDNA 2610018105 gene (2610018105Rik), mRNA [NM_183279]	NM_183279	9.77006	1.01E-17
Nrarp	Notch-regulated ankyrin repeat protein (Nrarp), mRNA	NM_025980	9.74784	4.38E-07
Eml5	Mus musculus echinoderm microtubule associated protein like 5, mRNA (cDNA clone MGC:40838 IMAGE:5368750), complete cds.	BC030361	9.71342	1.76E-27
Slc26a4	Pendrin (Pds)	NM_011867	9.7024	2.38E-37
Sdfr1	Stromal cell derived factor receptor 1 (Sdfr1), mRNA	AK039616	9.69602	1.98E-06
A43010505Rik	B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730031B04 product: Serine-threonine kinase (Fragment) homolog [Rattus norvegicus], full insert sequence	AK040531	9.69534	3.56E-18
Dgat2	Diacylglycerol O-acyltransferase 2 (Dgat2), mRNA	NM_026384	9.69276	2.73E-35
W29301	2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230029K24 product: hypothetical protein, full insert sequence	W29301	9.68389	1.54E-44
Gng8	Guanine nucleotide binding protein (G protein), gamma 8 subunit (Gng8), mRNA	NM_010320	9.68159	4.39E-19
Ppifbp2	Protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein 2, mRNA (cDNA clone IMAGE:3488375)	NM_008905	9.67203	0.00004
Aplp2	Amyloid beta (A4) precursor-like protein 2, mRNA (cDNA clone IMAGE:4504805)	NM_009691	9.54457	8.29E-26
4921524J17Rik	RIKEN cDNA 4921524J17 gene (4921524J17Rik), mRNA	AK006764	9.52196	0.00001

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Nppb	Natriuretic peptide precursor type B (Nppb), mRNA	NM_008726	9.5214	2.01E-10
AK082626	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone: C230071E14 product: unclassifiable, full insert sequence	AK082626	9.49805	0.00002
Ccp1	Cell cycle progression 1, mRNA (cDNA clone MGC:12151 IMAGE:3711012)	NM_028181	9.49574	1.25E-22
4933401N24Rik	RIKEN cDNA 4933401N24 gene (4933401N24Rik), mRNA	NM_175367	9.48097	1.88E-15
Eiv5	Ets variant gene 5, mRNA (cDNA clone MGC:28414 IMAGE:4036564)	NM_023794	9.46181	1.65E-37
Upp1	Ureidopropionase, beta, mRNA (cDNA clone IMAGE:4974180)	NM_133995	9.45902	7.68E-06
AK041503	PREDICTED: Mus musculus hypothetical protein LOC (LOC545502), mRNA	AK041503	9.45271	0.00022
Arc	Activity regulated cytoskeletal-associated protein, mRNA (cDNA clone MGC:27890 IMAGE:3498057)	NM_018790	9.4495	6.20E-31
4931406B18Rik	RIKEN cDNA 4931406B18 gene (4931406B18Rik), mRNA	NM_028737	9.44613	0.00004
Atg12	App12	NM_026217	9.43954	2.67E-16
Zswim5	Zinc finger, SWIM domain containing 5 (Zswim5), mRNA	AK046815	9.43427	0.00003
Pacsin3	Protein kinase C and casein kinase II substrate 3 (Pacsin3)	AK014830	9.42759	4.14E-13
AW125688	Expressed sequence AW125688 (AW125688), mRNA	NM_001001885	9.37585	5.66E-26
Odz2	ODZ2 (Odz2)	AK083775	9.36205	0.00002
Smpd3	Spingomyelin phosphodiesterase 3, neutral (Smpd3), mRNA	NM_021491	9.34228	2.30E-12
Ceacam2	CEA-related cell adhesion molecule 2, mRNA (cDNA clone MGC:18435 IMAGE:4241449)	NM_007543	9.33621	5.14E-12
Mmp10	Matrix metalloproteinase 10 (Mmp10), mRNA	NM_019471	9.28633	1.13E-07
BC013712	CDNA sequence BC013712, mRNA (cDNA clone IMAGE:3155889)	BC013712	9.27602	1.41E-15
Cfh	Complement component factor h (Cfh), mRNA	NM_009888	9.21081	1.00E-18
H2-Oa	Histocompatibility 2, O region alpha locus (H2-Oa), mRNA	NM_008206	9.20769	2.53E-16
Cacng5	Calcium channel, voltage-dependent, gamma subunit 5 (Cacng5), mRNA	NM_080644	9.20551	4.94E-09
Slc28a2	Purine-selective Na <sup>+</sup> nucleoside cotransporter (Cnt2)	NM_172980	9.20316	2.97E-09
AK089607	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830004H11 product: unclassifiable, full insert sequence.	AK089607	9.1922	0.00004
Gent1	Glucosaminyl (N-acetyl) transferase 1, core 2, mRNA (cDNA clone MGC:11452 IMAGE:3154671)	NM_010265	9.17498	8.19E-10
Serp1b1a	E1A (Serp1b1)	NM_025429	9.17307	6.72E-18
Ccbl2	Cysteine conjugate-beta lyase 2 (Ccbl2), mRNA	NM_173763	9.15601	3.33E-11
Nscn1	Mus musculus non-selective cation channel 1 (Nscn1), mRNA [NM_010940]	NM_010940	9.15204	0.0001
Hrc	Histidine rich calcium binding protein (Hrc), mRNA	NM_010473	9.13879	6.63E-24
H2-DMb2	Histocompatibility 2, class II, locus Mb1, mRNA (cDNA clone MGC:5741 IMAGE:3486844)	NM_010388	9.10407	1.15E-27
Rgl1	Ral guanine nucleotide dissociation stimulator-like 1, mRNA (cDNA clone MGC:18430 IMAGE:4241244)	NM_016846	9.0778	1.59E-41

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<i>Dapk2</i>	Death-associated kinase 2, mRNA (cDNA clone MGC:13742 IMAGE:4016911)	NM_0100019	9.06365	4.58E-16
<i>Lmk2</i>	Lemur tyrosine kinase 2, mRNA (cDNA clone IMAGE:6407188)	AK039738	9.05942	1.27E-38
<i>Cfh</i>	Complement component factor h, mRNA (cDNA clone IMAGE:5132971)	M29010	8.96985	2.80E-06
<i>Spry1</i>	Sprouty homolog 1 (Drosophila), mRNA (cDNA clone MGC:18307 IMAGE:3672353)	NM_011896	8.96343	8.83E-21
<i>Gm693</i>	PREDICTED: similar to novel protein [Mus musculus], mRNA sequence	XM_204104	8.95937	1.91E-21
<i>Ryr1</i>	RyR1 mRNA for skeletal muscle ryanodine receptor	AK042482	8.94761	2.14E-13
8430437N05Rik	DACH protein (Dach)	AK018473	8.93946	0.00004
<i>Ahl5c</i>	ADP-ribosylation factor-like 12 (Ahl12), mRNA	NM_207231	8.93395	2.10E-19
<i>Rasip1</i>	Ras interacting protein 1, mRNA (cDNA clone IMAGE:1245387)	AK033276	8.93241	7.99E-10
<i>Adam25</i>	Testase 2 (Adam-25)	NM_011781	8.91583	0.00004
4930579G22Rik	RIKEN cDNA 4930579G22 gene (4930579G22Rik), mRNA	NM_026916	8.91564	1.40E-14
NAP062857-1	Unknown		8.89087	0.0001
<i>Pbx3</i>	Pre B-cell leukemia transcription factor 3 (Pbx3), mRNA	AK052017	8.85804	0.00004
<i>Kcnip1</i>	A-type potassium channel modulatory protein 1.2 (Kchip1.2)	NM_027398	8.84607	0.00004
<i>Pard6b</i>	Par-6 (partitioning defective 6) homolog beta (C. elegans), mRNA (cDNA clone MGC:35871 IMAGE:2655658)	NM_021409	8.83071	3.85E-15
<i>Fli13</i>	Strain C57BL/6xCBA fibronectin leucine rich transmembrane protein 3 (Flrt3)	NM_178382	8.81882	2.05E-14
AK032440	Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430547C23 product: unclassifiable, full insert sequence	AK032440	8.80642	0.00004
<i>Cpn1</i>	Carboxypeptidase N, polypeptide 1, mRNA (cDNA clone MGC:25883 IMAGE:4211169)	NM_030703	8.79262	7.85E-18
2810405K02Rik	RIKEN cDNA 2810405K02 gene, mRNA (cDNA clone MGC:40622 IMAGE:5401948)	NM_025582	8.78415	0.00006
9230110K08Rik	Adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230110K08 product: hypothetical HMG-I and HMG-Y DNA-binding domain (A+T-hook) containing protein, full insert sequence	AK020331	8.77293	4.72E-29
<i>Igsf1</i>	Immunoglobulin superfamily, member 1, transcript variant 2, mRNA (cDNA clone IMAGE:30249729)	NM_183336	8.75732	0.00008
<i>Ndrg4</i>	N-myc downstream regulated gene 4 (Ndrg4), mRNA	NM_145602	8.75653	6.57E-36
<i>Mst1r</i>	Macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (Mst1r), mRNA	NM_009074	8.71853	6.63E-18
<i>Cdon</i>	Cell adhesion molecule-related/down-regulated by oncogenes (Cdon), mRNA	NM_021339	8.71613	1.34E-16
<i>Serpine1</i>	Serine (or cysteine) peptidase inhibitor, clade E, member 1 (Serpine1), mRNA	NM_008871	8.66415	7.69E-24
<i>Aig12</i>	Apg12	NM_026217	8.66365	5.05E-14
AK051813	Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230004F15 product: unclassifiable, full insert sequence.	AK051813	8.6557	6.88E-09
F830010H11Rik	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830010H11 product: unclassifiable, full insert sequence.	AK089716	8.65219	0.00002
<i>Clu</i>	Clusterin (Clu), mRNA	NM_013492	8.64934	3.24E-12

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<b>Akap12</b>	<b>A kinase (PRKA) anchor protein (gravin) 12 (Akap12), mRNA</b>	<b>NM_031185</b>	<b>8.6406</b>	<b>1.71E-27</b>
Paecin1	Protein kinase C and casein kinase substrate in neurons 1, mRNA (cDNA clone MGC:25285 IMAGE:4527708)	NM_178365	8.62899	5.37E-08
4930449104Rik	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930449104 product: hypothetical protein, full insert sequence	AK015432	8.6266	3.24E-33
Ap3m2	Adaptor-related protein complex 3, mu 2 subunit, mRNA (cDNA clone MGC:40858 IMAGE:5369288)	NM_029505	8.62306	1.02E-10
Olfrl1383	Olfactory receptor 1383 (Olfrl1383), mRNA	NM_207574	8.60579	1.28E-24
Lip1	Lysosomal acid lipase 1 (Lip1), mRNA	AK083099	8.59815	2.87E-09
Ero1lb	ERO1-like beta (S. cerevisiae) (Ero1lb), mRNA	NM_026184	8.59729	5.41E-29
Zfp509	Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330031118 product: weakly similar to ZINC FINGER PROTEIN ZFP-93 (ZINC FINGER PROTEIN HZF6) (FRAGMENT) [Homo sapiens], full insert sequence.	AK054488	8.5938	1.99E-28
Fgd4	FYVE, RhoGEF and PH domain containing 4 (Fgd4), transcript variant beta, mRNA	AK043656	8.53643	5.81E-08
Il1rap	Interleukin 1 receptor accessory protein (Il1rap), transcript variant 2, mRNA	AK045686	8.52846	5.61E-45
1700109H08Rik	RIKEN cDNA 1700109H08 gene, mRNA (cDNA clone MGC:118394 IMAGE:30920581)	AK007150	8.52551	1.98E-13
Ptger4	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DI130004L12 product: prostaglandin E receptor 4 (subtype EP4), full insert sequence.	AK051137	8.52297	6.25E-26
4933408J17Rik	Small nuclear ribonucleoprotein polypeptide F, mRNA (cDNA clone MGC:118343 IMAGE:30917013)	AK016739	8.52005	0.00012
Jrkl	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430098H07 product: hypothetical protein, full insert sequence	AK079877	8.51387	4.41E-18
Cxc9	Chemokine (C-X-C motif) ligand 9, mRNA (cDNA clone MGC:6179 IMAGE:3257716)	NM_008599	8.50345	1.39E-17
Cfh	Complement component factor h (Cfh), mRNA	NM_009888	8.49969	1.56E-11
AK042806	Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730026C13 product: unclassifiable, full insert sequence.	AK042806	8.4994	1.23E-08
Gdps5	Glycerophosphodiester phosphodiesterase domain containing 5, mRNA (cDNA clone MGC:37148 IMAGE:4953174)	NM_201352	8.48545	5.38E-09
Tgm4	Experimental autoimmune prostatitis antigen 1 (Eapa1)	NM_177911	8.48033	0.00012
Btd5	BTB (POZ) domain containing 5, mRNA (cDNA clone MGC:47075 IMAGE:5347183)	NM_025707	8.46778	1.71E-15
Rtn4r	Reticulon 4 receptor (Rtn4r), mRNA	NM_022982	8.45249	7.05E-28
Ibrdc3	IBR domain containing 3, mRNA (cDNA clone IMAGE:5254400)	AK040902	8.4511	6.53E-22
Aldh1l2	Aldehyde dehydrogenase 1 family, member L2 (Aldh1l2), mRNA	AK085074	8.41092	2.26E-14
LOC433886	hypothetical gene supported by AK049058; BC025881	BC025881	8.39834	0.00022
<b>Ktss1</b>	<b>Golgi transport 1 homolog A (S. cerevisiae) (Golt1a), mRNA</b>	<b>NM_178260</b>	<b>8.39812</b>	<b>0.00014</b>
Egr3	Early growth response 3 (Egr3), mRNA	AK078299	8.39771	1.35E-12
NAP112027-1	Unknown		8.38015	1.69E-11
Myh3	PREDICTED: myosin, heavy polypeptide 3, skeletal muscle, embryonic [Mus musculus], mRNA sequence	M11154	8.3727	4.98E-25



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Vil1	Villin 1, mRNA (cDNA clone MGC:18506 IMAGE:4236751)	NM_009509	8.36524	5.30E-09
Aplp2	Amyloid beta (A4) precursor-like protein 2, mRNA (cDNA clone IMAGE:4504805)	NM_009691	8.36361	8.30E-43
Gats	Opposite strand transcription unit to Stag3 (Gats), mRNA	BC026208	8.35244	8.31E-10
Olfrl1052	Olfactory receptor 1052 (Olfrl1052), mRNA	NM_147010	8.34985	0.00013
Akap13	PREDICTED: hypothetical protein LOC75547 [Mus musculus], mRNA sequence	AK006382	8.31218	1.41E-14
Nanos1	Nanos homolog 1 (Drosophila), mRNA (cDNA clone MGC:102288 IMAGE:6849859)	BC056473	8.30066	1.94E-13
Eif2c3	Eukaryotic translation initiation factor 2C, 3 (Eif2c3), mRNA	AK087577	8.26887	1.33E-22
AK086157	Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930008M17 product: unclassifiable, full insert sequence.	AK086157	8.26126	0.00012
Art3	ART3 mono(ADP-ribosyl)transferase (art3 gene), splice variant 1	NM_181728	8.2485	9.93E-16
TC1085358	AF179867 STE20-like kinase [Homo sapiens], partial (56%) [TC1085358]		8.24529	1.54E-22
Eif2c3	Eukaryotic translation initiation factor 2C, 3 (Eif2c3), mRNA	BC060127	8.21917	1.00E-29
Cd52	CD52 antigen, mRNA (cDNA clone MGC:40993 IMAGE:1396480)	NM_013706	8.21899	0.00035
Slc25a29	Solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29, mRNA (cDNA clone MGC:7958 IMAGE:3584570)	NM_181328	8.20668	2.73E-17
Kif13b	MKIAA0639 protein	AK031370	8.20576	2.43E-10
Itpka	Inositol 1,4,5-trisphosphate 3-kinase A (Itpka), mRNA	NM_146125	8.20068	2.20E-07
Efhc1	EF hand domain containing 1, mRNA (cDNA clone MGC:28727 IMAGE:4459208)	NM_028889	8.18839	4.79E-24
Cepgl	Cell cycle progression 1, mRNA (cDNA clone MGC:12151 IMAGE:3711012)	BC006717	8.15286	2.83E-33
1810020D17Rik	RIKEN cDNA 1810020D17 gene, mRNA (cDNA clone MGC:36240 IMAGE:5027461)	AK031619	8.13287	0.00011
Ripk3	Receptor-interacting serine-threonine kinase 3, mRNA (cDNA clone MGC:35896 IMAGE:3590770)	NM_019955	8.12366	1.65E-15
Zdhhc15	Zinc finger, DHHC domain containing 15 (Zdhhc15), mRNA	BU610239	8.10685	0.00016
Scgblc1	PREDICTED: similar to RYD5 [Mus musculus], mRNA sequence	XM_355976	8.10518	1.20E-23
XM_356367	Mus musculus similar to cyclin-dependent kinase-like 5; serine/threonine kinase 9 (LOC382253), mRNA [XM_356367]	XM_356367	8.10486	1.44E-12
Rab3il1	Mus musculus RAB3A interacting protein (rab3il1)-like 1 (Rab3il1), mRNA.	NM_178881	8.09444	1.48E-10
Egfl5	MKIAA0818 protein	NM_172694	8.09398	1.04E-08
Csnd	Mus musculus 10 days lactation, adult female mammary gland cDNA, RIKEN full-length enriched library, clone:D730003B11 product: casein delta, full insert sequence.	AK052789	8.09332	0.00016
Fkbp6	FK506 binding protein 6 (Fkbp6), mRNA	NM_033571	8.09194	5.51E-33
Dll4	Dll-4 mRNA for Delta-4	NM_019454	8.08534	8.83E-21
Sema4g	Semaphorin subclass 4 member G (sema4g)	NM_011976	8.0833	5.15E-11
Rccd1	Protein regulator of cytokinesis 1 (Prc1), mRNA	AK047578	8.0818	4.76E-07
Cul4a	Cullin 4A (Cul4a), mRNA	AK084008	8.07649	0.00002

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Tec	Cytoplasmic tyrosine kinase, Dscr28c related (Drosophila), mRNA (cDNA clone MGC:46873 IMAGE:5029430)	NM_013689	8.06	3.75E-18
Enupd2	Ectonucleoside triphosphate diphosphohydrolase 2, mRNA (cDNA clone MGC:5806 IMAGE:3582550)	NM_009849	8.05603	1.54E-20
Krtap16-4	Keratin associated protein 16-4 (Krtap16-4), mRNA	NM_130873	8.05589	0.00004
Aqp11	Aquaporin 11, mRNA (cDNA clone IMAGE:5126527)	NM_175105	8.05418	1.48E-42
Cd36	CD36 antigen, mRNA (cDNA clone MGC:6068 IMAGE:3481681)	L23108	8.05303	7.36E-26
1700001G17Rik	RIKEN cDNA 1700001G17 gene (1700001G17Rik), mRNA	NM_026204	8.04819	1.22E-14
Pgr	Progesterone receptor (Pgr), mRNA	AK036862	8.04787	0.00003
Maf	c-maf-c-Maf protein {proto-oncogene} [mice, BALB/c, cerebellum, mRNA, 2736 nt].	S74567	8.03437	0.00007
Sdc4	Syndecan 4, mRNA (cDNA clone MGC:11456 IMAGE:3154160)	NM_011521	8.0206	1.74E-10
Aytl1	Hypothetical protein A330042H22 (A330042H22), mRNA	NM_173014	8.01654	7.00E-11
2310047O13Rik	RIKEN cDNA 2310047O13 gene, mRNA (cDNA clone MGC:28605 IMAGE:4217391)	AK049694	8.01005	1.88E-15
Trp73	P73 alpha protein (P73 gene)	AK014503	8.00474	0.00017
Tagln3	Transgelin 3 (Tagln3), mRNA	NM_019754	8.00047	0.00012
NAP052665-1	Unknown		7.99834	3.51E-13
Cd40	CD40 antigen (Cd40), transcript variant 5, mRNA	NM_170701	7.98914	2.13E-26
4732465E10Rik	MKIAA0716 protein	AK028870	7.98626	1.12E-30
1700109F18Rik	Homeo box D4 (Hoxd4), mRNA	AK006878	7.96332	0.00015
Slc25a29	Solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29, mRNA (cDNA clone MGC:7958 IMAGE:3584570)	NM_181328	7.95316	5.52E-28
Ebi3	Epstein-Barr virus induced gene 3, mRNA (cDNA clone MGC:11457 IMAGE:3154957)	NM_015766	7.94831	1.93E-15
D330017120Rik	Mus musculus RIKEN cDNA D330017120 gene (D330017120Rik), mRNA [NM_177204]	NM_177204	7.9325	1.86E-28
A930037G23Rik	RIKEN cDNA A930037G23 gene, mRNA (cDNA clone MGC:67253 IMAGE:6403474)	AK044382	7.92998	0.00002
Wdr47	WD repeat domain 47 (Wdr47), mRNA	NM_181400	7.92668	7.41E-15
Ppl	Periplakin (Ppl), mRNA	BC057152	7.88627	4.33E-13
3110021A11Rik	Rab6 interacting protein 2 (Rab6ip2), transcript variant 1, mRNA	AK052063	7.84546	0.00001
Dmn	MKIAA0353 protein	NM_201639	7.82763	3.07E-17
Olfir541	Olfactory receptor 541 (Olfir541), mRNA	NM_146962	7.82426	0.0002
Lgr4	PREDICTED: G protein-coupled receptor 48 [Mus musculus], mRNA sequence	AK044357	7.82294	1.53E-17
Star	Steroidogenic acute regulatory protein (Star), mRNA	NM_011485	7.81952	6.22E-16
Plekha7	Pleckstrin homology domain containing, family A member 7, mRNA (cDNA clone MGC:90927 IMAGE:3602481)	NM_172743	7.81937	5.45E-12
D330028D13Rik	RIKEN cDNA D330028D13 gene, mRNA (cDNA clone MGC:67688 IMAGE:4487036)	NM_172727	7.81506	3.42E-10
Rpm	Reprimo, TP53 dependent G2 arrest mediator candidate, mRNA (cDNA clone MGC:41066 IMAGE:1434823)	NM_023396	7.7925	1.35E-15

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Lcn12	Lipocalin 12 (Lcn12), mRNA	AK020307	7.78453	0.00011
Spire1	Spire homolog 1 (Drosophila), mRNA (cDNA clone MGC:106458 IMAGE:30535423)	AK053505	7.77423	9.18E-16
Glt25d2	Glycosyltransferase 25 domain containing 2, mRNA (cDNA clone MGC:92944 IMAGE:5706069)	NM_177756	7.7719	0.00026
<b>Ddit3</b>	<b>DNA-damage inducible transcript 3, mRNA (cDNA clone MGC:18641 IMAGE:4012433)</b>	<b>NM_007837</b>	<b>7.77126</b>	<b>3.83E-06</b>
Gab3	Growth factor receptor bound protein 2-associated protein 3 (Gab3), mRNA	NM_181584	7.75833	1.55E-13
I110031B11Rik	RIKEN cDNA I110031B11 gene (I110031B11Rik), mRNA	NM_026811	7.73455	0.00024
Tcf7	Transcription factor 7, T-cell specific (Tcf7), mRNA	NM_009331	7.7187	0.00008
Lcn5	Lipocalin 5 (Lcn5), mRNA	NM_007947	7.70424	0.00016
BB064041	Activated spleen cDNA, RIKEN full-length enriched library, clone:F830206M21 product: unclassifiable, full insert sequence	BB064041	7.6678	1.96E-26
Tagln	Transgelin, mRNA (cDNA clone MGC:6045 IMAGE:3600413)	NM_011526	7.64204	1.12E-11
Tktl1	Transketolase-like 1 (Tktl1), mRNA	NM_031379	7.63328	0.00021
Mlph	Melanophilin (Mlph), mRNA	NM_053015	7.6104	0.00021
Armc9	RIKEN cDNA 4930438005 gene (4930438005Rik), mRNA	NM_030184	7.59315	8.43E-21
9330102E08Rik	PREDICTED: hypothetical protein XP_489154 [Mus musculus], mRNA sequence	AK033854	7.58577	7.54E-14
Cbara1	Calcium binding atopy-related autoantigen 1 (Cbara1), mRNA	AK029884	7.57763	9.77E-14
Hispad2a	4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430315C20 product: hypothetical Histidine acid phosphatase containing protein, full insert sequence	AK046696	7.56076	1.42E-12
TC1052172	Unknown		7.55807	1.37E-10
Decun1d4	Expressed sequence A1836376, mRNA (cDNA clone IMAGE:3995042)	NM_178896	7.55542	4.88E-10
Ralgps1	Ral GEF with PH domain and SH3 binding motif 1, mRNA (cDNA clone MGC:99991 IMAGE:30536315)	AK129123	7.52544	1.74E-06
Flrt3	Strain C57BL/6xCBA fibronectin leucine rich transmembrane protein 3 (Flrt3)	NM_178382	7.51845	1.29E-33
Efnb2	Ephrin B2 (Efnb2), mRNA	NM_010111	7.50936	8.34E-13
Mum1l1	Melanoma associated antigen (mutated) 1-like 1, mRNA (cDNA clone IMAGE:30619674)	NM_175541	7.50527	4.98E-06
<b>Zfp185</b>	<b>Zinc finger protein 185, mRNA (cDNA clone MGC:49126 IMAGE:4191053)</b>	<b>NM_009549</b>	<b>7.50102</b>	<b>5.10E-06</b>
Epb4.115	Erythrocyte protein band 4.1-like 5 (Epb4.115), mRNA	AK079301	7.49371	1.30E-11
Tnfrap82	Tumor necrosis factor, alpha-induced protein 8-like 2 (Tnfrap82), mRNA	NM_027206	7.48745	3.98E-30
<b>Rad9b</b>	<b>RAD9 homolog B (S. cerevisiae) (Rad9b), mRNA</b>	<b>NM_144912</b>	<b>7.47671</b>	<b>3.20E-11</b>
Irf8	Interferon consensus sequence binding protein 1, mRNA (cDNA clone MGC:6194 IMAGE:3487214)	NM_008320	7.47332	6.42E-32
9430085L16Rik	Early B-cell factor 2 (Ebf2), mRNA	AK020505	7.46734	0.00033
9630050P21Rik	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630050P21 product: unclassifiable, full insert sequence	AK036274	7.46671	1.10E-07
Gpr155	G protein-coupled receptor 155, mRNA (cDNA clone IMAGE:4167684)	BC026382	7.45823	3.04E-31

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Habp4	Hyaluronic acid binding protein 4 (Habp4), mRNA	NM_019986	7.45096	7.37E-17
9830169C18Rik	RIKEN cDNA 9830169C18 gene, mRNA (cDNA clone MGC:69959 IMAGE:6509090)	NM_172581	7.4493	6.68E-15
<b>Lrp1b</b>	<b>Low density lipoprotein-related protein 1B (deleted in tumors) (Lrp1b), mRNA</b>	<b>AK034373</b>	<b>7.43347</b>	<b>0.00006</b>
Btg2	B-cell translocation gene 2, anti-proliferative (Btg2), mRNA	NM_007570	7.43345	2.06E-10
2410066E13Rik	RIKEN cDNA 2410066E13 gene (2410066E13Rik), mRNA	NM_026629	7.43071	6.08E-15
Got111	RIKEN cDNA 1700083M11 gene (1700083M11Rik), mRNA	AK006984	7.42792	8.13E-06
Mell1	Nephrilysin-like metalloproteinase 1 (Nll1)	NM_013783	7.41912	4.75E-11
Pde6c	Phosphodiesterase 6C, cGMP specific, cone, alpha prime, mRNA (cDNA clone MGC:38745 IMAGE:5358611)	NM_033614	7.40919	0.00024
3-Mar	Membrane-associated ring finger (C3HC4) 3 (March3), mRNA	AK036622	7.38467	0.00002
TC1013578	AF110520 NG28 [Mus musculus], partial (30%) [TC1013578]		7.37995	2.09E-06
2310046K01Rik	RIKEN cDNA 2310046K01 gene (2310046K01Rik), mRNA	NM_027172	7.37995	6.69E-29
Ldhc	Lactate dehydrogenase 3, C chain, sperm specific (Ldh3), mRNA	NM_013580	7.36571	3.03E-20
Mgst3	Microsomal glutathione S-transferase 3, mRNA (cDNA clone MGC:35738 IMAGE:5372427)	NM_025569	7.36371	7.31E-12
AK084877	0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130014I08 product: unclassifiable, full insert sequence	AK084877	7.35577	7.22E-23
4732467B22	hypothetical protein 4732467B22	NM_177822	7.33593	6.02E-12
Spib	Spi-B transcription factor (Spi-1/PU.1 related) (Spib), mRNA	U87620	7.32567	1.70E-08
Aldh1a1	Aldh-2=acetaldehyde dehydrogenase [nrice, BALB/c, livers, mRNA Partial, 1632 nt]	NM_013467	7.32059	1.68E-29
BB128963	Expressed sequence BB128963, mRNA (cDNA clone IMAGE:3964696)	AK088715	7.29587	3.02E-21
Samd8	Sterile alpha motif domain containing 8 (Samd8), mRNA	NM_026283	7.28944	2.04E-13
Dnmt3b	DNA cytosine methyltransferase 3b6 (Dnmt3b6) mRNA, complete cds; alternatively spliced	NM_010068	7.28075	1.55E-06
Txnip	Thioredoxin interacting protein, mRNA (cDNA clone MGC:25534 IMAGE:3591421)	AK004653	7.27867	6.51E-09
D930040F23Rik	Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430407I07 product: unclassifiable, full insert sequence.	AK032178	7.26988	3.49E-09
Wdr47	WD repeat domain 47 (Wdr47), mRNA	NM_181400	7.26652	1.73E-06
Pla2g5	Phospholipase A2, group V, mRNA (cDNA clone MGC:31537 IMAGE:4502326)	NM_011110	7.25852	7.82E-12
Tex101	Testis expressed gene 101 (Tex101), mRNA	NM_019981	7.22574	4.77E-20
Gprk5	G protein-coupled receptor kinase 5 (GRK5)	AK079806	7.217	0.00001
<b>Cty2</b>	<b>Cryptochrome 2 (photolyase-like), mRNA (cDNA clone IMAGE:5593948)</b>	<b>NM_009963</b>	<b>7.21232</b>	<b>4.87E-34</b>
Epb4.113	Protein 4.1B (Epb4.113)	AK086340	7.20588	0.00037
Cpeb4	Cytoplasmic polyadenylation element binding protein 4 (Cpeb4), mRNA	AY313775	7.18189	1.32E-08
Rasgef1b	RasGEF domain family, member 1B (Rasgef1b), transcript variant 1, mRNA	NM_181318	7.17597	4.25E-16

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Atrnl1	Attractin like 1, mRNA (cDNA clone IMAGE:4221668)	AK048968	7.15363	4.73E-28
Abfml1	Actin-binding LIM protein 1, mRNA (cDNA clone IMAGE:5523557)	AK031453	7.15289	6.91E-24
D930005D10Rik	MKIAA1849 protein	NM_178702	7.13213	5.89E-24
Rgl1	Ral guanine nucleotide dissociation stimulator,-like 1, mRNA (cDNA clone MGC:18430 IMAGE:4241244)	NM_016846	7.12829	2.93E-40
Olfir295	Olfactory receptor 295 (Olfir295), mRNA	NM_146851	7.12443	2.88E-06
Ccp1	Cell cycle progression 1, mRNA (cDNA clone MGC:12151 IMAGE:3711012)	BC006717	7.12363	1.51E-24
Zbtb10	PREDICTED: zinc finger and BTB domain containing 10 [Mus musculus], mRNA sequence	AK083443	7.11228	0.00061
Icosl	Icos ligand, mRNA (cDNA clone MGC:35971 IMAGE:4217333)	NM_015790	7.1024	0.0004
Mycn	Neuroblastoma myc-related oncogene 1, mRNA (cDNA clone MGC:6240 IMAGE:3495446)	NM_008709	7.10045	0.0004
D030074K08Rik	YY1 associated factor 2 (Yaf2), mRNA	AK083749	7.09956	0.00016
Slc6a18	Solute carrier family 6 (neurotransmitter transporter), member 18, mRNA (cDNA clone MGC:18346 IMAGE:4235659)	AK085473	7.09686	0.00038
Tex12	Testis protein TEX12 (Tex12)	NM_025687	7.09649	1.01E-10
Usp49	Ubiquitin specific peptidase 49 (Usp49), mRNA	NM_198421	7.09535	1.27E-14
Magi3	Membrane associated guanylate kinase, WW and PDZ domain containing 3 (Magi3), mRNA	NM_133853	7.08507	8.81E-28
Mgl1	Macrophage galactose N-acetyl-galactosamine specific lectin 1 (Mgl1), mRNA	NM_010796	7.07263	8.28E-25
Pdlim5	PDZ and LIM domain 5, mRNA (cDNA clone MGC:46824 IMAGE:4457868)	NM_019809	7.05824	9.20E-15
A630005I04Rik	RIKEN cDNA A630005I04 gene (A630005I04Rik), mRNA	AK088332	7.03002	2.01E-26
AK089990	RCB-0559 K-1. F1 cDNA, RIKEN full-length enriched library, clone:G430046I05 product: unclassifiable, full insert sequence	AK089990	7.0234	9.15E-19
Dmn	MKIAA0353 protein	NM_201639	7.0219	2.13E-11
Fabp4	Fatty acid binding protein 4, adipocyte (Fabp4), mRNA	NM_024406	7.02153	1.00E-18
4930463G05Rik	PREDICTED: Mus musculus RIKEN cDNA 4930463G05 gene (4930463G05Rik), mRNA	AK015217	7.02125	1.22E-42
Rshl3	PREDICTED: similar to radial spoke head-like 1 [Mus musculus], mRNA sequence	AK038980	7.01713	0.00039
Smpd3	Sphingomyelin phosphodiesterase 3, neutral (Smpd3), mRNA	NM_021491	7.00037	1.98E-09
A1931714	PREDICTED: hypothetical protein LOC102182 [Mus musculus], mRNA sequence	AK045296	7.00021	4.36E-14
Diras1	DIRAS family, GTP-binding RAS-like 1 (Diras1), mRNA	NM_145217	6.99843	8.46E-28
Olfir460	Olfactory receptor 460 (Olfir460), mRNA	NM_146383	6.98029	0.00004
Lphn3	Latrophilin 3, mRNA (cDNA clone IMAGE:30549106)	AK053210	6.97894	0.00044
1700026L06Rik	RIKEN cDNA 1700026L06 gene (1700026L06Rik), mRNA	BC055108	6.97247	2.83E-27
Kremen1	Kringle containing transmembrane protein 1 (Kremen1), mRNA	AK081707	6.95532	2.39E-24
B3gnt4	Beta1,3 N-acetylglucosaminyltransferase-4 (B3gnt4)	NM_198611	6.94475	2.02E-12
Hcn3	Hyperpolarization-activated, cyclic nucleotide-gated K+ 3 (Hcn3), mRNA	NM_008227	6.93488	8.78E-08

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Ptxdc1	Plexin domain containing 1 (Ptxdc1), mRNA	NM_028199	6.93463	8.74E-18
Meig1	Meiosis expressed gene 1 (Meig1), mRNA	NM_008579	6.92131	9.92E-14
Cdx1	Caudal type homeo box 1, mRNA (cDNA clone MGC:28644 IMAGE:4224352)	NM_009880	6.91978	0.00044
Zp3	Zona pellucida glycoprotein 3 (Zp3), mRNA	NM_011776	6.91854	8.16E-36
6530409C15Rik	PREDICTED: hypothetical protein LOC76224 [Mus musculus], mRNA sequence	AK018330	6.91722	0.00041
4930518F03Rik	Mus musculus RIKEN cDNA 4930518F03 gene (4930518F03Rik), mRNA [NM_177191]	NM_177191	6.91301	0.00073
Mmp2	Matrix metalloproteinase 2 (Mmp2), mRNA	BF147716	6.91006	1.84E-11
Herc5	Iduronato sulfatase	AK037442	6.90618	7.13E-07
Neud4	Clone m62 zinc finger protein neuro-d4 (neuro-d4)	NM_013874	6.90322	1.87E-11
Slc16a10	Solute carrier family 16 (monocarboxylic acid transporters), member 10, mRNA (cDNA clone MGC:60866 IMAGE:30046388)	AK011813	6.89975	2.58E-10
TC947784	SNAG_HUMAN Gamma-soluble NSF attachment protein (SNAP-gamma) (N-ethylmaleimide-sensitive factor attachment protein, gamma). [Human] [Homo sapiens], partial (13%) [TC947784]		6.88434	0.00048
Tmem64	Transmembrane protein 64, mRNA (cDNA clone MGC:40684 IMAGE:3661112)	AK035894	6.87747	0.00049
AK043237	Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730074B07 product: unclassifiable, full insert sequence.	AK043237	6.86471	0.00065
Gm172	PREDICTED: similar to hypothetical protein [Mus musculus], mRNA sequence	AV254918	6.86109	7.31E-13
Apobec2	Apolipoprotein B editing complex 2, mRNA (cDNA clone MGC:41184 IMAGE:1433092)	NM_009694	6.85954	0.0007
Bcl2l11	<b>BCL2-like 11 (apoptosis facilitator), transcript variant 1, mRNA (cDNA clone MGC:28730 IMAGE:4459720)</b>	<b>BC058175</b>	<b>6.85608</b>	<b>1.80E-13</b>
Gent1	Glucosaminyl (N-acetyl) transferase 1, core 2, mRNA (cDNA clone MGC:11452 IMAGE:3154671)	NM_173442	6.84626	6.17E-10
Fcgr3	Fc gamma receptor III (Fcgr3) mRNA, Fcgr3-b allele	NM_010188	6.844	1.64E-15
Zdhhc6	Zinc finger, DHHC domain containing 6, mRNA (cDNA clone MGC:30394 IMAGE:4459242)	NM_025883	6.84083	0.00001
Pbx4	Pre-B-cell leukemia transcription factor 4, mRNA (cDNA clone MGC:40990 IMAGE:1263363)	NM_030555	6.83768	6.20E-23
Eif2c3	Eukaryotic translation initiation factor 2C, 3 (Eif2c3), mRNA	BC060127	6.80015	7.50E-12
1810057P16Rik	RIKEN cDNA 1810057P16 gene (1810057P16Rik), mRNA	AK075801	6.77942	5.18E-12
Osbp18	Oxysterol binding protein-like 8 (Osbp18), transcript variant 2, mRNA	AK036477	6.77762	1.16E-17
Lysmd4	RIKEN cDNA 4930506D23 gene, mRNA (cDNA clone MGC:65434 IMAGE:4504057)	AK039294	6.75923	2.83E-18
Fsd1	Fibronectin type 3 and SPRY domain-containing protein (Fsd1), mRNA	NM_183178	6.74462	0.0004
Lcnt1	Leucine carboxyl methyltransferase 1, mRNA (cDNA clone IMAGE:3595687)	NM_025304	6.72952	3.34E-35
<b>Bach2</b>	<b>BTB and CNC homology 2 (Bach2), mRNA</b>	<b>NM_007521</b>	<b>6.72785</b>	<b>5.54E-12</b>
Kif17	Kinesin family member 17 (Kif17), mRNA	NM_010623	6.70819	8.92E-14
LOC195281	similar to Proton-associated sugar transporter A (PAST-A) (Deleted in neuroblastoma 5 protein) (DNb-5)	XM_111577	6.70613	4.14E-29
D330012F22Rik	RIKEN cDNA D330012F22 gene, mRNA (cDNA clone MGC:47349 IMAGE:4458984)	AK084531	6.70519	3.43E-07



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Athgf7	Rho guanine nucleotide exchange factor (GEF7) (Athgf7), mRNA	AK129064	6.70342	1.94E-21
D930046H04Rik	Mus musculus RIKEN cDNA D930046H04 gene (D930046H04Rik), mRNA [NM_176934]	NM_176934	6.70196	0.00005
Tmem24	Transmembrane protein 24, mRNA (cDNA clone IMAGE:5360163)	AK004920	6.68313	1.32E-19
Cyp46a1	Cytochrome P450, family 46, subfamily a, polypeptide 1, mRNA (cDNA clone MGC:18311 IMAGE:4195579)	NM_010010	6.67773	6.83E-22
Usp22	MKIAA1063 protein	AK086502	6.67222	1.15E-09
9530059J11Rik	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530059J11, product: weakly similar to 12 DAYS EMBRYO HEAD CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:3010005E14, FULL INSERT SEQUENCE [Mus musculus], full insert sequence.	AK020615	6.66825	1.21E-08
Mgst3	Microsomal glutathione S-transferase 3, mRNA (cDNA clone MGC:357738 IMAGE:5372427)	AK008211	6.65726	9.29E-09
9330107J05Rik	PREDICTED: hypothetical protein LOC73884 [Mus musculus], mRNA sequence	AK047625	6.65622	0.00061
Ghb7	Growth factor receptor bound protein 7, mRNA (cDNA clone MGC:5653 IMAGE:3583896)	NM_010346	6.65154	6.22E-12
Pros1	Protein S (alpha) (Pros1), mRNA	NM_011173	6.6501	9.72E-31
Usf1	M.musculus USF1 (non-coding exon 1).	X95315	6.64978	1.88E-09
Grin3b	Glutamate receptor, ionotropic, NMDA3B (Grin3b), mRNA	NM_130455	6.64959	3.38E-22
A730016F12Rik	Mus musculus RIKEN cDNA A730016F12 gene (A730016F12Rik), transcript variant 2, mRNA [NM_175079]	NM_175079	6.64561	1.08E-35
Cas2l	MKIAA3026 protein	AK010559	6.63118	9.68E-36
Nckap1l	NCK associated protein 1 like (Nckap1l), mRNA	NM_153505	6.62986	7.63E-07
AI324046	Immunoglobulin heavy chain 6 (heavy chain of IgM), mRNA (cDNA clone MGC:18788 IMAGE:4189350)	NM_198640	6.62565	0.00096
9530001N24Rik	Peroxiredoxin 1 (Prdx1), mRNA	AK020533	6.60763	2.92E-11
4732496G21Rik	RIKEN cDNA 4732496G21 gene (4732496G21Rik), mRNA	AK035094	6.59781	0.00384
Eyp1	Envoplakin, mRNA (cDNA clone IMAGE:3985477)	AK007353	6.59541	1.14E-40
Postn	Periostin, osteoblast specific factor, mRNA (cDNA clone MGC:25368 IMAGE:4457222)	NM_015784	6.59457	2.74E-12
Lyzs	Lysozyme, mRNA (cDNA clone IMAGE:2655292)	NM_017372	6.58874	0.00173
Apol2	PREDICTED: hypothetical protein XP_139463 [Mus musculus], mRNA sequence	AK036408	6.56783	8.71E-25
Paqr3	Progesterin and adipoQ receptor family member III (Paqr3), mRNA	NM_198422	6.56779	5.81E-14
4833421E05Rik	RIKEN cDNA 4833421E05 gene (4833421E05Rik), mRNA	AK014743	6.56384	7.26E-13
4930519L02Rik	PREDICTED: hypothetical protein LOC75085 [Mus musculus], mRNA sequence	AK015845	6.55752	0.00113
Hrb1	HIV-1 Rev binding protein-like (Hrb1), transcript variant 1, mRNA	NM_178162	6.55743	8.29E-31
Bai2	Brain-specific angiogenesis inhibitor 2, mRNA (cDNA clone MGC:66520 IMAGE:5705854)	NM_173071	6.5429	2.54E-10
Map2k6	MAP Kinase Kinase	NM_011943	6.53525	2.77E-11
Ttll1	Mus musculus tubulin tyrosine ligase-like 1 (Ttll1), mRNA.	NM_178869	6.52155	6.57E-30
Hand2	BHLH transcription factor dHand	NM_010402	6.51319	0.00064

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Cpeb4	Cytoplasmic polyadenylation element binding protein 4 (Cpeb4), mRNA	AK173229	6.50992	7.59E-11
C920005C14Rik	RIKEN cDNA C920005C14 gene (C920005C14Rik), mRNA	NM_177391	6.49949	0.0012
Fbp2	Fructose biphosphatase 2, mRNA (cDNA clone MGC:14060 IMAGE:4205515)	NM_007994	6.49091	1.69E-19
AK042798	Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730025J02 product: unclassifiable, full insert sequence.	AK042798	6.47491	0.00001
D930005D10Rik	MKIAA1849 protein	NM_178702	6.4664	3.36E-17
Irf6	Interferon regulatory factor 6, mRNA (cDNA clone MGC:5918 IMAGE:3592582)	NM_016851	6.46367	8.31E-13
A530064D06Rik	RIKEN cDNA A530064D06 gene (A530064D06Rik), mRNA	NM_178796	6.46325	0.00093
Fbxl16	PREDICTED: similar to spinal cord injury and regeneration related protein 1 [Mus musculus], mRNA sequence	XM_128530	6.46071	5.26E-11
1700013F07Rik	PREDICTED: hypothetical protein LOC75504 [Mus musculus], mRNA sequence	AK005946	6.44623	1.24E-23
Cdh15	Cadherin 15 (Cdh15), mRNA	NM_007662	6.44407	1.52E-22
AK033995	Mus musculus adult male dienecephalon cDNA, RIKEN full-length enriched library, clone:9330137C05 product: unclassifiable, full insert sequence.	AK033995	6.44198	2.74E-11
Slc36a2	Solute carrier family 36 (proton/amino acid symporter), member 2 (Slc36a2), mRNA	NM_153170	6.43572	4.47E-18
Agt	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8), mRNA (cDNA clone MGC:4194190)	NM_007428	6.43479	0.00014
4921513E08Rik	RIKEN cDNA 4921513E08 gene (4921513E08Rik), mRNA	NM_025725	6.42815	1.00E-30
Hey2	Basic helix-loop-helix factor 1 (CHFI)	AK048343	6.425	0.0015
Krtap6-1	Keratin associated protein 6-1 (Krtap6-1), mRNA	D86421	6.42422	0.0014
AK046930	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930004K07 product: histocompatibility 2, T region locus 18, full insert sequence	AK046930	6.42302	4.29E-12
Rif1	Gene trap locus 7, mRNA (cDNA clone IMAGE:6740526)	XM_283757	6.42082	3.63E-18
Raf122	Ring finger protein 122, mRNA (cDNA clone MGC:36976 IMAGE:4947596)	NM_175136	6.40147	0.00007
5730508B09Rik	RIKEN cDNA 5730508B09 gene (5730508B09Rik), mRNA	AK017758	6.39187	2.05E-39
D230014K01Rik	RIKEN cDNA D230014K01 gene (D230014K01Rik), mRNA	NM_172573	6.38975	1.69E-06
Spdef	SAM pointed domain containing ets transcription factor, mRNA (cDNA clone MGC:13763 IMAGE:4218741)	NM_013891	6.37865	8.43E-08
Adc	Arginine decarboxylase (Ade), mRNA	NM_172875	6.37788	6.03E-36
Adora2b	Adenosine A2b receptor (Adora2b), mRNA	NM_007413	6.37729	8.30E-10
TC949982	AF465729 cyclin fold protein 1 variant b (Homo sapiens), partial (83%) [TC949982]		6.36781	5.12E-29
Ccdc37	RIKEN cDNA C230069K22 gene, mRNA (cDNA clone MGC:90884 IMAGE:5693354)	NM_173775	6.36741	4.66E-17
Epas1	Endothelial PAS domain protein 1 (Epas1), mRNA	AK087208	6.35043	1.62E-18
9630020I17Rik	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530095L03 product: unclassifiable, full insert sequence	AK079318	6.34776	3.78E-06
ENSMUST00000055324	OLFATORY RECEPTOR GA_X6K02TP2PSCP-1637650-1636712 (FRAGMENT). [Source:SPTREMBL;Acc:Q7TRL0] [ENSMUST00000055324]		6.3429	0.00019

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Al646023	Expressed sequence Al646023 (Al646023), mRNA	NM_198860	6.3422	1.37E-12
Ptpn12	Protein tyrosine phosphatase, non-receptor type 12 (Ptpn12), mRNA	AK087609	6.32927	0.00114
Wdr40b	WD repeat domain 40B, mRNA (cDNA clone MGC:76797 IMAGE:30431243)	NM_178739	6.32111	0.00162
Rap2ip	Rap2 interacting protein (Rap2ip), mRNA	AK007019	6.3115	4.38E-17
6230427J02Rik	RIKEN cDNA 6230427J02 gene (6230427J02Rik), mRNA	AK020090	6.30412	4.72E-38
5730420B22Rik	RIKEN cDNA 5730420B22 gene, mRNA (cDNA clone IMAGE:5356411)	NM_172597	6.29909	2.99E-13
Zhx1	Zinc fingers and homeoboxes protein 1 (Zhx1), mRNA	AK051410	6.29396	3.18E-08
Lmtk2	Lemur tyrosine kinase 2, mRNA (cDNA clone IMAGE:6407188)	BC058653	6.2919	1.25E-23
2410003J06Rik	RIKEN cDNA 2410003J06 gene, mRNA (cDNA clone MGC:60956 IMAGE:30007513)	AK010362	6.2909	1.27E-08
Dgat2	Diacylglycerol O-acyltransferase 2 (Dgat2), mRNA	NM_026384	6.28587	3.72E-19
Rab3d	RAB3D, member RAS oncogene family, mRNA (cDNA clone MGC:6707 IMAGE:3584902)	NM_031874	6.28515	3.96E-08
2610031L17Rik	RIKEN cDNA 2610031L17 gene, mRNA (cDNA clone MGC:38351 IMAGE:5344332)	AK043897	6.2836	0.00003
Jmjd2d	Hypothetical protein 4932416A15 (4932416A15), mRNA	NM_173433	6.27488	2.19E-07
1700023A16Rik	PREDICTED: hypothetical protein LOC69371 [Mus musculus], mRNA sequence	AK006257	6.27378	2.95E-13
Tncc3	Transmembrane and coiled coil domains 3, mRNA (cDNA clone MGC:30586 IMAGE:3660220)	NM_172051	6.27294	9.85E-06
Clec2e	C-type lectin domain family 2, member e (Clec2e), mRNA	NM_153506	6.27057	0.0012
H2-DMa	Histocompatibility 2, class II, locus DMA, mRNA (cDNA clone MGC:5743 IMAGE:3591389)	NM_010386	6.26974	1.31E-33
Habp4	Hyaluronic acid binding protein 4 (Habp4), mRNA	NM_019986	6.26891	6.44E-11
LOC434018	hypothetical gene supported by AK029757	AK029757	6.2591	0.0016
2700038N03Rik	RIKEN cDNA 2700038N03 gene, mRNA (cDNA clone MGC:27927 IMAGE:3584484)	NM_027356	6.2369	1.38E-30
3526402J09Rik	RIKEN cDNA 3526402J09 gene, mRNA (cDNA clone IMAGE:30544810)	AK028312	6.23264	3.49E-06
Dlgap1	Discs, large (Drosophila) homolog-associated protein 1 (Dlgap1), transcript variant 2, mRNA	AK034215	6.21769	1.54E-06
9230116B18Rik	PREDICTED: hypothetical protein LOC78245 [Mus musculus], mRNA sequence	AK020348	6.21758	3.02E-09
H2-Ke6	H2-K region expressed gene 6 (H2-Ke6), mRNA	NM_013543	6.21346	6.39E-38
Prdx1	Peroxiredoxin 1 (Prdx1), mRNA	AK083642	6.21182	3.67E-17
4930550L24Rik	Mus musculus RIKEN cDNA 4930550L24 gene (4930550L24Rik), mRNA [NM_023774]	NM_023774	6.21139	6.89E-09
Trim62	Tripartite motif-containing 62 (Trim62), mRNA	NM_178110	6.20606	8.48E-07
NAP044566-1	Unknown		6.20486	9.69E-13
Brsk2	BR serine/threonine kinase 2 (Brsk2), transcript variant 2, mRNA	BC056498	6.18857	0.00023
9630019E01Rik	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DI130045C05 product: unclassifiable, full insert sequence.	AK051384	6.17974	2.17E-15

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Iiga6	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230112G01 product: integrin alpha 6, full insert sequence.	AK045391	6.17009	2.44E-07
Acox1	Acy1-Coenzyme A oxidase-like (Acox1), mRNA	AV282483	6.16545	1.07E-07
C030014L02	hypothetical protein C030014L02	AK047704	6.15908	0.00132
4921515A04Rik	Mus musculus RIKEN cDNA 4921515A04 gene (4921515A04Rik), mRNA [NM_172939]	NM_172939	6.15587	2.02E-16
Frat1	Frequently rearranged in advanced T-cell lymphomas (Frat1), mRNA	NM_008043	6.14419	9.07E-08
D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed (D5Wsu178e), mRNA	AK046608	6.14236	5.29E-09
AK012034	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610315N17 product: unclassifiable, full insert sequence.	AK012034	6.1156	2.54E-08
Tax1bp1	Tax1 (human T-cell leukemia virus type I) binding protein 1, mRNA (cDNA clone MGC:11692 IMAGE:3962810)	AK051030	6.11319	0.00526
Syce1	PREDICTED: Mus musculus RIKEN cDNA 4933406107 gene (4933406107Rik), mRNA	AK016694	6.1065	1.56E-15
A430091O22Rik	RIKEN cDNA A430091O22 gene (A430091O22Rik), mRNA	AK039072	6.10372	0.00337
Scrib	<b>Scribbled homolog (Drosophila), mRNA (cDNA clone IMAGE:4459388)</b>	AK084936	6.1006	8.84E-14
Rhov	Ras homolog gene family, member V (Rhov), mRNA	NM_145530	6.0999	1.54E-23
AK040776	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530024117 product: unclassifiable, full insert sequence	AK040776	6.09753	1.78E-38
D330014H01Rik	Mus musculus RIKEN cDNA D330014H01 gene (D330014H01Rik), mRNA [NM_177617]	NM_177617	6.08754	1.59E-14
D0H4S114	DNA segment, human D4S114 (D0H4S114), mRNA	NM_053078	6.08447	0.00133
Herc1	Hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1, mRNA (cDNA clone MGC:7618 IMAGE:3494753)	AK083444	6.08322	4.90E-24
1700065D16Rik	Protein kinase ATR (Atr)	AK030118	6.07886	0.00004
Ppp1r13b	Protein phosphatase 1, regulatory (inhibitor) subunit 13B (Ppp1r13b), mRNA	NM_011625	6.0768	9.44E-25
LOC213402	hypothetical LOC213402	XM_136978	6.07669	6.10E-19
Capns2	Hypothetical protein A330042H22 (A330042H22), mRNA	AK009171	6.0641	6.40E-07
NM_027559	Mus musculus RIKEN cDNA 4930463G05 gene (4930463G05Rik), mRNA [NM_027559]	NM_027559	6.05992	8.61E-10
2810427I04Rik	RIKEN cDNA 2810427I04 gene (2810427I04Rik), mRNA	NM_028146	6.05072	3.51E-08
Mycbp	C-myc binding protein, mRNA (cDNA clone MGC:13820 IMAGE:3985166)	NM_019660	6.0454	3.53E-09
D130076A03Rik	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130076A03 product: unclassifiable, full insert sequence.	AK084007	6.04495	1.01E-16
AA919669	Adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900016J10 product: unclassifiable, full insert sequence	AA919669	6.04404	1.08E-19
Ifrd1	Interferon-related developmental regulator 1 (Ifrd1), mRNA	NM_013562	6.04347	2.10E-09
Ddit4l	DNA-damage-inducible transcript 4-like, mRNA (cDNA clone MGC:47974 IMAGE:5254530)	NM_030143	6.04198	0.00184
Gsdm1	Gasdermin 1 (Gsdm1), mRNA	NM_021347	6.04098	2.79E-13

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3110057012Rik	RIKEN cDNA 3110057012 gene, mRNA (cDNA clone IMAGE:4007705)	NM_026622	6.04095	1.90E-12
Pdpk1	Phosphoinositide-dependent protein kinase-1 beta (Pdk1beta)	NM_011062	6.03733	3.77E-31
Zp3	Zona pellucida glycoprotein 3 (Zp3), mRNA	NM_011776	6.02738	1.28E-12
TC984987	NDK6_HUMAN Nucleoside diphosphate kinase 6 (NDK 6) (NDP kinase 6) (nm23-H6) (Inhibitor of p53-induced apoptosis-alpha) (PIA-alpha). [Human] [Homo sapiens], partial (14%) [TC984987]		6.02678	0.00023
1700011E04Rik	PREDICTED: Mus musculus RIKEN cDNA 1700011E04 gene (1700011E04Rik), mRNA	AK005860	6.02661	6.11E-06
Sstr2	Somatostatin receptor 2 (Sstr2), mRNA	NM_009217	6.0182	1.48E-11
Pgm2l1	Phosphoglucomutase 2-like 1, mRNA (cDNA clone MGC:29299 IMAGE:5004308)	NM_027629	6.01695	1.89E-15
BE646931	Transcribed locus	BE646931	6.00062	1.38E-15
Ccdc37	ZXD family zinc finger C, mRNA (cDNA clone MGC:7160 IMAGE:3256958)	AK021139	5.99479	5.23E-06
Timd4	T-cell immunoglobulin and mucin domain containing 4, mRNA (cDNA clone MGC:41117 IMAGE:1195144)	NM_178759	5.98633	0.00165
Ap3m2	Adaptor-related protein complex 3, mu 2 subunit, mRNA (cDNA clone MGC:40858 IMAGE:5369288)	NM_029505	5.97689	1.24E-08
Htr2b	5-hydroxytryptamine (serotonin) receptor 2B, mRNA (cDNA clone MGC:36132 IMAGE:5344328)	NM_008311	5.97448	0.00018
Tfdp2	DP-3=protein regulating cell cycle transcription factor DRTF1/E2F [mice, pl-2, F9 EC, mRNA, 1380 nt].	S79780	5.97116	4.82E-07
Rybp	RING1 and YY1 binding protein (Rybp), mRNA	NM_019743	5.97057	9.26E-38
Sema3b	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B (Sema3b), mRNA	NM_009153	5.9703	2.43E-22
Dcn	Decorin (Dcn), mRNA	NM_007833	5.96766	2.08E-06
Lhx2	LIM-homeodomain protein MLHX2 (Lhx2)	NM_010710	5.96324	1.93E-11
Fbxo33	F-box only protein 33, mRNA (cDNA clone IMAGE:3661715)	BC020022	5.96152	1.82E-17
Cfh	Complement component factor h (Cfh), mRNA	M12660	5.95652	0.00006
Psd2	Pleckstrin and Sec7 domain containing 2 (Psd2), mRNA	NM_028707	5.95334	6.23E-14
Ncoa1	Nuclear receptor coactivator 1 (Ncoa1), mRNA	AA738860	5.94761	1.72E-25
Robo2	MKI6A1568 protein	BC055333	5.94552	0.00019
AW125753	Expressed sequence AW125753 (AW125753), mRNA	NM_029007	5.94357	1.90E-15
Cfh	Complement component factor h (Cfh), mRNA	NM_009888	5.94161	6.84E-07
1700014D04Rik	PREDICTED: hypothetical protein LOC74224 [Mus musculus], mRNA sequence	AK077007	5.93902	9.40E-15
6-Sep	Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920001C06 product: hypothetical protein, full insert sequence.	AK083302	5.93827	0.00283
Pdpk1	Phosphoinositide-dependent protein kinase-1 beta (Pdk1beta)	NM_011062	5.93442	2.75E-36
BC048651	CIDNA sequence BC048651 (BC048651), mRNA	NM_207258	5.93022	1.19E-13
Metml	Meteorin, glial cell differentiation regulator-like (Metml), mRNA	AK053718	5.9294	3.74E-21
LOC229608	Histone 2, H2bb (His2h2bb), mRNA	BC019122	5.92838	4.58E-08

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Ah15b	ADP-ribosylation factor-like 8 (Ah18), mRNA	NM_029466	5.92634	1.03E-09
Olfir987	Olfactory receptor 987 (Olfir987), mRNA	CB174485	5.92041	0.00266
Malat1	Adult male stomach cDNA, RIKEN full-length enriched library, clone:2210407K09 product: receptor (calcitonin) activity modifying protein 2, full insert sequence	AK020483	5.91958	6.65E-15
Mall	CDNA sequence BC012256 (BC012256), mRNA	NM_145532	5.91692	8.22E-08
Phf2	Putative homeodomain transcription factor 2, mRNA (cDNA clone MGC:60851 IMAGE:30050876)	NM_172992	5.91568	1.02E-30
D330028D13Rik	RIKEN cDNA D330028D13 gene, mRNA (cDNA clone MGC:67688 IMAGE:4487036)	NM_172727	5.91051	1.54E-22
Rhpn2	Rhopilin, Rho GTPase binding protein 2 (Rhpn2), mRNA	NM_027897	5.90122	2.02E-22
3526402J09Rik	8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730590C14 product: unclassifiable, full insert sequence	AK019982	5.89752	1.80E-24
Tigd5	Tigger transposable element derived 5 (Tigd5), mRNA	NM_178646	5.89512	9.40E-16
C230078M08Rik	RIKEN cDNA C230078M08 gene (C230078M08Rik), mRNA	NM_176995	5.88686	6.61E-06
D930001I22Rik	RIKEN cDNA D930001I22 gene, mRNA (cDNA clone MGC:107602 IMAGE:6750721)	AK052945	5.86474	5.89E-43
Tcf15	Transcription factor 15, mRNA (cDNA clone MGC:41210 IMAGE:5143248)	NM_009328	5.86455	2.79E-14
Wif1	Wnt inhibitory factor 1, mRNA (cDNA clone MGC:13706 IMAGE:3984128)	NM_011915	5.85749	1.02E-06
Egfl5	MKIAA0818 protein	AK122378	5.85619	1.22E-10
Fcer1g	Fc receptor, IgE, high affinity I, gamma polypeptide, mRNA (cDNA clone MGC:36077 IMAGE:5065647)	A1326608	5.85071	2.00E-10
Mtap2	Mus musculus microtubule-associated protein 2 (Mtap2), mRNA [NM_008632]	NM_008632	5.85052	5.98E-13
Uros	Uroporphyrinogen III synthase (Uros), mRNA	NM_009479	5.84947	1.39E-29
3110098I04Rik	Transmembrane protein 49, mRNA (cDNA clone MGC:7590 IMAGE:3493738)	AK019443	5.84922	1.23E-18
Snai3	Snail-related zinc finger protein SMUC (Smuc)	NM_013914	5.84401	6.78E-12
Arzc	Mus musculus hypothetical protein (Arzc) mRNA, complete cds.	AY344585	5.83844	1.81E-12
BE987854	Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830003K21 product: unclassifiable, full insert sequence	BE987854	5.8367	3.15E-09
Npc111	Mus musculus NPC1-like 1 (Npc111), mRNA.	XM_137497	5.83041	2.18E-14
Etv1	Ets variant gene 1, mRNA (cDNA clone MGC:6207 IMAGE:3257346)	NM_007960	5.82656	0.00003
AK041974	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630050C01 product: unclassifiable, full insert sequence	AK041974	5.82616	0.00025
Atp11b	ATPase, Class VI, type 11B (Atp11b), mRNA	AK041684	5.82607	3.61E-08
Pgm211	Phosphoglucomutase 2-like 1, mRNA (cDNA clone MGC:29299 IMAGE:5004308)	NM_027629	5.81964	0.0001
Ppp1r13b	Protein phosphatase 1, regulatory (inhibitor) subunit 13B (Ppp1r13b), mRNA	NM_011625	5.81761	4.07E-12
2310068J10Rik	Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310068J10 product: unclassifiable, full insert sequence	AK075917	5.81515	5.55E-09
Nos3	Nitric oxide synthase 3, endothelial cell (Nos3), mRNA	NM_008713	5.80909	1.30E-07



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Spsb1	SplA/ryanodine receptor domain and SOCS box containing 1 (Spsb1), mRNA	NM_029035	5.80869	5.16E-13
8430416H19Rik	RIKEN cDNA 8430416H19 gene (8430416H19Rik), mRNA	NM_198636	5.80743	1.09E-11
Gpr111	PREDICTED: similar to G-protein coupled receptor 111 [Mus musculus], mRNA sequence	AY255579	5.79653	0.00225
Pla2g4f	RIKEN cDNA 4732472I07 gene (4732472I07Rik), mRNA	BC039947	5.7812	5.59E-15
Rfx2	Regulatory factor X, 2 (influences HLA class II expression), mRNA (cDNA clone MGC:6105 IMAGE:3497910)	NM_009056	5.77832	1.13E-11
Dpf3	D4, zinc and double PHD fingers, family 3 (Dpf3), mRNA	NM_058212	5.77719	9.83E-15
Zfp654	Zinc finger protein 654, mRNA (cDNA clone IMAGE:5346461)	NM_028059	5.77371	1.78E-35
Rnu1	RNA, U transporter 1, mRNA (cDNA clone MGC:74414 IMAGE:30251661)	NM_178374	5.76909	7.92E-16
Mpp7	Membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7), mRNA (cDNA clone IMAGE:6532780)	AK017344	5.76872	3.39E-11
Cx3cl1	Mus musculus mRNA, complete cds, clone: 1-53.	AB030188	5.75894	0.00037
Map2k6	Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930047J04 product: mitogen activated protein kinase kinase 6, full insert sequence.	AK086722	5.74548	2.97E-08
Gsto2	Glutathione S-transferase omega 2 (Gsto2), mRNA	NM_026619	5.73514	3.96E-07
A030009H04Rik	RIKEN cDNA A030009H04 gene, mRNA (cDNA clone MGC:35887 IMAGE:5352453)	NM_020591	5.73374	2.63E-12
Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast), mRNA (cDNA clone MGC:41183 IMAGE:1328907)	AK089832	5.73109	2.04E-11
Map2k6	MAP Kinase Kinase	NM_011943	5.72903	0.00035
Bmp2k	BMP2 inducible kinase (Bmp2k), mRNA	NM_080708	5.72563	2.28E-11
St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5 (St3gal5), mRNA	A1464789	5.72266	0.0001
Rasd1	RAS, dexamethasone-induced 1, mRNA (cDNA clone MGC:36188 IMAGE:4989312)	NM_009026	5.71641	9.16E-11
C330001K17Rik	RIKEN cDNA C330001K17 gene (C330001K17Rik), mRNA	AK031175	5.70009	1.16E-08
Olig2	Olig2 bHLH protein	BC051967	5.69272	0.00135
Zfp422-rs1	zinc finger protein 422, related sequence 1	NM_029952	5.68877	7.93E-14
Ccni	Cyclin I, mRNA (cDNA clone MGC:5636 IMAGE:3583418)	AK083496	5.68864	0.00337
AK028719	10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732444B01 product: unclassifiable, full insert sequence	AK028719	5.68121	0.00073
5730469D23Rik	RIKEN cDNA 5730469D23 gene, mRNA (cDNA clone MGC:66555 IMAGE:6825308)	AK017687	5.67016	6.96E-16
Tspan1	Tetraspan 1 (Tspan1), mRNA	NM_133681	5.66843	7.35E-08
Ebfl	Early B-cell factor 1 (Ebf1), mRNA	AK036716	5.66713	0.00329
Susd2	Sushi domain containing 2 (Susd2), mRNA	NM_027890	5.66242	2.96E-08
XM_131928	Mus musculus myeloid/lymphoid or mixed-lineage leukemia 3 (Mll3), mRNA [XM_131928]	XM_131928	5.65966	0.00033
Tfrf2	Transferrin receptor 2, mRNA (cDNA clone MGC:18814 IMAGE:4196597)	NM_015799	5.65881	2.39E-07
Tspyl4	Mus musculus TSPY-like 4 (Tspyl4), mRNA.	NM_133745	5.65493	1.21E-11



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Hgf	Hepatocyte growth factor	AK082461	5.65072	0.00111
Txnip	Thioredoxin interacting protein, mRNA (cDNA clone MGC:25534 IMAGE:3591421)	AK004653	5.6496	1.05E-06
Angptl2	Angiopoietin-like 2 (Angptl2), mRNA	AK035967	5.64678	9.32E-12
Dos	Downstream of SIK1 (Dos), mRNA	AK035824	5.6364	2.23E-11
Mars2	Methionine-tRNA synthetase 2 (mitochondrial), mRNA (cDNA clone MGC:106216 IMAGE:3153138)	NM_175439	5.62867	1.35E-27
Hamp1	Prohepcidin (hepc1)	NM_032541	5.62597	1.61E-09
BC049806	CDNA sequence BC049806, mRNA (cDNA clone MGC:76460 IMAGE:30431671)	NM_172513	5.62361	6.88E-34
Sbsn	suprabasin	NM_172205	5.62177	3.83E-18
FHOS2	formin-family protein FHOS2	NM_175276	5.62016	0.00001
Ais2	Amniotrophic lateral sclerosis 2 (juvenile) homolog (human), mRNA (cDNA clone MGC:27807 IMAGE:3257574)	NM_028717	5.61726	6.41E-30
5330420D20Rik	RIKEN cDNA 5330420D20 gene (5330420D20Rik), mRNA	NM_027442	5.61363	0.00005
Gdap5	Dishevelled associated activator of morphogenesis 1 (Daam1), mRNA	Y17854	5.61177	1.02E-26
E030003N13Rik	Fibroblast growth factor receptor substrate 2, mRNA (cDNA clone MGC:64739 IMAGE:6830555)	AK051267	5.61074	0.00191
Zfp59	Zinc finger protein 59 (Zfp59), mRNA	AK042484	5.60473	0.00217
Rnd1	Rho family GTPase 1, mRNA (cDNA clone MGC:58446 IMAGE:6535763)	BC048531	5.60436	2.78E-39
Ypel4	Ypel4 mRNA for yippe-like 4	AK043577	5.60118	0.00005
Hbld2	HESB like domain containing 2 (Hbld2), mRNA	NM_026921	5.59811	1.03E-15
Plekhk1	Membrane-bound factor MBF1 (Mbf)	AY036116	5.59772	2.32E-19
Asb11	Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030022F06 product: ankyrin repeat and SOCS box-containing protein 11, full insert sequence.	AK078851	5.59544	0.00382
TC996139	Unknown		5.59089	1.46E-07
Bai2	Brain-specific angiogenesis inhibitor 2, mRNA (cDNA clone MGC:66520 IMAGE:5705854)	NM_173071	5.57838	0.00002
Rnf17	Ring finger protein 17 (Rnf17), transcript variant 1, mRNA	NM_013894	5.57648	0.00408
Scoc	Short coiled-coil protein, mRNA (cDNA clone MGC:28845 IMAGE:4506964)	NM_019708	5.57413	1.02E-21
Lama3	Laminin-5, alpha3B chain	X84014	5.56979	1.47E-30
Bmp6	Bone morphogenetic protein 6 (Bmp6), mRNA	NM_007556	5.5686	6.55E-09
Dffa	DNA fragmentation factor, alpha subunit (Dffa), transcript variant 2, mRNA	AK051011	5.55806	2.27E-19
Nf1ac4	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4, mRNA (cDNA clone MGC:25538 IMAGE:3670623)	AK014164	5.55789	1.20E-09
Klc3	Kinesin light chain 3 (Klc3), mRNA	NM_146182	5.55558	2.85E-09
Kif17	Kinesin family member 17 (Kif17), mRNA	NM_010623	5.5494	0.00022
Btd10	BTB (POZ) domain containing 10, mRNA (cDNA clone IMAGE:3484902)	AK052335	5.54822	4.06E-10

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Slc25a35	Solute carrier family 25, member 35 (Slc25a35), mRNA	NM_028048	5.54317	9.37E-07
AK076567	Adult male testis cDNA, RIKEN full-length enriched library, clone:4921513101 product: unclassifiable, full insert sequence	AK076567	5.54169	4.56E-17
Kif17	Kinesin family member 17 (Kif17), mRNA	NM_010623	5.53068	7.65E-13
Trpt1	TRNA phosphotransferase 1 (Trpt1), mRNA	NM_153597	5.52301	1.26E-44
C030032016Rik	Putative homeodomain transcription factor 1 (Phf1), mRNA	AK021115	5.52287	0.00004
NAP050738-1	Unknown		5.51793	0.00143
Slc40a1	Solute carrier family 40 (iron-regulated transporter), member 1, mRNA (cDNA clone MGC:6489 IMAGE:2647365)	NM_016917	5.51526	5.26E-10
Mll3	Mixed-lineage leukemia 3 protein (Mll3)	XM_355579	5.51391	1.75E-19
Ablim3	Actin binding LIM protein family, member 3, mRNA (cDNA clone MGC:106450 IMAGE:30534236)	NM_198649	5.51387	4.79E-12
Dmxl1	Dmx-like 1, mRNA (cDNA clone MGC:28386 IMAGE:4022096)	AK082851	5.51375	9.31E-09
Hivep3	Clone 5TRACE1 ZAS3 (Krc) mRNA, 5' UTR	AK013707	5.51275	3.18E-26
Fhl2	Four and a half LIM domains 2, mRNA (cDNA clone MGC:29060 IMAGE:5066565)	AK081770	5.51184	0.00028
Arl5b	ADP-ribosylation factor-like 8 (Arl5b), mRNA	NM_029466	5.50628	6.74E-06
Usp53	Ubiquitin specific peptidase 53, mRNA (cDNA clone IMAGE:4236151)	AK030317	5.5048	6.73E-16
Eaf2	Testosterone regulated apoptosis inducer and tumor suppressor (Traits)	NM_134111	5.49779	6.28E-07
Lmbr1	Limb region 1, mRNA (cDNA clone MGC:28737 IMAGE:4481088)	AK030631	5.49689	1.41E-08
F730023N20	hypothetical protein F730023N20	NM_183158	5.48167	0.00469
Vamp1	Vesicle-associated membrane protein 1 (Vamp1), mRNA	NM_009496	5.47901	7.04E-22
Abcc10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10 (Abcc10), transcript variant mmp7B, mRNA	NM_145140	5.47864	1.39E-10
BG080473	Transcribed locus	BG080473	5.47538	0.00524
Ppp1r9a	Protein phosphatase 1, regulatory (inhibitor) subunit 9A, mRNA (cDNA clone MGC:59493 IMAGE:6331919)	NM_181595	5.47417	4.82E-07
TC1012618	RGS2_MOUSE Regulator of G-protein signaling 2 (RGS2), [Mouse] [Mus musculus], partial (43%) [TC1012618]		5.46503	6.76E-10
Smarcad1	MRNA of enhancer-trap-locus 1	AK088163	5.4628	3.56E-06
Malat1	Adult male stomach cDNA, RIKEN full-length enriched library, clone:2210407K09 product: receptor (calcitonin) activity modifying protein 2, full insert sequence	BC004722	5.46155	1.11E-09
Big2	B-cell translocation gene 2, anti-proliferative (Big2), mRNA	NM_007570	5.46006	1.64E-08
Malat1	Adult male stomach cDNA, RIKEN full-length enriched library, clone:2210407K09 product: receptor (calcitonin) activity modifying protein 2, full insert sequence	AK090111	5.45534	2.16E-21
Kcnk7	Dpkch3 mRNA for double-pore K channel 3	AF110521	5.45419	0.00021
XM_358570	Mus musculus LOC381415 (LOC381415), mRNA [XM_358570]	XM_358570	5.4508	0.00001
Tnrc15	Trinucleotide repeat containing 15 (Tnrc15), mRNA	AK034426	5.44852	9.38E-14
D16H22S680E	DNA segment, Chr 16, human D22S680E, expressed (D16H22S680E), mRNA	NM_138583	5.4478	6.43E-27

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Cxxx5	CXXC finger 5 (Cxxx5), mRNA	NM_133687	5.44654	0.00002
Pbx4	Pre-B-cell leukemia transcription factor 4, mRNA (cDNA clone MGC:40990 IMAGE:1263363)	NM_030555	5.4461	4.76E-13
Gm1418	PREDICTED: similar to Ig kappa chain precursor V region - mouse [Mus musculus], mRNA sequence	J04610	5.44288	0.0003
Slc25a2	Mutant ornithine transporter 2 (Ornt2)	AK077159	5.43766	3.03E-14
Hist3h2bb	Histone 3, H2bb (Hist3h2bb), mRNA	NM_206882	5.43583	1.97E-33
Ralgps2	Ral GEF with PH domain and SH3 binding motif 2 (Ralgps2), mRNA	NM_023884	5.43465	0.0001
Lao1	L-amino acid oxidase 1 (Lao1), mRNA	NM_133892	5.43168	0.00322
Hist1h2bm	Histone 1, H2bm (Hist1h2bm), mRNA	NM_178200	5.42961	1.25E-36
Zfp422-rs1	zinc finger protein 422, related sequence 1	AK020746	5.42824	3.08E-44
Spire1	Spire homolog 1 (Drosophila), mRNA (cDNA clone MGC:106458 IMAGE:30535423)	NM_176832	5.42537	9.41E-07
Matn3	Matrin 3 (Matn3), mRNA	NM_010770	5.42402	0.00001
Zfp422-rs1	zinc finger protein 422, related sequence 1	NM_029952	5.42321	2.97E-17
<b>Pcdh10</b>	<b>OL-protocadherin isoform (Pcdh10) mRNA, complete cds; alternatively spliced</b>	<b>AK122503</b>	<b>5.42181</b>	<b>5.94E-28</b>
NAP042178-1	Unknown		5.41306	8.92E-21
Ranbp6	RAN binding protein 6 (Ranbp6), mRNA	AK083089	5.41102	0.00015
Myh3	PREDICTED: myosin, heavy polypeptide 3, skeletal muscle, embryonic [Mus musculus], mRNA sequence	XM_354614	5.39493	3.95E-11
Vill	Villin-like (Vill), mRNA	U27681	5.39006	1.44E-17
<b>Ephb3</b>	<b>Eph receptor B3, mRNA (cDNA clone MGC:18409 IMAGE:3673003)</b>	<b>NM_010143</b>	<b>5.38235</b>	<b>1.15E-08</b>
Xpr1	Xenotropic and polytropic murine retrovirus receptor (Xpr1)	NM_011273	5.38141	1.81E-13
Bank1	B-cell scaffold protein with ankyrin repeats 1 (Bank1), mRNA	AK041242	5.37887	0.00416
TC1066872	S3A1_HUMAN Splicing factor 3 subunit 1 (Spliceosome associated protein 114) (SAP 114) (SF3a120), [Human] [Homo sapiens], partial (3%) [TC1066872]		5.3751	0.00537
Wdr37	MKIAA0982 protein	AK044740	5.36656	0.00008
Mtap2	Microtubule-associated protein 2, mRNA (cDNA clone MGC:65400 IMAGE:6412797)	BC052446	5.36496	7.87E-18
ABI12350	NAPE-PLD mRNA for N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	NM_178728	5.36332	3.14E-16
Malat1	Adult male stomach cDNA, RIKEN full-length enriched library, clone:2210407K09 product: receptor (calcitonin) activity modifying protein 2, full insert sequence	AK020134	5.36328	6.17E-11
A1464131	MKIAA1161 protein	BC036141	5.36291	4.74E-15
H1f0	H1 histone family, member 0, mRNA (cDNA clone MGC:19309 IMAGE:4166167)	NM_008197	5.35386	2.93E-07
4933404M02Rik	RIKEN cDNA 4933404M02 gene (4933404M02Rik), mRNA	AK017113	5.35281	0.00005
Adarb1	Adenosine deaminase, RNA-specific, B1 (Adarb1), transcript variant 1, mRNA	AF403109	5.3483	1.65E-15
Tcf7	Transcription factor 7, T-cell specific (Tcf7), mRNA	NM_009331	5.34121	1.40E-08

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Strbp	Spermatid perinuclear RNA binding protein, mRNA (cDNA clone MGC:25337 IMAGE:4502840)	AK081780	5.33831	0.00004
<b>Foxj1</b>	<b>Forkhead Box j1 (Foxj1)</b>	<b>NM_008240</b>	<b>5.33683</b>	<b>3.52E-08</b>
Vill	Villin-like (Vil), mRNA	NM_011700	5.33523	2.17E-10
A_51_P170529	Unknown		5.32731	0.00598
2310047013Rik	RIKEN cDNA 2310047013 gene, mRNA (cDNA clone MGC:28605 IMAGE:4217391)	AK083925	5.32579	5.06E-32
Ccdc28a	Coiled-coil domain containing 28A (Ccdc28a), mRNA	NM_144820	5.32149	2.42E-10
NAP057224-1	Unknown		5.32046	8.05E-06
Arl5b	ADP-ribosylation factor-like 8 (Arl8), mRNA	NM_029466	5.31107	0.00004
Zfp40	Zinc finger protein 40 (Zfp40), mRNA	NM_009555	5.30822	4.36E-10
Thns1	Threonine synthase-like 1 (bacterial), mRNA (cDNA clone IMAGE:5037172)	NM_177588	5.30806	7.21E-20
4932411G14Rik	RIKEN cDNA 4932411G14 gene (4932411G14Rik), mRNA	NM_177711	5.30751	3.12E-11
Map3k14	Mitogen-activated protein kinase kinase kinase 14 (Map3k14), mRNA	NM_016896	5.30704	5.21E-18
1700110N18Rik	PREDICTED: hypothetical protein LOC73569 [Mus musculus], mRNA sequence	XM_283372	5.3057	1.79E-09
ENSMUST0000050440	Unknown		5.30328	1.74E-27
Rapgef6	Rap guanine nucleotide exchange factor (GEF) 6, mRNA (cDNA clone IMAGE:5321951)	AK040089	5.30322	2.62E-11
Arlgap26	MKIAA0621 protein	AK129176	5.30199	0.00026
Wnt9a	Wingless-type MMTV integration site 9A (Wnt9a), mRNA	BC066165	5.3003	0.00003
Hist1h2ba	Histone 1, H2ba (Hist1h2ba), mRNA	NM_175663	5.29806	2.18E-27
Linc	lung-inducible neuralized-related C3HC4 RING domain protein	NM_153408	5.29767	1.15E-07
B230105J10	hypothetical protein B230105J10	AK045359	5.29449	1.35E-06
TC984274	Unknown		5.29254	2.02E-17
5730553K21	5'-AMP-ACTIVATED PROTEIN KINASE, BETA-2 SUBUNIT (AMPK BETA-2 CHAIN) homolog [Rattus norvegicus] [5730553K21]		5.29004	4.53E-13
Nek1	PREDICTED: Mus musculus NIMA (never in mitosis gene a)-related expressed kinase 1 (Nek1), mRNA	AK049625	5.28832	1.68E-17
AK086484	Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D93003J116 product: microtubule-associated protein 2, full insert sequence.	AK086484	5.28708	1.64E-12
<b>Rbl</b>	<b>Retinoblastoma 1 (Rb1), mRNA</b>	<b>NM_009029</b>	<b>5.27516</b>	<b>1.41E-07</b>
Olfml3	Olfactomedin-like 3 (Olfml3), mRNA	NM_133859	5.26799	3.38E-15
Etv3	ETS-domain transcriptional repressor PE1 (PE1)	NM_012051	5.26705	2.17E-29
<b>Ptpn13</b>	<b>Protein tyrosine phosphatase, non-receptor type 13 (Ptpn13), mRNA</b>	<b>NM_011204</b>	<b>5.26698</b>	<b>1.95E-21</b>
<b>Tfdp2</b>	<b>Transcription factor Dp 2, mRNA (cDNA clone IMAGE:30604420)</b>	<b>NM_178667</b>	<b>5.26621</b>	<b>2.69E-06</b>
TC970961	AFI 69692 protocadherin-9 (Homo sapiens), partial (9%) [TC970961]		5.2653	5.85E-08

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Plekhk1	Membrane-bound factor MBF1 (Mbf)	AY036116	5.25979	2.22E-16
Tmcc3	Transmembrane and coiled coil domains 3, mRNA (cDNA clone MGC:30586 IMAGE:3660220)	AK083129	5.25708	2.98E-07
Prph1	Peripherin 1 (Prph1), mRNA	NM_013639	5.25389	4.55E-08
Tbc1d1	TBC1 domain family, member 1, mRNA (cDNA clone IMAGE:3500261)	NM_019636	5.2511	2.50E-15
Map3k1	MAP kinase kinase kinase 1 (Mekk1)	NM_011945	5.25036	0.00004
1810053B23Rik	10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810053B23 product: unclassifiable, full insert sequence	AK007854	5.24933	0.00479
Ppp1r2	Protein phosphatase 1, regulatory (inhibitor) subunit 2 (Ppp1r2), mRNA	AK037804	5.2492	8.39E-28
Rnf24	Ring finger protein 24, mRNA (cDNA clone MGC:106607 IMAGE:6406985)	NM_178607	5.24766	3.12E-31
Bhlhb8	Basic helix-loop-helix domain containing, class B, 8, mRNA (cDNA clone MGC:19046 IMAGE:4189225)	NM_010800	5.24479	8.19E-09
A230105L22Rik	Cytochrome P450, family 4, subfamily f, polypeptide 18, mRNA (cDNA clone MGC:19144 IMAGE:4218398)	AK020714	5.24224	0.00468
Herc1	Hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1, mRNA (cDNA clone MGC:7618 IMAGE:3494753)	BC004027	5.23497	5.02E-14
Upk3b	Uroplakin 3B, mRNA (cDNA clone IMAGE:30297822)	NM_175309	5.22777	0.00453
Pja2	Praja 2, RING-H2 motif containing (Pja2), transcript variant 2, mRNA	AK122282	5.22623	2.64E-30
Usp2	Ubiquitin specific peptidase 2, mRNA (cDNA clone MGC:27630 IMAGE:4506362)	NM_016808	5.22394	9.53E-08
Pak3	P21-activated kinase 3 (pak3 gene)	NM_008778	5.22033	7.00E-06
0610008C08Rik	RIKEN cDNA 0610008C08 gene (0610008C08Rik), mRNA	AK029224	5.21977	0.00125
6330416L11Rik	RIKEN cDNA 6330416L11 gene (6330416L11Rik), mRNA	NM_027518	5.21346	3.01E-07
Homer1	Homer homolog 1 (Drosophila) (Homer1), transcript variant L, mRNA	AK035139	5.20561	0.00057
Armc8	Armadillo repeat containing 8, mRNA (cDNA clone MGC:47965 IMAGE:1230321)	AK078280	5.20529	6.30E-35
Lipg	Lipase, endothelial, mRNA (cDNA clone MGC:13719 IMAGE:3981856)	NM_010720	5.20391	0.00001
Dnahc2	Axonemal dynein heavy chain (partial, ID mdhc5)	ZR3813	5.20226	0.00081
Cotl1	Coactosin-like 1 (Dictyostelium) (Cot1), mRNA	NM_028071	5.20139	3.70E-07
2700050L05Rik	RIKEN cDNA 2700050L05 gene (2700050L05Rik), transcript variant 1, mRNA	NM_145995	5.19216	5.70E-15
Rab11fip4	MKIAA1821 protein	AK122559	5.19174	0.00128
Eml5	Echinoderm microtubule associated protein like 5, mRNA (cDNA clone IMAGE:4953665)	AK047762	5.19141	0.00003
Ptpn13	Protein tyrosine phosphatase, non-receptor type 13 (Ptpn13), mRNA	NM_011204	5.19002	1.54E-26
3-Mar	Membrane-associated ring finger (C3HC4) 3 (March3), mRNA	NM_177115	5.18876	3.33E-22
Synpo2	Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530006G20 product: unclassifiable, full insert sequence	AK035258	5.18793	9.93E-06
Zfp36	Zinc finger protein 36, mRNA (cDNA clone MGC:29129 IMAGE:5053664)	NM_011756	5.18672	4.78E-06
Epb4.115	Erythrocyte protein band 4.1-like 5 (Epb4.115), mRNA	NM_145506	5.18616	1.68E-43

Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Pip5k3	Phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III (Pip5k3), mRNA	NM_011086	5.18443	1.80E-10
Tec	Cytoplasmic tyrosine kinase, Dscr28C related (Drosophila), mRNA (cDNA clone MGC:46873 IMAGE:5029430)	NM_013689	5.1779	7.22E-11
C130065N10Rik	PREDICTED: hypothetical protein XP_488897 [Mus musculus], mRNA sequence	AK048435	5.17772	1.71E-43
Petk2	PCTAIRE-motif protein kinase 2 (Petk2), mRNA	NM_146239	5.17294	1.41E-12
A130019P10Rik	Eukaryotic translation initiation factor 4E binding protein 2, mRNA (cDNA clone MGC:13950 IMAGE:4218820)	AK037456	5.17158	7.10E-27
C920006C10Rik	RIKEN cDNA C920006C10 gene (C920006C10Rik), mRNA	AK052176	5.17083	1.37E-21
Camkk1	Calcium/calmodulin-dependent protein kinase kinase 1, alpha, mRNA (cDNA clone MGC:27706 IMAGE:4924656)	NM_018883	5.17034	0.0001
<b>Tusc2</b>	<b>Tumor suppressor candidate 2 (Tusc2), mRNA</b>	<b>NM_019742</b>	<b>5.16901</b>	<b>1.18E-25</b>
AK048541	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:CI30071D07 product: ATPase, Cu++ transporting, alpha polypeptide, full insert sequence.	AK048541	5.16848	1.68E-13
Golph3	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4733401N08 product: golgi phosphoprotein 3, full insert sequence.	AK014644	5.16802	3.09E-33
Fa2h	Fatty acid 2-hydroxylase, mRNA (cDNA clone IMAGE:4983638)	NM_178086	5.16055	2.45E-15
<b>Sesn3</b>	<b>Sestrin 3 (Sesn3), mRNA</b>	<b>NM_030261</b>	<b>5.15972</b>	<b>4.03E-09</b>
D030022P07Rik	RIKEN cDNA 4930451A13 gene, mRNA (cDNA clone MGC:25849 IMAGE:4194266)	AK045169	5.15849	2.37E-16
Spock2	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2 (Spock2), mRNA	NM_052994	5.15198	5.72E-12
Elavl3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C) (Elavl3), mRNA	NM_010487	5.14832	3.61E-06
LOC620630	similar to Contactin 5 precursor (Neural recognition molecule NB-2)	XM_146640	5.14694	0.0002
Ptxna3	Plexin A3 (Ptxna3), mRNA	NM_008883	5.14348	1.78E-10
2200001115Rik	RIKEN cDNA 2200001115 gene (2200001115Rik), mRNA	NM_183278	5.12983	9.01E-11
Stk38l	Serine/threonine kinase 38 like, mRNA (cDNA clone MGC:70096 IMAGE:30135051)	NM_172734	5.12867	1.65E-13
NAP092202-001	Unknown		5.12151	9.54E-32
Dock4	MKIAA0716 protein	AK049953	5.10798	0.0001
Nek1	Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030407P11 product: NIMA (never in mitosis gene a)-related expressed kinase 1, full insert sequence.	AK031330	5.1072	1.46E-15
Rgs2	Regulator of G-protein signaling 2, mRNA (cDNA clone MGC:36187 IMAGE:5365271)	NM_009061	5.10596	4.25E-10
Mapk8ip1	JNK interacting protein-1b (JIP-1b)	NM_011162	5.10563	1.85E-29
Pard6b	Par-6 (partitioning defective 6) homolog beta (C. elegans), mRNA (cDNA clone MGC:35871 IMAGE:2655658)	BC025147	5.1056	2.16E-21
H1f0	H1 histone family, member 0, mRNA (cDNA clone MGC:19309 IMAGE:4166167)	NM_008197	5.10476	2.71E-06
Dmp1	Dentin matrix protein 1 (Dmp1), mRNA	NM_016779	5.10461	0.0003
<b>Usf1</b>	<b>M.musculus USF1 (non-coding exon 1).</b>	<b>X95315</b>	<b>5.1015</b>	<b>0.00002</b>
2810453I06Rik	RIKEN cDNA 2810453I06 gene (2810453I06Rik), mRNA	NM_026050	5.08664	2.86E-23
Ndrg3	N-myc downstream regulated gene 3, mRNA (cDNA clone MGC:21649 IMAGE:4500970)	NM_013865	5.08321	3.05E-26



Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
2810013E07Rik	RIKEN cDNA 2810013E07 gene, mRNA (cDNA clone MGC:67555 IMAGE:6402150)	AK036255	5.08237	0.0059
6330406L22Rik	RIKEN cDNA 6330406L22 gene, mRNA (cDNA clone MGC:59510 IMAGE:6333971)	AK041380	5.07511	0.00009
Tubgcp5	Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430028E06 product: unclassifiable, full insert sequence.	AK034715	5.07129	0.00549
AK037544	Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130024K02 product: hypothetical proteinase inhibitor I4, serpin containing protein, full insert sequence.	AK037544	5.07051	5.67E-11
Creb3l3	CAMP responsive element binding protein 3-like 3 (Creb3l3), mRNA	NM_145365	5.06499	2.30E-13
Mfp3l	Microfibrillar-associated protein 3-like, mRNA (cDNA clone MGC:106286 IMAGE:5025281)	AK122332	5.0638	0.00006
Ddah2	Dimethylarginine dimethylaminohydrolase 2, mRNA (cDNA clone MGC:5866 IMAGE:3158175)	NM_016765	5.06334	6.63E-30
Il1rap	Interleukin 1 receptor accessory protein (Il1rap), transcript variant 2, mRNA	NM_134103	5.06296	4.72E-21
Cox7a1	Cytochrome c oxidase, subunit VIIa 1 (Cox7a1), mRNA	NM_009944	5.06261	3.37E-27
Unc13a	Glycosyltransferase 25 domain containing 1 (Glt25d1), mRNA	AK083196	5.06174	6.78E-08
Mdm1	Transformed mouse 3T3 cell double minute 1 (Mdm1), transcript variant 2, mRNA	NM_148922	5.0613	3.82E-13
Flywch1	FLYWCH-type zinc finger 1 (Flywch1), mRNA	BC025645	5.06097	8.55E-16
2410116G06Rik	RIKEN cDNA 2410116G06 gene (2410116G06Rik), mRNA	NM_026630	5.05623	7.14E-06
AK087708	Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330009M13 product: unclassifiable, full insert sequence.	AK087708	5.05545	0.00228
Hist1h2bk	Histone 1, H2bk (Hist1h2bk), mRNA	NM_175665	5.0523	1.47E-33
Dffa	DNA fragmentation factor, alpha subunit (Dffa), transcript variant 2, mRNA	NM_010044	5.05211	4.21E-08
Gpr155	G protein-coupled receptor 155, mRNA (cDNA clone IMAGE:4167684)	AY255560	5.05096	5.00E-13
Cntn3	Contactin 3 (Cntn3), mRNA	NM_008779	5.05051	8.40E-08
Trpc6	Transient receptor potential cation channel, subfamily C, member 6 (Trpc6), mRNA	NM_013838	5.04168	0.00005
Xpr1	Xenotropic and polytropic murine retrovirus receptor (Xpr1)	AK047436	5.0407	5.27E-29
BC052046	CDNA sequence BC052046 (BC052046), mRNA	NM_183177	5.03591	1.47E-06
Scnn1g	Sodium channel, nonvoltage-gated 1 gamma, mRNA (cDNA clone MGC:29058 IMAGE:5042876)	NM_011326	5.0338	0.00021
Rab11fip1	MFLJ00294 protein	AK008412	5.03263	6.56E-16
Zfpml	Zinc finger protein, multitype 1 (Zfpml), mRNA	NM_009569	5.02713	4.89E-09
Serp1b1c	Serine (or cysteine) peptidase inhibitor, clade B, member 1c (Serp1b1c), mRNA	NM_173051	5.02704	1.26E-06
Ablim3	Actin binding LIM protein family, member 3, mRNA (cDNA clone MGC:106450 IMAGE:30534236)	NM_198649	5.01635	0.00514
Hic2	Hypermethylated in cancer 2 protein (Hic2)	NM_178922	5.01624	5.56E-27
Vkorc1	Vitamin K epoxide reductase complex, subunit 1, mRNA (cDNA clone MGC:25747 IMAGE:3991412)	NM_178600	5.01352	1.91E-06
3-Mar	Membrane-associated ring finger (C3HC4) 3 (March3), mRNA	AK018160	5.01164	0.00268
Kcnh1	Potassium voltage-gated channel, subfamily H (eag-related), member 1 (Kcnh1), mRNA	NM_010600	5.00508	2.36E-08



Primary Sequence Name	Sequence Description	Accession #	Fold Change	P-value
Rab37	RAB37, member of RAS oncogene family (Rab37), mRNA	NM_021411	5.00277	1.08E-09
Hist3h2a	Histone 3, H2a, mRNA (cDNA clone MGC:70265 IMAGE:6493838)	NM_178218	5.00243	0.00002
Atp6v1b2	ATPase, H+ transporting, V1 subunit B, isoform 2, mRNA (cDNA clone MGC:21587 IMAGE:4500843)	BB633273	5.00183	2.44E-07

**Table V**

Confirmed/Putative TSGs identified in our screen that contain CpG islands in both human and mouse forms of the gene.

Gene	CpG Island M/H	RT-PCR*	MSP** M/H
<i>Tspan33</i>	+/+	+	-/-
<i>Cabc1</i>	+/+	+	-/-
<i>Dusp2</i>	+/+	+	+/+
<i>Nlk</i>	+/+	+	-/-
<i>Timp3</i>	+/+	+	+/+
<i>Dbccr1</i>	+/+	-	-/-
<i>Klf2</i>	+/+	-	-/-
<i>Dock4</i>	+/+	-	-/-
<i>Cacna1g</i>	+/+	+	-/-
<i>Atp1b2</i>	+/+	+	+/+
<i>Egr1</i>	+/+	-	-/-
<i>Smpd3</i>	+/+	+	+/+
<i>Akap12</i>	+/+	-	-/-
<i>Rprm</i>	+/+	+	+/+
<i>Zfp185</i>	+/+	-	-/-
<i>Cry2</i>	+/+	-	-/-
<i>Scrib</i>	+/+	-	-/-
<i>Btg2</i>	+/+	-	-/-
<i>Foxj1</i>	+/+	+	+/+
<i>Sesn3</i>	+/+	-	-/-
<i>Kremen1</i>	+/+	+	-/-
<i>Bach2</i>	+/+	+	-/-
<i>Rb1</i>	+/+	-	-/-
<i>Ddit3</i>	+/+	-	-/-
<i>Irf6</i>	+/+	-	-/-
<i>Bcl2l11</i>	+/+	-	-/-
<i>Tusc2</i>	+/+	ND	ND
<i>Tfdp2</i>	+/+	ND	ND
<i>Ptpn13</i>	+/+	ND	ND
<i>Ephb3</i>	+/+	ND	ND
<i>Pcdh10</i>	+/+	ND	ND
<i>Eaf2</i>	+/+	ND	ND
<i>Sema3b</i>	+/+	ND	ND
<i>Lrp1b</i>	+/+	ND	ND
<i>Rad9b</i>	+/+	ND	ND

Gene	CpG Island M/H	RT-PCR*	MSP** M/H
<i>Cdh15</i>	+/+	ND	ND
<i>Dapk2</i>	+/+	ND	ND

M: mouse, H: human

ND: not done

\* For RT-PCR assays, + = increased gene expression in 5-azadC/TSA treated EMT6 cells

\*\* For MSP assays, + = gene methylation in any mouse mammary or human breast tumor line studied