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Contextual fear conditioning induces differential alternative splicing

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Abstract

The process of memory consolidation requires transcription and translation to form long-term memories. Significant effort has been dedicated to understanding changes in hippocampal gene expression after contextual fear conditioning. However, alternative splicing by differential transcript regulation during this time period has received less attention. Here, we use RNA-seq to determine exon-level changes in expression after contextual fear conditioning and retrieval. Our work reveals that a short variant of Homer1, *Ania-3*, is regulated by contextual fear conditioning. The ribosome biogenesis regulator *Las1l*, small nucleolar RNA *Snord14e*, and the RNA-binding protein *Rbm3* also change specific transcript usage after fear conditioning. The changes in *Ania-3* and *Las1l* are specific to either the new context or the context-shock association, while the changes in *Rbm3* occur after context or shock only. Our analysis revealed novel transcript regulation of previously undetected changes after learning, revealing the importance of high throughput sequencing approaches in the study of gene expression changes after learning.

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Conflict of interest

None.

Keywords

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1. Introduction

Contextual fear conditioning requires two waves of transcription and protein synthesis in the hippocampus to form long-term memory (Bourtchouladze et al., 1998; Igaz, Vianna, Medina, & Izquierdo, 2002). Our lab and others have focused on discovering the genes regulated during these transcriptional waves using both candidate gene and genome-wide approaches. Our microarray-based studies have indicated that the first wave of transcription induces the largest change in gene expression 30 min after contextual learning (Peixoto, Wimmer et al., 2015). However, gene regulation is a complex process that has multiple layers of control. Levels of particular mRNA isoforms can be regulated by alternative start sites, differential splicing including exon skipping and intron retention, and alternative poly(A) site selection (Leff, Rosenfeld, & Evans, 1986; Raj & Blencowe, 2015). Alternative splicing can lead to distinct protein function and interactions (Ellis et al., 2012) or regulate mRNA localization (Ehlers, Fung, O'Brien, & Haganir, 1998; Jaskolski et al., 2004; Papandrikopoulou, Doll, Tucker, Garner, & Matus, 1989), and thus is expected to be particularly important in neurons, which need to traffic mRNA to their long cellular processes.

Most previous research studying genome-wide gene expression in the hippocampus after contextual learning has relied on microarray technology (Barnes, Kirtley, & Thomas, 2012; Cavallaro, D'Agata, Manickam, Dufour, & Alkon, 2002; Keeley et al., 2006; Klur et al., 2009; Levenson et al., 2004; Mei et al., 2005; Peixoto, Wimmer et al., 2015). Although microarrays are a reliable tool to measure changes in gene expression, they are unable to distinguish exon-level effects that are indicative of alternative splicing. RNA-seq provides numerous advantages over microarrays (Peixoto, Risso et al., 2015), including the ability to study exon-level changes in gene expression. Isoform-specific gene expression changes are known to occur after fear conditioning, including upregulation of *Bdnf IV*, but not other *Bdnf* isoforms (Lubin, Roth, & Sweatt, 2008; Mizuno, Dempster, Mill, & Giese, 2012), and *Homer1a*, but not *Homer1c* (Mahan et al., 2012) in response to strong, three shock training protocols. The different *Bdnf* isoforms have distinct transcription start sites, while the expression of *Homer1* isoforms is controlled by the splicing regulator SRp20 (Wang, Chikina, Pincas, & Sealfon, 2014), which is upregulated after learning (Antunes-Martins, Mizuno, Irvine, Lepicard, & Giese, 2007). These examples indicate that gene regulation after learning is more complex than gene-level differences and can be highly selective for particular isoforms of a gene.

Therefore, we used RNA-seq to study differential alternative splicing 30 min after contextual fear conditioning and 30 min after memory retrieval. Applying Remove Unwanted Variation (RUV), a recently designed normalization algorithm (Peixoto, Risso et al., 2015; Risso, Ngai, Speed, & Dudoit, 2014), to our data, we discovered 171 bins, corresponding to either an entire exon or any portion of a gene, across 138 genes that showed differential expression

after learning independent of changes at the gene-level. After memory retrieval 450 differentially expressed bins corresponding to 311 unique genes were discovered. These bins include retained introns, unique start/end sites, or small RNA not yet spliced out of the polyadenylated mRNA. The differences include *Snord14e*, a small nucleolar RNA, which our lab has previously shown to be regulated at this time point (Peixoto, Wimmer et al., 2015). Sno-RNAs, which are commonly found within introns of genes, regulate RNA processing and have been implicated in memory consolidation (Rogelj, Hartmann, Yeo, Hunt, & Giese, 2003). In addition, *Ania-3*, an alternative short form of Homer1 that has not previously been linked to learning, ribosome biogenesis regulator *Las1l*, and the RNA-binding protein *Rbm3* were also regulated by contextual fear conditioning. These findings demonstrate that alternative splicing is regulated by contextual learning on a genome-wide scale and also identify novel candidate isoforms that may be pertinent to memory consolidation.

2. Materials and methods

2.1. Subjects

C57Bl/6J mice were maintained under standard conditions with food and water available *ad libitum*. Adult male mice 2 months of age were kept on a 12-h light/12-h dark cycle with lights on at 7AM. All behavioral and biochemical experiments were performed during the light cycle with training starting at 10AM (ZT3). All animal experiments were approved by the Institutional Animal Care and Use Committee of the University of Pennsylvania and were consistent with National Institutes of Health guidelines.

2.2. Behavior

Contextual fear conditioning was performed as previously described (Hawk et al., 2012; Vecsey et al., 2007) with handling for 3 days prior to conditioning. Briefly, the conditioning protocol entailed a single 2-s, 1.5 mA footshock terminating at 2.5 min after placement of the mouse in the chamber. Mice were left in the chamber for an additional 30 s and then returned to their homecage. One mouse per behavioral group (homecage, fear conditioned) was trained per day over 10 days to reduce unwanted variation caused by training and sacrifice times. One mouse was also tested the next day to ensure proper freezing levels (Peixoto, Wimmer et al., 2015).

2.3. RNA isolation

Hippocampi were dissected either from homecage mice or 30 min after training and placed into RNeasy lysis buffer (Qiagen Valencia, CA) and frozen on dry ice. Tissue was homogenized using a TissueLyser system and RNA was extracted using the RNeasy Microarray Tissue kit (Qiagen) according to the manufacturer's instructions. Samples were DNase treated using the RNase-Free DNase kit (Qiagen) off-column by incubating 5 μ l DNase and 35 μ l Buffer RDD for 25 min at RT with each sample. Samples were then ethanol precipitated and resuspended in water.

2.4. RNA-seq library preparation and sequencing

2 µg of RNA from n = 5 homecage and fear conditioned mice was used in the TruSeq RNA Sample Prep Kit (Illumina San Diego, CA) according to the manufacturer's instructions with polyA selection. Completed libraries were size-selected on an agarose gel to remove any high basepair fragments, quantified by qPCR (KAPA Biosystems Boston, MA), and submitted to the PGFI sequencing core at the University of Pennsylvania. An Illumina HiSeq 2000 sequenced the libraries in paired-end 100 bp reads. 3 libraries were sequenced per lane on an Illumina HiSeq 2000, resulting in an average of 67,011,105 reads per sample in the homecage mice and 62,115,805 reads per sample after fear conditioning. Reads had good unique concordance (86.9% in homecage, 85.5% after fear conditioning) and mapping (90.7% of unique concordant reads in homecage and 93.1% after fear conditioning). RNA-seq data is available through GEO (GSE63412) (Peixoto, Risso et al., 2015).

2.5. Data analysis

Sequencing reads were aligned to the mouse mm9 genome using GSNAP (Wu & Nacu, 2010) (<http://share.gene.com/gmap>). An exon-level count table was produced by counting reads into unique, non-overlapping "bins" using Ensembl gene models and HTSeq (Anders, Reyes, & Huber, 2012) (<http://www-huber.embl.de/users/anders/HTSeq/doc/overview.html>). A "bin" can either be any part of a gene or an entire exon depending on the uniqueness of the region. Bin counts were normalized using upper-quartile scaling implemented in edgeR (Robinson, McCarthy, & Smyth, 2010) followed by RUVs, which corrects for unwanted variation using replicate/negative control samples (Risso et al., 2014). Additionally, we used 8897 bins residing in 625 genes identified as unchanged from a previous microarray experiment as negative controls for RUV under the assumption that these bins are also not changing (Peixoto, Risso et al., 2015; Peixoto, Wimmer et al., 2015). We discovered that four factors of unwanted variation ($k = 4$) need to be adjusted for to resolve the differences caused by contextual fear, which was chosen using the method described by Peixoto, Risso et al. (2015). Differential splicing analysis was performed with the limma Bioconductor package, using the voom and diffSplice functions (Law, Chen, Shi, & Smyth, 2014; Ritchie et al., 2015). Functional annotation was performed through DAVID (Huang da, Sherman, & Lempicki, 2009a, 2009b) (<http://david.abcc.ncifcrf.gov/>). The annotation was limited to the following sources: GO Biological process, GO Molecular Function, KEGG pathways, and SwissProt and Protein Information Resource keywords and an EASE score restriction of 0.1.

2.6. qPCR analysis

RNA was isolated from a separate cohort of fear conditioned, immediate shock, or context only mice following the same behavioral paradigms described above. Immediate shock consisted of placing the mouse in the context with the footshock on and immediate removal, while context involved placing the mouse in the context for the same time as contextual conditioning with no shock. RNA was converted to cDNA using the RETROscript kit (Ambion) according to the manufacturer's instructions. cDNA reactions were diluted to 200 µl and 2.25 µl was combined with 0.25 µl 5 µM primer mix and 2.5 µl SYBR Select Master Mix (Life Technologies Carlsbad, CA) and run on a Viia7 Real Time PCR system. The Ct method was used for analysis (Poplawski et al., 2014), with all primers showing >90%

efficiency. The primers used were: Ania1F-AGTGGCTGGTTTTCTTGGACT, Ania1R-GGGAGGTGGATTGGTGACAA, Homer1Bin21F-CTGGAGTCCACTGCCAATGT, Homer1Bin21R-CTCTGCTTCCTCCTGGTACG, Las11Bin15F-TCAAAGTCAGAGGGGTCGGA, Las11Bin15R-AGACTTCGCTCTTGCTGCTT, Las11Bin17F-TGCTGGAGAAACACAGGCAT, Las11Bin17R-ACATTGTACACGTGGGGAAAGA, Rbm3Bin2F-ACCTGAGTTTTGGAGGCTGG, Rbm3Bin2R-ACAACAGCGGACCATAGG, Rbm3Bin7F-GGTGGCTATGACCGCTACTC, Rbm3Bin7R-TTTTGTGTGCATGCCCCATC, Rbm3Bin22F-TGCCCTGGCAGACATAGAG, Rbm3Bin22R-GTCTGCCACTTTCTTCGTTCTTT. The comparison between three groups (homecage, immediate shock, context only) was analyzed using an ANOVA. The effect of bin ($F(7, 160) = 11.90$), condition ($F(2, 160) = 7.835$) and interaction ($F(14, 160) = 3.719$) were all significant, and Tukey tests were used to determine the significance of each bin.

3. Results

RNA-seq has the advantage of distinguishing exon-level reads that are difficult to identify by any other method, and therefore it is an ideal technique to study alternative splicing. We used RNA-seq to study gene expression in the hippocampus 30 min after contextual fear conditioning, a time point our lab has previously determined to show robust expression changes after fear conditioning (Peixoto, Wimmer et al., 2015). We used GSNAP (Wu & Nacu, 2010) to align reads to the mm9 mouse genome and HTSeq (Anders, Pyl, & Huber, 2015) to count reads into bins (Anders et al., 2012) using Ensembl gene models. Bins are separated based on overlap of Ensembl gene models, with any unique section of a transcriptional unit split into a separate bins. Therefore, a bin can represent either a whole exon or any other unique portion of the gene model. Thus, differential start sites, 3' ends, or retained introns can be observed as unique bins if they are part of the Ensembl database. So as not to bias ourselves using gene models, we considered every bin as a potential site for alternative regulation. RUVs normalization performed as described (Risso et al., 2014), adjusting for four factors of unwanted variation (which can include biological and technical noise), was found to control for fear conditioning as the primary effector of variation between samples. Bioconductor package limma was then used to determine differential bin usage independent of gene-level changes (Ritchie et al., 2015). We identified 171 bins across 138 genes that displayed differential usage ($FDR < 0.05$) after contextual fear conditioning (Table 1). 129 of these bins were upregulated and 42 were downregulated, consistent with the general increase in gene expression after fear conditioning (Peixoto, Wimmer et al., 2015). We performed functional classification of genes showing at least 1 bin-specific change after fear conditioning. The SwissProt and Protein Information Resource keywords “phosphoprotein” and “alternative splicing” were enriched in our data set, indicating that our exon-level analysis discovers alternative splicing as expected. Clusters corresponding to protein catabolic processes and nucleotide binding were also enriched. The same analysis was performed on samples 30 min after memory retrieval (testing). In this analysis, we found 450 bins corresponding to 311 unique genes (Table 2). This list of genes contains 70 of the 138 genes observed to change after fear conditioning, highlighting the overlap between memory consolidation and retrieval (Peixoto, Wimmer et al., 2015).

Upregulated bins during memory consolidation included *Snord14e*, which reside in the introns of the *Hspa8* gene. We have recently validated *Snord14e* upregulation after detecting differences by microarray (Peixoto, Wimmer et al., 2015). We also discovered that a poorly studied short isoform of *Homer1* known as *Ania-3* (*Ensembl Homer1-005*) (Bottai et al., 2002) is upregulated after contextual fear conditioning. *Homer1a* has previously been shown to be upregulated by fear conditioning (Mahan et al., 2012), but *Ania-3* has not been studied. To validate our results, we performed qPCR in a separate cohort of mice, comparing the bins observed to change to a bin of the same gene that was unchanged. *Ania-3* was found to be upregulated independently of the entire *Homer1* gene (Fig. 1a). Ribosome biogenesis protein *Las1l* exhibited bin-specific downregulation in response to contextual fear conditioning and this was also confirmed by qPCR (Fig. 1b). RNA-binding protein *Rbm3*, which our lab has shown to change in the hippocampus after sleep deprivation (Vecsey et al., 2012), displays complex regulation with both upregulated and downregulated bins after learning. Both the upregulated and downregulated bins were confirmed by qPCR in a separate cohort of animals (Fig. 1c). In all cases, the bin predicted to change was significantly regulated while a control bin in the same gene was unchanged.

To test whether these changes are specific to the association of context and shock, a separate cohort of animals were either immediately shocked or exposed to the context with no footshock. Expression of *Ania-3* shows a change in response to context only, but not after immediate shock (Fig. 2). This is not surprising given the overlap of gene expression between fear conditioning and spatial training (Keeley et al., 2006; Poplawski et al., 2014). An increase in *Ania-3* may represent splicing changes in response to a novel environment. *Las1l* displays a non-significant trend toward a reduction in the context only, but not immediate shock (Fig. 2). *Las1l* bin 15 may represent a splicing change that occurs only with a context-shock association. *Rbm3* bin 2 expression shows changes in both the immediate shock and context only conditions, (Fig. 2), suggesting that this alternative splicing occurs with minimal perturbation and may not reflect a learning event. *Rbm3* bin 22 showed only a trend toward a decrease in both cases. Therefore, changes in *Rbm3* bin 2 may represent any activity within the hippocampus, while *Rbm3* bin 22 could be specific to context-shock associations. These results indicate that alternative splicing can occur in response to a variety of factors and may be a specific marker in the hippocampus of recent behavioral stimuli.

4. Discussion

In this study, we provide the first evidence of genome-wide regulation of alternative splicing after learning in the hippocampus. Using bin counts produced by HTSeq and the limma Bioconductor package, we compared bins representing a unique piece of a gene against expression of that entire gene to create a list of bin-level changes. We were able to detect significant gene expression changes at 171 bins occurring in response to contextual fear conditioning at 138 genes. The exact number of potential splicing sites is not known in neurons, and splicing studies have identified as low as 3110 splicing events in neurons (Zhang et al., 2014) or as high as 92–94% of all genes (Wang et al., 2008). We suspect that 138 genes showing changes is only a small fraction of the potential change. It is unclear at this time why memory retrieval shows a larger set of changes than memory consolidation.

This study used whole hippocampus, so only a small fraction of all cells in the sample are being activated by learning. However, our RUV analysis removes unwanted variation including that from nonresponsive cells, so we believe that the changes observed are due to activated neurons.

Although individual examples of alternative splicing have been observed during memory consolidation (Lubin et al., 2008; Mahan et al., 2012; Rozic, Lupowitz, Piontkewitz, & Zisapel, 2011), no studies have explored this phenomenon genome-wide. We also identified candidate genes displaying alternative regulation that may be important for learning. As previously reported (Peixoto, Wimmer et al., 2015), we confirmed that *Snord14e*, which exists within an intron of *Hspa8*, is regulated by fear conditioning. It is unclear why *Snord14e* increases in polyadenylated RNA, but it could be due increases in intron retention during transcription or splicing and polyadenylation of a *Snord14e* precursor. We also implicate the selective alternative splicing of *Homer1* isoform *Ania-3*, RNA-binding protein *Rbm3* and ribosome biogenesis regulator *Las1l* in learning for the first time. These results emphasize the importance of using genome-wide binning techniques to identify subtle changes in splicing following fear conditioning, which would be overlooked with standard RNA-seq analysis.

It is interesting that we observed different results for *Rbm3* alternative splicing in the context only and immediate shock controls. At the gene-level, gene expression changes after contextual and spatial learning are known to overlap (Poplawski et al., 2014). Previous work from our lab has highlighted similar gene expression between fear conditioning and context-only exposure in the hippocampus, but not the amygdala (Keeley et al., 2006). Thus, we anticipated similar results between our fear conditioning results and the context only control, as was the case with all splicing events tested. This confirms our previous findings that exposure to a context is sufficient to elicit similar gene expression changes that occur when context is paired with shock.

However, we found that *Rbm3* had a unique response to the components of fear conditioning, with an immediate shock being able to alter alternative splicing of bin 2 of this gene. Immediate shock does not provide the subject enough time to form a contextual representation of the space, and therefore is generally thought not to cause expression changes in the hippocampus (Huff et al., 2006). Thus, the change after immediate shock in *Rbm3* may suggest that splicing of *Rbm3* bin 2 in the hippocampus is altered by many brain stimuli. In contrast, *Rbm3* bin 22, *Ania-3* and *Las1l* may be specific to exposure to a novel context or context-shock association. Thus, splicing changes in *Rbm3* bin 2 may not be involved in forming long-term contextual fear memories, while splicing in *Ania-3* and *Las1l* may have a role in encoding these types of memories. We hypothesize that this may be an instance of a broader phenomenon in neuronal plasticity, where certain splicing events are regulated by any neuronal activity while others only respond to specific stimuli.

In the present study, we did not determine the type of splicing that is occurring at each of these bins, which will be the subject of future analyses. Each bin observed could be the result of many types of regulation, including exon skipping, intron retention, or alternative start/stop sites. *Ania-3* has previously been reported as an alternative isoform of *Homer1* that

responds like an immediate early gene (Bottai et al., 2002), and the change we detect here corresponds to the unique *Ania-3* exon. Whether *Ania-3* splicing is regulated by SRp20, as is the case for *Homer1a* (Wang et al., 2014), is a subject for future investigation. *Las1*/bin 15 appears to be a retained intron, but whether this is part of the canonical *Las1* mRNA or part of a different isoform is unknown. It is also possible that this could be a small RNA that is spliced out of the final polyadenylated mRNA. *Rbm3* bin 2 is one of several potential transcriptional termination sites of *Rbm3* while bin 22 could either be an early termination site or a retained intron. Further study will be required to determine the exact identity and function of the isoforms that are regulated by contextual fear conditioning.

The mechanism that drives this alternative splicing is not studied within these experiments, although transcription of certain splicing proteins such as SRp20 is known to change after fear conditioning (Antunes-Martins et al., 2007). Recent studies have also highlighted the importance of Rbfox1 in splicing and mRNA regulation in neurons (Lee et al., 2016). Our data indicates regulation of a specific isoform of splicing factor *Sfpq*. However, it is unclear whether these transcriptional changes would be translated into protein and affect splicing by 30 min after training. The mechanism by which alternative regulation of transcripts is controlled during memory consolidation is an important question for future studies. It is possible that changes in epigenetic modifications are regulating this selective transcript usage (Zhou, Luo, Wise, & Lou, 2014), including H3K36me3 and H4K20me1 (Luco et al., 2010; Zhu, Wang, Liu, & Wang, 2013). It would be interesting to observe whether the differential bins discovered in this study show differential histone modifications as well. We hope our findings and this unique analysis method drive further study into the mechanisms of isoform-specific changes in gene expression during memory consolidation.

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References

- Anders S, Pyl PT, Huber W. HTSeq — A Python framework to work with high-throughput sequencing data. *Bioinformatics*. 2015; 31(2):166–169. [PubMed: 25260700]
- Anders S, Reyes A, Huber W. Detecting differential usage of exons from RNA-seq data. *Genome Research*. 2012; 22:2008–2017. [PubMed: 22722343]
- Antunes-Martins A, Mizuno K, Irvine EE, Lopicard EM, Giese KP. Sex-dependent up-regulation of two splicing factors, Psf and Srp20, during hippocampal memory formation. *Learning & Memory*. 2007; 14:693–702. [PubMed: 17911373]
- Barnes P, Kirtley A, Thomas KL. Quantitatively and qualitatively different cellular processes are engaged in CA1 during the consolidation and reconsolidation of contextual fear memory. *Hippocampus*. 2012; 22:149–171. [PubMed: 21080409]
- Bottai D, Guzowski JF, Schwarz MK, Kang SH, Xiao B, Lanahan A, Worley PF, Seeburg PH. Synaptic activity-induced conversion of intronic to exonic sequence in *Homer 1* immediate early gene expression. *Journal of Neuroscience*. 2002; 22:167–175. [PubMed: 11756499]
- Bourtchouladze R, Abel T, Berman N, Gordon R, Lapidus K, Kandel ER. Different training procedures recruit either one or two critical periods for contextual memory consolidation, each of which requires protein synthesis and PKA. *Learning & Memory*. 1998; 5:365–374. [PubMed: 10454361]

- Cavallaro S, D'Agata V, Manickam P, Dufour F, Alkon DL. Memory-specific temporal profiles of gene expression in the hippocampus. *Proceedings of the National Academy of Sciences of the United States of America*. 2002; 99:16279–16284. [PubMed: 12461180]
- Ehlers MD, Fung ET, O'Brien RJ, Huganir RL. Splice variant-specific interaction of the NMDA receptor subunit NR1 with neuronal intermediate filaments. *Journal of Neuroscience*. 1998; 18:720–730. [PubMed: 9425014]
- Ellis JD, Barrios-Rodiles M, Colak R, Irimia M, Kim T, Calarco JA, Blencowe BJ. Tissue-specific alternative splicing remodels protein–protein interaction networks. *Molecular Cell*. 2012; 46:884–892. [PubMed: 22749401]
- Hawk JD, Bookout AL, Poplawski SG, Bridi M, Rao AJ, Sulewski ME, Kroener BT, Manglesdorf DJ, Abel T. NR4A nuclear receptors support memory enhancement by histone deacetylase inhibitors. *The Journal of Clinical Investigation*. 2012; 122:3593–3602. [PubMed: 22996661]
- Huang da W, Sherman BT, Lempicki RA. Bioinformatics enrichment tools: Paths toward the comprehensive functional analysis of large gene lists. *Nucleic Acids Research*. 2009a; 37:1–13. [PubMed: 19033363]
- Huang da W, Sherman BT, Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. *Nature Protocols*. 2009b; 4:44–57. [PubMed: 19131956]
- Huff NC, Frank M, Wright-Hardesty K, Sprunger D, Matus-Amat P, Higgins E, Rudy JW. Amygdala regulation of immediate-early gene expression in the hippocampus induced by contextual fear conditioning. *Journal of Neuroscience*. 2006; 26:1616–1623. [PubMed: 16452685]
- Igaz LM, Vianna MR, Medina JH, Izquierdo I. Two time periods of hippocampal mRNA synthesis are required for memory consolidation of fear-motivated learning. *Journal of Neuroscience*. 2002; 22:6781–6789. [PubMed: 12151558]
- Jaskolski F, Coussen F, Nagarajan N, Normand E, Rosenmund C, Mulle C. Subunit composition and alternative splicing regulate membrane delivery of kainate receptors. *Journal of Neuroscience*. 2004; 24:2506–2515. [PubMed: 15014126]
- Keeley MB, Wood MA, Isiegas C, Stein J, Hellman K, Hannenhalli S, Abel T. Differential transcriptional response to nonassociative and associative components of classical fear conditioning in the amygdala and hippocampus. *Learning & Memory*. 2006; 13:135–142. [PubMed: 16547164]
- Klur S, Muller C, Pereira de Vasconcelos A, Ballard T, Lopez J, Galani R, Certa U, Cassel JC. Hippocampal-dependent spatial memory functions might be lateralized in rats: An approach combining gene expression profiling and reversible inactivation. *Hippocampus*. 2009; 19:800–816. [PubMed: 19235229]
- Law CW, Chen Y, Shi W, Smyth GK. Voom: Precision weights unlock linear model analysis tools for RNA-seq read counts. *Genome Biology*. 2014; 15:R29. [PubMed: 24485249]
- Lee JA, Damianov A, Lin CH, Fontes M, Parikshak NN, Anderson ES, Geschwind DH, Black DL, Martin KC. Cytoplasmic Rbfox1 regulates the expression of synaptic and autism-related genes. *Neuron*. 2016; 89:113–128. [PubMed: 26687839]
- Leff SE, Rosenfeld MG, Evans RM. Complex transcriptional units: Diversity in gene expression by alternative RNA processing. *Annual Review of Biochemistry*. 1986; 55:1091–1117.
- Levenson JM, Choi S, Lee SY, Cao YA, Ahn HJ, Worley KC, Pizzi M, Liou HC, Sweatt JD. A bioinformatics analysis of memory consolidation reveals involvement of the transcription factor c-rel. *Journal of Neuroscience*. 2004; 24:3933–3943. [PubMed: 15102909]
- Lubin FD, Roth TL, Sweatt JD. Epigenetic regulation of BDNF gene transcription in the consolidation of fear memory. *Journal of Neuroscience*. 2008; 28:10576–10586. [PubMed: 18923034]
- Luco RF, Pan Q, Tominaga K, Blencowe BJ, Pereira-Smith OM, Misteli T. Regulation of alternative splicing by histone modifications. *Science*. 2010; 327:996–1000. [PubMed: 20133523]
- Mahan AL, Mou L, Shah N, Hu JH, Worley PF, Ressler KJ. Epigenetic modulation of *Homer1a* transcription regulation in amygdala and hippocampus with pavlovian fear conditioning. *Journal of Neuroscience*. 2012; 32:4651–4659. [PubMed: 22457511]
- Mei B, Li C, Dong S, Jiang CH, Wang H, Hu Y. Distinct gene expression profiles in hippocampus and amygdala after fear conditioning. *Brain Research Bulletin*. 2005; 67:1–12. [PubMed: 16140156]

- Mizuno K, Dempster E, Mill J, Giese KP. Long-lasting regulation of hippocampal *Bdnf* gene transcription after contextual fear conditioning. *Genes, Brain and Behavior*. 2012; 11:651–659.
- Papandrikopoulou A, Doll T, Tucker RP, Garner CC, Matus A. Embryonic MAP2 lacks the cross-linking sidearm sequences and dendritic targeting signal of adult MAP2. *Nature*. 1989; 340:650–652. [PubMed: 2770869]
- Peixoto L, Risso D, Poplawski SG, Wimmer ME, Speed TP, Wood MA, Abel T. How data analysis affects power, reproducibility and biological insight of RNA-seq studies in complex datasets. *Nucleic Acids Research*. 2015; 43:7664–7674. [PubMed: 26202970]
- Peixoto LL, Wimmer ME, Poplawski SG, Tudor JC, Kenworthy CA, Liu S, Abel T. Memory acquisition and retrieval impact different epigenetic processes that regulate gene expression. *BMC Genomics*. 2015; 16(Suppl. 5):S5. [PubMed: 26040834]
- Poplawski SG, Schoch H, Wimmer ME, Hawk JD, Walsh JL, Giese KP, Abel T. Object-location training elicits an overlapping but temporally distinct transcriptional profile from contextual fear conditioning. *Neurobiology of Learning and Memory*. 2014; 116:90–95. [PubMed: 25242102]
- Raj B, Blencowe BJ. Alternative splicing in the mammalian nervous system: Recent insights into mechanisms and functional roles. *Neuron*. 2015; 87:14–27. [PubMed: 26139367]
- Risso D, Ngai J, Speed TP, Dudoit S. Normalization of RNA-seq data using factor analysis of control genes or samples. *Nature Biotechnology*. 2014; 32:896–902.
- Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, Smyth GK. Limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic Acids Research*. 2015; 43:e47. [PubMed: 25605792]
- Robinson MD, McCarthy DJ, Smyth GK. EdgeR: A bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics*. 2010; 26:139–140. [PubMed: 19910308]
- Rogelj B, Hartmann CE, Yeo CH, Hunt SP, Giese KP. Contextual fear conditioning regulates the expression of brain-specific small nucleolar RNAs in hippocampus. *The European Journal of Neuroscience*. 2003; 18:3089–3096. [PubMed: 14656304]
- Rozic G, Lupowitz Z, Piontkewitz Y, Zisapel N. Dynamic changes in neurexins' alternative splicing: Role of Rho-associated protein kinases and relevance to memory formation. *PLoS ONE*. 2011; 6
- Vecsey CG, Hawk JD, Lattal KM, Stein JM, Fabian SA, Attner MA, Wood MA. Histone deacetylase inhibitors enhance memory and synaptic plasticity via CREB:CBP-dependent transcriptional activation. *Journal of Neuroscience*. 2007; 27:6128–6140. [PubMed: 17553985]
- Vecsey CG, Peixoto L, Choi JH, Wimmer M, Jaganath D, Hernandez PJ, Abel T. Genomic analysis of sleep deprivation reveals translational regulation in the hippocampus. *Physiological Genomics*. 2012; 44:981–991. [PubMed: 22930738]
- Wang Q, Chikina MD, Pincas H, Sealton SC. *Homer1* alternative splicing is regulated by gonadotropin-releasing hormone and modulates gonadotropin gene expression. *Molecular and Cellular Biology*. 2014; 34:1747–1756. [PubMed: 24591653]
- Wang ET, Sandberg R, Luo S, Khrebtkova I, Zhang L, Mayr C, Kingsmore SF, Schroth GP, Burge CB. Alternative isoform regulation in human tissue transcriptomes. *Nature*. 2008; 456:470–476. [PubMed: 18978772]
- Wu TD, Nacu S. Fast and SNP-tolerant detection of complex variants and splicing in short reads. *Bioinformatics*. 2010; 26:873–881. [PubMed: 20147302]
- Zhang Y, Chen K, Sloan SA, Bennett ML, Scholze AR, O'Keefe S, Wu JQ. An RNA-sequencing transcriptome and splicing database of glia, neurons, and vascular cells of the cerebral cortex. *Journal of Neuroscience*. 2014; 34:11929–11947. [PubMed: 25186741]
- Zhou HL, Luo G, Wise JA, Lou H. Regulation of alternative splicing by local histone modifications: Potential roles for RNA-guided mechanisms. *Nucleic Acids Research*. 2014; 42:701–713. [PubMed: 24081581]
- Zhu S, Wang G, Liu B, Wang Y. Modeling exon expression using histone modifications. *PLoS ONE*. 2013; 8:e67448. [PubMed: 23825663]

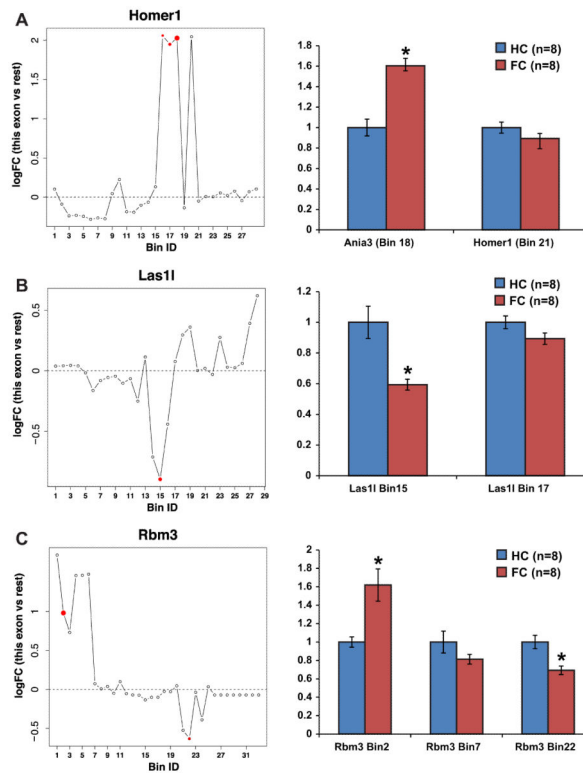


Fig. 1. Bin-specific regulation of *Homer1* (*Ania-3*), *Las11*, and *Rbm3*. (A) (left) diffSplice result showing the predicted significant bin changes of the *Homer1* gene in red on a log₂ scale. Bins 16–18 indicate the *Ania-3* isoform. (right) qPCR validation of the change in Bin18 in an independent cohort of mice. Bin 21 expression was compared as a control. (B) (left) diffSplice result showing the predicted significant bin changes of the *Las11* gene in red on a log₂ scale. (right) qPCR validation of the change in Bin 15 in an independent cohort of mice. Expression of Bin 17 was used as a control. (C) (left) diffSplice result showing the predicted significant bin changes of the *Rbm3* gene in red on a log₂ scale. (right) qPCR validation of the changes in Bin 2 and Bin 22 an independent cohort of mice. Expression of Bin 7 was used as a control. HC = homecage, FC = fear conditioned. * denotes a p-value of <0.05. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

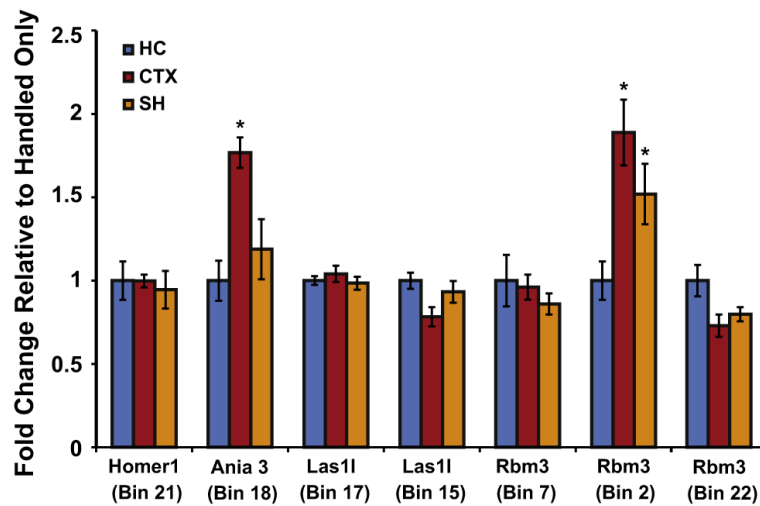


Fig. 2.

Alternative splicing changes variably in response to either component of fear conditioning alone. The same primers used in Fig. 1 were used to test gene expression after context only ($n = 8$) or immediate shock controls ($n = 8$) or homecage animals ($n = 7$) and analyzed by ANOVA. *Ania-3* and *Las1l* changes in response to the context only control and *Rbm3* changes with all manipulations. This may suggest *Ania-3* and *Las1l* are markers of contextual novelty while *Rbm3* responds to many stimuli. No control bins change with either context-only or immediate shock controls. HC = homecage, CTX = context only, SH = shock only. * denotes significance below an alpha of 0.05.

List of bins showing differential expression after fear conditioning. Each differential bin contains the chromosome, start position, and end position for easy reference.

Table 1

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG00000007617	Homer1	018	chr13	94136356	94137083	+	2.0	14.1	1.4E-33	3.7E-28
ENSMUSG00000029657	Hsph1	012	chr5	150423259	150426039	-	1.1	10.3	2.4E-21	3.3E-16
ENSMUSG00000039801	2410089E03Rik	053	chr15	8201065	8202148	+	-1.1	-9.2	9.6E-19	8.6E-14
ENSMUSG00000031167	Rbm3	002	chrX	7717104	7717909	-	1.0	9.0	3.5E-17	2.3E-12
ENSMUSG00000007617	Homer1	017	chr13	94136233	94136355	+	1.9	8.4	3.5E-15	1.9E-10
ENSMUSG00000020431	Adey1	024	chr11	7072883	7078509	+	-0.4	-8.4	5.5E-15	2.4E-10
ENSMUSG00000025372	Baiap2	027	chr11	119867673	119868096	+	0.5	7.7	3.5E-13	1.3E-08
ENSMUSG00000034083	C130022K22Rik	009	chr6	91835401	91838063	+	1.0	7.8	4.5E-13	1.5E-08
ENSMUSG00000008153	Clstn3	004	chr6	124383426	124383521	-	1.2	7.4	1.5E-12	4.5E-08
ENSMUSG00000043872	Zmym1	001	chr4	126724338	126724885	-	1.1	7.3	6.6E-12	1.8E-07
ENSMUSG00000005089	Slc1a2	036	chr2	102621901	102630941	+	-0.3	-6.7	8.4E-11	2.0E-06
ENSMUSG00000020287	Mpg	010	chr11	32130054	32131244	+	-0.6	-7.1	1.5E-10	3.3E-06
ENSMUSG00000024576	Csnk1a1	028	chr18	61745286	61746152	+	0.6	6.5	4.2E-10	8.5E-06
ENSMUSG00000063077	Kif1b	001	chr4	148550428	148552126	-	-0.2	-6.3	7.6E-10	1.5E-05
ENSMUSG00000035206	3110056O03Rik	016	chr10	80329406	80330144	+	0.4	6.5	9.0E-10	1.6E-05
ENSMUSG00000059495	Arhgef12	002	chr9	42771926	42776264	-	-0.3	-6.3	1.0E-09	1.7E-05
ENSMUSG00000022710	Usp7	020	chr16	8697013	8697568	-	0.8	6.2	1.4E-09	2.1E-05
ENSMUSG00000025372	Baiap2	026	chr11	119864352	119864399	+	0.6	6.3	1.6E-09	2.4E-05
ENSMUSG00000024576	Csnk1a1	027	chr18	61744853	61745285	+	0.6	6.2	2.3E-09	3.2E-05
ENSMUSG00000063077	Kif1b	002	chr4	148552127	148552971	-	-0.3	-6.0	4.0E-09	5.3E-05
ENSMUSG00000041879	Ipo9	036	chr1	137302594	137303043	-	-0.7	-5.9	5.5E-09	7.0E-05
ENSMUSG00000057421	Las11	015	chrX	931443543	93144773	-	-0.9	-6.0	6.0E-09	7.3E-05
ENSMUSG00000034656	Caenala	068	chr8	87163334	87163334	+	1.4	5.9	7.4E-09	8.6E-05
ENSMUSG00000031878	Nae1	015	chr8	107042164	107043101	-	1.1	5.9	8.2E-09	9.1E-05
ENSMUSG00000023033	Scn8a	030	chr15	100869972	100876360	+	-0.2	-5.9	9.3E-09	1.0E-04
ENSMUSG00000075876 + ENSMUSG00000064791 + ENSMUSG00000075924 + ENSMUSG00000015656	Snord14c/ Snord14e/ Snord14d/Hspa8	038	chr9	40612831	40612920	+	1.4	5.9	9.7E-09	1.0E-04

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG000000027523	Gnas	027	chr2	174155788	174155935	+	1.0	5.8	1.0E-08	1.0E-04
ENSMUSG000000071984	Fnde1	001	chr17	7931434	7932195	-	0.4	5.8	2.0E-08	1.9E-04
ENSMUSG000000038383	Pigu	004	chr2	155104386	155108131	-	0.5	5.8	2.6E-08	2.4E-04
ENSMUSG000000028053	Ash11	002	chr3	88785155	88789712	+	0.4	5.7	3.0E-08	2.6E-04
ENSMUSG000000028826	Tmem57	002	chr4	134360480	134362431	-	-0.4	-5.7	3.9E-08	3.4E-04
ENSMUSG000000075876 + ENSMUSG000000064791 + ENSMUSG000000075924 + ENSMUSG000000015656	Snord14c/ Snord14e/ Snord14d/Hspa8	037	chr9	40612779	40612830	+	1.4	5.6	4.3E-08	3.6E-04
ENSMUSG000000024576	Csnk1a1	025	chr18	61742498	61744058	+	0.5	5.6	4.5E-08	3.7E-04
ENSMUSG000000023952	Gtpbp2	035	chr17	46303816	46303936	+	0.9	5.6	4.6E-08	3.7E-04
ENSMUSG000000007617	Homer1	016	chr13	94136198	94136232	+	2.1	5.6	5.4E-08	4.1E-04
ENSMUSG000000027429	Sec23b	030	chr2	144405140	144406851	+	0.9	5.5	6.4E-08	4.8E-04
ENSMUSG000000036052	Dnajb5	011	chr4	42963816	42965965	+	0.4	5.7	6.8E-08	4.9E-04
ENSMUSG000000013033	Lphn1	001	chr8	86424004	86424471	+	0.7	5.5	8.0E-08	5.6E-04
ENSMUSG000000035640	Dos	014	chr10	79598293	79598333	-	1.6	5.5	8.3E-08	5.7E-04
ENSMUSG000000028488	Sh3gl2	016	chr4	85033579	85035284	+	0.2	5.5	1.1E-07	7.5E-04
ENSMUSG000000027569	1600027N09Rik	010	chr2	180318228	180319110	+	0.4	5.5	1.5E-07	9.7E-04
ENSMUSG000000008153	C12n3	005	chr6	124386790	124386835	-	1.4	5.3	2.1E-07	1.3E-03
ENSMUSG000000014873	Surf2	009	chr2	26773052	26774384	+	0.3	5.4	2.3E-07	1.5E-03
ENSMUSG000000063160 + ENSMUSG00000003762	Numbl/Adck4	037	chr7	28047272	28049894	+	0.4	5.2	2.9E-07	1.8E-03
ENSMUSG000000024777	Ppp2f5b	006	chr19	6230276	6230385	-	0.5	5.3	3.1E-07	1.8E-03
ENSMUSG000000031167	Rbm3	022	chrX	7721600	7721698	-	-0.6	-5.2	3.1E-07	1.8E-03
ENSMUSG000000053580	Tanc2	043	chr11	105786047	105790613	+	-0.3	-5.2	3.3E-07	1.9E-03
ENSMUSG000000028161	Ppp3ca	030	chr3	136598842	136598864	+	0.7	5.2	3.5E-07	1.9E-03
ENSMUSG000000029765	Pitxna4	001	chr6	32094565	32095925	-	-0.3	-5.2	3.7E-07	2.0E-03
ENSMUSG000000075003 + ENSMUSG000000037876	Jmj1c/Jmj1c	041	chr10	66707622	66708166	+	0.7	5.1	4.2E-07	2.3E-03
ENSMUSG000000027799	Nbea	062	chr3	55986894	55987623	-	0.6	5.1	4.4E-07	2.3E-03
ENSMUSG000000023952	Gtpbp2	031	chr17	46302947	46303259	+	0.4	5.1	5.3E-07	2.7E-03
ENSMUSG000000042605	Atxn2	051	chr5	122261639	122261939	+	0.6	5.1	5.6E-07	2.8E-03
ENSMUSG000000003269	Cytl2	023	chr7	53068527	53069248	-	0.4	5.1	5.9E-07	2.9E-03
ENSMUSG000000022451	Twf1	001	chr15	944408382	94410096	-	0.2	5.2	6.1E-07	3.0E-03

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG000000072647 + ENSMUSG000000029454	Adam1a/Mapkapk5	002	chr5	121968622	121969392	-	0.4	5.1	6.9E-07	3.3E-03
ENSMUSG000000038664	Here1	095	chr9	66348328	66348982	+	-0.6	-5.0	7.3E-07	3.4E-03
ENSMUSG000000030082	Sec61a1	014	chr6	88463896	88464200	-	0.8	5.1	7.6E-07	3.5E-03
ENSMUSG000000032855	Pkd1	017	chr17	24709563	24711715	+	0.5	5.0	8.4E-07	3.8E-03
ENSMUSG000000040929	Rfx3	001	chr19	27836211	27840930	-	-0.3	-5.0	9.7E-07	4.3E-03
ENSMUSG000000038762	Abcf1	037	chr17	36105913	36106178	-	1.4	4.9	1.3E-06	5.6E-03
ENSMUSG000000023952	Gipbp2	044	chr17	46304840	46304970	+	0.4	4.9	1.3E-06	5.7E-03
ENSMUSG000000006676	Usp19	027	chr9	108403525	108404028	+	0.2	5.0	1.4E-06	5.8E-03
ENSMUSG000000078789 + ENSMUSG000000038268	Dph1/Ovca2	001	chr11	74989444	74991144	-	0.3	5.0	1.4E-06	5.8E-03
ENSMUSG000000040896	Kend3	009	chr3	105468465	105469879	+	1.0	5.0	1.4E-06	5.9E-03
ENSMUSG000000030207	8430419L09Rik	017	chr6	135182873	135183273	+	-0.5	-4.9	1.7E-06	6.9E-03
ENSMUSG000000029587	Zip12	004	chr5	143997458	143997932	+	1.0	5.0	1.7E-06	6.9E-03
ENSMUSG000000021097	Cimn	001	chr12	106001324	106010173	-	-0.2	-5.0	1.8E-06	7.0E-03
ENSMUSG000000015536	Mocs2	015	chr13	115615731	115616365	+	0.6	4.9	2.0E-06	7.8E-03
ENSMUSG000000045482	Trap	027	chr5	145557830	145558030	+	0.9	4.8	2.0E-06	7.8E-03
ENSMUSG000000085832	D430036J16Rik	004	chr9	81530442	81530544	+	-1.8	-5.1	2.1E-06	7.8E-03
ENSMUSG000000020612	Pkar1a	011	chr11	109522664	109523067	+	0.4	4.9	2.2E-06	8.2E-03
ENSMUSG000000053470	Kdm3a	017	chr6	71558999	71559041	-	2.5	4.8	2.6E-06	9.3E-03
ENSMUSG000000042042	Csgalnact2	007	chr6	118074432	118076139	-	1.2	4.9	2.8E-06	1.0E-02
ENSMUSG000000004070	Hmox2	004	chr16	4756845	4756902	+	1.1	4.9	2.8E-06	1.0E-02
ENSMUSG000000040479	Dgkz	011	chr2	91774090	91774212	-	0.5	4.7	3.1E-06	1.1E-02
ENSMUSG000000021327	Zkscan3	009	chr13	21481162	21485100	-	0.3	4.8	3.1E-06	1.1E-02
ENSMUSG000000055491	Ppre1	039	chr19	46146825	46147038	+	0.9	4.7	3.4E-06	1.2E-02
ENSMUSG000000074247	Dda1	013	chr8	73996515	73996681	+	0.7	4.8	3.6E-06	1.2E-02
ENSMUSG000000020654	Adcy3	032	chr12	4210892	4211481	+	0.5	4.7	3.6E-06	1.2E-02
ENSMUSG000000022565 + ENSMUSG000000063268	Plec/Parp10	003	chr15	76001406	6005809	-	-0.2	-4.7	3.7E-06	1.2E-02
ENSMUSG000000062296	Trank1	011	chr9	111267179	111270052	+	0.4	4.8	3.9E-06	1.3E-02
ENSMUSG000000057897	Camk2b	049	chr11	5965662	5965745	-	1.3	4.7	4.0E-06	1.3E-02
ENSMUSG000000050357	Rltpr	040	chr8	108219675	108220760	+	0.4	4.7	4.2E-06	1.3E-02
ENSMUSG000000000416	Cttnbp2	029	chr6	18381940	18383819	-	0.4	4.7	4.2E-06	1.3E-02

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG000000028161	Ppp3ca	029	chr3	136598744	136598841	+	0.6	4.7	4.4E-06	1.4E-02
ENSMUSG000000024826	Dpf2	011	chr19	5902769	5903332	-	0.4	4.7	4.4E-06	1.4E-02
ENSMUSG000000034171	Faah	014	chr4	115672694	115673391	-	0.3	4.7	4.6E-06	1.4E-02
ENSMUSG000000015869	Prpsap1	009	chr11	116338662	116339053	-	0.5	4.7	4.8E-06	1.4E-02
ENSMUSG000000053483	Usp21	037	chr1	173215746	173216480	-	0.4	4.6	4.8E-06	1.4E-02
ENSMUSG000000004947	Dlx2	015	chr5	136495428	136497624	+	0.9	4.7	5.0E-06	1.5E-02
ENSMUSG000000025155	Dus11	009	chr11	120651195	120651761	-	0.4	4.6	5.1E-06	1.5E-02
ENSMUSG000000006920	Ezh1	022	chr11	101068968	101069435	-	1.2	4.6	5.3E-06	1.5E-02
ENSMUSG000000004110	Cacna1e	001	chr1	156239649	156246065	-	-0.3	-4.6	5.5E-06	1.5E-02
ENSMUSG000000019254	Ppp1r12c	052	chr7	4453132	4453266	-	0.9	4.6	5.6E-06	1.5E-02
ENSMUSG000000068221 + ENSMUSG000000022436	Pdxp/Sh3bp1	031	chr15	78744349	78744961	+	0.3	4.6	5.6E-06	1.5E-02
ENSMUSG000000063077	Kif1b	004	chr4	148552981	148554344	-	-0.2	-4.6	5.6E-06	1.5E-02
ENSMUSG0000000074247	Dda1	012	chr8	73996275	73996514	+	0.7	4.7	5.7E-06	1.5E-02
ENSMUSG000000024012	Mitch1	030	chr17	29484705	29484849	-	0.7	4.6	5.7E-06	1.5E-02
ENSMUSG000000053141	Piprt	001	chr2	161347726	161352092	-	-0.3	-4.6	5.7E-06	1.5E-02
ENSMUSG000000039838	Slc45a1	002	chr4	150004156	150005026	-	0.4	4.8	5.7E-06	1.5E-02
ENSMUSG000000000441	Raf1	007	chr6	115570346	115571833	-	0.2	4.6	5.7E-06	1.5E-02
ENSMUSG000000054263	Lifr	025	chr15	7141744	7147489	+	-0.3	-4.6	5.9E-06	1.5E-02
ENSMUSG000000063160 + ENSMUSG000000003762	Numbl/Adck4	035	chr7	28046397	28047186	+	0.5	4.6	6.1E-06	1.6E-02
ENSMUSG000000038406	Scaf1	010	chr7	52266722	52267492	-	0.7	4.6	6.5E-06	1.6E-02
ENSMUSG000000020978	Klhdc2	002	chr12	70397709	70397741	+	0.8	4.6	6.8E-06	1.7E-02
ENSMUSG000000019877	Serinc1	001	chr10	57235580	57237098	-	0.1	4.6	7.3E-06	1.8E-02
ENSMUSG000000069045	Ddx3y	001	chrY	597158	599810	-	0.3	4.6	7.4E-06	1.8E-02
ENSMUSG000000027893	Alcyl1	007	chr3	107468310	107468433	-	0.8	4.6	7.4E-06	1.8E-02
ENSMUSG000000021830	Txndc16	017	chr14	45787030	45787898	-	1.7	4.5	7.5E-06	1.8E-02
ENSMUSG000000042726	Traf1d1	010	chr5	121825256	121825804	-	-0.4	-4.5	8.4E-06	2.0E-02
ENSMUSG000000052593	Adam17	007	chr12	21333841	21333900	-	2.5	4.5	9.0E-06	2.1E-02
ENSMUSG000000022199	Slc22a17	005	chr14	55526468	55526722	-	0.4	4.6	9.2E-06	2.2E-02
ENSMUSG000000060216	Arrb2	011	chr11	70249075	70249498	+	0.7	4.5	9.4E-06	2.2E-02
ENSMUSG000000027185	Nat10	027	chr2	103574683	103575022	-	0.8	4.5	9.4E-06	2.2E-02
ENSMUSG000000002280	Narf1	018	chr17	25917898	25918137	+	-0.5	-4.5	9.4E-06	2.2E-02

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG000000032540	Abhd5	002	chr9	122260848	122260957	+	-0.9	-4.7	9.8E-06	2.2E-02
ENSMUSG000000047342	Zip286	003	chr11	62591891	62593106	-	0.4	4.5	9.9E-06	2.2E-02
ENSMUSG000000038324	Trpc4ap	013	chr2	155464719	155465208	-	0.5	4.5	1.0E-05	2.3E-02
ENSMUSG000000063659	Zip238	002	chr1	179375952	179377219	+	0.4	5.1	1.0E-05	2.3E-02
ENSMUSG000000034739 + ENSMUSG000000079592	Mfrp/C1qmf5	030	chr9	43915789	43916054	+	-1.1	-4.5	1.0E-05	2.3E-02
ENSMUSG0000000223087	Cem4l	003	chr3	51044128	51051726	+	0.5	4.7	1.1E-05	2.3E-02
ENSMUSG000000029765	Pixna4	002	chr6	32095926	32100584	-	-0.2	-4.5	1.1E-05	2.4E-02
ENSMUSG000000040225	Prrc2c	029	chr1	164640414	164640960	-	0.5	4.5	1.1E-05	2.4E-02
ENSMUSG000000034675	Dbn1	011	chr13	55577678	55577992	-	0.3	4.5	1.1E-05	2.4E-02
ENSMUSG000000028782	Bai2	046	chr4	129698499	129698806	+	0.3	4.4	1.3E-05	2.7E-02
ENSMUSG000000039953	Cistm1	001	chr4	148960577	148960746	+	1.2	4.5	1.3E-05	2.7E-02
ENSMUSG000000061751	Kalrn	052	chr16	34152121	34152180	-	0.4	4.4	1.4E-05	2.9E-02
ENSMUSG000000033059	Pygb	019	chr2	150649343	150649711	+	0.9	4.4	1.4E-05	2.9E-02
ENSMUSG000000035847	Ids	002	chrX	67596247	67599848	-	0.2	4.5	1.4E-05	2.9E-02
ENSMUSG000000030603	Psmc4	021	chr7	28834222	28834719	-	0.5	4.5	1.4E-05	2.9E-02
ENSMUSG000000021196	Pfkfb	021	chr13	6594283	6595229	-	0.6	4.4	1.5E-05	3.0E-02
ENSMUSG000000040479	Dgkz	010	chr2	91774000	91774089	-	0.5	4.4	1.5E-05	3.1E-02
ENSMUSG000000029713 + ENSMUSG000000029711	Gnb2/Epo	041	chr5	137972128	137972202	-	0.4	4.4	1.6E-05	3.1E-02
ENSMUSG000000048148	Nwd1	031	chr8	75235492	75238645	+	-0.3	-4.4	1.6E-05	3.1E-02
ENSMUSG000000022514	Il1rap	028	chr16	26728315	26730203	+	-0.3	-4.4	1.7E-05	3.3E-02
ENSMUSG000000044783	Hjupr	023	chr1	90171673	90173793	-	0.5	4.4	1.7E-05	3.3E-02
ENSMUSG000000045482	Trap	013	chr5	145545127	145545215	+	1.3	4.3	1.7E-05	3.3E-02
ENSMUSG000000005378	Wbscr22	030	chr5	135537215	135537339	-	0.9	4.4	1.7E-05	3.3E-02
ENSMUSG000000084896 + ENSMUSG000000020883	Gm11632/Fbxl20	014	chr11	97956818	97958242	-	-0.6	-4.4	1.7E-05	3.3E-02
ENSMUSG000000052423	B4gal3	014	chr1	173201505	173201770	+	-0.8	-4.4	1.8E-05	3.4E-02
ENSMUSG000000031878	Nae1	009	chr8	107040890	107040949	-	1.0	4.3	1.8E-05	3.4E-02
ENSMUSG000000037996	Sic24a2	002	chr4	86629033	86637076	-	-0.2	-4.4	1.9E-05	3.5E-02
ENSMUSG000000028703	Lrrc4l	005	chr4	115751487	115751587	+	1.1	4.4	1.9E-05	3.5E-02
ENSMUSG000000060206	Zip462	005	chr4	55021187	55024237	+	0.4	4.4	1.9E-05	3.6E-02
ENSMUSG000000037017	Zscan21	015	chr5	138575442	138575442	+	2.3	4.4	2.0E-05	3.6E-02
ENSMUSG000000020716	Nf1	029	chr11	79258526	79258648	+	1.2	4.3	2.0E-05	3.6E-02

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG0000000031389 + ENSMUSG0000000031388 + ENSMUSG0000000031391	Arhgap4/Naa10/L1cam	132	chrX	71163408	71164840	-	0.4	4.3	2.1E-05	3.7E-02
ENSMUSG0000000032589	Bsn	010	chr9	108012745	108018857	-	0.4	4.4	2.1E-05	3.7E-02
ENSMUSG0000000091471 + ENSMUSG0000000025204 + ENSMUSG0000000051984	Gm20538/Ndubf8/Sec3lb	015	chr19	44599966	44600144	-	-2.8	-4.3	2.1E-05	3.7E-02
ENSMUSG0000000020894	Vamp2	013	chr11	68903553	68903678	+	0.5	4.4	2.1E-05	3.8E-02
ENSMUSG0000000001763	Tspan33	001	chr6	29644222	29644233	+	1.9	4.4	2.3E-05	4.0E-02
ENSMUSG0000000026596	Abl2	018	chr1	158572848	158579699	+	-0.3	-4.4	2.3E-05	4.0E-02
ENSMUSG0000000050875	A730017C20Rik	012	chr18	59232072	59234318	+	-0.6	-4.4	2.3E-05	4.0E-02
ENSMUSG0000000030082	Sec61a1	012	chr6	88462600	88463804	-	0.5	4.3	2.4E-05	4.2E-02
ENSMUSG0000000040447	Spns2	007	chr11	72266618	72267055	-	0.5	4.3	2.4E-05	4.2E-02
ENSMUSG0000000048078	Odz4	055	chr7	104057065	104059603	+	-0.2	-4.3	2.5E-05	4.2E-02
ENSMUSG0000000057236	Rbbp4	016	chr4	129002068	129005831	-	0.4	4.3	2.5E-05	4.2E-02
ENSMUSG0000000044308	Ubr3	054	chr2	69858185	69858507	+	-0.5	-4.3	2.5E-05	4.2E-02
ENSMUSG0000000040209	Zfp704	001	chr3	9427011	9438898	-	-0.4	-4.4	2.6E-05	4.3E-02
ENSMUSG0000000023026	Dip2b	023	chr15	100011740	100011867	+	0.6	4.2	2.8E-05	4.6E-02
ENSMUSG0000000056602	Fry	027	chr5	151198318	151198442	+	0.5	4.2	2.8E-05	4.7E-02
ENSMUSG0000000051306	Usp42	023	chr5	144483224	144483814	-	1.8	4.3	2.9E-05	4.7E-02
ENSMUSG0000000035027	Map2k2	009	chr10	80581357	80581721	+	-0.9	-4.3	2.9E-05	4.7E-02
ENSMUSG0000000007850	Hnrnp1	046	chr11	50199824	50199891	+	0.6	4.2	2.9E-05	4.7E-02
ENSMUSG0000000029578	Wipi2	016	chr5	143140444	143140598	+	0.7	4.3	3.0E-05	4.8E-02
ENSMUSG0000000027797	Dcl1	009	chr3	55270495	55275239	+	0.3	4.3	3.0E-05	4.8E-02
ENSMUSG0000000028943	Espn	001	chr4	151494440	151494444	-	0.8	4.2	3.0E-05	4.8E-02
ENSMUSG0000000042625	Satb2	026	chr17	56708446	56708857	-	0.4	4.2	3.1E-05	4.8E-02
ENSMUSG0000000058624	Gda	010	chr19	21493215	21493863	-	1.6	4.3	3.1E-05	4.9E-02

Table 2

List of bins showing differential expression 30 min after memory retrieval. Each differential bin contains the chromosome, start position, and end position for easy reference.

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG00000029657	Hsph1	012	chr5	150423259	150426039	-	1.2	12.8	1.7E-29	4.7E-24
ENSMUSG000000031167	Rbm3	002	chrX	7717909	7717909	-	1.2	11.8	3.5E-26	4.6E-21
ENSMUSG000000007617	Homert1	018	chr13	94136356	94137083	+	1.5	10.5	1.6E-21	1.4E-16
ENSMUSG000000039801	2410089E03Rik	053	chr15	8201065	8202148	+	-1.0	-9.2	1.1E-18	7.3E-14
ENSMUSG000000041879	Ipo9	036	chr1	137302594	137303043	-	-1.1	-9.0	6.4E-18	3.4E-13
ENSMUSG000000034083	C130022K22Rik	009	chr6	91835401	91838063	+	1.1	9.1	1.2E-16	5.5E-12
ENSMUSG000000027523	Gnas	027	chr2	174155788	174155935	+	1.3	8.2	3.8E-15	1.4E-10
ENSMUSG000000034656	Caenala	068	chr8	87163334	87163334	+	1.7	7.9	1.2E-14	4.0E-10
ENSMUSG000000057897	Camk2b	049	chr11	5965662	5965745	-	2.2	7.6	1.9E-13	5.6E-09
ENSMUSG000000035206	3110056O03Rik	016	chr10	80329406	80330144	+	0.5	8.0	2.4E-13	6.5E-09
ENSMUSG000000035640	Dos	014	chr10	79598293	79598333	-	2.1	7.6	2.8E-13	6.8E-09
ENSMUSG000000039953	Clstml	001	chr4	148960577	148960746	+	1.9	7.5	1.6E-12	3.6E-08
ENSMUSG000000008153	Clstm3	004	chr6	124383426	124383521	-	1.1	7.4	2.0E-12	4.0E-08
ENSMUSG00000075876 + ENSMUSG00000064791 + ENSMUSG00000075924 + ENSMUSG00000015656	Snord14c/ Snord14e/ Snord14d/Hspa8	038	chr9	40612831	40612920	+	1.6	7.1	6.7E-12	1.3E-07
ENSMUSG000000031167	Rbm3	022	chrX	7721600	7721698	-	-0.8	-7.1	8.5E-12	1.5E-07
ENSMUSG000000057421	Las1l	015	chrX	93143543	93144773	-	-1.0	-7.1	1.1E-11	1.8E-07
ENSMUSG000000036052	Dnajb5	011	chr4	42963816	42965965	+	0.4	7.3	1.1E-11	1.8E-07
ENSMUSG000000031878	Nae1	015	chr8	107042164	107043101	-	1.2	6.9	1.7E-11	2.5E-07
ENSMUSG000000022199	Slc22a17	005	chr14	55526468	55526722	-	0.5	7.1	4.1E-11	5.8E-07
ENSMUSG00000075876 + ENSMUSG00000064791 + ENSMUSG00000075924 + ENSMUSG00000015656	Snord14c/ Snord14e/ Snord14d/Hspa8	037	chr9	40612779	40612830	+	1.4	6.7	9.5E-11	1.3E-06
ENSMUSG00000075003 + ENSMUSG000000037876	Jmjd1c/Jmjd1c	041	chr10	66707622	66708166	+	0.9	6.6	1.1E-10	1.3E-06
ENSMUSG000000031167	Rbm3	003	chrX	7717910	7718334	-	1.1	6.7	1.5E-10	1.9E-06
ENSMUSG000000023965	Fbxl17	017	chr17	63848374	63849366	-	0.5	6.8	1.9E-10	2.2E-06
ENSMUSG000000028826	Tmem57	002	chr4	134360480	134362431	-	-0.5	-6.6	3.8E-10	4.2E-06
ENSMUSG000000038664	Herc1	093	chr9	66346564	66348060	+	-0.7	-6.3	4.3E-10	4.6E-06

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG00000019254	Ppp1r12c	052	chr7	4453132	4453266	-	1.1	6.4	5.3E-10	5.4E-06
ENSMUSG00000028797 + ENSMUSG000000086797	2510006D16Rik/ Gm12965	034	chr4	129284424	129284574	+	1.1	6.3	7.6E-10	7.5E-06
ENSMUSG00000028782	Bai2	001	chr4	129662114	129662407	+	0.6	6.3	8.8E-10	8.4E-06
ENSMUSG00000024012	Mitch1	030	chr17	29484705	29484849	-	0.8	6.3	1.2E-09	1.1E-05
ENSMUSG00000024576	Csnk1a1	028	chr18	61745286	61746152	+	0.5	6.3	1.4E-09	1.2E-05
ENSMUSG00000027569	1600027N09Rik	010	chr2	180318228	180319110	+	0.5	6.5	1.4E-09	1.2E-05
ENSMUSG00000031660	Brd7	032	chr8	90885914	90886093	-	1.1	6.3	1.5E-09	1.3E-05
ENSMUSG00000046667	Rbm12b	012	chr4	12072176	12073847	+	0.8	6.5	1.6E-09	1.3E-05
ENSMUSG00000024392	Bag6	032	chr17	35277897	35278103	+	0.8	6.1	2.0E-09	1.5E-05
ENSMUSG00000052423	B4gal13	014	chr1	173201505	173201770	+	-1.0	-6.2	2.0E-09	1.5E-05
ENSMUSG00000019854	Reps1	001	chr10	17775667	17775711	+	1.1	6.1	2.5E-09	1.8E-05
ENSMUSG00000061887	Ssbp3	003	chr4	106584116	106584137	+	1.8	6.1	2.7E-09	2.0E-05
ENSMUSG00000074247	Dda1	012	chr8	73996275	73996514	+	0.9	6.3	2.9E-09	2.0E-05
ENSMUSG00000056413	Adap1	022	chr5	139801419	139801576	-	1.8	6.2	3.2E-09	2.2E-05
ENSMUSG00000026090	2010300C02Rik	018	chr1	37776641	37776930	-	1.5	6.3	3.4E-09	2.3E-05
ENSMUSG00000007617	Homer1	017	chr13	94136233	94136355	+	1.4	6.0	5.7E-09	3.7E-05
ENSMUSG00000037266	D4Wsu53e	022	chr4	134481737	134481940	+	-0.4	-6.0	5.9E-09	3.8E-05
ENSMUSG00000037266	D4Wsu53e	024	chr4	134482066	134482649	+	-0.4	-6.0	6.1E-09	3.8E-05
ENSMUSG00000037098	Rab11fip3	027	chr17	26206181	26206354	-	0.9	6.0	6.7E-09	4.1E-05
ENSMUSG00000043872	Znmy1	001	chr4	126724338	126724885	-	0.9	6.1	7.1E-09	4.2E-05
ENSMUSG00000024826	Dpf2	011	chr19	5902769	5903332	-	0.5	6.0	8.4E-09	4.9E-05
ENSMUSG00000025372	Baiap2	027	chr11	119867673	119868096	+	0.3	6.0	8.6E-09	4.9E-05
ENSMUSG00000037266	D4Wsu53e	021	chr4	134481701	134481736	+	-0.5	-5.9	1.1E-08	6.3E-05
ENSMUSG00000013033	Lphn1	001	chr8	86424004	86424471	+	0.8	5.8	1.3E-08	7.3E-05
ENSMUSG00000040479	Dgkz	011	chr2	91774090	91774212	-	0.6	5.8	1.4E-08	7.5E-05
ENSMUSG00000027893	Ahcy11	007	chr3	107468310	107468433	-	1.0	5.8	1.7E-08	9.0E-05
ENSMUSG00000001729	Akt1	034	chr12	113912418	113912487	-	1.4	5.8	1.8E-08	9.3E-05
ENSMUSG00000037266	D4Wsu53e	020	chr4	134481692	134481700	+	-0.5	-5.8	2.0E-08	1.0E-04
ENSMUSG00000031167	Rbm3	021	chrX	7721572	7721599	-	-0.8	-5.8	2.1E-08	1.0E-04
ENSMUSG00000055491	Pprc1	039	chr19	46146825	46147038	+	1.0	5.7	2.2E-08	1.1E-04

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG000000021327	Zkscan3	009	chr13	21481162	21485100	-	0.4	5.8	2.2E-08	1.1E-04
ENSMUSG000000021262	Evl	001	chr12	109792930	109793423	+	0.5	5.9	2.3E-08	1.1E-04
ENSMUSG000000015869	Prpsap1	009	chr11	116338662	116339053	-	0.6	5.8	2.5E-08	1.1E-04
ENSMUSG000000014873	Surf2	009	chr2	26773052	26774384	+	0.3	5.8	2.5E-08	1.1E-04
ENSMUSG000000038383	Pigu	004	chr2	155104386	155108131	-	0.4	5.8	2.8E-08	1.3E-04
ENSMUSG000000022514	Il1rap	028	chr16	26728315	26730203	+	-0.4	-5.7	3.0E-08	1.3E-04
ENSMUSG000000004929	Thop1	013	chr10	80541613	80542202	+	0.6	5.8	3.2E-08	1.4E-04
ENSMUSG000000021040	1810035L17Rik	009	chr12	88790351	88790753	+	0.6	5.9	3.3E-08	1.4E-04
ENSMUSG000000023353	Agap3	002	chr5	23958025	23958073	+	1.8	5.7	3.3E-08	1.4E-04
ENSMUSG000000050875	A730017C20Rik	012	chr18	59232072	59234318	+	-0.7	-5.8	3.4E-08	1.4E-04
ENSMUSG000000001729	Akt1	033	chr12	113912211	113912417	-	0.7	5.7	3.6E-08	1.4E-04
ENSMUSG000000093290 + ENSMUSG0000000035632	Mir3572/Cnot3	026	chr7	3610347	3610426	+	0.6	5.7	3.7E-08	1.5E-04
ENSMUSG000000009073	Nf2	014	chr11	4684567	4685110	-	0.9	5.6	3.8E-08	1.5E-04
ENSMUSG000000084708 + ENSMUSG000000065862 + ENSMUSG000000059796	/Eif4a1	040	chr11	69485107	69485232	-	0.8	5.6	4.0E-08	1.5E-04
ENSMUSG000000037266	D4Wau53e	019	chr4	134481361	134481691	+	-0.4	-5.7	4.0E-08	1.5E-04
ENSMUSG000000015536	Mocs2	015	chr13	115615731	115616365	+	0.6	5.7	4.7E-08	1.8E-04
ENSMUSG000000034675	Dbn1	011	chr13	55577678	55577992	-	0.3	5.6	4.8E-08	1.8E-04
ENSMUSG000000003269	Cytb2	023	chr7	53068527	53069248	-	0.4	5.6	5.0E-08	1.8E-04
ENSMUSG000000031065	Cdk16	027	chrX	20274091	20274245	+	0.5	5.6	5.6E-08	2.0E-04
ENSMUSG000000025499	Hras1	021	chr7	148379860	148379893	-	3.4	5.6	5.9E-08	2.1E-04
ENSMUSG000000080683 + ENSMUSG0000000087376 + ENSMUSG000000080352 + ENSMUSG000000045411	/Gm15517//2410002F23Rik	030	chr7	51503682	51504911	+	0.4	5.5	7.4E-08	2.6E-04
ENSMUSG000000009549	Srp14	005	chr2	118304301	118304567	-	0.8	5.7	8.4E-08	2.9E-04
ENSMUSG000000031392 + ENSMUSG000000076127 + ENSMUSG000000092907	Irak1/Mir718/Mir5132	056	chrX	71269148	71269165	-	1.7	5.4	8.6E-08	2.9E-04
ENSMUSG000000078789 + ENSMUSG000000038268	Dphi/Ovca2	001	chr11	74989444	74991144	-	0.3	5.5	1.1E-07	3.6E-04
ENSMUSG000000031660	Brd7	031	chr8	90885805	90885913	-	0.7	5.4	1.2E-07	3.9E-04
ENSMUSG000000020923	Ubf1	012	chr11	102169844	102170012	-	1.3	5.4	1.2E-07	4.1E-04
ENSMUSG000000032047	Acat1	004	chr9	53391700	53391862	-	0.7	5.6	1.3E-07	4.2E-04
ENSMUSG000000003345	Csnk1g2	001	chr10	80085525	80085695	+	0.6	5.5	1.3E-07	4.3E-04

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG000000072770 + ENSMUSG000000030330	Acrbp/Ing4	042	chr6	125003508	125003819	+	0.5	5.4	1.4E-07	4.4E-04
ENSMUSG000000028796	Phc2	020	chr4	128404926	128404953	+	2.3	5.4	1.4E-07	4.4E-04
ENSMUSG000000002393	Nr2f6	023	chr8	73905806	73905859	-	1.7	5.5	1.5E-07	4.6E-04
ENSMUSG000000037266	D4Wau53e	023	chr4	134481941	134482065	+	-0.4	-5.4	1.5E-07	4.6E-04
ENSMUSG000000006575	Rundc3a	019	chr11	102261951	102261974	+	0.4	5.4	1.6E-07	4.9E-04
ENSMUSG000000092679 + ENSMUSG000000026872	Mir129/Zeb2	001	chr2	44839154	44842640	-	-0.2	-5.4	1.8E-07	5.3E-04
ENSMUSG000000001211	Agpat3	029	chr10	77814958	77815187	-	0.5	5.4	1.8E-07	5.4E-04
ENSMUSG00000016933	Pleg1	004	chr2	160557454	160557468	+	0.9	5.3	2.0E-07	5.9E-04
ENSMUSG000000042625	Safb2	026	chr17	56708446	56708857	-	0.4	5.3	2.1E-07	6.2E-04
ENSMUSG000000027546	Aip9a	040	chr2	168567301	168567462	-	0.7	5.3	2.6E-07	7.4E-04
ENSMUSG000000027367	Stard7	014	chr2	127115811	127116507	+	0.5	5.3	2.8E-07	7.9E-04
ENSMUSG000000038644	Pold1	018	chr7	51789560	51789754	-	1.7	5.2	2.8E-07	7.9E-04
ENSMUSG000000002812	Flii	019	chr11	60532729	60533194	-	0.5	5.2	3.1E-07	8.5E-04
ENSMUSG000000042605	Auxn2	051	chr5	122261639	122261939	+	0.6	5.2	3.1E-07	8.6E-04
ENSMUSG000000040479	Dgkz	054	chr2	91803443	91803814	-	0.3	5.2	3.2E-07	8.8E-04
ENSMUSG000000059995	Atnx7f3	020	chr11	102157717	102157943	-	0.7	5.3	3.3E-07	8.9E-04
ENSMUSG000000092870 + ENSMUSG000000020349	Mir3061/Ppp2ca	001	chr11	51912183	51912652	+	0.9	5.5	3.3E-07	8.9E-04
ENSMUSG000000027303	Ptpnra	001	chr2	130276014	130276279	+	0.6	5.3	3.5E-07	9.2E-04
ENSMUSG000000023353	Agap3	001	chr5	23957995	23958024	+	1.6	5.3	3.6E-07	9.4E-04
ENSMUSG000000028484	Psp1	026	chr4	83132179	83132357	-	0.5	5.2	3.9E-07	1.0E-03
ENSMUSG000000033423	Eri3	004	chr4	117223367	117225214	+	-0.5	-5.2	4.3E-07	1.1E-03
ENSMUSG000000026277	Stk25	009	chr1	95522184	95522357	-	0.3	5.2	4.7E-07	1.2E-03
ENSMUSG000000037907	Ankrd13b	036	chr11	77303169	77303180	-	2.3	5.1	4.8E-07	1.2E-03
ENSMUSG000000038664	Herc1	095	chr9	66348328	66348982	+	-0.5	-5.0	5.6E-07	1.4E-03
ENSMUSG000000034254	Agpat1	012	chr17	34747951	34748122	+	0.4	5.1	5.8E-07	1.4E-03
ENSMUSG000000040479	Dgkz	010	chr2	91774000	91774089	-	0.5	5.1	5.8E-07	1.4E-03
ENSMUSG000000024858	Adrbk1	046	chr19	4306215	4306222	-	1.6	5.1	5.9E-07	1.4E-03
ENSMUSG000000004929	Thop1	012	chr10	80541376	80541500	+	0.8	5.2	5.9E-07	1.4E-03
ENSMUSG000000084708 + ENSMUSG000000065862 + ENSMUSG000000059796	//Eif4a1	037	chr11	69484479	69484603	-	0.5	5.1	6.1E-07	1.5E-03
ENSMUSG000000038324	Trpc4ap	013	chr2	155464719	155465208	-	0.5	5.1	6.6E-07	1.6E-03

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG00000038546	Ranbp9	018	chr13	43576298	43576342	-	1.6	5.2	7.1E-07	1.7E-03
ENSMUSG00000025499	Hras1	020	chr7	148379782	148379859	-	1.0	5.1	7.3E-07	1.7E-03
ENSMUSG00000034730 + ENSMUSG000000093340	Bai1/	020	chr15	74394251	74394282	+	0.8	5.0	7.6E-07	1.7E-03
ENSMUSG00000068267 + ENSMUSG000000027329	Cenpb/Spef1	018	chr2	131005613	131005803	-	0.9	5.1	7.6E-07	1.7E-03
ENSMUSG00000029571	Tmem106b	020	chr6	13034188	13039269	+	0.2	5.1	7.7E-07	1.7E-03
ENSMUSG00000025964	Adam23	005	chr1	63492509	63492986	+	0.5	5.0	8.2E-07	1.8E-03
ENSMUSG00000025372	Baiap2	026	chr11	119864352	119864399	+	0.4	5.1	8.2E-07	1.8E-03
ENSMUSG00000020894	Vamp2	013	chr11	68903553	68903678	+	0.5	5.1	8.6E-07	1.9E-03
ENSMUSG00000031065	Cdk16	003	chrX	20265544	20265932	+	0.2	5.0	8.6E-07	1.9E-03
ENSMUSG00000036555	Iqce	001	chr5	141137781	141139458	-	0.5	5.0	9.1E-07	2.0E-03
ENSMUSG00000016503	Gtf3a	004	chr5	147761583	147762108	+	0.5	5.1	9.1E-07	2.0E-03
ENSMUSG00000001366	Fbxo9	006	chr9	77933505	77933713	-	0.7	5.1	9.3E-07	2.0E-03
ENSMUSG00000037098	Rab11fip3	026	chr17	26206123	26206180	-	0.7	5.0	9.3E-07	2.0E-03
ENSMUSG00000004071	5730403B10Rik	008	chr16	4769309	4769639	-	-0.4	-5.1	9.4E-07	2.0E-03
ENSMUSG00000020612	Prkar1a	011	chr11	109522664	109523067	+	0.3	5.1	9.8E-07	2.0E-03
ENSMUSG00000018861	Fdxd	018	chr11	115137497	115138038	-	0.6	5.1	9.9E-07	2.1E-03
ENSMUSG00000034730 + ENSMUSG000000093340	Bai1/	021	chr15	74394283	74394341	+	0.7	5.0	1.0E-06	2.1E-03
ENSMUSG00000024533	Spir1	022	chr18	67770059	67770443	-	0.7	5.1	1.0E-06	2.1E-03
ENSMUSG00000024576	Csnk1a1	027	chr18	61744853	61745285	+	0.5	5.0	1.1E-06	2.1E-03
ENSMUSG00000028412	Slc44a1	001	chr4	53453285	53453542	+	0.9	5.0	1.1E-06	2.3E-03
ENSMUSG00000026074	Map4k4	001	chr1	39957758	39958024	+	0.7	5.0	1.1E-06	2.3E-03
ENSMUSG00000026977	March7	022	chr2	60083318	60085399	+	0.4	5.0	1.1E-06	2.3E-03
ENSMUSG00000002949	Timm44	019	chr8	4267402	4267540	-	-0.6	-5.0	1.2E-06	2.4E-03
ENSMUSG00000027634	Ndrp3	005	chr2	156756888	156756951	-	1.0	4.9	1.2E-06	2.4E-03
ENSMUSG000000074247	Dda1	011	chr8	73996146	73996274	+	0.8	5.1	1.3E-06	2.5E-03
ENSMUSG00000024392	Bag6	033	chr17	35278104	35278338	+	0.7	4.9	1.4E-06	2.7E-03
ENSMUSG00000057522	Spop	019	chr11	95346773	95346850	+	-1.2	-5.0	1.4E-06	2.7E-03
ENSMUSG000000022771	Ppil2	003	chr16	17087409	17088082	-	0.4	4.9	1.6E-06	2.9E-03
ENSMUSG00000035202	Lars2	021	chr9	123370617	123371782	+	-0.6	-5.0	1.6E-06	2.9E-03
ENSMUSG00000052423	B4gal3	015	chr1	173201771	173201773	+	-1.3	-4.9	1.6E-06	3.0E-03
ENSMUSG00000016346	Kcnq2	047	chr2	180869912	180869948	-	1.4	4.9	1.8E-06	3.3E-03

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ENSMUSG00000020402	Ydac1	013	chr11	52199869	52199973	+	-0.6	-4.9	1.8E-06	3.3E-03
ENSMUSG00000003279	Dlgap1	004	chr17	70318713	70318741	+	0.7	4.8	1.8E-06	3.4E-03
ENSMUSG00000018040	Rip7a	009	chr15	82948605	82948776	-	0.7	5.0	1.9E-06	3.4E-03
ENSMUSG00000042042	Csgalact2	007	chr6	118074432	118076139	-	1.2	5.0	2.0E-06	3.5E-03
ENSMUSG00000030189	Csda	018	chr6	131338232	131338468	-	1.2	4.9	2.0E-06	3.6E-03
ENSMUSG00000026918	Brd3	013	chr2	27308971	27309832	-	-1.2	-4.8	2.0E-06	3.6E-03
ENSMUSG00000021830	Txndc16	017	chr14	45787030	45787898	-	1.7	4.8	2.1E-06	3.7E-03
ENSMUSG00000065452 + ENSMUSG00000028410	Mir207/Dnaj1	027	chr4	40678833	40679108	+	0.5	4.9	2.1E-06	3.7E-03
ENSMUSG00000059552	Trp53	018	chr11	69403365	69404007	+	0.7	4.9	2.2E-06	3.8E-03
ENSMUSG00000037058	Paip2	010	chr18	35769938	35770524	+	0.3	4.9	2.2E-06	3.8E-03
ENSMUSG00000068221 + ENSMUSG00000022436	Pdxp/Sh3bp1	031	chr15	78744349	78744961	+	0.3	4.8	2.2E-06	3.8E-03
ENSMUSG00000028796	Phc2	019	chr4	128404829	128404925	+	2.0	4.8	2.3E-06	3.9E-03
ENSMUSG00000039219	Arid4b	042	chr13	14283524	14284215	+	-0.8	-4.8	2.3E-06	3.9E-03
ENSMUSG00000027655	Dhx35	035	chr2	158676365	158676477	+	1.4	4.8	2.3E-06	3.9E-03
ENSMUSG00000024163 + ENSMUSG00000073436	Mapk8ip3/Eme2	062	chr17	25038763	25039222	-	0.3	4.7	2.4E-06	4.0E-03
ENSMUSG00000039470	Zdhhc2	004	chr8	41509194	41509212	+	1.5	4.8	2.4E-06	4.0E-03
ENSMUSG00000068921	Dap3	001	chr3	88724725	88727556	-	-0.3	-4.8	2.4E-06	4.0E-03
ENSMUSG00000042605	Axn2	002	chr5	122161618	122162285	+	0.7	4.8	2.4E-06	4.0E-03
ENSMUSG00000006024	Napa	016	chr7	16698993	16699469	+	0.3	4.8	2.5E-06	4.1E-03
ENSMUSG00000066900	Suds3	014	chr5	117565681	117566002	-	0.3	4.9	2.6E-06	4.2E-03
ENSMUSG00000050530	Fam171a1	002	chr2	3035654	3035684	+	2.0	4.9	2.6E-06	4.2E-03
ENSMUSG00000038291	Snx25	029	chr8	47237136	47237511	-	1.9	4.8	2.8E-06	4.5E-03
ENSMUSG00000039108	Lsm14b	001	chr2	179759692	179760017	+	0.5	4.9	2.8E-06	4.5E-03
ENSMUSG00000084896 + ENSMUSG00000020883	Gm11632/Fbxl20	014	chr11	97956818	97958242	-	-0.6	-4.8	2.9E-06	4.7E-03
ENSMUSG00000017412	Cacnb4	001	chr2	52283845	52290269	-	0.3	4.8	3.0E-06	4.8E-03
ENSMUSG00000002984	Tomn40	008	chr7	20288492	20288617	-	0.6	4.8	3.2E-06	5.0E-03
ENSMUSG00000039759	Thap3	004	chr4	151359568	151359777	-	-0.5	-5.0	3.3E-06	5.2E-03
ENSMUSG00000038822	Hacel	010	chr10	45325391	45325393	+	2.1	4.7	3.4E-06	5.3E-03
ENSMUSG00000052373	Mpp3	012	chr11	101870999	101871520	-	0.7	4.7	3.4E-06	5.3E-03
ENSMUSG00000084708 + ENSMUSG00000065862 + ENSMUSG00000059796	//Eif4a1	038	chr11	69484604	69484724	-	0.5	4.7	3.4E-06	5.3E-03

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ENSMUSG00000025155	Dus11	009	chr11	120651195	120651761	-	0.4	4.7	3.5E-06	5.3E-03
ENSMUSG00000036545	Adams2	028	chr11	50617071	50621075	+	-0.8	-4.8	3.5E-06	5.3E-03
ENSMUSG00000038429	Usp5	025	chr6	124772861	124773037	-	0.7	4.7	3.5E-06	5.3E-03
ENSMUSG00000061887	Ssbp3	002	chr4	106584075	106584115	+	1.9	4.7	3.7E-06	5.6E-03
ENSMUSG00000084708 + ENSMUSG00000065862 + ENSMUSG00000059796	//Eif4a1	039	chr11	69484725	69484952	-	0.5	4.7	3.8E-06	5.6E-03
ENSMUSG00000021087	Rtn1	003	chr12	73313276	73313276	-	-0.2	-4.8	3.8E-06	5.6E-03
ENSMUSG00000024012	Mtch1	029	chr17	29484412	29484704	-	0.3	4.7	3.8E-06	5.6E-03
ENSMUSG00000026885	Tull1	024	chr2	35835145	35835286	-	0.6	4.7	3.9E-06	5.6E-03
ENSMUSG00000040896	Kend3	009	chr3	105468465	105469879	+	0.9	4.8	3.9E-06	5.6E-03
ENSMUSG00000040859	Bsdcl	017	chr4	129146293	129147418	+	0.7	4.7	3.9E-06	5.7E-03
ENSMUSG00000028063	Lmna	005	chr3	88286535	88286786	-	0.6	4.7	4.0E-06	5.7E-03
ENSMUSG00000053046 + ENSMUSG000000092652	Brsk2/Mir3104	002	chr7	149135751	149135911	+	0.9	4.7	4.0E-06	5.7E-03
ENSMUSG00000032997 + ENSMUSG00000026211	Chpf/Obsl1	060	chr1	75499791	75499941	-	-2.6	-4.7	4.0E-06	5.8E-03
ENSMUSG00000023952	Gtpbp2	035	chr17	46303816	46303936	+	0.7	4.7	4.2E-06	6.0E-03
ENSMUSG00000050989	Sepr1	019	chr4	134107852	134108081	-	1.2	4.8	4.3E-06	6.1E-03
ENSMUSG00000027223	Mapk8ip1	018	chr2	92241186	92241420	-	0.4	4.8	4.3E-06	6.1E-03
ENSMUSG00000031167	Rbm3	005	chrX	7719487	7719493	-	1.7	4.7	4.4E-06	6.1E-03
ENSMUSG00000047617	BC029214	024	chr2	25316142	25316174	-	-0.7	-4.7	4.4E-06	6.1E-03
ENSMUSG00000030447	Cytip1	051	chr7	63185842	63185868	+	-0.8	-4.6	4.5E-06	6.3E-03
ENSMUSG00000013593	Ndufr2	015	chr1	173170159	173170186	-	0.8	4.7	4.7E-06	6.4E-03
ENSMUSG00000000441	Raf1	007	chr6	115570346	115571833	-	0.2	4.7	4.7E-06	6.5E-03
ENSMUSG00000027001 + ENSMUSG00000026999	Dusp19/Nup35	032	chr2	80496235	80497345	+	-0.9	-4.7	5.0E-06	6.7E-03
ENSMUSG00000038822	Hacel	034	chr10	45420831	45429686	+	-0.3	-4.6	5.0E-06	6.7E-03
ENSMUSG00000073174 + ENSMUSG00000040003	Magi2/Magi2	030	chr5	20208194	20208297	+	0.8	4.7	5.0E-06	6.7E-03
ENSMUSG00000025487	Psmcl3	024	chr7	148076311	148076393	+	0.8	4.6	5.0E-06	6.7E-03
ENSMUSG00000036067	Slc2a6	009	chr2	26879856	26880104	-	-0.6	-4.7	5.1E-06	6.8E-03
ENSMUSG00000057236	Rbbp4	016	chr4	129002068	129005831	-	0.5	4.7	5.1E-06	6.8E-03
ENSMUSG00000031511	Arhgef7	028	chr8	11830238	11831492	+	0.3	4.7	5.1E-06	6.8E-03
ENSMUSG00000030207	8430419L09Rik	017	chr6	135182873	135183273	+	-0.4	-4.7	5.2E-06	6.8E-03
ENSMUSG00000026977	March7	025	chr2	60085570	60085946	+	0.6	4.7	5.3E-06	6.9E-03

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ENSMUSG00000028782	Bai2	046	chr4	129698499	129698806	+	0.3	4.6	5.4E-06	7.1E-03
ENSMUSG00000021772	Nkiras1	014	chr14	19109961	19110079	+	0.7	4.7	5.5E-06	7.1E-03
ENSMUSG00000027674	Pex5l	032	chr3	33042005	33042169	-	0.7	4.6	5.5E-06	7.1E-03
ENSMUSG00000074886	Grk6	001	chr13	55546695	55546921	+	0.5	4.7	5.5E-06	7.1E-03
ENSMUSG00000031392 + ENSMUSG00000076127 + ENSMUSG00000092907	Irak1/Mir718/Mir5132	057	chrX	71269166	71269170	-	1.9	4.6	5.6E-06	7.2E-03
ENSMUSG00000025134	Alyref	011	chr11	120459546	120459679	-	1.4	4.8	5.6E-06	7.2E-03
ENSMUSG00000023952	Gpbbp2	036	chr17	46303937	46304171	+	0.5	4.6	5.7E-06	7.2E-03
ENSMUSG00000024392	Bag6	034	chr17	35278339	35278370	+	0.8	4.6	5.7E-06	7.2E-03
ENSMUSG00000005469	Prkaca	001	chr8	86496877	86497131	+	0.5	4.8	5.9E-06	7.3E-03
ENSMUSG00000031167	Rbm3	004	chrX	7719485	7719486	-	1.7	4.6	5.9E-06	7.3E-03
ENSMUSG00000031878	Nae1	008	chr8	107040635	107040889	-	0.7	4.6	6.1E-06	7.6E-03
ENSMUSG00000008348	Ubc	003	chr5	125866669	125866896	-	-0.3	-4.8	6.1E-06	7.6E-03
ENSMUSG00000022514	Illrap	019	chr16	26722520	26723017	+	0.3	4.6	6.1E-06	7.6E-03
ENSMUSG00000001847	Rac1	011	chr5	144288631	144288861	-	0.5	4.7	6.3E-06	7.7E-03
ENSMUSG00000038244	Mical2	037	chr7	119497490	119498460	+	0.2	4.6	6.4E-06	7.8E-03
ENSMUSG00000027429	Sec23b	030	chr2	144405140	144406851	+	0.7	4.6	6.5E-06	7.9E-03
ENSMUSG00000042726	Traf1d1	024	chr5	121835049	121835317	-	0.6	4.6	6.7E-06	8.1E-03
ENSMUSG00000092367 + ENSMUSG00000011751 + ENSMUSG00000089832	Gm20479/Spnb4/Shkbp1	007	chr7	28127780	28127940	-	0.4	4.5	6.8E-06	8.1E-03
ENSMUSG00000003808	Farsa	027	chr8	87391986	87392122	+	0.4	4.6	6.8E-06	8.1E-03
ENSMUSG00000049327	Setd8	006	chr5	124895592	124895672	+	1.4	4.6	6.8E-06	8.1E-03
ENSMUSG00000006392	Med8	007	chr4	118082953	118083489	+	0.6	4.6	6.8E-06	8.1E-03
ENSMUSG00000031167	Rbm3	006	chrX	7719494	7719666	-	1.7	4.6	7.6E-06	8.9E-03
ENSMUSG00000033184 + ENSMUSG00000056130	Tmed7/Ticam2	012	chr18	46756969	46757170	-	0.6	4.7	7.9E-06	9.2E-03
ENSMUSG00000032301	Psm4	007	chr9	54799151	54799235	+	-0.8	-4.6	7.9E-06	9.3E-03
ENSMUSG0000007670	Khsrp	026	chr17	57170571	57170930	-	0.5	4.6	8.2E-06	9.5E-03
ENSMUSG00000034064	Poglut1	008	chr16	38531927	38532578	-	0.5	4.6	8.2E-06	9.6E-03
ENSMUSG00000022514	Illrap	020	chr16	26723018	26723306	+	0.5	4.5	8.6E-06	9.9E-03
ENSMUSG00000047617	BC029214	023	chr2	25316015	25316141	-	-0.5	-4.5	8.7E-06	1.0E-02
ENSMUSG00000026209	Dnpep	004	chr1	75305285	75305873	-	0.4	4.6	8.7E-06	1.0E-02
ENSMUSG00000029047	Pex10	012	chr4	154443226	154444495	+	0.6	4.6	9.0E-06	1.0E-02

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ENSMUSG00000026103	Gls	052	chr1	52289656	52290067	-	0.4	4.5	9.1E-06	1.0E-02
ENSMUSG00000006958	Chrd	016	chr16	20736516	20736981	+	-0.4	-4.5	9.1E-06	1.0E-02
ENSMUSG00000023952	Gipbp2	031	chr17	46302947	46303259	+	0.4	4.5	9.2E-06	1.0E-02
ENSMUSG00000020376	Rnf130	001	chr11	49838848	49838849	+	2.8	4.6	9.4E-06	1.1E-02
ENSMUSG00000022433	Csnk1e	035	chr15	79272430	79272432	-	0.8	4.5	9.4E-06	1.1E-02
ENSMUSG00000018501	Ncor1	099	chr11	62270650	62270825	-	0.8	4.5	9.5E-06	1.1E-02
ENSMUSG00000079737 + ENSMUSG00000022684	3110001122Rik/Bfar	006	chr16	13676927	13678498	+	0.5	4.6	9.6E-06	1.1E-02
ENSMUSG00000030852	Tacc2	003	chr7	137765235	137770355	+	1.3	4.5	9.6E-06	1.1E-02
ENSMUSG00000020684	Rasl10b	003	chr11	83223190	83223383	+	0.6	4.7	9.7E-06	1.1E-02
ENSMUSG00000030058	Copg	028	chr6	87852761	87853478	+	0.4	4.5	9.7E-06	1.1E-02
ENSMUSG00000023984 + ENSMUSG00000090115 + ENSMUSG00000092558	Gm20517/Usp49/Med20	013	chr17	47756513	47759833	+	0.4	4.5	9.9E-06	1.1E-02
ENSMUSG00000090213 + ENSMUSG00000089739 + ENSMUSG00000078923	Tmem189/Gm20431/Ube2v1	032	chr2	167487055	167487056	-	1.9	4.5	9.9E-06	1.1E-02
ENSMUSG00000071984	Fndc1	001	chr17	7931434	7932195	-	0.3	4.5	1.0E-05	1.1E-02
ENSMUSG00000027674	Pex5l	031	chr3	33041999	33042004	-	0.7	4.5	1.1E-05	1.1E-02
ENSMUSG00000029550	Splp3	002	chr5	115461155	115461624	+	0.4	4.5	1.1E-05	1.1E-02
ENSMUSG00000036940	Kdmla	039	chr4	136158224	136158602	-	0.5	4.5	1.1E-05	1.1E-02
ENSMUSG00000030603	Psmc4	021	chr7	28834222	28834719	-	0.4	4.5	1.1E-05	1.2E-02
ENSMUSG00000050357	Rlpr	040	chr8	108219675	108220760	+	0.3	4.5	1.1E-05	1.2E-02
ENSMUSG00000028041	Adam15	014	chr3	89144102	89144274	-	0.4	4.4	1.1E-05	1.2E-02
ENSMUSG00000091509 + ENSMUSG00000022119	Gm17066/Rbm26	013	chr14	105515352	105516202	-	-0.7	-4.5	1.1E-05	1.2E-02
ENSMUSG00000022456	Sept3	002	chr15	82105677	82105916	+	0.3	4.6	1.1E-05	1.2E-02
ENSMUSG00000030204	Ddx47	025	chr6	134969130	134970633	+	-0.4	-4.5	1.2E-05	1.2E-02
ENSMUSG00000023952	Gipbp2	045	chr17	46304971	46305094	+	0.3	4.4	1.2E-05	1.2E-02
ENSMUSG00000021018	Polr2h	002	chr16	20718245	20718742	+	0.6	4.7	1.2E-05	1.2E-02
ENSMUSG00000015467 + ENSMUSG00000015474 + ENSMUSG00000092176	Egfl8/Ppt2/Gm20460	020	chr17	34752267	34752276	-	2.4	4.4	1.2E-05	1.2E-02
ENSMUSG00000039219	Arid4b	044	chr13	14284369	14285632	+	-0.5	-4.4	1.3E-05	1.4E-02
ENSMUSG00000057672	Pkn1	043	chr8	86223035	86223066	-	1.4	4.4	1.3E-05	1.4E-02

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ENSMUSG00000034863	Ano8	001	chr8	73999922	74000820	-	0.3	4.5	1.3E-05	1.4E-02
ENSMUSG00000003778	Brd8	025	chr18	34771145	34772690	-	-1.1	-4.4	1.3E-05	1.4E-02
ENSMUSG00000004947	Dcx2	015	chr5	136495428	136497624	+	0.8	4.4	1.3E-05	1.4E-02
ENSMUSG000000068917	Clk2	019	chr3	88976087	88977298	+	0.8	4.4	1.4E-05	1.4E-02
ENSMUSG000000064267	Hvcn1	013	chr5	122688520	122688646	+	0.5	4.5	1.4E-05	1.4E-02
ENSMUSG000000057788	Dux49	011	chr8	72819719	72820281	-	0.4	4.5	1.4E-05	1.4E-02
ENSMUSG000000057672	Pkn1	042	chr8	86222997	86223034	-	1.2	4.4	1.4E-05	1.4E-02
ENSMUSG000000027710	Acad9	015	chr3	35979219	35979628	+	0.8	4.4	1.5E-05	1.4E-02
ENSMUSG000000031447	Lamp1	001	chr8	13159135	13159434	+	0.6	4.6	1.5E-05	1.4E-02
ENSMUSG000000039470	Zdhhc2	005	chr8	41509213	41509353	+	0.9	4.4	1.5E-05	1.4E-02
ENSMUSG000000021493	Pellm7	021	chr13	55609242	55609568	-	0.3	4.4	1.5E-05	1.4E-02
ENSMUSG000000071793	2610005L07Rik	002	chr8	19981360	19983980	-	0.3	4.5	1.5E-05	1.4E-02
ENSMUSG000000044060 + ENSMUSG000000089798	A830010M20Rik/ 1700028K03Rik	003	chr5	107926397	107926739	+	1.6	4.4	1.5E-05	1.4E-02
ENSMUSG000000058301	Upf1	024	chr8	72876677	72877172	-	0.4	4.4	1.5E-05	1.5E-02
ENSMUSG000000008976	Gabpa	011	chr16	84856285	84856706	+	1.1	4.4	1.5E-05	1.5E-02
ENSMUSG000000007617	Homer1	016	chr13	94136198	94136232	+	1.6	4.4	1.5E-05	1.5E-02
ENSMUSG000000074247	Dda1	013	chr8	73996515	73996681	+	0.6	4.5	1.5E-05	1.5E-02
ENSMUSG000000029478	Ncor2	011	chr5	125503295	125503590	-	1.3	4.3	1.6E-05	1.5E-02
ENSMUSG000000055805	Fnnl1	035	chr11	103059093	103059190	+	0.4	4.4	1.6E-05	1.5E-02
ENSMUSG000000036459	Wtip	014	chr7	34917838	34918287	-	1.5	4.5	1.6E-05	1.5E-02
ENSMUSG000000028041	Adam15	027	chr3	89146654	89147034	-	0.5	4.4	1.6E-05	1.6E-02
ENSMUSG000000035569	Ankrd11	023	chr8	125565849	125565897	-	0.7	4.4	1.6E-05	1.6E-02
ENSMUSG000000024068	Spast	001	chr17	74738327	74738785	+	0.4	4.4	1.7E-05	1.6E-02
ENSMUSG000000038502	Prox1	035	chr7	52124721	52125158	-	0.3	4.4	1.7E-05	1.6E-02
ENSMUSG000000002010	Idh3g	029	chrX	71027708	71028013	-	0.4	4.4	1.7E-05	1.6E-02
ENSMUSG000000028967	Errf1	003	chr4	150229577	150229923	+	-1.6	-4.6	1.7E-05	1.6E-02
ENSMUSG000000089704 + ENSMUSG000000031826 + ENSMUSG000000092329	Gaint2/Usp10/ Gm20388	031	chr8	122478834	122479217	+	0.5	4.3	1.8E-05	1.7E-02
ENSMUSG000000022514	Il1rap	027	chr16	26728019	26728314	+	-0.5	-4.4	1.9E-05	1.7E-02
ENSMUSG000000089012 + ENSMUSG000000017421	/Zfp207	026	chr11	80211918	80211972	+	-0.4	-4.4	1.9E-05	1.7E-02

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ENSMUSG00000031392 + ENSMUSG000000076127 + ENSMUSG000000092907	Irak1/Mir718/Mir5132	058	chrX	71269171	71269187	-	1.9	4.3	1.9E-05	1.7E-02
ENSMUSG000000045009	Prr3	002	chr6	113446294	113446925	-	0.5	4.6	1.9E-05	1.7E-02
ENSMUSG000000022710	Usp7	020	chr16	8697013	8697568	-	0.5	4.3	1.9E-05	1.8E-02
ENSMUSG000000037300	Ttc13	021	chr8	127206060	127206430	-	-0.5	-4.3	1.9E-05	1.8E-02
ENSMUSG00000089661 + ENSMUSG000000053291 + ENSMUSG000000093348	Mial1/Rab4b/Mir3101	022	chr7	27961113	27961176	-	-0.6	-4.3	1.9E-05	1.8E-02
ENSMUSG000000050640	Tmem150c	004	chr5	100512966	100515024	-	-0.3	-4.4	2.0E-05	1.8E-02
ENSMUSG000000027692	Tmik	046	chr3	28565151	28565371	+	-0.5	-4.3	2.0E-05	1.8E-02
ENSMUSG000000092367 + ENSMUSG000000011751 + ENSMUSG000000089832	Gm20479/Spnb4/Shkbp1	015	chr7	28132192	28132473	-	0.7	4.3	2.0E-05	1.8E-02
ENSMUSG000000029064	Gnb1	001	chr4	154865470	154865478	+	1.9	4.4	2.1E-05	1.8E-02
ENSMUSG000000032737	Inpp1l	010	chr7	108976713	108976802	-	-0.4	-4.3	2.1E-05	1.8E-02
ENSMUSG000000044857	Lemd2	009	chr17	27340604	27341383	-	0.6	4.5	2.1E-05	1.8E-02
ENSMUSG000000055313	Pgbd1	008	chr13	21526220	21526540	-	-1.2	-4.4	2.1E-05	1.8E-02
ENSMUSG000000021910	Nisch	032	chr14	31994136	31994656	-	0.3	4.3	2.1E-05	1.8E-02
ENSMUSG000000025060	Sik	001	chr19	47654168	47654508	+	1.2	4.3	2.1E-05	1.9E-02
ENSMUSG000000052423	B4gal3	011	chr1	173201123	173201236	+	-0.6	-4.3	2.2E-05	1.9E-02
ENSMUSG000000071644	Eef1g	008	chr19	9044478	9044691	+	-0.8	-4.4	2.2E-05	1.9E-02
ENSMUSG000000001763	Tspan33	001	chr6	29644222	29644233	+	1.7	4.4	2.2E-05	1.9E-02
ENSMUSG000000022656	Pvr13	027	chr16	46496966	46497080	-	2.0	4.3	2.2E-05	1.9E-02
ENSMUSG000000035901	Denmd5a	034	chr7	117103791	117103837	-	1.1	4.3	2.2E-05	1.9E-02
ENSMUSG000000019854	Reps1	002	chr10	17775712	17775745	+	0.8	4.3	2.2E-05	1.9E-02
ENSMUSG000000000568	Hmnpd	009	chr5	100391153	100391223	-	0.4	4.3	2.2E-05	1.9E-02
ENSMUSG000000089715 + ENSMUSG000000089837 + ENSMUSG000000022421	Cbx6/Npcd/Npnr	012	chr15	79634889	79635058	-	0.9	4.3	2.3E-05	1.9E-02
ENSMUSG000000026839	Upp2	002	chr2	58419729	58419797	+	0.9	4.4	2.3E-05	2.0E-02
ENSMUSG000000026426	Arl8a	001	chr1	137043401	137043677	+	0.2	4.4	2.3E-05	2.0E-02
ENSMUSG000000028381	Usgg	001	chr4	59202129	59202429	+	1.7	4.4	2.4E-05	2.0E-02
ENSMUSG000000041506	Rip9	023	chr9	106386851	106387407	+	0.4	4.3	2.5E-05	2.1E-02
ENSMUSG0000000054934	Kcnmb4	001	chr10	115854917	115855462	-	-0.6	-4.5	2.5E-05	2.1E-02
ENSMUSG000000063160 + ENSMUSG000000003762	Numbl/Adck4	037	chr7	28047272	28049894	+	0.3	4.3	2.5E-05	2.1E-02

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ENSMUSG00000072770 + ENSMUSG00000030330	Acrbp/Ing4	037	chr6	125001261	125001378	+	0.5	4.3	2.6E-05	2.2E-02
ENSMUSG00000024182	Axin1	004	chr17	26275848	26275894	+	1.3	4.3	2.6E-05	2.2E-02
ENSMUSG00000024835	Coro1b	021	chr19	4152580	4152808	+	-0.3	-4.3	2.6E-05	2.2E-02
ENSMUSG00000033059	Pygb	019	chr2	150649343	150649711	+	0.8	4.3	2.6E-05	2.2E-02
ENSMUSG00000025571	Tnrc6c	016	chr11	117603815	117604240	+	-0.6	-4.3	2.6E-05	2.2E-02
ENSMUSG00000035953	Tmem55b	005	chr14	51547713	51548495	-	0.3	4.3	2.6E-05	2.2E-02
ENSMUSG00000059248	Sept9	021	chr11	117218024	117218313	+	0.9	4.3	2.7E-05	2.2E-02
ENSMUSG00000048446 + ENSMUSG00000076240	Plod3/Mir702	033	chr5	137470929	137471047	+	0.7	4.3	2.7E-05	2.2E-02
ENSMUSG00000039069	Gtpbp5	017	chr2	179818166	179818768	+	0.4	4.3	2.8E-05	2.2E-02
ENSMUSG00000031979	Cog2	014	chr8	127066851	127067909	+	0.4	4.3	2.8E-05	2.3E-02
ENSMUSG00000031392 + ENSMUSG00000076127 + ENSMUSG00000092907	Irak1/Mir718/Mir5132	055	chrX	71269085	71269147	-	0.9	4.2	2.8E-05	2.3E-02
ENSMUSG00000009207	Lnp	022	chr2	74389952	74393044	-	-0.7	-4.2	2.8E-05	2.3E-02
ENSMUSG00000030374	Stmn4	021	chr7	17417980	17418274	+	0.3	4.2	2.8E-05	2.3E-02
ENSMUSG00000019927	Ube2d1	008	chr10	70722568	70724831	-	0.3	4.4	2.8E-05	2.3E-02
ENSMUSG00000052949	Rnf157	037	chr11	116274319	116274346	-	1.7	4.2	2.9E-05	2.4E-02
ENSMUSG00000036052	Dnajb5	003	chr4	42962786	42962876	+	-0.4	-4.3	3.0E-05	2.4E-02
ENSMUSG00000040048	Ndufb10	002	chr17	24859166	24859325	-	0.5	4.3	3.0E-05	2.4E-02
ENSMUSG00000038848	Ythdf1	009	chr2	180655389	180655654	-	0.8	4.4	3.0E-05	2.4E-02
ENSMUSG00000020610	Amz2	020	chr11	109298566	109299462	+	0.2	4.3	3.0E-05	2.4E-02
ENSMUSG00000075876 + ENSMUSG00000064791 + ENSMUSG00000075924 + ENSMUSG00000015656	Snord14c/Snord14e/Snord14d/Hspa8	024	chr9	40611297	40611462	+	-0.6	-4.2	3.1E-05	2.4E-02
ENSMUSG00000063659	Zfp238	002	chr1	179375952	179377219	+	0.4	4.7	3.1E-05	2.4E-02
ENSMUSG00000004865	Srpki	026	chr17	28757088	28757398	-	2.6	4.2	3.1E-05	2.4E-02
ENSMUSG0000002325 + ENSMUSG00000047098	Irf9/Rnf31	062	chr14	56227758	56228864	+	0.3	4.2	3.1E-05	2.4E-02
ENSMUSG00000038244	Mical2	012	chr7	119459543	119461899	+	-0.5	-4.2	3.1E-05	2.5E-02
ENSMUSG000000041740	Rnf10	012	chr5	115693701	115694029	-	0.6	4.2	3.2E-05	2.5E-02
ENSMUSG00000045205	Dpy19l4	001	chr4	11188462	11192225	-	0.3	4.2	3.2E-05	2.5E-02
ENSMUSG00000026860	Sh3glb2	023	chr2	30205260	30205807	-	0.4	4.2	3.2E-05	2.5E-02
ENSMUSG00000022974	Gcfc1	033	chr16	91044251	91044409	-	0.7	4.2	3.2E-05	2.5E-02
ENSMUSG00000028863	Meaf6	014	chr4	124780674	124780747	+	0.6	4.2	3.2E-05	2.5E-02

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ENSMUSG00000052997	Uba2	007	chr7	34927894	34928288	-	0.5	4.2	3.3E-05	2.5E-02
ENSMUSG00000001911	Nfix	031	chr8	87324040	87324243	-	2.5	4.2	3.3E-05	2.5E-02
ENSMUSG00000034656	Cacna1a	067	chr8	87163145	87163333	+	0.4	4.2	3.3E-05	2.5E-02
ENSMUSG00000019843	Fyn	004	chr10	39089609	39089996	+	0.3	4.2	3.3E-05	2.5E-02
ENSMUSG00000031167	Rbm3	001	chrX	7716101	7716103	-	2.0	4.2	3.6E-05	2.7E-02
ENSMUSG00000022514	Il1rap	026	chr16	26727733	26728018	+	-0.5	-4.2	3.6E-05	2.8E-02
ENSMUSG00000004233	Wars2	014	chr3	9039402	9040231	+	2.3	4.2	3.7E-05	2.8E-02
ENSMUSG00000024571 + ENSMUSG000000057130	Gm16286/Txnl4a	017	chr18	80404083	80404423	+	-0.7	-4.2	3.7E-05	2.8E-02
ENSMUSG00000020978	Klhdcc2	002	chr12	70397709	70397741	+	0.7	4.2	3.7E-05	2.8E-02
ENSMUSG00000024335	Brd2	037	chr17	34258693	34258933	-	2.3	4.2	3.8E-05	2.9E-02
ENSMUSG00000026155	Smap1	025	chr1	23928877	23929156	-	0.3	4.2	3.8E-05	2.9E-02
ENSMUSG0000004561 + ENSMUSG000000072572	Mettl17/Sic39a2	055	chr14	52514182	52514573	+	0.3	4.2	3.8E-05	2.9E-02
ENSMUSG00000019254	Ppp1r12c	053	chr7	4453267	4453282	-	1.1	4.2	3.9E-05	2.9E-02
ENSMUSG00000040331	Nsmce4a	020	chr7	137690506	137690895	-	0.3	4.2	3.9E-05	2.9E-02
ENSMUSG0000005882	Uqcc	030	chr2	155736341	155737476	-	-0.7	-4.2	4.0E-05	2.9E-02
ENSMUSG00000021234	Fam161b	004	chr12	85687442	85687736	-	0.6	4.2	4.0E-05	3.0E-02
ENSMUSG00000008153	Cistin3	005	chr6	124386790	124386835	-	1.0	4.2	4.1E-05	3.0E-02
ENSMUSG00000021610	C1ptm11	001	chr13	73741554	73741847	+	0.2	4.2	4.3E-05	3.1E-02
ENSMUSG00000027303	Ptpra	002	chr2	130276280	130276294	+	0.5	4.2	4.3E-05	3.2E-02
ENSMUSG00000038546	Ranbp9	017	chr13	43576247	43576297	-	1.7	4.2	4.4E-05	3.2E-02
ENSMUSG00000030374	Strn4	020	chr7	17416930	17416988	+	0.5	4.1	4.4E-05	3.2E-02
ENSMUSG00000025198	Erlin1	024	chr19	44144181	44144186	-	-1.0	-4.2	4.4E-05	3.2E-02
ENSMUSG00000031292	Cdkl5	021	chrX	157432523	157432634	-	-1.8	-4.2	4.5E-05	3.3E-02
ENSMUSG00000086285	D630044L22Rik	006	chr17	26099007	26099155	+	-1.4	-4.3	4.6E-05	3.3E-02
ENSMUSG00000019189	Rnf145	012	chr11	44365322	44368479	+	-0.5	-4.2	4.6E-05	3.3E-02
ENSMUSG00000028849	Mtap7d1	017	chr4	125914140	125914303	-	0.2	4.1	4.6E-05	3.3E-02
ENSMUSG00000027642	Rpn2	034	chr2	157147897	157148207	+	0.4	4.1	4.6E-05	3.3E-02
ENSMUSG00000053907	Mat2a	002	chr6	72384390	72384538	-	0.3	4.2	4.6E-05	3.3E-02
ENSMUSG00000001416	Cct3	008	chr3	88103326	88104721	+	0.5	4.1	4.6E-05	3.3E-02
ENSMUSG00000022265	Ank	001	chr15	27396432	27396854	+	0.3	4.2	4.6E-05	3.3E-02
ENSMUSG00000025103	Btdl1	008	chr7	88973859	88974317	-	0.3	4.3	4.7E-05	3.3E-02

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ENSMUSG00000085609	170001Gp03Rik	002	chr11	74987480	74987663	+	1.4	4.6	4.7E-05	3.3E-02
ENSMUSG00000044783	Hljurp	023	chr1	90171673	90173793	-	0.5	4.1	4.7E-05	3.3E-02
ENSMUSG00000031245	Hmgn5	001	chrX	106199873	106201410	-	0.4	4.4	4.7E-05	3.3E-02
ENSMUSG00000034135	Sik3	002	chr9	45820947	45821082	+	0.8	4.1	4.8E-05	3.3E-02
ENSMUSG00000029364	Wsb2	001	chr5	117807313	117807313	+	2.2	4.2	4.8E-05	3.4E-02
ENSMUSG0000000568	Hnmpd	008	chr5	100391117	100391152	-	0.4	4.1	4.9E-05	3.4E-02
ENSMUSG00000028347	Tmeff1	002	chr4	48598065	48598236	+	1.1	4.2	4.9E-05	3.4E-02
ENSMUSG00000025198	Erlin1	025	chr19	44144187	44144234	-	-1.0	-4.1	4.9E-05	3.4E-02
ENSMUSG00000033904	6330503K22Rik	022	chr7	125876487	125878781	+	0.3	4.1	4.9E-05	3.4E-02
ENSMUSG00000023087	Cern4l	003	chr3	51044128	51051726	+	0.4	4.3	4.9E-05	3.4E-02
ENSMUSG00000067713	Prkag1	001	chr15	98643229	98643911	-	-0.3	-4.2	4.9E-05	3.4E-02
ENSMUSG00000090266 + ENSMUSG00000020818	1110005A03Rik/ Mfsd11	033	chr11	116719896	116720427	+	-0.8	-4.1	5.0E-05	3.4E-02
ENSMUSG00000028412	Slc44a1	002	chr4	53453543	53453555	+	0.7	4.1	5.0E-05	3.4E-02
ENSMUSG00000027351	Spred1	001	chr2	116947110	116947373	+	0.8	4.3	5.0E-05	3.4E-02
ENSMUSG00000028047	Thbs3	020	chr3	89025074	89025135	+	1.1	4.1	5.1E-05	3.5E-02
ENSMUSG0000003279	Dlgap1	005	chr17	70318742	70318760	+	0.6	4.1	5.3E-05	3.6E-02
ENSMUSG00000030584	Dpfl	006	chr7	30093118	30093973	+	0.5	4.1	5.3E-05	3.6E-02
ENSMUSG00000045994	B3gat1	002	chr9	26541388	26541408	+	1.9	4.1	5.3E-05	3.6E-02
ENSMUSG0000003360	Ddx23	020	chr15	98482970	98483318	-	0.5	4.1	5.4E-05	3.6E-02
ENSMUSG0000004994	Ccdc130	011	chr8	86785700	86785805	-	0.9	4.1	5.4E-05	3.6E-02
ENSMUSG00000063873	Slc24a3	002	chr2	144993655	144993933	+	0.4	4.1	5.6E-05	3.7E-02
ENSMUSG00000078919 + ENSMUSG000000051149	Dpm1/Adnp	009	chr2	168032210	168032422	-	0.9	4.1	5.6E-05	3.7E-02
ENSMUSG00000052423	B4gal3	030	chr1	173204520	173206012	+	0.3	4.1	5.6E-05	3.7E-02
ENSMUSG00000058239	Usf2	007	chr7	31731875	31731898	-	-0.3	-4.1	5.7E-05	3.7E-02
ENSMUSG00000027639	Samhd1	004	chr2	156925240	156927056	-	0.4	4.1	5.7E-05	3.7E-02
ENSMUSG00000032557	Uba5	016	chr9	103962489	103962547	-	0.8	4.1	5.7E-05	3.8E-02
ENSMUSG00000049092	Gpr137c	001	chr14	45839394	45839667	+	1.2	4.2	5.8E-05	3.8E-02
ENSMUSG00000019970	Sgk1	002	chr10	21602175	21602513	+	-0.5	-4.1	5.8E-05	3.8E-02
ENSMUSG00000072770 + ENSMUSG00000030330	Acrbp/Ing4	041	chr6	125001872	125001908	+	2.4	4.1	5.8E-05	3.8E-02
ENSMUSG00000024843	Chka	032	chr19	3889989	3891730	+	0.4	4.1	5.9E-05	3.8E-02

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
ENSMUSG00000063873	Slc24a3	001	chr2	144993490	144993654	+	0.8	4.1	5.9E-05	3.9E-02
ENSMUSG00000020719 + ENSMUSG000000093273 + ENSMUSG000000093133	Ddx5/Mir3064/	020	chr11	106645047	106645272	-	0.2	4.1	6.0E-05	3.9E-02
ENSMUSG00000020893	Per1	026	chr11	68919799	68919954	+	0.8	4.1	6.0E-05	3.9E-02
ENSMUSG00000058239	Usf2	021	chr7	31741401	31741447	-	0.4	4.1	6.2E-05	4.0E-02
ENSMUSG00000003438	Timm50	013	chr7	29094525	29095097	-	0.7	4.1	6.2E-05	4.0E-02
ENSMUSG00000019254	Ppp1r12c	051	chr7	4452964	4453131	-	0.4	4.0	6.3E-05	4.0E-02
ENSMUSG00000032382	Snx1	006	chr9	65938538	65939154	-	0.3	4.1	6.3E-05	4.0E-02
ENSMUSG00000000902	Smnrcb1	009	chr10	75367320	75368774	-	-0.4	-4.1	6.4E-05	4.1E-02
ENSMUSG00000015467 + ENSMUSG000000015474 + ENSMUSG000000092176	Egfl8/Ppt2/Gm20460	019	chr17	34752266	34752266	-	2.2	4.0	6.6E-05	4.2E-02
ENSMUSG00000056692	D17W ^{su92e}	009	chr17	27957437	27957487	-	1.4	4.2	6.6E-05	4.2E-02
ENSMUSG00000020719 + ENSMUSG000000093273 + ENSMUSG000000093133	Ddx5/Mir3064/	015	chr11	106644586	106644625	-	0.2	4.0	6.6E-05	4.2E-02
ENSMUSG00000060216	Arrb2	011	chr11	70249075	70249498	+	0.6	4.0	6.7E-05	4.3E-02
ENSMUSG00000047030	Spata2	002	chr2	167306933	167307058	-	-0.6	-4.1	6.7E-05	4.3E-02
ENSMUSG00000020128	Vps54	001	chr11	21138892	21139283	+	0.7	4.0	6.8E-05	4.3E-02
ENSMUSG00000047368	Fam108b	001	chr19	21727799	21728083	+	0.7	4.4	7.0E-05	4.4E-02
ENSMUSG00000038084	Opal	047	chr16	29652577	29654970	+	0.2	4.0	7.0E-05	4.4E-02
ENSMUSG00000020333	Acs16	029	chr11	54150651	54151230	+	0.4	4.0	7.1E-05	4.5E-02
ENSMUSG00000032322	Pstpip1	008	chr9	55969742	55969829	+	2.1	4.0	7.1E-05	4.5E-02
ENSMUSG00000061207	Stk19	010	chr17	34961794	34962547	-	0.3	4.1	7.2E-05	4.5E-02
ENSMUSG00000022974	Gefc1	034	chr16	91044410	91044599	-	0.7	4.0	7.2E-05	4.5E-02
ENSMUSG00000016933	Pleg1	002	chr2	160557046	160557080	+	0.8	4.0	7.4E-05	4.6E-02
ENSMUSG00000020333	Acs16	030	chr11	54151231	54151913	+	0.4	4.0	7.5E-05	4.6E-02
ENSMUSG00000059316	Slc27a4	004	chr2	29662518	29662875	+	0.4	4.1	7.5E-05	4.6E-02
ENSMUSG00000003848	Nob1	013	chr8	109942343	109942566	-	0.8	4.0	7.5E-05	4.7E-02
ENSMUSG00000078789 + ENSMUSG000000038268	Dphi/Ovca2	016	chr11	74994164	74994191	-	-0.8	-4.0	7.6E-05	4.7E-02
ENSMUSG00000004929	Thop1	006	chr10	80536111	80537622	+	0.6	4.0	7.6E-05	4.7E-02
ENSMUSG00000038644	Pold1	017	chr7	51789557	51789559	-	1.7	4.0	7.7E-05	4.7E-02
ENSMUSG00000035901	Demd5a	035	chr7	117103838	117103914	-	1.0	4.0	7.9E-05	4.8E-02
ENSMUSG00000089715 + ENSMUSG000000089837	Cbx6/Npcd/Npxr	014	chr15	79635063	79635194	-	1.0	4.0	7.9E-05	4.8E-02

GeneID	Gene name	Bin #	Chr	Start	Stop	Strand	logFC	t	P value	FDR
+ ENSMUSG00000022421										
ENSMUSG000000075876 + ENSMUSG000000064791	Snord14c/ Snord14e/ Snord14d/Hspa8	031	chr9	40612078	40612163	+	1.5	4.0	7.9E-05	4.8E-02
+ ENSMUSG000000075924 + ENSMUSG000000015656										
ENSMUSG000000037266	D4Wsu53e	018	chr4	134481348	134481360	+	-0.3	-4.0	7.9E-05	4.8E-02
ENSMUSG000000044700	Tmem201	003	chr4	149091187	149092128	-	0.4	4.0	8.0E-05	4.9E-02
ENSMUSG000000027692	Tnik	051	chr3	28569508	28574780	+	-0.2	-4.0	8.1E-05	4.9E-02
ENSMUSG000000093290 + ENSMUSG000000035632	Mir3572/Cnot3	029	chr7	3611109	3612278	+	0.3	4.0	8.1E-05	4.9E-02
ENSMUSG000000009394	Syn2	001	chr6	115084920	115085478	+	0.2	4.1	8.1E-05	4.9E-02
ENSMUSG000000053754	Chd8	006	chr14	52821423	52821818	-	-0.5	-4.0	8.2E-05	4.9E-02
ENSMUSG000000037331	Larp1	001	chr11	57822566	57823049	+	0.5	4.0	8.2E-05	4.9E-02
ENSMUSG000000011658	Fuz	044	chr7	52157792	52158001	+	0.4	4.0	8.3E-05	4.9E-02
ENSMUSG000000074657	Kif5a	002	chr10	126666106	126666800	-	0.5	4.0	8.3E-05	4.9E-02
ENSMUSG000000022394	L3mbtl2	004	chr15	81494386	81494430	+	-0.5	-4.0	8.3E-05	4.9E-02
ENSMUSG000000038453	Srcin1	034	chr11	97436441	97436529	-	1.8	4.0	8.3E-05	4.9E-02
ENSMUSG000000065438 + ENSMUSG000000065497 + ENSMUSG000000065561 + ENSMUSG000000091158 + ENSMUSG000000065570	Mir377/Mir410/ Mir369/Mirg/ Mir412	018	chr12	110987305	110987665	+	-0.3	-4.0	8.4E-05	5.0E-02