

## Genome-Wide DNA Methylation Changes in a Mouse Model of Infection-Mediated Neurodevelopmental Disorders

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## ABSTRACT

**Background:** Prenatal exposure to infectious or inflammatory insults increases the risk of neurodevelopmental disorders. Using a well-established mouse model of prenatal viral-like immune activation, we examined whether this pathological association involves genome-wide DNA methylation differences at single nucleotide resolution.

**Methods:** Prenatal immune activation was induced by maternal treatment with the viral mimetic poly(I:C) in middle (gestation day 9) or late (gestation day 17) gestation. Following behavioral and cognitive characterization of the adult offspring, unbiased capture array bisulfite sequencing was combined with subsequent matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and quantitative real-time PCR analyses to quantify DNA methylation changes and transcriptional abnormalities in the medial prefrontal cortex of immune-challenged and control offspring. GO term enrichment analysis was used to explore shared functional pathways of genes with differential DNA methylation.

**Results:** Adult offspring of immune-challenged mothers displayed hyper- and hypomethylated CpGs at numerous loci and at distinct genomic regions, including genes relevant for GABAergic differentiation and signaling (e.g., DLX1, LHX5, LHX8), Wnt signaling (WNT3, WNT8A, WNT7B), and neural development (e.g., EFNB3, MID1, NLGN1, NRX2). Altered DNA methylation was associated with transcriptional changes of the corresponding genes. The epigenetic and transcriptional effects were dependent on the offspring's age and were markedly influenced by the precise timing of prenatal immune activation.

**Conclusions:** Prenatal viral-like immune activation is capable of inducing stable DNA methylation changes in the medial prefrontal cortex. These long-term epigenetic modifications are a plausible mechanism underlying the disruption of prefrontal gene transcription and behavioral functions in subjects with prenatal infectious histories.

## **INTRODUCTION**

Prenatal exposure to infectious or inflammatory insults is an environmental risk factor for brain disorders with neurodevelopmental components, including schizophrenia (1,2), autism (3,4), and bipolar disorder (5,6). This epidemiological association is further supported by translational work in animal models demonstrating abnormal brain development and behavioral dysfunctions following prenatal administration of infectious pathogens or immune activating agents (7-10). Cytokine-associated inflammatory events, together with downstream pathophysiological effects such as oxidative stress and (temporary) macronutrient and micronutrient deficiency, seem to be critical in mediating the adverse effects of maternal infection on the fetal system (2,11,12). These pathological processes can affect somatic cell development and change the offspring's neurodevelopmental trajectories, which in turn can lead to the emergence of behavioral and cognitive disturbances in later life (13-16).

Epigenetic modifications may be critical for mediating alterations in brain development and behavioral functions in response to in-utero immune challenges. Epigenetic mechanisms stably program genome activity and gene expression without altering the DNA sequence (17-19). Rodent models of prenatal immune activation now begin to reveal epigenetic alterations in the offspring's brain and have already provided evidence for altered DNA methylation (20,21), histone modifications (22,23), and micro-RNA expression (24) that persist into adolescence and/or adulthood. Some of the epigenetic modifications induced by prenatal immune activation have been found to correlate with altered transcription of the corresponding genes and with behavioral deficits (21). These studies, however, were based on targeted approaches and did not assess global DNA methylation profiles across the entire genome. Hence, it remains unknown whether prenatal immune activation may cause altered DNA methylation in selected genomic regions or loci, or alternatively, whether such changes extend to the entire genome.

The present study is the first to examine genome-wide DNA methylation differences at single nucleotide resolution by capture array bisulfite sequencing of promoters and

enhancers using a well-established mouse model of prenatal viral-like immune activation. The model is based on maternal administration of the viral mimetic poly(I:C) (= *polyriboinosinic-polyribocytidilic acid*), which induces a cytokine-associated viral-like acute phase response in maternal and fetal compartments, including the fetal brain (10). Prenatal poly(I:C) treatment in rodents leads to multiple behavioral and cognitive disturbances in offspring, many of which are implicated in developmental psychiatric disorders such as schizophrenia and autism (7-12). The prenatal poly(I:C) exposure model thus offers a unique opportunity to explore genome-wide DNA methylation changes following prenatal exposure to an etiologically relevant risk factor of developmental psychiatric disorders. Since the precise timing of prenatal immune activation can critically influence the nature and/or severity of the long-term brain abnormalities (25-27), we compared alterations in DNA methylation in response to prenatal immune activation in [middle](#) and late gestation. We focused on DNA methylation profiles in the prefrontal cortex (PFC) in view of its role in developmental psychiatric disorders such as schizophrenia and autism (28-30).

## MATERIALS AND METHODS

### Animals and Prenatal Immune Activation

C57Bl6/N mice were used throughout the study. Female mice were subjected to a timed mating procedure as established previously (31,32). [As described in the Supplementary Information](#), pregnant dams on gestation day (GD) 9 or 17 were randomly assigned to receiving either a single injection of poly(I:C) (potassium salt; Sigma–Aldrich, Buchs, St. Gallen, Switzerland) or vehicle. Poly(I:C) (5 mg/kg) was dissolved in sterile pyrogen-free 0.9% NaCl (vehicle) solution to yield a final concentration of 1 mg/ml and was administered intravenously (i.v.) into the tail vein under mild physical constraint. [The two gestational windows \(i.e., GD 9 and 17\)](#) were selected based on our previous studies assessing the influence of the precise timing of prenatal viral-like immune activation (25,26). [GD 9 in the mouse roughly corresponds to human gestational weeks 4 to 5 in](#)

terms of limbic neurogenesis, whereas GD 17 corresponds to human gestational weeks 28 to 29 in terms of cortical neurogenesis (<http://translatingtime.net/translate>).

The allocation and housing of neonatal and adult offspring of dams injected with poly(I:C) on GD 9 (POL-GD9 offspring) or GD 17 (POL-GD17 offspring) and vehicle-exposed control offspring (CON offspring) are described in the **Supplementary Information**. All procedures described in the present study had been previously approved by the Cantonal Veterinarian's Office of Zurich, and all efforts were made to minimize the number of animals used and their suffering.

### ***Behavioral Testing***

Behavioral testing in adult offspring started on postnatal day (PND) 100. The tests included paradigms assessing spatial recognition memory, social interaction, and prepulse inhibition (PPI) of the acoustic startle reflex. These tests were selected based on their relevance to neurodevelopmental disorders with infectious and inflammatory components, including schizophrenia and autism (33,34). A detailed description of the test apparatuses and procedures is provided in the **Supplementary Information**. Each animal underwent each behavioral test in the following order: (i) spatial recognition memory test, (ii) social interaction test, and (iii) PPI test. A test-free resting period of 2 days was imposed between individual tests.

### ***Collection of Brain Samples***

All adult offspring were first subjected to behavioral testing prior to the molecular analyses (**Supplementary Information**). They were killed by decapitation two weeks after completion of behavioral testing. The brains were rapidly extracted from the skull (within < 20 s) and placed on an ice-chilled plate. Coronal sections were prepared using razorblade cuts along the following coordinates with respect to bregma: anterior–posterior: +2.0 to +1.0, +1.0 to 0.0, 0.0 to –1.0, –1.0 to –2.0, and –2.0 to –3.0 mm. Discrete brain regions were then collected using a micropunch needle (1 mm in diameter) generating

micropunches of distinct brain areas as described previously (35). In the present study, we focused on PFC specimens (bregma: +2.0 to +1.0 mm; including anterior cingulate, prelimbic and dorsal parts of the infralimbic subregions), which were collected in 96-well microtiter plates kept on dry ice and allowed to freeze before storage at  $-80^{\circ}\text{C}$  until further use. Neonatal offspring were killed by decapitation on PND 1; and neonatal PFC specimens were prepared as described for adult offspring.

### **DNA and RNA Isolation and Quantitative Real-Time PCR Analyses**

Total DNA and RNA were isolated using the Qiagen AllPrep DNA and RNA Mini kit (Qiagen, Italy) according as described in the **Supplementary Information**. mRNA levels were quantified by TaqMan qRT-PCR (CFX384 real-time system, Bio-Rad Laboratories) using the iScript one-step RT-PCR kit for probes (Bio-Rad Laboratories) (see **Supplementary Information**).

### **SureSelectXT Capture Sequencing Assay**

Genomic DNA was converted into bisulfite-sequencing samples for the Illumina paired-end multiplexed sequencing platform (Illumina, Canada) as described in the **Supplementary Information**. Bisulfite-converted samples were amplified with PCR using Takara EpiTaq HS enzyme (Clontech, Canada) and further processed to obtain a purified bisulfite-treated library, which was sequenced with Illumina HiSeq2000 (**Supplementary Information**).

### **Data Processing and Differential Methylation Detection**

After sequencing, an average of 31 million reads per sample was obtained (150 to 180 million reads per condition). These were aligned to the mouse genome (mm9 build/assembly) using Bismark (<http://www.bioinformatics.babraham.ac.uk/projects/bismark/>), leading to an average of 26.6 million reads per sample. 25% of the reads was then removed, as they were duplicate reads. Cytosine methylation states were determined using Bismark.

The BAM files generated by Bismark were then used to calculate the methylation differences at different context cytosine-phosphodiester-guanine (CpG) regions. For this last passage, the BAM files were loaded into R using the methylKit package that took into account methylation information of cytosines with at least 10 reads for each animal. In a first step, logistic regression was applied to identify methylation differences at 1000 sliding base-pair regions using corrected P-values (sliding linear model) (36) set at a 20% threshold ( $q < 0.2$ ). Subsequently, methylation differences at single CpG resolution were determined by considering those CpGs that were significant ( $q < 0.2$ ) in the preceding analysis of the 1000 sliding base-pair regions. [Hierarchical clustering of differentially methylated CpGs was performed using Partek Genomics Suite \(Partek, USA; see Supplementary Information\)](#)

### **Validation of Methylation Differences by EpiTYPER**

To validate methylation differences observed with the SureSelectXT capture sequencing assay, specific CpGs were analyzed using EpiTYPER. This technique detects and quantifies DNA methylation using base-specific cleavage and Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS) (37). Genomic DNA was treated and analyzed as fully described in the **Supplementary Information**.

### **Statistical Analyses**

All behavioral and RT-PCR data were analyzed using analysis of variance (ANOVA) followed by Fisher's least significant difference (FLSD) post-hoc comparisons or restricted ANOVAs whenever appropriate. All statistical analyses for the behavioral tests and RT-PCR analyses were performed using the statistical software SPSS (version 13.0), and statistical significance was set at  $p < 0.05$ . In the capture-sequencing assay, FDR-corrected ( $q < 0.2$ ) methylation differences were calculated using the Benjamini-Hochberg correction. Methylation levels measured at selected genomic regions using EpiTYPER

were analyzed using ANOVA followed by FLSD post-hoc comparisons whenever appropriate, and statistical significance was set at  $p < 0.05$ .

## RESULTS

### Behavioral and Cognitive Deficits Following Prenatal Immune Activation in Middle or Late Gestation

First, we ascertained the effects of prenatal immune activation in middle or late gestation on adult behavioral and cognitive functions. Consistent with previous studies (22,26), we found that prenatal immune activation in late but not middle gestation impaired performance in a Y-maze spatial recognition memory test. In this test, the critical measure of spatial recognition memory is the relative time spent in the novel (previously unexplored) arm during the choice phase. CON and POL-GD9 offspring displayed a noticeable preference towards the novel arm, indicating intact spatial recognition memory in these groups (**Figure 1A**). In contrast, POL-GD17 offspring exhibited a marked reduction in this measure and performed below chance level (**Figure 1A**). There were no group differences with respect to the total distance moved (**Supplementary Figure 2A**), indicating that the negative effects of late prenatal immune activation on spatial recognition memory were not confounded by possible differences in basal locomotor activity.

In line with previous studies (21,32,38), offspring exposed to prenatal immune activation also displayed impaired sociability in a social interaction test, in which they were allowed to concomitantly explore an inanimate dummy object and an unfamiliar live mouse (**Figure 1B**). Whereas CON offspring showed a clear preference for the live mouse versus the inanimate dummy object, POL-GD9 and POL-GD17 offspring did not display such a preference (**Figure 1B**). There were no group differences with respect to the total distance moved during the social interaction test (**Supplementary Figure 2B**),



suggesting that prenatal immune activation leads to genuine deficits in social approach behavior regardless of the precise prenatal timing.

Prenatal immune activation further caused deficits in sensorimotor gating as assessed using PPI of the acoustic startle reflex. Consistent with previous reports (26,27,32,39), a significant PPI impairment emerged only after prenatal poly(I:C)-induced immune activation in **middle** (GD 9) but not late (GD 17) gestation (**Figure 1C**). The prenatal manipulations did not affect startle reactivity per se: The reactivities (mean  $\pm$  s.e.m., in arbitrary units) to pulse-alone trials were  $106.06 \pm 7.72$  in controls,  $111.26 \pm 11.29$  in offspring exposed to poly(I:C) treatment on GD 9, and  $126.97 \pm 12.20$  in offspring exposed to poly(I:C) treatment on GD 17.

### **Genome-wide DNA Methylation Profiles Following Prenatal Immune Activation in Middle or Late Gestation**

Using the behaviorally characterized cohort of poly(I:C)-exposed and control offspring, we then sought to identify genome-wide DNA methylation changes in the **adult** PFC. Using capture-sequencing techniques, we first performed regional analysis to detect significant methylation differences in 1000 base-pair sliding regions ( $q < 0.2$ ) and then detected differences at single CpG resolution ( $q < 0.2$ ) by focusing on those significant 1000 base-pair regions. 9488 sliding regions were differentially methylated in POL-GD9 offspring **relative CON offspring (Supplementary Table 1)**, and 10360 sliding regions were differentially methylated in POL-GD17 offspring **compared to CON offspring (Supplementary Table 2)**. Within those regions, 2365 and 3361 single CpG sites were differentially ( $q < 0.2$ ) methylated in POL-GD9 and POL-GD17 offspring, respectively (**Supplementary Table 3 and 4**). These single-base methylation changes clustered according to the prenatal treatment conditions (**Figure 2A**). Among the 2365 differentially methylated sites present in POL-GD9 offspring, 65% were hypomethylated and 35% were hypermethylated (**Table 1**). A similar global methylation profile was found in POL-GD17 offspring, where 63% and 37% of the 3361 CpG sites were hypo- and hypermethylated,

respectively (**Table 1**). Comparable global methylation profiles were also observed when considering the 1000 base-pair sliding regions (**Supplementary Table 5**).

There was a positive correlation between all CpG sites that were differentially methylated in POL-GD9 (2365 sites) or POL-GD17 (3361 sites) offspring (**Supplementary Figure 4**), suggesting a similar direction of methylation changes between the two prenatal treatment conditions. However, only 335 single CpG sites (and 2499 sliding regions) were commonly affected by both prenatal manipulations, as confirmed by hypergeometric distribution testing (**Figure 2B, Supplementary Table 6**). The direction of methylation changes in these common CpG sites correlated between the two prenatal treatment conditions: Those regions or sites that were hypermethylated (or hypomethylated) in POL-GD9 offspring were also hypermethylated (or hypomethylated) in POL-GD17 offspring (**Figure 2B, Supplementary Figure 4**).

To validate the findings obtained by capture sequencing, we measured methylation levels at individual CpG sites using an EpiTYPER assay that quantifies differential CpG methylation using MALDI-TOF mass spectrometry (38). First, we measured the methylation levels of individual CpGs within three distinct regions of the midline 1 (MID1) gene. MID1 stood out as the gene showing the most extensive changes in adult methylation, with a predominance of hypermethylated regions in correspondence of both the gene body and various transcription enhancer sites (**Supplementary Figure 5, Supplementary Table 8**). These effects appeared to be more pronounced in POL-GD17 relative to GD9-POL offspring (**Supplementary Figure 5, Supplementary Table 8**). Analyzing methylation profiles using EpiTYPER confirmed that prenatal immune activation caused hypermethylation of multiple CpGs sites in distinct MID1 gene segments (**Figure 3A**). Consistent with the findings revealed by capture sequencing, EpiTYPER showed that prenatal immune activation in late (GD 17) gestation caused more extensive methylation changes in different MID1 gene segments compared to prenatal immune activation in middle (GD 9) gestation (**Figure 3A**). Importantly, the two techniques used to assess DNA

methylation (bisulfite capture sequencing and EpiTYPER) yielded consistent results in terms of differential methylation of MID1 (see **Supplementary Table 9**).

In addition to MID1, we further validated the methylation differences of a number of other specific CpGs using EpiTYPER, including sites annotating to wingless-type MMTV integration site family member 3 (WNT3), distal-less homeobox 1 (DLX1), neuroligin 1 (NLGN1), and neurofibromin 2 (NF2). Initial bisulfite capture-sequencing showed that WNT3 and DLX1 were hypomethylated specifically in POL-GD9 and POL-GD17 offspring, respectively, whereas differential methylation of NLGN1 and NF2 occurred in both prenatal treatment conditions relative to controls (**Supplementary Table 3,4**). Consistent with these results, EpiTYPER revealed that WNT3 was hypomethylated selectively in POL-GD9 offspring relative to controls (**Figure 3B**), whereas reduced methylation of DLX1 occurred specifically in POL-GD17 offspring (**Figure 3C**). EpiTYPER further confirmed that both prenatal treatment conditions showed reduced and increased methylation levels at NLGN1 (**Figure 3D**) and NF2 (**Figure 3E**) gene segments, respectively, as predicted by capture sequencing (**Supplementary Table 9**).

### **Enrichment of Genes Affected by Prenatal Immune Activation in Middle or Late Gestation**

The 2365 CpGs affected by prenatal immune activation in middle gestation (GD 9) matched to 1408 unique genes, whereas the 3361 CpGs affected by the late (GD 17) prenatal manipulation corresponded to 1756 unique genes. We incorporated these genes into GO term enrichment analysis to explore whether the affected genes in POL-GD9 and POL-GD17 offspring share specific functional features. For both prenatal treatment conditions, the most significant enrichment occurred in GO-term category “biological process” involving genes annotating with the term “single organism cellular process”, followed by “cell differentiation” (**Supplementary Table 11**). Within the latter, “neuronal differentiation” resulted as the biological process characterized by the highest enrichment score in both prenatal treatment conditions (**Figure 4**). However, different sets of genes

annotating with “neuronal differentiation” were affected by prenatal immune activation in middle (GD 9) and late (GD 17) gestation (Figure 4). For example, late prenatal immune activation changed the methylation profiles of various genes that are involved in the differentiation of  $\gamma$ -aminobutyric acid (GABA) (Figure 4B; Supplementary Tables 4 and 11), including members of the LIM homeobox (Lhx) and distal-less homeobox (Dlx) transcription factor families (40-42). In contrast, genes included in the canonical Wnt signaling pathway (Figure 4A) were affected primarily by prenatal immune activation in middle gestation (Figure 4A, Supplementary Tables 3 and 12).

Besides these timing-dependent effects, however, prenatal immune activation in middle and late gestation also affected a number of common genes: the 335 CpG sites that were commonly affected by the two prenatal manipulations matched to 167 genes (Supplementary Tables 3 and 4). Notably, some of the commonly affected genes have previously been associated with neurodevelopmental disorders, including neuregulin 1 (NRGN1) (43,44), neurexin 2 (NRXN2) (45,46), neuronal differentiation 6 (NEUROD6) (47), and ephrin-B3 (EFNB3) (48,49). GO enrichment analysis of the commonly affected genes further revealed a strong enrichment of genes annotated with the term “neuron part” under the GO-term category “cellular component” (Supplementary Table 13). This term encompasses several neuronal elements such as neuronal projection, presynaptic and postsynaptic membranes, and axonal parts (Figure 5A), the development of which are under the control of genes commonly affected by prenatal immune activation in middle and late gestation (Figure 5B).

### Altered Gene Transcription Following Prenatal Immune Activation in Middle or Late Gestation

We examined whether the identified DNA methylation changes translate into altered gene expression (17-19,50). First, we measured the mRNA levels of those genes, for which DNA methylation differences were validated using EpiTYPER (i.e., MID1, WNT3, DLX1, NLGN1, and NF2; see Figure 3). As predicted by the preceding DNA methylation

analyses, the mRNA levels of WNT3 were altered selectively in POL-GD9 offspring, whereas DLX1 mRNA levels were altered specifically in POL-GD17 offspring (**Figure 6**). On the other hand, the mRNA levels of MID1, NLGN1 and NF2, which were differentially methylated in both prenatal treatment groups (**Figure 3, Supplementary Tables 3 and 4**), were similarly altered in POL-GD9 and POL-GD17 offspring (**Figure 6**).

We further confirmed that the mRNA levels of several genes, which were differentially methylated according to the initial genome-wide capture sequencing approach, were altered in prenatally infected offspring relative to controls (**Supplementary Figure 6**). These included genes that are part of the canonical Wnt signaling pathway, GABAergic cell differentiation, and neuronal development (**Supplementary Figure 6**).

### **Ontogeny of Altered DNA Methylation Following Prenatal Immune Activation in Middle or Late Gestation**

To explore the ontogeny of the DNA methylation changes that are manifest in adult offspring of infected mothers, we assessed possible methylation differences in neonatal (PND 1) offspring of immune-challenged and control offspring. To this end, we focused on MID1, NLGN1 and NF2, all of which were differentially methylated in the adult offspring of infected mothers. EpiTYPER analyses showed that there were no significant group differences in neonatal DNA methylation levels (**Figure 7**). Consistent with these findings, there were also no group differences with respect to mRNA levels of MID1, NLGN1 and NF2 during the neonatal stage of development (**Figure 7**).

## **DISCUSSION**

The present study shows that maternal immune activation causes long-term and genome-wide changes in the offspring's prefrontal DNA methylome. These changes are characterized by hyper- and hypomethylated CpGs at numerous loci and at distinct genomic regions. Hence, the epigenetic effects of prenatal immune activation are not restricted to specific DNA sequences but readily extend to the entire genome. **These**

epigenetic modifications likely have functional consequences in terms of modulating the transcription of the corresponding genes. Indeed, we found altered mRNA levels of various genes showing differential methylation levels in prenatally infected offspring relative to controls. Consistent with the repressive effects of DNA hypermethylation on gene transcription (50-52), the mRNA levels of predominantly hypermethylated genes, including MID1 and NF2, were decreased in adult offspring of infected mothers, whereas the mRNA levels of some genes with a predominance of hypomethylated regions (e.g., WNT3 and NTM) were increased. Interestingly, however, the mRNA levels of several hypomethylated genes, including DLX1, LMO4, FEZF2, SOX1 and SOX5, were decreased rather than increased in adult offspring exposed to prenatal immune activation. These effects are consistent with recent lines of evidence suggesting that the functional impact of DNA methylation on gene transcription is critically determined by the genomic location at which methylation occurs (50-52).

Our study further shows that the effects on the adult DNA methylome are influenced by the precise timing of the prenatal immune challenge. Whilst immune activation in middle (GD 9) and late (GD 17) gestation affected a relatively small number of common genes, the two prenatal conditions mostly showed methylation differences in distinct loci. The differential epigenetic effects of middle versus late prenatal immune activation may, at least in part, be accounted for by differences in the precise maternal and fetal immune responses to poly(I:C) at the selected gestational time points (**Supplementary Discussion**). One intriguing distinction between the epigenetic effects of the two manipulations relates to methylation differences in genes that are crucial for GABAergic cell development and functions. We show that the late prenatal insult leads to differential methylation and transcription of members of the Lhx and Dlx transcription factor families, whereas similar effects were absent following prenatal immune activation in middle gestation. Lhx and Dlx transcription factors play pivotal roles in the phenotypic specification, migration, and/or survival of GABAergic cell populations (41-43,54). Previous work in rodent models has repeatedly demonstrated that prenatal immune

challenge can induce functional and structural abnormalities in prefrontal (and other) GABAergic systems (16,26,54,55), and these tend to be more pronounced following immune activation in late as compared to middle gestation (26,35,56). For example, prenatal poly(I:C)-induced immune activation has been shown to reduce basal GABA contents in the offspring's brains when the exposure takes place in late (GD 17) gestation (35), whereas identical immune activation in middle (GD 9) gestation fails to do so (56). Mice prenatally exposed to poly(I:C) on GD 17 also show an overall reduction in the GABA-synthesizing enzymes GAD<sub>65</sub> and GAD<sub>67</sub> in prefrontal and hippocampal regions (16,57), whereas similar effects are absent (58) or appear to be cell-specific (59) when the same immune exposure takes place on GD 9. Despite this, however, prenatal immune activation in middle gestation can still alter GABAergic neurotransmission, even in the absence of overt morphological abnormalities (59). The current state of research thus suggests that discrete GABAergic functions may be impaired by prenatal immune activation regardless of the precise prenatal timing, whereas late prenatal immune activation may have more overt effects on (prefrontal) GABAergic cell morphology and gene expression compared to identical exposures during earlier gestational periods. Against this background, our findings indicate that GABAergic abnormalities following late prenatal immune activation may involve methylation-related epigenetic modifications of transcription factors that are critical for GABAergic cell development and functions.

On the contrary, Wnt signaling stood out as one of the pathways markedly affected by prenatal immune activation in middle gestation. Wnt signaling is fundamental in embryogenesis and controls various early events in the developing nervous system, including specification of the anterior-posterior axis of the neural plate, neural tube formation, neuronal polarization, and early development of neural circuitries (60). Wnt signaling also participates in later stages of brain development and various adult brain functions, including synapse formation and remodeling, neuroplasticity, and neurotransmission (61,62). Given that Wnt signaling is disrupted more extensively by prenatal immune activation in middle as compared to late gestation, one may speculate

that the earlier exposure leads to more severe neurodevelopmental deficits compared to the later prenatal exposure. In support of this notion, it has previously been shown that prenatal poly(I:C)-induced immune activation in middle gestation (GD 9), but not in late gestation (GD 17), leads to enlarged lateral ventricles in adulthood (27). Moreover, adult mice prenatally exposed to poly(I:C) on GD 9 show more extensive changes in white matter microstructure compared to mice exposed to the same insult on GD17 (63). These findings tentatively suggest that immune activation at earlier fetal stages may indeed be associated with more pronounced brain morphological changes compared to immune activation at later fetal stages. However, additional studies are warranted to further examine this hypothesis and to ascertain whether (methylation-induced) changes in Wnt signaling contribute to these effects.

The differential effects of prenatal immune activation in middle and late gestation on the prefrontal methylome are consistent with and extend previous findings emphasizing a critical influence of the precise prenatal timing in shaping the specificity of long-term behavioral and cognitive abnormalities (22,25-27,35). Here, the inclusion of two prenatal time points of immune activation allowed us to identify possible relationships between differential DNA methylation profiles and specific behavioral and cognitive deficits. On speculative grounds, altered methylation of GABA-related genes may contribute to the emergence of cognitive deficits in offspring exposed to late prenatal immune activation, whereas altered Wnt signaling may contribute to the sensorimotor gating impairments in offspring exposed to immune activation in middle gestation (see **Supplementary Discussion**).

Despite these possible associations, it should be pointed out that prenatal immune activation appears to cause differential methylation of a large number of genes, which in turn likely affects the differentiation and/or functional properties of various other neuronal subtypes. One of the genes that were markedly affected by both prenatal manipulations was MID1. MID1 was first identified as part of the genetic basis of Opitz BBB/G syndrome, a rare hereditary disorder characterized by ventral midline malformations (64). Since then,



MID1 has been associated with numerous cellular and developmental functions, many of which relate to brain development and maturation (65). Of particular interest is MID1's involvement in axonal growth, cerebellar development, and corpus callosum formation (66,67), the disruption of which likely plays an important role in neurodevelopmental disorders such as schizophrenia and autism (68-71). Moreover, both prenatal treatment conditions caused differential methylation of genes relevant for the differentiation of dopaminergic neurons. The latter effects support previous findings indicating that prenatal immune activation affects dopaminergic development (14,72) and further suggest that multiple neurotransmitter systems and pathways may contribute to the emergence of behavioral and cognitive abnormalities in prenatally infected offspring.

Another intriguing finding of our study is that the pattern of prefrontal DNA methylation in prenatally infected offspring changes over time. We found that MID1, NLGN1 and NF2, all of which were differentially methylated in the adult offspring of infected mothers, did not show abnormal methylation patterns in the neonatal offspring. It therefore seems that the changes in the adult DNA methylome are not the direct consequence of the maternal immune response. Rather, our findings suggest the involvement of dynamic and age-dependent epigenetic processes in infection-mediated neurodevelopmental pathologies. According to this notion, prenatal immune activation may interfere with epigenetic programs that are crucial for normal brain maturation and may disrupt the developmentally regulated expression of factors governing DNA methylation at different stages of brain development (18,73). For example, prenatal immune activation may lead to age-dependent changes in the expression of DNA-methylating enzymes such as DNA methyltransferases (17,18,50), which in turn may modulate the prefrontal methylome in an age-dependent manner. Additional research is needed to examine this hypothesis.

Our study has a number of limitations. Firstly, we only assessed genome-wide DNA methylation profiles in the PFC. It thus remains elusive whether the identified epigenetic changes induced by prenatal immune activation are specific to the PFC, or alternatively, whether they can be extended to other brain regions or even peripheral tissues. Secondly,

we focused on epigenetic modifications in the form of DNA methylation. Prenatal immune activation, like various other early-life adversities such as prenatal or neonatal stress (74-76), might further induce various other epigenetic modifications across the entire genome, which would not have been captured here. **Thirdly, even though we find a striking correspondence between altered DNA methylation and transcriptional activity for selected genes, our study does not provide circumspect statistical analyses of the overall relationship between altered DNA methylation and gene expression following prenatal immune activation. Finally, additional research will be needed to validate our findings at the protein level and in peripheral tissues such as blood, the latter of which may help to define methylation-related biomarkers for prenatal infection-induced pathologies.**

There is increasing recognition of and evidence for altered DNA methylation in the pathogenesis of neurodevelopmental disorders, including schizophrenia, autism, and bipolar disorder (50,77-83). Against these backgrounds, our findings raise the intriguing possibility that prenatal exposure to immune challenges may be one of the environmental factors causing genome-wide methylation abnormalities in these disabling brain disorders. Since at least some of these epigenetic modifications may be modifiable throughout life (17,84), our data may help to open new avenues for symptomatic or even preventive treatments in subjects with prenatal infectious histories.

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## TABLES & FIGURES LEGENDS

**Table 1.** Genomic distribution of differentially methylated CpGs (single base resolution) measured by capture sequencing in **adult** offspring exposed to poly(I:C)-induced immune activation in **middle** (POL-GD9) or late (POL-GD17) gestation relative to **adult** control offspring (CON). The columns describe the number of affected genomic regions, the enrichment of each affected region relative to the total number of affected regions, and the percentage of hyper- and hypo-methylated regions. Promoter defined as -1kb to +100 bp to TSS.

**Figure 1.** Cognitive and behavioral deficits in **adult offspring exposed to** prenatal immune activation in **middle** or late gestation. Mice were subjected to prenatal poly(I:C) treatment on gestation day 9 (POL-GD9) or 17 (POL-GD17), or they were exposed to prenatal control (CON) treatment. **(A)** Percent time spent in the novel arm during the Y-maze working memory test.  $*p < 0.05$  and  $**p < 0.01$ , based on post-hoc comparisons following significance ( $F_{(2,33)} = 6.85$ ,  $p < 0.01$ ) in one-way ANOVA. **(B)** Percent time spent with an unfamiliar live mouse, relative to an inanimate dummy object, during the social interaction test.  $*p < 0.05$  and  $**p < 0.01$ , based on post-hoc comparisons following significance ( $F_{(2,33)} = 5.63$ ,  $p < 0.01$ ) in one-way ANOVA. **(C)** The line plot shows percent prepulse inhibition as a function of different prepulse intensities, and the bar plot depicts mean prepulse inhibition across all prepulse levels.  $*p < 0.05$  and  $**p < 0.01$ , based on post-hoc comparisons following the presence of a significant main effect of prenatal treatment ( $F_{(2,33)} = 4.96$ ,  $p < 0.05$ ) in the initial  $3 \times 5$  (prenatal treatment  $\times$  prepulse intensity) ANOVA.  $N = 12$  in each group and test; all data are means  $\pm$  s.e.m.

**Figure 2.** Unique and common DNA methylation differences in **adult offspring exposed to** prenatal immune activation in **middle** or late gestation as revealed by capture sequencing. Mice were subjected to prenatal poly(I:C) treatment on gestation day 9 (POL-GD9) or 17 (POL-GD17), or they were exposed to prenatal control (CON) treatment. **(A)** Hierarchical clustering of differentially methylated CpGs in POL-GD9 and POL-GD17 offspring relative to CON offspring. Hypo- and hypermethylated CpGs are represented in purple and yellow color, respectively. **(B)** Venn Diagram depicting the number of CpGs that are uniquely and commonly affected in POL-GD9 and POL-GD17 offspring (**hypergeometric distribution test for common sites:  $p = 3.86E-2830$** ). The commonly affected CpGs show a significant positive correlation between the two prenatal treatment conditions. **The inter-replicate correlations for each group are given in Supplementary Table 7.** All data are based on  $N(\text{CON}) = 6$ ,  $N(\text{POL-GD9}) = 5$ , and  $N(\text{POL-GD17}) = 5$ .

**Figure 3.** EpiTYPER validation of DNA methylation differences in adult offspring exposed to prenatal immune activation in middle or late gestation. Mice were subjected to prenatal poly(I:C) treatment on gestation day 9 (POL-GD9) or 17 (POL-GD17), or they were exposed to prenatal control (CON) treatment. The line plots depict percent DNA methylation of specific CpGs in selected amplicons, and the bar plots show the mean percent DNA methylation across all individual CpGs included in the corresponding amplicon. Amplicon sequences and position of CpGs in each amplicon are provided in *Supplementary Table 10*. **(A)** MID1:  $^+p < 0.05$  between individual CpGs of CON and POL-GD9 or POL-GD17 offspring,  $^{\#}p < 0.001$  between individual CpGs of CON and POL-GD17 offspring,  $^{\S}p < 0.01$  between individual CpGs of POL-GD17 and CON or POL-GD9 offspring, and  $^{\circ}p < 0.01$  between individual CpGs of POL-GD9 and POL-GD17 offspring based on post-hoc tests following the presence of a significant interaction between prenatal treatment and position in ANOVA (Amplicon 1:  $F_{(6,39)} = 2.34$ ,  $p < 0.05$ ; Amplicon 2:  $F_{(4,26)} = 2.43$ ,  $p < 0.05$ ; Amplicon 3:  $F_{(12,72)} = 2.913$ ,  $p < 0.001$ ).  $^*p < 0.05$ , reflecting group differences in mean percent DNA methylation based on post-hoc tests. **(B)** WNT3:  $^*p < 0.05$ , reflecting group differences in mean percent DNA methylation based on post-hoc tests following the presence of a significant main effect in ANOVA ( $F_{(2,13)} = 4.47$ ,  $p < 0.05$ ). **(C)** DLX1:  $^*p < 0.05$  and  $^{**}p < 0.01$ , reflecting group differences in mean percent DNA methylation based on post-hoc tests following the presence of a significant main effect in ANOVA ( $F_{(2,13)} = 6.20$ ,  $p < 0.05$ ). **(D)** NLGN1:  $^*p < 0.05$ , reflecting group differences in mean percent DNA methylation based on post-hoc tests following the presence of a significant main effect in ANOVA ( $F_{(2,13)} = 5.23$ ,  $p < 0.05$ ). **(E)** NF2:  $^+p < 0.05$  and between  $^{\dagger}p < 0.001$  individual CpGs of CON and POL-GD9 or POL-GD17 offspring based on post-hoc tests following the presence of a significant interaction between prenatal treatment and position in ANOVA ( $F_{(8,52)} = 6.39$ ,  $p < 0.001$ ).  $^*p < 0.05$  and  $^*p < 0.01$ , reflecting group differences in mean percent DNA methylation based on post-hoc tests. All data are means $\pm$ s.e.m.;  $N(\text{CON}) = 6$ ,  $N(\text{POL-GD9}) = 5$ , and  $N(\text{POL-GD17}) = 5$ .

**Figure 4.** GO enrichment analysis of genes showing differential methylation in adult offspring exposed to prenatal immune activation in middle **(A)** and late **(B)** gestation. The bar plots summarize the 10 most enriched processes encompassed by the term “cell differentiation” under the category “biological processes”. “Neuronal differentiation” (highlighted as filled red bars) showed the highest enrichment score in both prenatal treatment conditions. The networks (generated by the Ingenuity Pathway Analysis software) illustrate the interactions between the individual genes that are encompassed as

sub-terms (displayed as bars with diagonal red patterning) in the term “neuronal differentiation”. Hypo- and hypermethylated genes are represented in purple and yellow color, respectively.

**Figure 5.** GO enrichment analysis of genes showing common methylation differences following prenatal immune activation in middle and late gestation. **(A)** The bar plots summarize the 10 most enriched terms encompassed by the category “cellular component”. “Neuron projection” (highlighted as filled red bar) showed the highest enrichment score and included genes enriched for dendrite, axonal and spine development (displayed as bars with diagonal red patterning). **(B)** The network (generated by the Ingenuity Pathway Analysis software) illustrates the interactions between individual genes in relation to their biological functions they are enriched in.

**Figure 6.** Expression of selected genes that were differentially methylated in adult offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation relative to adult control (CON) offspring. The scatter dot plots show individual mRNA levels in terms of fold changes measured by TaqMan qRT-PCR. \* $p < 0.05$ , \*\* $p < 0.01$ , and \*\*\* $p < 0.001$ , based on post-hoc test following one-way ANOVA (DLX1:  $F_{(6,39)} = 2.34$ ,  $p < 0.05$ ; NF2:  $F_{(4,26)} = 2.43$ ,  $p < 0.05$ ; NLGN1:  $F_{(12,72)} = 2.913$ ,  $p < 0.001$ ; MID1:  $F_{(12,72)} = 2.913$ ,  $p < 0.001$ ; WNT3:  $F_{(4,26)} = 2.43$ ,  $p < 0.05$ ).  $N = 9-12$  per group.

**Figure 7.** DNA methylation and gene expression profiles in neonatal offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation relative to adult control (CON) offspring. Mice were subjected to prenatal poly(I:C) treatment on gestation day 9 (POL-GD9) or 17 (POL-GD17), or they were exposed to prenatal control (CON) treatment. DNA methylation and gene expression of selected genes were measured on postnatal day 1 using EpiTYPER and TaqMan qRT-PCR, respectively. The line plots depict percent DNA methylation (means $\pm$ s.e.m) of specific CpGs in selected amplicons, and the bar plots show the mean percent DNA methylation (means $\pm$ s.e.m) across all individual CpGs included in the corresponding amplicon. Amplicon sequences and position of CpGs in each amplicon are provided in *Supplementary Table 10*. The scatter dot plots show individual mRNA levels in terms of fold changes. For EpiTYPER,  $N(\text{CON}) = 6$ ,  $N(\text{POL-GD9}) = 5$ , and  $N(\text{POL-GD17}) = 5$ ; for qRT-PCR,  $N(\text{CON}) = 8$ ,  $N(\text{POL-GD9}) = 7$ , and  $N(\text{POL-GD17}) = 8$ .

**Table 1**

<b>POL-GD9 versus CON offspring</b>				
<b>Genomic regions</b>	<b>Number of regions</b>	<b>Percent of total regions (%)</b>	<b>Hyper-methylated (%)</b>	<b>Hypo-methylated (%)</b>
Total	2365	100.0	35	65
CpG islands	69	2.9	45	55
Promoter	178	7.5	48	52
Introns	1001	42.5	34	66
Exons	140	5.9	35	65
Intergenic	793	33.5	33	67
Other	184	7.7	36	64
<b>POL-GD17 versus CON offspring</b>				
<b>Genomic regions</b>	<b>Number of regions</b>	<b>Percent of total regions (%)</b>	<b>Hyper-methylated (%)</b>	<b>Hypo-methylated (%)</b>
Total	3361	100.0	37	63
CpG islands	75	2.3	63	37
Promoter	278	8.3	40	60
Introns	1518	45.2	37	63
Exons	204	6.0	34	66
Intergenic	1233	36.6	36	64
Other	53	1.6	39	61

Figure 1  
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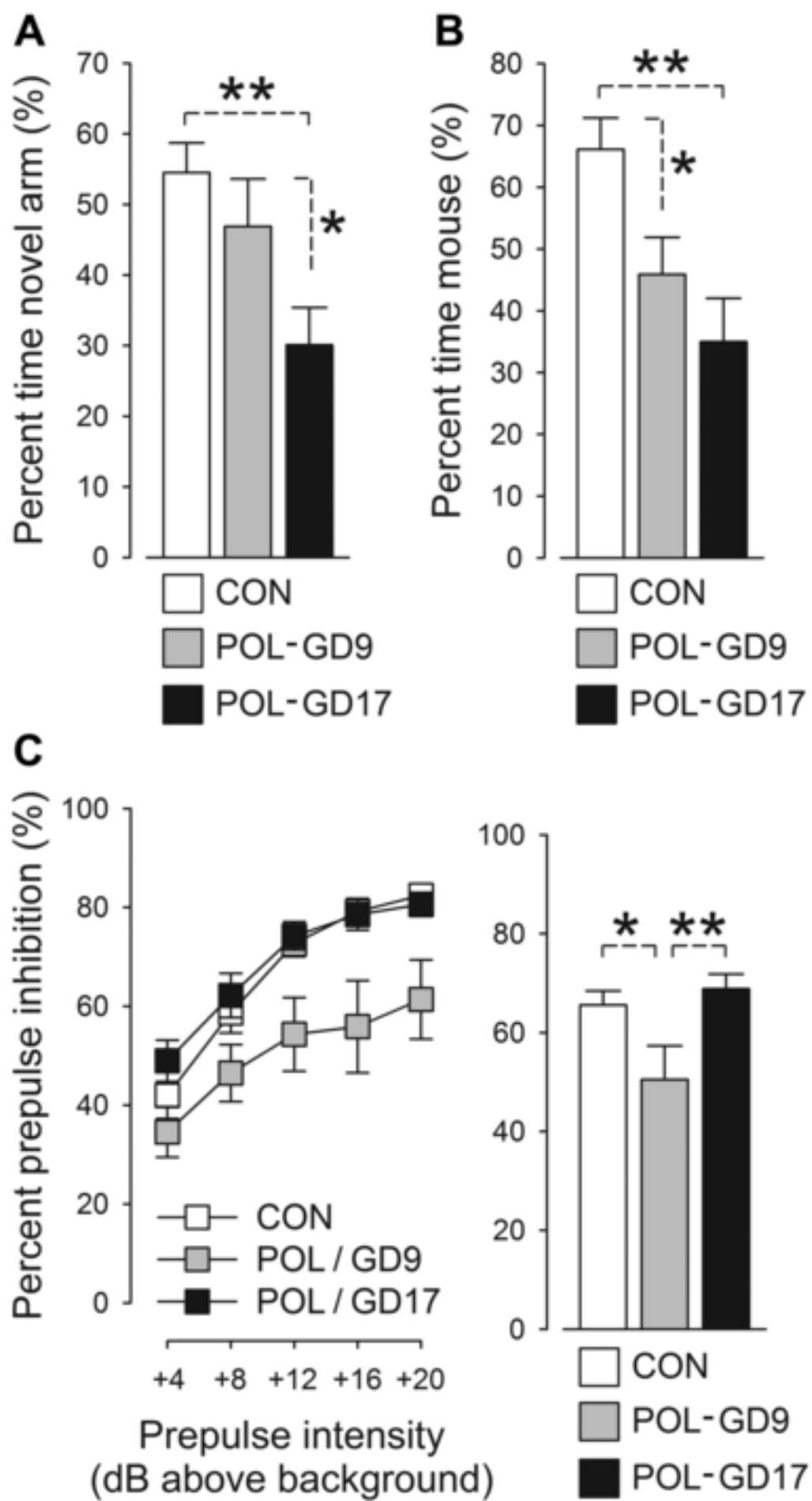
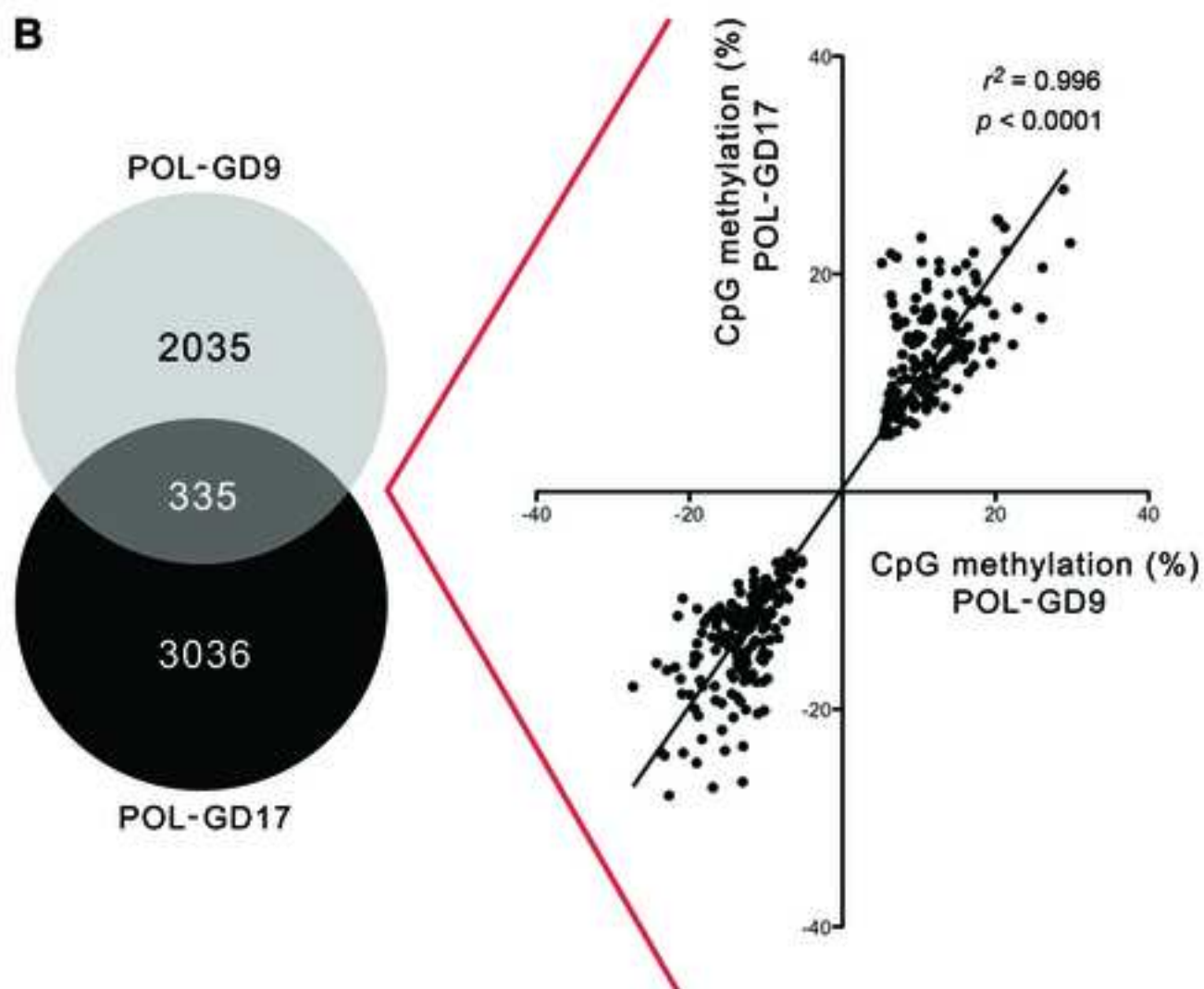
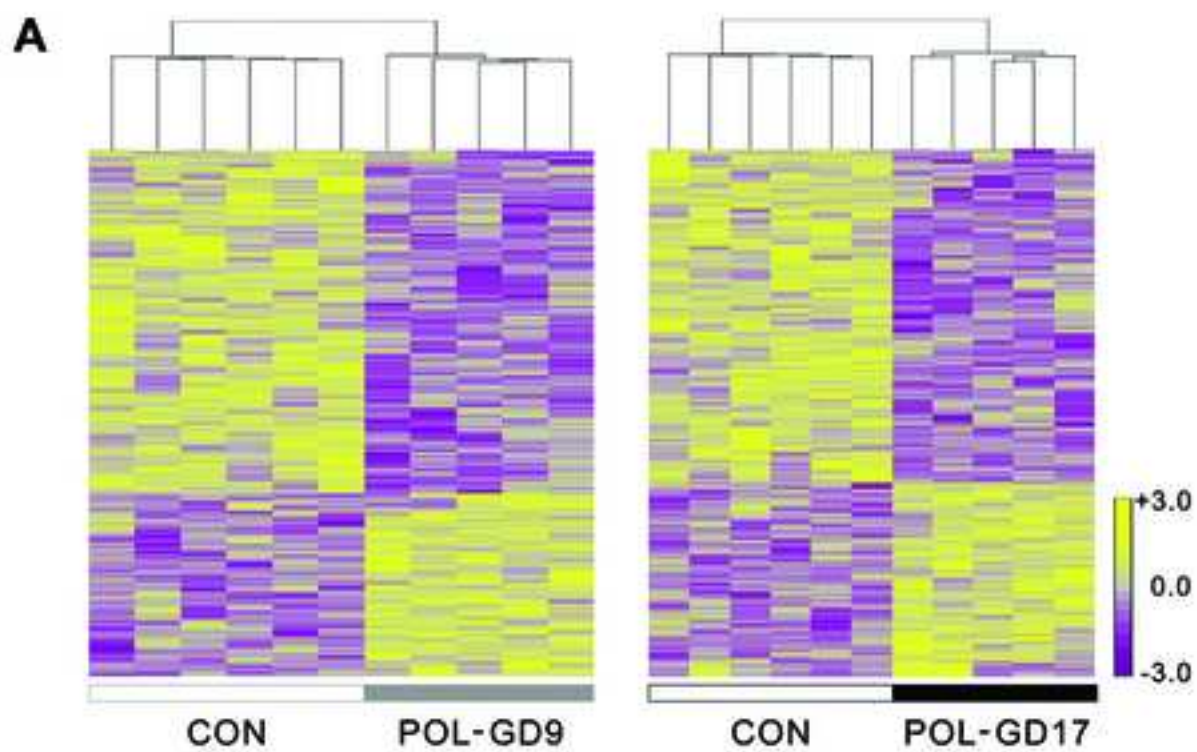
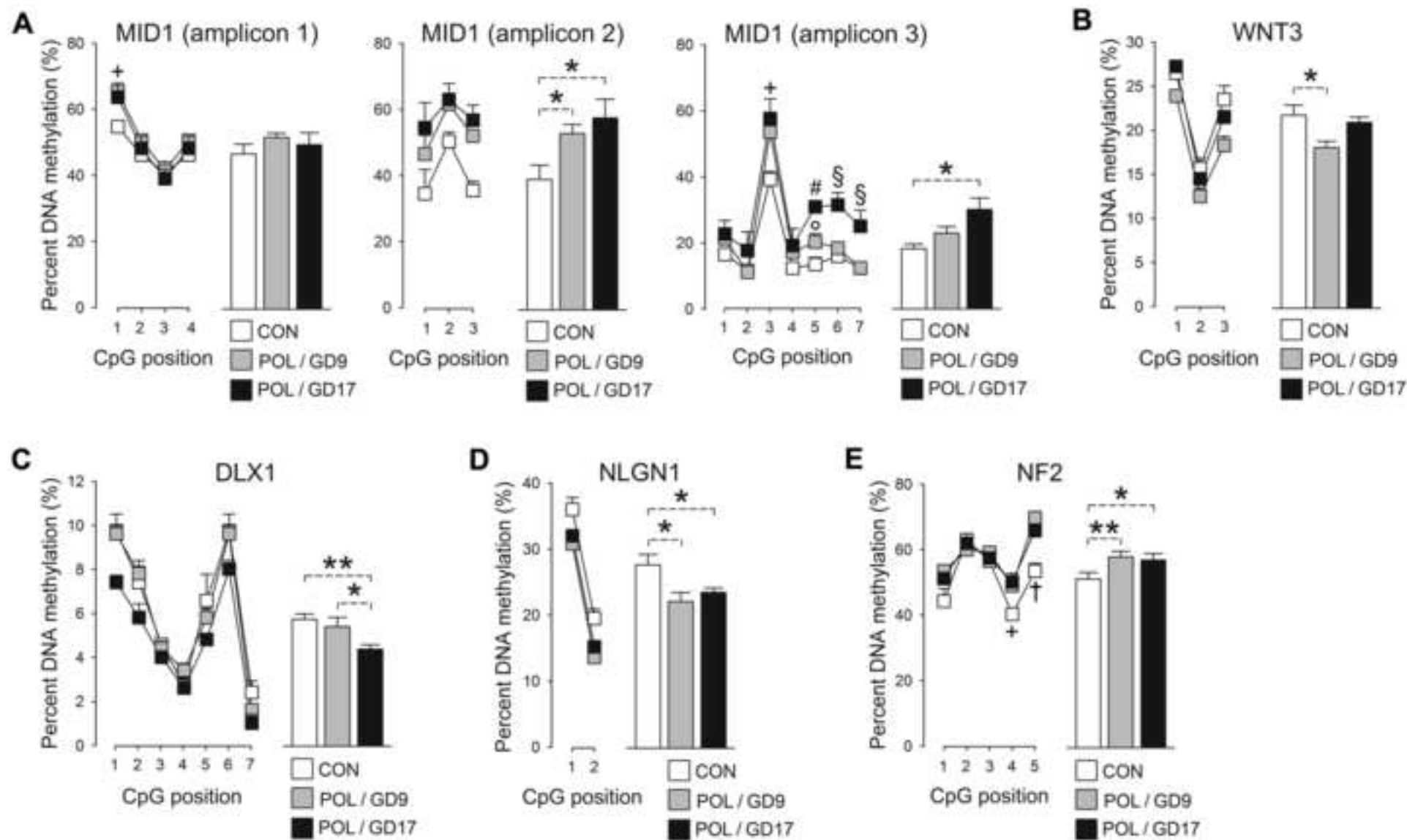


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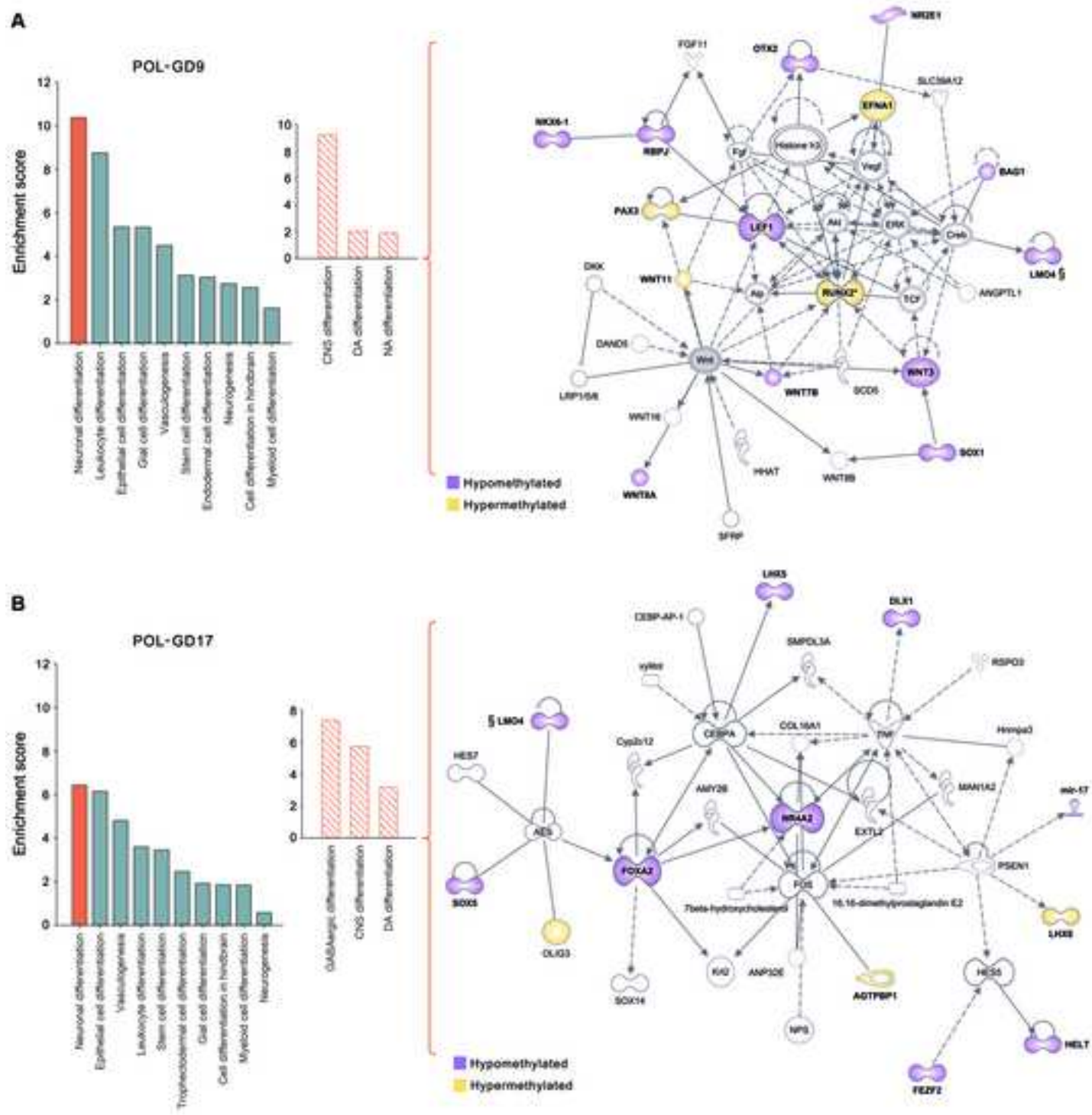




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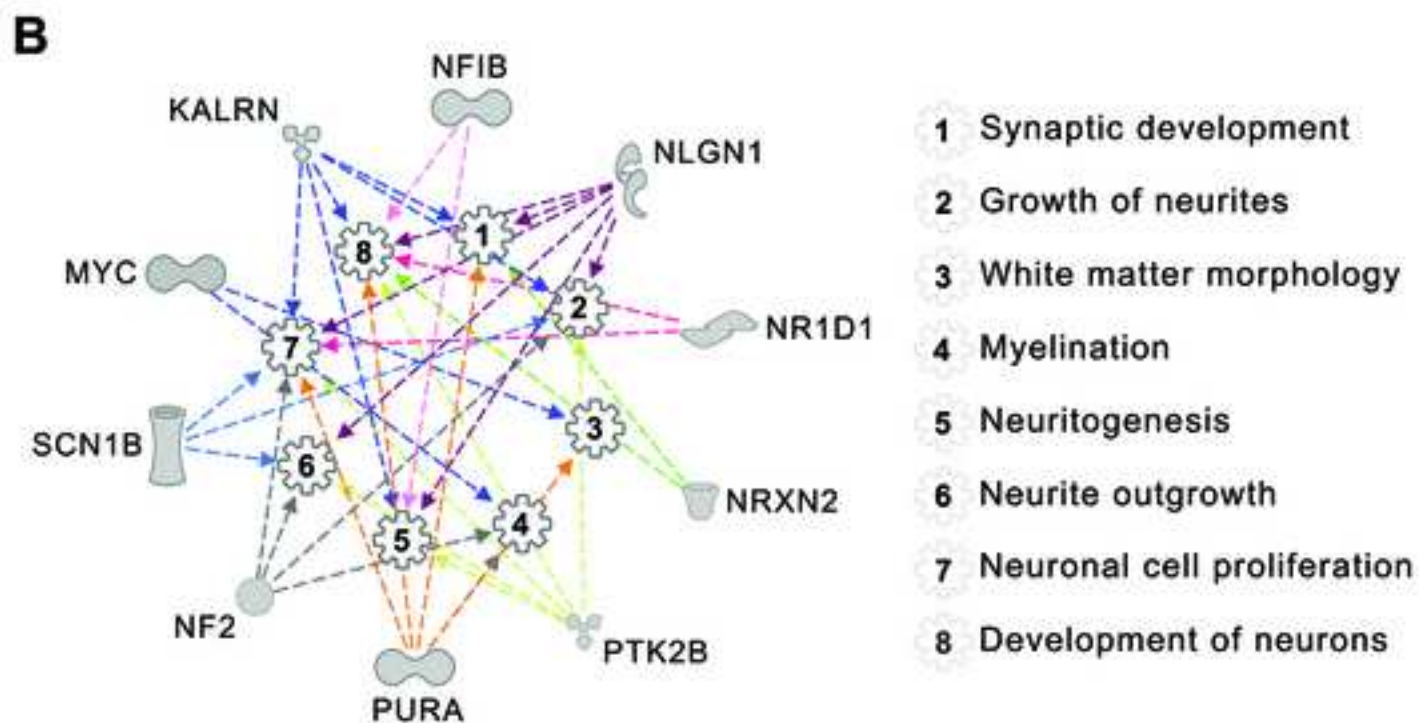
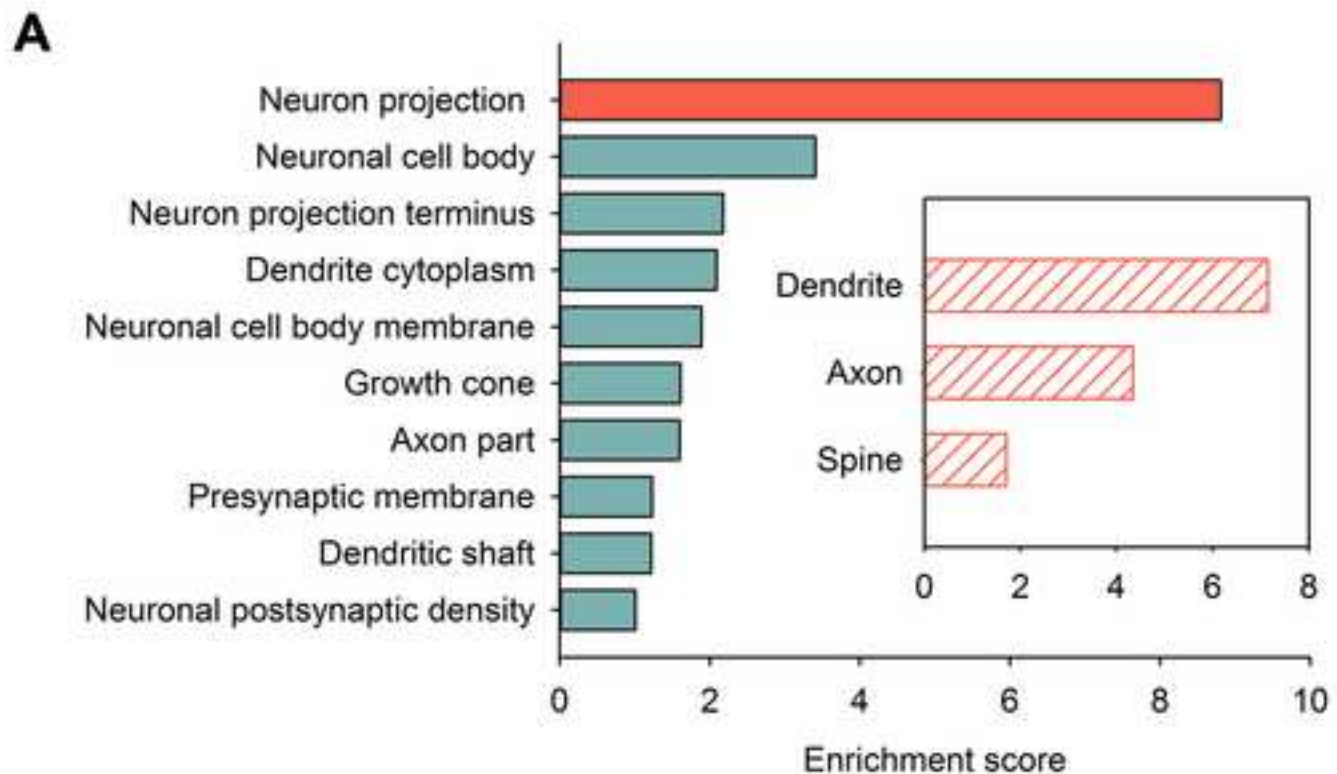


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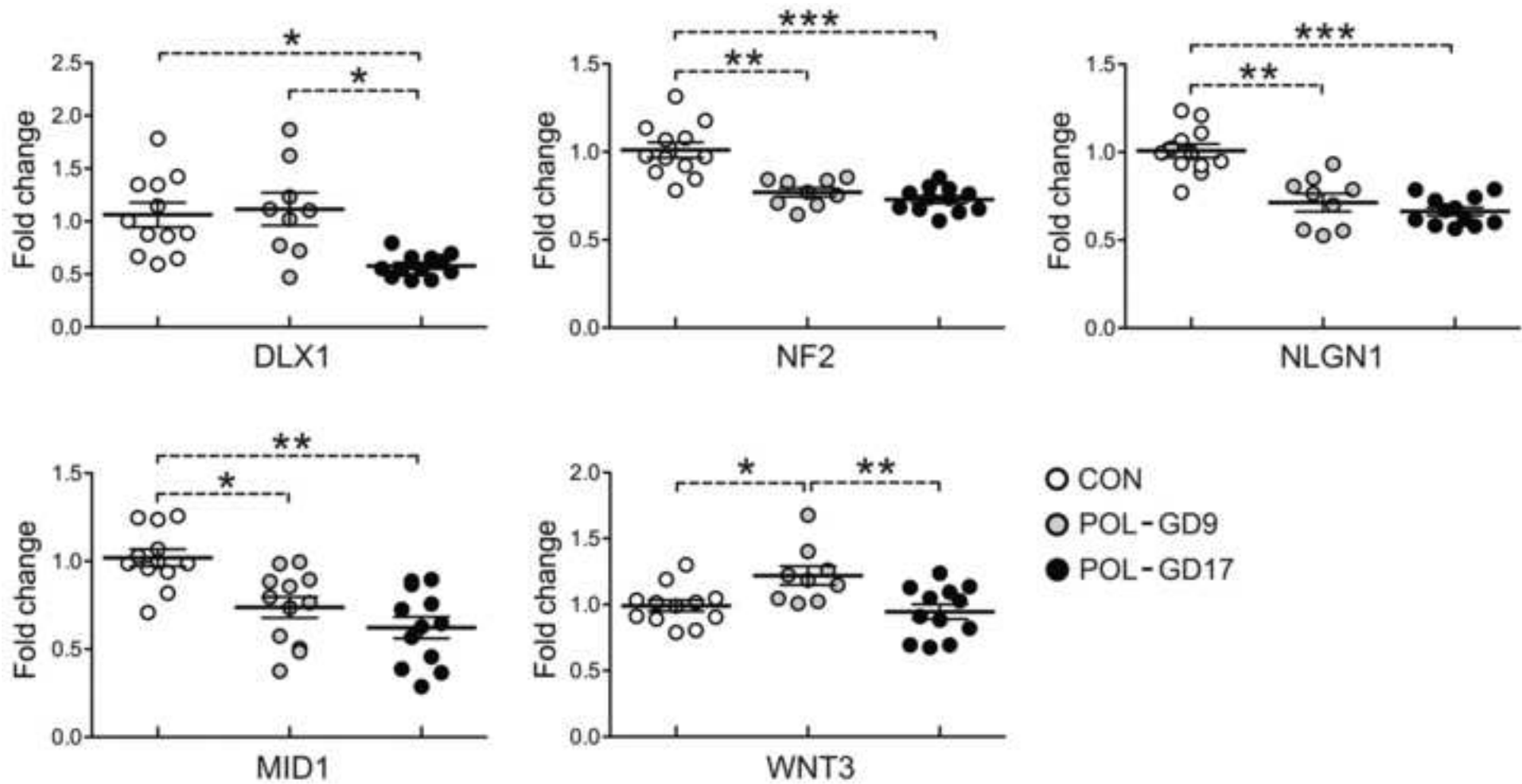
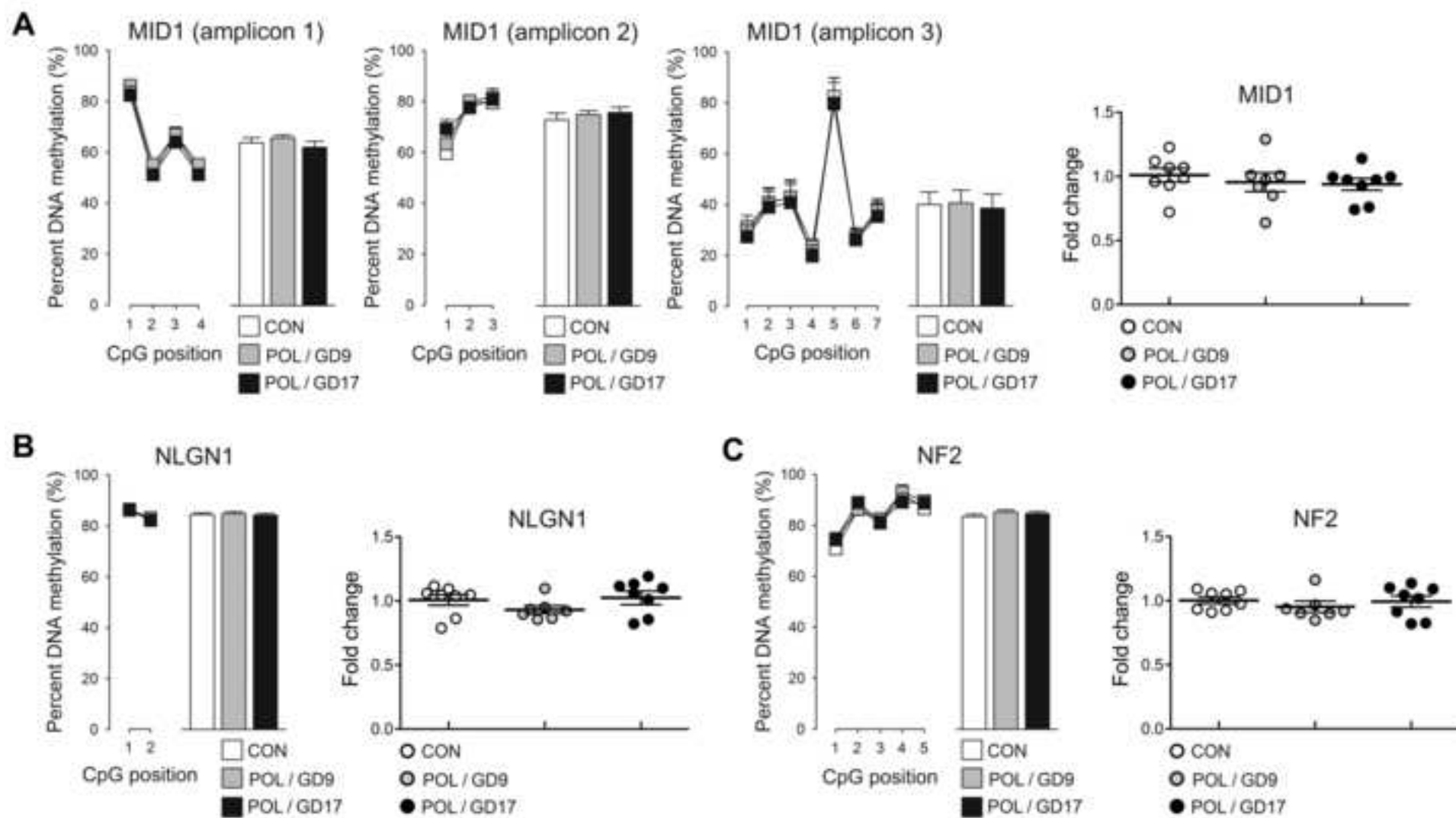


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## SUPPLEMENTARY INFORMATION

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### Genome-Wide DNA Methylation Changes in a Mouse Model of Infection-Mediated Neurodevelopmental Disorders

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# SUPPLEMENTARY MATERIAL AND METHODS

## ***Animals***

C57Bl6/N mice were obtained from Charles River Laboratories (Germany) and kept in our in-house specific-pathogen-free (SPF) facility until breeding began to generate poly(I:C)-exposed and control offspring (see below). All animal breeding and holding rooms were temperature- and humidity-controlled ( $21 \pm 1$  °C,  $55 \pm 5\%$ ) and kept under a reversed light–dark cycle (lights off: 7:00 A.M. to 7:00 P.M.). All animals had *ad libitum* access to food (Kliba 3430, Kaiseraugst, Switzerland) and water throughout the entire study.

## ***Prenatal Immune Activation***

Female mice were subjected to a timed mating procedure as established and described previously (1). Pregnant dams on gestation day (GD) 9 or 17 were randomly assigned to receiving either a single injection of poly(I:C) (potassium salt; Sigma–Aldrich, Buchs, St. Gallen, Switzerland) or vehicle. Poly(I:C) (5 mg/kg; calculated based on the pure form of poly(I:C)) was dissolved in sterile pyrogen-free 0.9% NaCl (vehicle) solution to yield a final concentration of 1 mg/ml and was administered intravenously (i.v.) into the tail vein under mild physical constraint. The dose of poly(I:C) was selected based on previous dose-response studies (1). 12 pregnant dams were injected with poly(I:C) on GD 9, 12 were injected with poly(I:C) on GD 17, and another 12 were injected with vehicle solution. We previously verified that poly(I:C) administration at these gestational time points are effective in terms of eliciting cytokine-associated inflammatory response in maternal and fetal tissues (2). Half of the vehicle-treated dams were injected on GD 9, and the other half on GD 17, in order to control for the two timings of poly(I:C) injections. The two vehicle groups were combined into a single control group as they did not differ from each other in terms of behavioral and cognitive performances (see **Supplementary Figure 1**) and genome-wide methylation levels (see **Supplementary Figure 3**).

### ***Allocation of Offspring***

Except when used for molecular analyses during neonatal stages (see below), offspring of dams injected with poly(I:C) on GD 9 (POL-GD9 offspring) or GD 17 (POL-GD17 offspring) and vehicle-exposed control offspring (CON offspring) were weaned and sexed on postnatal day (PND) 21. Littermates of the same sex were caged separately and maintained in groups of 3 to 4 animals per cage. Only male animals were included in all experiments because our previous research using the mouse prenatal poly(I:C) administration model did not reveal sex-dependent effects on behavioral and cognitive functions of primary interest, including social interaction, prepulse inhibition, and short-term spatial memory (1,3,4) For adult testing, 1 male offspring per litter was randomly selected for the subsequent behavioral and molecular analyses in order to avoid litter effects (5,6). This led to initial group sizes of  $N = 12$  adult offspring per experimental group, which were used for behavioral tests and gene expression analyses (see below). All DNA methylation analyses in adult offspring were performed using a subset of animals. The group sizes in these latter analyses were  $N(\text{CON}) = 6$ ,  $N(\text{POL-GD9}) = 5$ , and  $N(\text{POL-GD17}) = 5$ . For adult investigations, all animals were first subjected to behavioral testing prior to the molecular analyses.

Neonatal CON ( $N = 8$ ), POL-GD9 ( $N = 7$ ) and POL-GD17 ( $N = 8$ ) offspring were generated as described above and were killed for molecular analyses on PND 1. The neonatal DNA methylation analyses were performed using a subset of animals, yielding a group size of  $N(\text{CON}) = 6$ ,  $N(\text{POL-GD9}) = 5$ , and  $N(\text{POL-GD17}) = 5$  offspring. The neonatal gene expression analyses were conducted using all offspring (i.e.,  $N = 7-8$  per neonatal group).

### ***Spatial Recognition Memory Test***

Spatial recognition memory was assessed using the Y-maze as established and validated before (7,8). This test uses the natural tendency of rodents to explore novel over familiar spatial environments. The apparatus was made of transparent Plexiglas and consisted of three identical arms (50 × 9 cm; length × width) surrounded by 10-cm high transparent

Plexiglas walls. The three arms radiated from a central triangle (8 cm on each side) and were spaced 120° from each other. A removable opaque barrier wall was used to block access to each arm from the central area. The floor of the maze was covered with sawdust bedding, which was changed between sample and choice phases. The maze was elevated 90 cm above the floor and was positioned in a well-lit room enriched with distal spatial cues. A digital camera was mounted above the Y-maze apparatus. Images were captured at a rate of 5 Hz and transmitted to a PC running the EthoVision tracking system (Noldus Information Technology, The Netherlands), which calculated the time spent and distance moved in the three arms and center zone of the Y-maze.

The spatial recognition memory test consisted of two phases, called the sample and choice phases. The allocation of arms (start, familiar, and novel arm) to a specific spatial location was counterbalanced across the experimental conditions.

Sample phase: The animals were allowed to explore two arms (referred to as “start arm” and “familiar arm”). Access to the remaining arm (“novel arm”) was blocked by the opaque barrier wall. To begin a trial, the animal was introduced at the end of the start arm and was allowed to freely explore both the start and the familiar arms for 5 min. Test timing was initiated once the subject had made an entry into the central triangular area, as detected by the EthoVision tracking system. The animal was then removed and kept in a holding cage prior to commencement of the choice phase. The barrier door was removed and the sawdust flooring changed to avoid olfactory cues.

Choice phase: The animal was introduced to the maze following a retention interval of 1 min. During the choice phase, the barrier wall was removed so that the animals could freely explore all arms of the maze for 2 min. The animal was then removed from the maze and returned to the home cage. The sawdust flooring was changed in preparation for the next trial.

On each trial, the time spent in each of the three arms was recorded. The relative time spent in the novel arm during the choice phase was calculated by the formula ( $[\text{time spent in the novel arm}] / [\text{time spent in all arms}] \times 100$ ) and used as the index for short-term spatial

recognition memory. In addition, total distance moved on the entire maze was recorded and analyzed in order to assess general locomotor activity.

### ***Social Interaction Test***

Social interaction was assessed by analyzing the relative exploration time between an unfamiliar congenic mouse and an inanimate dummy object using methods established before (4,9). The test apparatus was made of Plexiglas and consisted of three identical arms (50 cm × 9 cm; length × width) surrounded by 10-cm high Plexiglas walls. The three arms radiated from a central triangle (8 cm on each side) and spaced 120° from each other. The Plexiglas walls of apparatus were covered by brown self-adhesive paper. Two out of the three arms contained a rectangular wire grid cages (13 cm × 8 cm × 10 cm, length × width × height; bars horizontally and vertically spaced 9 mm apart). The third arm did not contain a metal wire cage and served as the start zone (see below).

All animals were first habituated to the test apparatus on the day before social interaction testing. This served to familiarize the test animals with the apparatus and to reduce novelty-related locomotor hyperactivity, which may potentially confound social interaction during the critical test phase. The rectangular wire cages (located at the end of two arms) were left empty during the habituation phase. During habituation, each test mouse was gently placed in the start arm and allowed to explore the apparatus for 10 min.

The critical test phase took place one day after the habituation day. During the test phase, one metal wire cage contained an unfamiliar male C57BL6/N mouse (10-12 weeks of age), whereas the other wire cage contained an inanimate dummy object. The latter was made of black LEGO™ bricks and took the shape of a mouse. The allocation of the unfamiliar live mouse and inanimate dummy object to the two wire cages was counterbalanced across experimental groups. To start a test trial, the test mouse was gently placed in the start arm and allowed to explore freely for 5 min. Behavioral observations were made by an experimenter blind to the experimental conditions, and social interaction was defined as nose contact within a 2-cm interaction zone. The relative time spent with the live



mouse was calculated by the formula  $([\text{time spent with the mouse}]/[\text{time spent with the inanimate object} + \text{time spent with the mouse}]) \times 100$  and used to compare the relative exploration time between the unfamiliar mouse and the inanimate dummy object. The animals were placed back to their home cages following completion of the social interaction test.

### ***Prepulse Inhibition Test***

Sensorimotor gating was assessed using the paradigm of prepulse inhibition (PPI) of the acoustic startle reflex. PPI of the acoustic startle reflex refers to the reduction in startle reaction in response to a startle-eliciting pulse stimulus when it is shortly preceded by a weak prepulse stimulus (1). The apparatus consisted of four startle chambers for mice (San Diego Instruments, San Diego, CA, USA) and has been fully described elsewhere (1). During a 45-min test session, the animals were presented with a series of discrete test trials comprising a mixture of four trial-types as fully described previously (1). In brief, these trial stimuli included pulse-alone, prepulse-plus-pulse and prepulse-alone trials, as well as no-stimulus trials in which no discrete stimulus other than the constant background noise (65 dB<sub>A</sub>) was presented. The startle program consisted of one 40-ms pulse of white noise (120 dB<sub>A</sub>) combined with five different pre-pulses. Pre-pulses were a 20-ms burst of white noise at five different intensities (69, 73, 77, 81, and 85 dB<sub>A</sub>, which corresponded to 4, 8, 12, 16, and 20 dB<sub>A</sub> above background). The stimulus onset asynchrony (SOA) of the pre-pulse and pulse stimuli in prepulse-plus-pulse trials was 100 ms. Following a 2-min acclimatization period, 6 consecutive pulse-alone trials were presented in order to habituate and stabilize the animals' startle response. Subsequent to this startle habituation phase, each trial stimulus was presented 12 times in a pseudorandom order with an average interval between successive trials (ITI) of  $15 \pm 5$  s. The session was concluded with 6 consecutive pulse-alone trials. Boxes were cleansed with warm tap water and dried between each animal. For each animal and at each of the 5 possible prepulse intensities, PPI was indexed by percent inhibition of startle response obtained in the prepulse-plus-pulse-trials compared to pulse-alone trials by

following expression:  $[1 - (\text{mean reactivity on prepulse-plus-pulse trials} / \text{mean reactivity on pulse-alone trials}) \times 1/100]$ . The first and last six trials were not included in the calculation and analysis of percent PPI. In addition to PPI, the reactivity to pulse-alone trials was also analyzed.

### ***DNA and RNA Isolation and Quantitative Real-Time PCR Analyses***

Total DNA and RNA were isolated using the Qiagen AllPrep DNA and RNA Mini kit (Qiagen, Italy) according to the manufacturer's instructions, and quantified by spectrophotometric analysis. An aliquot of each RNA sample was then treated with DNase to avoid DNA contamination. RNA was analysed by TaqMan qRT-PCR instrument (CFX384 real-time system, Bio-Rad Laboratories) using the iScript one-step RT-PCR kit for probes (Bio-Rad Laboratories). The samples were run in 384-well formats in triplicates as multiplexed reactions with a normalizing internal control (36B4). We choose 36B4 as internal standard for gene expression analyses since its expression was not affected by the prenatal treatments (10).

Thermal cycling was initiated with an incubation at 50°C for 10 min (RNA retrotranscription) and then at 95°C for 5 min (TaqMan polymerase activation). After this initial step, 39 cycles of PCR were performed. Each PCR cycle consisted of heating the samples at 95°C for 10 s to enable the melting process and then for 30 s at 60°C for the annealing and extension reaction. Relative target gene expression was calculated according to the  $2^{-(\Delta\Delta C(T))}$  method (11). Custom-designed probe and primer sequences used for the various genes of interest and reference gene (36B4) are summarized below (see *next page*) and were purchased from Eurofins Genomics GmbH (Germany).

Gene	Forward Primer	Reverse Primer	Probe
<i>MID1</i>	5'-CCCAGGTCCTAATTCCCAGAAAT-3'	5'-GGGTTGGGAGCTGTTAGGTAAT-3'	5'-TTGCCTTGGATTTTTCCCGG-3'
<i>NTM</i>	5'-CCATCCCAAATTTTCATCGGTCC-3'	5'-ACTTCATGACACACGCGACT-3'	5'-ACAGAGCAAGAAACAAGGGC-3'
<i>WNT3</i>	5'-ACTTTTGTGAGCCCAACCCA-3'	5'-TCCTTCCGTTTCTCCGCCT-3'	5'-CTTGCAATGTCACCTCCAC-3'
<i>NLGN1</i>	5'-CCGATACCACATAGCCTTTGGA-3'	5'-CAAACCTCAACCCTTCCCCTTG-3'	5'-ACCAGATGACCCTCAGATACTG-3'
<i>NF2</i>	5'-ACCTGGTTCTTTGGACTGCA-3'	5'-CTCCTCCTCAGCATTTCAGGA-3'	5'-CAGTTACCTTCACTTCTGGC-3'
<i>NR1D1</i>	5'-AAGTGTCTCTCCGTTGGCAT-3'	5'-AGGCTGCTCAGTTGGTTGT-3'	5'-CAAGAGAGAGAAGCAACGGATG-3'
<i>PURA</i>	5'-CAAGCTCATCGACGACTATGGA-3'	5'-TCGCATAAACACGCCGACT-3'	5'-CTTCTTCTCGATGTGGGTTCC-3'
<i>SCN1B</i>	5'-TATGAGCACAACACCAGCGT-3'	5'-CAACACCACAATGAGCACGT-3'	5'-GACAAGGCCAACAGAGATATGG-3'
<i>LMO4</i>	5'-CGGGAGATCGGTTTCACTACA-3'	5'-TGACCTCTCAGCAGACCTTCT-3'	5'-CACTTCAGAGCAATCCACTACTG-3'
<i>SOX1</i>	5'-AAGATGGCCAGGAAAACCC-3'	5'-GTGTTCTTCATGTGCAGCG-3'	5'-AGTGAAGGTCATGTCCGAG-3'
<i>SOX5</i>	5'-TGGTGTGGGCGAAAGATGAA-3'	5'-GGCTGTTTCTCTAGGTTGGTCA-3'	5'-CCCGACATGCACAATCCAA-3'
<i>DLX1</i>	5'-GAAGAGATGACCATGACCACCA-3'	5'-GAAGGAGACATTTGCTGGTTGG-3'	5'-CTGTGTTTATGGAGTTGGGCC-3'
<i>FEZF2</i>	5'-CAAGAACTGCTCAACCTCTGC-3'	5'-GCTCTCCAGAACTCCGAGTAA-3'	5'-TATGATCCCTCTCCAGCCTCTA-3'
<i>36B4</i>	5'-AGATGCAGCAGATCCGCAT-3'	5'-GTTCTTGCCCATCAGCACC-3'	5'-CGCTCCGAGGGAAGGCCG-3'

### SureSelectXT Capture Sequencing Assay

DNA concentrations of the samples were measured with a Qbit Fluorometer (Thermo Fisher Scientific, Canada). Genomic DNA was converted into bisulfite-sequencing samples for the Illumina paired-end multiplexed sequencing platform (Illumina, Canada) according to the manufacturer's instructions. Briefly, gDNA was sheared to fragments of 150-200 bp using a focused-ultrasonicator Covaris according to manufacturer's parameters (Covaris, D-Mark Biosciences Inc., Canada). Methylated adaptors were ligated according to SureSelect Methyl-Seq Capture protocol (Agilent, Canada). Samples were then hybridized for 24 hrs using the SureSelectXT Methyl-Seq kit, captured with streptavidin beads and eluted. Purified samples were then bisulfite converted with EZ DNA Methylation-Lightning kit (Zymo Research, Canada) and amplified with PCR using Takara EpiTaq HS enzyme (Clontech, Canada). The amplified bisulfite-treated library was then purified using AMPure XP beads (Agilent, Canada). The modified libraries were then indexed by PCR amplification and pooled

for multiplexed sequence analysis (16 samples on 3 lanes of flowcell). Purified libraries were then amplified on the Illumina flow cell with TruSeq PE Cluster Kit v3-cBot-HS (Illumina) and sequenced with Illumina HiSeq2000 (2 x 50 cycles). All the Illumina quality controls were found to be in order, including sample-independent controls, sample-dependent controls, staining controls, extension controls, target removal controls, hybridization controls, bisulphite conversion I and II controls, specificity controls, non-polymorphic controls and negative controls.

### ***Hierarchical Clustering of Differentially Methylated CpGs***

The methylation values of differentially methylated CpGs ( $q < 0.2$ ) were loaded into Partek Genomics Suite (Partek, USA) and were clustered according to the Hierarchical Clustering function of Partek Genomics Suite (4). For this purpose, the data was normalized with standardization (each column mean is zero, and the standard deviation is scaled to one), and then multidimensional scaling with a Euclidian distance metric was performed on the normalized samples to allow visualization of the distance between them.

### ***Validation of Methylation Differences by EpiTYPER***

To validate the methylation differences observed using the SureSelectXT capture-sequencing assay (see above), specific CpGs were analyzed with EpiTYPER for the detection and quantitative analysis of DNA methylation using base-specific cleavage and Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS) (12). Genomic DNA was treated and analyzed according to manufacturers' instructions (Agena Bioscience, Germany). Briefly, genomic DNA was treated with bisulfite and amplified by PCR with primers specific to genomic regions of the genes of interest (DLX1, MID1, NF2, NLGN1, and WNT3): 95°C for 2 min, followed by 49 repeated cycles (95.0°C for 40 s, 56.0°C for 40 s, 72.0°C for 40 s) and a last step at 72.0 °C for 5 min. Unincorporated dNTPs leftover from amplification were neutralized using shrimp alkaline phosphatase (SAP). Then, to obtain fragmented RNA molecules, in-vitro RNA transcription with subsequent base-specific

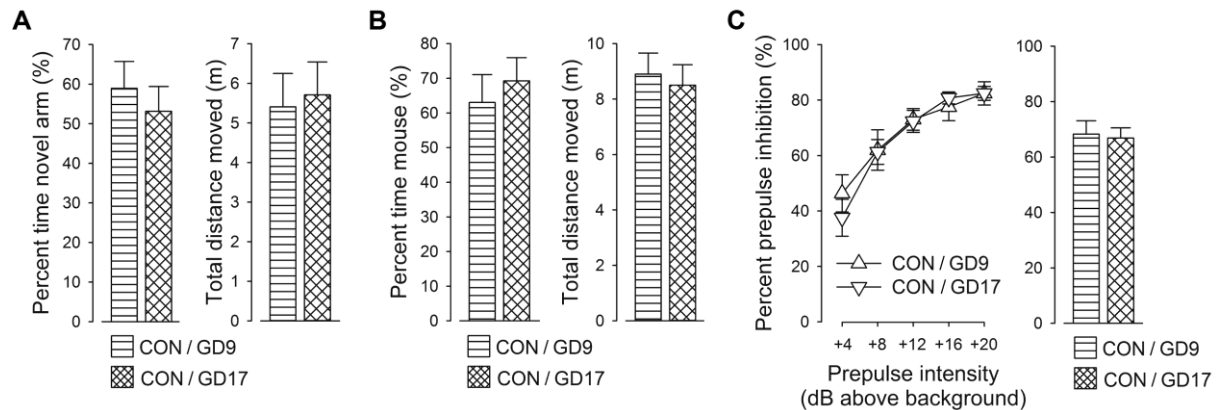
cleavage using RNase A was performed. Both methylated and non-methylated regions were cleaved at every T to produce fragments that are identical in length and differ only in their nucleotide composition. The samples were then conditioned so that the products could be processed in the MALDI-TOF mass spectrometer and could be analyzed by their mass spectra. In analyzing the mass spectrum, the relative amount of methylation can be calculated by comparing the difference in signal intensity between mass signals derived from methylated and non-methylated template DNA (12).

The primer sequences used to amplify specific genomic regions of the genes of interest (DLX1, MID1, NF2, NLGN1, and WNT3) were as follows:

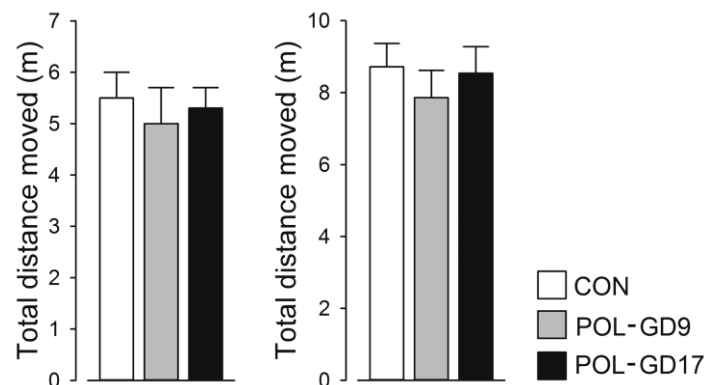
<b>Amplicon</b>	<b>Forward Primer (<i>bold letters: gene specific</i>)</b>	<b>Reverse Primer (<i>bold letters: gene specific</i>)</b>
<b>MID1-A1</b>	5'-aggaagagag <b>GTGGTTGGAAGTATAGGTATGGTTG</b> -3'	5'-gggagaaggct <b>CCTCAAACCTCAAACCTAAAATTTACC</b> -3'
<b>MID1-A2</b>	5'-aggaagagag <b>TTTTTGGTAAATTTTAGTTTTGAGG</b> -3'	5'-ggagaaggct <b>ACTCCAATAATTTACTTCTACTTTCCC</b> -3'
<b>MID1-A3</b>	5'-aggaagagag <b>AAGTAGGGGGTTTATTGTGAGTGAT</b> -3'	5'-gagaaggct <b>AAAACCAAACCTTCCCAAC</b> -3'
<b>WNT3</b>	5'-aggaagagag <b>TTTTATTTTTGAATTTGGGTTTGA</b> -3'	5'-ggagaaggct <b>ACAACATCTTCAACCATAACTACCC</b> -3'
<b>DLX</b>	5'-aggaagagag <b>AAAGGTAGTGTAGTATTAATAAGGGTTTTT</b> -3'	5'-ggagaaggct <b>TCAAACCTACAACCTCAAACCTAAAATAAA</b> -3'
<b>NLGN1</b>	5'-aggaagagag <b>ATATGATTGATATTAGATATGGGGG</b> -3'	5'-ggagaaggct <b>AACTAAAATCCTTAACCTCAAACCA</b> -3'
<b>NF2</b>	5'-aggaagagag <b>TTTTTGTTTTTGATGATTTTTGTG</b> -3'	5'-ggagaaggct <b>AAAACAACCTCACCTAACTCTACCC</b> -3'

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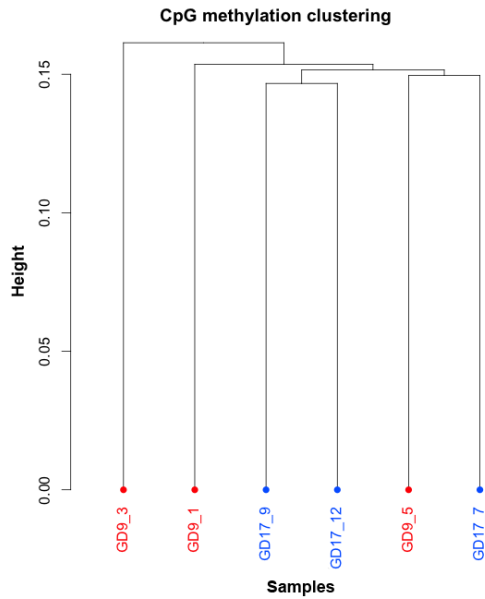
## SUPPLEMENTARY RESULTS



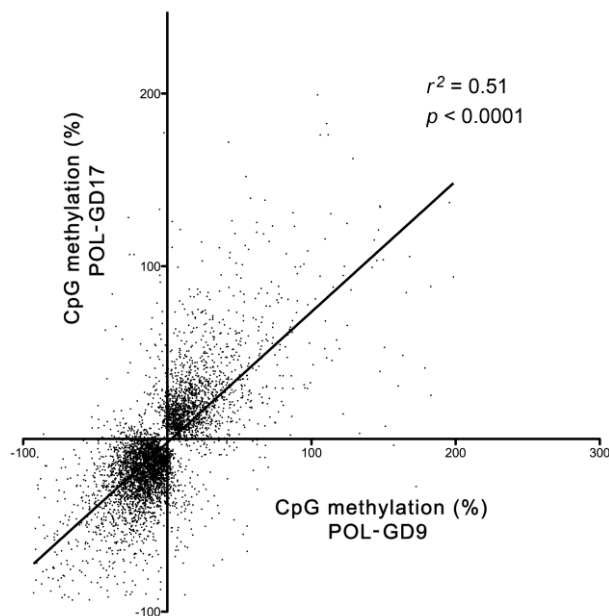
**Supplementary Figure 1.** Behavioral and cognitive performances of the two vehicle-exposed control subgroups. In order to control for the two timings of poly(I:C) injection, half of the vehicle-treated dams were injected on GD 9, and the other half on GD 17, resulting in CON/GD9 and CON/GD17 control offspring. The graphs show the performances of the two control subgroups in adulthood. **(A)** Percent time spent in the novel arm and total distance moved in the Y-maze test of spatial recognition memory. **(B)** Percent time spent with an unfamiliar mouse and total distance moved during the social interaction test. **(C)** Percent prepulse inhibition (PPI) as function of different prepulse intensities (line plot) and mean percent PPI (bar plot).  $N(\text{CON/GD9}) = 6$  and  $N(\text{CON/GD17}) = 6$ ; all data are means  $\pm$  s.e.m.



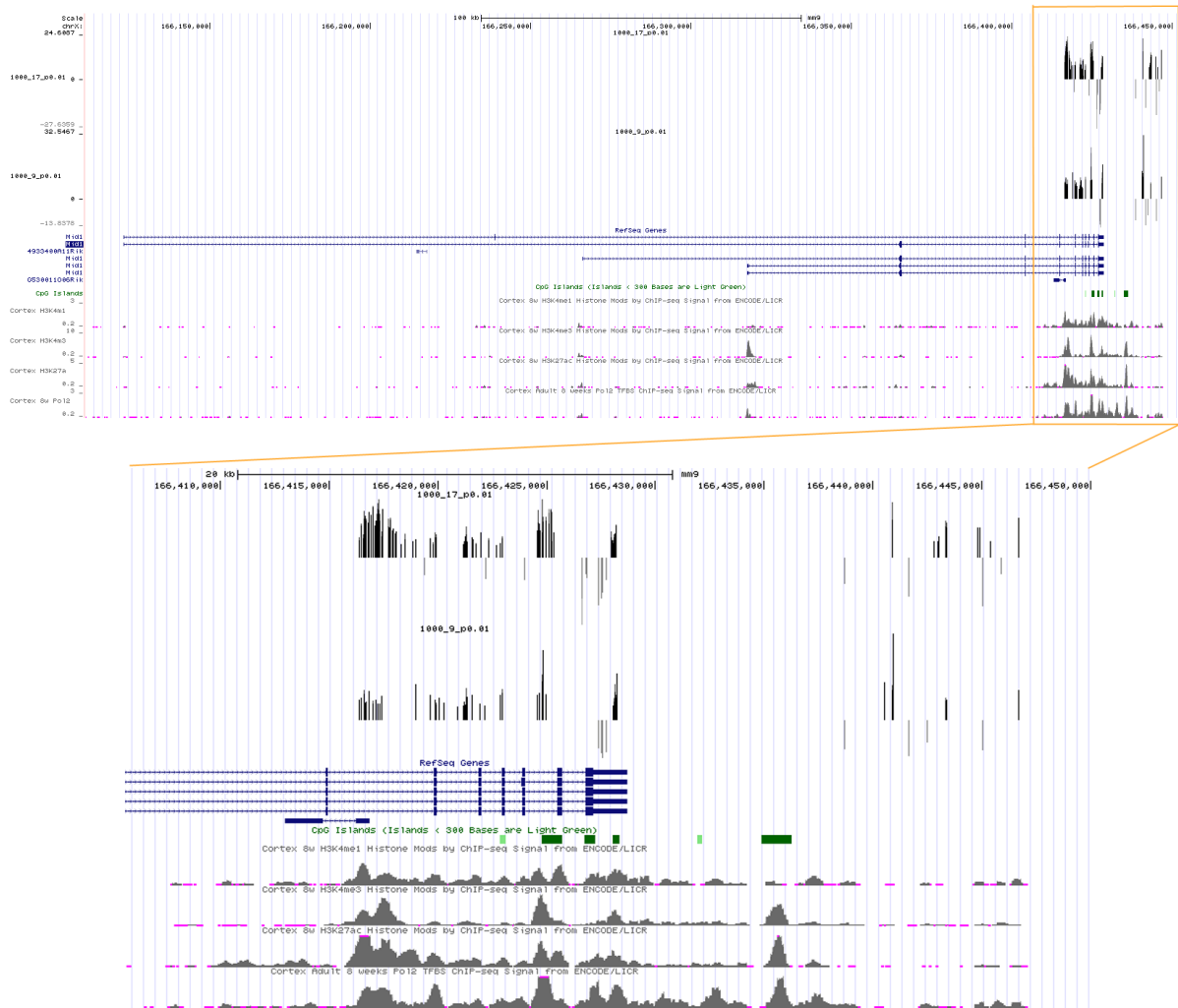
**Supplementary Figure 2.** Locomotor activity in adult control (CON) offspring and adult offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation. **(A)** Total distance moved during the working memory test in the Y-maze, corresponding to *Main Figure 1A* **(B)** Total distance moved during the social interaction test, corresponding to *Main Figure 1B*.  $N = 12$  males in each group; all data are means  $\pm$  s.e.m.



**Supplementary Figure 3.** CpG methylation clustering of individual samples that were included the merged prenatal control group. In order to control for the two timings of poly(I:C) injection, half of the vehicle-treated dams were injected on GD 9, and the other half on GD 17. The graph shows that there was no clustering between adult offspring of dams injected with vehicle control solution on GD9 (red color; sample GD9\_1, GD9\_3, and GD9\_5) and offspring of dams injected with vehicle control solution on GD17 (blue color; sample GD17\_7, GD17\_9, and GD17\_12). Therefore, offspring born to GD9-injected and GD17-injected control dams were merged into a single control group for the final analyses presented throughout the manuscript.

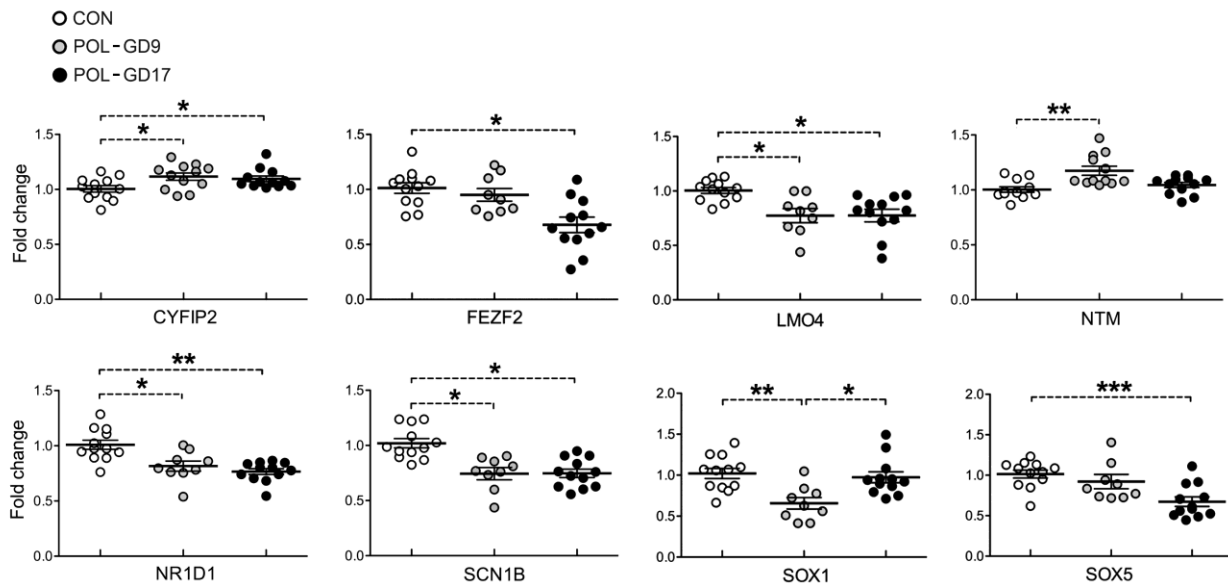


**Supplementary Figure 4.** Correlation between single CpG sites that were either affected by poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation. 2365 CpG sites were significantly affected in POL-GD9 relative to CON offspring, and 3361 CpGs were significantly affected in POL-GD17 relative to CON offspring. Each dot represents a single CpG site, which was significantly affected in POL-GD9 and/or POL-GD17 offspring. The data are expressed as percent methylation differences from control offspring (CON,  $N = 6$ ) and are based on  $N(\text{POL-GD9}) = 5$  and  $N(\text{POL-GD17}) = 5$ .



**Supplementary Figure 5.** Graphical representation of differentially methylated CpGs in the MID1 gene of adult offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation. The figure was created by the online genome browser hosted by the University of California, Santa Cruz (UCSC) and highlights the differentially methylated CpGs revealed by the capture sequencing analysis in the context of different RefSeq isoforms of the MID1 gene (represented by blue lines). The black and grey bars represent hyper- and hypomethylated CpGs, respectively. The length of the bars indicates the magnitude of the methylation difference. The highlighted area (orange color) is given at higher magnification. Bottom tracks show genomic enhancer sites and polymerase II binding sites in the cortex of 8 weeks old mice (H3K4m1, H3K4m3, H3K27a and Pol2 tracks as given by the ENCODE/LICR database). CpG islands are also indicated in the green track.





**Supplementary Figure 6.** mRNA expression levels of selected genes that were differentially methylated in adult offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation relative to adult control (CON). Differential methylation of these genes was revealed by the genome-wide capture sequencing approach (see *Supplementary Tables 1-4*) but was not validated by EpiTYPER. The genes were selected based on their involvement in GABAergic cell differentiation and functions (FEZF2, SOX5), Wnt signaling (LMO4, SOX1), and neural development (CYFIP2, NTM, NR1D1, SCN1B). \* $p < 0.05$ , \*\* $p < 0.01$ , and \*\*\* $p < 0.001$ , based on Fisher's post-hoc test following one-way ANOVA.

Supplementary Table 1 (ST1) is provided as a separate file under the online Supplementary Material. The corresponding data are also provided in *bedGraph* format and can be uploaded to the genome browser of the University of California, Santa Cruz (UCSC).

**Supplementary Table 1.** Differentially methylated genes that are affected in adult offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) gestation. The table summarizes CpG methylation differences that were revealed by genome-wide capture sequencing at a resolution of 1000 base-pair sliding regions. The columns describe the location of the 1000 base-pair sliding region, the magnitude of methylation difference (percent change from controls), the *q*-values, and the corresponding gene to which the changes annotate. The regions are sorted according to gene names.

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Supplementary Table 2 (ST2) is provided as a separate file under the online Supplementary Material. The corresponding data are also provided in *bedGraph* format and can be uploaded to the genome browser of the University of California, Santa Cruz (UCSC).

**Supplementary Table 2.** Differentially methylated genes that are affected in adult offspring exposed to poly(I:C)-induced immune activation in late (POL-GD17) gestation. The table summarizes CpG methylation differences that were revealed by genome-wide capture sequencing at a resolution of 1000 base-pair sliding regions. The columns describe the location of the 1000 base-pair sliding region, the magnitude of methylation difference (percent change from controls), the *q*-values, and the corresponding gene to which the changes annotate. The regions are sorted according to gene names.

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Supplementary Table 3 (ST3) is provided as a separate file under the online Supplementary Material. The corresponding data are also provided in *bedGraph* format and can be uploaded to the genome browser of the University of California, Santa Cruz (UCSC).

**Supplementary Table 3.** Differentially methylated genes that are affected in adult offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) gestation. The table summarizes CpG methylation differences that were revealed by genome-wide capture sequencing at at single-base resolution. The columns describe the location of the specific CpGs affected, the magnitude of methylation difference (percent change from controls), the *q*-values, and the corresponding gene to which the changes annotate. The CpGs are sorted according to gene names.

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Supplementary Table 4 (ST4) is provided as a separate file under the online Supplementary Material. The corresponding data are also provided in *bedGraph* format and can be uploaded to the genome browser of the University of California, Santa Cruz (UCSC).

**Supplementary Table 4.** Differentially methylated genes that are affected in adult offspring exposed to poly(I:C)-induced immune activation in late (POL-GD17) gestation. The table summarizes CpG methylation differences that were revealed by genome-wide capture sequencing at at single-base resolution. The columns describe the location of the specific CpGs affected, the magnitude of methylation difference (percent change from controls), the *q*-values, and the corresponding gene to which the changes annotate. The CpGs are sorted according to gene names.

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<b>POL-GD9 versus CON offspring – 1000bp sliding regions</b>				
<b>Genomic regions</b>	<b>Number of regions</b>	<b>Percent of total regions (%)</b>	<b>Hyper-methylated (%)</b>	<b>Hypo-methylated (%)</b>
Total	9488	100.0	40	60
CpG islands	173	1.8	38	62
Promoter	1097	11.6	41	59
Introns	3375	35.6	40	60
Exons	636	6.7	41	59
Intergenic	2764	29.1	40	60
Other	1443	15.2	39	61
<b>POL-GD17 versus CON offspring – 1000bp sliding regions</b>				
<b>Genomic regions</b>	<b>Number of regions</b>	<b>Percent of total regions (%)</b>	<b>Hyper-methylated (%)</b>	<b>Hypo-methylated (%)</b>
Total	10630	100.0	42	58
CpG islands	174	1.6	41	59
Promoter	1195	11.2	45	55
Introns	3738	35.1	40	60
Exons	661	6.2	46	54
Intergenic	3153	29.9	42	58
Other	1709	16.0	41	59

**Supplementary Table 5.** Genomic distribution of differentially methylated 1000 base-pair (bp) sliding regions measured by genome-wide capture sequencing in adult offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation relative to control offspring (CON). The columns describe the number of affected genomic regions, the enrichment of each affected region relative to the total number of affected regions, and the percentage of hyper- and hypo-methylated regions.

<b>Genomic location</b>	<b>Methylation difference POL-GD9</b>	<b>q-value POL-GD9</b>	<b>Methylation difference POL-GD17</b>	<b>q-value POL-GD17</b>	<b>Gene Name</b>
chr5 64263485	12.260	0.129	11.377	0.141	0610040J01Rik
chr12 20821051	-10.307	0.117	-9.802	0.118	1700030C10Rik
chr12 20821302	-7.853	0.111	-9.734	0.048	1700030C10Rik
chr12 20821969	-7.532	0.127	-11.867	0.023	1700030C10Rik
chr10 67908977	-8.287	0.165	-7.389	0.194	1700040L02Rik
chr15 63660525	7.182	0.166	9.120	0.073	1700065I16Rik
chr15 63660727	-10.321	0.129	-17.450	0.015	1700065I16Rik
chr15 63660729	-9.532	0.156	-13.639	0.049	1700065I16Rik
chr15 63660733	-13.317	0.06	-19.289	0.009	1700065I16Rik
chr16 6350486	-13.685	0.137	-15.848	0.071	1700123O21Rik
chr16 6350606	-14.551	0.054	-16.703	0.029	1700123O21Rik
chr16 6350645	-11.563	0.073	-8.152	0.178	1700123O21Rik
chr16 6350715	-10.540	0.088	-8.977	0.122	1700123O21Rik
chr13 63057769	10.519	0.132	9.081	0.192	2010111I01Rik
chr7 87120197	-13.274	0.037	-12.002	0.046	2610034B18Rik
chr11 16761370	-19.064	0.065	-24.936	0.020	2810442I21Rik
chr11 16761442	-11.018	0.129	-11.303	0.106	2810442I21Rik
chr7 26178170	15.584	0.06	14.607	0.077	4732471J01Rik
chr7 26178229	11.224	0.2	15.770	0.066	4732471J01Rik
chr13 91881580	-12.986	0.153	-23.411	0.010	4833422C13Rik
chr12 72530574	13.297	0.078	11.469	0.111	4930404H11Rik
chr5 127078719	15.657	0.082	12.778	0.116	4933438B17Rik
chr19 57584445	-12.626	0.139	-20.040	0.028	6720468P15Rik

chr19	57584467	-10.271	0.149	-15.558	0.041	6720468P15Rik
chr16	30039631	12.268	0.155	10.615	0.182	9030404E10Rik
chr16	30039633	15.043	0.063	9.425	0.184	9030404E10Rik
chr16	30039640	14.220	0.061	12.433	0.095	9030404E10Rik
chr19	57172873	-10.183	0.136	-9.071	0.144	Ablim1
chr19	57269834	-13.177	0.157	-15.207	0.115	Ablim1
chr19	57269983	-18.964	0.02	-10.781	0.139	Ablim1
chr5	114649374	-11.869	0.107	-11.305	0.123	Acacb
chr12	36693372	-9.237	0.185	-11.235	0.113	Agr2
chr12	36693596	-13.043	0.155	-26.680	0.012	Agr2
chr3	152220241	-9.261	0.175	-9.281	0.160	AI115009
chr14	26681480	-13.017	0.185	-14.892	0.133	Anxa11
chr5	97145523	15.316	0.133	13.367	0.176	Anxa3
chr3	62153526	14.238	0.147	14.543	0.109	Arhgef26
chr3	62153601	10.675	0.196	11.606	0.165	Arhgef26
chr3	62153612	11.050	0.185	12.584	0.125	Arhgef26
chr4	135771099	10.372	0.198	21.097	0.007	Asap3
chr1	140224422	-12.641	0.093	-11.533	0.110	Atp6v1g3
chr1	140224686	-7.085	0.173	-9.861	0.053	Atp6v1g3
chr12	34029889	-13.975	0.018	-11.269	0.043	Atxn711
chr10	126605306	-11.572	0.071	-8.698	0.144	B4galnt1
chr10	126605469	-11.757	0.19	-16.739	0.065	B4galnt1
chr7	116863127	-20.826	0.046	-24.017	0.029	BC051019
chr1	88268495	-7.692	0.018	-6.364	0.023	C130036L24Rik
chr2	60121326	-16.029	0.035	-10.634	0.149	Cd302
chr2	60121468	-14.319	0.031	-14.329	0.021	Cd302
chr1	196765680	-13.175	0.12	-11.098	0.158	Cd34
chr1	196765761	-15.646	0.039	-11.146	0.122	Cd34
chr8	101924785	-23.255	0.034	-24.263	0.030	Cdh8
chr1	191510145	-13.375	0.048	-14.788	0.039	Cenpf
chr15	86007718	-16.698	0.093	-17.883	0.061	Cerk
chr8	106833408	-10.984	0.102	-11.636	0.092	Cmtm1
chr6	104934441	21.201	0.048	24.280	0.020	Cntn6
chr1	137583296	-10.363	0.144	-14.752	0.039	Csrp1
chr11	87959167	-9.708	0.164	-14.971	0.048	Cuedc1
chr11	46123224	13.377	0.039	13.917	0.031	Cyfip2
chr11	46123237	11.279	0.108	8.878	0.176	Cyfip2
chr11	46123240	12.045	0.089	8.359	0.194	Cyfip2
chr10	45527004	16.495	0.064	10.978	0.169	D030045P18Rik
chr10	45527211	14.074	0.117	14.816	0.078	D030045P18Rik
chr15	98643188	-14.214	0.073	-12.126	0.105	Ddn
chr9	64637324	-12.953	0.105	-13.016	0.096	Dennd4a
chr9	64637343	-12.039	0.131	-11.393	0.138	Dennd4a
chr16	22622206	14.695	0.043	12.808	0.077	Dgkg
chr16	22622343	19.783	0.036	16.270	0.087	Dgkg
chr8	14114113	-18.263	0.068	-17.889	0.065	Dlgap2
chr11	101844806	-10.547	0.071	-11.043	0.052	Dusp3

chr11	101844865	-13.278	0.035	-13.432	0.034	Dusp3
chr19	53608746	-18.829	0.038	-15.171	0.065	Dusp5
chr11	69371137	8.310	0.094	10.382	0.048	Efnb3
chr11	69371281	11.000	0.061	7.543	0.144	Efnb3
chr9	83698172	-12.569	0.183	-15.840	0.095	Elovl4
chr4	149605279	-16.094	0.064	-13.774	0.096	Eno1
chr17	39980024	6.329	0.058	7.532	0.029	Esp38
chr17	39981174	7.642	0.035	6.988	0.043	Esp38
chr17	39981197	6.089	0.027	5.582	0.034	Esp38
chr17	39985208	8.183	0.191	8.386	0.146	Esp38
chr16	22398702	15.823	0.064	12.193	0.150	Etv5
chr7	50509199	-7.334	0.171	-6.833	0.176	EU599041
chr16	90830125	12.646	0.166	11.298	0.184	Eva1c
chr16	90830138	14.922	0.089	20.317	0.031	Eva1c
chr2	172172479	17.314	0.014	20.000	0.001	Fam210b
chr19	45768769	16.713	0.039	13.495	0.077	Fbxw4
chr17	88842101	-14.601	0.054	-11.860	0.090	Foxn2
chr17	88842146	-8.094	0.192	-8.595	0.166	Foxn2
chr19	41899642	-12.728	0.065	-11.076	0.090	Frat1
chr3	151729721	-7.699	0.103	-7.149	0.117	Gipc2
chr3	85692272	-6.248	0.19	-6.511	0.167	Glt28d2
chr3	85692282	-12.428	0.122	-14.633	0.054	Glt28d2
chr4	88417543	-11.034	0.035	-8.965	0.059	Gm13290
chr3	96373517	-16.570	0.122	-19.193	0.064	Gm15441
chr7	105313295	-21.171	0.044	-17.210	0.086	Gm16938
chr5	64991333	-11.667	0.089	-10.190	0.136	Gm3716
chr16	49987368	-8.592	0.057	-6.540	0.122	Gm6936
chr13	120276412	21.415	0.074	22.121	0.050	Gm7120
chr13	120276435	28.914	0.012	27.778	0.011	Gm7120
chr13	120276557	20.420	0.02	24.897	0.003	Gm7120
chr13	120277524	12.111	0.037	9.554	0.096	Gm7120
chr13	120277538	8.931	0.082	8.753	0.096	Gm7120
chr13	120277548	9.255	0.063	8.403	0.097	Gm7120
chr13	120277563	10.978	0.034	8.157	0.115	Gm7120
chr13	120277667	7.137	0.004	5.539	0.031	Gm7120
chr13	120277669	5.668	0.031	6.307	0.014	Gm7120
chr13	120277680	5.822	0.031	6.787	0.009	Gm7120
chr13	120277733	5.393	0.034	5.178	0.037	Gm7120
chr10	98006609	15.814	0.043	12.767	0.096	Gm8633
chr19	43573483	-15.589	0.114	-13.800	0.136	Got1
chr19	43573558	-19.189	0.108	-15.081	0.155	Got1
chr8	122974080	15.578	0.125	13.593	0.160	Gse1
chr8	122974144	11.563	0.105	11.998	0.086	Gse1
chr7	149766284	29.778	0.012	22.848	0.036	H19
chr7	149766288	26.149	0.024	20.602	0.053	H19
chr10	20972204	-14.267	0.155	-20.758	0.036	Hbs1l
chr10	20972214	-20.957	0.035	-18.595	0.048	Hbs1l

chr9	24905727	5.449	0.185	5.736	0.105	Herpud2
chr9	24905740	6.180	0.13	5.189	0.155	Herpud2
chr16	94399111	-10.739	0.19	-9.759	0.196	Hlcs
chr16	94399225	-11.410	0.171	-13.684	0.095	Hlcs
chr16	94399235	-12.699	0.158	-15.295	0.080	Hlcs
chr14	65503827	-10.427	0.107	-13.862	0.033	Hmbox1
chr14	65503905	-9.905	0.078	-8.041	0.138	Hmbox1
chr17	80416876	-13.369	0.054	-9.264	0.166	HnrnpII
chr4	128797143	-7.757	0.192	-8.025	0.183	Hpca
chr4	128797168	-11.380	0.07	-10.456	0.095	Hpca
chr1	156906858	-10.436	0.173	-12.651	0.076	Ier5
chr1	156906939	-14.321	0.045	-11.898	0.095	Ier5
chr9	100202396	-17.010	0.077	-13.383	0.127	Il20rb
chr9	118542057	-14.810	0.12	-13.154	0.147	Itga9
chr16	34400527	-12.822	0.177	-17.414	0.053	Kalrn
chr2	163993554	-27.380	0.009	-17.919	0.069	Kcns1
chr1	183853472	-12.745	0.196	-16.996	0.108	Lbr
chr1	183853843	-16.266	0.048	-11.689	0.123	Lbr
chr9	56480413	-12.267	0.109	-12.121	0.102	Lingo1
chr3	88297691	-15.776	0.109	-19.450	0.048	Lmna
chr3	88297695	-18.332	0.068	-22.755	0.028	Lmna
chr3	88297699	-23.758	0.024	-23.967	0.019	Lmna
chr10	63549273	-16.844	0.053	-11.061	0.171	Lrrtm3
chr7	25413890	13.708	0.122	16.551	0.051	Lypd3
chr8	122088089	20.231	0.044	25.010	0.001	Mbtps1
chr10	117113780	-10.694	0.139	-15.368	0.031	Mdm2
chr10	117113794	-9.835	0.107	-11.535	0.053	Mdm2
chr2	115887557	-7.222	0.118	-8.000	0.070	Meis2
chr2	115887638	-13.880	0.032	-13.509	0.033	Meis2
chr2	115887667	-13.725	0.089	-18.895	0.011	Meis2
chr6	121079703	-11.263	0.1	-11.849	0.085	Mical3
chr8	41406942	13.636	0.041	16.132	0.018	Micu3
chr8	41406944	12.898	0.071	14.596	0.044	Micu3
chrX	166416412	7.855	0.117	6.386	0.192	Mid1
chrX	166416485	8.545	0.127	13.872	0.014	Mid1
chrX	166416621	11.017	0.031	18.613	0.000	Mid1
chrX	166416628	8.632	0.08	14.235	0.007	Mid1
chrX	166416645	6.548	0.167	17.303	0.000	Mid1
chrX	166416709	6.954	0.178	16.027	0.004	Mid1
chrX	166416828	10.966	0.162	19.195	0.020	Mid1
chrX	166417000	7.086	0.089	21.553	0.000	Mid1
chrX	166417010	5.158	0.181	21.010	0.000	Mid1
chrX	166417136	7.632	0.034	15.476	0.000	Mid1
chrX	166417256	6.347	0.107	21.885	0.000	Mid1
chrX	166417315	6.324	0.163	18.028	0.000	Mid1
chrX	166417427	9.336	0.092	10.272	0.066	Mid1
chrX	166419008	13.398	0.031	7.738	0.183	Mid1

chrX	166419668	9.696	0.038	7.921	0.079	Mid1
chrX	166419899	7.651	0.068	10.207	0.013	Mid1
chrX	166419908	6.034	0.161	8.147	0.055	Mid1
chrX	166419927	5.668	0.155	7.427	0.058	Mid1
chrX	166419931	6.503	0.122	9.709	0.021	Mid1
chrX	166421197	5.504	0.033	5.667	0.021	Mid1
chrX	166421242	7.008	0.061	6.774	0.062	Mid1
chrX	166421255	6.074	0.1	8.939	0.017	Mid1
chrX	166421293	6.813	0.077	7.271	0.054	Mid1
chrX	166421313	11.146	0.034	12.067	0.019	Mid1
chrX	166421338	8.820	0.076	6.464	0.169	Mid1
chrX	166422857	9.458	0.001	6.183	0.043	Mid1
chrX	166422944	11.305	0	8.538	0.014	Mid1
chrX	166422977	9.381	0.006	7.692	0.027	Mid1
chrX	166424584	9.438	0.16	11.255	0.072	Mid1
chrX	166424685	10.398	0.191	14.208	0.072	Mid1
chrX	166424805	12.657	0.122	21.115	0.012	Mid1
chrX	166424813	16.411	0.043	17.618	0.029	Mid1
chrX	166424826	26.032	0	15.970	0.033	Mid1
chrX	166424980	9.472	0.178	16.738	0.027	Mid1
chrX	166424984	9.764	0.171	14.422	0.050	Mid1
chrX	166427373	-10.220	0.069	-20.121	0.000	Mid1
chrX	166427536	-12.370	0	-17.299	0.000	Mid1
chrX	166427567	-13.838	0	-14.739	0.000	Mid1
chrX	166427753	-11.903	0.026	-9.623	0.036	Mid1
chrX	166428095	5.973	0.155	6.801	0.111	Mid1
chrX	166428106	8.329	0.043	8.292	0.045	Mid1
chrX	166428120	6.317	0.104	9.159	0.022	Mid1
chrX	166428147	10.699	0.035	10.136	0.040	Mid1
chrX	166428153	13.356	0.02	9.946	0.068	Mid1
chrX	166428186	9.236	0.118	13.550	0.027	Mid1
chrX	166438684	-10.723	0	-11.199	0.000	Mid1
chrX	166440873	10.321	0.017	23.363	0.000	Mid1
chrX	166440879	12.703	0	20.242	0.000	Mid1
chrX	166441665	-13.187	0.001	-16.399	0.000	Mid1
chrX	166443343	7.835	0.049	12.624	0.003	Mid1
chrX	166443349	8.148	0.031	15.600	0.000	Mid1
chrX	166443368	6.597	0.035	10.923	0.000	Mid1
chrX	166443375	7.887	0.019	11.310	0.061	Mid1
chrX	166445032	-11.076	0	-20.405	0.000	Mid1
chrX	166446717	11.427	0.01	16.842	0.033	Mid1
chr11	86407208	13.968	0.13	12.072	0.185	Mir21
chr11	86407229	16.950	0.105	17.253	0.095	Mir21
chr1	34466960	-13.632	0.044	-8.502	0.175	Mir5103
chr1	34466972	-8.472	0.177	-9.723	0.106	Mir5103
chr6	102730933	7.716	0.038	7.745	0.036	Mir6373
chr13	62861544	12.419	0.088	11.100	0.088	Mir713

chr15	73906292	-13.658	0.103	-15.853	0.057	Mroh5
chr15	73906416	-11.595	0.042	-7.331	0.185	Mroh5
chr15	61831575	-13.596	0.038	-16.154	0.018	Myc
chr9	71454574	-12.579	0.057	-15.659	0.018	Myzap
chr15	37720396	-19.414	0.08	-15.836	0.115	Ncald
chr15	37720725	-10.210	0.078	-8.108	0.122	Ncald
chr6	55629630	-18.971	0.034	-13.968	0.098	Neurod6
chr11	4706269	14.596	0.135	14.900	0.111	Nf2
chr11	4706313	18.622	0.018	13.895	0.054	Nf2
chr11	4706641	12.244	0.137	13.583	0.107	Nf2
chr4	82184801	-12.698	0.05	-16.714	0.009	Nfib
chr7	139788577	-9.517	0.112	-11.141	0.056	Nkx1-2
chr3	26129152	-16.373	0.064	-11.944	0.135	Nlgn1
chr3	26129259	-11.221	0.198	-17.529	0.043	Nlgn1
chr11	107126663	-16.499	0.075	-12.299	0.155	Nol11
chr18	12392723	11.991	0.075	8.194	0.180	Npc1
chr11	98632164	-13.235	0.138	-12.500	0.152	Nr1d1
chr11	98632921	10.879	0.159	16.582	0.049	Nr1d1
chr19	6421306	-21.868	0.044	-16.154	0.119	Nrxn2
chr19	47043650	-9.540	0.071	-11.337	0.034	Nt5c2
chr1	172574266	14.286	0.012	15.385	0.004	Olfml2b
chr9	39419905	-16.937	0.065	-27.200	0.006	Olf148
chr15	41280655	-12.929	0.192	-15.954	0.098	Oxr1
chr15	41280787	-11.836	0.196	-11.976	0.157	Oxr1
chr18	37979970	-10.000	0.182	-11.800	0.115	Pcdhgc5
chr13	75365565	18.798	0.082	17.484	0.085	Pcsk1
chr13	75365567	16.483	0.128	13.147	0.183	Pcsk1
chr15	92427583	6.314	0.193	6.941	0.168	Pdzrn4
chr15	92427590	11.236	0.136	9.874	0.178	Pdzrn4
chr15	92427602	13.346	0.046	11.609	0.066	Pdzrn4
chr15	92427608	11.709	0.089	16.286	0.029	Pdzrn4
chr13	43023513	-13.756	0.134	-10.784	0.196	Phactr1
chr13	43023529	-12.257	0.146	-11.131	0.169	Phactr1
chr4	104876528	-15.942	0.08	-13.418	0.107	Ppap2b
chr17	36008178	-9.461	0.139	-9.226	0.135	Ppp1r18
chr17	36008186	-11.900	0.068	-10.899	0.085	Ppp1r18
chr15	93582438	-22.970	0.024	-16.420	0.097	Prickle1
chr15	93582443	-19.921	0.035	-18.681	0.046	Prickle1
chr15	93582483	-19.302	0.026	-19.939	0.021	Prickle1
chr15	93582486	-10.903	0.174	-10.793	0.169	Prickle1
chr15	93582558	-12.944	0.102	-14.948	0.053	Prickle1
chr5	24590639	-11.721	0.189	-14.120	0.126	Prkag2
chr5	24590768	-19.318	0.019	-15.031	0.050	Prkag2
chr8	98123729	19.929	0.055	14.155	0.117	Prss54
chr19	17200097	-9.946	0.178	-12.305	0.108	Prune2
chr14	66884471	-15.347	0.129	-23.808	0.025	Ptk2b
chr14	66884698	-14.621	0.094	-13.227	0.112	Ptk2b



chr7	52123407	14.452	0.064	12.156	0.096	Ptov1
chr18	36444107	-13.725	0.117	-15.217	0.064	Pura
chr18	36444323	-15.735	0.122	-21.929	0.031	Pura
chr15	94348535	-11.806	0.146	-12.254	0.108	Pus7l
chr15	94348594	-13.583	0.095	-11.825	0.119	Pus7l
chr15	94348602	-14.469	0.084	-18.571	0.027	Pus7l
chr14	8932273	9.630	0.182	17.784	0.031	Pxk
chr14	8932540	14.451	0.089	16.211	0.059	Pxk
chr15	10617507	9.656	0.161	11.715	0.084	Rai14
chr2	131865604	-20.873	0.026	-9.821	0.196	Rassf2
chr2	131865606	-15.134	0.088	-11.148	0.163	Rassf2
chr8	35098500	10.438	0.185	15.811	0.041	Rbpms
chr12	83719280	-17.620	0.031	-11.582	0.104	Rgs6
chr10	84371891	-18.834	0.052	-20.625	0.031	Ric8b
chr6	47631815	-5.476	0.188	-8.433	0.043	Rn4.5s
chr6	47694526	-5.367	0.181	-6.319	0.122	Rn4.5s
chr6	47694538	-6.865	0.071	-5.664	0.134	Rn4.5s
chr6	47703548	-6.628	0.093	-6.838	0.078	Rn4.5s
chr11	87478802	9.836	0.133	13.793	0.034	Rnf43
chr11	87478838	12.636	0.074	13.819	0.053	Rnf43
chr15	97337818	-8.751	0.167	-12.599	0.039	Rpap3
chr15	97337832	-12.153	0.076	-12.650	0.045	Rpap3
chr4	33083081	7.050	0.113	8.254	0.033	Rragd
chr7	31909678	-18.568	0.064	-17.341	0.095	Scn1b
chr2	164267709	9.615	0.165	10.124	0.137	Sdc4
chr11	116978079	-13.333	0.064	-11.944	0.098	Sec14l1
chr11	116978112	-14.877	0.016	-11.602	0.059	Sec14l1
chr14	76969138	-10.765	0.12	-11.249	0.115	Serp2
chr14	76969324	-6.479	0.193	-7.074	0.164	Serp2
chr14	76969363	-14.475	0.02	-10.312	0.081	Serp2
chr17	31909193	15.742	0.069	18.420	0.035	Sik1
chr17	86089237	-7.572	0.196	-9.444	0.111	Six2
chr4	45440495	10.186	0.077	11.531	0.041	Slc25a51
chr4	45440598	9.206	0.101	12.207	0.031	Slc25a51
chr15	96628123	-15.974	0.074	-10.727	0.194	Slc38a2
chr15	96886126	11.671	0.18	12.092	0.184	Slc38a4
chr15	96886130	18.488	0.052	13.129	0.167	Slc38a4
chr15	96886142	17.201	0.063	11.564	0.200	Slc38a4
chr15	96886150	19.449	0.042	11.805	0.192	Slc38a4
chr15	96886168	13.781	0.163	18.132	0.084	Slc38a4
chr15	96886170	17.160	0.097	21.993	0.042	Slc38a4
chr15	96886250	16.469	0.106	15.165	0.129	Slc38a4
chr15	96886308	14.673	0.157	13.807	0.136	Slc38a4
chr8	81886426	-24.294	0.018	-15.782	0.101	Smad1
chr6	146783138	17.892	0.038	17.734	0.033	Smco2
chr19	53489186	-8.425	0.155	-10.246	0.094	Smndc1
chr19	53489933	-22.656	0.06	-27.936	0.016	Smndc1

chr1	191744361	-10.163	0.161	-11.311	0.115	Smyd2
chr6	28433001	13.371	0.035	11.920	0.049	Snd1
chr13	114396610	-18.056	0.056	-12.077	0.158	Snx18
chr13	114396622	-21.517	0.026	-11.426	0.158	Snx18
chr8	46682217	-18.379	0.036	-13.003	0.100	Sorbs2
chr10	74721884	-9.790	0.106	-17.196	0.017	Specc1l
chr11	19879596	-9.555	0.173	-9.540	0.165	Spred2
chr2	151938855	-9.405	0.188	-8.574	0.199	Srxn1
chr3	102750789	14.073	0.147	14.775	0.106	Sycp1
chr17	71222778	7.158	0.196	15.241	0.025	Tgif1
chr17	81340727	-14.912	0.116	-14.208	0.111	Tmem178
chr17	81340739	-16.582	0.075	-14.557	0.099	Tmem178
chr17	6452022	-9.168	0.198	-9.142	0.159	Tmem181b-ps
chr17	6452040	-13.535	0.063	-13.783	0.040	Tmem181b-ps
chr15	72865231	-14.243	0.182	-17.109	0.113	Trappc9
chr5	73154593	-8.353	0.168	-13.467	0.049	Txk
chr5	86609931	-14.141	0.134	-12.323	0.165	Uba6
chr4	105872668	22.843	0.026	16.841	0.073	Usp24
chr4	105872673	22.271	0.036	13.505	0.166	Usp24
chr4	105872678	16.162	0.11	20.915	0.043	Usp24
chr16	77027348	-15.773	0.082	-13.097	0.121	Usp25
chr19	46681492	-5.286	0.199	-6.547	0.114	Wbp1l
chr2	73389266	-9.317	0.121	-10.965	0.053	Wipf1
chr2	73389271	-10.320	0.07	-9.964	0.062	Wipf1
chr8	111223764	9.979	0.129	9.459	0.117	Zfhx3
chr8	111223825	10.162	0.03	9.651	0.028	Zfhx3
chr18	82874731	-9.437	0.135	-13.589	0.031	Zfp236
chr18	82874817	-13.294	0.063	-12.068	0.096	Zfp236
chr11	95640412	17.577	0.065	19.316	0.039	Zfp652

**Supplementary Table 6.** Differentially methylated genes that are commonly affected in adult offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation. The table summarizes methylation differences that were revealed by the analysis of CpG methylation at single-base resolution. The columns describe the location of the specific CpGs affected, the magnitude of methylation differences (percent change from controls), the  $q$ -values, and the corresponding gene to which the changes annotate. The CpGs are sorted according to gene names.

	CON_1	CON_2	CON_3	CON_4	CON_5	CON_6
CON_1	1.0000000	0.8334601	0.8568496	0.8225162	0.8657010	0.8451711
CON_2	0.8334601	1.0000000	0.8615622	0.8510367	0.8521754	0.8509176
CON_3	0.8568496	0.8615622	1.0000000	0.8269721	0.8666168	0.8558773
CON_4	0.8225162	0.8510367	0.8269721	1.0000000	0.8385426	0.7879279
CON_5	0.8657010	0.8521754	0.8666168	0.8385426	1.0000000	0.8398989
CON_6	0.8451711	0.8509176	0.8558773	0.7879279	0.8398989	1.0000000
	GD9_1	GD9_2	GD9_3	GD9_4	GD9_5	
GD9_1	1.0000000	0.8339739	0.8211404	0.8860356	0.8702147	
GD9_2	0.8339739	1.0000000	0.8794656	0.8245801	0.8712609	
GD9_3	0.8211404	0.8794656	1.0000000	0.8280647	0.8632152	
GD9_4	0.8860356	0.8245801	0.8280647	1.0000000	0.8682256	
GD9_5	0.8702147	0.8712609	0.8632152	0.8682256	1.0000000	
	GD17_1	GD17_2	GD17_3	GD17_4	GD17_5	
GD17_1	1.0000000	0.8860938	0.8301068	0.7969081	0.7843140	
GD17_2	0.8860938	1.0000000	0.8086783	0.7995635	0.7621425	
GD17_3	0.8301068	0.8086783	1.0000000	0.8621250	0.8534399	
GD17_4	0.7969081	0.7995635	0.8621250	1.0000000	0.8632177	
GD17_5	0.7843140	0.7621425	0.8534399	0.8632177	1.0000000	

**Supplementary Table 7.** Summary of the inter-replicate methylation level correlations (at single CpG resolution;  $r^2$ ) between individual samples obtained from adult offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation and adult control (CON) offspring.

Genomic location	Methylation difference POL-GD9	q-value POL-GD9	Methylation difference POL-GD17	q-value POL-GD17	Annotation
chrX 166416383			7.973	0.122	Intron (NM_010797 4 of 9)
chrX 166416412	7.855	0.117	6.386	0.192	Intron (NM_010797 4 of 9)
chrX 166416485	8.545	0.127	13.872	0.014	Intron (NM_010797 4 of 9)
chrX 166416503			13.212	0.009	Intron (NM_010797 4 of 9)
chrX 166416554			7.260	0.147	Intron (NM_010797 4 of 9)
chrX 166416588			9.129	0.072	Intron (NM_010797 4 of 9)
chrX 166416621	11.017	0.031	18.613	0.000	Intron (NM_010797 4 of 9)
chrX 166416628	8.632	0.080	14.235	0.007	Intron (NM_010797 4 of 9)
chrX 166416645	6.548	0.167	17.303	0.000	Intron (NM_010797 4 of 9)
chrX 166416709	6.954	0.178	16.027	0.004	Intron (NM_010797 4 of 9)
chrX 166416722			14.704	0.012	Intron (NM_010797 4 of 9)
chrX 166416812			14.465	0.036	Intron (NM_010797 4 of 9)
chrX 166416828	10.966	0.162	19.195	0.020	Intron (NM_010797 4 of 9)
chrX 166416931			17.720	0.027	Intron (NM_010797 4 of 9)
chrX 166417000	7.086	0.089	21.553	0.000	Intron (NM_010797 4 of 9)
chrX 166417010	5.158	0.181	21.010	0.000	Intron (NM_010797 4 of 9)
chrX 166417102			13.531	0.000	Intron (NM_010797 4 of 9)
chrX 166417136	7.632	0.034	15.476	0.000	Intron (NM_010797 4 of 9)
chrX 166417185			18.197	0.000	Intron (NM_010797 4 of 9)
chrX 166417210			12.865	0.002	Intron (NM_010797 4 of 9)
chrX 166417213			15.797	0.000	Intron (NM_010797 4 of 9)
chrX 166417225			17.584	0.000	Intron (NM_010797 4 of 9)
chrX 166417232			18.941	0.000	Intron (NM_010797 4 of 9)
chrX 166417253			22.318	0.000	Intron (NM_010797 4 of 9)
chrX 166417256	6.347	0.107	21.885	0.000	Intron (NM_010797 4 of 9)
chrX 166417260			21.793	0.000	Intron (NM_010797 4 of 9)
chrX 166417266			20.651	0.000	Intron (NM_010797 4 of 9)
chrX 166417270			24.609	0.000	Intron (NM_010797 4 of 9)
chrX 166417309			14.225	0.002	Intron (NM_010797 4 of 9)
chrX 166417315	6.324	0.163	18.028	0.000	Intron (NM_010797 4 of 9)
chrX 166417340			17.427	0.000	Intron (NM_010797 4 of 9)
chrX 166417346			11.931	0.014	Intron (NM_010797 4 of 9)
chrX 166417350			15.105	0.002	Intron (NM_010797 4 of 9)
chrX 166417402			7.664	0.128	Intron (NM_010797 4 of 9)
chrX 166417427	9.336	0.092	10.272	0.066	Intron (NM_010797 4 of 9)
chrX 166417467			20.456	0.001	Intron (NM_010797 4 of 9)
chrX 166417729			10.831	0.111	Intron (NM_010797 4 of 9)
chrX 166417752			15.156	0.018	Intron (NM_010797 4 of 9)
chrX 166417787			12.635	0.036	Intron (NM_010797 4 of 9)
chrX 166417808			16.423	0.003	Intron (NM_010797 4 of 9)
chrX 166417817			15.398	0.003	Intron (NM_010797 4 of 9)
chrX 166417900			11.281	0.018	Intron (NM_010797 4 of 9)
chrX 166417970			11.956	0.013	Intron (NM_010797 4 of 9)
chrX 166418049			10.059	0.039	Intron (NM_010797 4 of 9)
chrX 166418087			10.912	0.007	Intron (NM_010797 4 of 9)

chrX	166418312			5.778	0.053	Intron (NM_010797 4 of 9)
chrX	166418487			5.861	0.066	Intron (NM_010797 4 of 9)
chrX	166418492			6.969	0.028	Intron (NM_010797 4 of 9)
chrX	166418508			9.939	0.004	Intron (NM_010797 4 of 9)
chrX	166418837			6.746	0.171	Intron (NM_010797 4 of 9)
chrX	166419008	13.398	0.031	7.738	0.183	Intron (NM_010797 4 of 9)
chrX	166419395			-7.603	0.030	Intron (NM_010797 4 of 9)
chrX	166419668	9.696	0.038	7.921	0.079	Intron (NM_010797 4 of 9)
chrX	166419771			5.370	0.087	Intron (NM_010797 4 of 9)
chrX	166419809			6.263	0.182	Intron (NM_010797 4 of 9)
chrX	166419884			5.912	0.146	Exon (NM_010797 5 of 10)
chrX	166419893			8.856	0.030	Exon (NM_010797 5 of 10)
chrX	166419899	7.651	0.068	10.207	0.013	Exon (NM_010797 5 of 10)
chrX	166419908	6.034	0.161	8.147	0.055	Exon (NM_010797 5 of 10)
chrX	166419927	5.668	0.155	7.427	0.058	Exon (NM_010797 5 of 10)
chrX	166419931	6.503	0.122	9.709	0.021	Exon (NM_010797 5 of 10)
chrX	166420047	8.272	0.067			Intron (NM_010797 5 of 9)
chrX	166420265	6.813	0.034			Intron (NM_010797 5 of 9)
chrX	166420929	5.202	0.046			Intron (NM_010797 5 of 9)
chrX	166421197	5.504	0.033	5.667	0.021	Intron (NM_010797 5 of 9)
chrX	166421234			6.680	0.022	Intron (NM_010797 5 of 9)
chrX	166421242	7.008	0.061	6.774	0.062	Intron (NM_010797 5 of 9)
chrX	166421255	6.074	0.100	8.939	0.017	Intron (NM_010797 5 of 9)
chrX	166421293	6.813	0.077	7.271	0.054	Intron (NM_010797 5 of 9)
chrX	166421313	11.146	0.034	12.067	0.019	Intron (NM_010797 5 of 9)
chrX	166421338	8.820	0.076	6.464	0.169	Intron (NM_010797 5 of 9)
chrX	166421346			6.769	0.167	Intron (NM_010797 5 of 9)
chrX	166421583	9.501	0.108			Intron (NM_010797 5 of 9)
chrX	166421599			8.477	0.095	Intron (NM_010797 5 of 9)
chrX	166421604			7.687	0.092	Intron (NM_010797 5 of 9)
chrX	166421746			5.003	0.185	Intron (NM_010797 5 of 9)
chrX	166421759			5.964	0.131	Intron (NM_010797 5 of 9)
chrX	166421947	6.140	0.104			Exon (NM_010797 6 of 10)
chrX	166421976			10.457	0.007	Exon (NM_010797 6 of 10)
chrX	166422164	5.523	0.041			Intron (NM_010797 6 of 9)
chrX	166422217			-9.168	0.000	Intron (NM_010797 6 of 9)
chrX	166422320			6.587	0.048	Intron (NM_010797 6 of 9)
chrX	166422355			7.983	0.049	Intron (NM_010797 6 of 9)
chrX	166422691			5.132	0.045	Intron (NM_010797 6 of 9)
chrX	166422857	9.458	0.001	6.183	0.043	CpG
chrX	166422944	11.305	0.000	8.538	0.014	Exon (NM_010797 7 of 10)
chrX	166422977	9.381	0.006	7.692	0.027	Exon (NM_010797 7 of 10)
chrX	166424010			-9.340	0.087	Exon (NM_010797 7 of 10)
chrX	166424584	9.438	0.160	11.255	0.072	Intron (NM_010797 8 of 9)
chrX	166424620			18.292	0.013	Intron (NM_010797 8 of 9)
chrX	166424639			10.796	0.130	Intron (NM_010797 8 of 9)
chrX	166424685	10.398	0.191	14.208	0.072	Intron (NM_010797 8 of 9)

chrX	166424692			11.514	0.133	Intron (NM_010797 8 of 9)
chrX	166424805	12.657	0.122	21.115	0.012	CpG
chrX	166424811			-6.730	0.059	CpG
chrX	166424813	16.411	0.043	17.618	0.029	CpG
chrX	166424826	26.032	0.000	15.970	0.033	CpG
chrX	166424840			16.616	0.029	CpG
chrX	166424842			12.810	0.079	CpG
chrX	166424980	9.472	0.178	16.738	0.027	CpG
chrX	166424984	9.764	0.171	14.422	0.050	CpG
chrX	166425097			13.894	0.099	CpG
chrX	166425100			20.395	0.006	CpG
chrX	166425112			10.861	0.096	CpG
chrX	166425119			11.502	0.062	CpG
chrX	166425197			19.455	0.000	CpG
chrX	166425203			20.172	0.000	CpG
chrX	166425228			10.967	0.096	CpG
chrX	166425234			16.408	0.016	CpG
chrX	166425255			-7.163	0.064	CpG
chrX	166425352			10.417	0.071	CpG
chrX	166426612			-27.636	0.000	Intron (NM_010797 9 of 9)
chrX	166426624			-6.526	0.073	Intron (NM_010797 9 of 9)
chrX	166426824			-7.008	0.180	exon (NM_010797, exon 10 of 10)
chrX	166426834			-8.838	0.081	exon (NM_010797, exon 10 of 10)
chrX	166427373	-10.220	0.069	-20.121	0.000	3' UTR (NM_010797, exon 10 of 10)
chrX	166427536	-12.370	0.000	-17.299	0.000	3' UTR (NM_010797, exon 10 of 10)
chrX	166427567	-13.838	0.000	-14.739	0.000	3' UTR (NM_010797, exon 10 of 10)
chrX	166427753	-11.903	0.026	-9.623	0.036	3' UTR (NM_010797, exon 10 of 10)
chrX	166427973			6.726	0.118	3' UTR (NM_010797, exon 10 of 10)
chrX	166427992			10.316	0.022	3' UTR (NM_010797, exon 10 of 10)
chrX	166428001			7.242	0.098	3' UTR (NM_010797, exon 10 of 10)
chrX	166428047	5.371	0.164			3' UTR (NM_010797, exon 10 of 10)
chrX	166428050			7.035	0.085	3' UTR (NM_010797, exon 10 of 10)
chrX	166428056	5.391	0.190			3' UTR (NM_010797, exon 10 of 10)
chrX	166428059			5.225	0.171	3' UTR (NM_010797, exon 10 of 10)
chrX	166428095	5.973	0.155	6.801	0.111	3' UTR (NM_010797, exon 10 of 10)
chrX	166428100			9.580	0.038	3' UTR (NM_010797, exon 10 of 10)
chrX	166428106	8.329	0.043	8.292	0.045	3' UTR (NM_010797, exon 10 of 10)
chrX	166428120	6.317	0.104	9.159	0.022	3' UTR (NM_010797, exon 10 of 10)
chrX	166428147	10.699	0.035	10.136	0.040	3' UTR (NM_010797, exon 10 of 10)
chrX	166428153	13.356	0.020	9.946	0.068	3' UTR (NM_010797, exon 10 of 10)
chrX	166428157	7.854	0.141			3' UTR (NM_010797, exon 10 of 10)
chrX	166428172			10.073	0.086	3' UTR (NM_010797, exon 10 of 10)
chrX	166428175	7.647	0.190			3' UTR (NM_010797, exon 10 of 10)

						10 of 10)
chrX	166428186			13.550	0.027	3' UTR (NM_010797, exon 10 of 10)
chrX	166428195			13.441	0.031	3' UTR (NM_010797, exon 10 of 10)
chrX	166428214			13.098	0.064	3' UTR (NM_010797, exon 10 of 10)
chrX	166428254	17.399	0.043			3' UTR (NM_010797, exon 10 of 10)
chrX	166438684	-10.723	-	-11.199	0.000	Intergenic
chrX	166440542	14.163	0.157			Intergenic
chrX	166440873	10.321	0.017	23.363	0.000	Intergenic
chrX	166440879	12.703	0.000	20.242	0.000	Intergenic
chrX	166440898			13.475	0.000	Intergenic
chrX	166440905			7.056	0.098	Intergenic
chrX	166440939	32.547	0.002			Intergenic
chrX	166441665	-13.187	0.001	-16.399	0.000	Intergenic
chrX	166442484	-8.183	0.053			Intergenic
chrX	166442831			6.810	0.024	Intergenic
chrX	166443013			6.863	0.122	Intergenic
chrX	166443025			8.904	0.030	Intergenic
chrX	166443343	7.835	0.049	12.624	0.003	Intergenic
chrX	166443349	8.148	0.031	15.600	0.000	Intergenic
chrX	166443368	6.597	0.035	10.923	0.000	Intergenic
chrX	166443375	7.887	0.019	11.310	0.061	Intergenic
chrX	166443409			13.950	0.048	Intergenic
chrX	166444809			12.493	0.003	Intergenic
chrX	166444934			12.744	0.027	Intergenic
chrX	166445032	-11.076	0.000	-20.405	0.000	Intergenic
chrX	166445429			6.934	0.100	Intergenic
chrX	166445879			-7.101	0.036	Intergenic
chrX	166446717	11.427	0.010	16.842	0.033	Intergenic

**Supplementary Table 8.** Differentially methylated CpG sites in the MID1 gene (chromosome X) of offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation. The table summarizes methylation differences that were revealed by the analysis of CpG methylation at single-base resolution. The columns describe the location of the specific CpGs affected, the magnitude of methylation difference (percent change from controls), and the *q*-values.

CpG Site		Methylation Difference in POL-GD9 (Percent from CON)		Methylation Difference in POL-GD17 (Percent from CON)	
EpiTYPER	Capture-S	EpiTYPER	Capture-S	EpiTYPER	Capture-S
<b>MID1 (Amplicon 1)</b>					
CpG1	ChrX.166416485	10.7 <sup>(*)</sup>	8.5 <sup>(*)</sup>	8.9 <sup>(*)</sup>	13.8 <sup>(*)</sup>
CpG2	ChrX.166416503	ns	ns	ns	13.2 <sup>(*)</sup>
CpG3	ChrX.166416588	ns	ns	ns	9.1 <sup>(*)</sup>
CpG4	ChrX.166416645	4.5 <sup>(*)</sup>	6.5 <sup>(*)</sup>	2.1	17.3 <sup>(*)</sup>
<b>MID1 (Amplicon 2)</b>					
CpG1	ChrX.166416709	12.0 <sup>(*)</sup>	6.9 <sup>(*)</sup>	20.0 <sup>(*)</sup>	16.0 <sup>(*)</sup>
CpG2	ChrX.166416828	11.3 <sup>(*)</sup>	10.9 <sup>(*)</sup>	12.7 <sup>(*)</sup>	19.1 <sup>(*)</sup>
CpG3	ChrX.166416812	16.5 <sup>(*)</sup>	ns	21.2 <sup>(*)</sup>	14.4 <sup>(*)</sup>
<b>MID1 (Amplicon 3)</b>					
CpG1	ChrX.166443289	ns	ns	ns	ns
CpG2	ChrX.166443304	ns	ns	ns	ns
CpG3	ChrX.166443343	14.3 <sup>(*)</sup>	7.8 <sup>(*)</sup>	18.5 <sup>(*)</sup>	12.6 <sup>(*)</sup>
CpG4	ChrX.166443349	4.9 <sup>(*)</sup>	8.1 <sup>(*)</sup>	6.9 <sup>(*)</sup>	15.5 <sup>(*)</sup>
CpG5	ChrX.166443368	6.8 <sup>(*)</sup>	6.5 <sup>(*)</sup>	17.4 <sup>(*)</sup>	10.9 <sup>(*)</sup>
CpG6	ChrX.166443375	2.4 <sup>(*)</sup>	7.8 <sup>(*)</sup>	15.5 <sup>(*)</sup>	11.3 <sup>(*)</sup>
CpG7	ChrX.166443409	ns	ns	12.7 <sup>(*)</sup>	13.9 <sup>(*)</sup>
<b>WNT3</b>					
CpG1	Chr11.103672108	-2.6 <sup>(a)</sup>	ns	ns	ns
CpG2	Chr11.103672126	-3.1 <sup>(a)</sup>	-24.6 <sup>(*)</sup>	ns	ns
CpG3	Chr11.103672133 Chr11.103672141	-5.3 <sup>(a)</sup>	-17.9 <sup>(*)</sup> -18.3 <sup>(*)</sup>	ns	ns
<b>NLGN1</b>					
CpG1	Chr3.26129152	-5.2 <sup>(a)</sup>	-16.3 <sup>(*)</sup>	-4 <sup>(a)</sup>	-11.9 <sup>(*)</sup>
CpG2	Chr3.26129259	-5.9 <sup>(a)</sup>	-11.2 <sup>(*)</sup>	-4.3 <sup>(a)</sup>	-17.5 <sup>(*)</sup>
<b>NF2</b>					
CpG1	Chr11.4706269	9.3 <sup>(a)</sup>	14.5 <sup>(*)</sup>	6.9 <sup>(a)</sup>	14.9 <sup>(*)</sup>
CpG2	Chr11.4706277	ns	ns	ns	ns
CpG3	Chr11.4706289	2.7 <sup>(a)</sup>	ns	1.1 <sup>(a)</sup>	ns
CpG4	Chr11.4706313	8.7 <sup>(a)</sup>	18.6 <sup>(*)</sup>	9.9 <sup>(a)</sup>	13.8 <sup>(*)</sup>
CpG5	Chr11.4706641	16.3 <sup>(a)</sup>	12.2 <sup>(*)</sup>	12.3 <sup>(a)</sup>	13.5 <sup>(*)</sup>
<b>DLX1</b>					
CpG1	Chr2.71369017	ns	ns	-3.1 <sup>(a)</sup>	-10.8 <sup>(*)</sup>
CpG2	Chr2.71369024	ns	ns	-1.6 <sup>(a)</sup>	-5.1 <sup>(*)</sup>
CpG3	Chr2.71369035	ns	ns	-2.6 <sup>(a)</sup>	-5.2 <sup>(*)</sup>
CpG 4/5	Chr2.71369048 Chr2.71369051	ns	ns	-0.1 <sup>(a)</sup>	ns
CpG6	Chr2.71369058	ns	ns	-1.7 <sup>(a)</sup>	ns
CpG7	Chr2.71369066	ns	ns	-1.7 <sup>(a)</sup>	ns
CpG8	Chr2.71369085	ns	ns	-1.4 <sup>(a)</sup>	ns

**Supplementary Table 9.** Comparison between the bisulfite capture-sequencing (Capture-S) and EpiTYPER techniques used to assess differential DNA methylation in adult offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation. The columns describe the specific CpG affected in each of the selected genes (corresponding to *main Figure 3*), the specific genomic location of each CpG, and the differences between immune-challenged relative to control (CON) offspring as measured with the two techniques. Symbol <sup>(\*)</sup> indicates significance at specific CpG sites; symbol <sup>(a)</sup> indicates a significant main effect of prenatal immune activation across all CpG sites (see *main Figure 3*); ns = no significance. The precise genomic location of the CpG sites measured with EpiTYPER is provided the *Supplementary Table 10*.



<b>MID1 (Amplicon 1)</b>
GTGGCTGGAAGCACAGGCATGGTTGAAGAGATAC <b>CG</b> <sup>1</sup> GGCATGCCTGCAGTT <b>CG</b> <sup>2</sup> ATGCCGTGCCTAAAAACATCCTGGA AGAATCTGGAATTGCTTTGGATCGGATGGAAGGCAGAAACCAGGCCTGTGCCTCAG <b>CG</b> <sup>3</sup> CCACAGAC TGCAGAAAGCTTCTTATTATTACAGGGACGGGAAAAGAGATTG <b>CG</b> <sup>4</sup> ATGTCTGCCTGGCATCATAGCTTTGGCAAAC TTCAGTTCTGAGGTTCTGG
<b>MID1 (Amplicon 2)</b>
CTTTTGGCAAACCTCAGTTCTGAGGTTCTGGAACAAGTCAGT <b>CG</b> <sup>1</sup> TTAAGAGGACCCGTACTCCAATTCTATTATCACAC CAGACAGGTGCCTCAGAGGCACAGAGATGAGACAGGAGTCCACAGTGAGATTGGATTGCAGAG <b>CG</b> <sup>2</sup> CTGAGCCCAGGAGC <b>CG</b> <sup>3</sup> GTTAGGGGAAAGCAGAAGTAAAACCATTGGAGC
<b>MID1 (Amplicon 3)</b>
GGAACCAAGCCCTCCCCAGCC <b>CG</b> <sup>1</sup> GGGGCTGCCTGG <b>CG</b> <sup>2</sup> CCTGCCTCGCCATGG <b>CG</b> <sup>3</sup> CACAGGGAGGAGACACAGAGCC <b>G</b> <sup>3</sup> CTCC <b>CG</b> <sup>4</sup> CCAGGGGTCATGGAGG <b>CG</b> <sup>5</sup> TCCAG <b>CG</b> <sup>6</sup> GCCTGGGGGGAGGGAGCCTCAGAACTCACT <b>CG</b> <sup>7</sup> CAGTCAACC CCCAGCCTCATATATTCACCCACAGTGATCCACCTGCCTCAGAAAATCACTCGCAGTCATCCCCCTGCCTCAGAAATTCAC TACAGTCATCCCCCTGCCTCAGAAAATCACTCACAGTCATCCCCCTGCCTCAGAAAATCACTCACAGTGAGCCCCCTGCTT CAGAAAATCACTTACAGT
<b>WNT3</b>
TCTCATCTCTGAACCCTGGGCTGAGG <b>CG</b> <sup>1</sup> AGAACTGCCTTGTCT <b>CG</b> <sup>2</sup> ACCCT <b>CG</b> <sup>3/4</sup> TGGCTT <b>CG</b> <sup>3/4</sup> TAGGAGGAGGGCAA GAAATGGGCAGCCATGGCTGAAGATGCTGC
<b>NLGN1</b>
ACATGACTGACACCAGACATGGGG <b>CG</b> <sup>1</sup> TATGAGTCAGCACATTATGGCTTATACCAGATGTCCAGGGAAACCC AAAGTAAATAGTCAAGTAATCTGTTATACAATTATTCTGGGTAGAGTACCACTTTTGT <b>CG</b> <sup>2</sup> ATTCTGCATACTTATGGCCTTG AGGTCAAGGACTTTAGCC
<b>NF2</b>
GAAGCAGCCTCACCTGGCTCTGCC <b>CG</b> <sup>1</sup> GTGCT <b>CG</b> <sup>2</sup> CATACCAAGCC <b>CG</b> <sup>3</sup> TAATTCTCTCCTCCACATTT <b>CG</b> <sup>4</sup> GAGTCATC TGATAGAGATTTATCACCTACCAAAGACAGCAAAAGAAAAGCCACATGCAAAGCAAGTCTGGGTATTGTTGCCATTTT ATTATTATGGCTCATTTTTACAAAACAACAGAGCTATTTTTAAAAGCTGCATGCAGGGAGAGGCACACATAGAGGTGGGTG TGTAACAAGCACTGTTCCACTAGAGCAGCAACCGGAGAGCTGCAGGATGCCTCTAGCCTAAGTACACTCCTGGGCTAGG AGTGCCCTTTTGGCTGCTGGGGCTGTTTCTCAGGGACCACCTGACAGTAGAGCAATGCTTACTCACTGGCC <b>CG</b> <sup>5</sup> TCAC TGCACAGAAGTCATCAAAGGACAAGGA
<b>DLX1</b>
AAAGGCAGTGCAGCATTAAAGGGTCTCTGCTTCTGTTGTCCCTCCAGGG <b>CG</b> <sup>1</sup> GACT <b>CG</b> <sup>2</sup> AGAAGAGTAC <b>CG</b> <sup>3</sup> GTGGTG GAAGG <b>CG</b> <sup>4/5</sup> <b>CG</b> <sup>4/5</sup> AGGT <b>CG</b> <sup>6</sup> CTTAA <b>CG</b> <sup>7</sup> GCAAAGGGAAAAGAT <b>CG</b> <sup>8</sup> TAAACCCAGGACAATTTATTCCAGTTTGCAGTT GCAGGCTTTGA

**Supplementary Table 10.** Sequences of the selected amplicons assessed with EpiTYPER and position of CpGs in each amplicon. Methylation of the numbered CpGs (in bold font) was accessible to quantification by EpiTYPER and corresponds to the CpG numbers presented in main *Figure 3* and *Figure 7*. The underlined CpGs were not measurable for technical reasons.

<b>POL-GD9 versus CON offspring</b>		
<b>Biological process</b>	<b>Enrichment score</b>	<b>Enrichment p-value</b>
Cellular Process	66.83	9.39E-30
Single Organism Cellular Process	58.38	4.40E-26
Cellular Developmental Process	36.37	1.59E-16
Cell Differentiation	29.83	1.10E-13
Neuron Differentiation	10.36	3.14E-05
<b>POL-GD17 versus CON offspring</b>		
<b>Biological process</b>	<b>Enrichment score</b>	<b>Enrichment p-value</b>
Cellular Process	57.61	9.50E-26
Single Organism Cellular Process	48.98	5.31E-22
Cellular Developmental Process	19.92	2.23E-09
Cell Differentiation	15.38	2.09E-07
Neuron Differentiation	6.16	2.10E-03

**Supplementary Table 11.** GO enrichment analysis of genes affected by methylation differences in offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation. For both prenatal treatment conditions, the most significant enrichment occurred in GO-term category “biological process” involving genes annotating with the terms listed in the table. The table also specifies the enrichment score and the enrichment *p*-value for each term.

<b>GO term NEURON DIFFERENTIATION POL-GD9</b>			
<b>Gene Name</b>	<b>CpG</b>	<b>Methylation Difference</b>	<b>q-value</b>
Otx2	chr14.49274059	-26.850	0.020
Lef1	chr3.130787703	-22.923	0.029
Lmx1a	chr1.169857064	12.134	0.036
Efna1	chr3.89080559	-12.638	0.038
Wnt3	chr11.103672126	-24.691	0.038
Bag1	chr4.40893758	-10.793	0.040
Wnt11	chr7.105919349	11.884	0.043
Lef1	chr3.130787575	-16.726	0.044
Ttc26	chr6.38332287	17.341	0.049
Gdpd5	chr7.106528869	-14.807	0.052
Wnt7b	chr15.85446192	-17.416	0.057
Runx2	chr17.44610012	14.659	0.064
Olig3	chr10.19179542	15.038	0.065
Sox1	chr8.12401489	-9.454	0.069
Nr2e1	chr10.42321583	-18.757	0.070
Lef1	chr3.130787898	-13.484	0.071
Nkx6-1	chr5.102087602	-10.446	0.073
Rbpj	chr5.53900396	-11.357	0.079
Nr2e1	chr10.42321599	-18.116	0.082
Wnt11	chr7.105919523	10.688	0.088
Tulp3	chr6.128304861	8.729	0.090
Rbpj	chr5.53900945	-12.783	0.090
Wnt8a	chr18.34708934	-18.509	0.091
Wnt3	chr11.103672141	-17.920	0.092
Tulp3	chr6.128304767	19.067	0.095
Lef1	chr3.130816157	15.219	0.106
Wnt3	chr11.103672133	-18.354	0.109
Lmo4	chr3.143856160	-12.614	0.117
Agtpbp1	chr13.59355118	-17.282	0.117
Tulp3	chr6.128304627	15.256	0.120
Pax3	chr1.78078405	11.340	0.122
Olig3	chr10.19179537	10.900	0.122
Phox2b	chr5.67530422	12.498	0.126
Lef1	chr3.130787884	-10.165	0.131
Sox1	chr8.12401618	-6.391	0.132
Lmo4	chr3.143851190	-12.629	0.136
Nkx6-1	chr5.102087595	-10.140	0.137
Pax3	chr1.78078542	10.922	0.139
Agtpbp1	chr13.59355019	-11.224	0.142
Cbln1	chr8.89993378	14.333	0.144
Adnp2	chr18.80315479	-14.074	0.146
Lmo4	chr3.143851107	-11.262	0.146
Adnp2	chr18.80315510	-11.269	0.155
Otx2	chr14.49274274	-11.670	0.160
Lef1	chr3.130787699	-12.945	0.161
Lef1	chr3.130787695	-12.815	0.163

Runx2	chr17.44610021	9.407	0.167
Tulp3	chr6.128304959	7.911	0.169
Wnt7b	chr15.85446220	-10.952	0.170
Cbln1	chr8.89993265	14.323	0.179
Lmo4	chr3.143856559	-8.718	0.181
Phox2b	chr5.67530030	8.672	0.185
Ttc26	chr6.38332105	13.098	0.188
Wnt3	chr11.103672558	-11.377	0.194
Wnt7b	chr15.85446204	-11.515	0.195
Lhx4	chr1.157575064	10.326	0.195
Efna1	chr3.89080319	-11.039	0.195
Lmo4	chr3.143851424	-6.623	0.199
Efna1	chr3.89080909	-7.355	0.199
Tbx20	chr9.24574486	-8.527	0.199

GO term NEURON DIFFERENTIATION POL-GD17			
Gene Name	CpG	Methylation Difference	q-value
Olig3	chr10.19124131	26.659	0.006
Sox5	chr6.144006054	-24.099	0.017
Irx5	chr8.94983861	-18.317	0.020
Dlx1	chr2.71369036	-10.879	0.026
Nr4a2	chr2.56970305	-6.612	0.032
Ntrk2	chr13.58911381	20.180	0.037
Agtpbp1	chr13.59601953	13.103	0.039
Ntrk2	chr13.58911375	18.206	0.039
Fezf2	chr14.13174084	-7.527	0.041
Barhl2	chr5.106846162	-15.503	0.042
Kcnma1	chr14.24382686	-16.777	0.042
Tlx3	chr11.33096862	13.351	0.045
Sox8	chr17.25705353	19.643	0.049
Ush1c	chr7.53491362	11.960	0.067
Dfna5	chr6.50204947	-9.591	0.068
Kcnma1	chr14.24382692	-15.231	0.073
Barhl2	chr5.106846151	-13.952	0.076
Ntf3	chr6.126059016	-7.783	0.084
Sox8	chr17.25705369	11.338	0.097
Mir17	chr14.115348130	-13.740	0.099
Lmo4	chr3.143858284	-9.643	0.103
Helt	chr8.47426429	-10.767	0.106
Lhx5	chr5.120781974	-14.301	0.106
Lhx2	chr2.38215493	15.303	0.116
Ryk	chr9.102762694	-9.037	0.116
Sox5	chr6.144006006	-13.647	0.118
Cux1	chr5.137069363	8.162	0.118
Lhx8	chr3.153889705	11.795	0.122
Lhx2	chr2.38215432	13.931	0.123
Lmo4	chr3.143858229	-8.787	0.123
Agtpbp1	chr13.59601118	9.505	0.124
Mir17	chr14.115348147	-12.725	0.131
Fezf2	chr14.13174859	-14.816	0.131
Lmo4	chr3.143858828	-11.794	0.133
Fezf2	chr14.13174107	-6.910	0.136
Lhx8	chr3.153889730	9.806	0.137
Dfna5	chr6.50204934	-8.693	0.138
Helt	chr8.47426318	-8.584	0.157
Ush1c	chr7.53491426	9.391	0.160
Ntf3	chr6.126059203	-9.532	0.162
Dlx1	chr2.71369018	-5.126	0.165
Cux1	chr5.137069408	7.070	0.168
Foxa2	chr2.147908009	-8.905	0.170
Lhx5	chr5.120781971	-11.389	0.178
Ntrk2	chr13.58911368	11.035	0.184
Foxa2	chr2.147908385	-13.087	0.185
Ush1c	chr7.53491306	7.543	0.189
Lhx5	chr5.120781994	-11.463	0.192
Foxa2	chr2.147908468	-9.552	0.194
Dlx1	chr2.71369025	-5.207	0.198

**Supplementary Table 12.** List of affected genes that annotate to the GO term ‘neuron differentiation’ in offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation. Each column describes the affected gene, the genomic location of the differentially methylated CpGs, the methylation difference (percent change from controls) and the *q*-value of the methylation difference.

<b>GO Term</b>		
<b>Cellular Component</b>	<b>Enrichment score</b>	<b>Enrichment p-value</b>
Cell Part	7.80459	4.07E-05
Neuron Part	11.2713	1.27E-05
Neuron Projection	8.81076	1.49E-05

**Supplementary Table 13.** GO enrichment analysis of genes with methylation differences commonly found in offspring exposed to poly(I:C)-induced immune activation in middle (POL-GD9) or late (POL-GD17) gestation. The most significant enrichment occurred in GO-term category “cellular component” involving genes annotating with the terms listed in the table. The table also specifies the enrichment score and the enrichment *p*-value for each term.

## SUPPLEMENTARY DISCUSSION

Our study demonstrates that the effects on the adult DNA methylome are influenced by the precise timing of prenatal immune challenge. These differential epigenetic effects may, at least in part, be accounted for by differences in the precise maternal and fetal immune responses to poly(I:C) at the selected gestational time points. Using the same maternal immune activation model and mouse strain, we previously found that the effects of maternal immune challenge between middle and late gestational periods are dissociable in terms of the pro- and anti-inflammatory cytokine responses to maternal poly(I:C) treatment (2). For example, whereas maternal poly(I:C) treatment on GD9 leads to more extensive maternal and fetal IL-6 responses compared to poly(I:C) treatment on GD17, the maternal and fetal IL-10 responses to poly(I:C) are protracted when the immune-stimulating agent is given on GD17 as compared to GD9 (2). Interestingly, different cytokine classes are known to modulate different epigenetic processes such as DNA methylation (13,14). Therefore, the specificity of poly(I:C)-induced inflammatory responses may be critical in determining the nature of long-term epigenetic effects in the offspring. Additional studies are warranted in order to examine this hypothesis more thoroughly.

The differential effects of middle versus late prenatal immune activation on the adult prefrontal methylome and gene expression profiles may also explain some of the differences in behavioral and cognitive outcomes that are induced by the two prenatal manipulations. The present study confirms that poly(I:C)-induced immune activation on GD 9 causes sensorimotor gating deficiency (1,4,15-17), whereas the same manipulation on GD 17 impaired performance in a Y-maze spatial recognition memory test similarly to what has been reported before (7,8,18,19). The latter test is often taken to index spatial working memory (7), suggesting that prenatal immune activation in late gestation leads to deficits in this cognitive domain. There is an ongoing debate, however, as to whether the Y-maze test measures spatial working memory or habituation (20,21). Hence, the poly(I:C)-induced impairments in Y-maze test might reflect abnormal spatial habituation rather than genuine deficits in spatial working memory. Whilst this hypothesis warrants further examination, it

should be pointed out adult mice prenatally exposed to poly(I:C) in late gestation (GD 17) were found to be impaired in other tests that more readily measure (spatial) working memory (7,19,22). Hence, whether or not captured by the current Y-maze test, accumulating evidence supports the notion that prenatal immune activation during late fetal periods can lead to working memory impairments in the adult offspring. In the present study, we used the Y-maze test primarily because it is associated with only minimal stress for the test animals, as it does not involve any major deviations from general housing conditions (such as single caging and/or food and water deprivation) or exposure to adverse stimuli such as foot shock. Our study followed a within-subjects design, in which all animals were first characterized at the behavioral/cognitive level before the initiation of the molecular analyses. This experimental approach necessitated the use of tests that are characterized by a relatively low amount of stress in order to minimize stress-induced confounds on methylation and gene expression profiles.

Whatever precise neurocognitive and -psychological constructs involved in the Y-maze test, the inclusion of two prenatal time points of immune activation allowed us to identify possible relationships between differential DNA methylation profiles and specific behavioral and cognitive deficits. In view of the proposed role of prefrontal GABAergic signaling in cognitive functions (23-26), altered methylation of GABA-related genes may readily contribute to the emergence of cognitive deficits in offspring prenatally exposed to immune activation in late gestation. On the other hand, methylation-induced changes in Wnt gene transcription and signaling may contribute to the emergence of sensorimotor gating impairments, as highlighted by previous studies (27,28). These possible associations, however, should be interpreted with caution and should be further explored using approaches that can determine causality. Furthermore, it should be pointed out that prenatal immune activation caused differential methylation of a large number of genes, which in turn likely affects the differentiation and/or functional properties of various other neuronal subtypes. Hence, abnormalities in multiple neurotransmitter systems and pathways may

contribute to the emergence of behavioral and cognitive dysfunctions in prenatally infected offspring, as previously suggested (29).

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## Supplementary Table ST1

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concatanate	chr	start	end	qvalue	meth.diff
chr12:87164001-87165000	chr12	87164001	87165000	0.131559118	-14.11732456
chr12:81774001-81775000	chr12	81774001	81775000	0.053644715	-6.955780336
chr11:120210001-120211000	chr11	120210001	120211000	5.70E-09	-4.883995862
chr6:72298001-72299000	chr6	72298001	72299000	0.032480639	9.165081349
chr8:80016001-80017000	chr8	80016001	80017000	0.049869475	-9.216646267
chr6:108484001-108485000	chr6	108484001	108485000	0.17396422	4.329748416
chr6:108526001-108527000	chr6	108526001	108527000	0.065677613	-8.878602048
chr5:64212001-64213000	chr5	64212001	64213000	0.036036406	-13.55798601
chr5:64263001-64264000	chr5	64263001	64264000	0.020869845	7.781784489
chr5:64278001-64279000	chr5	64278001	64279000	0.015833106	8.122444755
chr13:49310001-49311000	chr13	49310001	49311000	0.147344616	5.698355355
chr13:49311001-49312000	chr13	49311001	49312000	0.145734734	-3.277310457
chr5:121055001-121056000	chr5	121055001	121056000	0.136370029	-0.955409646
chr11:87523001-87524000	chr11	87523001	87524000	0.171724555	10.01386001
chr3:68672001-68673000	chr3	68672001	68673000	0.131572223	-6.423760058
chr17:35090001-35091000	chr17	35090001	35091000	0.154087981	12.91952195
chr16:24394001-24395000	chr16	24394001	24395000	0.111364218	5.3741274
chr1:24012001-24013000	chr1	24012001	24013000	0.164945751	1.179472151
chr19:21725001-21726000	chr19	21725001	21726000	0.110130047	-6.721311475
chr19:21726001-21727000	chr19	21726001	21727000	0.162750148	2.466116458
chr6:134876001-134877000	chr6	134876001	134877000	0.128443991	3.305820884
chr6:134877001-134878000	chr6	134877001	134878000	0.06583798	2.176619135
chr8:123156001-123157000	chr8	123156001	123157000	0.144394825	12.80487805
chr16:21795001-21796000	chr16	21795001	21796000	0.159669598	-3.251623402
chr15:82090001-82091000	chr15	82090001	82091000	0.021049232	-7.931234734
chr10:83181001-83182000	chr10	83181001	83182000	0.187024617	-4.925576766
chr10:83186001-83187000	chr10	83186001	83187000	0.065550642	-4.338993329
chr10:83519001-83520000	chr10	83519001	83520000	0.076183272	-12.43970673
chr5:115245001-115246000	chr5	115245001	115246000	0.171633446	-7.121730289
chr2:127617001-127618000	chr2	127617001	127618000	0.026530935	1.864596687
chr19:36751001-36752000	chr19	36751001	36752000	0.000580826	6.917261223
chr19:36752001-36753000	chr19	36752001	36753000	0.039637921	11.46335334
chr17:24353001-24354000	chr17	24353001	24354000	0.197793218	-11.30952381
chr7:38946001-38947000	chr7	38946001	38947000	0.027187092	-4.508473939
chr7:38968001-38969000	chr7	38968001	38969000	0.151860684	-3.656836244
chr17:45861001-45862000	chr17	45861001	45862000	0.085167319	-4.056444057
chr17:45871001-45872000	chr17	45871001	45872000	0.10226966	-11.45783036
chr17:45879001-45880000	chr17	45879001	45880000	0.123338396	-9.600672136
chr17:45985001-45986000	chr17	45985001	45986000	0.058531307	-9.926645883
chr17:46004001-46005000	chr17	46004001	46005000	0.107451688	-7.731325999
chrX:82325001-82326000	chrX	82325001	82326000	0.138486481	-8.144394061
chr9:50041001-50042000	chr9	50041001	50042000	0.036632436	9.712048291
chr9:50246001-50247000	chr9	50246001	50247000	0.017932526	-12.2277842

## Supplementary Table ST2

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concatanate	chr	start	end	qvalue	meth.diff
chrM:13001-14000	chrM	13001	14000	0.140320961	-0.045749646
chrM:5001-6000	chrM	5001	6000	0.045498128	-0.072054698
chr12:87164001-87165000	chr12	87164001	87165000	0.143059783	-12.84189805
chr12:87165001-87166000	chr12	87165001	87166000	0.135477917	-0.39304226
chr11:120210001-120211000	chr11	120210001	120211000	0.001889132	-3.458341117
chr16:31947001-31948000	chr16	31947001	31948000	0.138014923	3.050725917
chr8:80007001-80008000	chr8	80007001	80008000	0.171402214	4.989291996
chr6:108516001-108517000	chr6	108516001	108517000	0.034003577	-9.50042207
chr6:108563001-108564000	chr6	108563001	108564000	0.179441802	-9.143724484
chr6:108613001-108614000	chr6	108613001	108614000	0.146326902	-6.759177101
chr6:108616001-108617000	chr6	108616001	108617000	0.002778402	-13.00061092
chr6:108619001-108620000	chr6	108619001	108620000	0.037660936	-16.64222874
chr5:64239001-64240000	chr5	64239001	64240000	0.112617329	-4.887098279
chr5:64263001-64264000	chr5	64263001	64264000	0.015420279	8.072174739
chr7:123264001-123265000	chr7	123264001	123265000	0.173783873	5.603804797
chr5:116081001-116082000	chr5	116081001	116082000	0.062943203	-5.123073722
chr2:156689001-156690000	chr2	156689001	156690000	0.101000358	2.531547181
chr5:121057001-121058000	chr5	121057001	121058000	0.149084528	5.231534601
chr2:32235001-32236000	chr2	32235001	32236000	0.008615245	14.81292321
chrX:67638001-67639000	chrX	67638001	67639000	0.165300998	-1.212728759
chr17:85356001-85357000	chr17	85356001	85357000	0.183352922	0.549686066
chr8:109097001-109098000	chr8	109097001	109098000	0.025914431	-9.781383611
chr11:95573001-95574000	chr11	95573001	95574000	0.127070433	1.431619953
chr17:35089001-35090000	chr17	35089001	35090000	0.17657808	0.922901821
chr17:35090001-35091000	chr17	35090001	35091000	0.013973222	18.0923653
chr16:24394001-24395000	chr16	24394001	24395000	0.012418026	7.39673913
chr6:134877001-134878000	chr6	134877001	134878000	0.007492245	2.927329582
chr9:94437001-94438000	chr9	94437001	94438000	0.149469205	1.783099355
chr16:21815001-21816000	chr16	21815001	21816000	0.166412833	-6.353614668
chr16:21818001-21819000	chr16	21818001	21819000	0.042353631	12.05473428
chr16:21836001-21837000	chr16	21836001	21837000	0.129409753	-15.48322051
chr4:45880001-45881000	chr4	45880001	45881000	0.045111313	7.850720532
chr10:83181001-83182000	chr10	83181001	83182000	0.195171095	-4.833216219
chr10:83459001-83460000	chr10	83459001	83460000	0.184733483	-5.920646005
chr10:83482001-83483000	chr10	83482001	83483000	0.01004167	6.051036155
chr5:115245001-115246000	chr5	115245001	115246000	0.118195171	-7.519579752
chr2:166878001-166879000	chr2	166878001	166879000	0.162223594	-8.996511773
chr19:36751001-36752000	chr19	36751001	36752000	0.176421833	3.621196068
chr16:96082001-96083000	chr16	96082001	96083000	0.025327985	-9.191516378
chr7:38946001-38947000	chr7	38946001	38947000	0.137873967	-2.930888276
chr17:45871001-45872000	chr17	45871001	45872000	0.01919748	-13.9367174
chr17:45927001-45928000	chr17	45927001	45928000	0.054409557	-24.31446541
chr17:45985001-45986000	chr17	45985001	45986000	0.011945932	-11.46213598

## Supplementary Table 3 (ST3)

Differentially methylated CpGs in POL-GD9 Offspring				
Base	Methylation Difference	q-value	Gene Name	Detailed Annotation
chr11 120210756	-7.477	0.035	0610009L18Rik	promoter-TSS (NM_009609)
chr8 80016478	-11.470	0.067	0610038B21Rik	intron (NM_030113, intron 1 of 22)
chr5 64263485	12.260	0.129	0610040J01Rik	intron (NM_029554, intron 1 of 3)
chr5 64263366	12.041	0.138	0610040J01Rik	intron (NM_029554, intron 1 of 3)
chr5 64263371	10.924	0.177	0610040J01Rik	intron (NM_029554, intron 1 of 3)
chr2 127617983	6.944	0.060	1500011K16Rik	non-coding (NR_015476, exon 1 of 2)
chr17 24354161	-15.338	0.035	1600002H07Rik	intron (NM_028056, intron 8 of 9)
chr7 38946855	-8.257	0.020	1600014C10Rik	Intergenic
chrX 82325176	-14.458	0.101	1600014K23Rik	intron (NM_007868, intron 63 of 78)
chrX 82325238	-12.381	0.118	1600014K23Rik	intron (NM_007868, intron 63 of 78)
chr13 119386112	-6.977	0.048	1700003P14Rik	Intergenic
chr13 119386050	-6.911	0.073	1700003P14Rik	Intergenic
chr3 6675623	8.201	0.130	1700008P02Rik	Intergenic
chr1 173054776	-11.129	0.126	1700009P17Rik	ID4_ SINE ID
chr1 173054804	-11.423	0.180	1700009P17Rik	ID4_ SINE ID
chr7 118446067	-20.806	0.010	1700012D14Rik	Intergenic
chr8 11666672	-8.442	0.165	1700016D06Rik	intron (NM_024271, intron 1 of 5)
chr3 40421696	19.216	0.089	1700017G19Rik	non-coding (NR_040445, exon 1 of 6)
chr3 40421965	12.969	0.123	1700017G19Rik	promoter-TSS (NR_040445)
chr3 40421975	12.988	0.146	1700017G19Rik	promoter-TSS (NR_040445)
chr3 40421725	11.440	0.166	1700017G19Rik	non-coding (NR_040445, exon 1 of 6)
chr6 85854771	-13.678	0.037	1700019G17Rik	5' UTR (NM_029331, exon 1 of 4)
chr6 85854794	-16.077	0.038	1700019G17Rik	5' UTR (NM_029331, exon 1 of 4)
chr6 85854775	-13.512	0.058	1700019G17Rik	5' UTR (NM_029331, exon 1 of 4)
chr6 85854815	-8.287	0.188	1700019G17Rik	5' UTR (NM_029331, exon 1 of 4)
chr19 58890758	-30.104	0.016	1700019N19Rik	intron (NM_175199, intron 6 of 11)
chr19 58890770	-23.739	0.035	1700019N19Rik	intron (NM_175199, intron 6 of 11)
chr9 120808863	-11.147	0.029	1700020M21Rik	Intergenic
chr1 153800562	-12.538	0.095	1700025G04Rik	intron (NM_197990, intron 3 of 5)
chr1 153800653	-8.030	0.135	1700025G04Rik	intron (NM_197990, intron 3 of 5)
chr12 19887673	-12.556	0.099	1700030C10Rik	Intergenic
chr12 20318834	-11.787	0.107	1700030C10Rik	Intergenic
chr12 19887798	-7.573	0.109	1700030C10Rik	Intergenic
chr12 20821302	-7.853	0.111	1700030C10Rik	non-coding (NR_015521, exon 1 of 2)
chr12 20821051	-10.307	0.117	1700030C10Rik	CpG
chr12 20821969	-7.532	0.127	1700030C10Rik	promoter-TSS (NR_015521)
chr12 20821909	-11.077	0.132	1700030C10Rik	promoter-TSS (NR_015521)
chr12 20318405	-10.455	0.133	1700030C10Rik	CpG
chr12 20318452	-9.902	0.147	1700030C10Rik	CpG
chr12 20820900	-11.035	0.148	1700030C10Rik	intron (NR_015521, intron 1 of 1)
chr12 19887775	-8.385	0.150	1700030C10Rik	Intergenic
chr12 20820885	-9.863	0.155	1700030C10Rik	intron (NR_015521, intron 1 of 1)

chr12	20318519	-11.954	0.157	1700030C10Rik	CpG
chr1	193733028	-11.170	0.187	1700034H15Rik	exon (NM_009579, exon 2 of 2)
chr10	67908977	-8.287	0.165	1700040L02Rik	intron (NM_028491, intron 5 of 7)
chr4	115855708	-14.147	0.035	1700042G07Rik	Intergenic
chr4	124074167	-14.770	0.139	1700057H15Rik	Intergenic
chr4	124074186	-12.254	0.150	1700057H15Rik	Intergenic
chr6	143461914	-15.838	0.026	1700060C16Rik	Intergenic
chr9	41004151	-17.264	0.091	1700063D05Rik	Intergenic
chr15	63660733	-13.317	0.060	1700065I16Rik	intron (NM_177912, intron 5 of 11)
chr15	63660727	-10.321	0.129	1700065I16Rik	intron (NM_177912, intron 5 of 11)
chr15	63660729	-9.532	0.156	1700065I16Rik	intron (NM_177912, intron 5 of 11)
chr15	63660525	7.182	0.166	1700065I16Rik	intron (NM_177912, intron 5 of 11)
chr6	75247937	-7.436	0.075	1700065L07Rik	Intergenic
chr6	75247542	-9.418	0.123	1700065L07Rik	Intergenic
chr6	75247827	-5.028	0.180	1700065L07Rik	Intergenic
chrX	49333402	-14.149	0.039	1700080O16Rik	Intergenic
chr4	145587292	-12.919	0.044	1700095A21Rik	(CTTG)n Simple_repeat Simple_repeat
chr17	3570957	5.646	0.063	1700102H20Rik	Intergenic
chr17	3570803	-14.166	0.155	1700102H20Rik	Intergenic
chr12	55384975	-21.721	0.041	1700104L18Rik	Intergenic
chr17	10522509	12.748	0.064	1700110C19Rik	TTS (NR_045461)
chr17	10522684	7.988	0.195	1700110C19Rik	TTS (NR_045461)
chr1	186219466	-19.444	0.098	1700112H15Rik	Intergenic
chr1	186219150	-14.141	0.165	1700112H15Rik	Intergenic
chr12	107716780	5.344	0.034	1700121N20Rik	Intergenic
chr12	107716590	-7.411	0.044	1700121N20Rik	Intergenic
chr12	107716577	-6.723	0.157	1700121N20Rik	Intergenic
chr12	107716554	-8.233	0.162	1700121N20Rik	Intergenic
chr17	48138400	-10.849	0.155	1700122O11Rik	Intergenic
chr16	6350606	-14.551	0.054	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6350645	-11.563	0.073	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6350715	-10.540	0.088	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6350486	-13.685	0.137	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6350718	-8.533	0.155	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr1	100171057	-14.052	0.063	1810006J02Rik	Intergenic
chr18	75422547	-9.123	0.161	2010010A06Rik	intron (NM_027727, intron 16 of 16)
chr18	75422493	-10.713	0.189	2010010A06Rik	intron (NM_027727, intron 16 of 16)
chr18	75422699	-9.518	0.199	2010010A06Rik	intron (NM_027727, intron 16 of 16)
chr6	34944182	-7.972	0.049	2010107G12Rik	Intergenic
chr6	34944172	-9.641	0.065	2010107G12Rik	Intergenic
chr13	63057769	10.519	0.132	2010111I01Rik	URR1B DNA MER1_type
chr13	63057885	6.728	0.133	2010111I01Rik	Intergenic
chr9	63340426	-19.006	0.064	2300009A05Rik	intron (NM_030068, intron 15 of 21)
chr16	21654744	24.306	0.031	2510009E07Rik	intron (NM_001001881, intron 1 of 1)
chr4	125589182	-17.008	0.065	2610028E06Rik	intron (NR_015560, intron 2 of 5)
chr4	125589216	-17.143	0.116	2610028E06Rik	intron (NR_015560, intron 2 of 5)

chr7	87120197	-13.274	0.037	2610034B18Rik	Intergenic
chr2	84509731	12.776	0.074	2700094K13Rik	TTS (NM_001145100)
chr2	84509727	10.480	0.188	2700094K13Rik	TTS (NM_001145100)
chr11	116909311	-8.576	0.104	2810008D09Rik	Intergenic
chr11	116861313	15.787	0.143	2810008D09Rik	Intergenic
chr11	116909263	-10.194	0.146	2810008D09Rik	Intergenic
chr11	116909273	-9.534	0.190	2810008D09Rik	Intergenic
chr11	16761370	-19.064	0.065	2810442I21Rik	intron (NM_007912, intron 3 of 15)
chr11	16761442	-11.018	0.129	2810442I21Rik	intron (NM_007912, intron 3 of 15)
chr11	16761364	-15.091	0.155	2810442I21Rik	intron (NM_007912, intron 3 of 15)
chr11	28595088	-17.750	0.012	2810471M01Rik	Intergenic
chr5	113566077	-11.833	0.147	2900026A02Rik	intron (NM_172884, intron 1 of 7)
chr5	113566087	-9.487	0.192	2900026A02Rik	intron (NM_172884, intron 1 of 7)
chr7	26178170	15.584	0.060	4732471J01Rik	intron (NM_010719, intron 1 of 9)
chr7	26178229	11.224	0.200	4732471J01Rik	intron (NM_010719, intron 1 of 9)
chr17	12528862	-19.137	0.056	4732491K20Rik	Intergenic
chr17	12528871	-16.736	0.088	4732491K20Rik	Intergenic
chr13	91881588	-14.286	0.064	4833422C13Rik	promoter-TSS (NR_028314)
chr13	91881580	-12.986	0.153	4833422C13Rik	promoter-TSS (NR_028314)
chr9	50910228	-25.714	0.020	4833427G06Rik	promoter-TSS (NM_177702)
chr2	25471482	-15.700	0.117	4921530D09Rik	intron (NM_029859, intron 4 of 13)
chr2	25471682	-14.449	0.131	4921530D09Rik	exon (NM_029859, exon 4 of 14)
chr2	25471221	-9.985	0.200	4921530D09Rik	intron (NM_029859, intron 4 of 13)
chr4	102926651	-6.356	0.180	4921539E11Rik	intron (NM_001163494, intron 4 of 7)
chr13	31438899	-8.482	0.088	4930401O12Rik	Intergenic
chr13	31438755	-7.825	0.090	4930401O12Rik	Intergenic
chr2	35252925	-13.829	0.099	4930402F06Rik	promoter-TSS (NM_001272040)
chr2	35252959	-9.040	0.170	4930402F06Rik	promoter-TSS (NM_001272040)
chr12	72530516	15.856	0.039	4930404H11Rik	Intergenic
chr12	72561546	-12.152	0.065	4930404H11Rik	Intergenic
chr12	72530574	13.297	0.078	4930404H11Rik	Intergenic
chr11	11428754	-10.075	0.169	4930415F15Rik	Intergenic
chr2	74264850	14.303	0.088	4930441J16Rik	Intergenic
chr2	74264859	13.975	0.095	4930441J16Rik	Intergenic
chr2	74264832	9.816	0.184	4930441J16Rik	Intergenic
chr13	18265911	-13.583	0.031	4930448F12Rik	intron (NM_175006, intron 3 of 7)
chr18	28236195	14.642	0.093	4930474G06Rik	Intergenic
chrX	35352590	12.632	0.019	4930525M21Rik	Intergenic
chr19	55769156	18.349	0.048	4930552P12Rik	intron (NR_045318, intron 2 of 3)
chr19	55638729	15.109	0.069	4930552P12Rik	intron (NM_016862, intron 7 of 7)
chr19	55638563	8.520	0.149	4930552P12Rik	intron (NM_016862, intron 7 of 7)
chr19	55769172	11.701	0.193	4930552P12Rik	intron (NR_045318, intron 2 of 3)
chr16	84446600	-6.087	0.039	4930553E22Rik	Intergenic
chr7	125387839	6.816	0.199	4930583K01Rik	promoter-TSS (NM_001031814)
chr1	141053096	-6.763	0.035	4930596I21Rik	intron (NM_181347, intron 18 of 20)
chr19	37312553	-8.475	0.042	4931408D14Rik	Intergenic

chr9	40761552	-14.913	0.091	4931429I11Rik	intron (NM_001081121, intron 2 of 8)
chr9	40761404	-8.642	0.191	4931429I11Rik	intron (NM_001081121, intron 2 of 8)
chr13	48222191	9.110	0.180	4931429P17Rik	intron (NR_102303, intron 1 of 2)
chr13	48222041	10.957	0.190	4931429P17Rik	intron (NR_102303, intron 1 of 2)
chr1	91585641	-11.653	0.036	4933400F21Rik	intron (NM_001037136, intron 9 of 16)
chr1	91585678	-11.097	0.092	4933400F21Rik	intron (NM_001037136, intron 9 of 16)
chr11	25596308	14.502	0.053	4933427E13Rik	intron (NR_027973, intron 2 of 5)
chr5	127078877	11.035	0.079	4933438B17Rik	Intergenic
chr5	127078719	15.657	0.082	4933438B17Rik	Intergenic
chr14	75452513	10.621	0.186	5031414D18Rik	TTS (NM_198642)
chr2	131633623	20.475	0.049	5330413P13Rik	(CAT)n Simple_repeat Simple_repeat
chr2	131633687	13.758	0.146	5330413P13Rik	Intergenic
chr13	81079829	15.504	0.084	5430425K12Rik	non-coding (NR_103550, exon 1 of 5)
chr13	81079835	14.431	0.133	5430425K12Rik	non-coding (NR_103550, exon 1 of 5)
chr13	81079818	12.079	0.155	5430425K12Rik	non-coding (NR_103550, exon 1 of 5)
chr12	18394014	-10.372	0.052	5730507C01Rik	CpG
chr12	19294755	-11.747	0.078	5730507C01Rik	CpG
chr12	19294933	-9.490	0.089	5730507C01Rik	CpG
chr12	18394668	-11.348	0.093	5730507C01Rik	CpG
chr12	18394841	-10.973	0.094	5730507C01Rik	CpG
chr12	18394583	-9.265	0.116	5730507C01Rik	CpG
chr12	19294744	-9.390	0.120	5730507C01Rik	CpG
chr12	19294943	-8.605	0.122	5730507C01Rik	CpG
chr12	19294136	-6.989	0.125	5730507C01Rik	CpG
chr12	19182042	-12.038	0.134	5730507C01Rik	CpG
chr12	19294802	-10.945	0.135	5730507C01Rik	CpG
chr12	19294959	-8.691	0.149	5730507C01Rik	CpG
chr12	19182090	-10.013	0.154	5730507C01Rik	CpG
chr12	19182072	-9.070	0.159	5730507C01Rik	CpG
chr12	19294763	-8.004	0.173	5730507C01Rik	CpG
chr12	19294267	-6.523	0.174	5730507C01Rik	CpG
chr12	19294937	-6.659	0.188	5730507C01Rik	CpG
chr12	19294860	-9.105	0.192	5730507C01Rik	CpG
chr15	12753442	-10.951	0.062	6030458C11Rik	exon (NM_001166360, exon 2 of 3)
chr8	126232699	-16.299	0.089	6030466F02Rik	Intergenic
chr17	9355107	-14.345	0.063	6530411M01Rik	intron (NR_027881, intron 1 of 2)
chr17	9355194	-8.409	0.126	6530411M01Rik	intron (NR_027881, intron 1 of 2)
chr19	57584445	-12.626	0.139	6720468P15Rik	intron (NR_040306, intron 2 of 3)
chr19	57584467	-10.271	0.149	6720468P15Rik	intron (NR_040306, intron 2 of 3)
chr19	57584475	-10.403	0.167	6720468P15Rik	intron (NR_040306, intron 2 of 3)
chr8	19991227	-5.880	0.044	6820431F20Rik	TTS (NR_030708).2
chr8	19991123	-6.470	0.153	6820431F20Rik	TTS (NR_030708).2
chr8	19892404	-5.964	0.160	6820431F20Rik	intron (NR_030708, intron 1 of 4)
chr8	19892837	7.947	0.176	6820431F20Rik	CpG
chr2	11297045	17.638	0.076	8030442B05Rik	intron (NR_040615, intron 1 of 2)
chr2	11297004	12.911	0.167	8030442B05Rik	intron (NR_040615, intron 1 of 2)

chr4	7241605	-22.810	0.023	8430436N08Rik	Intergenic
chr16	30039640	14.220	0.061	9030404E10Rik	promoter-TSS (NR_045878)
chr16	30039633	15.043	0.063	9030404E10Rik	promoter-TSS (NR_045878)
chr16	30039631	12.268	0.155	9030404E10Rik	promoter-TSS (NR_045878)
chr13	44389594	-15.126	0.079	A330076C08Rik	Intergenic
chr13	44389638	-14.368	0.179	A330076C08Rik	Intergenic
chr13	29370505	13.321	0.102	A330102I10Rik	Intergenic
chr13	29370486	12.019	0.136	A330102I10Rik	Intergenic
chr13	29370530	11.076	0.191	A330102I10Rik	Intergenic
chr19	56851834	-12.688	0.052	A630007B06Rik	Intergenic
chr19	56874840	-17.190	0.065	A630007B06Rik	intron (NM_170757, intron 8 of 14)
chr19	56851752	-9.369	0.164	A630007B06Rik	Intergenic
chr3	65156775	-5.761	0.108	A730090N16Rik	intron (NM_010597, intron 8 of 13)
chr18	44818684	-17.035	0.034	A930012L18Rik	intron (NM_001085373, intron 3 of 18)
chr18	44818483	-11.660	0.151	A930012L18Rik	intron (NM_001085373, intron 3 of 18)
chr10	39619399	12.738	0.117	AA474331	promoter-TSS (NR_033628)
chr10	39619451	10.007	0.129	AA474331	promoter-TSS (NR_033628)
chr2	156359105	23.496	0.037	Aar2	intron (NM_001003815, intron 17 of 21)
chr11	84256032	-13.979	0.040	Aatf	intron (NM_019816, intron 12 of 12)
chr11	84256200	-10.812	0.101	Aatf	intron (NM_019816, intron 11 of 12)
chr4	53209745	20.271	0.035	Abca1	Intergenic
chr4	53209411	-7.645	0.045	Abca1	Intergenic
chr4	53209642	13.527	0.129	Abca1	Intergenic
chr4	53209527	8.495	0.172	Abca1	Intergenic
chr3	121814393	15.655	0.077	Abca4	intron (NM_007378, intron 15 of 49)
chr3	121814397	14.973	0.100	Abca4	intron (NM_007378, intron 15 of 49)
chr1	75177331	-13.316	0.057	Abcb6	promoter-TSS (NM_023732)
chr14	119072693	-8.640	0.140	Abcc4	intron (NM_001033336, intron 1 of 30)
chr14	119072706	-8.998	0.153	Abcc4	intron (NM_001033336, intron 1 of 30)
chr14	119072612	-6.325	0.172	Abcc4	intron (NM_001033336, intron 1 of 30)
chr6	142666924	-11.272	0.122	Abcc9	Intergenic
chr6	142666785	-11.602	0.180	Abcc9	Intergenic
chr2	150728309	13.166	0.184	Abhd12	intron (NM_024465, intron 1 of 12)
chr7	86400977	-17.826	0.047	Abhd2	Intergenic
chr7	86400960	-10.957	0.162	Abhd2	Intergenic
chr19	57269983	-18.964	0.020	Ablim1	intron (NM_178688, intron 1 of 24)
chr19	57172873	-10.183	0.136	Ablim1	intron (NM_001103177, intron 6 of 21)
chr19	57269834	-13.177	0.157	Ablim1	intron (NM_178688, intron 1 of 24)
chr5	114649174	-13.055	0.093	Acacb	intron (NM_133904, intron 12 of 51)
chr5	114649374	-11.869	0.107	Acacb	intron (NM_133904, intron 12 of 51)
chr5	114649799	-13.689	0.157	Acacb	intron (NM_133904, intron 12 of 51)
chr5	114649064	-15.116	0.179	Acacb	intron (NM_133904, intron 12 of 51)
chr12	81358861	-11.253	0.081	Actn1	intron (NM_134156, intron 1 of 20)
chr12	81358698	-12.193	0.146	Actn1	intron (NM_134156, intron 1 of 20)
chr18	58997677	16.045	0.089	Adamts19	exon (NM_175506, exon 2 of 23)
chr11	6967982	-11.316	0.065	Adcy1	intron (NM_009622, intron 1 of 19)



chr11	6967975	-9.528	0.117	Adcy1	intron (NM_009622, intron 1 of 19)
chr19	53203299	-12.641	0.094	Add3	Intergenic
chr19	53203264	-13.710	0.106	Add3	Intergenic
chr18	80315479	-14.074	0.146	Adnp2	3' UTR (NM_053117, exon 3 of 3)
chr18	80315510	-11.269	0.155	Adnp2	3' UTR (NM_053117, exon 3 of 3)
chr10	67021424	-17.374	0.053	Ado	Intergenic
chr10	74736025	-7.295	0.102	Adora2a	intron (NM_001145826, intron 13 of 18)
chr10	74736036	-6.433	0.141	Adora2a	intron (NM_001145826, intron 13 of 18)
chr3	105703046	-12.094	0.055	Adora3	intron (NM_027025, intron 1 of 6)
chr3	105703091	-19.527	0.089	Adora3	URR1B DNA MER1_type
chr18	62338779	-9.312	0.143	Adrb2	exon (NM_007420, exon 1 of 1)
chr18	62338860	-9.722	0.157	Adrb2	exon (NM_007420, exon 1 of 1)
chr18	62338848	-8.951	0.192	Adrb2	exon (NM_007420, exon 1 of 1)
chr10	77835390	-15.436	0.134	Agpat3	Intergenic
chr12	36693596	-13.043	0.155	Agr2	Intergenic
chr12	36693566	-10.162	0.176	Agr2	Intergenic
chr12	36693372	-9.237	0.185	Agr2	Intergenic
chr4	155562760	-20.142	0.061	Agrn	intron (NM_021604, intron 2 of 35)
chr4	155562623	-12.216	0.149	Agrn	intron (NM_021604, intron 2 of 35)
chr13	59355118	-17.282	0.117	Agtppb1	Intergenic
chr13	59355019	-11.224	0.142	Agtppb1	Intergenic
chr10	20635574	-13.661	0.184	Ahi1	Intergenic
chr16	22881704	-12.578	0.089	Ahsg	Intergenic
chr16	22881539	-14.719	0.179	Ahsg	Intergenic
chr3	152220241	-9.261	0.175	Al115009	intron (NM_001081277, intron 6 of 13)
chr9	55155754	9.859	0.024	Al118078	Intergenic
chr9	55155632	10.950	0.117	Al118078	Intergenic
chr10	39726694	16.812	0.039	Al317395	intron (NM_144821, intron 2 of 3)
chr10	39726669	9.511	0.194	Al317395	intron (NM_144821, intron 2 of 3)
chr3	154040516	16.242	0.038	Al606473	Intergenic
chr7	86708945	-11.570	0.153	Al854517	Intergenic
chr14	55194382	11.256	0.165	Ajuba	intron (NM_010590, intron 1 of 7)
chr14	55194362	8.775	0.193	Ajuba	intron (NM_010590, intron 1 of 7)
chr10	24918868	-13.471	0.089	Akap7	intron (NM_018747, intron 7 of 7)
chr10	24918405	-9.592	0.143	Akap7	intron (NM_018747, intron 7 of 7)
chr10	24918624	-8.053	0.164	Akap7	intron (NM_018747, intron 7 of 7)
chr8	96534992	8.003	0.130	Amfr	intron (NM_011787, intron 1 of 13)
chr8	96534890	9.416	0.157	Amfr	intron (NM_011787, intron 1 of 13)
chr15	97173263	-16.712	0.061	Amigo2	intron (NM_172293, intron 3 of 5)
chr15	97146006	16.928	0.065	Amigo2	intron (NM_172293, intron 3 of 5)
chr15	97173237	-14.341	0.075	Amigo2	intron (NM_172293, intron 3 of 5)
chr15	97146010	15.524	0.104	Amigo2	intron (NM_172293, intron 3 of 5)
chr3	102889892	12.859	0.065	Ampd1	intron (NM_001033303, intron 5 of 15)
chr15	42204838	-15.472	0.035	Angpt1	Intergenic
chr8	24049854	16.963	0.027	Ank1	exon (NM_001081149, exon 18 of 18)
chr10	69250557	7.368	0.103	Ank3	intron (NM_170730, intron 1 of 17)

chr10	69250529	12.526	0.134	Ank3	intron (NM_170730, intron 1 of 17)
chr10	69250533	11.908	0.172	Ank3	intron (NM_170730, intron 1 of 17)
chr10	69250377	9.519	0.173	Ank3	intron (NM_170730, intron 1 of 17)
chr13	99045714	-13.558	0.114	Ankra2	Intergenic
chr13	99045479	-14.160	0.134	Ankra2	TTS (NM_001271389)
chr13	99045522	-11.773	0.145	Ankra2	TTS (NM_001271389)
chr13	99045725	-10.618	0.182	Ankra2	Intergenic
chr15	36371460	-11.889	0.107	Ankrd46	Intergenic
chr15	36371561	-10.556	0.163	Ankrd46	Intergenic
chr14	26681480	-13.017	0.185	Anxa11	intron (NM_013469, intron 1 of 14)
chr14	26681444	-13.021	0.185	Anxa11	intron (NM_013469, intron 1 of 14)
chr14	26681564	-11.905	0.188	Anxa11	intron (NM_013469, intron 1 of 14)
chr5	97145523	15.316	0.133	Anxa3	intron (NM_175473, intron 47 of 73)
chr5	97145352	13.342	0.157	Anxa3	intron (NM_175473, intron 47 of 73)
chr10	90490854	-24.005	0.014	Apaf1	intron (NM_001042558, intron 17 of 26)
chr2	22602795	-15.913	0.041	Apbb1ip	Intergenic
chr5	66804606	-12.967	0.101	Apbb2	intron (NM_001201414, intron 5 of 15)
chr5	66804585	-9.292	0.191	Apbb2	intron (NM_001201414, intron 5 of 15)
chr2	94364862	15.741	0.114	Api5	Intergenic
chr2	94364866	12.591	0.192	Api5	Intergenic
chr9	30984389	13.214	0.200	Aplp2	intron (NM_001102456, intron 3 of 16)
chr12	7957477	-12.143	0.134	Apob	Intergenic
chr12	7957408	-11.073	0.134	Apob	Intergenic
chr12	7957480	-11.593	0.147	Apob	Intergenic
chr9	71014594	-15.861	0.043	Aqp9	(TCCA)n Simple_repeat Simple_repeat
chr18	5985033	-8.559	0.031	Arhgap12	Intergenic
chr18	39194798	-18.188	0.102	Arhgap26	MIRb SINE MIR
chr11	103224303	6.579	0.056	Arhgap27	intron (NM_183288, intron 1 of 2)
chr16	38673485	11.857	0.092	Arhgap31	intron (NM_020260, intron 1 of 11)
chr2	158375826	7.895	0.038	Arhgap40	MER5A DNA MER1_type
chr11	68761152	-13.711	0.035	Arhgef15	exon (NM_177566, exon 11 of 16)
chr11	68761308	-11.401	0.106	Arhgef15	exon (NM_177566, exon 10 of 16)
chr11	68761139	-10.236	0.143	Arhgef15	exon (NM_177566, exon 11 of 16)
chr11	68761297	-11.031	0.159	Arhgef15	exon (NM_177566, exon 10 of 16)
chr3	62153526	14.238	0.147	Arhgef26	intron (NM_001081295, intron 3 of 13)
chr3	62153612	11.050	0.185	Arhgef26	intron (NM_001081295, intron 3 of 13)
chr3	62153601	10.675	0.196	Arhgef26	intron (NM_001081295, intron 3 of 13)
chr4	135771062	10.886	0.079	Asap3	intron (NM_001008232, intron 1 of 24)
chr4	135771099	10.372	0.198	Asap3	MIRb SINE MIR
chr13	3645079	17.467	0.064	Asb13	intron (NM_178283, intron 4 of 5)
chr10	59444643	16.429	0.039	Ascc1	Intergenic
chr10	59444628	10.167	0.184	Ascc1	Intergenic
chr11	69905978	-10.131	0.109	Asgr2	promoter-TSS (NM_007493)
chr11	69905957	-11.930	0.128	Asgr2	promoter-TSS (NM_007493)
chr2	31262077	-8.451	0.146	Ass1	Intergenic
chr2	31262047	-6.618	0.194	Ass1	Intergenic

chr6	136415954	-19.268	0.013	Atf7ip	Intergenic
chr6	136415819	-16.034	0.133	Atf7ip	Intergenic
chr14	48141956	10.227	0.036	Atg14	intron (NR_027414, intron 4 of 5)
chr5	23885777	-19.453	0.035	Atg9b	exon (NM_008713, exon 18 of 26)
chr5	23885756	-20.989	0.036	Atg9b	intron (NM_008713, intron 17 of 25)
chr10	62562334	-15.409	0.106	Atoh7	promoter-TSS (NM_016864)
chr6	72194479	-14.247	0.063	Atoh8	Intergenic
chr6	72194460	-8.983	0.177	Atoh8	Intergenic
chr6	72194472	-10.632	0.185	Atoh8	Intergenic
chr7	25791933	-11.904	0.107	Atp1a3	Intergenic
chr11	69416601	-15.615	0.073	Atp1b2	exon (NM_013415, exon 3 of 7)
chr11	69416508	-9.656	0.199	Atp1b2	intron (NM_013415, intron 3 of 6)
chr10	98237823	-18.974	0.035	Atp2b1	Intergenic
chr10	98237390	-9.435	0.173	Atp2b1	Intergenic
chr10	127518753	-19.165	0.034	Atp5b	B3A SINE B2
chr13	91011406	22.087	0.031	Atp6ap1l	Intergenic
chr1	140224436	-13.538	0.048	Atp6v1g3	Intergenic
chr1	140224508	-10.491	0.082	Atp6v1g3	Intergenic
chr1	140224422	-12.641	0.093	Atp6v1g3	Intergenic
chr1	140224686	-7.085	0.173	Atp6v1g3	Intergenic
chr2	168559467	-28.398	0.027	Atp9a	intron (NM_015731, intron 1 of 27)
chr13	46119035	14.112	0.065	Atxn1	Intergenic
chr12	34029889	-13.975	0.018	Atxn7l1	intron (NM_001033436, intron 4 of 7)
chr12	34030890	-15.575	0.148	Atxn7l1	exon (NM_001033436, exon 5 of 8)
chr9	117836842	-15.518	0.089	Azi2	Intergenic
chr9	117836680	-12.080	0.177	Azi2	Intergenic
chr7	105343842	-8.471	0.184	B3gnt6	intron (NM_001081167, intron 1 of 1)
chr10	126605306	-11.572	0.071	B4galnt1	3' UTR (NM_001244618, exon 5 of 5)
chr10	126605170	-8.938	0.170	B4galnt1	3' UTR (NM_001244618, exon 5 of 5)
chr10	126605469	-11.757	0.190	B4galnt1	3' UTR (NM_001244618, exon 5 of 5)
chr8	35754218	5.714	0.113	B930018H19Rik	Intergenic
chr8	35754224	9.633	0.133	B930018H19Rik	Intergenic
chr4	155071399	-21.363	0.045	B930041F14Rik	TTS (NM_178699)
chr9	61141542	13.254	0.174	B930092H01Rik	promoter-TSS (NR_045334)
chr9	61141232	9.928	0.177	B930092H01Rik	intron (NR_045334, intron 1 of 4)
chr15	38717184	-11.179	0.119	Baalc	Intergenic
chr4	32610196	6.540	0.114	Bach2os	intron (NM_001109661, intron 2 of 4)
chr4	32610205	7.832	0.146	Bach2os	intron (NM_001109661, intron 2 of 4)
chr4	40893758	-10.793	0.040	Bag1	intron (NM_001171739, intron 1 of 6)
chr7	135666715	-16.941	0.065	Bag3	promoter-TSS (NM_013863)
chr11	120114042	-16.474	0.039	Bahcc1	intron (NM_198423, intron 2 of 27)
chr8	15047185	17.246	0.048	BB014433	Intergenic
chr13	52924232	8.502	0.108	BB123696	Intergenic
chr13	52924168	6.026	0.122	BB123696	Intergenic
chr13	52924234	7.140	0.170	BB123696	Intergenic
chr8	96613691	-13.039	0.099	Bbs2	exon (NM_026116, exon 3 of 17)

chr16	45653192	-15.288	0.072	BC016579	intron (NM_145389, intron 1 of 5)
chr1	159380225	-18.022	0.106	BC026585	Intergenic
chr1	159380229	-14.624	0.174	BC026585	Intergenic
chr3	95695709	14.565	0.088	BC028528	intron (NM_153513, intron 1 of 4)
chr7	127839008	21.505	0.018	BC030336	intron (NM_001164580, intron 1 of 2)
chr7	116863127	-20.826	0.046	BC051019	intron (NM_001040700, intron 3 of 5)
chr7	116863183	-18.796	0.058	BC051019	intron (NM_001040700, intron 3 of 5)
chr13	61905349	-10.485	0.173	BC052688	Intergenic
chr6	120824106	-13.031	0.122	Bcl2l13	intron (NM_153516, intron 5 of 6)
chr6	120824100	-12.756	0.129	Bcl2l13	intron (NM_153516, intron 5 of 6)
chr6	134380738	-13.042	0.034	Bcl2l14	intron (NM_025778, intron 5 of 6)
chr6	134380776	-7.975	0.144	Bcl2l14	intron (NM_025778, intron 5 of 6)
chr12	106799917	-16.534	0.106	Bdkrb2	Intergenic
chr12	106799952	-15.872	0.124	Bdkrb2	Intergenic
chr14	70501464	14.336	0.133	Bin3	intron (NM_021328, intron 1 of 8)
chr5	97383152	18.868	0.100	Bmp2k	Intergenic
chr13	38412336	-16.218	0.047	Bmp6	Intergenic
chr13	38412590	-14.288	0.182	Bmp6	Intergenic
chr13	38412379	-9.533	0.199	Bmp6	Intergenic
chr4	84167657	-11.841	0.036	Bnc2	intron (NM_172870, intron 2 of 5)
chr4	84167695	-10.306	0.129	Bnc2	intron (NM_172870, intron 2 of 5)
chr11	31577335	-16.154	0.043	Bod1	Intergenic
chr11	31577467	-10.775	0.196	Bod1	Intergenic
chr6	34421595	-13.438	0.046	Bpgm	Intergenic
chr6	34421635	-10.176	0.079	Bpgm	Intergenic
chr1	160273672	20.357	0.047	Brinp2	intron (NM_207583, intron 1 of 7)
chr1	160273850	18.873	0.050	Brinp2	intron (NM_207583, intron 1 of 7)
chr7	120511080	14.770	0.088	Btbd10	intron (NM_133700, intron 2 of 10)
chr7	120511434	8.250	0.132	Btbd10	intron (NM_133700, intron 2 of 10)
chr10	84973265	17.849	0.044	Btbd11	intron (NM_028709, intron 1 of 16)
chr10	85112442	-7.295	0.158	Btbd11	intron (NM_001017525, intron 12 of 14)
chr10	85112453	-10.656	0.162	Btbd11	intron (NM_001017525, intron 12 of 14)
chr1	88268495	-7.692	0.018	C130036L24Rik	Intergenic
chr13	83855941	-6.358	0.035	C130071C03Rik	Intergenic
chr13	83855928	-5.947	0.143	C130071C03Rik	Intergenic
chr1	186707694	-17.376	0.049	C130074G19Rik	promoter-TSS (NM_178692)
chr11	102809216	-11.955	0.102	C1q1	Intergenic
chr11	102809111	-13.478	0.157	C1q1	Intergenic
chr6	143059206	-21.023	0.035	C2cd5	Intergenic
chr7	129771077	-17.790	0.045	Cacng3	intron (NM_008855, intron 16 of 16)
chr7	129771015	-10.303	0.149	Cacng3	intron (NM_008855, intron 16 of 16)
chr7	129771073	-11.810	0.172	Cacng3	intron (NM_008855, intron 16 of 16)
chr11	107727745	7.395	0.096	Cacng5	Intergenic
chr6	23787111	-16.526	0.077	Cadps2	intron (NM_001252106, intron 1 of 28)
chr6	23787629	-8.834	0.161	Cadps2	intron (NM_001252106, intron 1 of 28)
chr5	131019094	-19.072	0.034	Caln1	B1F SINE Alu

chr13	100619696	9.852	0.185	Cartpt	Intergenic
chr13	100619706	9.653	0.189	Cartpt	Intergenic
chr19	56472338	-21.977	0.020	Casp7	intron (NM_007611, intron 1 of 6)
chr19	56472312	-13.572	0.112	Casp7	intron (NM_007611, intron 1 of 6)
chr8	89993378	14.333	0.144	Cbln1	3' UTR (NM_019626, exon 3 of 3)
chr8	89993265	14.322	0.179	Cbln1	3' UTR (NM_019626, exon 3 of 3)
chr9	110575412	9.619	0.154	Ccdc12	intron (NM_028312, intron 1 of 6)
chr9	110575410	7.378	0.161	Ccdc12	intron (NM_028312, intron 1 of 6)
chr19	48014439	11.775	0.127	Ccdc147	intron (NM_001163267, intron 1 of 17)
chr5	52907227	10.540	0.154	Ccdc149	Intergenic
chr9	70264338	-15.433	0.104	Ccnb2	intron (NM_007630, intron 3 of 8)
chr17	47706303	16.950	0.069	Ccnd3	intron (NM_001081636, intron 1 of 6)
chr1	64751889	-13.747	0.102	Ccnyl1	intron (NM_001097644, intron 3 of 9)
chr13	103455749	12.562	0.138	Cd180	Intergenic
chr13	103455742	10.478	0.189	Cd180	Intergenic
chr10	43302445	-15.587	0.101	Cd24a	exon (NM_009846, exon 2 of 2)
chr10	43302438	-11.362	0.194	Cd24a	exon (NM_009846, exon 2 of 2)
chr10	43302484	-11.725	0.199	Cd24a	exon (NM_009846, exon 2 of 2)
chr1	60881494	-14.588	0.094	Cd28	URR1B DNA MER1_type
chr1	60881640	-8.664	0.155	Cd28	Intergenic
chr2	60121468	-14.319	0.031	Cd302	intron (NM_025422, intron 1 of 4)
chr2	60121326	-16.029	0.035	Cd302	intron (NM_025422, intron 1 of 4)
chr2	60121585	-14.236	0.099	Cd302	intron (NM_025422, intron 1 of 4)
chr1	196765761	-15.646	0.039	Cd34	intron (NM_133654, intron 1 of 7)
chr1	196765680	-13.175	0.120	Cd34	intron (NM_133654, intron 1 of 7)
chr16	49792916	-8.973	0.105	Cd47	Intergenic
chr12	119045908	-10.377	0.154	Cdca7l	Intergenic
chr12	119045883	-9.192	0.164	Cdca7l	Intergenic
chr15	21460658	-14.947	0.036	Cdh12	intron (NM_001008420, intron 6 of 11)
chr18	16923062	5.390	0.171	Cdh2	intron (NM_007664, intron 2 of 15)
chr18	16923153	8.186	0.177	Cdh2	intron (NM_007664, intron 2 of 15)
chr8	106623171	-16.667	0.070	Cdh5	Intergenic
chr8	106623427	-13.886	0.199	Cdh5	Intergenic
chr8	101924785	-23.255	0.034	Cdh8	exon (NM_001285913, exon 2 of 13)
chr10	68769766	26.576	0.028	Cdk1	Intergenic
chr10	68769756	15.613	0.153	Cdk1	Intergenic
chr10	128140986	9.750	0.139	Cdk2	exon (NM_183417, exon 2 of 8)
chr10	128140949	11.480	0.155	Cdk2	intron (NM_016756, intron 2 of 6)
chr5	3146501	13.014	0.157	Cdk6	Intergenic
chr5	3146538	6.432	0.176	Cdk6	Intergenic
chr11	51730455	-24.581	0.012	Cdkn2aipnl	Intergenic
chr11	51730390	-6.783	0.072	Cdkn2aipnl	Intergenic
chr7	20452112	-17.530	0.036	Ceacam16	Intergenic
chr1	191510145	-13.375	0.048	Cenpf	intron (NM_001081363, intron 1 of 17)
chr16	32114904	10.053	0.153	Cep19	Intergenic
chr16	32114889	9.788	0.164	Cep19	Intergenic

chr1	157842884	-12.081	0.101	Cep350	Intergenic
chr1	157842982	-8.297	0.155	Cep350	Intergenic
chr10	53118208	-9.423	0.116	Cep85l	Intergenic
chr10	53118258	-11.641	0.178	Cep85l	Intergenic
chr10	53118263	-10.505	0.189	Cep85l	Intergenic
chr15	86007718	-16.698	0.093	Cerk	intron (NM_145475, intron 1 of 12)
chr6	125036516	10.185	0.093	Chd4	Intergenic
chr5	110564419	-12.105	0.166	Chfr	promoter-TSS (NM_172717)
chr19	3842403	11.274	0.117	Chka	Intergenic
chr19	3842301	9.415	0.176	Chka	Intergenic
chr7	13618993	-9.402	0.109	Chmp2a	intron (NM_026885, intron 2 of 5)
chr10	82450505	13.486	0.184	Chst11	intron (NM_021439, intron 1 of 2)
chr10	82450629	10.482	0.190	Chst11	intron (NM_021439, intron 1 of 2)
chr10	82450689	10.152	0.192	Chst11	intron (NM_021439, intron 1 of 2)
chr8	72409630	14.010	0.072	Cilp2	intron (NM_026818, intron 3 of 7)
chr8	72409698	9.772	0.166	Cilp2	intron (NM_026818, intron 3 of 7)
chr15	102615900	15.422	0.081	Cistr-act	Intergenic
chr15	102615946	12.206	0.157	Cistr-act	Intergenic
chr15	102615913	12.352	0.174	Cistr-act	Intergenic
chr3	144471820	-10.601	0.101	Clca2	intron (NM_030601, intron 7 of 13)
chr3	144471620	-13.529	0.177	Clca2	exon (NM_030601, exon 8 of 14)
chr16	10639525	-26.227	0.031	Clec16a	intron (NM_001204229, intron 17 of 22)
chr16	10639515	-16.941	0.133	Clec16a	intron (NM_001204229, intron 17 of 22)
chr4	134848603	-17.646	0.040	Clic4	Intergenic
chr4	134848610	-14.593	0.088	Clic4	Intergenic
chr4	134848615	-8.261	0.153	Clic4	Intergenic
chr9	57615028	-14.545	0.043	Clk3	Intergenic
chr8	106833408	-10.984	0.102	Cmtm1	exon (NM_181990, exon 1 of 4)
chr8	106833387	-10.153	0.106	Cmtm1	exon (NM_181990, exon 1 of 4)
chr9	114752259	-12.066	0.111	Cmtm8	intron (NM_027294, intron 1 of 3)
chr9	114752221	-13.988	0.117	Cmtm8	intron (NM_027294, intron 1 of 3)
chr1	37269614	-11.893	0.133	Cnga3	Intergenic
chr1	37269654	-11.521	0.163	Cnga3	Intergenic
chr19	43502774	-15.176	0.062	Cnnm1	Intergenic
chr19	43502870	-12.225	0.153	Cnnm1	Intergenic
chr15	91783154	-14.320	0.044	Cntn1	Intergenic
chr6	104934441	21.201	0.048	Cntn6	Intergenic
chr17	58003699	10.223	0.153	Cntnap5c	intron (NM_001081653, intron 1 of 23)
chr2	153433801	16.393	0.109	Commmd7	Intergenic
chr2	153433722	11.542	0.129	Commmd7	Intergenic
chr2	153433827	14.613	0.147	Commmd7	Intergenic
chr2	153433773	12.540	0.173	Commmd7	Intergenic
chr7	88600699	-18.429	0.101	Cpeb1	Intergenic
chr7	88600701	-15.729	0.153	Cpeb1	Intergenic
chr7	88600920	-5.929	0.177	Cpeb1	Intergenic
chr10	116996765	15.656	0.045	Cpm	Intergenic

chr10	116996747	14.793	0.069	Cpm	Intergenic
chr10	116996844	16.597	0.087	Cpm	Intergenic
chr11	113559558	-15.556	0.138	Cpsf4l	TTS (NM_001164532)
chr11	113559617	-13.307	0.150	Cpsf4l	3' UTR (NM_001164532, exon 8 of 8)
chr2	130189644	18.699	0.010	Cpxm1	intron (NM_001110513, intron 14 of 16)
chr2	130189633	11.753	0.102	Cpxm1	intron (NM_001110513, intron 14 of 16)
chr1	197067996	-5.527	0.104	Cr2	CpG
chr10	94670162	-21.748	0.043	Cradd	intron (NM_009950, intron 2 of 2)
chr10	94670174	-17.486	0.120	Cradd	intron (NM_009950, intron 2 of 2)
chr2	91905534	-15.994	0.053	Creb3l1	Intergenic
chr2	91905554	-11.089	0.149	Creb3l1	Intergenic
chr15	48808077	-6.060	0.132	Csmd3	Intergenic
chr15	48808193	-7.898	0.146	Csmd3	Intergenic
chr1	137564880	-10.085	0.026	Csrp1	Intergenic
chr1	137583204	-12.306	0.071	Csrp1	Intergenic
chr1	137583296	-10.363	0.144	Csrp1	Intergenic
chr1	137583303	-8.815	0.161	Csrp1	Intergenic
chr2	150397586	19.314	0.016	Cst7	intron (NM_009977, intron 1 of 3)
chr10	126387822	11.343	0.033	Ctdsp2	Intergenic
chr10	126387810	10.735	0.129	Ctdsp2	Intergenic
chr7	151600773	15.674	0.093	Cttn	intron (NM_001113373, intron 15 of 15)
chr7	151600762	14.925	0.094	Cttn	intron (NM_001113373, intron 15 of 15)
chr7	151600752	15.583	0.096	Cttn	intron (NM_001113373, intron 15 of 15)
chr11	87959175	-15.308	0.019	Cuedc1	intron (NM_198013, intron 1 of 10)
chr11	87959167	-9.708	0.164	Cuedc1	intron (NM_198013, intron 1 of 10)
chr17	46659156	16.174	0.151	Cul9	exon (NM_001081335, exon 19 of 41)
chr17	46659071	11.035	0.193	Cul9	exon (NM_001081335, exon 19 of 41)
chr5	122417077	-21.933	0.049	Cux2	intron (NM_007804, intron 2 of 22)
chr11	46123224	13.377	0.039	Cyfip2	intron (NM_001252459, intron 1 of 30)
chr11	46122742	-10.530	0.044	Cyfip2	intron (NM_001252459, intron 1 of 30)
chr11	46112679	-12.139	0.085	Cyfip2	intron (NM_001252459, intron 1 of 30)
chr11	46123240	12.045	0.089	Cyfip2	intron (NM_001252459, intron 1 of 30)
chr11	46122724	-9.979	0.103	Cyfip2	intron (NM_001252459, intron 1 of 30)
chr11	46123237	11.279	0.108	Cyfip2	intron (NM_001252459, intron 1 of 30)
chr11	46122942	-10.462	0.136	Cyfip2	intron (NM_001252459, intron 1 of 30)
chr11	46122754	-9.450	0.146	Cyfip2	intron (NM_001252459, intron 1 of 30)
chr11	46122163	-13.421	0.152	Cyfip2	intron (NM_001252459, intron 1 of 30)
chr15	82595440	-6.092	0.092	Cyp2d40	promoter-TSS (NM_023623)
chr15	82595334	-13.534	0.139	Cyp2d40	promoter-TSS (NM_023623)
chr5	144381865	-13.822	0.101	Cyth3	Intergenic
chr5	144381706	-9.150	0.179	Cyth3	Intergenic
chr10	45527004	16.495	0.064	D030045P18Rik	promoter-TSS (NR_040624)
chr10	45527211	14.074	0.117	D030045P18Rik	promoter-TSS (NR_040624)
chr10	45527072	10.843	0.176	D030045P18Rik	promoter-TSS (NR_040624)
chr14	28210809	-14.325	0.078	D14Abb1e	exon (NM_027871, exon 9 of 11)
chr14	28210801	-11.250	0.145	D14Abb1e	exon (NM_027871, exon 9 of 11)

chr17	12143334	-20.556	0.034	D17Ert648e	intron (NM_016694, intron 9 of 11)
chr17	12143340	-14.375	0.166	D17Ert648e	intron (NM_016694, intron 9 of 11)
chr1	188746711	15.536	0.069	D1Pas1	Intergenic
chr2	116774376	14.867	0.060	D330050G23Rik	Intergenic
chr2	104253627	-22.839	0.031	D430041D05Rik	Intergenic
chr2	158056842	-11.340	0.150	D630003M21Rik	Intergenic
chr2	158056839	-11.843	0.177	D630003M21Rik	Intergenic
chr6	143363880	-21.774	0.038	D6Ert474e	Intergenic
chr6	143363897	-15.789	0.133	D6Ert474e	Intergenic
chr6	143363764	-16.181	0.141	D6Ert474e	Intergenic
chr6	143363757	-14.035	0.182	D6Ert474e	Intergenic
chr19	28724296	13.883	0.138	D930032P07Rik	intron (NM_175459, intron 2 of 10)
chr1	132239420	-11.449	0.079	Daf2	Intergenic
chr1	132239378	-11.458	0.126	Daf2	Intergenic
chr1	132239380	-9.927	0.155	Daf2	Intergenic
chr3	116215413	8.311	0.076	Dbt	promoter-TSS (NM_010022)
chr7	56777934	19.118	0.037	Dbx1	intron (NM_175272, intron 11 of 37)
chr7	56724118	-19.390	0.061	Dbx1	intron (NM_175272, intron 10 of 37)
chr7	56724145	-18.329	0.079	Dbx1	intron (NM_175272, intron 10 of 37)
chr15	98643352	-15.503	0.070	Ddn	3' UTR (NM_016781, exon 12 of 12)
chr15	98643188	-14.214	0.073	Ddn	TTS (NM_016781)
chr15	98643346	-10.512	0.161	Ddn	3' UTR (NM_016781, exon 12 of 12)
chr15	98643350	-11.259	0.165	Ddn	3' UTR (NM_016781, exon 12 of 12)
chr2	130489652	-9.899	0.166	Ddrgk1	intron (NM_029832, intron 1 of 8)
chr2	130489614	-12.558	0.176	Ddrgk1	intron (NM_029832, intron 1 of 8)
chr17	66583912	-19.960	0.037	Ddx11	Intergenic
chr17	66583889	-15.139	0.104	Ddx11	Intergenic
chr17	66583926	-15.556	0.107	Ddx11	Intergenic
chr8	108534382	21.701	0.034	Ddx28	exon (NM_028038, exon 1 of 1)
chr8	64481752	-11.251	0.038	Ddx60	intron (NM_001081215, intron 29 of 38)
chr17	28346395	-18.056	0.103	Def6	intron (NM_027185, intron 1 of 10)
chr17	28346390	-15.235	0.149	Def6	intron (NM_027185, intron 1 of 10)
chr13	47174375	-18.098	0.076	Dek	intron (NM_172262, intron 18 of 20)
chr3	102943827	-15.374	0.035	Dennd2c	intron (NM_177857, intron 5 of 18)
chr3	102943901	-11.138	0.138	Dennd2c	intron (NM_177857, intron 5 of 18)
chr9	64637324	-12.953	0.105	Dennd4a	Intergenic
chr9	64637343	-12.039	0.131	Dennd4a	Intergenic
chr15	89029882	-18.144	0.042	Dennd6b	Intergenic
chr5	124356877	-12.384	0.144	Denr	promoter-TSS (NM_026603)
chr16	22622343	19.783	0.036	Dgkg	5' UTR (NM_138650, exon 2 of 25)
chr16	22622206	14.695	0.043	Dgkg	intron (NM_138650, intron 2 of 24)
chr14	79070121	-8.420	0.116	Dgkh	MTC LTR MaLR
chr14	79070129	-10.368	0.161	Dgkh	intron (NM_001081336, intron 1 of 28)
chr15	99922177	-17.511	0.050	Dip2b	intron (NM_001159361, intron 1 of 37)
chr2	118605698	6.696	0.155	Disp2	intron (NM_170593, intron 1 of 7)
chr8	14114113	-18.263	0.068	Dlgap2	intron (NM_001145965, intron 1 of 14)



chr8	14114209	-14.474	0.155	Dlgap2	intron (NM_001145965, intron 1 of 14)
chr6	6830462	-6.977	0.038	Dlx5	intron (NM_010056, intron 1 of 2)
chr3	151852612	-19.723	0.029	Dnajb4	intron (NM_027287, intron 2 of 3)
chr3	151855419	-13.137	0.063	Dnajb4	intron (NM_027287, intron 2 of 3)
chr3	151852279	-14.583	0.151	Dnajb4	intron (NM_027287, intron 2 of 3)
chr4	42963925	9.265	0.093	Dnajb5	Intergenic
chr4	42963837	10.784	0.117	Dnajb5	Intergenic
chr18	36932024	-6.905	0.065	Dnd1	exon (NM_008214, exon 5 of 13)
chr18	36932261	-12.347	0.106	Dnd1	intron (NM_008214, intron 4 of 12)
chr12	84826020	-8.989	0.050	Dpf3	intron (NM_001267625, intron 1 of 10)
chr12	84826016	-8.780	0.053	Dpf3	intron (NM_001267625, intron 1 of 10)
chr12	84826061	-5.028	0.119	Dpf3	intron (NM_001267625, intron 1 of 10)
chr2	62229076	-10.490	0.044	Dpp4	intron (NM_001159543, intron 2 of 24)
chr2	62229078	-9.506	0.103	Dpp4	intron (NM_001159543, intron 2 of 24)
chr6	122609667	13.487	0.162	Dppa3	Intergenic
chr6	122609787	13.937	0.172	Dppa3	Intergenic
chr9	49162718	-6.976	0.054	Drd2	intron (NM_010077, intron 1 of 7)
chr1	34197653	18.387	0.088	Dst	intron (NM_134448, intron 6 of 97)
chr17	56904882	-8.046	0.061	Dus3l	intron (NM_144858, intron 1 of 12)
chr17	26662002	-12.149	0.145	Dusp1	Intergenic
chr1	185924265	-8.063	0.106	Dusp10	Intergenic
chr1	185924277	-9.508	0.136	Dusp10	Intergenic
chr11	101844865	-13.278	0.035	Dusp3	intron (NM_028207, intron 1 of 2)
chr11	101844806	-10.547	0.071	Dusp3	intron (NM_028207, intron 1 of 2)
chr11	101844895	-9.392	0.129	Dusp3	intron (NM_028207, intron 1 of 2)
chr19	53608746	-18.829	0.038	Dusp5	intron (NM_001085390, intron 2 of 3)
chr2	125055181	-11.027	0.043	Dut	3' UTR (NM_183354, exon 27 of 27)
chr2	12222866	12.146	0.129	E030013I19Rik	promoter-TSS (NR_040353)
chr2	12222879	8.849	0.176	E030013I19Rik	promoter-TSS (NR_040353)
chr2	12222930	9.015	0.190	E030013I19Rik	promoter-TSS (NR_040353)
chr10	39394860	17.989	0.089	E130307A14Rik	intron (NR_038037, intron 2 of 2)
chr10	39394704	11.811	0.160	E130307A14Rik	intron (NR_038037, intron 2 of 2)
chr13	30138089	18.700	0.039	E2f3	Intergenic
chr16	78217264	-19.364	0.030	E330011O21Rik	Intergenic
chr16	78217257	-13.366	0.095	E330011O21Rik	Intergenic
chr14	44675763	-7.899	0.131	Ear2	Intergenic
chr10	95241369	-20.994	0.031	Eea1	Intergenic
chr10	95241330	-11.200	0.076	Eea1	Intergenic
chr10	95241427	-18.202	0.081	Eea1	Intergenic
chr4	141424402	-16.138	0.065	Efhd2	intron (NM_025994, intron 1 of 3)
chr3	89080559	-12.638	0.038	Efna1	intron (NM_001162425, intron 1 of 4)
chr3	89080319	-11.039	0.195	Efna1	exon (NM_010107, exon 2 of 5)
chr3	89080909	-7.355	0.199	Efna1	intron (NM_001162425, intron 1 of 4)
chr17	62642397	-6.803	0.153	Efna5	Intergenic
chr11	69371281	11.000	0.061	Efnb3	intron (NM_007911, intron 1 of 4)
chr11	69371137	8.310	0.094	Efnb3	intron (NM_007911, intron 1 of 4)

chr18	35014231	-16.017	0.071	Egr1	ID_B1 SINE B4
chrY	346867	-18.963	0.029	Eif2s3y	promoter-TSS (NM_012011)
chrY	346523	-12.743	0.188	Eif2s3y	promoter-TSS (NM_012011)
chr9	83698355	-9.417	0.156	Elovl4	intron (NM_148941, intron 1 of 5)
chr9	83698172	-12.569	0.183	Elovl4	intron (NM_148941, intron 1 of 5)
chr9	83698395	-7.952	0.190	Elovl4	intron (NM_148941, intron 1 of 5)
chr3	129237986	14.461	0.026	Elovl6	intron (NM_130450, intron 2 of 4)
chr3	129237516	19.979	0.057	Elovl6	intron (NM_130450, intron 2 of 4)
chr3	129237740	10.675	0.143	Elovl6	intron (NM_130450, intron 2 of 4)
chr13	109004118	9.449	0.180	Elovl7	promoter-TSS (NM_029001)
chr2	112179956	-7.246	0.039	Emc4	intron (NM_133648, intron 8 of 24)
chr17	71658645	11.663	0.060	Emilin2	intron (NM_145158, intron 2 of 7)
chr17	71658708	10.982	0.063	Emilin2	intron (NM_145158, intron 2 of 7)
chr17	71658944	-16.412	0.080	Emilin2	intron (NM_145158, intron 2 of 7)
chr17	71658368	-13.293	0.129	Emilin2	intron (NM_145158, intron 2 of 7)
chr17	71658648	9.254	0.131	Emilin2	intron (NM_145158, intron 2 of 7)
chr17	71658739	9.658	0.152	Emilin2	intron (NM_145158, intron 2 of 7)
chr17	71639016	-13.984	0.174	Emilin2	intron (NM_145158, intron 2 of 7)
chr15	97548072	-12.281	0.160	Endou	intron (NM_001168693, intron 6 of 9)
chr15	97548200	-9.641	0.180	Endou	intron (NM_001168693, intron 6 of 9)
chr4	149605279	-16.094	0.064	Eno1	Intergenic
chr4	149605266	-11.865	0.135	Eno1	Intergenic
chr4	149605214	-11.301	0.136	Eno1	Intergenic
chr15	44258549	10.647	0.196	Eny2	intron (NM_001113554, intron 1 of 9)
chr14	78326604	-17.919	0.054	Epsti1	intron (NM_029495, intron 1 of 11)
chr5	30560254	-12.346	0.073	Ept1	intron (NM_027652, intron 1 of 9)
chr5	30560750	-9.947	0.143	Ept1	intron (NM_027652, intron 1 of 9)
chr5	30560741	-9.444	0.149	Ept1	intron (NM_027652, intron 1 of 9)
chr4	48286267	-17.669	0.117	Erp44	intron (NM_029572, intron 1 of 11)
chr18	10532879	-20.856	0.038	Esco1	exon (NM_001083628, exon 19 of 33)
chr18	10532887	-19.319	0.061	Esco1	exon (NM_001083628, exon 19 of 33)
chr18	10532925	-14.739	0.147	Esco1	exon (NM_001083628, exon 19 of 33)
chr14	75133080	-10.947	0.105	Esd	intron (NM_001285423, intron 1 of 8)
chr14	75133573	-12.285	0.129	Esd	intron (NM_001285423, intron 1 of 8)
chr14	75133225	-10.556	0.194	Esd	intron (NM_001285423, intron 1 of 8)
chr17	39981197	6.089	0.027	Esp38	CpG
chr17	39981174	7.642	0.035	Esp38	CpG
chr17	39980024	6.329	0.058	Esp38	FordPrefect DNA Tip100
chr17	39981838	7.829	0.109	Esp38	CpG
chr17	39981982	5.148	0.185	Esp38	CpG
chr17	39985208	8.183	0.191	Esp38	CpG
chr17	39981886	7.376	0.191	Esp38	CpG
chr11	18051993	23.401	0.025	Etaa1	Intergenic
chr7	50699697	-5.824	0.076	Etfb	intron (NM_026695, intron 1 of 5)
chr6	143114765	11.302	0.165	Etnk1	promoter-TSS (NM_029250)
chr6	143114767	10.873	0.170	Etnk1	promoter-TSS (NM_029250)

chr9	32501696	-8.254	0.158	Ets1	Intergenic
chr9	32501777	-8.931	0.194	Ets1	Intergenic
chr16	22398535	7.236	0.038	Etv5	intron (NM_023794, intron 9 of 12)
chr16	22398702	15.823	0.064	Etv5	intron (NM_023794, intron 9 of 12)
chr16	22398496	6.690	0.138	Etv5	intron (NM_023794, intron 9 of 12)
chr16	22398650	10.297	0.146	Etv5	intron (NM_023794, intron 9 of 12)
chr6	133989463	-15.098	0.058	Etv6	intron (NM_007961, intron 1 of 7)
chr6	133989582	-10.269	0.152	Etv6	intron (NM_007961, intron 1 of 7)
chr6	134070885	-8.250	0.169	Etv6	intron (NM_007961, intron 1 of 7)
chr6	134070973	-9.783	0.177	Etv6	intron (NM_007961, intron 1 of 7)
chr7	50509277	-9.913	0.128	EU599041	Intergenic
chr7	50509294	-10.606	0.141	EU599041	Intergenic
chr7	50509199	-7.334	0.171	EU599041	Intergenic
chr16	90830138	14.922	0.089	Eva1c	promoter-TSS (NM_001199210)
chr16	90830125	12.646	0.166	Eva1c	promoter-TSS (NM_001199210)
chr5	37719353	-17.179	0.050	Evc	intron (NM_021292, intron 3 of 20)
chr15	53387892	19.030	0.020	Ext1	intron (NM_177225, intron 4 of 4)
chr15	52922485	19.146	0.024	Ext1	intron (NM_010162, intron 5 of 10)
chr15	52922463	10.657	0.188	Ext1	intron (NM_010162, intron 5 of 10)
chr17	7009134	-10.215	0.072	Ezr	Intergenic
chr17	7009136	-6.908	0.147	Ezr	Intergenic
chr17	7009096	-8.408	0.149	Ezr	Intergenic
chr17	7009047	-6.488	0.185	Ezr	Intergenic
chr3	108800596	9.572	0.108	Fam102b	intron (NM_001163567, intron 2 of 10)
chr3	108800675	10.050	0.122	Fam102b	intron (NM_001163567, intron 2 of 10)
chr15	27612660	-11.187	0.124	Fam105a	Intergenic
chr15	27589569	5.077	0.155	Fam105a	intron (NM_001242424, intron 6 of 8)
chr15	27589862	10.214	0.186	Fam105a	intron (NM_198301, intron 4 of 6)
chr12	31772321	-15.026	0.052	Fam110c	Intergenic
chr19	12649752	-15.078	0.037	Fam111a	intron (NM_026640, intron 1 of 3)
chr3	85581267	-14.948	0.108	Fam160a1	Intergenic
chr12	104539859	22.720	0.030	Fam181a	Intergenic
chr2	172172479	17.314	0.014	Fam210b	intron (NM_025912, intron 1 of 2)
chr14	35171559	12.091	0.153	Fam25c	Intergenic
chr9	85217903	-15.278	0.064	Fam46a	3' UTR (NM_001160379, exon 3 of 3)
chr9	85217761	-11.575	0.131	Fam46a	3' UTR (NM_001160379, exon 3 of 3)
chr15	63835573	-11.498	0.165	Fam49b	intron (NM_144846, intron 1 of 11)
chr15	63835430	-8.780	0.171	Fam49b	intron (NM_144846, intron 1 of 11)
chr1	133445750	-12.241	0.173	Fam72a	Intergenic
chr1	133445758	-10.134	0.198	Fam72a	Intergenic
chr11	120682987	12.459	0.184	Fasn	intron (NM_007988, intron 3 of 42)
chr8	107788961	6.911	0.039	Fbxl8	promoter-TSS (NM_001033161)
chr8	107788927	6.054	0.177	Fbxl8	promoter-TSS (NM_001033161)
chr1	84848467	13.835	0.051	Fbxo36	intron (NM_025386, intron 1 of 3)
chr1	84848538	12.456	0.138	Fbxo36	intron (NM_025386, intron 1 of 3)
chr19	45768769	16.713	0.039	Fbxw4	Intergenic

chr13	99573975	-12.053	0.065	Fcho2	intron (NM_172591, intron 2 of 25)
chr7	108209895	14.980	0.125	Fchsd2	Intergenic
chr7	108209801	13.685	0.169	Fchsd2	Intergenic
chr7	108209820	13.249	0.172	Fchsd2	Intergenic
chr14	63796149	9.282	0.096	Fdft1	intron (NM_010191, intron 1 of 7)
chr18	64660839	-20.080	0.016	Fech	intron (NM_001142950, intron 14 of 14)
chr18	64660901	-10.046	0.142	Fech	intron (NM_001142950, intron 14 of 14)
chr2	132796566	-16.688	0.039	Fermt1	Intergenic
chr16	28555644	-23.630	0.038	Fgf12	intron (NM_010199, intron 2 of 5)
chr7	137342028	-8.395	0.043	Fgfr2	exon (NM_010207, exon 8 of 18)
chr5	109149249	12.320	0.016	Fgfr1	Intergenic
chr5	109149182	6.486	0.139	Fgfr1	Intergenic
chr4	53726644	15.282	0.056	Fktn	promoter-TSS (NM_139309)
chr14	8662414	-10.309	0.140	Flnb	intron (NM_134080, intron 1 of 45)
chr14	8662630	-8.419	0.156	Flnb	intron (NM_134080, intron 1 of 45)
chr5	148493648	-14.871	0.099	Flt1	intron (NM_010228, intron 4 of 29)
chr5	148493698	-14.177	0.122	Flt1	intron (NM_010228, intron 4 of 29)
chr5	148493610	-12.788	0.161	Flt1	intron (NM_010228, intron 4 of 29)
chr5	148220562	-11.849	0.198	Flt3	Intergenic
chr2	30916894	13.403	0.119	Fnbp1	intron (NM_001038700, intron 6 of 14)
chr3	122338355	14.903	0.140	Fnbp11	Intergenic
chr3	122338479	14.778	0.192	Fnbp11	Intergenic
chr8	123644996	-13.037	0.132	Foxc2	Intergenic
chr8	123644992	-9.387	0.138	Foxc2	Intergenic
chr8	123644982	-9.156	0.187	Foxc2	Intergenic
chr17	88842101	-14.601	0.054	Foxn2	intron (NM_180974, intron 1 of 5)
chr17	88803895	-16.380	0.064	Foxn2	Intergenic
chr17	88803837	-16.538	0.096	Foxn2	Intergenic
chr17	88803874	-13.205	0.103	Foxn2	Intergenic
chr17	88842146	-8.094	0.192	Foxn2	intron (NM_180974, intron 1 of 5)
chr12	100584180	-19.017	0.064	Foxn3	intron (NM_183186, intron 2 of 5)
chr6	98974786	-12.925	0.127	Foxp1	intron (NM_001197321, intron 4 of 17)
chr6	98942860	-11.102	0.128	Foxp1	intron (NM_001197321, intron 8 of 17)
chr6	98974332	9.421	0.193	Foxp1	intron (NM_001197321, intron 4 of 17)
chr19	41899642	-12.728	0.065	Frat1	Intergenic
chr19	41899616	-11.343	0.086	Frat1	Intergenic
chr10	34618830	-5.703	0.137	Frk	Intergenic
chr10	34618884	-7.096	0.154	Frk	Intergenic
chr10	34618881	-6.439	0.182	Frk	Intergenic
chr4	57072000	9.211	0.060	Frrs1l	Intergenic
chr4	57072097	6.811	0.143	Frrs1l	Intergenic
chr19	10016878	-13.001	0.059	Fth1	Intergenic
chr7	52704219	15.125	0.036	Ftl1	intron (NM_030678, intron 12 of 15)
chr3	151874649	11.782	0.087	Fubp1	intron (NM_057172, intron 1 of 19)
chr2	31426421	-14.703	0.070	Fubp3	Intergenic
chr2	31426279	-12.051	0.180	Fubp3	Intergenic

chr9	45179403	-9.182	0.136	Fxyd6	intron (NM_022004, intron 1 of 7)
chr9	45179549	-7.964	0.154	Fxyd6	intron (NM_022004, intron 1 of 7)
chr7	96551601	-15.620	0.052	Fzd4	Intergenic
chr7	96551528	-12.335	0.149	Fzd4	Intergenic
chr7	96551632	-11.676	0.184	Fzd4	Intergenic
chr4	47000476	-11.994	0.063	Gabbr2	intron (NM_001081141, intron 1 of 18)
chr4	47000612	-10.850	0.155	Gabbr2	intron (NM_001081141, intron 1 of 18)
chr11	33479257	15.223	0.038	Gabrp	promoter-TSS (NM_146017)
chr11	33479119	11.020	0.136	Gabrp	promoter-TSS (NM_146017)
chr7	118926027	10.098	0.093	Galnt18	Intergenic
chr7	118926033	6.749	0.193	Galnt18	Intergenic
chr15	100550610	7.865	0.178	Galnt6	5' UTR (NM_001161767, exon 2 of 12)
chr15	100550552	6.757	0.180	Galnt6	5' UTR (NM_001161767, exon 2 of 12)
chr8	60625979	-11.458	0.020	Galnt7	intron (NM_175032, intron 4 of 11)
chr18	11039985	10.465	0.024	Gata6	Intergenic
chr18	11039823	7.735	0.060	Gata6	Intergenic
chr11	4106454	-11.818	0.078	Gatsl3	intron (NM_134023, intron 2 of 8)
chr11	4106508	-8.789	0.174	Gatsl3	intron (NM_134023, intron 2 of 8)
chr13	40956595	-6.859	0.072	Gcnt2	exon (NM_023887, exon 1 of 3)
chr13	40956446	-6.475	0.144	Gcnt2	exon (NM_023887, exon 1 of 3)
chr8	119552568	16.753	0.065	Gcsh	intron (NM_029686, intron 29 of 42)
chr8	119552594	10.856	0.135	Gcsh	intron (NM_029686, intron 29 of 42)
chr8	73156017	6.504	0.064	Gdf15	promoter-TSS (NM_011819)
chr8	73156634	6.200	0.184	Gdf15	Intergenic
chr7	106528869	-14.807	0.052	Gdpd5	Intergenic
chr6	48706047	-20.356	0.019	Gimap5	Intergenic
chr3	151777095	15.277	0.041	Gipc2	intron (NM_016867, intron 3 of 5)
chr3	151729721	-7.699	0.103	Gipc2	Intergenic
chr3	151729676	-10.522	0.106	Gipc2	Intergenic
chr3	151729739	-5.846	0.172	Gipc2	Intergenic
chr5	128295799	-16.408	0.106	Glt1d1	intron (NM_172885, intron 5 of 8)
chr5	128188699	-13.596	0.148	Glt1d1	TTS (NM_177005)
chr5	128188668	-11.842	0.166	Glt1d1	TTS (NM_177005)
chr3	85692282	-12.428	0.122	Glt28d2	promoter-TSS (NM_177130)
chr3	85692272	-6.248	0.190	Glt28d2	promoter-TSS (NM_177130)
chr9	106062577	10.294	0.020	Glyctk	Intergenic
chr9	106062737	6.925	0.119	Glyctk	Intergenic
chr12	118398943	-13.410	0.155	Gm10421	intron (NM_011215, intron 12 of 22)
chr12	118398922	-12.385	0.167	Gm10421	intron (NM_011215, intron 12 of 22)
chr12	118398941	-13.731	0.168	Gm10421	intron (NM_011215, intron 12 of 22)
chr9	56918815	13.047	0.043	Gm10658	intron (NR_045886, intron 1 of 2)
chr11	119410014	-12.607	0.057	Gm11762	promoter-TSS (NM_008730)
chr4	14888031	14.131	0.050	Gm11837	intron (NM_178617, intron 10 of 12)
chr4	14888029	12.260	0.081	Gm11837	intron (NM_178617, intron 10 of 12)
chr4	140502131	-13.971	0.103	Gm13031	intron (NM_008812, intron 13 of 15)
chr4	140502182	-16.793	0.106	Gm13031	intron (NM_008812, intron 13 of 15)

chr4	145175617	-11.649	0.064	Gm13212	Intergenic
chr4	145175080	5.913	0.122	Gm13212	Intergenic
chr4	145175335	-7.773	0.129	Gm13212	Intergenic
chr4	88417543	-11.034	0.035	Gm13290	Intergenic
chr4	88417583	-12.004	0.049	Gm13290	Intergenic
chr2	177631981	-14.787	0.019	Gm14327	RMER17B LTR ERVK
chr2	177631826	-17.046	0.020	Gm14327	promoter-TSS (NR_038101)
chr2	177631902	-9.117	0.106	Gm14327	promoter-TSS (NR_038101)
chr2	177631990	-9.098	0.133	Gm14327	RMER17B LTR ERVK
chr2	176858724	-5.835	0.077	Gm14405	Intergenic
chr2	176958182	-10.570	0.091	Gm14405	Intergenic
chr2	176858905	-5.712	0.137	Gm14405	Intergenic
chr2	177183001	-5.537	0.134	Gm14420	Intergenic
chr3	96373741	-16.214	0.103	Gm15441	Intergenic
chr3	96373517	-16.570	0.122	Gm15441	Intergenic
chr14	78173475	-12.952	0.039	Gm1587	Intergenic
chr4	154998303	-7.609	0.036	Gm16023	promoter-TSS (NM_007661)
chr6	8294124	-15.063	0.034	Gm16039	intron (NR_033518, intron 2 of 3)
chr15	39645520	-11.710	0.103	Gm16291	intron (NM_022722, intron 7 of 9)
chr13	63382102	-19.026	0.066	Gm16907	intron (NM_028079, intron 12 of 14)
chr13	63348206	-12.560	0.102	Gm16907	intron (NM_028079, intron 12 of 14)
chr13	63348048	-10.153	0.179	Gm16907	intron (NM_028079, intron 12 of 14)
chr13	63382112	-14.189	0.183	Gm16907	intron (NM_028079, intron 12 of 14)
chr7	105313295	-21.171	0.044	Gm16938	intron (NM_007602, intron 1 of 12)
chr3	79221382	14.296	0.037	Gm17359	intron (NM_001142953, intron 2 of 4)
chr10	92828361	21.190	0.063	Gm17745	Intergenic
chr10	92799014	-13.303	0.104	Gm17745	promoter-TSS (NR_038014)
chr10	92799019	-11.253	0.155	Gm17745	promoter-TSS (NR_038014)
chr10	92828156	13.698	0.160	Gm17745	Intergenic
chr10	92828357	15.764	0.171	Gm17745	Intergenic
chr10	92828929	-5.456	0.177	Gm17745	Intergenic
chr19	47568145	18.720	0.057	Gm19557	Intergenic
chr19	47568115	11.746	0.165	Gm19557	Intergenic
chr10	16758574	-15.702	0.104	Gm20125	intron (NR_038020, intron 1 of 8)
chr15	84606303	10.369	0.134	Gm20556	Intergenic
chr3	52762756	-11.717	0.146	Gm20750	Intergenic
chr3	52762829	-9.422	0.151	Gm20750	Intergenic
chr8	19684379	-7.236	0.123	Gm21119	(TG)n Simple_repeat Simple_repeat
chr8	19684389	-7.299	0.169	Gm21119	(TG)n Simple_repeat Simple_repeat
chr8	19684383	-6.387	0.190	Gm21119	(TG)n Simple_repeat Simple_repeat
chr7	46583859	-26.470	0.030	Gm21276	Intergenic
chr14	4959005	8.597	0.063	Gm3264	CpG
chr14	4959042	9.141	0.068	Gm3264	CpG
chr14	4959019	8.132	0.082	Gm3264	CpG
chr14	4959082	5.244	0.172	Gm3264	CpG
chr14	4959284	6.995	0.174	Gm3264	CpG

chr5	64991351	-11.824	0.061	Gm3716	intron (NR_045078, intron 3 of 3)
chr5	64993257	-13.571	0.064	Gm3716	non-coding (NR_045078, exon 3 of 4)
chr5	64993251	-13.088	0.070	Gm3716	non-coding (NR_045078, exon 3 of 4)
chr5	64991333	-11.667	0.089	Gm3716	intron (NR_045078, intron 3 of 3)
chr5	64991369	-5.815	0.195	Gm3716	intron (NR_045078, intron 3 of 3)
chr10	93819825	-17.896	0.054	Gm4792	Intergenic
chr10	93819735	-15.839	0.094	Gm4792	Intergenic
chr10	93861189	15.363	0.143	Gm4792	Intergenic
chr10	93861203	15.674	0.155	Gm4792	Intergenic
chr10	93819832	-12.009	0.183	Gm4792	Intergenic
chr9	49035798	-16.923	0.058	Gm4894	Intergenic
chr9	49035789	-13.549	0.096	Gm4894	Intergenic
chr9	49035802	-14.018	0.101	Gm4894	Intergenic
chr9	49035824	-12.177	0.152	Gm4894	Intergenic
chr9	49035853	-11.202	0.184	Gm4894	Intergenic
chr14	122805656	-8.807	0.104	Gm5089	intron (NR_033326, intron 1 of 3)
chr14	122805681	-7.199	0.122	Gm5089	intron (NR_033326, intron 1 of 3)
chr14	122805641	-9.551	0.180	Gm5089	intron (NR_033326, intron 1 of 3)
chr13	62887450	-6.816	0.171	Gm5141	promoter-TSS (NM_001256065)
chrX	25546568	-22.151	0.023	Gm5168	Intergenic
chrX	25546663	-7.017	0.157	Gm5168	Intergenic
chr5	139300480	-12.332	0.125	Gm5294	Intergenic
chr5	139300504	-11.124	0.149	Gm5294	Intergenic
chr11	96113343	5.660	0.041	Gm53	CpG
chr11	96113890	6.557	0.153	Gm53	intron (NR_037977, intron 1 of 2)
chr8	12383241	-13.895	0.065	Gm5607	Intergenic
chr8	12383407	-13.543	0.100	Gm5607	Intergenic
chr8	12382877	-11.005	0.155	Gm5607	Intergenic
chr8	12383383	-8.978	0.167	Gm5607	Intergenic
chr14	4122157	7.307	0.019	Gm5796	CpG
chr14	4122975	9.343	0.051	Gm5796	Intergenic
chr14	4122144	5.290	0.188	Gm5796	CpG
chr5	112928376	-12.272	0.065	Gm6588	intron (NM_019982, intron 1 of 16)
chr16	49987368	-8.592	0.057	Gm6936	intron (NR_045001, intron 1 of 3)
chr16	49987364	-5.566	0.169	Gm6936	intron (NR_045001, intron 1 of 3)
chr13	120276286	28.858	0.000	Gm7120	promoter-TSS (NM_001039244)
chr13	120277667	7.137	0.004	Gm7120	promoter-TSS (NM_001177666)
chr13	120276435	28.914	0.012	Gm7120	promoter-TSS (NM_001039244)
chr13	120277742	5.758	0.019	Gm7120	promoter-TSS (NM_001177666)
chr13	120277756	5.531	0.020	Gm7120	promoter-TSS (NM_001177666)
chr13	120276557	20.420	0.020	Gm7120	promoter-TSS (NM_001039244)
chr13	120277680	5.822	0.031	Gm7120	promoter-TSS (NM_001177666)
chr13	120277669	5.668	0.031	Gm7120	promoter-TSS (NM_001177666)
chr13	120277733	5.393	0.034	Gm7120	promoter-TSS (NM_001177666)
chr13	120277563	10.978	0.034	Gm7120	promoter-TSS (NM_001177666)
chr13	120277524	12.111	0.037	Gm7120	promoter-TSS (NM_001177666)

chr13	120277754	5.051	0.054	Gm7120	promoter-TSS (NM_001177666)
chr13	120277548	9.255	0.063	Gm7120	promoter-TSS (NM_001177666)
chr13	120277556	8.961	0.064	Gm7120	promoter-TSS (NM_001177666)
chr13	120276412	21.415	0.074	Gm7120	promoter-TSS (NM_001039244)
chr13	120277543	9.177	0.076	Gm7120	promoter-TSS (NM_001177666)
chr13	120277538	8.931	0.082	Gm7120	promoter-TSS (NM_001177666)
chr1	85194154	-11.393	0.034	Gm7609	Intergenic
chr1	85194052	-8.885	0.137	Gm7609	Intergenic
chr6	3133313	13.381	0.136	Gm8579	Intergenic
chr6	3133227	-8.376	0.159	Gm8579	Intergenic
chr10	98006609	15.814	0.043	Gm8633	Intergenic
chr4	59053929	-18.868	0.042	Gng10	intron (NM_025277, intron 2 of 2)
chr4	59053938	-14.009	0.135	Gng10	intron (NM_025277, intron 2 of 2)
chr10	87852561	-24.142	0.034	Gnptab	intron (NM_001004164, intron 1 of 20)
chr12	103745038	-20.333	0.031	Golga5	ID4 SINE ID
chr19	43573493	-17.174	0.078	Got1	TTS (NM_010324)
chr19	43573558	-19.189	0.108	Got1	TTS (NM_010324)
chr19	43573483	-15.589	0.114	Got1	TTS (NM_010324)
chr1	168068340	-8.501	0.135	Gpa33	intron (NM_021610, intron 1 of 6)
chr14	116608632	-12.844	0.103	Gpc6	intron (NM_175500, intron 7 of 7)
chr14	116608549	-10.575	0.161	Gpc6	intron (NM_175500, intron 7 of 7)
chr14	116608638	-10.679	0.162	Gpc6	intron (NM_175500, intron 7 of 7)
chr3	62408427	-13.796	0.163	Gpr149	exon (NM_177346, exon 1 of 4)
chr3	62408360	-16.051	0.164	Gpr149	exon (NM_177346, exon 1 of 4)
chr3	62408552	-10.927	0.167	Gpr149	5' UTR (NM_177346, exon 1 of 4)
chr2	73291693	7.636	0.154	Gpr155	intron (NM_153138, intron 1 of 7)
chr6	134827051	-16.958	0.093	Gpr19	intron (NM_001167694, intron 3 of 3)
chr6	134827004	-16.079	0.148	Gpr19	intron (NM_001167694, intron 3 of 3)
chr7	139011133	20.093	0.038	Gpr26	Intergenic
chr7	139011051	13.921	0.151	Gpr26	Intergenic
chr12	53139440	-10.216	0.172	Gpr33	Intergenic
chr12	53139380	-10.116	0.193	Gpr33	Intergenic
chr8	122895441	-10.048	0.065	Gse1	Intergenic
chr8	122974144	11.563	0.105	Gse1	CpG
chr8	122895410	-10.726	0.106	Gse1	Intergenic
chr8	122974080	15.578	0.125	Gse1	CpG
chr8	122974129	11.305	0.166	Gse1	CpG
chr10	75294875	-22.253	0.010	Gstt2	intron (NM_010361, intron 4 of 4)
chr2	44783853	-17.312	0.043	Gtdc1	Intergenic
chr12	92879319	-14.648	0.065	Gtf2a1	intron (NM_175367, intron 6 of 6)
chr12	92879286	-9.241	0.157	Gtf2a1	intron (NM_175367, intron 6 of 6)
chr16	44746825	-10.203	0.080	Gtpbp8	promoter-TSS (NM_025332)
chr16	44746798	-9.295	0.129	Gtpbp8	promoter-TSS (NM_025332)
chr16	44746768	-11.348	0.146	Gtpbp8	promoter-TSS (NM_025332)
chr16	44746932	-11.127	0.174	Gtpbp8	promoter-TSS (NM_025332)
chr16	44746831	-7.936	0.185	Gtpbp8	promoter-TSS (NM_025332)



chr16	44746909	-12.779	0.191	Gtpbp8	promoter-TSS (NM_025332)
chr6	100655767	10.369	0.034	Gxylt2	intron (NM_198612, intron 1 of 6)
chr6	100655748	11.645	0.094	Gxylt2	intron (NM_198612, intron 1 of 6)
chr7	149766284	29.778	0.012	H19	Intergenic
chr7	149766288	26.149	0.024	H19	Intergenic
chr7	149766297	24.437	0.034	H19	Intergenic
chr7	149766280	15.909	0.138	H19	Intergenic
chr7	149766266	14.145	0.194	H19	Intergenic
chr15	78859950	11.397	0.100	H1f0	3' UTR (NM_008197, exon 1 of 1)
chr15	78859685	10.415	0.149	H1f0	exon (NM_008197, exon 1 of 1)
chr15	78859609	14.286	0.167	H1f0	exon (NM_008197, exon 1 of 1)
chr2	134282282	14.398	0.131	Hao1	Intergenic
chr2	134282285	13.308	0.152	Hao1	Intergenic
chr12	32686773	-11.094	0.043	Hbp1	intron (NM_011158, intron 2 of 10)
chr12	32686726	-9.460	0.122	Hbp1	intron (NM_011158, intron 2 of 10)
chr10	20972214	-20.957	0.035	Hbs1l	Intergenic
chr10	20972204	-14.267	0.155	Hbs1l	Intergenic
chr13	118393409	-13.356	0.094	Hcn1	intron (NM_010408, intron 1 of 7)
chr9	37192133	-5.093	0.127	Hepacam	exon (NM_175189, exon 7 of 7)
chr9	24905621	12.976	0.112	Herpud2	Intergenic
chr9	24905740	6.180	0.130	Herpud2	Intergenic
chr9	24905727	5.449	0.185	Herpud2	Intergenic
chr11	68934495	-16.324	0.118	Hes7	intron (NM_033041, intron 1 of 3)
chr3	8664034	-10.433	0.161	Hey1	3' UTR (NM_010423, exon 5 of 5)
chr16	37564657	-9.489	0.124	Hgd	intron (NM_001042499, intron 5 of 7)
chr12	109555334	-28.121	0.005	Hhip1	intron (NM_001044380, intron 3 of 8)
chr12	109555336	-20.383	0.034	Hhip1	intron (NM_001044380, intron 3 of 8)
chr12	109555322	-15.313	0.133	Hhip1	intron (NM_001044380, intron 3 of 8)
chr12	109555338	-13.925	0.143	Hhip1	intron (NM_001044380, intron 3 of 8)
chr4	119594175	-11.284	0.120	Hivep3	intron (NM_010657, intron 1 of 8)
chr16	94399238	-16.679	0.078	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94449386	19.512	0.080	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94399235	-12.699	0.158	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94399225	-11.410	0.171	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94399111	-10.739	0.190	Hlcs	intron (NM_139145, intron 5 of 9)
chr1	186549643	18.366	0.073	Hlx	Intergenic
chr1	186549159	6.527	0.077	Hlx	Intergenic
chr1	186549064	8.740	0.146	Hlx	Intergenic
chr14	65503905	-9.905	0.078	Hmbox1	intron (NM_177338, intron 4 of 9)
chr14	65503827	-10.427	0.107	Hmbox1	intron (NM_177338, intron 4 of 9)
chr14	65503768	-8.717	0.162	Hmbox1	intron (NM_177338, intron 4 of 9)
chr7	138684678	-5.155	0.092	Hmx3	Intergenic
chr5	100351402	8.538	0.171	Hnrnpd	Intergenic
chr17	80416876	-13.369	0.054	Hnrnp1l	Intergenic
chr17	80416880	-13.268	0.090	Hnrnp1l	Intergenic
chr17	80413761	-15.765	0.139	Hnrnp1l	Intergenic

chr17	80416883	-8.209	0.182	Hnrnp1l	Intergenic
chr7	88871331	-14.993	0.088	Homer2	Intergenic
chr7	88871352	-14.853	0.123	Homer2	Intergenic
chr11	4397575	-15.557	0.031	Hormad2	intron (NM_028860, intron 10 of 17)
chr11	4397555	-10.078	0.098	Hormad2	intron (NM_028860, intron 10 of 17)
chr4	128799626	-18.005	0.034	Hpca	promoter-TSS (NM_001286081)
chr4	128799617	-11.327	0.070	Hpca	promoter-TSS (NM_001286081)
chr4	128797168	-11.380	0.070	Hpca	intron (NM_001286081, intron 1 of 3)
chr4	128797143	-7.757	0.192	Hpca	intron (NM_001286081, intron 1 of 3)
chr19	42966355	8.866	0.045	Hps1	intron (NM_001081257, intron 9 of 11)
chr19	42966410	11.585	0.056	Hps1	intron (NM_001081257, intron 9 of 11)
chr7	52595609	11.537	0.172	Hrc	exon (NM_029741, exon 29 of 30)
chr7	52595506	10.232	0.179	Hrc	intron (NM_029741, intron 29 of 29)
chr6	114351030	16.634	0.153	Hrh1	intron (NM_008285, intron 1 of 2)
chr6	114351014	14.450	0.171	Hrh1	intron (NM_008285, intron 1 of 2)
chr11	63770391	-17.268	0.035	Hs3st3b1	Intergenic
chr14	119654698	-24.130	0.018	Hs6st3	intron (NM_015820, intron 1 of 1)
chr8	120221406	-13.698	0.065	Hsd17b2	Intergenic
chr8	120221322	-16.159	0.065	Hsd17b2	Intergenic
chr8	120221350	-18.019	0.096	Hsd17b2	Intergenic
chr5	136384504	15.254	0.112	Hspb1	3' UTR (NM_018871, exon 2 of 2)
chr5	136384502	13.548	0.147	Hspb1	3' UTR (NM_018871, exon 2 of 2)
chr11	100576565	-16.961	0.061	Hspb9	TTS (NM_024456)
chr16	65104997	12.616	0.129	Htr1f	intron (NM_008310, intron 1 of 2)
chr11	115269811	26.530	0.031	Ict1	intron (NM_026729, intron 2 of 5)
chr1	156906939	-14.321	0.045	Ier5	Intergenic
chr1	156906858	-10.436	0.173	Ier5	Intergenic
chr2	30320117	-15.629	0.089	Ier5l	Intergenic
chr4	139770530	-15.416	0.018	Igsf21	intron (NM_198610, intron 1 of 9)
chr4	139770512	-9.206	0.099	Igsf21	intron (NM_198610, intron 1 of 9)
chr4	139770417	-13.388	0.157	Igsf21	intron (NM_198610, intron 1 of 9)
chr8	84908689	14.742	0.095	Il15	intron (NM_001254747, intron 1 of 7)
chr14	58162669	-15.517	0.014	Il17d	TTS (NM_145837)
chr9	100202396	-17.010	0.077	Il20rb	Intergenic
chr9	100202393	-14.445	0.174	Il20rb	Intergenic
chr13	113375010	14.629	0.035	Il31ra	Intergenic
chr1	89545407	-16.388	0.039	Inpp5d	intron (NM_010566, intron 2 of 26)
chr1	89545400	-16.659	0.045	Inpp5d	intron (NM_010566, intron 2 of 26)
chr1	89545354	-13.003	0.128	Inpp5d	intron (NM_010566, intron 2 of 26)
chr1	89545372	-12.618	0.132	Inpp5d	intron (NM_010566, intron 2 of 26)
chr12	56754057	-12.697	0.050	Insm2	intron (NM_001286263, intron 37 of 41)
chr12	56754044	-10.178	0.090	Insm2	intron (NM_001286263, intron 37 of 41)
chr12	56754213	-8.830	0.128	Insm2	intron (NM_001286263, intron 37 of 41)
chr7	104628983	14.722	0.039	Ints4	promoter-TSS (NM_027256)
chr14	121229353	-11.216	0.093	Ipo5	Intergenic
chr14	121229521	-8.214	0.176	Ipo5	Intergenic

chr12	88207376	10.047	0.043	Irf2bpl	Intergenic
chr13	72336204	16.882	0.064	Irx1	Intergenic
chr13	72336356	10.907	0.175	Irx1	Intergenic
chr13	72336344	10.524	0.198	Irx1	Intergenic
chr9	118542069	-15.248	0.118	Itga9	intron (NM_133721, intron 3 of 27)
chr9	118542057	-14.810	0.120	Itga9	intron (NM_133721, intron 3 of 27)
chr2	83533042	-13.805	0.089	Itgav	Intergenic
chr2	83533162	-16.932	0.090	Itgav	RMER10A LTR ERVL
chr8	131048090	-10.101	0.070	Itgb1	Intergenic
chr2	119567112	-14.441	0.111	Itpka	promoter-TSS (NM_146125)
chr2	119567299	-14.863	0.141	Itpka	promoter-TSS (NM_146125)
chr6	146409703	-12.302	0.069	Itpr2	intron (NM_019923, intron 2 of 56)
chr6	146409674	-15.111	0.074	Itpr2	intron (NM_019923, intron 2 of 56)
chr1	153097804	-22.112	0.020	Ivns1abp	Intergenic
chr1	153097814	-22.854	0.026	Ivns1abp	Intergenic
chr3	41403630	-19.720	0.034	Jade1	intron (NM_172303, intron 6 of 10)
chr12	86961040	12.661	0.071	Jdp2	intron (NM_001205052, intron 2 of 3)
chr12	86961027	13.399	0.072	Jdp2	intron (NM_001205052, intron 2 of 3)
chr12	86961003	10.239	0.178	Jdp2	intron (NM_001205052, intron 2 of 3)
chr12	86961055	9.740	0.194	Jdp2	intron (NM_001205052, intron 2 of 3)
chr10	66645409	-12.734	0.065	Jmjd1c	intron (NM_207221, intron 2 of 25)
chr1	17081668	8.861	0.043	Jph1	exon (NM_020604, exon 2 of 5)
chr8	124258322	-12.805	0.103	Jph3	intron (NM_020605, intron 1 of 4)
chr8	124258326	-12.788	0.120	Jph3	intron (NM_020605, intron 1 of 4)
chr16	34400527	-12.822	0.177	Kalrn	intron (NM_177357, intron 1 of 59)
chr8	15012606	6.724	0.085	Kbtbd11	intron (NM_029116, intron 1 of 1)
chr8	15012794	8.854	0.133	Kbtbd11	intron (NM_029116, intron 1 of 1)
chr8	15012831	8.694	0.173	Kbtbd11	intron (NM_029116, intron 1 of 1)
chr8	15012733	5.083	0.178	Kbtbd11	intron (NM_029116, intron 1 of 1)
chr9	65240626	-25.165	0.036	Kbtbd13	Intergenic
chr2	107814081	14.186	0.036	Kcna4	Intergenic
chr11	111397671	7.769	0.094	Kcnj2	Intergenic
chr11	33810817	-16.569	0.091	Kcnmb1	intron (NM_001190886, intron 1 of 7)
chr11	33810972	-6.201	0.116	Kcnmb1	intron (NM_001190886, intron 1 of 7)
chr2	163993554	-27.380	0.009	Kcns1	exon (NM_008435, exon 3 of 4)
chr1	190627562	-18.942	0.013	Kctd3	intron (NM_021408, intron 49 of 70)
chr14	9039073	-21.548	0.065	Kctd6	Intergenic
chr7	53129517	-21.804	0.040	Kdelr1	exon (NM_133950, exon 3 of 5)
chr7	53129514	-12.323	0.190	Kdelr1	exon (NM_133950, exon 3 of 5)
chr6	39208087	20.227	0.043	Kdm7a	Intergenic
chr5	76440263	-10.011	0.188	Kdr	Intergenic
chr12	25644215	-12.515	0.035	Kidins220	3' UTR (NM_026037, exon 13 of 13)
chr2	10024008	8.114	0.061	Kin	(TG)n Simple_repeat Simple_repeat
chr2	10024012	13.598	0.071	Kin	(TG)n Simple_repeat Simple_repeat
chr2	10024000	7.863	0.120	Kin	(TG)n Simple_repeat Simple_repeat
chr5	76091400	-12.863	0.110	Kit	Intergenic

chr5	151858333	-9.466	0.112	Kl	intron (NM_146258, intron 7 of 13)
chr14	99983803	21.222	0.038	Klf5	Intergenic
chr6	30387006	-7.827	0.195	Klhdc10	intron (NM_029742, intron 2 of 9)
chr1	134184973	14.299	0.061	Klhdc8a	Intergenic
chr5	65522648	14.134	0.065	Klhl5	exon (NM_175174, exon 1 of 11)
chr5	65522614	9.451	0.139	Klhl5	5' UTR (NM_175174, exon 1 of 11)
chr5	65522622	7.645	0.188	Klhl5	5' UTR (NM_175174, exon 1 of 11)
chr16	19980210	-21.791	0.034	Klhl6	intron (NM_183390, intron 1 of 6)
chr4	88364580	10.236	0.057	Klhl9	3' UTR (NM_172871, exon 1 of 1)
chr11	99292121	19.755	0.038	Krt20	exon (NM_023256, exon 6 of 8)
chr11	99292094	17.213	0.077	Krt20	exon (NM_023256, exon 6 of 8)
chr11	99292163	12.438	0.170	Krt20	exon (NM_023256, exon 6 of 8)
chr16	89524792	-6.134	0.148	Krtap7-1	Intergenic
chr17	68526221	-15.138	0.118	L3mbtl4	Intergenic
chr14	77274952	-12.782	0.117	Lacc1	Intergenic
chr14	77274058	-13.686	0.130	Lacc1	Intergenic
chr14	77274454	-9.996	0.190	Lacc1	Intergenic
chr3	107064675	16.700	0.064	Lamtor5	Intergenic
chr3	107064650	13.487	0.182	Lamtor5	Intergenic
chr1	183853843	-16.266	0.048	Lbr	exon (NM_001083120, exon 5 of 14)
chr1	183853867	-14.190	0.064	Lbr	exon (NM_001083120, exon 5 of 14)
chr1	183853472	-12.745	0.196	Lbr	intron (NM_010135, intron 6 of 14)
chr18	68226220	-11.892	0.073	Ldlrad4	intron (NM_172631, intron 2 of 5)
chr4	134316664	-12.373	0.103	Ldlrap1	intron (NM_145554, intron 1 of 8)
chr4	134316254	-13.525	0.105	Ldlrap1	intron (NM_145554, intron 1 of 8)
chr4	134316974	-12.137	0.125	Ldlrap1	intron (NM_145554, intron 1 of 8)
chr3	130787703	-22.923	0.029	Lef1	Intergenic
chr3	130787575	-16.726	0.044	Lef1	Intergenic
chr3	130787898	-13.484	0.071	Lef1	Intergenic
chr3	130816157	15.219	0.106	Lef1	intron (NM_001276403, intron 1 of 11)
chr3	130787884	-10.165	0.131	Lef1	Intergenic
chr3	130787699	-12.945	0.161	Lef1	Intergenic
chr3	130787695	-12.815	0.163	Lef1	Intergenic
chr9	75279481	-14.602	0.123	Leo1	Intergenic
chr16	26041765	12.650	0.108	Leprel1	intron (NM_173379, intron 1 of 14)
chr16	26041738	10.835	0.191	Leprel1	intron (NM_173379, intron 1 of 14)
chr12	103623249	14.677	0.075	Lgmn	intron (NM_177620, intron 8 of 9)
chr12	103623273	9.330	0.186	Lgmn	intron (NM_177620, intron 8 of 9)
chr3	52848762	-26.447	0.021	Lhfp	intron (NM_175386, intron 2 of 3)
chr3	52848786	-13.173	0.196	Lhfp	intron (NM_175386, intron 2 of 3)
chr1	157575064	10.326	0.195	Lhx4	intron (NM_010712, intron 1 of 5)
chr1	140738284	6.276	0.151	Lhx9	CpG
chr9	123388367	17.165	0.077	Limd1	exon (NM_013860, exon 1 of 8)
chr9	123388338	13.414	0.149	Limd1	5' UTR (NM_013860, exon 1 of 8)
chr5	100919414	-14.746	0.037	Lin54	intron (NM_172714, intron 1 of 12)
chr5	100919424	-12.278	0.068	Lin54	intron (NM_172714, intron 1 of 12)

chr5	100919344	-9.258	0.183	Lin54	intron (NM_172714, intron 1 of 12)
chr9	56480471	-12.714	0.104	Lingo1	intron (NM_181074, intron 3 of 3)
chr9	56480413	-12.267	0.109	Lingo1	intron (NM_181074, intron 3 of 3)
chr9	56480491	-10.962	0.186	Lingo1	intron (NM_181074, intron 3 of 3)
chr3	88297699	-23.758	0.024	Lmna	promoter-TSS (NM_019390)
chr3	88297768	-16.251	0.064	Lmna	promoter-TSS (NM_019390)
chr3	88297695	-18.332	0.068	Lmna	promoter-TSS (NM_019390)
chr3	88297691	-15.776	0.109	Lmna	promoter-TSS (NM_019390)
chr3	143856160	-12.614	0.117	Lmo4	intron (NM_010723, intron 4 of 4)
chr3	143851190	-12.629	0.136	Lmo4	TTS (NM_001161770)
chr3	143851107	-11.262	0.146	Lmo4	TTS (NM_001161770)
chr3	143856559	-8.718	0.181	Lmo4	intron (NM_010723, intron 4 of 4)
chr3	143851424	-6.623	0.199	Lmo4	TTS (NM_001161770)
chr1	169857064	12.134	0.036	Lmx1a	Intergenic
chr14	70031515	13.398	0.048	Loxl2	intron (NM_033325, intron 1 of 13)
chr14	70031535	10.853	0.166	Loxl2	intron (NM_033325, intron 1 of 13)
chr4	58522481	8.285	0.036	Lpar1	intron (NM_010336, intron 1 of 3)
chr6	124615527	11.774	0.089	Lpcat3	intron (NM_145130, intron 1 of 12)
chr6	124615470	14.725	0.092	Lpcat3	intron (NM_145130, intron 1 of 12)
chr6	124615334	9.793	0.122	Lpcat3	intron (NM_145130, intron 1 of 12)
chr1	193517442	12.036	0.106	Lpgat1	Intergenic
chr1	193517451	10.409	0.177	Lpgat1	Intergenic
chr8	86438417	-19.158	0.059	Lphn1	intron (NM_181039, intron 1 of 22)
chr8	86438860	-12.875	0.187	Lphn1	intron (NM_181039, intron 1 of 22)
chr3	148081459	19.846	0.031	Lphn2	Intergenic
chr7	31148592	-14.613	0.123	Lrfn3	promoter-TSS (NM_175478)
chr5	123948163	-6.218	0.073	Lrrc43	intron (NM_001033461, intron 4 of 11)
chr5	123948252	-6.405	0.162	Lrrc43	intron (NM_001033461, intron 4 of 11)
chr2	120496151	11.993	0.144	Lrrc57	Intergenic
chr10	63549273	-16.844	0.053	Lrrtm3	intron (NM_178678, intron 2 of 2)
chr10	63549051	-18.049	0.122	Lrrtm3	intron (NM_178678, intron 2 of 2)
chr10	63549042	-16.631	0.157	Lrrtm3	intron (NM_178678, intron 2 of 2)
chr10	63549262	-10.884	0.192	Lrrtm3	intron (NM_178678, intron 2 of 2)
chr14	30042300	9.176	0.146	Lrtm1	intron (NM_009785, intron 11 of 37)
chr17	35357285	-18.866	0.036	Lta	3' UTR (NM_010909, exon 4 of 4)
chr17	35357269	-18.138	0.103	Lta	3' UTR (NM_010909, exon 4 of 4)
chr7	25413890	13.708	0.122	Lypd3	exon (NM_001102613, exon 15 of 15)
chr7	25413876	12.173	0.189	Lypd3	exon (NM_001102613, exon 15 of 15)
chr2	49642972	-13.062	0.091	Lypd6b	promoter-TSS (NM_027990)
chr2	49642858	-12.101	0.157	Lypd6b	promoter-TSS (NM_027990)
chr2	49642941	-6.136	0.165	Lypd6b	promoter-TSS (NM_027990)
chr6	145160460	-18.612	0.072	Lym5	promoter-TSS (NM_177222)
chr9	121526069	13.291	0.057	Lyzl4	intron (NM_026915, intron 1 of 5)
chr19	45104745	9.802	0.063	Lzts2	exon (NM_001195265, exon 11 of 16)
chr19	23476443	15.867	0.034	Mamdc2	intron (NM_174857, intron 2 of 13)
chr19	23542727	16.683	0.038	Mamdc2	Intergenic

chr19	23476497	15.000	0.068	Mamdc2	intron (NM_174857, intron 2 of 13)
chr19	23476445	12.282	0.091	Mamdc2	intron (NM_174857, intron 2 of 13)
chr3	51833708	-12.646	0.141	Maml3	intron (NM_001004176, intron 1 of 4)
chr3	51833817	-12.611	0.160	Maml3	intron (NM_001004176, intron 1 of 4)
chr3	51833931	-9.167	0.178	Maml3	intron (NM_001004176, intron 1 of 4)
chr13	112719528	-9.323	0.192	Map3k1	Intergenic
chr4	32249885	-10.906	0.045	Map3k7	Intergenic
chr4	32249753	-10.794	0.062	Map3k7	Intergenic
chr1	40036221	17.742	0.035	Map4k4	intron (NM_001252202, intron 5 of 29)
chr1	40036255	14.579	0.092	Map4k4	intron (NM_001252202, intron 5 of 29)
chr1	40036272	11.131	0.167	Map4k4	intron (NM_001252202, intron 5 of 29)
chr9	107182011	19.162	0.060	Mapkapk3	intron (NM_178907, intron 2 of 10)
chr9	107182835	12.559	0.126	Mapkapk3	intron (NM_178907, intron 2 of 10)
chr9	107182983	-6.273	0.148	Mapkapk3	intron (NM_178907, intron 2 of 10)
chr9	107182992	8.549	0.148	Mapkapk3	intron (NM_178907, intron 2 of 10)
chr11	104167273	-16.281	0.031	Mapt	intron (NM_001038609, intron 6 of 11)
chr11	104167243	-13.727	0.146	Mapt	intron (NM_001038609, intron 6 of 11)
chr8	122088028	10.671	0.040	Mbtps1	exon (NM_175185, exon 5 of 5)
chr8	122088089	20.231	0.044	Mbtps1	intron (NM_175185, intron 4 of 4)
chr8	12883649	-17.312	0.096	Mcf2l	Intergenic
chr8	12883644	-16.215	0.106	Mcf2l	Intergenic
chr15	81067672	-25.796	0.024	Mchr1	exon (NM_145132, exon 2 of 2)
chr10	117113434	-10.317	0.079	Mdm2	intron (NM_027468, intron 7 of 8)
chr10	117113794	-9.835	0.107	Mdm2	intron (NM_027468, intron 7 of 8)
chr10	117113780	-10.694	0.139	Mdm2	intron (NM_027468, intron 7 of 8)
chr10	117113330	-8.658	0.190	Mdm2	intron (NM_027468, intron 7 of 8)
chr11	86218446	-14.952	0.035	Med13	Intergenic
chr2	29202935	-13.218	0.053	Med27	intron (NM_026896, intron 1 of 7)
chr2	115887638	-13.880	0.032	Meis2	intron (NM_001159568, intron 2 of 11)
chr2	115887667	-13.725	0.089	Meis2	intron (NM_001159568, intron 2 of 11)
chr2	115887557	-7.222	0.118	Meis2	intron (NM_001159568, intron 2 of 11)
chr3	123074671	-11.181	0.040	Mettl14	intron (NM_201638, intron 9 of 10)
chr3	123074644	-8.290	0.128	Mettl14	intron (NM_201638, intron 9 of 10)
chr10	40458183	-14.827	0.122	Mettl24	intron (NM_177793, intron 3 of 4)
chr11	49065181	14.047	0.055	Mgat1	intron (NM_001110150, intron 2 of 2)
chr1	37596358	-12.444	0.054	Mgat4a	Intergenic
chr1	37596987	-12.839	0.104	Mgat4a	Intergenic
chr1	37596796	-8.346	0.174	Mgat4a	Intergenic
chr1	37596388	-7.051	0.192	Mgat4a	Intergenic
chr1	37596155	-8.223	0.197	Mgat4a	Intergenic
chr1	129260723	-19.630	0.041	Mgat5	intron (NM_145128, intron 4 of 17)
chr3	51655707	19.687	0.018	Mgst2	intron (NM_001004176, intron 2 of 4)
chr3	51655469	6.338	0.180	Mgst2	intron (NM_001004176, intron 2 of 4)
chr6	121040026	8.525	0.088	Mical3	intron (NM_001270475, intron 1 of 31)
chr6	121040055	7.110	0.095	Mical3	intron (NM_001270475, intron 1 of 31)
chr6	121079854	-6.665	0.098	Mical3	intron (NM_001270475, intron 1 of 31)

chr6	121079703	-11.263	0.100	Mical3	intron (NM_001270475, intron 1 of 31)
chr6	121040095	6.736	0.153	Mical3	intron (NM_001270475, intron 1 of 31)
chr8	41406942	13.636	0.041	Micu3	intron (NM_030110, intron 1 of 14)
chr8	41406944	12.898	0.071	Micu3	intron (NM_030110, intron 1 of 14)
chrX	166438684	-10.723	0.000	Mid1	Intergenic
chrX	166427567	-13.838	0.000	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166445032	-11.076	0.000	Mid1	Intergenic
chrX	166440879	12.703	0.000	Mid1	Intergenic
chrX	166427536	-12.370	0.000	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166422944	11.305	0.000	Mid1	exon (NM_010797, exon 7 of 10)
chrX	166424826	26.032	0.000	Mid1	CpG
chrX	166422857	9.458	0.001	Mid1	CpG
chrX	166441665	-13.187	0.001	Mid1	Intergenic
chrX	166440939	32.547	0.002	Mid1	Intergenic
chrX	166422977	9.381	0.006	Mid1	exon (NM_010797, exon 7 of 10)
chrX	166446717	11.427	0.010	Mid1	Intergenic
chrX	166440873	10.321	0.017	Mid1	Intergenic
chrX	166443375	7.887	0.019	Mid1	Intergenic
chrX	166428153	13.356	0.020	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166427753	-11.903	0.026	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166443349	8.148	0.031	Mid1	Intergenic
chrX	166419008	13.398	0.031	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166416621	11.017	0.031	Mid1	Intron (NM_010797, intron 4 of 9)
chrX	166421197	5.504	0.033	Mid1	intron (NM_010797, 5 of 9)
chrX	166417136	7.632	0.034	Mid1	Intron (NM_010797 4 of 9)
chrX	166421313	11.146	0.034	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166420265	6.813	0.034	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166443368	6.597	0.035	Mid1	Intergenic
chrX	166428147	10.699	0.035	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166419668	9.696	0.038	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166422164	5.523	0.041	Mid1	intron (NM_010797, intron 6 of 9)
chrX	166424813	16.411	0.043	Mid1	CpG
chrX	166428106	8.329	0.043	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166428254	17.399	0.043	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166420929	5.202	0.046	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166443343	7.835	0.049	Mid1	Intergenic
chrX	166442484	-8.183	0.053	Mid1	Intergenic
chrX	166421242	7.008	0.061	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166420047	8.272	0.067	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166419899	7.651	0.068	Mid1	exon (NM_010797, exon 5 of 10)
chrX	166427373	-10.220	0.069	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166421338	8.820	0.076	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166421293	6.813	0.077	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166416628	8.632	0.080	Mid1	Intron (NM_010797 4 of 9)
chrX	166417000	7.086	0.089	Mid1	Intron (NM_010797 4 of 9)
chrX	166417427	9.336	0.092	Mid1	Intron (NM_010797 4 of 9)

chrX	166421255	6.074	0.100	Mid1	intron (010797, intron 5 of 9)
chrX	166421947	6.140	0.104	Mid1	exon (NM_010797, exon 6 of 10)
chrX	166428120	6.317	0.104	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166417256	6.347	0.107	Mid1	Intron (NM_010797 4 of 9)
chrX	166421583	9.501	0.108	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166416412	7.855	0.117	Mid1	Intron (NM_010797 4 of 9)
chrX	166428186	9.236	0.118	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166424805	12.657	0.122	Mid1	CpG
chrX	166419931	6.503	0.122	Mid1	exon (NM_010797, exon 5 of 10)
chrX	166416485	8.545	0.127	Mid1	Intron (NM_010797 4 of 9)
chrX	166428157	7.854	0.141	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166419927	5.668	0.155	Mid1	exon (NM_010797, exon 5 of 10)
chrX	166428095	5.973	0.155	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166440542	14.163	0.157	Mid1	Intergenic
chrX	166424584	9.438	0.160	Mid1	intron (NM_010797, intron 8 of 9)
chrX	166419908	6.034	0.161	Mid1	exon (NM_010797, exon 5 of 10)
chrX	166416828	10.966	0.162	Mid1	Intron (NM_010797 4 of 9)
chrX	166417315	6.324	0.163	Mid1	Intron (NM_010797 4 of 9)
chrX	166428047	5.371	0.164	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166416645	6.548	0.167	Mid1	Intron (NM_010797 4 of 9)
chrX	166424984	9.764	0.171	Mid1	CpG
chrX	166416709	6.954	0.178	Mid1	Intron (NM_010797 4 of 9)
chrX	166424980	9.472	0.178	Mid1	CpG
chrX	166417010	5.158	0.181	Mid1	Intron (NM_010797 4 of 9)
chrX	166428175	7.647	0.190	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166428056	5.391	0.190	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166424685	10.398	0.191	Mid1	intron (NM_010797, intron 8 of 9)
chr9	3030193	-14.082	0.052	Mir101c	GSAT_MM Satellite Satellite
chr12	102245866	-17.077	0.064	Mir1190	intron (NM_026681, intron 3 of 29)
chr12	102245859	-19.702	0.064	Mir1190	intron (NM_026681, intron 3 of 29)
chr8	86710747	-8.508	0.105	Mir181c	Intergenic
chr8	86710866	-8.167	0.146	Mir181c	Intergenic
chr18	6456677	10.789	0.151	Mir1893	intron (NM_027497, intron 2 of 13)
chr18	6456567	9.422	0.158	Mir1893	intron (NM_027497, intron 2 of 13)
chr13	110697878	-14.270	0.072	Mir1904	intron (NM_011056, intron 8 of 16)
chr13	110504076	15.076	0.100	Mir1904	intron (NM_011056, intron 3 of 16)
chr13	110697868	-9.070	0.133	Mir1904	intron (NM_011056, intron 8 of 16)
chr13	110697829	-8.501	0.140	Mir1904	intron (NM_011056, intron 8 of 16)
chr13	110504354	12.878	0.143	Mir1904	intron (NM_011056, intron 3 of 16)
chr10	44100879	-12.432	0.171	Mir1929	Intergenic
chr10	44100500	-12.066	0.176	Mir1929	Intergenic
chr2	115549946	-9.561	0.076	Mir1951	intron (NM_207264, intron 10 of 10)
chr2	115549521	-14.712	0.132	Mir1951	intron (NM_207264, intron 10 of 10)
chr13	22007646	-15.127	0.120	Mir1983	Intergenic
chr13	22007431	-14.243	0.172	Mir1983	ID4 SINE ID
chr11	86399968	21.337	0.044	Mir21	intron (NM_029478, intron 11 of 11)



chr11	86399928	12.700	0.054	Mir21	intron (NM_029478, intron 11 of 11)
chr11	86400870	16.538	0.064	Mir21	intron (NM_029478, intron 10 of 11)
chr11	86407229	16.950	0.105	Mir21	intron (NM_029478, intron 10 of 11)
chr11	86407208	13.968	0.130	Mir21	intron (NM_029478, intron 10 of 11)
chr11	86400892	12.814	0.147	Mir21	intron (NM_029478, intron 10 of 11)
chr7	71371921	-17.695	0.068	Mir211	intron (NM_001039104, intron 16 of 26)
chr9	104311621	11.449	0.115	Mir2136	Intergenic
chr9	104311654	14.872	0.127	Mir2136	Intergenic
chr12	17399956	-14.199	0.147	Mir3066	intron (NM_001008421, intron 13 of 20)
chr12	17399953	-14.819	0.157	Mir3066	intron (NM_001008421, intron 13 of 20)
chr12	110847239	-18.573	0.063	Mir341	intron (NR_028261, intron 2 of 20)
chr12	110847462	-15.559	0.088	Mir341	intron (NR_028261, intron 2 of 20)
chr11	79585364	5.641	0.177	Mir365-2	Intergenic
chr11	79585405	5.006	0.188	Mir365-2	Intergenic
chr1	34466960	-13.632	0.044	Mir5103	Intergenic
chr1	34467018	-16.152	0.060	Mir5103	Intergenic
chr1	34467027	-13.354	0.099	Mir5103	Intergenic
chr1	34466972	-8.472	0.177	Mir5103	Intergenic
chr19	44372971	-16.836	0.038	Mir5114	intron (NM_009128, intron 3 of 5)
chr16	43547799	12.163	0.079	Mir568	intron (NM_019778, intron 3 of 8)
chr16	43547797	8.813	0.193	Mir568	intron (NM_019778, intron 3 of 8)
chr13	110021087	-11.778	0.065	Mir582	intron (NM_011056, intron 3 of 16)
chr13	110021110	-12.667	0.074	Mir582	intron (NM_011056, intron 3 of 16)
chr14	64300608	13.948	0.107	Mir598	intron (NM_173393, intron 1 of 2)
chr14	64300731	12.773	0.128	Mir598	intron (NM_173393, intron 1 of 2)
chr14	64300595	12.420	0.167	Mir598	intron (NM_173393, intron 1 of 2)
chr2	166389463	20.805	0.045	Mir6364	Intergenic
chr2	166389454	13.430	0.148	Mir6364	Intergenic
chr6	102730933	7.716	0.038	Mir6373	Intergenic
chr12	15808106	22.321	0.037	Mir6387	promoter-TSS (NR_105809)
chr12	15808101	14.176	0.060	Mir6387	promoter-TSS (NR_105809)
chr14	118884936	-5.345	0.035	Mir6391	intron (NM_001033336, intron 30 of 30)
chr12	27001385	-11.122	0.122	Mir6538	intron (NM_001081977, intron 8 of 9)
chr12	27001465	-13.770	0.149	Mir6538	intron (NM_001081977, intron 8 of 9)
chr12	70862165	-12.342	0.078	Mir681	intron (NM_183294, intron 3 of 9)
chr12	70862230	-14.606	0.108	Mir681	intron (NM_183294, intron 3 of 9)
chr12	70862199	-10.050	0.149	Mir681	intron (NM_183294, intron 3 of 9)
chr12	70862224	-10.313	0.199	Mir681	intron (NM_183294, intron 3 of 9)
chr11	59999533	-16.705	0.038	Mir6921	exon (NM_009021, exon 3 of 6)
chr11	59999409	-19.231	0.069	Mir6921	exon (NM_009021, exon 3 of 6)
chr11	59999581	-12.542	0.148	Mir6921	exon (NM_009021, exon 3 of 6)
chr11	120208936	-7.801	0.019	Mir6935	promoter-TSS (NR_105900)
chr11	120208909	-9.470	0.029	Mir6935	promoter-TSS (NR_105900)
chr11	120208914	-10.919	0.032	Mir6935	promoter-TSS (NR_105900)
chr11	120208869	-6.243	0.046	Mir6935	promoter-TSS (NR_105900)
chr11	120208953	-5.566	0.181	Mir6935	promoter-TSS (NR_105900)

chr14	30809435	-14.519	0.103	Mir6947	TTS (NM_019583)
chr14	30809442	-11.296	0.188	Mir6947	TTS (NM_019583)
chr2	29866348	-12.243	0.135	Mir6997	intron (NM_001076554, intron 31 of 56)
chr3	95536474	-17.480	0.035	Mir7014	Intergenic
chr3	95536454	-12.176	0.149	Mir7014	Intergenic
chr7	50720399	-11.009	0.155	Mir7051	CpG
chr7	103391732	5.862	0.057	Mir708	intron (NM_011858, intron 1 of 32)
chr7	103391641	8.274	0.118	Mir708	intron (NM_011858, intron 1 of 32)
chr12	115785398	-14.611	0.035	Mir7094-2	Intergenic
chr4	126241221	-17.286	0.035	Mir7119	exon (NM_175554, exon 5 of 26)
chr13	62861544	12.419	0.088	Mir713	promoter-TSS (NR_030493)
chr14	24953685	-11.316	0.068	Mir7210	3' UTR (NM_027726, exon 31 of 31)
chr14	24953719	-10.179	0.181	Mir7210	3' UTR (NM_027726, exon 31 of 31)
chr7	134810622	-19.161	0.051	Mir762	Intergenic
chr11	53573012	-19.946	0.014	Mir7671	Intergenic
chr11	53573819	-12.015	0.197	Mir7671	Intergenic
chr15	78098562	-22.403	0.020	Mir7676-2	Intergenic
chr10	122136258	-9.321	0.139	Mir8104	intron (NM_001110218, intron 1 of 9)
chr10	122136340	-7.996	0.193	Mir8104	intron (NM_001110218, intron 1 of 9)
chr10	122370265	-16.203	0.064	Mirlet7i	intron (NM_001110218, intron 9 of 9)
chr10	122370173	-11.846	0.155	Mirlet7i	intron (NM_001110218, intron 9 of 9)
chr6	31340876	-16.922	0.091	Mkln1os	intron (NR_040300, intron 2 of 2)
chr6	31340872	-12.678	0.169	Mkln1os	intron (NR_040300, intron 2 of 2)
chr7	69565631	19.781	0.004	Mkrn3	promoter-TSS (NM_011746)
chr7	69565740	8.315	0.160	Mkrn3	promoter-TSS (NM_011746)
chr7	69565226	6.610	0.173	Mkrn3	promoter-TSS (NM_011746)
chr3	67177163	-14.332	0.154	Mif1	promoter-TSS (NM_010801)
chr4	3797752	-14.657	0.139	Mos	TTS (NM_020021)
chr10	24037022	-16.897	0.074	Moxd1	Intergenic
chr9	99333490	-19.134	0.094	Mras	intron (NM_008624, intron 1 of 5)
chr9	99322634	-14.364	0.129	Mras	intron (NM_008624, intron 1 of 5)
chr9	99322599	-8.267	0.195	Mras	intron (NM_008624, intron 1 of 5)
chr15	73906416	-11.595	0.042	Mroh5	Intergenic
chr15	73906327	-15.267	0.046	Mroh5	Intergenic
chr15	73906292	-13.658	0.103	Mroh5	Intergenic
chr15	73906606	-8.174	0.166	Mroh5	Intergenic
chr1	165021916	-17.929	0.070	Mroh9	Intergenic
chr11	5606883	-6.129	0.091	Mrps24	intron (NM_026080, intron 3 of 3)
chr11	5606522	-15.036	0.137	Mrps24	intron (NM_026080, intron 3 of 3)
chr13	25099817	12.344	0.055	Mrs2	intron (NM_001013389, intron 2 of 10)
chr13	25099888	9.656	0.124	Mrs2	IAPLTR3-int LTR ERVK
chr13	25099892	9.636	0.133	Mrs2	IAPLTR3-int LTR ERVK
chr13	25099903	10.449	0.161	Mrs2	IAPLTR3-int LTR ERVK
chr17	35176422	-16.888	0.110	Msh5	intron (NM_001146215, intron 10 of 24)
chr14	64160092	-20.109	0.043	Mtmr9	intron (NM_177594, intron 2 of 9)
chr4	61505835	11.763	0.040	Mup5	Intergenic

chr13	55429425	-14.673	0.079	Mxd3	intron (NM_016662, intron 4 of 5)
chr10	20821626	15.696	0.040	Myb	Intergenic
chr2	162881035	11.987	0.075	Mybl2	CpG
chr2	162881023	5.374	0.157	Mybl2	CpG
chr2	162881368	14.491	0.177	Mybl2	intron (NM_008652, intron 1 of 13)
chr15	61831575	-13.596	0.038	Myc	Intergenic
chr2	69967966	10.224	0.129	Myo3b	intron (NM_177376, intron 8 of 34)
chr2	69967945	9.386	0.157	Myo3b	intron (NM_177376, intron 8 of 34)
chr9	71454574	-12.579	0.057	Myzap	Intergenic
chr9	71454663	-9.798	0.139	Myzap	Intergenic
chr4	154943220	7.662	0.039	Nadk	intron (NM_001159637, intron 1 of 11)
chrX	100381082	6.945	0.183	Nap1l2	exon (NM_008671, exon 1 of 1)
chr7	56654609	-17.078	0.056	Nav2	intron (NM_175272, intron 4 of 37)
chr7	56654689	-13.376	0.096	Nav2	intron (NM_175272, intron 4 of 37)
chr15	37385518	-16.105	0.052	Ncald	intron (NM_001170867, intron 1 of 4)
chr15	37720725	-10.210	0.078	Ncald	intron (NM_134094, intron 1 of 6)
chr15	37720396	-19.414	0.080	Ncald	intron (NM_134094, intron 1 of 6)
chr15	37385539	-13.099	0.096	Ncald	intron (NM_001170867, intron 1 of 4)
chr15	37720549	-9.831	0.143	Ncald	intron (NM_134094, intron 1 of 6)
chr15	37720691	-9.540	0.169	Ncald	intron (NM_134094, intron 1 of 6)
chr2	80419264	-9.745	0.104	Nckap1	intron (NM_016965, intron 1 of 30)
chr2	80419664	-9.514	0.172	Nckap1	intron (NM_016965, intron 1 of 30)
chr5	125618115	-12.929	0.089	Ncor2	intron (NM_011424, intron 1 of 46)
chr5	125618126	-9.865	0.117	Ncor2	intron (NM_011424, intron 1 of 46)
chr5	125618109	-10.742	0.119	Ncor2	intron (NM_011424, intron 1 of 46)
chr15	58820549	14.503	0.107	Ndufb9	intron (NM_144800, intron 3 of 14)
chr19	5844632	-25.287	0.001	Neat1	non-coding (NR_003513, exon 1 of 1)
chr19	5844636	-21.326	0.014	Neat1	non-coding (NR_003513, exon 1 of 1)
chr19	5844514	-19.993	0.040	Neat1	non-coding (NR_003513, exon 1 of 1)
chr19	5844519	-15.749	0.068	Neat1	non-coding (NR_003513, exon 1 of 1)
chr18	65161027	16.787	0.088	Nedd4l	intron (NM_001114386, intron 2 of 30)
chr18	65161217	7.909	0.123	Nedd4l	intron (NM_001114386, intron 2 of 30)
chr1	36326332	-20.611	0.053	Neur13	exon (NM_153408, exon 2 of 4)
chr1	36326037	-14.196	0.089	Neur13	intron (NM_153408, intron 2 of 3)
chr1	36326160	-12.016	0.098	Neur13	exon (NM_153408, exon 2 of 4)
chr1	36326278	-12.318	0.175	Neur13	exon (NM_153408, exon 2 of 4)
chr6	55629630	-18.971	0.034	Neurod6	exon (NM_009717, exon 2 of 2)
chr3	151925038	-19.541	0.030	Nexn	intron (NM_199465, intron 1 of 12)
chr3	151925042	-10.719	0.188	Nexn	intron (NM_199465, intron 1 of 12)
chr11	4706313	18.622	0.018	Nf2	exon (NM_010898, exon 6 of 16)
chr11	4706269	14.596	0.135	Nf2	exon (NM_010898, exon 6 of 16)
chr11	4706641	12.244	0.137	Nf2	intron (NM_001252250, intron 5 of 16)
chr1	134492979	-17.633	0.070	Nfasc	intron (NM_001160318, intron 22 of 26)
chr1	134492415	-14.044	0.136	Nfasc	intron (NM_001160318, intron 22 of 26)
chr4	82184801	-12.698	0.050	Nfib	Intergenic
chr12	88443158	10.322	0.092	Ngb	exon (NM_022414, exon 1 of 4)

chr1	75063756	-9.356	0.066	Nhej1	intron (NM_029342, intron 3 of 5)
chr12	71210859	20.213	0.062	Nin	intron (NM_001286079, intron 1 of 28)
chr6	120141918	-14.944	0.076	Ninj2	intron (NM_016718, intron 1 of 3)
chr7	139788329	-14.660	0.088	Nkx1-2	3' UTR (NM_009123, exon 2 of 2)
chr7	139788577	-9.517	0.112	Nkx1-2	3' UTR (NM_009123, exon 2 of 2)
chr7	139788612	-8.394	0.180	Nkx1-2	3' UTR (NM_009123, exon 2 of 2)
chr5	102087602	-10.446	0.073	Nkx6-1	TTS (NM_144955)
chr5	102087595	-10.140	0.137	Nkx6-1	TTS (NM_144955)
chr3	26215139	-12.905	0.057	Nlgn1	PB1D10 SINE Alu
chr3	26129152	-16.373	0.064	Nlgn1	intron (NM_138666, intron 1 of 7)
chr3	26129259	-11.221	0.198	Nlgn1	intron (NM_138666, intron 1 of 7)
chr7	88064072	-11.638	0.062	Nmb	intron (NM_019951, intron 4 of 5)
chr16	4718549	7.402	0.153	Nmral1	intron (NM_026393, intron 1 of 5)
chr16	4718484	8.352	0.155	Nmral1	intron (NM_026393, intron 1 of 5)
chr16	4718505	7.111	0.157	Nmral1	intron (NM_026393, intron 1 of 5)
chr11	107126663	-16.499	0.075	Nol11	intron (NM_145823, intron 5 of 9)
chr11	107126652	-13.445	0.151	Nol11	intron (NM_145823, intron 5 of 9)
chr11	78736616	-23.087	0.043	Nos2	intron (NM_010927, intron 2 of 26)
chr11	78736667	-12.556	0.068	Nos2	intron (NM_010927, intron 2 of 26)
chr18	12392723	11.991	0.075	Npc1	intron (NM_008720, intron 1 of 24)
chr18	12392850	11.990	0.094	Npc1	intron (NM_008720, intron 1 of 24)
chr18	12392214	13.850	0.129	Npc1	intron (NM_008720, intron 1 of 24)
chr18	12392219	12.893	0.134	Npc1	intron (NM_008720, intron 1 of 24)
chr18	12392366	12.808	0.146	Npc1	intron (NM_008720, intron 1 of 24)
chr18	12392915	9.574	0.147	Npc1	intron (NM_008720, intron 1 of 24)
chr18	12392909	9.760	0.198	Npc1	intron (NM_008720, intron 1 of 24)
chr5	145309612	-14.739	0.147	Nptx2	intron (NM_016789, intron 2 of 4)
chr11	98632164	-13.235	0.138	Nr1d1	intron (NM_145434, intron 4 of 7)
chr11	98632921	10.879	0.159	Nr1d1	intron (NM_145434, intron 2 of 7)
chr10	42321583	-18.756	0.070	Nr2e1	Intergenic
chr10	42321599	-18.116	0.082	Nr2e1	Intergenic
chr7	77316578	12.741	0.096	Nr2f2	Intergenic
chr7	77316531	11.836	0.120	Nr2f2	Intergenic
chr1	139101192	-7.132	0.180	Nr5a2	Intergenic
chr1	139101200	-6.736	0.190	Nr5a2	Intergenic
chr1	138846582	11.570	0.193	Nr5a2	intron (NM_030676, intron 2 of 8)
chr18	36357451	6.250	0.051	Nrg2	promoter-TSS (NM_001167891)
chr18	36353484	-11.897	0.095	Nrg2	intron (NM_001167891, intron 1 of 9)
chr18	36353657	-7.691	0.167	Nrg2	intron (NM_001167891, intron 1 of 9)
chr18	36353555	-7.152	0.192	Nrg2	intron (NM_001167891, intron 1 of 9)
chr13	36817985	-15.517	0.014	Nrn1	3' UTR (NM_153529, exon 3 of 3)
chr13	36817682	-15.500	0.044	Nrn1	3' UTR (NM_153529, exon 3 of 3)
chr13	36817998	-8.884	0.144	Nrn1	3' UTR (NM_153529, exon 3 of 3)
chr13	36817904	9.823	0.166	Nrn1	3' UTR (NM_153529, exon 3 of 3)
chr2	33657565	14.424	0.089	Nron	intron (NM_175184, intron 7 of 9)
chr2	33657378	13.540	0.135	Nron	intron (NM_175184, intron 7 of 9)

chr2	33657551	11.580	0.177	Nron	intron (NM_175184, intron 7 of 9)
chr17	92031170	-17.460	0.033	Nrxn1	Intergenic
chr19	6421306	-21.868	0.044	Nrxn2	intron (NM_020253, intron 1 of 22)
chr19	6421169	-13.836	0.115	Nrxn2	intron (NM_020253, intron 1 of 22)
chr19	6421067	-13.267	0.159	Nrxn2	intron (NM_020253, intron 1 of 22)
chr5	38549600	13.105	0.105	Nsg1	intron (NM_010942, intron 2 of 4)
chr5	38549592	9.847	0.117	Nsg1	intron (NM_010942, intron 2 of 4)
chr5	38549510	10.702	0.155	Nsg1	intron (NM_010942, intron 2 of 4)
chr4	6440554	-13.701	0.089	Nsmaf	Intergenic
chr4	6440541	-10.473	0.145	Nsmaf	Intergenic
chr4	6440593	-12.393	0.174	Nsmaf	Intergenic
chr19	47043666	-16.429	0.064	Nt5c2	intron (NM_001164363, intron 1 of 17)
chr19	47043650	-9.540	0.071	Nt5c2	intron (NM_001164363, intron 1 of 17)
chr9	29557806	-18.666	0.059	Ntm	intron (NM_172290, intron 1 of 7)
chr11	68212880	-12.187	0.079	Ntn1	Intergenic
chr11	68212819	-10.124	0.101	Ntn1	Intergenic
chr11	68212795	-9.558	0.171	Ntn1	Intergenic
chr7	28046762	-14.632	0.158	Numbl	intron (NM_010950, intron 1 of 9)
chr2	90492274	-10.542	0.100	Nup160	Intergenic
chr2	90492287	-10.309	0.127	Nup160	Intergenic
chr2	90518891	-9.695	0.133	Nup160	intron (NM_021512, intron 1 of 36)
chr2	90518956	-5.030	0.192	Nup160	intron (NM_021512, intron 1 of 36)
chr11	76173989	-14.448	0.065	Nxn	intron (NM_008750, intron 1 of 7)
chr11	76194926	-9.062	0.162	Nxn	intron (NM_008750, intron 1 of 7)
chr11	76194939	-8.998	0.177	Nxn	intron (NM_008750, intron 1 of 7)
chr11	76173982	-9.390	0.190	Nxn	intron (NM_008750, intron 1 of 7)
chr11	76194902	-8.011	0.197	Nxn	intron (NM_008750, intron 1 of 7)
chr5	121287378	-14.300	0.044	Oas1f	Intergenic
chr10	58965150	18.075	0.049	Oit3	intron (NM_001033259, intron 1 of 7)
chr10	58965232	15.899	0.188	Oit3	intron (NM_001033259, intron 1 of 7)
chr1	172574266	14.286	0.012	Olfml2b	promoter-TSS (NM_177068)
chr3	103562579	13.991	0.154	Olfml3	exon (NM_010432, exon 8 of 16)
chr3	103562573	14.180	0.156	Olfml3	exon (NM_010432, exon 8 of 16)
chr9	39419905	-16.937	0.065	Olfr148	Intergenic
chr10	19179542	15.038	0.065	Olig3	Intergenic
chr10	19179537	10.900	0.122	Olig3	Intergenic
chr7	134910373	-14.667	0.039	Orai3	intron (NM_172748, intron 9 of 10)
chr18	13039127	22.772	0.031	Osbpl1a	promoter-TSS (NM_001252489)
chr15	6853953	8.346	0.069	Osmr	Intergenic
chr15	6853914	5.643	0.177	Osmr	Intergenic
chr14	49274059	-26.850	0.020	Otx2	Intergenic
chr14	49274274	-11.670	0.160	Otx2	Intergenic
chr15	41281054	-22.200	0.038	Oxr1	intron (NM_001130166, intron 1 of 16)
chr15	41267703	-12.521	0.131	Oxr1	intron (NR_106195, intron 3 of 4)
chr15	41267883	-11.135	0.135	Oxr1	intron (NR_106195, intron 3 of 4)
chr15	41280655	-12.929	0.192	Oxr1	intron (NM_001130166, intron 1 of 16)

chr15	41280787	-11.836	0.196	Oxr1	intron (NM_001130166, intron 1 of 16)
chr15	36579716	-14.079	0.071	Pabpc1	Intergenic
chr19	32713123	19.555	0.045	Papss2	intron (NM_011864, intron 4 of 12)
chr19	32713018	16.098	0.107	Papss2	intron (NM_011864, intron 4 of 12)
chr9	95452496	15.625	0.143	Paqr9	Intergenic
chr9	95452506	15.539	0.152	Paqr9	Intergenic
chr15	84061923	-8.209	0.071	Parvb	promoter-TSS (NM_133167)
chr15	84061937	-6.320	0.148	Parvb	promoter-TSS (NM_133167)
chr15	84114321	-14.280	0.115	Parvg	intron (NM_133167, intron 4 of 12)
chr15	84114413	-5.624	0.125	Parvg	intron (NM_133167, intron 4 of 12)
chr10	107891888	13.590	0.153	Pawr	Intergenic
chr1	78078405	11.340	0.122	Pax3	Intergenic
chr1	78078542	10.922	0.139	Pax3	Intergenic
chr2	24328596	-10.106	0.089	Pax8	intron (NM_011040, intron 2 of 11)
chr18	38293003	-20.181	0.028	Pcdh1	Intergenic
chr18	37516757	-14.133	0.136	Pcdhb8	exon (NM_053133, exon 1 of 1)
chr18	37979756	-12.089	0.180	Pcdhgc5	exon (NM_033583, exon 1 of 4)
chr18	37979970	-10.000	0.182	Pcdhgc5	exon (NM_033583, exon 1 of 4)
chr15	97035095	15.320	0.098	Pced1b	Intergenic
chr15	97035190	8.352	0.129	Pced1b	Intergenic
chr12	82946132	-11.058	0.173	Pcnx	Intergenic
chr13	75365565	18.798	0.082	Pcsk1	Intergenic
chr13	75365567	16.483	0.128	Pcsk1	Intergenic
chr2	79967237	12.297	0.045	Pde1a	intron (NM_001159582, intron 2 of 15)
chr2	79967160	9.553	0.146	Pde1a	intron (NM_001159582, intron 2 of 15)
chr9	20988058	16.148	0.065	Pde4a	intron (NM_183408, intron 1 of 14)
chr9	20988076	16.965	0.105	Pde4a	intron (NM_183408, intron 1 of 14)
chr4	102330050	-17.292	0.134	Pde4b	Intergenic
chr4	102330052	-15.711	0.147	Pde4b	Intergenic
chr4	102330061	-13.889	0.148	Pde4b	Intergenic
chr3	97607867	-13.765	0.054	Pde4dip	intron (NM_001039376, intron 4 of 46)
chr1	88468624	-14.474	0.065	Pde6d	intron (NM_008801, intron 1 of 4)
chr1	88468071	-10.961	0.101	Pde6d	intron (NM_008801, intron 1 of 4)
chr1	88468594	-10.427	0.146	Pde6d	intron (NM_008801, intron 1 of 4)
chr4	11892345	12.539	0.162	Pdp1	intron (NM_001033453, intron 1 of 1)
chr4	11892119	13.808	0.175	Pdp1	intron (NM_001033453, intron 1 of 1)
chr2	129574053	-12.284	0.161	Pdyn	Intergenic
chr2	129574073	-12.304	0.171	Pdyn	Intergenic
chr6	101167856	14.868	0.042	Pdzrn3	intron (NM_018884, intron 3 of 9)
chr6	101167882	10.643	0.128	Pdzrn3	intron (NM_018884, intron 3 of 9)
chr6	101167890	10.827	0.184	Pdzrn3	intron (NM_018884, intron 3 of 9)
chr15	92427602	13.346	0.046	Pdzrn4	promoter-TSS (NM_001164594)
chr15	92427608	11.709	0.089	Pdzrn4	promoter-TSS (NM_001164594)
chr15	92427590	11.236	0.136	Pdzrn4	promoter-TSS (NM_001164594)
chr15	92427583	6.314	0.193	Pdzrn4	promoter-TSS (NM_001164594)
chr8	126894447	-13.483	0.155	Pgbd5	exon (NM_171824, exon 7 of 7)

chr13	43023486	-15.143	0.114	Phactr1	intron (NM_001005740, intron 1 of 12)
chr13	43023513	-13.756	0.134	Phactr1	intron (NM_001005740, intron 1 of 12)
chr13	43023529	-12.257	0.146	Phactr1	intron (NM_001005740, intron 1 of 12)
chr13	48873474	-24.055	0.027	Phf2	Intergenic
chr7	25404661	15.528	0.102	Phldb3	intron (NM_001102613, intron 7 of 14)
chr5	67530422	12.498	0.126	Phox2b	Intergenic
chr5	67530030	8.672	0.185	Phox2b	Intergenic
chr4	133230582	-10.611	0.155	Pigv	Intergenic
chr4	133230393	-10.791	0.183	Pigv	Intergenic
chr11	84693007	-10.149	0.034	Pigw	promoter-TSS (NM_025414)
chr13	102522342	-19.768	0.053	Pik3r1	intron (NM_001077495, intron 2 of 15)
chr9	14502338	-14.620	0.047	Piwil4	Intergenic
chr3	142599123	19.539	0.035	Pkn2	Intergenic
chr3	142599005	14.250	0.077	Pkn2	Intergenic
chr3	142599106	13.302	0.153	Pkn2	Intergenic
chr16	16197518	-12.486	0.098	Pkp2	Intergenic
chr16	16197494	-17.122	0.118	Pkp2	Intergenic
chr16	16197571	-10.832	0.192	Pkp2	Intergenic
chr3	129566330	-8.425	0.170	Pla2g12a	intron (NM_007686, intron 8 of 13)
chr1	151808030	-9.647	0.057	Pla2g4a	intron (NM_008869, intron 1 of 17)
chr1	151808932	-8.230	0.095	Pla2g4a	promoter-TSS (NM_008869)
chr1	151808919	-7.859	0.126	Pla2g4a	promoter-TSS (NM_008869)
chr1	151808542	-14.264	0.126	Pla2g4a	promoter-TSS (NM_008869)
chr15	79164127	-20.615	0.035	Pla2g6	Intergenic
chr15	79164134	-16.123	0.083	Pla2g6	Intergenic
chr9	50041309	11.667	0.043	Plet1	Intergenic
chr13	111191591	-19.661	0.036	Plk2	TTS (NM_152804)
chr13	111188641	-10.740	0.082	Plk2	exon (NM_152804, exon 9 of 14)
chr13	111191085	-13.344	0.162	Plk2	TTS (NM_152804)
chr13	111188711	-9.591	0.177	Plk2	intron (NM_152804, intron 9 of 13)
chr13	111191277	-8.972	0.185	Plk2	TTS (NM_152804)
chr13	111191474	10.898	0.186	Plk2	TTS (NM_152804)
chr6	32589121	-9.062	0.183	Plxna4	Intergenic
chr9	58090183	-16.204	0.036	Pml	intron (NM_178087, intron 2 of 8)
chr9	58090198	-13.466	0.106	Pml	intron (NM_178087, intron 2 of 8)
chr14	51563904	-6.481	0.042	Pnp	promoter-TSS (NM_013632)
chr8	23780437	14.110	0.076	Polb	PB1D7 SINE Alu
chr8	23780491	12.761	0.103	Polb	PB1D7 SINE Alu
chr8	23780394	9.423	0.192	Polb	intron (NM_001159774, intron 12 of 21)
chr5	115690215	-14.000	0.159	Pop5	exon (NM_026398, exon 4 of 6)
chr5	136145887	23.318	0.020	Por	Intergenic
chr1	167792006	19.666	0.048	Pou2f1	3' UTR (NM_001113391, exon 8 of 8)
chr3	133002334	-12.980	0.088	Ppa2	intron (NM_146141, intron 6 of 11)
chr3	133002331	-11.161	0.135	Ppa2	intron (NM_146141, intron 6 of 11)
chr3	133002325	-9.432	0.171	Ppa2	intron (NM_146141, intron 6 of 11)
chr13	113622257	9.812	0.071	Ppap2a	CpG

chr13	113622406	6.259	0.141	Ppap2a	CpG
chr4	104876528	-15.942	0.080	Ppap2b	intron (NM_080555, intron 2 of 5)
chr4	104918635	-9.100	0.157	Ppap2b	Intergenic
chr10	6938887	-8.236	0.060	Ppp1r14c	intron (NM_133485, intron 1 of 3)
chr17	36008186	-11.900	0.068	Ppp1r18	intron (NM_001146710, intron 2 of 3)
chr17	36008178	-9.461	0.139	Ppp1r18	intron (NM_001146710, intron 2 of 3)
chr8	36497022	-29.648	0.010	Ppp1r3b	Intergenic
chr14	55494542	-18.685	0.071	Ppp1r3e	3' UTR (NM_001167908, exon 2 of 2)
chr14	55494825	-6.583	0.114	Ppp1r3e	3' UTR (NM_001167908, exon 2 of 2)
chr14	55494546	-16.071	0.117	Ppp1r3e	3' UTR (NM_001167908, exon 2 of 2)
chrX	7148003	17.862	0.074	Ppp1r3fos	intron (NM_138605, intron 1 of 3)
chr14	67688741	-12.030	0.152	Ppp2r2a	intron (NM_028032, intron 2 of 9)
chr3	136406060	-16.058	0.121	Ppp3ca	intron (NM_008913, intron 1 of 13)
chr4	142828646	-13.800	0.063	Prdm2	Intergenic
chr10	44571165	7.960	0.056	Prep	Intergenic
chr17	85487799	-9.118	0.034	Prepl	exon (NM_001163622, exon 2 of 15)
chr17	85487953	-15.476	0.035	Prepl	5' UTR (NM_001163622, exon 2 of 15)
chr17	85487807	-8.922	0.071	Prepl	exon (NM_001163622, exon 2 of 15)
chr17	85487802	-7.735	0.193	Prepl	exon (NM_001163622, exon 2 of 15)
chr15	93582438	-22.970	0.024	Prickle1	Intergenic
chr15	93582483	-19.302	0.026	Prickle1	Intergenic
chr15	93582443	-19.921	0.035	Prickle1	Intergenic
chr15	93582558	-12.944	0.102	Prickle1	Intergenic
chr15	93582403	-15.043	0.173	Prickle1	Intergenic
chr15	93582486	-10.903	0.174	Prickle1	Intergenic
chr15	93582703	12.642	0.183	Prickle1	Intergenic
chr6	92678443	7.302	0.088	Prickle2	Intergenic
chr6	92678439	6.035	0.129	Prickle2	Intergenic
chr5	116412150	-22.745	0.038	Prkab1	intron (NM_007708, intron 23 of 46)
chr5	24590768	-19.318	0.019	Prkag2	intron (NM_145401, intron 1 of 15)
chr5	24412739	-10.532	0.155	Prkag2	TTS (NR_040684)
chr5	24590639	-11.721	0.189	Prkag2	intron (NM_145401, intron 1 of 15)
chr11	108105374	-14.211	0.131	Prkca	intron (NM_011101, intron 2 of 16)
chr17	79391968	18.686	0.094	Prkd3	intron (NM_001171004, intron 2 of 18)
chr11	75301237	-14.901	0.060	Prpf8	exon (NM_138659, exon 2 of 42)
chr11	75301270	-11.011	0.161	Prpf8	exon (NM_138659, exon 2 of 42)
chr2	101591701	23.058	0.035	Prr5l	intron (NM_001110849, intron 5 of 9)
chr8	98123722	31.545	0.008	Prss54	Intergenic
chr8	98123729	19.929	0.055	Prss54	Intergenic
chr8	98123709	13.521	0.191	Prss54	Intergenic
chr19	17200111	-10.808	0.157	Prune2	exon (NM_181348, exon 9 of 20)
chr19	17200097	-9.946	0.178	Prune2	exon (NM_181348, exon 9 of 20)
chr9	55923502	-11.779	0.168	Pstpip1	Intergenic
chr3	119647267	28.128	0.002	Ptbp2	Intergenic
chr2	30774465	-15.652	0.108	Ptges	Intergenic
chr2	30774222	-14.574	0.127	Ptges	Intergenic



chr2	30774345	-12.479	0.140	Ptges	Intergenic
chr2	30774482	-10.089	0.185	Ptges	Intergenic
chr14	66884698	-14.621	0.094	Ptk2b	intron (NM_001162365, intron 1 of 30)
chr14	66884471	-15.347	0.129	Ptk2b	intron (NM_001162365, intron 1 of 30)
chr7	52123407	14.452	0.064	Ptov1	intron (NM_133949, intron 1 of 11)
chr10	107185032	8.317	0.130	Ptprq	Intergenic
chr18	36444107	-13.725	0.117	Pura	intron (NM_008989, intron 1 of 1)
chr18	36444323	-15.735	0.122	Pura	intron (NM_008989, intron 1 of 1)
chr15	94348602	-14.469	0.084	Pus7l	Intergenic
chr15	94309606	-16.071	0.089	Pus7l	Intergenic
chr15	94309323	-14.172	0.089	Pus7l	Intergenic
chr15	94348594	-13.583	0.095	Pus7l	Intergenic
chr15	94309373	-14.402	0.136	Pus7l	Intergenic
chr15	94309366	-15.246	0.139	Pus7l	Intergenic
chr15	94348535	-11.806	0.146	Pus7l	Intergenic
chr15	94309351	-13.710	0.171	Pus7l	Intergenic
chr15	94309454	13.391	0.192	Pus7l	Intergenic
chr15	61870840	-16.676	0.075	Pvt1	intron (NR_003368, intron 1 of 8)
chr15	61870953	-13.040	0.122	Pvt1	intron (NR_003368, intron 1 of 8)
chr14	8932540	14.451	0.089	Pxk	intron (NM_178279, intron 1 of 18)
chr14	8932273	9.630	0.182	Pxk	intron (NM_178279, intron 1 of 18)
chr1	157653143	-10.190	0.135	Qsox1	intron (NM_001024945, intron 1 of 11)
chr1	157653033	-9.357	0.138	Qsox1	intron (NM_001024945, intron 1 of 11)
chr1	157653022	-8.227	0.186	Qsox1	intron (NM_001024945, intron 1 of 11)
chr1	157653026	-7.983	0.197	Qsox1	intron (NM_001024945, intron 1 of 11)
chr1	157653131	-8.195	0.198	Qsox1	intron (NM_001024945, intron 1 of 11)
chr17	26204488	17.542	0.028	Rab11fip3	intron (NM_001162868, intron 1 of 13)
chr17	66857072	10.212	0.133	Rab12	intron (NM_024448, intron 1 of 5)
chr17	66857102	13.145	0.139	Rab12	intron (NM_024448, intron 1 of 5)
chr1	187029247	-21.246	0.020	Rab3gap2	intron (NM_001163754, intron 1 of 34)
chr8	126347836	18.196	0.078	Rab4a	intron (NM_009003, intron 2 of 7)
chr8	126347747	16.236	0.087	Rab4a	exon (NM_009003, exon 2 of 8)
chr8	126322010	10.880	0.092	Rab4a	Intergenic
chr8	126322076	9.348	0.129	Rab4a	Intergenic
chr8	126322245	10.438	0.152	Rab4a	Intergenic
chr8	126347739	11.753	0.174	Rab4a	exon (NM_009003, exon 2 of 8)
chr8	126347867	13.986	0.190	Rab4a	intron (NM_009003, intron 2 of 7)
chr7	133571962	-6.657	0.064	Rabep2	promoter-TSS (NM_030566)
chr15	10617507	9.656	0.161	Rai14	intron (NM_001166408, intron 2 of 17)
chr15	10617582	13.184	0.182	Rai14	intron (NM_001166408, intron 2 of 17)
chr2	158234993	-14.644	0.089	Ralgapb	promoter-TSS (NM_177658)
chr2	158234843	-13.434	0.167	Ralgapb	promoter-TSS (NM_177658)
chr2	158234982	-9.990	0.198	Ralgapb	promoter-TSS (NM_177658)
chr1	158925646	11.315	0.137	Ralgps2	Intergenic
chr5	129524650	-14.963	0.031	Ran	Intergenic
chr5	129524808	-14.412	0.139	Ran	Intergenic

chr4	137221657	-17.057	0.103	Rap1gap	intron (NM_029563, intron 1 of 23)
chr11	98697734	6.951	0.193	Rapgef11	promoter-TSS (NM_001080925)
chr14	17406811	-14.888	0.095	Rarb	intron (NM_011243, intron 1 of 7)
chr14	17406753	-10.615	0.114	Rarb	intron (NM_011243, intron 1 of 7)
chr14	17406842	-12.087	0.153	Rarb	intron (NM_011243, intron 1 of 7)
chr2	131865604	-20.873	0.026	Rassf2	Intergenic
chr2	131865606	-15.134	0.088	Rassf2	Intergenic
chr2	131865630	-15.014	0.113	Rassf2	Intergenic
chr2	131865619	-12.864	0.183	Rassf2	Intergenic
chr6	145675719	-9.670	0.139	Rassf8	Intergenic
chr6	145675781	-5.747	0.181	Rassf8	Intergenic
chr16	7049696	-19.859	0.051	Rbfox1	intron (NM_021477, intron 5 of 16)
chr8	93502918	-8.611	0.065	Rbl2	intron (NM_177224, intron 9 of 39)
chr8	93605826	-11.444	0.065	Rbl2	intron (NM_001282000, intron 4 of 20)
chr8	93605723	-11.780	0.145	Rbl2	intron (NM_001282000, intron 4 of 20)
chr8	93502489	-12.007	0.176	Rbl2	intron (NM_177224, intron 8 of 39)
chr13	46456902	-14.961	0.133	Rbm24	Intergenic
chr13	46456151	-11.439	0.192	Rbm24	Intergenic
chr5	66470671	12.245	0.020	Rbm47	intron (NM_001127382, intron 3 of 7)
chr5	53900396	-11.357	0.079	Rbpj	Intergenic
chr5	53900945	-12.783	0.090	Rbpj	Intergenic
chr8	35098500	10.438	0.185	Rbpms	Intergenic
chr16	92421193	-10.767	0.146	Rcan1	intron (NM_001081549, intron 1 of 3)
chr16	92421882	-11.254	0.147	Rcan1	intron (NM_001081549, intron 1 of 3)
chr10	66568177	-21.096	0.031	Reep3	Intergenic
chr10	66568144	-14.977	0.104	Reep3	Intergenic
chr10	66568150	-14.446	0.113	Reep3	Intergenic
chr14	79731519	13.545	0.137	Rgcc	Intergenic
chr7	135562617	-7.704	0.106	Rgs10	promoter-TSS (NM_026418)
chr1	145763773	-24.814	0.037	Rgs2	Intergenic
chr12	83719280	-17.620	0.031	Rgs6	intron (NM_001282061, intron 1 of 16)
chr12	83719278	-18.554	0.035	Rgs6	intron (NM_001282061, intron 1 of 16)
chr12	83719288	-13.039	0.129	Rgs6	intron (NM_001282061, intron 1 of 16)
chr11	32121105	-16.818	0.029	Rhbdf1	intron (NM_010117, intron 1 of 17)
chr11	32121126	-8.035	0.199	Rhbdf1	intron (NM_010117, intron 1 of 17)
chr10	84371891	-18.834	0.052	Ric8b	Intergenic
chr10	84372004	13.108	0.106	Ric8b	Intergenic
chr10	84372096	15.491	0.122	Ric8b	Intergenic
chr10	84372099	14.646	0.150	Ric8b	Intergenic
chr2	163742363	-18.259	0.043	Rims4	intron (NM_183023, intron 1 of 5)
chr2	163742823	-13.611	0.146	Rims4	intron (NM_183023, intron 1 of 5)
chr2	163742376	-12.189	0.198	Rims4	intron (NM_183023, intron 1 of 5)
chr8	108213645	-15.025	0.153	Rltpr	Intergenic
chr8	108213635	-14.192	0.176	Rltpr	Intergenic
chr8	108213655	-12.471	0.196	Rltpr	Intergenic
chr6	47713991	-7.410	0.026	Rn4.5s	CpG

chr6	47694588	-8.177	0.028	Rn4.5s	promoter-TSS (NR_002841).10
chr6	47714308	-21.805	0.030	Rn4.5s	RMER12B LTR ERVK
chr6	47694538	-6.865	0.071	Rn4.5s	promoter-TSS (NR_002841).10
chr6	47703548	-6.628	0.093	Rn4.5s	promoter-TSS (NR_002841).6
chr6	47694636	-5.056	0.101	Rn4.5s	promoter-TSS (NR_002841).10
chr6	47610482	-9.434	0.113	Rn4.5s	RMER12B LTR ERVK
chr6	47694552	-5.647	0.113	Rn4.5s	promoter-TSS (NR_002841).10
chr6	47714022	-5.532	0.115	Rn4.5s	CpG
chr6	47714297	-13.924	0.127	Rn4.5s	Intergenic
chr6	47694816	-5.273	0.135	Rn4.5s	promoter-TSS (NR_002841).10
chr6	47694545	-5.386	0.139	Rn4.5s	promoter-TSS (NR_002841).10
chr6	47614714	7.990	0.157	Rn4.5s	promoter-TSS (NR_002841).3
chr6	47714081	-12.776	0.161	Rn4.5s	CpG
chr6	47694526	-5.367	0.181	Rn4.5s	promoter-TSS (NR_002841).10
chr6	47714075	-10.855	0.185	Rn4.5s	CpG
chr6	47631815	-5.476	0.188	Rn4.5s	promoter-TSS (NR_002841).8
chr6	47610287	-10.253	0.189	Rn4.5s	promoter-TSS (NR_002841).2
chr6	47703576	-6.286	0.190	Rn4.5s	promoter-TSS (NR_002841).6
chr6	47703528	-5.167	0.195	Rn4.5s	promoter-TSS (NR_002841).6
chr6	47631948	-9.036	0.199	Rn4.5s	promoter-TSS (NR_002841).8
chr14	52549595	11.248	0.133	Rnase13	Intergenic
chr14	52549601	10.552	0.135	Rnase13	(CAGA)n Simple_repeat Simple_repeat
chr14	52549963	16.480	0.139	Rnase13	Intergenic
chr18	21120946	-12.133	0.146	Rnf125	intron (NM_026301, intron 1 of 5)
chr1	107071849	15.532	0.057	Rnf152	Intergenic
chr13	43710124	17.984	0.113	Rnf182	Intergenic
chr13	43710130	15.120	0.153	Rnf182	Intergenic
chr4	128735073	5.682	0.059	Rnf19b	promoter-TSS (NM_029219)
chr11	87478838	12.636	0.074	Rnf43	intron (NM_172448, intron 2 of 9)
chr11	87478802	9.836	0.133	Rnf43	intron (NM_172448, intron 2 of 9)
chr16	73106356	-10.746	0.171	Robo1	Intergenic
chr16	73106400	-11.484	0.171	Robo1	Intergenic
chr9	37192569	-12.308	0.177	Robo4	3' UTR (NM_175189, exon 7 of 7)
chr2	155971073	-8.170	0.062	Romo1	intron (NM_001164216, intron 2 of 2)
chr2	155971717	-10.582	0.101	Romo1	TTS (NM_025946)
chr15	97337832	-12.153	0.076	Rpap3	Intergenic
chr15	97337818	-8.751	0.167	Rpap3	Intergenic
chr15	97337800	-7.856	0.193	Rpap3	Intergenic
chr9	61517831	-14.364	0.045	Rplp1	Intergenic
chr9	61517844	-9.508	0.134	Rplp1	Intergenic
chr9	61517952	-7.061	0.169	Rplp1	Intergenic
chr4	133372366	-17.809	0.035	Rps6ka1	Intergenic
chr4	133372356	-13.117	0.153	Rps6ka1	Intergenic
chr4	33083081	7.050	0.113	Rragd	intron (NM_027491, intron 2 of 6)
chr4	33083076	7.016	0.180	Rragd	intron (NM_027491, intron 2 of 6)
chr7	121202529	-10.317	0.150	Rras2	exon (NM_025846, exon 3 of 6)

chr13	37946187	-13.179	0.038	Rreb1	intron (NM_001039188, intron 1 of 9)
chr13	38026910	14.811	0.096	Rreb1	3' UTR (NM_026830, exon 10 of 10)
chr13	37946195	-6.472	0.169	Rreb1	intron (NM_001039188, intron 1 of 9)
chr13	37946143	-9.124	0.175	Rreb1	intron (NM_001039188, intron 1 of 9)
chr13	37946206	-11.202	0.193	Rreb1	intron (NM_001039188, intron 1 of 9)
chr5	20458302	13.297	0.075	Rsb1l1	promoter-TSS (NM_001080977)
chr12	73334539	-21.082	0.023	Rtn1	intron (NM_001286448, intron 1 of 6)
chr12	73334340	-17.144	0.092	Rtn1	intron (NM_001286448, intron 1 of 6)
chr12	73507465	12.791	0.103	Rtn1	intron (NM_153457, intron 1 of 8)
chr12	73334562	-14.640	0.106	Rtn1	intron (NM_001286448, intron 1 of 6)
chr12	73507487	13.848	0.129	Rtn1	intron (NM_153457, intron 1 of 8)
chr12	73334335	-13.702	0.169	Rtn1	intron (NM_001286448, intron 1 of 6)
chr11	75068299	-13.154	0.048	Rtn4r1	intron (NM_177708, intron 1 of 1)
chr11	75068365	-12.389	0.132	Rtn4r1	intron (NM_177708, intron 1 of 1)
chr17	44610012	14.659	0.064	Runx2	Intergenic
chr17	44610021	9.407	0.167	Runx2	Intergenic
chr4	43420518	-15.975	0.091	Rusc2	intron (NM_199057, intron 1 of 11)
chr4	43420582	-12.678	0.134	Rusc2	intron (NM_199057, intron 1 of 11)
chr4	43420291	-13.112	0.174	Rusc2	intron (NM_199057, intron 1 of 11)
chr1	169481676	-14.087	0.106	Rxrg	Intergenic
chr6	100120784	-7.195	0.157	Rybp	Intergenic
chr3	93368573	13.117	0.034	S100a10	TTS (NM_009112)
chr9	20787627	-15.754	0.059	S1pr2	Intergenic
chr18	81248719	14.901	0.078	Sall3	Intergenic
chr17	51924148	16.329	0.101	Satb1	intron (NM_001163632, intron 6 of 10)
chr1	56907488	-28.257	0.024	Satb2	intron (NM_139146, intron 7 of 10)
chr1	56907475	-21.848	0.046	Satb2	intron (NM_139146, intron 7 of 10)
chr1	56907463	-14.238	0.180	Satb2	intron (NM_139146, intron 7 of 10)
chr17	3140789	-19.646	0.034	Scaf8	intron (NM_134123, intron 1 of 19)
chr12	40867331	-13.528	0.122	Scin	Intergenic
chr12	40867310	-10.113	0.153	Scin	Intergenic
chr2	66278074	-13.745	0.061	Scn1a	promoter-TSS (NR_033495)
chr2	66278027	-11.869	0.197	Scn1a	promoter-TSS (NR_033495)
chr7	31909678	-18.568	0.064	Scn1b	RSINE1 SINE B4
chr7	31909877	-12.808	0.129	Scn1b	PB1D10 SINE Alu
chr2	65506366	-9.524	0.031	Scn2a1	Intergenic
chr15	32660678	-19.639	0.063	Sdc2	Intergenic
chr2	164267512	16.154	0.093	Sdc4	intron (NM_011521, intron 1 of 4)
chr2	164267709	9.615	0.165	Sdc4	intron (NM_011521, intron 1 of 4)
chr10	127388688	11.596	0.116	Sdr9c7	Intergenic
chr10	127388763	6.050	0.194	Sdr9c7	Intergenic
chr18	65911780	-18.487	0.039	Sec11c	TTS (NM_177028)
chr18	65911888	-11.485	0.147	Sec11c	TTS (NM_177028)
chr18	65911772	-12.321	0.151	Sec11c	TTS (NM_177028)
chr11	116978112	-14.877	0.016	Sec14l1	intron (NM_001166507, intron 1 of 16)
chr11	116978079	-13.333	0.064	Sec14l1	intron (NM_001166507, intron 1 of 16)

chr3	94497141	6.104	0.049	Selenbp2	promoter-TSS (NM_019414)
chr3	94497559	-12.917	0.079	Selenbp2	promoter-TSS (NM_019414)
chr3	94497291	5.904	0.195	Selenbp2	promoter-TSS (NM_019414)
chr16	35604380	11.312	0.078	Sema5b	intron (NM_013661, intron 1 of 21)
chr16	35542934	-9.960	0.131	Sema5b	intron (NM_013661, intron 1 of 21)
chr3	94963353	-13.162	0.181	Sema6c	promoter-TSS (NM_001272024)
chr11	117021384	-23.011	0.018	Sep-09	TTS (NM_028777)
chr11	117021391	-16.087	0.078	Sep-09	TTS (NM_028777)
chr11	117021411	-13.413	0.139	Sep-09	TTS (NM_028777)
chr14	76969363	-14.475	0.020	Serp2	Intergenic
chr14	76969007	-12.679	0.043	Serp2	Intergenic
chr14	76969138	-10.765	0.120	Serp2	Intergenic
chr14	76969324	-6.479	0.193	Serp2	Intergenic
chr5	123603324	-7.937	0.078	Setd1b	intron (NM_001040398, intron 7 of 16)
chr1	167121982	-13.802	0.094	Sft2d2	intron (NM_145512, intron 1 of 7)
chr1	167121955	-10.091	0.163	Sft2d2	intron (NM_145512, intron 1 of 7)
chr1	167121968	-8.909	0.166	Sft2d2	intron (NM_145512, intron 1 of 7)
chr6	85236711	17.903	0.051	Sfxn5	intron (NM_178639, intron 6 of 13)
chr6	85236665	-14.257	0.088	Sfxn5	intron (NM_178639, intron 6 of 13)
chr6	85236539	-10.547	0.099	Sfxn5	intron (NM_178639, intron 6 of 13)
chr6	85236935	-10.983	0.177	Sfxn5	intron (NM_178639, intron 6 of 13)
chr6	85236442	-8.344	0.178	Sfxn5	intron (NM_178639, intron 6 of 13)
chr10	21717739	-17.253	0.038	Sgk1	exon (NM_001161849, exon 10 of 12)
chr10	21666652	-11.354	0.072	Sgk1	intron (NM_001161845, intron 2 of 13)
chr10	21717827	-14.452	0.075	Sgk1	exon (NM_001161849, exon 10 of 12)
chr10	21666720	-10.014	0.131	Sgk1	intron (NM_001161845, intron 2 of 13)
chr10	21666508	-7.900	0.184	Sgk1	intron (NM_001161845, intron 2 of 13)
chr10	21717708	-10.656	0.197	Sgk1	exon (NM_001161849, exon 10 of 12)
chr19	32333735	-10.962	0.035	Sgms1	intron (NM_144792, intron 3 of 9)
chr19	32270842	-14.712	0.089	Sgms1	intron (NM_001168525, intron 5 of 9)
chr19	32270754	-14.686	0.135	Sgms1	intron (NM_001168525, intron 5 of 9)
chr19	32270750	-9.985	0.153	Sgms1	intron (NM_001168525, intron 5 of 9)
chr19	32333765	-6.762	0.175	Sgms1	intron (NM_144792, intron 3 of 9)
chr7	133613812	-12.473	0.060	Sh2b1	intron (NM_001081459, intron 5 of 9)
chr8	70657159	26.621	0.025	Sh2d4a	Intergenic
chr1	90993008	14.851	0.089	Sh3bp4	intron (NM_133816, intron 1 of 5)
chr1	90993002	12.840	0.162	Sh3bp4	intron (NM_133816, intron 1 of 5)
chr11	32284445	13.116	0.113	Sh3pxd2b	intron (NM_177364, intron 3 of 12)
chr11	32284376	12.324	0.130	Sh3pxd2b	intron (NM_177364, intron 3 of 12)
chr11	32284273	7.766	0.143	Sh3pxd2b	intron (NM_177364, intron 3 of 12)
chr7	28153327	-13.174	0.086	Shkbp1	intron (NM_032610, intron 26 of 35)
chr7	28153306	-12.944	0.092	Shkbp1	intron (NM_032610, intron 26 of 35)
chr7	28153189	-9.806	0.178	Shkbp1	intron (NM_032610, intron 26 of 35)
chr7	28153211	-8.837	0.190	Shkbp1	intron (NM_032610, intron 26 of 35)
chr8	89281106	-10.686	0.030	Siah1a	Intergenic
chr8	89281420	-10.712	0.153	Siah1a	Intergenic

chr8	89281188	-8.955	0.161	Siah1a	Intergenic
chr8	89281624	-12.661	0.178	Siah1a	Intergenic
chrX	160513186	-21.047	0.036	Siah1b	intron (NM_009173, intron 2 of 3)
chr17	31909281	14.448	0.034	Sik1	Intergenic
chr17	31909193	15.742	0.069	Sik1	Intergenic
chr9	45836328	-11.901	0.065	Sik3	intron (NM_027498, intron 1 of 24)
chr17	86089237	-7.572	0.196	Six2	Intergenic
chr4	154609559	-9.639	0.036	Ski	Intergenic
chr4	154609556	-9.197	0.065	Ski	Intergenic
chr8	108483202	-13.818	0.063	Slc12a4	intron (NM_001253804, intron 3 of 23)
chr8	108483271	-9.379	0.185	Slc12a4	exon (NM_009195, exon 3 of 24)
chr16	33558247	-22.970	0.034	Slc12a8	intron (NM_001083902, intron 4 of 11)
chr10	124975695	20.285	0.034	Slc16a7	Intergenic
chr15	8545043	-17.006	0.024	Slc1a3	Intergenic
chr15	8545026	-13.930	0.045	Slc1a3	Intergenic
chr15	8545679	9.323	0.064	Slc1a3	Intergenic
chr11	20336739	-20.931	0.035	Slc1a4	Intergenic
chr17	12704182	7.749	0.054	Slc22a3	Intergenic
chr17	12704109	7.907	0.080	Slc22a3	Intergenic
chr2	124731123	15.805	0.035	Slc24a5	Intergenic
chr4	45440495	10.186	0.077	Slc25a51	intron (NM_001033306, intron 5 of 5)
chr4	45440598	9.206	0.101	Slc25a51	MIRc SINE MIR
chr5	21352772	-12.573	0.044	Slc26a5	MTE2a LTR MaLR
chr5	21352995	-11.039	0.130	Slc26a5	intron (NM_030727, intron 3 of 19)
chr5	21352991	-10.567	0.165	Slc26a5	intron (NM_030727, intron 3 of 19)
chr13	58615712	-16.565	0.061	Slc28a3	Intergenic
chr4	149537309	8.127	0.150	Slc2a7	exon (NM_001085529, exon 9 of 12)
chr5	38894339	-7.181	0.079	Slc2a9	promoter-TSS (NM_145559)
chr5	38894352	-8.162	0.119	Slc2a9	promoter-TSS (NM_145559)
chr13	101631915	14.565	0.035	Slc30a5	Intergenic
chr13	101631823	9.671	0.072	Slc30a5	Intergenic
chr19	38458460	13.225	0.035	Slc35g1	L1M3 LINE L1
chr19	38458465	13.106	0.052	Slc35g1	L1M3 LINE L1
chr19	38458444	7.332	0.099	Slc35g1	Intergenic
chr15	96528120	-15.310	0.040	Slc38a2	intron (NM_175121, intron 4 of 15)
chr15	96628096	-15.336	0.061	Slc38a2	Intergenic
chr15	96528530	-14.508	0.064	Slc38a2	intron (NM_175121, intron 3 of 15)
chr15	96628123	-15.974	0.074	Slc38a2	Intergenic
chr15	96525398	-12.339	0.102	Slc38a2	intron (NM_175121, intron 7 of 15)
chr15	96522831	-12.003	0.108	Slc38a2	exon (NM_175121, exon 12 of 16)
chr15	96528201	-9.500	0.133	Slc38a2	intron (NM_175121, intron 4 of 15)
chr15	96528050	-6.602	0.167	Slc38a2	intron (NM_175121, intron 4 of 15)
chr15	96522620	-9.905	0.175	Slc38a2	intron (NM_175121, intron 12 of 15)
chr15	96522745	-8.256	0.176	Slc38a2	exon (NM_175121, exon 12 of 16)
chr15	96886150	19.449	0.042	Slc38a4	intron (NM_027052, intron 1 of 15)
chr15	96886130	18.488	0.052	Slc38a4	intron (NM_027052, intron 1 of 15)

chr15	96886142	17.201	0.063	Slc38a4	intron (NM_027052, intron 1 of 15)
chr15	96886144	17.334	0.065	Slc38a4	intron (NM_027052, intron 1 of 15)
chr15	96886170	17.160	0.097	Slc38a4	(CA)n Simple_repeat Simple_repeat
chr15	96886250	16.469	0.106	Slc38a4	intron (NM_027052, intron 1 of 15)
chr15	96886146	14.355	0.119	Slc38a4	intron (NM_027052, intron 1 of 15)
chr15	96886172	15.710	0.133	Slc38a4	(CA)n Simple_repeat Simple_repeat
chr15	96886308	14.673	0.157	Slc38a4	promoter-TSS (NM_027052)
chr15	96886168	13.781	0.163	Slc38a4	(CA)n Simple_repeat Simple_repeat
chr15	96886126	11.671	0.180	Slc38a4	intron (NM_027052, intron 1 of 15)
chr8	98377002	-8.308	0.064	Slc38a7	intron (NM_172758, intron 1 of 11)
chr8	98377063	-6.611	0.197	Slc38a7	intron (NM_172758, intron 1 of 11)
chr19	8770091	13.505	0.144	Slc3a2	Intergenic
chr19	8770104	13.650	0.171	Slc3a2	Intergenic
chr1	45983547	-14.782	0.122	Slc40a1	Intergenic
chr1	45983437	-14.588	0.162	Slc40a1	promoter-TSS (NM_016917)
chr4	53451751	-19.359	0.035	Slc44a1	Intergenic
chr4	53399359	-10.908	0.185	Slc44a1	Intergenic
chr4	53399659	-13.197	0.192	Slc44a1	Intergenic
chr7	130342668	-15.005	0.047	Slc5a11	Intergenic
chr7	130342788	-15.200	0.095	Slc5a11	Intergenic
chr7	57163845	-5.714	0.060	Slc6a5	Intergenic
chr7	57163928	-5.275	0.129	Slc6a5	Intergenic
chr18	67625455	12.030	0.107	Slmo1	intron (NM_144867, intron 1 of 6)
chr18	67625427	13.540	0.113	Slmo1	intron (NM_144867, intron 1 of 6)
chr8	81886426	-24.294	0.018	Smad1	intron (NM_008539, intron 2 of 6)
chr5	24103690	-21.615	0.018	Smarcd3	intron (NM_025891, intron 2 of 12)
chrX	148452089	-6.821	0.056	Smc1a	intron (NM_019710, intron 1 of 24)
chr6	146783138	17.892	0.038	Smco2	Intergenic
chr19	53489933	-22.656	0.060	Smndc1	Intergenic
chr19	53489186	-8.425	0.155	Smndc1	Intergenic
chr17	13630938	-11.976	0.034	Smok4a	Intergenic
chr17	13630904	-10.139	0.200	Smok4a	Intergenic
chr5	145709674	-22.939	0.038	Smurf1	(CGGA)n Simple_repeat Simple_repeat
chr5	145709666	-16.643	0.096	Smurf1	(CGGA)n Simple_repeat Simple_repeat
chr5	145709670	-15.231	0.141	Smurf1	(CGGA)n Simple_repeat Simple_repeat
chr5	145709502	-12.089	0.171	Smurf1	intron (NM_001038627, intron 1 of 17)
chr1	191744366	-13.427	0.082	Smyd2	intron (NM_026796, intron 1 of 11)
chr1	191744386	-12.500	0.122	Smyd2	intron (NM_026796, intron 1 of 11)
chr1	191744361	-10.163	0.161	Smyd2	intron (NM_026796, intron 1 of 11)
chr6	28433001	13.371	0.035	Snd1	intron (NM_019776, intron 1 of 23)
chr2	158211932	-14.931	0.129	Shhg11	TTS (NM_175692)
chr2	158211911	-12.379	0.133	Shhg11	TTS (NM_175692)
chr10	80641948	-7.077	0.190	Snord37	TTS (NR_028549)
chr8	112377443	-7.014	0.162	Snord71	exon (NM_009677, exon 18 of 24)
chr8	112377484	-7.120	0.177	Snord71	exon (NM_009677, exon 18 of 24)
chr2	154245631	11.499	0.104	Snta1	Intergenic

chr13	114396622	-21.517	0.026	Snx18	intron (NM_130796, intron 1 of 1)
chr13	114396610	-18.056	0.056	Snx18	intron (NM_130796, intron 1 of 1)
chr13	114396511	-15.592	0.153	Snx18	intron (NM_130796, intron 1 of 1)
chr17	5887517	-11.914	0.105	Snx9	intron (NM_025664, intron 2 of 17)
chr17	5885419	15.127	0.147	Snx9	intron (NM_025664, intron 1 of 17)
chr11	117826735	-13.019	0.109	Socs3	TTS (NM_007707)
chr11	117826677	-9.587	0.123	Socs3	TTS (NM_007707)
chr17	66797048	-8.960	0.142	Soga2	intron (NM_172963, intron 1 of 13)
chr17	66797675	-5.600	0.146	Soga2	exon (NM_001114098, exon 1 of 15)
chr17	66797057	-7.814	0.148	Soga2	intron (NM_172963, intron 1 of 13)
chr17	66797679	-6.183	0.180	Soga2	exon (NM_001114098, exon 1 of 15)
chr8	46682217	-18.379	0.036	Sorbs2	intron (NM_172752, intron 1 of 22)
chr8	12401489	-9.454	0.069	Sox1	intron (NR_027975, intron 1 of 7)
chr8	12401618	-6.391	0.132	Sox1	intron (NR_027975, intron 1 of 7)
chr7	123047912	16.532	0.034	Sox6	intron (NM_001025560, intron 2 of 15)
chr7	123047704	6.884	0.167	Sox6	intron (NM_001025560, intron 2 of 15)
chr14	64561432	-17.262	0.102	Sox7	Intergenic
chr14	64561210	-12.011	0.173	Sox7	Intergenic
chr11	93897008	-17.171	0.104	Spag9	intron (NM_027569, intron 2 of 28)
chr11	93897231	-11.038	0.174	Spag9	intron (NM_027569, intron 2 of 28)
chr11	55203709	-5.808	0.107	Sparc	Intergenic
chr10	74721821	-13.917	0.101	Specc1l	exon (NM_153406, exon 7 of 16)
chr10	74721884	-9.790	0.106	Specc1l	exon (NM_153406, exon 7 of 16)
chr10	74721805	-13.517	0.133	Specc1l	exon (NM_153406, exon 7 of 16)
chr10	43955462	-6.931	0.174	Speer5-ps1	Intergenic
chr11	19614176	9.255	0.157	Spred2	Intergenic
chr11	19879596	-9.555	0.173	Spred2	intron (NM_033523, intron 1 of 5)
chr11	19614403	12.143	0.179	Spred2	Intergenic
chr5	136448662	17.999	0.086	Srcrb4d	intron (NM_001160366, intron 1 of 10)
chr13	69747810	-6.352	0.190	Srd5a1	intron (NM_175283, intron 1 of 4)
chr10	61980383	-16.428	0.041	Srgn	Intergenic
chr10	61980418	-10.981	0.154	Srgn	Intergenic
chr10	61980425	-10.556	0.171	Srgn	Intergenic
chr4	134869384	-12.281	0.180	Srrm1	MIRb SINE MIR
chr4	135416164	10.432	0.042	Srsf10	intron (NM_001080387, intron 2 of 5)
chr2	151938844	-9.582	0.172	Srxn1	Intergenic
chr2	151938855	-9.405	0.188	Srxn1	Intergenic
chr6	146060503	15.375	0.104	Sspn	intron (NM_019923, intron 56 of 56)
chr6	146060522	11.562	0.118	Sspn	intron (NM_019923, intron 56 of 56)
chr16	58467227	-13.900	0.078	St3gal6	3' UTR (NM_028523, exon 16 of 16)
chr16	58467126	-12.933	0.166	St3gal6	3' UTR (NM_028523, exon 16 of 16)
chr10	86483504	17.473	0.096	Stab2	Intergenic
chr5	152021400	19.809	0.037	Stard13	Intergenic
chr5	152021218	11.038	0.169	Stard13	Intergenic
chr11	31130236	13.407	0.127	Stc2	Intergenic
chr14	66943398	15.019	0.045	Stmn4	Intergenic



chr12	93007405	14.156	0.099	Ston2	intron (NM_175367, intron 1 of 6)
chr8	48257135	9.302	0.034	Stox2	Intergenic
chr1	157046706	10.038	0.161	Stx6	intron (NM_021433, intron 7 of 7)
chr1	157046700	8.627	0.199	Stx6	intron (NM_021433, intron 7 of 7)
chr3	102750789	14.073	0.147	Sycp1	intron (NM_201619, intron 8 of 10)
chr13	52693132	-16.239	0.034	Syk	intron (NM_011518, intron 1 of 13)
chr12	106257978	15.761	0.130	Syne3	Intergenic
chr12	106257625	14.370	0.143	Syne3	Intergenic
chr12	106257688	13.382	0.186	Syne3	Intergenic
chr17	8790660	-13.211	0.107	T	Intergenic
chr17	8790673	-9.618	0.153	T	Intergenic
chr10	127159189	-17.468	0.101	Tac2	Intergenic
chr10	127159182	-14.326	0.157	Tac2	Intergenic
chr10	127159201	-14.312	0.178	Tac2	Intergenic
chr12	25178487	14.815	0.070	Taf1b	CpG
chr12	25178410	16.850	0.100	Taf1b	CpG
chr2	59499943	-13.953	0.071	Tanc1	intron (NM_198294, intron 2 of 26)
chr17	34341209	21.576	0.049	Tap2	promoter-TSS (NM_011530)
chr17	34341216	19.434	0.057	Tap2	promoter-TSS (NM_011530)
chr5	64557006	-22.664	0.035	Tbc1d1	intron (NM_019636, intron 1 of 19)
chr10	120737153	-18.717	0.040	Tbc1d30	intron (NM_029057, intron 5 of 11)
chr1	39518900	-13.954	0.095	Tbc1d8	intron (NM_018775, intron 1 of 19)
chr1	39518805	-11.725	0.095	Tbc1d8	intron (NM_018775, intron 1 of 19)
chr1	39518931	-14.432	0.136	Tbc1d8	intron (NM_018775, intron 1 of 19)
chr1	39518896	-12.500	0.136	Tbc1d8	intron (NM_018775, intron 1 of 19)
chr1	39518894	-11.401	0.164	Tbc1d8	intron (NM_018775, intron 1 of 19)
chr3	99062222	8.476	0.060	Tbx15	intron (NM_009323, intron 1 of 7)
chr9	24574486	-8.527	0.199	Tbx20	intron (NM_194263, intron 2 of 7)
chr1	9958563	5.430	0.105	Tcf24	promoter-TSS (NM_001285425)
chr1	9958764	8.787	0.127	Tcf24	TTS (NM_145692)
chr18	69553107	-14.135	0.034	Tcf4	intron (NM_013685, intron 3 of 19)
chr18	69553262	-8.706	0.184	Tcf4	intron (NM_013685, intron 3 of 19)
chr7	119863580	-22.575	0.054	Tead1	intron (NM_001166584, intron 1 of 13)
chr7	119863642	-9.580	0.170	Tead1	intron (NM_001166584, intron 1 of 13)
chr7	119828452	-11.926	0.188	Tead1	intron (NM_001166584, intron 1 of 13)
chr5	73258515	-14.773	0.071	Tec	intron (NM_001113461, intron 1 of 17)
chr5	73258792	-17.581	0.100	Tec	intron (NM_001113461, intron 1 of 17)
chr5	73258850	-12.533	0.189	Tec	intron (NM_001113461, intron 1 of 17)
chr11	37050905	-11.739	0.102	Tenm2	Intergenic
chr3	133290041	-20.936	0.036	Tet2	Intergenic
chr12	77346190	-13.712	0.167	Tex21	5' UTR (NM_001159532, exon 2 of 9)
chr1	159007708	-17.851	0.065	Tex35	(CG)n Simple_repeat Simple_repeat
chr1	159007712	-17.778	0.078	Tex35	(CG)n Simple_repeat Simple_repeat
chr1	159007714	-14.680	0.157	Tex35	(CG)n Simple_repeat Simple_repeat
chr1	159007675	-11.422	0.180	Tex35	Intergenic
chr13	40796557	17.411	0.076	Tfap2a	Intergenic

chr6	16651866	-13.913	0.057	Tfec	Intergenic
chr6	16651758	-11.373	0.092	Tfec	Intergenic
chr6	16651975	-11.094	0.191	Tfec	Intergenic
chr7	26471773	15.119	0.070	Tgfb1	promoter-TSS (NM_011577)
chr7	26471653	13.669	0.130	Tgfb1	promoter-TSS (NM_011577)
chr17	71222710	7.454	0.053	Tgif1	Intergenic
chr17	71222778	7.158	0.196	Tgif1	Intergenic
chr2	148232644	-21.250	0.040	Thbd	exon (NM_009378, exon 1 of 1)
chr2	148232650	-17.032	0.108	Thbd	exon (NM_009378, exon 1 of 1)
chr2	148232483	-15.670	0.138	Thbd	exon (NM_009378, exon 1 of 1)
chr6	112997656	-14.944	0.122	Thumpd3	exon (NM_008188, exon 2 of 10)
chr16	89869185	-6.711	0.133	Tiam1	intron (NM_001145886, intron 6 of 27)
chr4	71500529	13.890	0.039	Tle1	Intergenic
chr19	14964902	15.556	0.182	Tle4	Intergenic
chr8	66683099	12.527	0.106	Tll1	intron (NM_009390, intron 1 of 20)
chr8	66683063	12.551	0.168	Tll1	intron (NM_009390, intron 1 of 20)
chr3	83671876	16.843	0.019	Tlr2	Intergenic
chr3	57109732	-17.602	0.054	Tm4sf1	Intergenic
chr3	57109582	-11.598	0.165	Tm4sf1	Intergenic
chr2	130034847	-9.732	0.088	Tmc2	intron (NM_138655, intron 4 of 19)
chr2	116647458	-14.578	0.078	Tmco5	Intergenic
chr2	116647314	-9.048	0.200	Tmco5	Intergenic
chr9	89600321	12.344	0.091	Tmed3	promoter-TSS (NM_025360)
chr9	89600315	9.888	0.190	Tmed3	promoter-TSS (NM_025360)
chr5	126115478	-25.034	0.004	Tmem132b	intron (NM_001190352, intron 2 of 8)
chr6	34819734	-17.539	0.057	Tmem140	intron (NM_197986, intron 1 of 1)
chr6	34819612	-14.263	0.078	Tmem140	intron (NM_197986, intron 1 of 1)
chr6	34819870	-10.893	0.155	Tmem140	intron (NM_197986, intron 1 of 1)
chr6	34819629	-10.287	0.171	Tmem140	intron (NM_197986, intron 1 of 1)
chr11	22522117	-14.146	0.062	Tmem17	Intergenic
chr17	81340739	-16.582	0.075	Tmem178	Intergenic
chr17	81340727	-14.912	0.116	Tmem178	Intergenic
chr17	6452040	-13.535	0.063	Tmem181b-ps	Intergenic
chr17	6452022	-9.168	0.198	Tmem181b-ps	Intergenic
chr9	59370772	-14.318	0.145	Tmem202	intron (NM_178388, intron 2 of 4)
chr9	59370669	-9.228	0.149	Tmem202	intron (NM_178388, intron 2 of 4)
chr17	87305975	-16.682	0.064	Tmem247	Intergenic
chr17	87305842	-6.771	0.178	Tmem247	Intergenic
chr19	24757915	-26.050	0.009	Tmem252	3' UTR (NM_175013, exon 11 of 11)
chr19	24747909	-14.460	0.129	Tmem252	promoter-TSS (NM_183160)
chr19	24747915	-13.131	0.164	Tmem252	promoter-TSS (NM_183160)
chr14	49135455	18.796	0.070	Tmem260	TTS (NM_172600)
chr14	49135340	13.369	0.098	Tmem260	TTS (NM_172600)
chr14	49135579	11.498	0.165	Tmem260	TTS (NM_172600)
chr16	38559682	17.341	0.063	Tmem39a	intron (NM_001205286, intron 1 of 8)
chr4	141632064	-8.651	0.101	Tmem51os1	intron (NM_145402, intron 1 of 2)

chr14	51549283	-11.823	0.106	Tmem55b	exon (NM_001033271, exon 3 of 7)
chr14	51549888	-7.204	0.174	Tmem55b	exon (NM_001033271, exon 2 of 7)
chr10	90699610	-10.221	0.063	Tmpo	Intergenic
chr10	104947181	20.169	0.034	Tmtc2	intron (NM_177368, intron 1 of 11)
chr10	104947082	14.220	0.123	Tmtc2	intron (NM_177368, intron 1 of 11)
chr10	18782024	-15.390	0.060	Tnfaip3	Intergenic
chr10	18782210	-9.842	0.194	Tnfaip3	Intergenic
chr1	107699645	-19.238	0.034	Tnfrsf11a	intron (NM_009399, intron 1 of 9)
chr6	125300672	13.599	0.077	Tnfrsf1a	intron (NM_011609, intron 1 of 9)
chr6	125300754	13.084	0.123	Tnfrsf1a	intron (NM_011609, intron 1 of 9)
chr8	10007727	15.158	0.157	Tnfsf13b	intron (NM_033622, intron 2 of 6)
chr8	10007723	12.900	0.192	Tnfsf13b	intron (NM_033622, intron 2 of 6)
chr7	4461871	-20.259	0.068	Tnnt1	intron (NM_001277903, intron 7 of 13)
chr1	161647485	-21.350	0.038	Tnr	intron (NM_022312, intron 1 of 22)
chr1	161647516	-11.775	0.168	Tnr	intron (NM_022312, intron 1 of 22)
chr1	161647658	-8.999	0.177	Tnr	intron (NM_022312, intron 1 of 22)
chr1	161647642	-8.190	0.191	Tnr	intron (NM_022312, intron 1 of 22)
chr11	8467537	-21.755	0.021	Tns3	intron (NM_001083587, intron 4 of 30)
chr11	8476749	6.794	0.122	Tns3	intron (NM_001083587, intron 4 of 30)
chr8	129376047	-16.257	0.055	Tomm20	Intergenic
chr10	31166365	-15.034	0.117	Tpd5211	promoter-TSS (NM_009413)
chr6	43608450	-18.575	0.046	Tpk1	intron (NM_013861, intron 2 of 8)
chr9	66868077	21.233	0.034	Tpm1	Intergenic
chr4	114143122	15.848	0.070	Trabd2b	intron (NM_001085549, intron 2 of 6)
chr4	114143141	10.243	0.161	Trabd2b	intron (NM_001085549, intron 2 of 6)
chr9	121323550	-10.102	0.165	Trak1	intron (NM_175114, intron 2 of 15)
chr15	72865229	-18.908	0.088	Trappc9	intron (NM_001164643, intron 4 of 8)
chr15	72865231	-14.243	0.182	Trappc9	intron (NM_001164643, intron 4 of 8)
chr15	72865284	-11.792	0.196	Trappc9	intron (NM_001164643, intron 4 of 8)
chr2	13480509	-21.055	0.052	Trdmt1	Intergenic
chr2	13480493	-18.352	0.065	Trdmt1	Intergenic
chr17	47311974	-15.813	0.093	Trerf1	intron (NM_001097623, intron 3 of 19)
chr6	92198357	11.367	0.135	Trh	Intergenic
chr6	92198293	12.942	0.179	Trh	Intergenic
chr15	59465055	11.968	0.154	Trib1	Intergenic
chr15	59465058	11.497	0.168	Trib1	Intergenic
chr7	111501772	-7.977	0.096	Trim12c	promoter-TSS (NM_175677)
chr3	84023930	-6.195	0.057	Trim2	intron (NM_001271726, intron 1 of 11)
chr9	88961795	-22.081	0.050	Trim43b	Intergenic
chr9	88961825	-17.520	0.085	Trim43b	Intergenic
chr9	88961895	-11.610	0.096	Trim43b	Intergenic
chr9	88961883	-8.192	0.192	Trim43b	Intergenic
chr9	88961875	-7.794	0.200	Trim43b	Intergenic
chr15	27812718	-18.936	0.039	Trio	intron (NM_001081302, intron 9 of 56)
chr15	27918306	-11.132	0.095	Trio	intron (NM_001081302, intron 1 of 56)
chr15	27812635	-16.267	0.099	Trio	intron (NM_001081302, intron 9 of 56)

chr4	133053357	-14.552	0.032	Trnp1	intron (NM_001081156, intron 1 of 1)
chr4	133053350	-13.768	0.043	Trnp1	intron (NM_001081156, intron 1 of 1)
chr1	145617460	10.669	0.167	Trove2	intron (NM_013835, intron 2 of 8)
chr1	145617480	9.689	0.193	Trove2	intron (NM_013835, intron 2 of 8)
chr8	127545153	-14.032	0.030	Tsnax	intron (NM_016909, intron 3 of 5)
chr8	127545417	-13.674	0.063	Tsnax	intron (NM_016909, intron 3 of 5)
chr8	127547211	-17.895	0.095	Tsnax	intron (NM_016909, intron 3 of 5)
chr8	127545371	-9.015	0.170	Tsnax	intron (NM_016909, intron 3 of 5)
chr8	127545635	-6.596	0.180	Tsnax	intron (NM_016909, intron 3 of 5)
chr8	127547295	-10.131	0.182	Tsnax	intron (NM_016909, intron 3 of 5)
chr8	127545857	-8.873	0.189	Tsnax	intron (NM_016909, intron 3 of 5)
chr14	41770259	-10.694	0.034	Tspan14	intron (NM_145928, intron 1 of 8)
chr14	41770082	-13.679	0.048	Tspan14	intron (NM_145928, intron 1 of 8)
chr14	41770444	-10.713	0.122	Tspan14	intron (NM_145928, intron 1 of 8)
chr15	78235215	13.023	0.035	Tst	intron (NM_009437, intron 1 of 1)
chr15	78235175	9.626	0.128	Tst	intron (NM_009437, intron 1 of 1)
chr6	38332287	17.341	0.049	Ttc26	intron (NM_153600, intron 2 of 17)
chr6	38332105	13.098	0.188	Ttc26	exon (NM_153600, exon 2 of 18)
chr17	75088213	11.918	0.052	Ttc27	intron (NM_007566, intron 65 of 72)
chr18	12802974	6.728	0.109	Ttc39c	intron (NM_028341, intron 1 of 13)
chr7	28440435	-9.876	0.138	Ttc9b	TTS (NM_001081292)
chr7	28440438	-8.835	0.173	Ttc9b	TTS (NM_001081292)
chr7	28440416	-8.170	0.193	Ttc9b	TTS (NM_001081292)
chr3	100767993	-22.302	0.034	Ttf2	exon (NM_001013026, exon 4 of 23)
chr11	114537637	-12.290	0.102	Ttyh2	intron (NM_053273, intron 1 of 13)
chr11	114537644	-6.957	0.186	Ttyh2	intron (NM_053273, intron 1 of 13)
chr13	34170530	-21.729	0.010	Tubb2a	promoter-TSS (NM_009450)
chr13	34170827	-13.218	0.147	Tubb2a	promoter-TSS (NM_009450)
chr13	34170788	-11.817	0.193	Tubb2a	promoter-TSS (NM_009450)
chr6	128304861	8.729	0.090	Tulp3	intron (NM_011657, intron 1 of 10)
chr6	128304767	19.067	0.095	Tulp3	intron (NM_011657, intron 1 of 10)
chr6	128304627	15.256	0.120	Tulp3	intron (NM_011657, intron 1 of 10)
chr6	128304959	7.911	0.169	Tulp3	intron (NM_011657, intron 1 of 10)
chr19	9026830	15.388	0.155	Tut1	TTS (NM_011842)
chr19	9026820	13.564	0.170	Tut1	TTS (NM_011842)
chr19	9026824	12.832	0.175	Tut1	TTS (NM_011842)
chr5	73154593	-8.353	0.168	Txk	intron (NM_001113464, intron 14 of 17)
chr9	20936907	-20.000	0.072	Tyk2	Intergenic
chr9	20936903	-14.035	0.175	Tyk2	Intergenic
chr5	130753865	-23.497	0.031	Tyw1	exon (NM_178897, exon 8 of 9)
chr5	130753745	-11.270	0.119	Tyw1	intron (NM_001015876, intron 7 of 15)
chr5	86609931	-14.141	0.134	Uba6	Intergenic
chr8	34747236	16.780	0.034	Ubxn8	intron (NM_178648, intron 2 of 7)
chr1	169191693	-21.818	0.034	Uck2	intron (NM_030724, intron 1 of 6)
chr1	169201618	18.313	0.061	Uck2	intron (NM_030724, intron 1 of 6)
chr1	169201608	17.391	0.072	Uck2	intron (NM_030724, intron 1 of 6)

chr13	4000904	-6.791	0.128	Ucn3	Intergenic
chr9	121223605	-15.278	0.153	Ulk4	CT-rich Low_complexity Low_complexity
chr9	121223425	-5.463	0.192	Ulk4	Intergenic
chr9	121223447	-10.217	0.194	Ulk4	Intergenic
chr16	34188325	11.060	0.105	Umps	intron (NM_177357, intron 26 of 59)
chr16	34188425	7.479	0.147	Umps	intron (NM_177357, intron 26 of 59)
chr5	115583608	-15.430	0.095	Unc119b	intron (NM_175352, intron 1 of 4)
chr5	115583600	-12.284	0.138	Unc119b	intron (NM_175352, intron 1 of 4)
chr5	115583606	-12.013	0.173	Unc119b	intron (NM_175352, intron 1 of 4)
chr10	60257553	16.146	0.028	Unc5b	intron (NM_029770, intron 1 of 16)
chr10	60257565	10.084	0.120	Unc5b	intron (NM_029770, intron 1 of 16)
chr13	66909382	-7.565	0.100	Uqcrb	Intergenic
chr13	66909455	-7.774	0.106	Uqcrb	Intergenic
chr10	122613019	-10.695	0.103	Usp15	exon (NM_027604, exon 3 of 22)
chr4	105872668	22.843	0.026	Usp24	Intergenic
chr4	106020518	9.238	0.035	Usp24	intron (NM_183225, intron 5 of 67)
chr4	105872673	22.271	0.036	Usp24	Intergenic
chr4	105872747	15.810	0.079	Usp24	Intergenic
chr4	105872678	16.162	0.110	Usp24	Intergenic
chr16	77027348	-15.773	0.082	Usp25	intron (NM_013918, intron 1 of 23)
chr16	77027439	-10.930	0.107	Usp25	intron (NM_013918, intron 1 of 23)
chr15	51708227	6.814	0.152	Utp23	promoter-TSS (NM_030132)
chr15	51708511	12.256	0.169	Utp23	promoter-TSS (NM_030132)
chr13	89883129	-14.122	0.105	Vcan	Intergenic
chr13	89883563	-6.707	0.152	Vcan	Intergenic
chr13	89883052	-12.461	0.152	Vcan	promoter-TSS (NM_172955)
chr3	66359825	-9.604	0.088	Veph1	Intergenic
chr3	66359990	-9.603	0.195	Veph1	Intergenic
chr17	78977294	-12.917	0.076	Vit	intron (NM_028813, intron 5 of 13)
chr17	79003830	5.921	0.169	Vit	intron (NM_028813, intron 9 of 13)
chr17	78977214	-12.060	0.196	Vit	intron (NM_028813, intron 5 of 13)
chr5	130407972	-11.857	0.034	Vkorc111	Intergenic
chr7	7230919	11.849	0.088	Vmn2r29	promoter-TSS (NR_003555)
chr10	129907422	-5.012	0.167	Vmn2r86	CpG
chr5	124497768	-17.773	0.049	Vps37b	Intergenic
chr5	124477799	-16.491	0.099	Vps37b	intron (NM_177876, intron 1 of 3)
chr5	124497776	-13.354	0.141	Vps37b	Intergenic
chr5	124477815	-14.135	0.145	Vps37b	intron (NM_177876, intron 1 of 3)
chr5	124477871	-13.072	0.157	Vps37b	intron (NM_177876, intron 1 of 3)
chr12	85983194	16.517	0.072	Vrtn	promoter-TSS (NM_001168588)
chr12	85983161	14.935	0.079	Vrtn	promoter-TSS (NM_001168588)
chr5	147214079	14.298	0.135	Wasf3	(CGAA)n Simple_repeat Simple_repeat
chr5	147214087	13.286	0.153	Wasf3	(CGAA)n Simple_repeat Simple_repeat
chr5	147214071	12.906	0.170	Wasf3	(CGAA)n Simple_repeat Simple_repeat
chr5	147214075	12.768	0.177	Wasf3	(CGAA)n Simple_repeat Simple_repeat
chr19	46681492	-5.286	0.199	Wbp11	intron (NM_001177812, intron 2 of 4)

chr2	121413588	-10.021	0.060	Wdr76	intron (NM_172673, intron 2 of 14)
chr2	73389271	-10.320	0.070	Wipf1	Intergenic
chr2	73389266	-9.317	0.121	Wipf1	Intergenic
chr7	105919349	11.884	0.043	Wnt11	Intergenic
chr7	105919523	10.688	0.088	Wnt11	Intergenic
chr11	103672126	-24.691	0.038	Wnt3	intron (NM_009521, intron 2 of 4)
chr11	103672141	-17.920	0.092	Wnt3	intron (NM_009521, intron 2 of 4)
chr11	103672133	-18.354	0.109	Wnt3	intron (NM_009521, intron 2 of 4)
chr11	103672558	-11.377	0.194	Wnt3	intron (NM_009521, intron 2 of 4)
chr15	85446192	-17.416	0.057	Wnt7b	Intergenic
chr15	85446220	-10.952	0.170	Wnt7b	Intergenic
chr15	85446204	-11.515	0.195	Wnt7b	Intergenic
chr18	34708934	-18.509	0.091	Wnt8a	Intergenic
chr11	35730360	-22.569	0.054	Wwc1	intron (NM_170779, intron 1 of 22)
chr3	57316100	13.369	0.067	Wwtr1	intron (NM_001168281, intron 2 of 6)
chr10	126128643	-12.111	0.068	Xrcc6bp1	Intergenic
chr10	126128624	-10.663	0.122	Xrcc6bp1	Intergenic
chr16	30873901	13.883	0.069	Xxylt1	Intergenic
chr12	21954869	-14.621	0.042	Ywhaq	CpG
chr12	21954530	-11.210	0.060	Ywhaq	Intergenic
chr12	21954840	-12.898	0.093	Ywhaq	CpG
chr12	21954695	-12.390	0.095	Ywhaq	CpG
chr12	22086394	-13.561	0.102	Ywhaq	CpG
chr12	21954708	-12.970	0.105	Ywhaq	CpG
chr12	21840554	-5.170	0.113	Ywhaq	CpG
chr12	22086474	-9.318	0.115	Ywhaq	CpG
chr12	21954505	-9.281	0.137	Ywhaq	Intergenic
chr12	21954697	-11.088	0.143	Ywhaq	CpG
chr12	21954751	-11.445	0.189	Ywhaq	CpG
chr18	84439809	-11.453	0.118	Zadh2	intron (NM_001033341, intron 8 of 8)
chr18	84439922	-11.848	0.143	Zadh2	intron (NM_001033341, intron 8 of 8)
chr18	84439880	-14.977	0.146	Zadh2	intron (NM_001033341, intron 8 of 8)
chr1	179388773	13.574	0.086	Zbtb18	Intergenic
chr1	179388804	10.925	0.190	Zbtb18	Intergenic
chr10	6010992	-15.502	0.030	Zbtb2	intron (NM_031185, intron 2 of 3)
chr10	6010940	-11.339	0.080	Zbtb2	intron (NM_031185, intron 2 of 3)
chr10	6011045	-12.226	0.099	Zbtb2	intron (NM_031185, intron 2 of 3)
chr10	6011071	-12.426	0.132	Zbtb2	intron (NM_031185, intron 2 of 3)
chr10	6011111	-14.990	0.133	Zbtb2	intron (NM_031185, intron 2 of 3)
chr10	6011063	-11.909	0.141	Zbtb2	intron (NM_031185, intron 2 of 3)
chr10	6010703	-12.732	0.183	Zbtb2	intron (NM_031185, intron 2 of 3)
chr12	113938668	-18.439	0.034	Zbtb42	Intergenic
chr12	113938582	-13.729	0.045	Zbtb42	Intergenic
chr12	113927043	-11.277	0.134	Zbtb42	Intergenic
chr12	113927274	-14.120	0.171	Zbtb42	Intergenic
chr6	38305989	-10.663	0.193	Zc3hav1	Intergenic

chr13	59937463	-20.996	0.024	Zcchc6	Intergenic
chr13	59937484	-9.614	0.133	Zcchc6	Intergenic
chr8	111223825	10.162	0.030	Zfhx3	Intergenic
chr8	111223764	9.979	0.129	Zfhx3	Intergenic
chr5	138899628	-16.989	0.044	Zfp157	3' UTR (NM_028130, exon 5 of 5)
chr18	82874817	-13.294	0.063	Zfp236	Intergenic
chr18	82874731	-9.437	0.135	Zfp236	Intergenic
chr12	80860101	13.384	0.095	Zfp3611	intron (NM_009014, intron 8 of 10)
chr12	80870737	-10.892	0.104	Zfp3611	intron (NM_009014, intron 9 of 10)
chr12	80860157	14.433	0.160	Zfp3611	intron (NM_009014, intron 8 of 10)
chr17	84584560	-11.922	0.187	Zfp3612	3' UTR (NM_001001806, exon 2 of 2)
chr7	30695418	17.828	0.103	Zfp383	intron (NM_001243908, intron 2 of 4)
chr7	30695254	11.700	0.174	Zfp383	exon (NM_001243908, exon 2 of 5)
chr8	90468021	17.965	0.019	Zfp423	intron (NM_033327, intron 1 of 7)
chr11	95640412	17.577	0.065	Zfp652	Intergenic
chr13	62356691	-10.299	0.102	Zfp808	Intergenic
chr13	62356879	-11.197	0.106	Zfp808	Intergenic
chr8	72073347	-11.420	0.191	Zfp868	ID_B1 SINE B4
chr9	91272230	-13.840	0.135	Zic4	intron (NM_009576, intron 2 of 4)
chr9	91272420	-13.649	0.146	Zic4	intron (NM_009576, intron 2 of 4)
chr13	9882312	-12.769	0.092	Zmynd11	intron (NM_033269, intron 4 of 4)
chr13	9882365	-11.394	0.127	Zmynd11	intron (NM_033269, intron 4 of 4)

## Supplementary Table 4 (ST4)

Differentially methylated CpGs POL-GD17 Offspring					
Base		Methylation Difference	q-value	Gene Name	Annotation
chr8	80007790	11.172	0.137	0610038B21Rik	intron (NM_030113, intron 1 of 22)
chr8	80007779	11.394	0.184	0610038B21Rik	intron (NM_030113, intron 1 of 22)
chr6	108616145	-21.160	0.039	0610040F04Rik	3' UTR (NM_011498, exon 5 of 5)
chr6	108616129	-17.334	0.068	0610040F04Rik	3' UTR (NM_011498, exon 5 of 5)
chr6	108616096	-12.308	0.163	0610040F04Rik	3' UTR (NM_011498, exon 5 of 5)
chr5	64263543	19.158	0.089	0610040J01Rik	intron (NM_029554, intron 1 of 3)
chr5	64263485	11.377	0.141	0610040J01Rik	intron (NM_029554, intron 1 of 3)
chr5	64263371	10.603	0.179	0610040J01Rik	intron (NM_029554, intron 1 of 3)
chr2	156689839	10.283	0.142	1110008F13Rik	intron (NM_026124, intron 1 of 3)
chr6	134877808	7.908	0.15	1190002F15Rik	Intergenic
chr10	83482584	12.500	0.166	1500009L16Rik	Intergenic
chr10	83482539	-13.504	0.167	1500009L16Rik	Intergenic
chr2	166878902	-14.362	0.134	1500012F01Rik	intron (NM_001033196, intron 3 of 13)
chr2	166878847	-12.037	0.148	1500012F01Rik	intron (NM_001033196, intron 3 of 13)
chr16	96082596	-24.847	0.032	1600002D24Rik	intron (NR_040484, intron 1 of 3)
chr16	96082660	-20.327	0.034	1600002D24Rik	intron (NR_040484, intron 1 of 3)
chr16	96082620	-12.399	0.181	1600002D24Rik	intron (NR_040484, intron 1 of 3)
chr17	45927934	-22.357	0.043	1600014C23Rik	Intergenic
chr15	67294322	-18.711	0.034	1700012I11Rik	Intergenic
chr8	11666362	13.625	0.055	1700016D06Rik	intron (NM_024271, intron 1 of 5)
chr8	11666237	10.373	0.062	1700016D06Rik	intron (NM_024271, intron 1 of 5)
chr8	11666378	13.453	0.077	1700016D06Rik	intron (NM_024271, intron 1 of 5)
chr10	100092422	15.361	0.031	1700017N19Rik	Intergenic
chr10	100092596	10.270	0.086	1700017N19Rik	Intergenic
chr10	100092445	6.234	0.181	1700017N19Rik	Intergenic
chr10	100092540	6.102	0.183	1700017N19Rik	Intergenic
chr6	5989323	-18.734	0.054	1700019G24Rik	Intergenic
chr6	5989311	-14.250	0.167	1700019G24Rik	Intergenic
chr4	104672557	-12.412	0.068	1700024P16Rik	intron (NR_104376, intron 12 of 20)
chr4	104672544	-13.249	0.087	1700024P16Rik	intron (NR_104376, intron 12 of 20)
chr2	164939065	-9.284	0.068	1700025C18Rik	intron (NM_174988, intron 11 of 11)
chr2	164939087	-7.966	0.075	1700025C18Rik	intron (NM_174988, intron 11 of 11)
chr6	39009722	-24.812	0.021	1700025N23Rik	intron (NM_011539, intron 9 of 12)
chr12	20821969	-11.867	0.023	1700030C10Rik	promoter-TSS (NR_015521)
chr12	20821302	-9.734	0.048	1700030C10Rik	non-coding (NR_015521, exon 1 of 2)
chr12	20821078	-12.522	0.066	1700030C10Rik	CpG
chr12	20821232	-12.306	0.084	1700030C10Rik	non-coding (NR_015521, exon 1 of 2)
chr12	19710153	8.753	0.102	1700030C10Rik	CpG
chr12	19710085	13.834	0.112	1700030C10Rik	CpG
chr12	20821051	-9.802	0.118	1700030C10Rik	CpG
chr12	19710261	10.881	0.119	1700030C10Rik	CpG
chr12	19710075	14.796	0.122	1700030C10Rik	CpG



chr12	19710295	12.163	0.126	1700030C10Rik	CpG
chr12	19710381	-9.015	0.126	1700030C10Rik	Intergenic
chr12	19710166	9.194	0.147	1700030C10Rik	CpG
chr12	20821088	-9.847	0.148	1700030C10Rik	CpG
chr12	19710131	10.651	0.155	1700030C10Rik	CpG
chr12	20422104	8.806	0.158	1700030C10Rik	CpG
chr12	20821876	-6.446	0.195	1700030C10Rik	promoter-TSS (NR_015521)
chr12	20422355	9.748	0.197	1700030C10Rik	CpG
chr6	117739221	-22.424	0.032	1700030F04Rik	Intergenic
chr12	53736642	-16.465	0.111	1700031P21Rik	Intergenic
chr12	53736803	-12.145	0.199	1700031P21Rik	Intergenic
chr10	67908683	-9.449	0.129	1700040L02Rik	intron (NM_028491, intron 5 of 7)
chr10	67908977	-7.389	0.194	1700040L02Rik	intron (NM_028491, intron 5 of 7)
chr10	67908822	-9.926	0.198	1700040L02Rik	intron (NM_028491, intron 5 of 7)
chr15	63660733	-19.289	0.009	1700065I16Rik	intron (NM_177912, intron 5 of 11)
chr15	63660717	-16.626	0.01	1700065I16Rik	intron (NM_177912, intron 5 of 11)
chr15	63660727	-17.450	0.015	1700065I16Rik	intron (NM_177912, intron 5 of 11)
chr15	63660729	-13.639	0.049	1700065I16Rik	intron (NM_177912, intron 5 of 11)
chr15	63660525	9.120	0.073	1700065I16Rik	intron (NM_177912, intron 5 of 11)
chr15	63660323	-13.751	0.18	1700065I16Rik	B3 SINE B2
chr13	26250690	-20.945	0.022	1700092E19Rik	Intergenic
chr12	55394460	-15.896	0.024	1700104L18Rik	Intergenic
chr14	77212219	15.763	0.077	1700108F19Rik	Intergenic
chr14	77212306	6.875	0.16	1700108F19Rik	Intergenic
chr17	10567632	8.955	0.066	1700110C19Rik	Intergenic
chr17	10522660	10.139	0.153	1700110C19Rik	TTS (NR_045461)
chr17	10522663	10.528	0.17	1700110C19Rik	TTS (NR_045461)
chr17	10567535	8.532	0.197	1700110C19Rik	Intergenic
chr14	101693974	17.544	0.052	1700110M21Rik	Intergenic
chr16	6350606	-16.703	0.029	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6351172	-13.782	0.043	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6350486	-15.848	0.071	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6350404	-19.060	0.08	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6350338	-12.865	0.116	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6350715	-8.977	0.122	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6351078	-13.852	0.169	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr16	6350645	-8.152	0.178	1700123O21Rik	intron (NM_021477, intron 2 of 16)
chr10	86100242	11.083	0.106	1810014B01Rik	Intergenic
chr10	86100199	7.828	0.118	1810014B01Rik	Intergenic
chr7	80760748	-22.386	0.012	1810026B05Rik	Intergenic
chr7	80760720	-16.739	0.1	1810026B05Rik	Intergenic
chr11	116531373	16.551	0.044	1810032O08Rik	Intergenic
chr11	116531364	11.594	0.166	1810032O08Rik	Intergenic
chr11	116531318	7.324	0.196	1810032O08Rik	Intergenic
chr6	35205085	-15.425	0.022	1810058I24Rik	intron (NR_027875, intron 1 of 2)
chr6	35205026	-8.295	0.142	1810058I24Rik	intron (NR_027875, intron 1 of 2)

chr6	35205121	-8.918	0.194	1810058I24Rik	intron (NR_027875, intron 1 of 2)
chr17	86857833	-13.292	0.078	2010106C02Rik	intron (NM_011104, intron 2 of 14)
chr13	63239630	-15.363	0.019	2010111I01Rik	intron (NM_028079, intron 4 of 14)
chr13	63057769	9.081	0.192	2010111I01Rik	URR1B DNA MER1_type
chr6	31169432	-17.722	0.053	2210408F21Rik	promoter-TSS (NR_040262)
chr6	31169229	-14.265	0.092	2210408F21Rik	Intergenic
chr17	35727870	-11.582	0.027	2300002M23Rik	Intergenic
chr17	35727910	-5.726	0.134	2300002M23Rik	Intergenic
chr2	154916650	11.917	0.062	2310005A03Rik	Intergenic
chr2	154916663	8.613	0.134	2310005A03Rik	Intergenic
chr13	50417358	-12.736	0.029	2310081J21Rik	Intergenic
chr13	50362972	-12.063	0.036	2310081J21Rik	Intergenic
chr17	69627073	-15.367	0.031	2410021H03Rik	promoter-TSS (NR_045428)
chr1	90670955	21.608	0.032	2410088K16Rik	Intergenic
chr1	90670951	10.672	0.197	2410088K16Rik	Intergenic
chr4	125516295	-20.967	0.025	2610028E06Rik	Intergenic
chr4	125516025	-10.025	0.187	2610028E06Rik	Intergenic
chr7	87120197	-12.002	0.046	2610034B18Rik	Intergenic
chr11	113035915	19.158	0.086	2610035D17Rik	intron (NR_015556, intron 1 of 2)
chr9	65739002	18.237	0.043	2810417H13Rik	intron (NM_026515, intron 2 of 3)
chr11	16761370	-24.936	0.02	2810442I21Rik	intron (NM_007912, intron 3 of 15)
chr11	16761442	-11.303	0.106	2810442I21Rik	intron (NM_007912, intron 3 of 15)
chr1	87942406	-6.897	0.034	2810459M11Rik	promoter-TSS (NM_001144993)
chr6	149282066	-7.199	0.06	2810474O19Rik	intron (NM_026054, intron 4 of 4)
chr6	149282040	-7.216	0.089	2810474O19Rik	intron (NM_026054, intron 4 of 4)
chr8	110699083	-8.563	0.09	3010033K07Rik	CpG
chr8	110699271	-9.408	0.102	3010033K07Rik	CpG
chr8	110699257	-9.923	0.197	3010033K07Rik	CpG
chr7	88934886	-9.903	0.09	3110040N11Rik	promoter-TSS (NM_026077)
chr7	88934865	-8.925	0.094	3110040N11Rik	promoter-TSS (NM_026077)
chr12	72104948	-13.593	0.032	3110056K07Rik	intron (NR_045055, intron 3 of 3)
chr7	26178229	15.770	0.066	4732471J01Rik	intron (NM_010719, intron 1 of 9)
chr7	26178170	14.607	0.077	4732471J01Rik	intron (NM_010719, intron 1 of 9)
chr7	26161927	-10.976	0.107	4732471J01Rik	promoter-TSS (NR_073027)
chr7	26161951	-10.653	0.113	4732471J01Rik	intron (NR_073027, intron 1 of 5)
chr13	91881580	-23.411	0.01	4833422C13Rik	promoter-TSS (NR_028314)
chr13	91889859	-14.289	0.059	4833422C13Rik	exon (NM_028790, exon 2 of 15)
chr13	91881613	-11.546	0.116	4833422C13Rik	promoter-TSS (NR_028314)
chr13	91889871	-9.064	0.134	4833422C13Rik	intron (NM_028790, intron 2 of 14)
chr12	58677592	-17.562	0.023	4921506M07Rik	exon (NM_001037743, exon 2 of 5)
chr12	58677416	-6.510	0.13	4921506M07Rik	exon (NM_001037743, exon 2 of 5)
chr3	79032006	6.780	0.033	4921511C10Rik	intron (NR_045502, intron 1 of 2)
chr15	17700187	9.884	0.15	4921515E04Rik	Intergenic
chr15	17700190	10.198	0.167	4921515E04Rik	Intergenic
chr13	52248585	-10.002	0.063	4921525O09Rik	Intergenic
chr13	52248908	-14.748	0.076	4921525O09Rik	Intergenic

chr13	52248612	8.049	0.106	4921525O09Rik	Intergenic
chr13	52248882	-16.147	0.107	4921525O09Rik	Intergenic
chr13	52248709	-9.375	0.178	4921525O09Rik	Intergenic
chr2	25471634	-14.043	0.095	4921530D09Rik	CpG
chr18	83639265	-9.589	0.023	4921531P14Rik	Intergenic
chr2	130658002	26.316	0.024	4930402H24Rik	MLT1J LTR MaLR
chr12	72530574	11.469	0.111	4930404H11Rik	Intergenic
chr14	23636858	-9.249	0.118	4930405A10Rik	intron (NM_028275, intron 5 of 6)
chr2	156506453	-16.718	0.065	4930405A21Rik	intron (NM_001277186, intron 2 of 12)
chr2	156506456	-14.777	0.095	4930405A21Rik	intron (NM_001277186, intron 2 of 12)
chr10	19922301	16.152	0.025	4930405J17Rik	promoter-TSS (NR_045350)
chr2	9802133	-9.428	0.052	4930412O13Rik	promoter-TSS (NR_024257)
chr7	130098792	-7.489	0.105	4930413G21Rik	Intergenic
chr7	130098794	-9.385	0.107	4930413G21Rik	Intergenic
chr7	130098800	-7.731	0.147	4930413G21Rik	Intergenic
chr7	130098684	-10.924	0.173	4930413G21Rik	B1_Mus SINE Alu
chr11	11423304	13.761	0.007	4930415F15Rik	Intergenic
chr9	115249809	14.939	0.095	4930428G15Rik	intron (NR_040730, intron 2 of 2)
chr3	32263311	15.777	0.123	4930429B21Rik	intron (NM_009517, intron 1 of 5)
chr3	32263769	5.573	0.178	4930429B21Rik	promoter-TSS (NR_027966)
chr3	32263809	8.263	0.179	4930429B21Rik	promoter-TSS (NR_027966)
chr9	79714097	20.633	0.039	4930429F24Rik	intron (NM_001081243, intron 2 of 5)
chr2	74265159	12.421	0.118	4930441J16Rik	Intergenic
chr2	74265117	12.155	0.182	4930441J16Rik	Intergenic
chr13	18149170	-11.541	0.036	4930448F12Rik	Intergenic
chr13	18149117	-8.150	0.198	4930448F12Rik	Intergenic
chr18	77953502	-6.818	0.128	4930465K10Rik	promoter-TSS (NM_178670)
chr18	77953504	-8.199	0.184	4930465K10Rik	promoter-TSS (NM_178670)
chr1	62856507	-15.006	0.039	4930487H11Rik	intron (NM_010939, intron 15 of 15)
chr1	62856585	-13.072	0.099	4930487H11Rik	intron (NM_010939, intron 15 of 15)
chr1	62816240	7.664	0.106	4930487H11Rik	intron (NM_001077407, intron 11 of 15)
chr1	62856521	-10.441	0.112	4930487H11Rik	intron (NM_010939, intron 15 of 15)
chr1	62816301	7.902	0.152	4930487H11Rik	intron (NM_001077407, intron 11 of 15)
chr8	96414903	-26.653	0.009	4930488L21Rik	intron (NM_001113384, intron 2 of 7)
chr11	84643124	-12.119	0.065	4930502E09Rik	promoter-TSS (NM_177564)
chr11	84643111	-7.040	0.116	4930502E09Rik	promoter-TSS (NM_177564)
chr11	84643108	-7.879	0.197	4930502E09Rik	promoter-TSS (NM_177564)
chr3	146344853	-13.642	0.096	4930503B20Rik	Intergenic
chr3	146344763	-5.372	0.185	4930503B20Rik	Intergenic
chr11	31848902	-16.911	0.024	4930524B15Rik	Intergenic
chr14	115190448	-19.051	0.06	4930524C18Rik	Intergenic
chr14	115190385	-13.327	0.149	4930524C18Rik	Intergenic
chr16	37995133	-17.771	0.033	4930542C21Rik	intron (NM_153394, intron 8 of 9)
chr16	37995092	-9.661	0.122	4930542C21Rik	intron (NM_153394, intron 8 of 9)
chr19	55769166	13.791	0.111	4930552P12Rik	intron (NR_045318, intron 2 of 3)
chr19	55769459	16.410	0.115	4930552P12Rik	intron (NR_045318, intron 2 of 3)

chr19	55769179	12.739	0.13	4930552P12Rik	intron (NR_045318, intron 2 of 3)
chr19	55769168	11.997	0.151	4930552P12Rik	intron (NR_045318, intron 2 of 3)
chr19	55630734	-11.384	0.158	4930552P12Rik	intron (NM_016862, intron 7 of 7)
chr19	55630747	-12.844	0.169	4930552P12Rik	intron (NM_016862, intron 7 of 7)
chr19	55630704	-11.403	0.193	4930552P12Rik	intron (NM_016862, intron 7 of 7)
chr17	45248442	-14.444	0.155	4930564C03Rik	intron (NM_178652, intron 11 of 11)
chr17	45248424	-13.496	0.2	4930564C03Rik	intron (NM_178652, intron 11 of 11)
chr9	34720760	13.167	0.186	4930581F22Rik	intron (NM_001190913, intron 2 of 13)
chr1	37532013	-8.069	0.031	4930594C11Rik	intron (NM_173870, intron 4 of 14)
chr14	26423967	14.047	0.16	4931406H21Rik	intron (NM_183208, intron 6 of 23)
chr14	26423951	12.915	0.17	4931406H21Rik	intron (NM_183208, intron 6 of 23)
chr11	114415370	-21.071	0.018	4932435O22Rik	Intergenic
chr11	114415398	-17.973	0.048	4932435O22Rik	Intergenic
chr11	114415388	-15.631	0.066	4932435O22Rik	Intergenic
chr11	114415412	-15.444	0.087	4932435O22Rik	Intergenic
chr16	91074284	23.292	0.033	4932438H23Rik	Intergenic
chr16	91074207	9.399	0.175	4932438H23Rik	Intergenic
chr4	33095042	11.020	0.057	4933421O10Rik	intron (NM_027491, intron 5 of 6)
chr4	33095004	5.296	0.196	4933421O10Rik	intron (NM_027491, intron 5 of 6)
chr11	97396590	-19.833	0.033	4933428G20Rik	exon (NM_018873, exon 8 of 20)
chr11	97396592	-19.042	0.039	4933428G20Rik	exon (NM_018873, exon 8 of 20)
chr11	97396585	-15.320	0.11	4933428G20Rik	exon (NM_018873, exon 8 of 20)
chr17	84516386	-9.202	0.047	4933433H22Rik	Intergenic
chr17	84516368	-6.939	0.157	4933433H22Rik	Intergenic
chr5	127078719	12.778	0.116	4933438B17Rik	Intergenic
chr5	127078203	13.742	0.194	4933438B17Rik	Intergenic
chr10	111073520	-7.208	0.191	4933440J02Rik	Intergenic
chr13	17756406	-13.293	0.052	5033411D12Rik	intron (NM_138654, intron 3 of 13)
chr13	17756369	-8.340	0.076	5033411D12Rik	intron (NM_138654, intron 3 of 13)
chr12	18785647	-9.704	0.047	5730507C01Rik	Intergenic
chr12	18785463	-15.287	0.051	5730507C01Rik	Intergenic
chr12	18785666	-6.543	0.142	5730507C01Rik	Intergenic
chr19	53512030	-12.951	0.086	5830416P10Rik	Intergenic
chr19	53512702	-10.268	0.104	5830416P10Rik	Intergenic
chr15	12704403	9.417	0.143	6030458C11Rik	Intergenic
chr15	12704296	7.761	0.178	6030458C11Rik	Intergenic
chr8	126241825	14.755	0.07	6030466F02Rik	Intergenic
chr8	126241830	12.634	0.108	6030466F02Rik	Intergenic
chr7	147164921	-9.557	0.124	6430531B16Rik	promoter-TSS (NM_001033465)
chr8	37612597	-20.023	0.017	6430573F11Rik	Intergenic
chr8	37596512	-23.631	0.028	6430573F11Rik	Intergenic
chr8	37514649	18.454	0.032	6430573F11Rik	Intergenic
chr8	37612533	-10.923	0.097	6430573F11Rik	Intergenic
chr8	37596461	-11.061	0.146	6430573F11Rik	Intergenic
chr8	37596678	-13.364	0.154	6430573F11Rik	Intergenic
chr8	37612583	-9.812	0.193	6430573F11Rik	Intergenic

chr2	29112948	-9.657	0.042	6530402F18Rik	Intergenic
chr2	29112959	-9.103	0.183	6530402F18Rik	Intergenic
chr19	57584445	-20.040	0.028	6720468P15Rik	intron (NR_040306, intron 2 of 3)
chr19	57584467	-15.558	0.041	6720468P15Rik	intron (NR_040306, intron 2 of 3)
chr19	57584602	-11.138	0.169	6720468P15Rik	non-coding (NR_040307, exon 2 of 3)
chr8	19892893	-7.564	0.048	6820431F20Rik	CpG
chr8	19892881	-6.290	0.107	6820431F20Rik	CpG
chr5	149777030	-15.715	0.053	8430423G03Rik	Intergenic
chr5	149776737	-18.309	0.061	8430423G03Rik	Intergenic
chr5	149777811	-14.111	0.068	8430423G03Rik	Intergenic
chr5	149776781	-13.629	0.08	8430423G03Rik	Intergenic
chr5	149776751	-16.207	0.085	8430423G03Rik	Intergenic
chr5	149776740	-16.365	0.096	8430423G03Rik	Intergenic
chr5	149766618	-14.608	0.122	8430423G03Rik	Intergenic
chr5	149777018	-12.118	0.128	8430423G03Rik	Intergenic
chr5	149777025	-11.566	0.132	8430423G03Rik	Intergenic
chr5	149766610	-12.996	0.138	8430423G03Rik	Intergenic
chr5	149766621	-11.401	0.192	8430423G03Rik	Intergenic
chr16	30039640	12.433	0.095	9030404E10Rik	promoter-TSS (NR_045878)
chr16	30039729	8.213	0.154	9030404E10Rik	promoter-TSS (NR_045878)
chr16	30039631	10.615	0.182	9030404E10Rik	promoter-TSS (NR_045878)
chr16	30039633	9.425	0.184	9030404E10Rik	promoter-TSS (NR_045878)
chr2	9820469	21.028	0.04	9230102O04Rik	Intergenic
chr9	68854737	-11.159	0.105	9530091C08Rik	intron (NM_013646, intron 1 of 10)
chr12	113548340	-9.967	0.102	A730018C14Rik	Intergenic
chr12	113548297	-14.112	0.127	A730018C14Rik	Intergenic
chr12	113548409	-8.497	0.131	A730018C14Rik	Intergenic
chr2	129066711	-22.187	0.022	A730036I17Rik	Intergenic
chr2	129066794	-16.667	0.106	A730036I17Rik	Intergenic
chr2	129066730	-14.201	0.15	A730036I17Rik	Intergenic
chr7	80545189	11.023	0.145	A730056A06Rik	intron (NM_177740, intron 2 of 3)
chr7	80545061	7.166	0.184	A730056A06Rik	intron (NM_177740, intron 2 of 3)
chr5	100123874	-16.847	0.073	A930011G23Rik	intron (NR_030692, intron 1 of 3)
chr5	100123864	-15.693	0.098	A930011G23Rik	intron (NR_030692, intron 1 of 3)
chr5	100123860	-12.544	0.172	A930011G23Rik	intron (NR_030692, intron 1 of 3)
chr4	119211578	-15.536	0.107	AA415398	promoter-TSS (NM_172699)
chr15	51985171	17.005	0.055	Aard	Intergenic
chr15	51985065	17.117	0.078	Aard	Intergenic
chr17	45642308	-12.219	0.113	Aars2	Intergenic
chr17	45642546	-12.602	0.128	Aars2	Intergenic
chr17	45642317	-9.144	0.183	Aars2	Intergenic
chr6	23077231	-12.546	0.07	Aass	intron (NM_013930, intron 1 of 23)
chr6	23077267	-9.764	0.135	Aass	intron (NM_013930, intron 1 of 23)
chr6	23077175	-11.380	0.183	Aass	intron (NM_013930, intron 1 of 23)
chr11	84323665	-8.738	0.033	Aatf	intron (NM_019816, intron 4 of 12)
chr4	53150908	15.747	0.01	Abca1	intron (NM_013454, intron 2 of 49)

chr4	53180217	-19.904	0.029	Abca1	Intergenic
chr4	53180330	-11.748	0.183	Abca1	Intergenic
chr4	53180256	-10.815	0.188	Abca1	Intergenic
chr11	94281853	-11.481	0.086	Abcc3	intron (NM_001112813, intron 25 of 34)
chr14	119107088	-6.863	0.024	Abcc4	Intergenic
chr14	119066669	-10.059	0.044	Abcc4	intron (NM_001033336, intron 3 of 30)
chr2	150729006	21.802	0.023	Abhd12	intron (NM_024465, intron 1 of 12)
chr2	150729345	9.695	0.126	Abhd12	intron (NM_024465, intron 1 of 12)
chr16	56457829	-17.125	0.055	Abi3bp	Intergenic
chr16	56457895	-10.912	0.182	Abi3bp	Intergenic
chr16	56457843	-10.310	0.195	Abi3bp	Intergenic
chr19	57172920	-10.967	0.068	Ablim1	intron (NM_001103177, intron 6 of 21)
chr19	57271111	-11.808	0.09	Ablim1	intron (NM_178688, intron 1 of 24)
chr19	57269834	-15.207	0.115	Ablim1	intron (NM_178688, intron 1 of 24)
chr19	57172939	-10.405	0.117	Ablim1	intron (NM_001103177, intron 6 of 21)
chr19	57269983	-10.781	0.139	Ablim1	intron (NM_178688, intron 1 of 24)
chr19	57172933	-9.357	0.143	Ablim1	intron (NM_001103177, intron 6 of 21)
chr19	57172873	-9.071	0.144	Ablim1	intron (NM_001103177, intron 6 of 21)
chr19	57269852	-11.966	0.189	Ablim1	intron (NM_178688, intron 1 of 24)
chr5	114649374	-11.305	0.123	Acacb	intron (NM_133904, intron 12 of 51)
chr5	114649529	-6.850	0.169	Acacb	intron (NM_133904, intron 12 of 51)
chr2	93709213	10.335	0.113	Accsl	promoter-TSS (NM_001033452)
chr11	100387694	10.239	0.119	Acly	intron (NM_001199296, intron 1 of 28)
chr11	100387700	9.978	0.126	Acly	intron (NM_001199296, intron 1 of 28)
chr11	100387584	7.407	0.129	Acly	intron (NM_001199296, intron 1 of 28)
chr6	6905610	-13.958	0.06	Acn9	promoter-TSS (NM_001077713)
chr6	6905602	-9.189	0.154	Acn9	promoter-TSS (NM_001077713)
chr15	89375959	-17.544	0.042	Acr	intron (NM_021423, intron 20 of 21)
chr15	89375001	-8.795	0.134	Acr	intron (NM_021423, intron 20 of 21)
chr8	47531913	-16.667	0.034	Acs11	Intergenic
chr8	47531916	-11.895	0.106	Acs11	Intergenic
chr8	47531751	-14.589	0.152	Acs11	Intergenic
chr19	55326047	-12.309	0.044	Acs15	Intergenic
chr5	143682231	-12.774	0.034	Actb	Intergenic
chr13	112086366	11.392	0.058	Actbl2	Intergenic
chr13	112086194	8.921	0.093	Actbl2	Intergenic
chr11	19947230	-13.017	0.07	Actr2	Intergenic
chr11	19947240	-13.312	0.107	Actr2	Intergenic
chr11	102636376	-7.712	0.072	Adam11	exon (NM_009613, exon 18 of 27)
chr11	45886157	-8.955	0.149	Adam19	intron (NM_009616, intron 3 of 22)
chr11	45886186	-6.559	0.16	Adam19	intron (NM_009616, intron 3 of 22)
chr14	66707969	9.943	0.115	Adam2	intron (NM_001271402, intron 13 of 18)
chr14	66707948	9.821	0.195	Adam2	intron (NM_001271402, intron 13 of 18)
chr8	57995186	-8.674	0.083	Adam29	Intergenic
chr8	57995569	-5.247	0.156	Adam29	Intergenic

chr8	57995020	6.126	0.17	Adam29	Intergenic
chr9	30693391	-16.341	0.037	Adamts15	Intergenic
chr9	30693371	-15.839	0.074	Adamts15	Intergenic
chr4	85692056	-25.847	0.018	Adamts1	Intergenic
chr4	128640234	6.453	0.065	Adc	promoter-TSS (NM_172875)
chr15	64599115	-25.095	0.016	Adcy8	intron (NM_009623, intron 8 of 17)
chr6	86078797	-11.672	0.146	Add2	Intergenic
chr14	67257550	-13.055	0.159	Adra1a	intron (NM_001271761, intron 2 of 2)
chr5	104166520	16.579	0.029	Aff1	Intergenic
chr5	104218763	-15.237	0.036	Aff1	intron (NM_001080798, intron 3 of 19)
chr5	104166698	16.348	0.106	Aff1	Intergenic
chr5	104218769	-11.022	0.144	Aff1	intron (NM_001080798, intron 3 of 19)
chr5	104218750	-9.481	0.179	Aff1	intron (NM_001080798, intron 3 of 19)
chr15	73077181	12.519	0.115	Ago2	intron (NM_001130409, intron 23 of 29)
chr15	73077322	11.308	0.12	Ago2	intron (NM_001130409, intron 23 of 29)
chr12	36693596	-26.680	0.012	Agr2	Intergenic
chr12	36693372	-11.235	0.113	Agr2	Intergenic
chr13	59601952	13.103	0.039	Agtbbp1	exon (NM_023328, exon 14 of 26)
chr13	59601117	9.505	0.124	Agtbbp1	intron (NM_001284219, intron 13 of 24)
chr6	29719657	-10.048	0.149	Ahcy12	intron (NM_001171000, intron 1 of 16)
chr3	152220241	-9.281	0.16	Al115009	intron (NM_001081277, intron 6 of 13)
chr3	152220538	-13.141	0.165	Al115009	intron (NM_001081277, intron 6 of 13)
chr12	77706947	19.948	0.011	Al463170	intron (NM_013675, intron 23 of 35)
chr11	71842920	-14.363	0.06	Aipl1	exon (NM_053245, exon 6 of 6)
chr11	71842953	-10.871	0.122	Aipl1	exon (NM_053245, exon 6 of 6)
chr11	71842962	-8.665	0.133	Aipl1	intron (NM_053245, intron 5 of 5)
chr11	71842928	-7.118	0.2	Aipl1	exon (NM_053245, exon 6 of 6)
chr17	12919056	-21.236	0.031	Airn	exon (NM_010515, exon 9 of 48)
chr14	78941158	-21.472	0.013	Akap11	Intergenic
chr14	78941302	-12.607	0.182	Akap11	Intergenic
chr12	54040465	-17.221	0.035	Akap6	intron (NM_198111, intron 7 of 13)
chr12	54040490	-12.844	0.122	Akap6	intron (NM_198111, intron 7 of 13)
chr12	54040395	-11.276	0.16	Akap6	intron (NM_198111, intron 7 of 13)
chr10	24919413	-13.127	0.02	Akap7	intron (NM_018747, intron 7 of 7)
chr10	24919542	-10.958	0.06	Akap7	intron (NM_018747, intron 7 of 7)
chr10	24919516	-9.206	0.068	Akap7	intron (NM_018747, intron 7 of 7)
chr10	24919171	7.867	0.143	Akap7	intron (NM_018747, intron 7 of 7)
chr10	24919229	-9.641	0.147	Akap7	intron (NM_018747, intron 7 of 7)
chr6	37449684	-14.475	0.028	Akr1d1	IAP-d-int LTR ERVK
chr6	37608167	10.899	0.116	Akr1d1	Intergenic
chr6	37608275	11.820	0.148	Akr1d1	Intergenic
chr5	122042316	-23.617	0.024	Aldh2	intron (NM_009656, intron 1 of 12)
chr5	122042268	-13.512	0.108	Aldh2	intron (NM_009656, intron 1 of 12)
chr3	120993673	-12.421	0.079	Alg14	Intergenic
chr3	120993977	-19.921	0.08	Alg14	promoter-TSS (NM_024178)

chr3	120993764	-10.577	0.153	Alg14	promoter-TSS (NM_024178)
chr3	54540205	-9.091	0.022	Alg5	promoter-TSS (NM_001163570)
chr3	54540272	-6.585	0.169	Alg5	promoter-TSS (NM_001163570)
chr11	70171195	-15.903	0.106	Alox15	Intergenic
chr11	70171042	-11.663	0.115	Alox15	Intergenic
chr5	150099247	-11.171	0.108	Alox5ap	exon (NM_009663, exon 5 of 5)
chr5	150099173	-9.533	0.133	Alox5ap	exon (NM_009663, exon 5 of 5)
chr5	150099586	-11.883	0.136	Alox5ap	TTS (NM_009663)
chr5	150099050	-10.471	0.155	Alox5ap	CpG
chr5	150099048	-7.331	0.199	Alox5ap	CpG
chr3	127461737	8.033	0.118	Alpk1	intron (NM_027808, intron 1 of 13)
chr3	127461742	13.525	0.133	Alpk1	intron (NM_027808, intron 1 of 13)
chr3	127461745	9.630	0.142	Alpk1	intron (NM_027808, intron 1 of 13)
chr1	34635685	-5.217	0.06	Amer3	promoter-TSS (NM_213727)
chr1	34635633	-10.928	0.129	Amer3	promoter-TSS (NM_213727)
chr15	97117365	-19.099	0.036	Amigo2	intron (NM_172293, intron 3 of 5)
chr15	97117261	-13.313	0.147	Amigo2	intron (NM_172293, intron 3 of 5)
chr9	102617293	-13.616	0.06	Amotl2	Intergenic
chr9	102617385	-13.854	0.135	Amotl2	Intergenic
chr13	19094322	-17.370	0.036	Amph	intron (NM_175007, intron 1 of 20)
chr13	19094613	-13.977	0.095	Amph	intron (NM_175007, intron 1 of 20)
chr3	126738949	-17.138	0.096	Ank2	Intergenic
chr3	126738940	-12.700	0.2	Ank2	Intergenic
chr10	68995090	13.225	0.04	Ank3	Intergenic
chr8	11633346	12.475	0.062	Ankrd10	intron (NM_001281974, intron 1 of 6)
chr17	66410944	20.817	0.032	Ankrd12	intron (NM_001025572, intron 1 of 12)
chr3	38296216	-9.849	0.134	Ankrd50	Intergenic
chr4	32950239	-12.589	0.165	Ankrd6	intron (NM_001012451, intron 1 of 15)
chr4	32950151	-9.923	0.182	Ankrd6	intron (NM_001012451, intron 1 of 15)
chr9	22177733	-14.151	0.059	Anln	exon (NM_028390, exon 6 of 24)
chr9	22177705	-9.151	0.153	Anln	exon (NM_028390, exon 6 of 24)
chr9	22177745	-9.374	0.182	Anln	exon (NM_028390, exon 6 of 24)
chr15	95628149	-9.713	0.066	Ano6	intron (NM_175344, intron 1 of 19)
chr15	95556634	-16.452	0.1	Ano6	Intergenic
chr15	95628147	-7.153	0.131	Ano6	intron (NM_175344, intron 1 of 19)
chr15	95556534	-8.808	0.194	Ano6	Intergenic
chr7	148308273	-18.676	0.048	Ano9	Intergenic
chr7	148308173	-13.327	0.048	Ano9	Intergenic
chr7	148308149	-9.973	0.095	Ano9	Intergenic
chr7	148308255	-11.436	0.18	Ano9	Intergenic
chr9	62186274	11.928	0.1	Anp32a	Intergenic
chr14	26681480	-14.892	0.133	Anxa11	intron (NM_013469, intron 1 of 14)
chr14	26681467	-13.319	0.178	Anxa11	intron (NM_013469, intron 1 of 14)
chr5	97145514	14.318	0.138	Anxa3	intron (NM_175473, intron 47 of 73)
chr5	97145523	13.367	0.176	Anxa3	intron (NM_175473, intron 47 of 73)
chr5	97145446	9.898	0.184	Anxa3	intron (NM_175473, intron 47 of 73)



chr11	54860449	10.869	0.041	Anxa6	Intergenic
chr2	94275343	-16.238	0.107	Api5	intron (NM_007466, intron 1 of 13)
chr2	94275599	-11.686	0.128	Api5	intron (NM_007466, intron 1 of 13)
chr16	85171188	-10.374	0.048	App	intron (NM_001198824, intron 1 of 16)
chr16	85171404	-7.559	0.098	App	intron (NM_001198824, intron 1 of 16)
chr16	85171618	-7.932	0.135	App	intron (NM_001198824, intron 1 of 16)
chr7	104898159	-13.798	0.059	Aqp11	Intergenic
chrX	95346863	-19.845	0.083	Ar	intron (NM_013476, intron 1 of 7)
chrX	20425186	-7.436	0.116	Araf	promoter-TSS (NM_009703)
chr14	34016333	-11.970	0.158	Arhgap22	Intergenic
chr14	34016380	-10.025	0.167	Arhgap22	Intergenic
chr5	102912513	-15.581	0.09	Arhgap24	intron (NM_146161, intron 1 of 8)
chr5	102912860	-13.139	0.18	Arhgap24	intron (NM_146161, intron 1 of 8)
chr6	87485677	-15.441	0.065	Arhgap25	Intergenic
chr6	87485355	-15.426	0.096	Arhgap25	Intergenic
chr6	87485448	-11.670	0.104	Arhgap25	Intergenic
chr6	87485372	-12.920	0.155	Arhgap25	Intergenic
chr6	87485671	-11.112	0.183	Arhgap25	Intergenic
chr11	64976992	-10.617	0.069	Arhgap44	promoter-TSS (NM_175003)
chr11	64976670	-11.069	0.1	Arhgap44	promoter-TSS (NM_175003)
chrX	165566097	-21.582	0.028	Arhgap6	intron (NM_001287530, intron 1 of 12)
chr3	62153526	14.543	0.109	Arhgef26	intron (NM_001081295, intron 3 of 13)
chr3	62153612	12.584	0.125	Arhgef26	intron (NM_001081295, intron 3 of 13)
chr3	62153601	11.606	0.165	Arhgef26	intron (NM_001081295, intron 3 of 13)
chr8	97173592	17.034	0.038	Arl2bp	intron (NM_026274, intron 11 of 14)
chr8	97173600	12.102	0.115	Arl2bp	intron (NM_026274, intron 11 of 14)
chr11	101523580	10.637	0.048	Arl4d	Intergenic
chr11	101528058	-15.087	0.11	Arl4d	exon (NM_025404, exon 2 of 2)
chr11	101523215	16.963	0.123	Arl4d	Intergenic
chr11	101528056	-13.587	0.124	Arl4d	exon (NM_025404, exon 2 of 2)
chr11	101528110	-11.667	0.187	Arl4d	exon (NM_025404, exon 2 of 2)
chr2	53063804	-11.000	0.02	Arl6ip6	intron (NM_022989, intron 3 of 3)
chr5	21179146	15.988	0.073	Armc10	intron (NM_178728, intron 3 of 4)
chr5	21179078	10.959	0.184	Armc10	intron (NM_178728, intron 3 of 4)
chr10	41768100	-11.328	0.029	Armc2	Intergenic
chr10	41775730	-10.810	0.049	Armc2	Intergenic
chr10	41775647	-11.889	0.069	Armc2	Intergenic
chr7	91556454	-14.268	0.046	Arnt2	intron (NM_007488, intron 1 of 18)
chr7	91556663	-10.780	0.136	Arnt2	intron (NM_007488, intron 1 of 18)
chr7	91556718	-8.114	0.176	Arnt2	intron (NM_007488, intron 1 of 18)
chr15	64133182	-17.465	0.042	Asap1	intron (NM_001276467, intron 3 of 29)
chr4	135771099	21.097	0.007	Asap3	MIRb SINE MIR
chr4	135771087	12.688	0.093	Asap3	MIRb SINE MIR
chr11	80962306	-14.447	0.027	Asic2	intron (NM_001034013, intron 1 of 9)
chr11	80962224	-7.734	0.155	Asic2	intron (NM_001034013, intron 1 of 9)
chr19	32801491	12.228	0.124	Atad1	Intergenic

chr1	172801927	-13.035	0.038	Atf6	Intergenic
chr13	91318085	27.060	0.012	Atg10	intron (NM_025770, intron 2 of 7)
chr13	91318095	19.694	0.043	Atg10	intron (NM_025770, intron 2 of 7)
chr18	46900241	20.548	0.063	Atg12	intron (NM_026217, intron 1 of 3)
chr6	114651226	-16.262	0.036	Atg7	exon (NM_001253717, exon 11 of 20)
chr6	114532249	-9.460	0.096	Atg7	Intergenic
chr6	114532253	-8.120	0.131	Atg7	Intergenic
chr6	114532093	-7.907	0.147	Atg7	Intergenic
chr6	114485794	-5.324	0.171	Atg7	Intergenic
chr6	114485729	-6.584	0.175	Atg7	Intergenic
chr1	174173922	22.666	0.039	Atp1a4	intron (NM_013734, intron 11 of 22)
chr1	166371083	-15.789	0.026	Atp1b1	intron (NM_009721, intron 4 of 5)
chr1	166371384	-13.901	0.076	Atp1b1	intron (NM_009721, intron 4 of 5)
chr1	166371355	-7.858	0.131	Atp1b1	intron (NM_009721, intron 4 of 5)
chr9	96299146	17.933	0.034	Atp1b3	Intergenic
chr10	98301958	-10.887	0.052	Atp2b1	Intergenic
chr10	98167733	-15.947	0.092	Atp2b1	Intergenic
chr10	98167770	-13.036	0.148	Atp2b1	Intergenic
chr1	135651165	21.965	0.036	Atp2b4	promoter-TSS (NM_001167949)
chr16	84876446	-10.658	0.054	Atp5j	Intergenic
chr8	71551827	9.328	0.107	Atp6v1b2	Intergenic
chr8	71551727	13.894	0.16	Atp6v1b2	Intergenic
chr8	71551900	7.667	0.196	Atp6v1b2	Intergenic
chr1	140224686	-9.861	0.053	Atp6v1g3	Intergenic
chr1	140224627	-9.814	0.072	Atp6v1g3	Intergenic
chr1	140224422	-11.533	0.11	Atp6v1g3	Intergenic
chr1	140224386	-12.412	0.146	Atp6v1g3	Intergenic
chr19	57635436	19.345	0.065	Atrnl1	Intergenic
chr13	45860686	-10.388	0.137	Atxn1	intron (NM_009124, intron 4 of 7)
chr13	45860632	-10.560	0.166	Atxn1	ID_B1 SINE B4
chr12	34029889	-11.269	0.043	Atxn711	intron (NM_001033436, intron 4 of 7)
chr12	34030857	-19.638	0.054	Atxn711	exon (NM_001033436, exon 5 of 8)
chr12	34029798	-16.841	0.071	Atxn711	exon (NM_001033436, exon 4 of 8)
chr12	33910236	11.971	0.088	Atxn711	intron (NM_028139, intron 3 of 3)
chr12	33910034	13.127	0.103	Atxn711	intron (NM_028139, intron 3 of 3)
chr12	34029918	-8.252	0.132	Atxn711	intron (NM_001033436, intron 4 of 7)
chr2	132421493	14.950	0.089	AU019990	Intergenic
chr2	132421417	12.902	0.158	AU019990	Intergenic
chr5	132875618	-20.730	0.043	Auts2	intron (NM_177047, intron 1 of 18)
chr15	88020983	-15.248	0.039	B230214G05Rik	Intergenic
chr6	83411433	17.454	0.014	B230319C09Rik	Intergenic
chr4	141100924	-8.320	0.07	B330016D10Rik	Intergenic
chr9	26567758	-18.686	0.052	B3gat1	3' UTR (NM_029792, exon 5 of 5)
chr9	26567685	-11.889	0.078	B3gat1	3' UTR (NM_029792, exon 5 of 5)
chr9	26567603	-15.388	0.108	B3gat1	3' UTR (NM_029792, exon 5 of 5)
chr1	23682253	14.787	0.004	B3gat2	Intergenic

chr1	88165756	13.261	0.045	B3gnt7	intron (NM_030184, intron 23 of 24)
chr1	88165499	8.833	0.171	B3gnt7	intron (NM_030184, intron 23 of 24)
chr10	126605469	-16.739	0.065	B4galnt1	3' UTR (NM_001244618, exon 5 of 5)
chr10	126607035	17.660	0.084	B4galnt1	exon (NM_027739, exon 7 of 10)
chr10	126603701	13.479	0.11	B4galnt1	intron (NM_008080, intron 2 of 10)
chr10	126607099	14.319	0.134	B4galnt1	exon (NM_027739, exon 7 of 10)
chr10	126607384	15.455	0.135	B4galnt1	intron (NM_008080, intron 8 of 10)
chr10	126605306	-8.698	0.144	B4galnt1	3' UTR (NM_001244618, exon 5 of 5)
chr10	126607235	14.281	0.146	B4galnt1	intron (NM_008080, intron 8 of 10)
chr10	126603636	7.286	0.188	B4galnt1	intron (NM_008080, intron 2 of 10)
chr10	126607136	11.699	0.189	B4galnt1	exon (NM_027739, exon 7 of 10)
chr4	40801925	10.701	0.152	B4galnt1	promoter-TSS (NM_022305)
chr4	40801913	14.103	0.181	B4galnt1	promoter-TSS (NM_022305)
chr4	40801899	13.919	0.184	B4galnt1	promoter-TSS (NM_022305)
chr8	10768485	-10.784	0.095	B930025P03Rik	Intergenic
chr9	61107573	20.707	0.038	B930092H01Rik	non-coding (NR_045334, exon 5 of 5)
chr9	61107587	12.293	0.194	B930092H01Rik	non-coding (NR_045334, exon 5 of 5)
chr4	32337522	-7.866	0.131	Bach2	Intergenic
chr4	32337826	-6.176	0.182	Bach2	Intergenic
chr4	32337734	-6.463	0.194	Bach2	Intergenic
chr1	25753954	-14.993	0.031	Bai3	intron (NM_175642, intron 2 of 30)
chr18	3481148	-12.291	0.109	Bambi	RLTR41 LTR ERV1
chr18	3481799	-6.005	0.195	Bambi	Intergenic
chr5	106846161	-15.503	0.042	Barhl2	Intergenic
chr5	106846150	-13.952	0.076	Barhl2	Intergenic
chr11	112594230	-14.527	0.064	BC006965	Intergenic
chr11	112594265	-17.200	0.065	BC006965	Intergenic
chr10	121232985	18.029	0.02	BC048403	intron (NM_001242411, intron 18 of 21)
chr10	121232948	9.852	0.111	BC048403	intron (NM_001242411, intron 18 of 21)
chr10	121232975	7.977	0.153	BC048403	intron (NM_001242411, intron 18 of 21)
chr8	124437614	-15.342	0.139	BC048644	intron (NM_001033485, intron 1 of 1)
chr7	116863127	-24.017	0.029	BC051019	intron (NM_001040700, intron 3 of 5)
chr7	116863140	-19.540	0.059	BC051019	intron (NM_001040700, intron 3 of 5)
chr5	123768000	-17.853	0.048	Bcl7a	Intergenic
chr5	123768028	-14.183	0.092	Bcl7a	Intergenic
chr5	123768107	-11.174	0.179	Bcl7a	Intergenic
chr10	70594248	19.545	0.034	Bicc1	intron (NM_031397, intron 1 of 20)
chr10	70623366	-13.514	0.085	Bicc1	promoter-TSS (NM_031397)
chr10	70594239	16.962	0.095	Bicc1	intron (NM_031397, intron 1 of 20)
chr10	70623278	-9.543	0.097	Bicc1	promoter-TSS (NM_031397)
chr10	70623438	-13.006	0.114	Bicc1	Intergenic
chr10	70594250	13.451	0.129	Bicc1	intron (NM_031397, intron 1 of 20)
chr10	70623487	-13.038	0.135	Bicc1	Intergenic
chr5	97340810	-14.317	0.043	Bmp2k	Intergenic
chr5	97340817	-11.252	0.147	Bmp2k	Intergenic

chr5	97340657	-9.151	0.172	Bmp2k	Intergenic
chr5	97340758	-9.975	0.199	Bmp2k	Intergenic
chr14	67618237	-5.426	0.169	Bnip3l	intron (NM_009761, intron 2 of 5)
chr14	67618550	-9.297	0.198	Bnip3l	intron (NM_009761, intron 1 of 5)
chr9	108066430	-16.599	0.093	Bsn	intron (NM_007567, intron 1 of 11)
chr9	108066484	-14.678	0.182	Bsn	intron (NM_007567, intron 1 of 11)
chr10	96200259	-24.107	0.039	Btg1	Intergenic
chr19	45404436	18.880	0.087	Btrc	Intergenic
chr19	45404445	14.861	0.148	Btrc	Intergenic
chr19	45404582	11.808	0.173	Btrc	Intergenic
chr19	45404485	11.923	0.185	Btrc	Intergenic
chr1	88268495	-6.364	0.023	C130036L24Rik	Intergenic
chr13	83853571	-6.030	0.087	C130071C03Rik	Intergenic
chr13	83853550	-6.827	0.088	C130071C03Rik	Intergenic
chr13	83853665	-7.090	0.166	C130071C03Rik	Intergenic
chr13	83853695	-6.652	0.199	C130071C03Rik	Intergenic
chr6	7793841	14.356	0.085	C1galt1	Intergenic
chr6	7793482	8.456	0.14	C1galt1	Intergenic
chr6	7793563	7.964	0.18	C1galt1	Intergenic
chr2	90710591	-7.828	0.173	C1qtnf4	Intergenic
chr13	23521852	16.408	0.1	C230035I16Rik	intron (NR_015492, intron 2 of 3)
chr16	98144638	-8.602	0.031	C2cd2	promoter-TSS (NM_174847)
chr4	104566965	-18.480	0.031	C8a	Intergenic
chr9	78012268	-9.087	0.102	C920006O11Rik	intron (NM_001163780, intron 11 of 13)
chr9	78012357	-6.900	0.135	C920006O11Rik	exon (NM_019987, exon 12 of 14)
chr2	24549981	-7.188	0.108	Cacna1b	intron (NM_007579, intron 15 of 45)
chr2	24549961	-8.886	0.164	Cacna1b	intron (NM_007579, intron 15 of 45)
chr15	80170753	18.421	0.024	Cacna1i	intron (NM_001044308, intron 5 of 36)
chr2	52434625	19.330	0.022	Cacnb4	intron (NM_001037099, intron 2 of 13)
chr2	52434800	12.607	0.057	Cacnb4	intron (NM_001037099, intron 2 of 13)
chr2	52434591	9.908	0.195	Cacnb4	intron (NM_001037099, intron 2 of 13)
chr9	47432878	-15.549	0.041	Cadm1	intron (NM_001025600, intron 1 of 8)
chr9	47340896	11.752	0.046	Cadm1	intron (NM_001025600, intron 1 of 8)
chr9	47432901	-12.593	0.111	Cadm1	intron (NM_001025600, intron 1 of 8)
chr16	67317733	-11.733	0.087	Cadm2	intron (NM_178721, intron 1 of 9)
chr16	67317982	-12.788	0.133	Cadm2	intron (NM_178721, intron 1 of 9)
chr16	67317943	-8.534	0.158	Cadm2	intron (NM_178721, intron 1 of 9)
chr7	25258025	-14.121	0.016	Cadm4	intron (NM_011113, intron 5 of 6)
chr8	74967328	-8.795	0.115	Calr3	promoter-TSS (NM_028170)
chr8	74967279	-10.185	0.143	Calr3	promoter-TSS (NM_028170)
chr8	74967224	-12.952	0.196	Calr3	promoter-TSS (NM_028170)
chr18	61137795	-16.735	0.043	Camk2a	intron (NM_177407, intron 15 of 17)
chr18	61137830	-11.721	0.118	Camk2a	intron (NM_177407, intron 15 of 17)
chr18	61137801	-10.720	0.13	Camk2a	intron (NM_177407, intron 15 of 17)
chr14	21615964	17.393	0.009	Camk2g	Intergenic
chr14	21616240	15.096	0.031	Camk2g	Intergenic

chr14	21615891	17.702	0.038	Camk2g	Intergenic
chr14	21616305	11.011	0.078	Camk2g	Intergenic
chr14	21616029	7.866	0.133	Camk2g	Intergenic
chr5	123250363	-15.991	0.043	Camkk2	intron (NM_021505, intron 10 of 16)
chr5	123250380	-12.843	0.096	Camkk2	intron (NM_021505, intron 10 of 16)
chr3	14679299	9.673	0.073	Car13	Intergenic
chr3	14679235	12.636	0.126	Car13	Intergenic
chr11	84757730	20.777	0.012	Car4	Intergenic
chr11	119171877	-13.202	0.151	Card14	Intergenic
chr11	119171894	-11.169	0.195	Card14	Intergenic
chr8	11542566	6.934	0.091	Cars2	exon (NM_024248, exon 4 of 15)
chr6	4602938	11.167	0.054	Casd1	Intergenic
chr6	4602947	5.671	0.167	Casd1	Intergenic
chr6	4602927	8.849	0.17	Casd1	Intergenic
chr1	174146963	-16.521	0.045	Casq1	exon (NM_009813, exon 3 of 11)
chr8	125200262	-9.787	0.165	Cbfa2t3	intron (NM_009824, intron 1 of 11)
chr8	63877069	-9.975	0.021	Cbr4	Intergenic
chr11	118919471	-6.649	0.123	Cbx8	Intergenic
chr11	118919492	-8.073	0.187	Cbx8	Intergenic
chr18	66450470	-16.095	0.012	Ccbe1	intron (NM_178793, intron 2 of 10)
chr18	66450633	-13.417	0.123	Ccbe1	intron (NM_178793, intron 2 of 10)
chr18	66450566	-7.094	0.159	Ccbe1	intron (NM_178793, intron 2 of 10)
chr18	66450378	-8.078	0.192	Ccbe1	intron (NM_178793, intron 2 of 10)
chr2	69604360	-10.315	0.031	Ccdc173	intron (NM_001077684, intron 7 of 8)
chr2	69604215	-11.203	0.075	Ccdc173	intron (NM_001077684, intron 7 of 8)
chr12	81836220	10.015	0.033	Ccdc177	Intergenic
chr12	81840794	11.819	0.033	Ccdc177	Intergenic
chr2	5326652	-9.346	0.02	Ccdc3	intron (NM_177343, intron 3 of 10)
chr2	5326642	-11.051	0.105	Ccdc3	intron (NM_177343, intron 3 of 10)
chr10	69516173	8.537	0.042	Ccdc6	Intergenic
chr3	65733695	-11.780	0.02	Ccnl1	Intergenic
chr4	155187652	19.120	0.05	Ccnl2	exon (NM_207678, exon 3 of 11)
chr18	9393279	-14.746	0.041	Ccny	intron (NM_026484, intron 1 of 9)
chr18	9393209	-11.515	0.1	Ccny	intron (NM_026484, intron 1 of 9)
chr10	116506248	-14.345	0.096	Cct2	TTS (NM_177798)
chr10	116506479	-11.800	0.108	Cct2	TTS (NM_177798)
chr13	103499099	5.303	0.036	Cd180	Intergenic
chr11	114932827	13.254	0.116	Cd300e	Intergenic
chr11	114932882	12.842	0.136	Cd300e	Intergenic
chr11	114913852	13.471	0.142	Cd300lh	3' UTR (NM_172050, exon 4 of 4)
chr11	114913734	14.426	0.157	Cd300lh	3' UTR (NM_172050, exon 4 of 4)
chr11	114913736	13.556	0.197	Cd300lh	3' UTR (NM_172050, exon 4 of 4)
chr2	60121468	-14.329	0.021	Cd302	intron (NM_025422, intron 1 of 4)
chr2	60121142	-18.398	0.075	Cd302	intron (NM_025422, intron 1 of 4)
chr2	60121326	-10.634	0.149	Cd302	intron (NM_025422, intron 1 of 4)
chr2	60121544	-7.610	0.183	Cd302	intron (NM_025422, intron 1 of 4)

chr2	60121554	-8.657	0.187	Cd302	intron (NM_025422, intron 1 of 4)
chr1	196765761	-11.146	0.122	Cd34	intron (NM_133654, intron 1 of 7)
chr1	196765680	-11.098	0.158	Cd34	intron (NM_133654, intron 1 of 7)
chr16	49792814	-6.888	0.04	Cd47	Intergenic
chr16	49792844	-6.848	0.075	Cd47	Intergenic
chr16	49792953	-10.552	0.095	Cd47	Intergenic
chr16	49792851	-7.308	0.13	Cd47	Intergenic
chr16	18799019	-22.237	0.043	Cdc45	intron (NM_001161623, intron 6 of 17)
chr11	98764399	14.714	0.073	Cdc6	3' UTR (NM_197940, exon 8 of 8)
chr11	98764361	11.169	0.182	Cdc6	3' UTR (NM_197940, exon 8 of 8)
chr11	98764405	9.135	0.188	Cdc6	3' UTR (NM_197940, exon 8 of 8)
chr2	72315767	11.144	0.114	Cdca7	intron (NM_025866, intron 1 of 8)
chr2	72315762	8.037	0.129	Cdca7	intron (NM_025866, intron 1 of 8)
chr2	72315646	12.264	0.19	Cdca7	intron (NM_025866, intron 1 of 8)
chr12	119186008	-15.050	0.029	Cdca7l	intron (NM_010060, intron 65 of 81)
chr8	105311220	-16.658	0.068	Cdh11	Intergenic
chr8	105311218	-12.441	0.135	Cdh11	Intergenic
chr4	11781090	16.463	0.123	Cdh17	Intergenic
chr8	101924785	-24.263	0.03	Cdh8	exon (NM_001285913, exon 2 of 13)
chr8	101924904	-17.064	0.074	Cdh8	5' UTR (NM_001285913, exon 2 of 13)
chr8	101924008	-11.409	0.093	Cdh8	intron (NM_001039154, intron 2 of 12)
chr8	100590024	-9.072	0.1	Cdh8	Intergenic
chr8	100590318	-10.925	0.15	Cdh8	Intergenic
chr8	100590414	-11.397	0.158	Cdh8	Intergenic
chr8	101924769	-12.256	0.185	Cdh8	exon (NM_001285913, exon 2 of 13)
chr5	5419943	-11.943	0.075	Cdk14	Intergenic
chr5	5419967	-8.641	0.16	Cdk14	Intergenic
chr6	134867131	-8.537	0.049	Cdkn1b	Intergenic
chr5	102276863	14.451	0.018	Cds1	intron (NM_172882, intron 62 of 66)
chr1	191510145	-14.788	0.039	Cenpf	intron (NM_001081363, intron 1 of 17)
chr9	45553820	21.220	0.042	Cep164	intron (NM_001081270, intron 26 of 32)
chr10	53084763	12.687	0.027	Cep85l	intron (NM_001204983, intron 1 of 12)
chr10	53084730	14.918	0.097	Cep85l	intron (NM_001204983, intron 1 of 12)
chr10	53120535	-10.772	0.107	Cep85l	Intergenic
chr10	53120507	-9.930	0.149	Cep85l	Intergenic
chr10	53084733	11.863	0.165	Cep85l	intron (NM_001204983, intron 1 of 12)
chr15	86007718	-17.883	0.061	Cerk	intron (NM_145475, intron 1 of 12)
chr6	103463194	-10.334	0.058	Chl1	intron (NM_007697, intron 1 of 26)
chr6	103699570	-13.364	0.141	Chl1	Intergenic
chr2	92445362	-17.821	0.089	Chst1	intron (NM_023850, intron 1 of 2)
chr2	92445356	-13.814	0.155	Chst1	intron (NM_023850, intron 1 of 2)
chr9	95305414	-12.185	0.182	Chst2	exon (NM_018763, exon 2 of 2)
chr9	95305363	-13.651	0.198	Chst2	exon (NM_018763, exon 2 of 2)
chr10	17268751	9.602	0.035	Cited2	Intergenic
chr4	120347256	16.893	0.041	Cited4	Intergenic
chr3	144471594	-17.241	0.095	Clca2	exon (NM_030601, exon 8 of 14)

chr3	144471615	-11.467	0.199	Clca2	exon (NM_030601, exon 8 of 14)
chr3	31057158	9.132	0.149	Cldn11	intron (NM_008770, intron 2 of 2)
chr16	94041488	10.977	0.19	Cldn14	Intergenic
chr5	135443473	13.331	0.104	Cldn3	Intergenic
chr7	51562380	-9.073	0.095	Clec11a	promoter-TSS (NM_009131)
chr7	51562393	-10.209	0.107	Clec11a	promoter-TSS (NM_009131)
chr17	44393520	-22.669	0.021	Clic5	intron (NM_172621, intron 4 of 5)
chr17	44381208	15.615	0.058	Clic5	intron (NM_172621, intron 3 of 5)
chr17	44393613	-7.467	0.17	Clic5	intron (NM_172621, intron 4 of 5)
chr16	92553266	-10.185	0.136	Clic6	Intergenic
chr16	92553257	-9.167	0.196	Clic6	Intergenic
chr5	134998887	-17.690	0.047	Clip2	exon (NM_009990, exon 3 of 17)
chr5	134998854	-13.900	0.087	Clip2	exon (NM_009990, exon 3 of 17)
chr17	72154977	10.732	0.033	Clip4	intron (NR_073185, intron 6 of 16)
chr17	72347247	-13.278	0.197	Clip4	intron (NM_007439, intron 5 of 28)
chr12	106146440	-11.013	0.138	Clmn	Intergenic
chr16	57583082	-7.813	0.09	Cmss1	intron (NM_025599, intron 1 of 9)
chr16	57583241	-7.842	0.115	Cmss1	intron (NM_025599, intron 1 of 9)
chr8	106833408	-11.636	0.092	Cmtm1	exon (NM_181990, exon 1 of 4)
chr8	106833375	-9.858	0.125	Cmtm1	intron (NM_181990, intron 1 of 3)
chr8	106833310	-8.574	0.152	Cmtm1	intron (NM_181990, intron 1 of 3)
chr6	87804666	9.807	0.049	Cnbp	Intergenic
chr6	87804683	8.097	0.155	Cnbp	Intergenic
chr6	87804718	6.160	0.167	Cnbp	Intergenic
chr10	3132898	-10.913	0.096	Cnksr3	Intergenic
chr10	3132960	-17.375	0.105	Cnksr3	Intergenic
chr19	43514226	-12.148	0.072	Cnnm1	promoter-TSS (NM_031396)
chr19	43514180	-10.609	0.1	Cnnm1	promoter-TSS (NM_031396)
chr19	43514223	-8.926	0.164	Cnnm1	promoter-TSS (NM_031396)
chr4	33803520	-12.983	0.127	Cnr1	Intergenic
chr9	10689703	15.095	0.033	Cntn5	intron (NM_001033359, intron 1 of 20)
chr6	104934441	24.280	0.02	Cntn6	Intergenic
chr6	47141819	13.697	0.116	Cntnap2	intron (NM_001004357, intron 20 of 23)
chr8	127054357	-20.192	0.055	Cog2	intron (NM_029746, intron 5 of 17)
chr8	127054418	-14.913	0.123	Cog2	intron (NM_029746, intron 5 of 17)
chr8	127054188	-10.679	0.135	Cog2	intron (NM_029746, intron 5 of 17)
chr7	129107335	-9.468	0.14	Cog7	intron (NM_001033318, intron 5 of 16)
chr15	71926844	16.818	0.031	Col22a1	Intergenic
chr11	51134691	13.524	0.036	Col23a1	intron (NM_153393, intron 2 of 28)
chr5	137339921	-11.700	0.103	Col26a1	intron (NM_024474, intron 1 of 12)
chr5	137339913	-9.080	0.196	Col26a1	intron (NM_024474, intron 1 of 12)
chr8	11308753	-11.362	0.11	Col4a1	intron (NM_009931, intron 1 of 51)
chr8	11184080	-12.747	0.113	Col4a1	Intergenic
chr8	11184097	-12.225	0.148	Col4a1	Intergenic
chr8	11308856	-11.136	0.149	Col4a1	intron (NM_009931, intron 1 of 51)
chr12	29307182	-17.987	0.018	Colec11	intron (NM_027866, intron 1 of 6)

chr2	101749217	-18.376	0.039	Commd9	Intergenic
chr2	101749220	-17.991	0.042	Commd9	Intergenic
chr9	62371000	-17.480	0.033	Coro2b	intron (NM_175484, intron 1 of 11)
chr1	180205746	-14.533	0.081	Cox20	Intergenic
chr1	180205729	-14.590	0.099	Cox20	Intergenic
chr6	30499700	15.114	0.038	Cpa2	intron (NM_001024698, intron 6 of 10)
chr11	31761443	8.312	0.062	Cpeb4	Intergenic
chr8	97073412	14.543	0.134	Cpne2	intron (NM_153507, intron 2 of 15)
chr8	97073502	11.063	0.151	Cpne2	intron (NM_153507, intron 2 of 15)
chr1	68153119	-9.179	0.195	Cps1	intron (NM_010154, intron 20 of 26)
chr10	94753969	14.643	0.007	Cradd	intron (NM_009950, intron 2 of 2)
chr10	94717071	14.250	0.061	Cradd	intron (NM_009950, intron 2 of 2)
chr2	91896551	-24.163	0.03	Creb3l1	Intergenic
chr2	91896553	-17.766	0.094	Creb3l1	Intergenic
chr2	91896545	-12.831	0.194	Creb3l1	Intergenic
chr7	87842020	11.101	0.08	Crtc3	Intergenic
chr7	87842077	16.159	0.124	Crtc3	Intergenic
chr7	127344417	15.192	0.046	Crym	intron (NM_016669, intron 2 of 7)
chr7	127344470	17.466	0.047	Crym	intron (NM_016669, intron 2 of 7)
chr7	127344320	16.687	0.049	Crym	intron (NM_016669, intron 2 of 7)
chr1	137583296	-14.752	0.039	Csrp1	Intergenic
chr1	137560838	-13.400	0.107	Csrp1	Intergenic
chr1	137583292	-8.139	0.172	Csrp1	Intergenic
chr1	137560684	-15.214	0.188	Csrp1	Intergenic
chr18	80692749	-14.837	0.062	Ctdp1	Intergenic
chr10	126418197	-7.057	0.1	Ctdsp2	intron (NM_001113470, intron 1 of 7)
chr15	38892987	8.427	0.036	Cthrc1	Intergenic
chr10	62918401	-14.483	0.118	Ctnna3	intron (NM_177612, intron 1 of 17)
chr10	62918293	-12.139	0.122	Ctnna3	intron (NM_177612, intron 1 of 17)
chr10	62918364	-8.859	0.158	Ctnna3	intron (NM_177612, intron 1 of 17)
chr15	30312963	14.238	0.118	Ctnnd2	intron (NM_008729, intron 2 of 22)
chr15	30312860	11.538	0.192	Ctnnd2	intron (NM_008729, intron 2 of 22)
chr3	95321273	21.140	0.02	Ctss	Intergenic
chr3	95321412	9.375	0.06	Ctss	Intergenic
chr6	18323269	12.842	0.115	Cttnbp2	intron (NM_080285, intron 22 of 22)
chr6	18323259	12.512	0.126	Cttnbp2	intron (NM_080285, intron 22 of 22)
chr11	87959167	-14.971	0.048	Cuedc1	intron (NM_198013, intron 1 of 10)
chr11	87959163	-10.457	0.127	Cuedc1	intron (NM_198013, intron 1 of 10)
chr5	137069362	8.162	0.118	Cux1	Intergenic
chr5	137069407	7.070	0.168	Cux1	Intergenic
chr5	122512851	-13.347	0.158	Cux2	Intergenic
chr5	122512963	-9.634	0.165	Cux2	Intergenic
chr5	122512930	-8.482	0.173	Cux2	Intergenic
chr5	122512991	-10.474	0.197	Cux2	Intergenic
chr13	105518118	-16.713	0.014	Cwc27	intron (NM_026072, intron 10 of 13)
chr1	130729713	11.474	0.16	Cxcr4	Intergenic



chr1	130729665	10.442	0.184	Cxcr4	Intergenic
chr1	130729128	12.702	0.197	Cxcr4	Intergenic
chr18	36032601	-19.802	0.05	Cxxc5	Intergenic
chr18	36032620	-12.165	0.181	Cxxc5	Intergenic
chr9	86917522	16.284	0.104	Cyb5r4	intron (NM_024195, intron 1 of 15)
chr8	124956196	-20.828	0.052	Cyba	intron (NM_007806, intron 1 of 5)
chr2	70980582	14.922	0.075	Cybrd1	3' UTR (NM_028593, exon 4 of 4)
chr2	70980613	11.348	0.18	Cybrd1	3' UTR (NM_028593, exon 4 of 4)
chr6	50472070	-7.016	0.027	Cyca	Intergenic
chr11	46123224	13.917	0.031	Cyfp2	intron (NM_001252459, intron 1 of 30)
chr11	46123237	8.878	0.176	Cyfp2	intron (NM_001252459, intron 1 of 30)
chr11	46123240	8.359	0.194	Cyfp2	intron (NM_001252459, intron 1 of 30)
chr19	37770157	-17.730	0.057	Cyp26a1	Intergenic
chr19	37770045	-12.544	0.074	Cyp26a1	Intergenic
chr19	37770038	-9.457	0.163	Cyp26a1	Intergenic
chr19	37770060	-8.593	0.189	Cyp26a1	Intergenic
chr15	82472193	8.217	0.16	Cyp2d13	intron (NR_003552, intron 1 of 8)
chr5	144399828	13.331	0.12	Cyth3	intron (NM_011182, intron 1 of 12)
chr5	144399621	12.809	0.149	Cyth3	intron (NM_011182, intron 1 of 12)
chr3	128223511	-14.651	0.068	D030025E07Rik	Intergenic
chr3	128223470	-9.109	0.155	D030025E07Rik	Intergenic
chr3	128223538	-11.364	0.177	D030025E07Rik	Intergenic
chr3	128223445	-9.294	0.19	D030025E07Rik	Intergenic
chr10	45527211	14.816	0.078	D030045P18Rik	promoter-TSS (NR_040624)
chr10	45527004	10.978	0.169	D030045P18Rik	promoter-TSS (NR_040624)
chr10	18381903	-16.973	0.027	D10Bwg1379e	intron (NM_001033258, intron 6 of 33)
chr2	104248715	13.175	0.069	D430041D05Rik	intron (NM_001033347, intron 1 of 20)
chr2	104248762	-11.008	0.155	D430041D05Rik	intron (NM_001033347, intron 1 of 20)
chr2	104248205	-8.777	0.196	D430041D05Rik	intron (NM_001033347, intron 1 of 20)
chr10	70197100	-20.169	0.026	D630013N20Rik	Intergenic
chr11	85085154	-9.627	0.142	D630032N06Rik	Intergenic
chr9	43071202	11.853	0.072	D630033O11Rik	intron (NM_001243261, intron 1 of 2)
chr9	43071240	8.838	0.176	D630033O11Rik	intron (NM_001243261, intron 1 of 2)
chr9	43071129	10.000	0.186	D630033O11Rik	intron (NM_001243261, intron 1 of 2)
chr15	79735885	12.479	0.122	D730005E14Rik	exon (NM_030255, exon 5 of 8)
chr15	79735875	11.481	0.14	D730005E14Rik	exon (NM_030255, exon 5 of 8)
chr15	79735926	13.875	0.174	D730005E14Rik	exon (NM_030255, exon 5 of 8)
chr15	79735909	13.071	0.197	D730005E14Rik	exon (NM_030255, exon 5 of 8)
chr7	141588495	10.800	0.188	D7Erd443e	Intergenic
chr7	141588615	6.223	0.189	D7Erd443e	Intergenic
chr8	37219199	12.438	0.162	D8Erd82e	Intergenic
chr3	83800236	7.502	0.044	D930015E06Rik	intron (NM_172681, intron 3 of 34)
chr3	83800248	8.865	0.115	D930015E06Rik	intron (NM_172681, intron 3 of 34)
chr3	83800175	6.714	0.125	D930015E06Rik	intron (NM_172681, intron 3 of 34)
chr10	121076602	13.911	0.087	D930020B18Rik	Intergenic
chr10	121076631	9.815	0.088	D930020B18Rik	Intergenic

chr10	121076669	9.980	0.107	D930020B18Rik	Intergenic
chr10	121076587	11.784	0.109	D930020B18Rik	Intergenic
chr10	121076909	11.090	0.17	D930020B18Rik	MIRc SINE MIR
chr10	121076626	7.529	0.193	D930020B18Rik	Intergenic
chr12	73010927	9.285	0.041	Daam1	intron (NM_172464, intron 2 of 25)
chr14	97957207	-11.095	0.048	Dach1	Intergenic
chr7	52963581	-11.464	0.087	Dbp	intron (NM_016974, intron 2 of 3)
chr7	52963567	-12.221	0.096	Dbp	intron (NM_016974, intron 2 of 3)
chr7	52963764	14.330	0.129	Dbp	exon (NM_016974, exon 3 of 4)
chr7	52963562	-10.147	0.147	Dbp	intron (NM_016974, intron 2 of 3)
chr7	52963611	-9.820	0.166	Dbp	intron (NM_016974, intron 2 of 3)
chr7	56717621	-10.713	0.131	Dbx1	intron (NM_175272, intron 9 of 37)
chr7	56717873	-8.743	0.155	Dbx1	intron (NM_175272, intron 9 of 37)
chr7	56717780	-8.133	0.19	Dbx1	intron (NM_175272, intron 9 of 37)
chr12	84861077	-17.041	0.025	Dcaf4	promoter-TSS (NM_030246)
chr12	84861071	-13.256	0.079	Dcaf4	promoter-TSS (NM_030246)
chr12	84861086	-12.733	0.095	Dcaf4	promoter-TSS (NM_030246)
chr12	84861103	-10.761	0.169	Dcaf4	promoter-TSS (NM_030246)
chr3	86657653	-14.657	0.038	Dclk2	intron (NM_001195496, intron 2 of 16)
chr3	86607105	-16.625	0.063	Dclk2	intron (NM_001195496, intron 11 of 16)
chr15	39602762	-12.048	0.061	Dcstamp	intron (NM_022722, intron 9 of 9)
chr15	39602785	-11.435	0.065	Dcstamp	intron (NM_022722, intron 9 of 9)
chr15	39602691	-9.381	0.13	Dcstamp	intron (NM_022722, intron 9 of 9)
chr3	145420879	-19.392	0.021	Ddah1	promoter-TSS (NM_026993)
chr11	11781133	8.347	0.148	Ddc	intron (NM_001190448, intron 1 of 14)
chr15	98643188	-12.126	0.105	Ddn	TTS (NM_016781)
chr15	98643325	-8.805	0.179	Ddn	TTS (NM_016781)
chr17	35862582	11.202	0.06	Ddr1	Intergenic
chr2	152272901	-18.624	0.075	Defb23	Intergenic
chr9	64637324	-13.016	0.096	Dennd4a	Intergenic
chr9	64637343	-11.393	0.138	Dennd4a	Intergenic
chr9	64637224	-10.288	0.18	Dennd4a	Intergenic
chr9	64637354	-9.609	0.185	Dennd4a	Intergenic
chr6	137722286	18.381	0.028	Dera	intron (NM_172733, intron 1 of 8)
chr6	137722293	12.187	0.053	Dera	intron (NM_172733, intron 1 of 8)
chr6	137722291	11.777	0.115	Dera	intron (NM_172733, intron 1 of 8)
chr6	50204946	-9.591	0.068	Dfna5	intron (NM_018769, intron 1 of 9)
chr6	50204933	-8.693	0.138	Dfna5	intron (NM_018769, intron 1 of 9)
chr10	128174682	12.683	0.028	Dgka	intron (NM_016811, intron 1 of 23)
chr10	128174676	14.175	0.029	Dgka	intron (NM_016811, intron 1 of 23)
chr10	128174690	10.230	0.192	Dgka	intron (NM_016811, intron 1 of 23)
chr16	22622206	12.808	0.077	Dgkg	intron (NM_138650, intron 2 of 24)
chr16	22622343	16.270	0.087	Dgkg	5' UTR (NM_138650, exon 2 of 25)
chr2	91788358	-13.878	0.108	Dgkz	intron (NM_001166597, intron 1 of 31)
chr4	133561691	17.464	0.074	Dhdds	3' UTR (NM_145833, exon 4 of 4)
chr4	133561698	13.684	0.148	Dhdds	3' UTR (NM_145833, exon 4 of 4)

chr4	133561769	14.286	0.168	Dhdds	3' UTR (NM_145833, exon 4 of 4)
chr11	67633804	-10.728	0.037	Dhrs7c	Intergenic
chr11	67633825	-6.215	0.175	Dhrs7c	Intergenic
chr2	158811455	-13.917	0.082	Dhx35	Intergenic
chr2	158811510	-15.037	0.09	Dhx35	Intergenic
chr2	158811471	-12.919	0.121	Dhx35	Intergenic
chr1	194949284	-14.747	0.095	Diexf	intron (NM_145415, intron 4 of 11)
chr1	194949362	-17.251	0.129	Diexf	intron (NM_145415, intron 4 of 11)
chr1	194949296	-12.045	0.149	Diexf	intron (NM_145415, intron 4 of 11)
chr1	194949119	-9.837	0.2	Diexf	intron (NM_145415, intron 4 of 11)
chr1	88597265	-25.859	0.01	Dis3l2	Intergenic
chr8	37644323	15.359	0.07	Dlc1	intron (NM_001194941, intron 6 of 13)
chr8	37644263	15.010	0.073	Dlc1	intron (NM_001194941, intron 6 of 13)
chr8	37644363	14.251	0.096	Dlc1	intron (NM_001194941, intron 6 of 13)
chr8	37677649	-15.460	0.171	Dlc1	promoter-TSS (NM_015802)
chr8	37677506	-8.577	0.186	Dlc1	promoter-TSS (NM_015802)
chr7	98860030	-11.690	0.095	Dlg2	intron (NM_011807, intron 2 of 22)
chr8	14114113	-17.889	0.065	Dlgap2	intron (NM_001145965, intron 1 of 14)
chr8	14114170	-16.901	0.09	Dlgap2	intron (NM_001145965, intron 1 of 14)
chr8	14114050	-13.010	0.135	Dlgap2	intron (NM_001145965, intron 1 of 14)
chr8	14114023	-10.165	0.2	Dlgap2	intron (NM_001145965, intron 1 of 14)
chr2	71369035	-10.879	0.026	Dlx1	exon (NM_010053, exon 2 of 3)
chr2	71369017	-5.126	0.165	Dlx1	exon (NM_010053, exon 2 of 3)
chr2	71369024	-5.207	0.198	Dlx1	exon (NM_010053, exon 2 of 3)
chr15	79436925	-14.410	0.077	Dmc1	Intergenic
chr15	79436705	-13.408	0.104	Dmc1	Intergenic
chr15	28119912	-13.121	0.108	Dnah5	Intergenic
chr15	28119781	-11.793	0.145	Dnah5	Intergenic
chr4	41523196	19.738	0.027	Dnaic1	intron (NM_175138, intron 1 of 19)
chr9	54546114	-12.847	0.004	Dnaja4	Intergenic
chr9	54546146	-8.836	0.18	Dnaja4	Intergenic
chr2	181256559	-6.729	0.104	Dnajc5	intron (NM_001271584, intron 2 of 5)
chr2	181256611	-8.090	0.122	Dnajc5	intron (NM_001271584, intron 2 of 5)
chr2	181256443	-11.632	0.133	Dnajc5	intron (NM_001271584, intron 2 of 5)
chr12	3691758	-10.607	0.159	Dnmt3a	intron (NM_001162465, intron 9 of 17)
chr12	3691791	-8.727	0.178	Dnmt3a	intron (NM_001162465, intron 9 of 17)
chr13	55629396	-17.490	0.049	Dok3	intron (NM_013739, intron 1 of 4)
chr13	55629379	-14.321	0.067	Dok3	intron (NM_013739, intron 1 of 4)
chr2	170597716	9.723	0.159	Dok5	intron (NM_029761, intron 1 of 7)
chr2	170597736	9.216	0.181	Dok5	intron (NM_029761, intron 1 of 7)
chr2	170597629	9.423	0.195	Dok5	intron (NM_029761, intron 1 of 7)
chr16	48303911	-11.817	0.066	Dppa2	Intergenic
chr16	48303947	-14.645	0.083	Dppa2	Intergenic
chr5	31011639	9.220	0.17	Dpysl5	Intergenic
chr15	12828086	-7.317	0.033	Drosha	intron (NM_026799, intron 22 of 34)
chr5	104582767	11.281	0.099	Dspp	Intergenic

chr5	104582823	8.209	0.099	Dspp	Intergenic
chr18	23573956	-13.819	0.031	Dtna	promoter-TSS (NM_010087)
chr18	23573939	-10.572	0.049	Dtna	promoter-TSS (NM_010087)
chr2	122112234	16.566	0.136	Duox2	exon (NM_177610, exon 21 of 32)
chr2	122112252	16.023	0.155	Duox2	exon (NM_177610, exon 21 of 32)
chr11	101844865	-13.432	0.034	Dusp3	intron (NM_028207, intron 1 of 2)
chr11	101844806	-11.043	0.052	Dusp3	intron (NM_028207, intron 1 of 2)
chr11	101844958	-12.162	0.153	Dusp3	intron (NM_028207, intron 1 of 2)
chr19	53608746	-15.171	0.065	Dusp5	intron (NM_001085390, intron 2 of 3)
chr11	87805139	-10.457	0.066	Dynll2	intron (NM_001168471, intron 1 of 2)
chr11	87805050	-9.051	0.089	Dynll2	intron (NM_001168471, intron 1 of 2)
chr11	87805391	10.977	0.134	Dynll2	intron (NM_001168471, intron 1 of 2)
chr11	87805298	-7.333	0.139	Dynll2	intron (NM_001168471, intron 1 of 2)
chr11	87805167	-5.336	0.2	Dynll2	intron (NM_001168471, intron 1 of 2)
chr14	119323951	-12.320	0.051	Dzip1	Intergenic
chr14	119323953	-12.981	0.096	Dzip1	Intergenic
chr14	119323959	-10.965	0.107	Dzip1	Intergenic
chr7	70903675	13.113	0.106	E030018B13Rik	3' UTR (NM_130880, exon 14 of 14)
chr7	70903710	13.117	0.129	E030018B13Rik	3' UTR (NM_130880, exon 14 of 14)
chr7	70903686	14.852	0.137	E030018B13Rik	3' UTR (NM_130880, exon 14 of 14)
chr7	70903683	12.972	0.169	E030018B13Rik	3' UTR (NM_130880, exon 14 of 14)
chr5	112294121	-14.989	0.157	E130006D01Rik	Intergenic
chr5	112294149	-12.533	0.175	E130006D01Rik	Intergenic
chr4	45896394	-14.185	0.031	E230008N13Rik	CpG
chr4	45896380	-9.892	0.124	E230008N13Rik	CpG
chr6	66967385	-10.895	0.027	E230016M11Rik	intron (NM_001177556, intron 3 of 3)
chr6	66985907	15.889	0.043	E230016M11Rik	promoter-TSS (NR_040278)
chr6	66985901	11.166	0.123	E230016M11Rik	promoter-TSS (NR_040278)
chr6	66985076	11.593	0.165	E230016M11Rik	TTS (NM_007836)
chr6	66985708	11.244	0.167	E230016M11Rik	promoter-TSS (NR_040278)
chr7	97211645	-7.007	0.136	E230029C05Rik	Intergenic
chr13	30138152	13.300	0.044	E2f3	Intergenic
chr13	30138093	10.457	0.19	E2f3	Intergenic
chr19	60222258	-10.848	0.124	E330013P04Rik	intron (NR_026942, intron 1 of 4)
chr19	60222829	-11.305	0.196	E330013P04Rik	intron (NR_026942, intron 1 of 4)
chr11	44430464	8.000	0.029	Ebf1	Intergenic
chr7	144504437	-5.875	0.141	Ebf3	intron (NM_001113415, intron 3 of 15)
chr2	6188542	-14.633	0.096	Echdc3	intron (NR_040333, intron 3 of 6)
chr2	6188544	-13.579	0.109	Echdc3	intron (NR_040333, intron 3 of 6)
chr2	6188595	-10.870	0.137	Echdc3	intron (NR_040333, intron 3 of 6)
chr13	35086647	-9.740	0.044	Eci2	promoter-TSS (NM_001110331)
chr13	35086653	-5.678	0.151	Eci2	promoter-TSS (NM_001110331)
chr9	25208998	-25.094	0.023	Eepd1	Intergenic
chr15	83710537	19.273	0.11	Efcab6	intron (NM_029946, intron 26 of 31)
chr15	83710615	17.232	0.128	Efcab6	intron (NM_029946, intron 26 of 31)
chr11	32405484	-9.582	0.183	Efcab9	intron (NM_173784, intron 2 of 2)

chr11	69371137	10.382	0.048	Efnb3	intron (NM_007911, intron 1 of 4)
chr11	69375229	10.195	0.127	Efnb3	TTS (NM_144824)
chr11	69371234	12.054	0.13	Efnb3	intron (NM_007911, intron 1 of 4)
chr11	69371281	7.543	0.144	Efnb3	intron (NM_007911, intron 1 of 4)
chr11	69375239	7.744	0.19	Efnb3	TTS (NM_144824)
chr15	65627432	-12.942	0.024	Efr3a	intron (NM_133766, intron 1 of 22)
chr16	21781960	12.269	0.028	Ehhadh	intron (NM_023737, intron 1 of 6)
chr2	24718753	-15.899	0.046	Ehmt1	exon (NM_001109686, exon 6 of 26)
chr16	20677730	-14.936	0.121	Eif4g1	intron (NM_001005331, intron 5 of 31)
chr16	20677694	-13.261	0.167	Eif4g1	intron (NM_001005331, intron 5 of 31)
chr3	51152845	10.549	0.095	Elf2	Intergenic
chr3	51152833	10.387	0.119	Elf2	Intergenic
chr5	140461120	-16.106	0.079	Elfn1	Intergenic
chr2	121260575	10.709	0.073	Ell3	exon (NM_007952, exon 10 of 13)
chr9	83698491	-9.960	0.076	Elovl4	intron (NM_148941, intron 1 of 5)
chr9	83698295	-14.096	0.087	Elovl4	intron (NM_148941, intron 1 of 5)
chr9	83698172	-15.840	0.095	Elovl4	intron (NM_148941, intron 1 of 5)
chr13	109004116	9.029	0.188	Elovl7	promoter-TSS (NM_029001)
chr6	124650668	-17.147	0.058	Emg1	intron (NM_145130, intron 5 of 12)
chr9	14155214	-14.058	0.033	Endod1	Intergenic
chr9	14155209	-12.725	0.119	Endod1	Intergenic
chr4	149605279	-13.774	0.096	Eno1	Intergenic
chr4	149605356	-11.863	0.144	Eno1	Intergenic
chr10	24478099	-15.703	0.1	Enpp1	Intergenic
chr10	24478058	-11.930	0.186	Enpp1	Intergenic
chr10	24478351	-11.079	0.196	Enpp1	Intergenic
chr15	54686353	-9.021	0.035	Enpp2	intron (NM_001285994, intron 19 of 25)
chr15	54686363	-8.705	0.039	Enpp2	intron (NM_001285994, intron 19 of 25)
chr2	150570963	13.733	0.038	Entpd6	Intergenic
chr17	86936137	-17.761	0.035	Epas1	intron (NM_011104, intron 10 of 14)
chr17	86936144	-16.727	0.048	Epas1	intron (NM_011104, intron 10 of 14)
chr4	131582011	16.184	0.04	Epb4.1	intron (NM_183428, intron 1 of 20)
chr10	25152662	-10.546	0.123	Epb4.1l2	intron (NM_013511, intron 1 of 19)
chr10	25152620	-9.033	0.182	Epb4.1l2	intron (NM_013511, intron 1 of 19)
chr10	25152549	-9.261	0.189	Epb4.1l2	intron (NM_013511, intron 1 of 19)
chr10	25152641	-8.260	0.191	Epb4.1l2	intron (NM_013511, intron 1 of 19)
chr16	63862888	-12.267	0.117	Epha3	intron (NM_010140, intron 1 of 16)
chr16	63862949	-10.570	0.134	Epha3	intron (NM_010140, intron 1 of 16)
chr16	63862989	-8.714	0.157	Epha3	intron (NM_010140, intron 1 of 16)
chr4	28708851	-18.190	0.041	Epha7	Intergenic
chr4	29018815	13.905	0.052	Epha7	Intergenic
chr4	29018828	9.698	0.152	Epha7	Intergenic
chr4	29018820	9.814	0.158	Epha7	Intergenic
chr9	21767715	-14.799	0.108	Epor	intron (NM_010149, intron 1 of 7)
chr6	137479126	-12.993	0.145	Eps8	intron (NM_001271595, intron 3 of 20)
chr6	137479237	-13.507	0.155	Eps8	intron (NM_001271595, intron 3 of 20)

chr13	104784230	-21.156	0.044	Erb2ip	Intergenic
chr13	104784255	-15.897	0.127	Erb2ip	Intergenic
chr16	95660747	-17.066	0.038	Erg	intron (NM_133659, intron 2 of 10)
chr16	95660741	-14.375	0.07	Erg	intron (NM_133659, intron 2 of 10)
chr16	95660755	-9.691	0.192	Erg	intron (NM_133659, intron 2 of 10)
chr4	117208715	12.894	0.1	Eri3	Intergenic
chr13	114055515	-8.481	0.095	Esm1	Intergenic
chr17	39981493	6.041	0.001	Esp38	CpG
chr17	39982181	6.561	0.009	Esp38	CpG
chr17	39980024	7.532	0.029	Esp38	FordPrefect DNA Tip100
chr17	39981156	7.668	0.033	Esp38	CpG
chr17	39981197	5.582	0.034	Esp38	CpG
chr17	39980037	6.231	0.035	Esp38	FordPrefect DNA Tip100
chr17	39981174	6.988	0.043	Esp38	CpG
chr17	39980017	7.824	0.043	Esp38	FordPrefect DNA Tip100
chr17	39981185	5.427	0.055	Esp38	CpG
chr17	39981147	7.227	0.078	Esp38	CpG
chr17	39983240	6.027	0.128	Esp38	CpG
chr17	39983370	6.063	0.131	Esp38	SSU-rRNA_Hsa rRNA rRNA
chr17	39985208	8.386	0.146	Esp38	CpG
chr17	39980004	6.235	0.147	Esp38	FordPrefect DNA Tip100
chr4	151514591	-13.977	0.117	Espn	intron (NM_207687, intron 2 of 15)
chr6	143101073	10.466	0.174	Etnk1	Intergenic
chr6	143101071	10.226	0.183	Etnk1	Intergenic
chr6	143101077	10.247	0.191	Etnk1	Intergenic
chr3	130336721	20.273	0.012	Etnppl	intron (NM_027907, intron 12 of 12)
chr9	32501677	-13.061	0.047	Ets1	Intergenic
chr9	32501476	-7.501	0.161	Ets1	Intergenic
chr16	22398702	12.193	0.15	Etv5	intron (NM_023794, intron 9 of 12)
chr16	22398485	5.779	0.165	Etv5	intron (NM_023794, intron 9 of 12)
chr7	50509216	-8.035	0.123	EU599041	Intergenic
chr7	50509160	-8.663	0.14	EU599041	Intergenic
chr7	50509229	-6.774	0.17	EU599041	Intergenic
chr7	50509199	-6.833	0.176	EU599041	Intergenic
chr16	90830138	20.317	0.031	Eva1c	promoter-TSS (NM_001199210)
chr16	90830125	11.298	0.184	Eva1c	promoter-TSS (NM_001199210)
chr8	107819600	-13.101	0.164	Exoc3l	5' UTR (NM_177788, exon 2 of 14)
chr8	107819450	-9.541	0.199	Exoc3l	intron (NM_177788, intron 2 of 13)
chr6	84832881	-7.685	0.133	Exoc6b	intron (NM_177077, intron 8 of 21)
chr9	53149497	-6.928	0.053	Exph5	intron (NM_176846, intron 3 of 5)
chr9	53149018	-6.911	0.08	Exph5	intron (NM_176846, intron 3 of 5)
chr3	10301797	-10.018	0.107	Fabp12	promoter-TSS (NM_029310)
chr3	10301877	-7.373	0.175	Fabp12	promoter-TSS (NM_029310)
chr19	10134889	14.392	0.063	Fads3	TTS (NM_021890)
chr19	10134872	14.423	0.096	Fads3	TTS (NM_021890)
chr19	10134930	17.595	0.1	Fads3	TTS (NM_021890)

chr11	57288918	-7.595	0.187	Fam114a2	Intergenic
chr2	32773507	-10.314	0.107	Fam129b	intron (NM_146119, intron 5 of 13)
chr2	32773380	-11.440	0.171	Fam129b	intron (NM_146119, intron 5 of 13)
chr16	20694056	-13.390	0.12	Fam131a	Intergenic
chr16	20694083	-15.798	0.122	Fam131a	Intergenic
chr16	20694026	-7.816	0.144	Fam131a	Intergenic
chr6	86299338	18.549	0.052	Fam136a	Intergenic
chr6	86299346	14.911	0.113	Fam136a	Intergenic
chr3	79798277	-10.288	0.081	Fam198b	Intergenic
chr3	79798155	-8.987	0.155	Fam198b	Intergenic
chr2	172172479	20.000	0.001	Fam210b	intron (NM_025912, intron 1 of 2)
chr11	62460849	-12.857	0.065	Fam211a	intron (NM_198861, intron 1 of 3)
chr11	62460968	-9.155	0.087	Fam211a	intron (NM_198861, intron 1 of 3)
chr9	74820979	-17.475	0.032	Fam214a	intron (NM_001113283, intron 2 of 12)
chr9	74820879	-16.489	0.056	Fam214a	intron (NM_001113283, intron 2 of 12)
chr9	57386886	16.923	0.042	Fam219b	intron (NM_175273, intron 3 of 3)
chr5	115026182	-24.990	0.037	Fam222a	intron (NM_001004180, intron 1 of 2)
chr5	115026175	-24.305	0.04	Fam222a	intron (NM_001004180, intron 1 of 2)
chr15	63949778	-8.673	0.138	Fam49b	intron (NM_001276463, intron 22 of 27)
chr15	63949939	-8.650	0.155	Fam49b	intron (NM_001276463, intron 22 of 27)
chr5	33861732	-14.962	0.144	Fam53a	Intergenic
chr5	33861744	-14.816	0.153	Fam53a	Intergenic
chr2	158570925	-7.463	0.039	Fam83d	intron (NM_153089, intron 3 of 10)
chr15	80512927	6.780	0.112	Fam83f	intron (NM_145986, intron 1 of 4)
chr15	75840667	-6.565	0.048	Fam83h	promoter-TSS (NM_001168253)
chr15	75840959	-13.511	0.05	Fam83h	intron (NM_134087, intron 1 of 4)
chr15	75840871	-8.389	0.173	Fam83h	promoter-TSS (NM_001168253)
chr8	46020072	7.273	0.017	Fat1	Intergenic
chr6	91251982	12.494	0.046	Fbln2	Intergenic
chr12	103101000	-17.014	0.01	Fbln5	intron (NM_028446, intron 15 of 20)
chr13	62961029	12.500	0.039	Fbp2	Intergenic
chr9	55063302	13.548	0.039	Fbxo22	intron (NM_028049, intron 4 of 6)
chr4	140721876	14.031	0.087	Fbxo42	intron (NM_172518, intron 1 of 9)
chr4	140721852	6.804	0.165	Fbxo42	intron (NM_172518, intron 1 of 9)
chr19	45768769	13.495	0.077	Fbxw4	Intergenic
chr19	45768754	12.692	0.158	Fbxw4	Intergenic
chr13	99573985	-12.362	0.088	Fcho2	intron (NM_172591, intron 2 of 25)
chr1	172864049	11.113	0.066	Fcrla	Intergenic
chr1	172864579	14.884	0.09	Fcrla	Intergenic
chr14	13174083	-7.527	0.041	Fezf2	TTS (NM_080433)
chr14	13174858	-14.816	0.131	Fezf2	3' UTR (NM_080433, exon 5 of 5)
chr14	13174106	-6.910	0.136	Fezf2	TTS (NM_080433)
chr17	29493244	12.553	0.099	Fgd2	Intergenic
chr17	29493251	9.360	0.112	Fgd2	Intergenic
chr17	29493480	12.542	0.116	Fgd2	Intergenic
chr6	127026933	-20.206	0.034	Fgf23	intron (NM_022657, intron 1 of 2)

chr14	11963467	-9.060	0.09	Fhit	intron (NM_010210, intron 1 of 8)
chr14	11963518	-9.344	0.126	Fhit	intron (NM_010210, intron 1 of 8)
chr2	102293851	-16.615	0.071	Fjx1	Intergenic
chr9	32318586	-13.185	0.041	Fli1	intron (NM_008026, intron 1 of 8)
chr14	8686388	17.243	0.1	Flnb	intron (NM_134080, intron 1 of 45)
chr14	72956007	11.736	0.095	Fndc3a	exon (NM_207636, exon 23 of 26)
chr14	72956074	9.580	0.14	Fndc3a	exon (NM_207636, exon 23 of 26)
chr3	27607928	12.766	0.06	Fndc3b	intron (NM_173182, intron 1 of 25)
chr3	27665052	-9.583	0.126	Fndc3b	Intergenic
chr3	27607911	8.670	0.17	Fndc3b	intron (NM_173182, intron 1 of 25)
chr11	46082618	-7.536	0.124	Fndc9	intron (NM_001252460, intron 11 of 30)
chr3	79324061	15.285	0.032	Fnip2	intron (NM_001162999, intron 1 of 16)
chr3	79324010	8.025	0.134	Fnip2	intron (NM_001162999, intron 1 of 16)
chr3	79324118	5.786	0.171	Fnip2	intron (NM_001162999, intron 1 of 16)
chr2	147908008	-8.905	0.17	Foxa2	Intergenic
chr2	147908384	-13.087	0.185	Foxa2	MLT2B2 LTR ERV1
chr2	147908467	-9.552	0.194	Foxa2	Intergenic
chr11	116233321	7.074	0.131	Foxj1	intron (NM_027258, intron 2 of 18)
chr11	116233288	7.197	0.139	Foxj1	intron (NM_027258, intron 2 of 18)
chr11	116233006	9.213	0.167	Foxj1	intron (NM_027258, intron 2 of 18)
chr5	142891589	21.705	0.025	Foxk1	intron (NM_199068, intron 1 of 8)
chr8	123753081	13.155	0.022	Foxl1	Intergenic
chr17	88842101	-11.860	0.09	Foxn2	intron (NM_180974, intron 1 of 5)
chr17	88842094	-8.197	0.156	Foxn2	intron (NM_180974, intron 1 of 5)
chr17	88842146	-8.595	0.166	Foxn2	intron (NM_180974, intron 1 of 5)
chr17	88842245	-11.312	0.196	Foxn2	intron (NM_180974, intron 1 of 5)
chr6	99215879	-15.605	0.011	Foxp1	intron (NM_053202, intron 2 of 18)
chr6	99215979	-11.635	0.046	Foxp1	intron (NM_053202, intron 2 of 18)
chr6	98974961	-14.985	0.055	Foxp1	intron (NM_001197321, intron 4 of 17)
chr6	99215831	-11.290	0.078	Foxp1	intron (NM_053202, intron 2 of 18)
chr6	98974986	-13.220	0.102	Foxp1	intron (NM_001197321, intron 4 of 17)
chr6	98974605	-9.665	0.128	Foxp1	intron (NM_001197321, intron 4 of 17)
chr17	48095485	-16.334	0.023	Foxp4	Intergenic
chr9	35017131	-22.793	0.031	Foxred1	intron (NM_172291, intron 2 of 10)
chr9	35017530	-9.910	0.135	Foxred1	exon (NM_172291, exon 2 of 11)
chr9	35017134	-13.972	0.155	Foxred1	intron (NM_172291, intron 2 of 10)
chr5	96734098	21.115	0.012	Fras1	Intergenic
chr5	96734178	16.579	0.053	Fras1	Intergenic
chr5	96734258	15.857	0.084	Fras1	Intergenic
chr5	96734264	13.599	0.153	Fras1	Intergenic
chr19	41899709	-10.563	0.037	Frat1	L1M5 LINE L1
chr19	41899642	-11.076	0.09	Frat1	Intergenic
chr7	52910037	-15.040	0.085	Fut2	intron (NM_018876, intron 1 of 1)
chr7	52910028	-12.711	0.194	Fut2	intron (NM_018876, intron 1 of 1)
chr19	24391437	18.283	0.051	Fxn	intron (NM_008846, intron 13 of 14)
chr19	24391537	13.496	0.159	Fxn	intron (NM_008846, intron 13 of 14)



chr15	6470796	-13.845	0.065	Fyb	Intergenic
chr10	39132802	-14.723	0.049	Fyn	intron (NM_001122892, intron 2 of 12)
chr10	39132835	-8.093	0.182	Fyn	intron (NM_001122892, intron 2 of 12)
chr7	96551542	-14.126	0.104	Fzd4	Intergenic
chr7	96551576	-9.916	0.19	Fzd4	Intergenic
chr10	39678373	-23.119	0.036	G630090E17Rik	3' UTR (NM_001113388, exon 4 of 4)
chr8	83337624	14.470	0.036	Gab1	(CAA)n Simple_repeat Simple_repeat
chr8	83337870	-12.688	0.117	Gab1	intron (NM_021356, intron 1 of 9)
chr8	83337391	7.387	0.158	Gab1	intron (NM_021356, intron 1 of 9)
chr8	83337627	8.507	0.174	Gab1	(CAA)n Simple_repeat Simple_repeat
chr7	104320485	-20.914	0.031	Gab2	intron (NM_010248, intron 1 of 9)
chr7	104320482	-19.672	0.044	Gab2	intron (NM_010248, intron 1 of 9)
chr7	104320491	-14.954	0.103	Gab2	intron (NM_010248, intron 1 of 9)
chr7	104320488	-14.286	0.128	Gab2	intron (NM_010248, intron 1 of 9)
chr4	47002207	-9.653	0.174	Gabbr2	intron (NM_001081141, intron 1 of 18)
chr3	95022459	21.051	0.015	Gabpb2	promoter-TSS (NM_172512)
chr6	67079478	-16.560	0.094	Gadd45a	Intergenic
chr6	67079455	-17.939	0.129	Gadd45a	Intergenic
chr17	80495456	12.684	0.115	Galm	Intergenic
chr17	80495584	9.850	0.126	Galm	Intergenic
chr8	126674414	5.733	0.041	Galnt2	Intergenic
chr4	41701876	-18.401	0.035	Galt	promoter-TSS (NM_016658)
chr11	4967944	-12.885	0.017	Gas2l1	Intergenic
chr8	126068330	8.028	0.07	Gas8	Intergenic
chr8	126093754	10.196	0.141	Gas8	Intergenic
chr5	133951251	-8.243	0.106	Gatsl2	Intergenic
chr5	133951299	-6.469	0.108	Gatsl2	Intergenic
chr13	40960089	12.292	0.048	Gcnt2	intron (NM_023887, intron 1 of 2)
chr13	40960018	10.446	0.115	Gcnt2	intron (NM_023887, intron 1 of 2)
chr17	80655031	-13.863	0.061	Gemin6	(CAA)n Simple_repeat Simple_repeat
chr17	80655035	-14.863	0.073	Gemin6	intron (NM_198942, intron 12 of 22)
chr13	43432257	-12.302	0.088	Gfod1	Intergenic
chr13	43432216	-9.453	0.102	Gfod1	Intergenic
chr11	49624430	-5.363	0.141	Gfpt2	intron (NM_013529, intron 4 of 18)
chr11	49624485	-6.083	0.158	Gfpt2	exon (NM_013529, exon 5 of 19)
chr6	54943437	-22.392	0.022	Ggct	promoter-TSS (NM_026637)
chr6	54943404	-18.048	0.028	Ggct	promoter-TSS (NM_026637)
chr3	151729721	-7.149	0.117	Gipc2	Intergenic
chr11	77312042	18.793	0.103	Git1	intron (NM_001004144, intron 1 of 19)
chr4	127006715	-19.123	0.018	Gjb3	promoter-TSS (NM_008126)
chr4	127006730	-13.656	0.082	Gjb3	promoter-TSS (NM_008126)
chr19	30199775	11.543	0.046	Gldc	intron (NM_138595, intron 15 of 24)
chr19	30199838	12.314	0.085	Gldc	intron (NM_138595, intron 15 of 24)
chr17	31026703	11.950	0.041	Glp1r	Intergenic
chr17	31026835	10.298	0.135	Glp1r	Intergenic
chr3	85692282	-14.633	0.054	Git28d2	promoter-TSS (NM_177130)

chr3	85692341	-14.039	0.118	Glt28d2	promoter-TSS (NM_177130)
chr3	85692272	-6.511	0.167	Glt28d2	promoter-TSS (NM_177130)
chr3	85692316	-11.937	0.19	Glt28d2	promoter-TSS (NM_177130)
chr18	5618974	11.358	0.086	Gm10125	intron (NM_011546, intron 1 of 7)
chr18	5618690	11.890	0.119	Gm10125	intron (NM_011546, intron 1 of 7)
chr18	5618669	9.664	0.147	Gm10125	intron (NM_011546, intron 1 of 7)
chr18	5618702	9.613	0.157	Gm10125	intron (NM_011546, intron 1 of 7)
chr18	5618793	6.850	0.194	Gm10125	intron (NM_011546, intron 1 of 7)
chr6	126322070	-14.299	0.084	Gm10415	Intergenic
chr6	126322060	-12.025	0.112	Gm10415	Intergenic
chr7	31946005	-14.627	0.045	Gm10640	Intergenic
chr19	43932076	17.163	0.051	Gm10768	intron (NM_028029, intron 10 of 15)
chr16	90074171	8.825	0.188	Gm10789	Intergenic
chr10	76684198	-18.530	0.036	Gm10941	Intergenic
chr11	78890315	-8.365	0.133	Gm11201	intron (NM_013571, intron 1 of 17)
chr11	78890344	-9.483	0.137	Gm11201	intron (NM_013571, intron 1 of 17)
chr11	82431979	-13.792	0.071	Gm11426	Intergenic
chr11	82431972	-8.306	0.15	Gm11426	Intergenic
chr3	36435266	20.850	0.033	Gm11549	Intergenic
chr3	36435275	14.427	0.102	Gm11549	Intergenic
chr11	102443636	11.040	0.087	Gm11627	Intergenic
chr11	102443596	8.272	0.183	Gm11627	Intergenic
chr11	102443752	11.343	0.193	Gm11627	Intergenic
chr4	146034519	12.904	0.115	Gm13034	promoter-TSS (NR_030771)
chr4	146035301	10.269	0.192	Gm13034	non-coding (NR_030771, exon 1 of 1)
chr4	146034488	10.135	0.194	Gm13034	promoter-TSS (NR_030771)
chr4	146649287	-6.155	0.119	Gm13152	CpG
chr4	146649375	7.485	0.144	Gm13152	CpG
chr4	146649531	8.252	0.187	Gm13152	CpG
chr4	146649525	9.573	0.189	Gm13152	CpG
chr4	88417698	11.320	0.033	Gm13289	Intergenic
chr4	88417543	-8.965	0.059	Gm13289	Intergenic
chr4	88417521	-6.826	0.126	Gm13289	Intergenic
chr2	50280108	20.244	0.014	Gm13483	intron (NR_040362, intron 1 of 2)
chr2	29547577	-12.523	0.068	Gm13547	intron (NM_001039086, intron 4 of 25)
chr2	60280011	-14.707	0.102	Gm13580	intron (NM_008867, intron 19 of 29)
chr2	60280198	-11.039	0.163	Gm13580	intron (NM_008867, intron 19 of 29)
chr2	128237958	-16.488	0.111	Gm14005	intron (NR_028591, intron 1 of 1)
chr2	128237945	-16.093	0.119	Gm14005	intron (NR_028591, intron 1 of 1)
chr2	128240465	-11.946	0.166	Gm14005	intron (NR_028591, intron 1 of 1)
chr2	176583455	-8.092	0.126	Gm14295	RMER17B LTR ERVK
chr2	176583452	-8.956	0.169	Gm14295	RMER17B LTR ERVK
chr2	176583446	-8.011	0.196	Gm14295	RMER17B LTR ERVK
chr2	177282696	-5.928	0.099	Gm14403	promoter-TSS (NR_036450)
chr2	176913962	18.954	0.018	Gm14405	Intergenic
chr6	72627724	-15.248	0.095	Gm15401	intron (NM_001079822, intron 3 of 12)

chr3	96373517	-19.193	0.064	Gm15441	Intergenic
chr3	96380586	-10.569	0.112	Gm15441	Intergenic
chr5	150388552	-12.364	0.155	Gm15997	intron (NM_029440, intron 14 of 22)
chr7	6362881	-17.333	0.039	Gm16532	Intergenic
chr7	6362879	-12.521	0.044	Gm16532	Intergenic
chr7	6362866	-13.214	0.064	Gm16532	Intergenic
chr7	6362863	-12.796	0.073	Gm16532	Intergenic
chr7	6362902	-10.521	0.102	Gm16532	Intergenic
chr7	6362896	-14.321	0.111	Gm16532	Intergenic
chr5	34326955	17.808	0.019	Gm1673	intron (NM_001033458, intron 3 of 3)
chr8	36655453	-8.587	0.107	Gm16793	intron (NM_001081279, intron 1 of 2)
chr8	36655445	-10.472	0.132	Gm16793	intron (NM_001081279, intron 1 of 2)
chr9	21212939	17.971	0.036	Gm16853	non-coding (NR_045742, exon 2 of 5)
chr9	21212632	9.749	0.13	Gm16853	intron (NR_045742, intron 2 of 4)
chr13	63348074	-12.781	0.056	Gm16907	intron (NM_028079, intron 12 of 14)
chr13	63398098	-6.851	0.142	Gm16907	intron (NR_045794, intron 1 of 2)
chr13	63398037	-7.438	0.17	Gm16907	intron (NR_045794, intron 1 of 2)
chr13	63348028	-10.229	0.185	Gm16907	intron (NM_028079, intron 12 of 14)
chr7	105313295	-17.210	0.086	Gm16938	intron (NM_007602, intron 1 of 12)
chr7	105313250	-12.335	0.091	Gm16938	intron (NM_007602, intron 1 of 12)
chr3	79089545	-10.187	0.039	Gm17359	Intergenic
chr3	79089358	-6.750	0.046	Gm17359	Intergenic
chr3	79089377	-6.039	0.085	Gm17359	Intergenic
chr3	79089473	-7.465	0.105	Gm17359	Intergenic
chr3	79089481	-7.157	0.127	Gm17359	Intergenic
chr1	12669601	-13.354	0.045	Gm17644	RMER10A LTR ERV1
chr12	25888542	-9.047	0.186	Gm17746	Intergenic
chr8	111940016	-14.610	0.114	Gm1943	Intergenic
chr8	111940752	-14.980	0.134	Gm1943	Intergenic
chr8	111775599	10.768	0.137	Gm1943	Intergenic
chr8	111775534	8.398	0.141	Gm1943	Intergenic
chr8	111775629	9.739	0.145	Gm1943	Intergenic
chr8	111775578	11.638	0.149	Gm1943	Intergenic
chr8	111775695	8.048	0.16	Gm1943	Intergenic
chr8	111940699	-14.526	0.166	Gm1943	Intergenic
chr8	111940543	-11.393	0.175	Gm1943	Intergenic
chr8	111940552	-10.841	0.196	Gm1943	Intergenic
chr16	42911816	14.312	0.011	Gm19522	intron (NM_001285805, intron 1 of 10)
chr1	90505701	10.824	0.163	Gm19589	Intergenic
chr1	90505715	5.444	0.167	Gm19589	Intergenic
chr12	57399488	18.548	0.068	Gm19990	Intergenic
chr12	57399474	19.091	0.079	Gm19990	Intergenic
chr10	18928197	11.262	0.092	Gm20139	TTS (NR_038021)
chr10	18928151	10.483	0.163	Gm20139	TTS (NR_038021)
chr8	124978555	-15.644	0.063	Gm20735	3' UTR (NM_013914, exon 3 of 3)
chr8	124978509	-9.052	0.112	Gm20735	3' UTR (NM_013914, exon 3 of 3)

chr8	19979392	9.756	0.028	Gm21119	Intergenic
chr8	112920475	15.848	0.075	Gm21283	intron (NM_172916, intron 12 of 86)
chr8	112920443	10.348	0.084	Gm21283	intron (NM_172916, intron 12 of 86)
chr14	6011226	-6.098	0.091	Gm3383	intron (NM_001270812, intron 1 of 7)
chr5	64991381	-7.222	0.108	Gm3716	intron (NR_045078, intron 3 of 3)
chr5	64991333	-10.190	0.136	Gm3716	intron (NR_045078, intron 3 of 3)
chr5	64988907	6.743	0.147	Gm3716	intron (NR_045078, intron 3 of 3)
chr5	64988762	5.366	0.155	Gm3716	intron (NR_045078, intron 3 of 3)
chr7	25514947	-6.161	0.147	Gm4763	Intergenic
chr1	31419803	16.956	0.012	Gm4850	Intergenic
chr9	49035744	-12.068	0.134	Gm4894	Intergenic
chrX	11211448	11.111	0.016	Gm4906	Intergenic
chr1	182295945	7.317	0.034	Gm5069	intron (NM_001081175, intron 2 of 7)
chr10	107962070	-19.161	0.025	Gm5136	intron (NM_009306, intron 9 of 10)
chr10	107962059	-11.579	0.106	Gm5136	intron (NM_009306, intron 9 of 10)
chr10	21496254	-12.868	0.093	Gm5420	Intergenic
chr10	21496226	-13.315	0.123	Gm5420	Intergenic
chr10	21496221	-13.380	0.137	Gm5420	Intergenic
chr10	21496300	-10.114	0.183	Gm5420	Intergenic
chr15	100254176	8.958	0.036	Gm5475	promoter-TSS (NM_008732)
chr8	12151857	13.126	0.114	Gm5607	Intergenic
chr8	12151848	13.727	0.144	Gm5607	Intergenic
chr16	44174469	-8.941	0.098	Gm608	intron (NM_001029889, intron 1 of 7)
chr16	44159681	-8.586	0.109	Gm608	exon (NM_028108, exon 5 of 5)
chr16	44159462	-6.110	0.124	Gm608	intron (NM_028108, intron 4 of 4)
chr16	44159683	-6.254	0.169	Gm608	exon (NM_028108, exon 5 of 5)
chr8	87666519	-8.466	0.087	Gm6531	Intergenic
chrX	61311597	-18.269	0.037	Gm6760	Intergenic
chr12	88143493	-9.127	0.085	Gm6772	Intergenic
chr12	88143664	-6.375	0.166	Gm6772	Intergenic
chr16	49987368	-6.540	0.122	Gm6936	intron (NR_045001, intron 1 of 3)
chr13	120276557	24.897	0.003	Gm7120	promoter-TSS (NM_001039244)
chr13	120277680	6.787	0.009	Gm7120	promoter-TSS (NM_001177666)
chr13	120276435	27.778	0.011	Gm7120	promoter-TSS (NM_001039244)
chr13	120277669	6.307	0.014	Gm7120	promoter-TSS (NM_001177666)
chr13	120277807	5.046	0.022	Gm7120	promoter-TSS (NR_027974)
chr13	120277667	5.539	0.031	Gm7120	promoter-TSS (NM_001177666)
chr13	120277733	5.178	0.037	Gm7120	promoter-TSS (NM_001177666)
chr13	120277642	5.400	0.049	Gm7120	promoter-TSS (NM_001177666)
chr13	120276412	22.121	0.05	Gm7120	promoter-TSS (NM_001039244)
chr13	120277538	8.753	0.096	Gm7120	promoter-TSS (NM_001177666)
chr13	120277524	9.554	0.096	Gm7120	promoter-TSS (NM_001177666)
chr13	120277548	8.403	0.097	Gm7120	promoter-TSS (NM_001177666)
chr13	120277563	8.157	0.115	Gm7120	promoter-TSS (NM_001177666)
chr17	45756607	-19.002	0.078	Gm7325	Intergenic
chr17	45756778	-14.425	0.102	Gm7325	Intergenic

chr17	45756638	-13.582	0.141	Gm7325	Intergenic
chr3	47830464	-8.475	0.046	Gm7977	non-coding (NR_040408, exon 1 of 1)
chr13	50559977	-9.511	0.076	Gm806	Intergenic
chr6	3291179	7.168	0.102	Gm8579	Intergenic
chr6	3291213	6.489	0.163	Gm8579	Intergenic
chr6	3291096	5.561	0.191	Gm8579	Intergenic
chr10	98006609	12.767	0.096	Gm8633	Intergenic
chr10	98006626	11.511	0.107	Gm8633	Intergenic
chr13	50721262	9.825	0.05	Gm904	Intergenic
chr13	50721289	12.373	0.067	Gm904	Intergenic
chr19	16566242	18.702	0.034	Gna14	intron (NM_008137, intron 1 of 6)
chr19	16566226	16.176	0.096	Gna14	intron (NM_008137, intron 1 of 6)
chr9	107538167	-14.487	0.038	Gnai2	promoter-TSS (NM_008138)
chr9	107533984	12.306	0.102	Gnai2	intron (NM_008138, intron 1 of 8)
chr9	107533740	12.226	0.128	Gnai2	intron (NM_008138, intron 1 of 8)
chr9	107538316	-11.807	0.165	Gnai2	promoter-TSS (NM_008138)
chr3	32557872	-11.427	0.125	Gnb4	Intergenic
chr3	32557928	-10.833	0.171	Gnb4	Intergenic
chr4	124714922	-7.907	0.19	Gnl2	intron (NM_145552, intron 4 of 15)
chr10	120811744	-25.519	0.007	Gns	intron (NM_029364, intron 3 of 13)
chr10	120811729	-18.166	0.052	Gns	intron (NM_029364, intron 3 of 13)
chr2	70467551	12.532	0.055	Gorasp2	Intergenic
chr2	70467557	10.664	0.113	Gorasp2	Intergenic
chr19	43573483	-13.800	0.136	Got1	TTS (NM_010324)
chr19	43573558	-15.081	0.155	Got1	TTS (NM_010324)
chr19	43573355	-9.751	0.161	Got1	TTS (NM_010324)
chr19	43573374	-9.290	0.182	Got1	TTS (NM_010324)
chr8	99775588	17.151	0.054	Got2	Intergenic
chr8	99775454	14.404	0.189	Got2	Intergenic
chr1	168068555	-15.113	0.093	Gpa33	intron (NM_021610, intron 1 of 6)
chr1	168068647	-10.448	0.099	Gpa33	intron (NM_021610, intron 1 of 6)
chr1	189057518	16.919	0.031	Gpatch2	intron (NM_026367, intron 4 of 9)
chr1	189057659	6.123	0.036	Gpatch2	exon (NM_026367, exon 5 of 10)
chr1	189106829	-15.640	0.074	Gpatch2	intron (NM_026367, intron 5 of 9)
chr17	43536015	13.459	0.083	Gpr116	intron (NM_001081178, intron 1 of 20)
chr17	43536101	10.074	0.13	Gpr116	intron (NM_001081178, intron 1 of 20)
chr17	43536097	7.966	0.143	Gpr116	intron (NM_001081178, intron 1 of 20)
chr17	43536021	10.096	0.17	Gpr116	intron (NM_001081178, intron 1 of 20)
chr5	147408616	14.338	0.064	Gpr12	Intergenic
chr5	147408637	13.105	0.115	Gpr12	Intergenic
chr5	147408631	9.978	0.175	Gpr12	Intergenic
chr12	73094024	7.923	0.057	Gpr135	TTS (NM_026102)
chr12	73094029	7.458	0.073	Gpr135	TTS (NM_026102)
chr7	126414533	11.646	0.163	Gpr139	Intergenic
chr6	59362388	15.411	0.134	Gprin3	intron (NM_183183, intron 1 of 1)
chr6	59362581	9.127	0.199	Gprin3	intron (NM_183183, intron 1 of 1)

chr13	21355983	-9.520	0.1	Gpx5	Intergenic
chr18	56574568	12.408	0.193	Gramd3	Intergenic
chr1	176672834	12.633	0.097	Grem2	intron (NM_019445, intron 14 of 17)
chr1	176672750	11.333	0.181	Grem2	intron (NM_019445, intron 14 of 17)
chr4	44966611	8.462	0.039	Grhpr	Intergenic
chr9	42753420	-18.363	0.033	Grik4	promoter-TSS (NM_175481)
chr9	42753495	-13.902	0.059	Grik4	Intergenic
chr9	42753547	-9.726	0.154	Grik4	Intergenic
chr18	66009893	-15.634	0.096	Grp	Intergenic
chr18	66009923	-11.086	0.166	Grp	Intergenic
chr8	122973078	21.333	0.033	Gse1	Intergenic
chr8	122974160	12.809	0.033	Gse1	CpG
chr8	122974144	11.998	0.086	Gse1	CpG
chr8	123055288	-18.201	0.088	Gse1	intron (NM_198671, intron 1 of 15)
chr8	122931491	-8.990	0.107	Gse1	Intergenic
chr8	122974080	13.593	0.16	Gse1	CpG
chr8	123055213	-11.178	0.182	Gse1	intron (NM_198671, intron 1 of 15)
chr8	122931465	-7.298	0.182	Gse1	Intergenic
chr19	4048039	5.120	0.054	Gstp2	Intergenic
chr8	82987560	-10.648	0.035	Gypa	Intergenic
chr8	82987565	-7.410	0.092	Gypa	Intergenic
chr7	149766284	22.848	0.036	H19	Intergenic
chr7	149766288	20.602	0.053	H19	Intergenic
chr17	34128628	17.625	0.1	H2-K1	Intergenic
chr17	34163633	13.344	0.051	H2-Ke6	exon (NM_013543, exon 7 of 9)
chr17	34163668	11.652	0.052	H2-Ke6	intron (NM_013543, intron 6 of 8)
chr4	149377129	11.129	0.061	H6pd	intron (NM_173371, intron 1 of 4)
chr17	84259794	-17.421	0.091	Hao	Intergenic
chr17	84259806	-12.337	0.178	Hao	Intergenic
chr17	84259876	-10.478	0.182	Hao	Intergenic
chr19	56266890	-20.309	0.033	Habp2	Intergenic
chr19	56362498	-12.468	0.121	Habp2	promoter-TSS (NM_146101)
chr19	56266912	-14.965	0.128	Habp2	Intergenic
chr19	56362515	-10.482	0.163	Habp2	promoter-TSS (NM_146101)
chr10	92964361	-8.734	0.083	Hal	intron (NM_010401, intron 14 of 19)
chr11	32187152	-8.816	0.119	Hbq1b	intron (NM_001033981, intron 1 of 2)
chr11	32187174	-14.598	0.127	Hbq1b	intron (NM_001033981, intron 1 of 2)
chr10	20972204	-20.758	0.036	Hbs1l	Intergenic
chr10	20972214	-18.595	0.048	Hbs1l	Intergenic
chr10	20972301	-13.910	0.102	Hbs1l	Intergenic
chr10	82159797	-9.359	0.179	Hcfc2	Intergenic
chr2	126462376	-11.273	0.158	Hdc	intron (NM_001271469, intron 3 of 3)
chr2	126462286	-8.361	0.179	Hdc	intron (NM_001271469, intron 3 of 3)
chr8	47426428	-10.767	0.106	Helt	Intergenic
chr8	47426317	-8.584	0.157	Helt	Intergenic
chr9	24905723	7.538	0.053	Herpud2	Intergenic

chr9	24905727	5.736	0.105	Herpud2	Intergenic
chr9	24905729	5.711	0.118	Herpud2	Intergenic
chr9	24905740	5.189	0.155	Herpud2	Intergenic
chr13	97966450	13.901	0.033	Hexb	intron (NM_010422, intron 1 of 13)
chr13	97966376	11.695	0.122	Hexb	intron (NM_010422, intron 1 of 13)
chr3	8664082	-9.917	0.131	Hey1	3' UTR (NM_010423, exon 5 of 5)
chr1	194346618	14.655	0.133	Hhat	intron (NM_144881, intron 11 of 11)
chr1	194346670	11.746	0.154	Hhat	intron (NM_144881, intron 11 of 11)
chr1	194346674	10.835	0.175	Hhat	intron (NM_144881, intron 11 of 11)
chr19	37546065	-12.976	0.064	Hhex	Intergenic
chr19	37546062	-13.119	0.112	Hhex	Intergenic
chr19	37522934	-14.463	0.14	Hhex	Intergenic
chr19	37522889	-11.614	0.195	Hhex	Intergenic
chr2	104335536	-14.046	0.098	Hipk3	promoter-TSS (NM_010434)
chr2	104335617	-16.347	0.115	Hipk3	promoter-TSS (NM_010434)
chr2	104335292	-11.936	0.131	Hipk3	promoter-TSS (NM_010434)
chr2	104335547	-11.465	0.155	Hipk3	promoter-TSS (NM_010434)
chr2	104335542	-6.181	0.16	Hipk3	promoter-TSS (NM_010434)
chr13	21839523	14.571	0.023	Hist1h4k	Intergenic
chr13	21839532	14.704	0.047	Hist1h4k	Intergenic
chr13	42122857	11.887	0.084	Hivep1	Intergenic
chr13	42122794	9.723	0.196	Hivep1	Intergenic
chr16	94399233	-16.300	0.057	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94449638	13.530	0.075	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94399235	-15.295	0.08	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94399191	-13.346	0.082	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94399225	-13.684	0.095	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94449271	10.863	0.132	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94400572	10.829	0.178	Hlcs	intron (NM_139145, intron 5 of 9)
chr16	94399111	-9.759	0.196	Hlcs	intron (NM_139145, intron 5 of 9)
chr14	65503827	-13.862	0.033	Hmbox1	intron (NM_177338, intron 4 of 9)
chr14	65503820	-10.289	0.13	Hmbox1	intron (NM_177338, intron 4 of 9)
chr14	65503905	-8.041	0.138	Hmbox1	intron (NM_177338, intron 4 of 9)
chr9	75848875	-15.882	0.049	Hmgcl1	Intergenic
chr9	75848873	-8.602	0.16	Hmgcl1	Intergenic
chr17	25098011	5.778	0.107	Hn1l	promoter-TSS (NM_198937)
chr17	25098418	12.208	0.136	Hn1l	promoter-TSS (NM_198937)
chr17	25098444	7.455	0.19	Hn1l	promoter-TSS (NM_198937)
chr3	3021854	13.682	0.031	Hnf4g	Intergenic
chr5	100423395	-15.095	0.066	Hnrnpd	Intergenic
chr5	100423474	-9.324	0.129	Hnrnpd	Intergenic
chr17	80416741	-8.824	0.165	Hnrnp1l	Intergenic
chr17	80416876	-9.264	0.166	Hnrnp1l	Intergenic
chr5	77544435	9.570	0.2	Hopx	promoter-TSS (NM_175606)
chr4	128797168	-10.456	0.095	Hpca	intron (NM_001286081, intron 1 of 3)
chr4	128797143	-8.025	0.183	Hpca	intron (NM_001286081, intron 1 of 3)

chr4	128797105	-6.875	0.184	Hpca	intron (NM_001286081, intron 1 of 3)
chr11	63730766	-11.016	0.144	Hs3st3b1	intron (NM_018805, intron 1 of 1)
chr11	63730797	-10.492	0.164	Hs3st3b1	intron (NM_018805, intron 1 of 1)
chr1	35889022	11.863	0.043	Hs6st1	Intergenic
chr1	36122876	-10.215	0.104	Hs6st1	Intergenic
chr1	36122847	-12.519	0.169	Hs6st1	Intergenic
chr18	80433755	14.636	0.044	Hsbp111	intron (NM_001136181, intron 1 of 4)
chr8	120224883	19.864	0.031	Hsd17b2	promoter-TSS (NM_008290)
chr1	56351340	18.707	0.023	Hsfy2	Intergenic
chr7	57019431	-17.682	0.055	Htati2	intron (NM_016865, intron 3 of 5)
chr7	57019414	-13.874	0.144	Htati2	intron (NM_016865, intron 3 of 5)
chr11	115270768	16.712	0.048	Ict1	intron (NM_026729, intron 2 of 5)
chr11	115270340	10.694	0.084	Ict1	intron (NM_026729, intron 2 of 5)
chr17	35951541	-14.127	0.043	Ier3	Intergenic
chr1	156944687	-16.552	0.018	Ier5	3' UTR (NM_010500, exon 1 of 1)
chr1	156906997	-14.313	0.067	Ier5	Intergenic
chr1	156906887	-15.036	0.075	Ier5	Intergenic
chr1	156906858	-12.651	0.076	Ier5	Intergenic
chr1	156906939	-11.898	0.095	Ier5	Intergenic
chr1	156944676	-8.970	0.116	Ier5	3' UTR (NM_010500, exon 1 of 1)
chr1	156944928	-7.379	0.126	Ier5	3' UTR (NM_010500, exon 1 of 1)
chr1	156906477	-10.000	0.164	Ier5	Intergenic
chr1	156906875	-9.354	0.189	Ier5	Intergenic
chr1	156906989	-7.286	0.199	Ier5	Intergenic
chr3	151438132	14.564	0.087	Iifi44i	Intergenic
chr3	151438419	16.196	0.107	Iifi44i	Intergenic
chr11	48900343	15.979	0.073	Iifi47	promoter-TSS (NM_001271676)
chr16	49775519	-14.190	0.087	Iift57	Intergenic
chr16	49775564	12.657	0.095	Iift57	Intergenic
chr16	49775504	-12.090	0.109	Iift57	Intergenic
chr16	49775321	-10.351	0.136	Iift57	Intergenic
chr16	49775296	-7.725	0.155	Iift57	Intergenic
chr16	49775917	-12.181	0.167	Iift57	Intergenic
chr7	75110221	-16.261	0.041	Igf1r	intron (NM_010513, intron 1 of 20)
chr7	75110215	-10.156	0.182	Igf1r	intron (NM_010513, intron 1 of 20)
chr4	45833033	-8.782	0.028	Igfbpl1	intron (NM_018741, intron 1 of 4)
chr16	38945560	12.752	0.059	Igsf11	intron (NM_170599, intron 1 of 6)
chr16	38945640	11.677	0.08	Igsf11	intron (NM_170599, intron 1 of 6)
chr4	139704424	-22.195	0.037	Igsf21	intron (NM_198610, intron 2 of 9)
chr4	139704433	-20.113	0.053	Igsf21	intron (NM_198610, intron 2 of 9)
chr4	139704397	-15.813	0.093	Igsf21	intron (NM_198610, intron 2 of 9)
chr4	139704460	-13.690	0.116	Igsf21	intron (NM_198610, intron 2 of 9)
chr3	68481154	-10.527	0.039	Ii12a	Intergenic
chr3	68481086	-12.868	0.09	Ii12a	Intergenic
chr14	58159479	-13.455	0.036	Ii17d	intron (NM_145837, intron 2 of 2)
chr14	58159100	-9.023	0.197	Ii17d	intron (NM_145837, intron 2 of 2)



chrX	133958942	23.697	0.028	Il1rapl2	Intergenic
chr1	40432481	-9.129	0.149	Il1rl2	Intergenic
chr1	40432446	-7.053	0.168	Il1rl2	Intergenic
chr10	19411955	-12.925	0.097	Il20ra	Intergenic
chr10	19411962	-11.055	0.178	Il20ra	Intergenic
chr9	100202396	-13.383	0.127	Il20rb	Intergenic
chr3	89676324	-20.613	0.04	Il6ra	intron (NM_010559, intron 9 of 9)
chr3	89676462	-17.961	0.095	Il6ra	intron (NM_010559, intron 9 of 9)
chr6	55127629	-12.925	0.066	Inmt	Intergenic
chr6	55127338	-8.209	0.168	Inmt	Intergenic
chr18	24270964	-9.359	0.033	Ino80c	intron (NM_172625, intron 3 of 4)
chr8	84528451	6.959	0.065	Inpp4b	intron (NM_001024617, intron 14 of 22)
chr14	121266141	-7.790	0.189	Ipo5	Intergenic
chr11	53615102	12.248	0.041	Irf1	intron (NR_033332, intron 3 of 3)
chr11	53582205	8.441	0.071	Irf1	Intergenic
chr11	53615092	5.728	0.183	Irf1	intron (NR_033332, intron 3 of 3)
chr7	19597088	-19.614	0.043	Irf2bp1	Intergenic
chr8	129124859	-17.526	0.057	Irf2bp2	Intergenic
chr12	88246985	14.286	0.098	Irf2bp1	Intergenic
chr12	88246343	-10.020	0.131	Irf2bp1	Intergenic
chr7	25317386	-8.576	0.068	Irgq	intron (NM_153134, intron 2 of 2)
chr7	25317479	-10.578	0.127	Irgq	intron (NM_153134, intron 2 of 2)
chr8	94983860	-18.317	0.02	Irx5	Intergenic
chr13	59869964	-15.375	0.058	Isca1	intron (NM_026921, intron 1 of 3)
chr13	59869961	-9.968	0.147	Isca1	intron (NM_026921, intron 1 of 3)
chr2	79068383	-17.201	0.044	Itga4	Intergenic
chr9	118542199	-20.476	0.064	Itga9	intron (NM_133721, intron 3 of 27)
chr9	118542057	-13.154	0.147	Itga9	intron (NM_133721, intron 3 of 27)
chr9	118542019	-11.657	0.185	Itga9	intron (NM_133721, intron 3 of 27)
chr6	108161898	-7.554	0.076	Itpr1	Intergenic
chr6	108161943	-10.983	0.094	Itpr1	Intergenic
chr11	51665657	13.366	0.035	Jade2	intron (NM_199299, intron 1 of 11)
chr11	51665660	9.750	0.049	Jade2	intron (NM_199299, intron 1 of 11)
chr11	51665654	12.901	0.073	Jade2	intron (NM_199299, intron 1 of 11)
chr16	34400527	-17.414	0.053	Kalrn	intron (NM_177357, intron 1 of 59)
chr16	34400612	-9.588	0.131	Kalrn	intron (NM_177357, intron 1 of 59)
chr17	33947117	-13.556	0.08	Kank3	promoter-TSS (NM_030697)
chr17	33947093	-10.656	0.199	Kank3	promoter-TSS (NM_030697)
chr11	104262219	-28.594	0.015	Kansl1	intron (NM_001081045, intron 2 of 13)
chr4	141898917	-14.053	0.115	Kazn	Intergenic
chr4	141898893	-15.015	0.134	Kazn	Intergenic
chr11	100614839	-14.789	0.066	Kcnh4	intron (NM_001081194, intron 6 of 16)
chr11	60836862	8.792	0.13	Kcnj12	intron (NM_001267593, intron 1 of 1)
chr16	95218323	-15.218	0.048	Kcnj6	intron (NM_001025585, intron 1 of 2)
chr16	95218094	-10.882	0.107	Kcnj6	intron (NM_001025585, intron 1 of 2)
chr2	163664225	20.140	0.039	Kcnk15	Intergenic

chr14	24382685	-16.777	0.042	Kcnma1	intron (NM_001253361, intron 5 of 30)
chr14	24382691	-15.231	0.073	Kcnma1	intron (NM_001253361, intron 5 of 30)
chr10	115872223	-9.540	0.08	Kcnmb4os1	intron (NM_021452, intron 2 of 2)
chr7	150291593	22.367	0.025	Kcnq1	Intergenic
chr7	150291653	12.037	0.106	Kcnq1	Intergenic
chr2	163993554	-17.919	0.069	Kcns1	exon (NM_008435, exon 3 of 4)
chr2	163993570	-16.687	0.095	Kcns1	exon (NM_008435, exon 3 of 4)
chr5	114808738	-15.885	0.041	Kctd10	intron (NM_001164573, intron 23 of 30)
chr5	114808750	-9.118	0.191	Kctd10	intron (NM_001164573, intron 23 of 30)
chr1	190851125	9.733	0.107	Kctd3	Intergenic
chr1	190851191	11.358	0.107	Kctd3	Intergenic
chr1	190851087	9.582	0.199	Kctd3	Intergenic
chr5	69731502	-8.913	0.099	Kctd8	intron (NM_175519, intron 1 of 1)
chr5	76231166	-9.986	0.081	Kdr	Intergenic
chr5	76231161	-8.813	0.116	Kdr	Intergenic
chr5	76231302	-8.376	0.123	Kdr	Intergenic
chr5	76231196	-8.789	0.158	Kdr	Intergenic
chr9	21034536	11.015	0.062	Keap1	3' UTR (NM_016679, exon 5 of 5)
chr13	46967871	16.444	0.097	Kif13a	intron (NM_010617, intron 2 of 37)
chr13	46967903	16.212	0.099	Kif13a	intron (NM_010617, intron 2 of 37)
chr2	109120503	-8.537	0.005	Kif18a	promoter-TSS (NM_139303)
chr5	76022638	-11.450	0.018	Kit	intron (NM_021099, intron 7 of 20)
chr14	100744352	-13.676	0.024	Klf12	Intergenic
chr14	100509032	22.791	0.044	Klf12	exon (NM_010636, exon 2 of 7)
chr14	100509070	14.699	0.131	Klf12	exon (NM_010636, exon 2 of 7)
chr13	5864892	-10.767	0.129	Klf6	intron (NM_011803, intron 2 of 3)
chr13	5864643	-11.652	0.141	Klf6	intron (NM_011803, intron 2 of 3)
chr13	5864515	-10.796	0.18	Klf6	exon (NM_011803, exon 2 of 4)
chr13	5864032	-10.094	0.183	Klf6	exon (NM_011803, exon 2 of 4)
chr1	134180608	-26.374	0.024	Klhdc8a	Intergenic
chr2	69662487	-11.493	0.126	Klhl23	exon (NM_177784, exon 2 of 4)
chr2	69662452	-11.249	0.179	Klhl23	exon (NM_177784, exon 2 of 4)
chr15	58175601	-8.665	0.107	Klhl38	intron (NM_027211, intron 8 of 8)
chr15	58175531	-10.628	0.136	Klhl38	intron (NM_027211, intron 8 of 8)
chr5	65486691	-20.430	0.028	Klhl5	Intergenic
chr5	65486524	-11.233	0.137	Klhl5	Intergenic
chr5	65486657	-10.264	0.16	Klhl5	Intergenic
chr11	99105858	10.551	0.162	Krt222	promoter-TSS (NM_172946)
chr9	102402973	11.375	0.044	Ky	Intergenic
chr1	155038778	15.665	0.036	Lamc2	Intergenic
chr1	155038762	11.481	0.199	Lamc2	Intergenic
chr1	183699665	-23.970	0.015	Lbr	Intergenic
chr1	183853454	-21.284	0.041	Lbr	intron (NM_010135, intron 6 of 14)
chr1	183853820	-14.464	0.07	Lbr	exon (NM_001083120, exon 5 of 14)
chr1	183699642	-14.575	0.079	Lbr	Intergenic
chr1	183853472	-16.996	0.108	Lbr	intron (NM_010135, intron 6 of 14)

chr1	183699663	-15.182	0.113	Lbr	Intergenic
chr1	183853843	-11.689	0.123	Lbr	exon (NM_001083120, exon 5 of 14)
chr1	183853813	-11.523	0.164	Lbr	exon (NM_001083120, exon 5 of 14)
chr14	75536456	-15.667	0.108	Lcp1	intron (NM_008879, intron 1 of 16)
chr14	75536436	-15.281	0.115	Lcp1	5' UTR (NM_008879, exon 1 of 17)
chr17	5295360	12.242	0.099	Ldhal6b	intron (NM_001085355, intron 8 of 19)
chr17	5295626	17.162	0.112	Ldhal6b	intron (NM_001085355, intron 8 of 19)
chr17	5295265	12.685	0.124	Ldhal6b	intron (NM_001085355, intron 8 of 19)
chr18	68218816	-5.517	0.198	Ldlrad4	intron (NM_172631, intron 1 of 5)
chr18	68218787	-6.999	0.198	Ldlrad4	intron (NM_172631, intron 1 of 5)
chr14	48003786	-11.951	0.103	Lgals3	intron (NM_001145953, intron 4 of 5)
chr14	48003793	-10.598	0.161	Lgals3	intron (NM_001145953, intron 4 of 5)
chr3	52906533	-17.544	0.049	Lhfp	intron (NM_175386, intron 2 of 3)
chr2	38215492	15.303	0.116	Lhx2	exon (NM_010710, exon 4 of 5)
chr2	38215431	13.931	0.123	Lhx2	exon (NM_010710, exon 4 of 5)
chr5	120781973	-14.301	0.106	Lhx5	Intergenic
chr5	120781970	-11.389	0.178	Lhx5	Intergenic
chr5	120781993	-11.462	0.192	Lhx5	Intergenic
chr3	153889704	11.795	0.122	Lhx8	intron (NM_001081263, intron 4 of 21)
chr3	153889729	9.806	0.137	Lhx8	intron (NM_001081263, intron 4 of 21)
chr15	99721305	-11.878	0.129	Lima1	Intergenic
chr15	99721302	-10.397	0.162	Lima1	Intergenic
chr10	106760842	-18.712	0.051	Lin7a	intron (NM_001284329, intron 1 of 5)
chr10	106760886	-12.486	0.121	Lin7a	intron (NM_001284329, intron 1 of 5)
chr9	56480413	-12.121	0.102	Lingo1	intron (NM_181074, intron 3 of 3)
chr19	34169634	15.407	0.05	Lipm	Intergenic
chr19	34169919	12.325	0.104	Lipm	MIR SINE MIR
chr3	88297699	-23.967	0.019	Lmna	promoter-TSS (NM_019390)
chr3	88297695	-22.755	0.028	Lmna	promoter-TSS (NM_019390)
chr3	88297691	-19.450	0.048	Lmna	promoter-TSS (NM_019390)
chr3	88297745	-15.186	0.068	Lmna	promoter-TSS (NM_019390)
chr2	103753225	-12.904	0.06	Lmo2	Intergenic
chr2	103753003	-8.646	0.121	Lmo2	Intergenic
chr3	143858283	-9.643	0.103	Lmo4	intron (NM_010723, intron 2 of 4)
chr3	143858228	-8.787	0.123	Lmo4	intron (NM_010723, intron 2 of 4)
chr3	143858827	-11.794	0.133	Lmo4	intron (NM_010723, intron 2 of 4)
chr5	75037258	-23.746	0.018	Lnx1	intron (NM_001159577, intron 2 of 10)
chr5	75015075	11.419	0.026	Lnx1	intron (NM_001159579, intron 5 of 9)
chr14	6239490	-5.645	0.177	LOC100861615	intron (NM_001270812, intron 1 of 7)
chr3	126817850	-10.696	0.095	LOC100862268	Intergenic
chr3	126817938	-8.621	0.131	LOC100862268	Intergenic
chr8	37354233	-12.581	0.048	Lonrf1	Intergenic
chr8	37354217	-6.917	0.117	Lonrf1	Intergenic
chr8	37354074	10.415	0.137	Lonrf1	Intergenic
chr8	37354357	-8.589	0.15	Lonrf1	Intergenic
chr8	37354370	-9.155	0.166	Lonrf1	Intergenic

chr18	77499614	-16.174	0.078	Loxhd1	Intergenic
chr18	77499914	-12.077	0.134	Loxhd1	Intergenic
chr18	77499546	-6.155	0.174	Loxhd1	Intergenic
chr3	145928538	13.143	0.066	Lpar3	intron (NM_022983, intron 2 of 2)
chr3	145928568	11.321	0.085	Lpar3	intron (NM_022983, intron 2 of 2)
chr5	81453876	-18.391	0.035	Lphn3	intron (NM_198702, intron 1 of 27)
chr5	82223596	-7.143	0.045	Lphn3	exon (NM_198702, exon 28 of 28)
chr5	82223601	-13.032	0.05	Lphn3	exon (NM_198702, exon 28 of 28)
chr5	81453765	-16.299	0.086	Lphn3	intron (NM_198702, intron 1 of 27)
chr5	82223515	-8.500	0.123	Lphn3	exon (NM_198702, exon 28 of 28)
chr5	82223599	-6.253	0.182	Lphn3	exon (NM_198702, exon 28 of 28)
chr6	94636122	-16.489	0.06	Lrig1	intron (NM_008377, intron 1 of 18)
chr6	94636095	-14.925	0.062	Lrig1	intron (NM_008377, intron 1 of 18)
chr10	127057029	-10.161	0.031	Lrp1	intron (NM_008512, intron 1 of 88)
chr10	127057053	-10.891	0.034	Lrp1	intron (NM_008512, intron 1 of 88)
chr10	127030204	-11.270	0.094	Lrp1	intron (NM_008512, intron 10 of 88)
chr10	127030208	-11.435	0.103	Lrp1	intron (NM_008512, intron 10 of 88)
chr10	127030275	-9.578	0.161	Lrp1	intron (NM_008512, intron 10 of 88)
chr9	77391300	-14.283	0.054	Lrrc1	intron (NM_001146048, intron 1 of 13)
chr9	77391157	-11.246	0.127	Lrrc1	intron (NM_001146048, intron 1 of 13)
chr9	77391168	-11.239	0.134	Lrrc1	intron (NM_001146048, intron 1 of 13)
chr9	77391488	7.474	0.137	Lrrc1	intron (NM_001146048, intron 1 of 13)
chr9	77391229	-8.354	0.176	Lrrc1	intron (NM_001146048, intron 1 of 13)
chr7	74709457	-19.618	0.046	Lrrc28	intron (NM_175124, intron 5 of 9)
chr8	107955835	14.182	0.02	Lrrc36	intron (NM_001033371, intron 2 of 10)
chr8	107955813	17.141	0.037	Lrrc36	intron (NM_001033371, intron 2 of 10)
chr8	107955838	9.815	0.127	Lrrc36	intron (NM_001033371, intron 2 of 10)
chr4	106923294	6.749	0.102	Lrrc42	intron (NM_029985, intron 1 of 7)
chr2	97308553	7.413	0.196	Lrrc4c	5' UTR (NM_178725, exon 1 of 3)
chr10	63549155	-18.092	0.032	Lrrtm3	intron (NM_178678, intron 2 of 2)
chr10	63549144	-16.362	0.043	Lrrtm3	intron (NM_178678, intron 2 of 2)
chr10	63549195	-12.635	0.142	Lrrtm3	intron (NM_178678, intron 2 of 2)
chr10	63549273	-11.061	0.171	Lrrtm3	intron (NM_178678, intron 2 of 2)
chr8	81344313	-6.046	0.035	Lsm6	intron (NM_001191004, intron 1 of 4)
chr10	92901110	-26.136	0.019	Lta4h	MLT1A-int LTR MaLR
chr10	92901133	-12.031	0.17	Lta4h	MLT1A-int LTR MaLR
chr17	75367631	-15.011	0.015	Ltbp1	Intergenic
chr17	75367646	-11.652	0.048	Ltbp1	Intergenic
chr17	75474538	17.592	0.087	Ltbp1	intron (NM_019919, intron 3 of 33)
chr19	5744253	-15.755	0.034	Ltbp3	intron (NM_008520, intron 2 of 27)
chr7	25413890	16.551	0.051	Lypd3	exon (NM_001102613, exon 15 of 15)
chr3	86327244	-18.056	0.061	Mab21l2	ID4_SINE ID
chr4	123340528	-17.070	0.036	Macf1	intron (NM_001199136, intron 1 of 97)
chr19	7143004	19.811	0.052	Macrocl1	intron (NM_134147, intron 3 of 10)
chr15	79179033	14.004	0.058	Maff	intron (NM_010755, intron 1 of 2)
chr15	79179049	12.581	0.095	Maff	intron (NM_010755, intron 1 of 2)

chr13	41173676	11.619	0.105	Mak	intron (NM_001145802, intron 1 of 11)
chr13	41173638	10.350	0.172	Mak	intron (NM_001145802, intron 1 of 11)
chr13	41173682	10.200	0.184	Mak	intron (NM_001145802, intron 1 of 11)
chr6	49066002	14.261	0.053	Malsu1	intron (NM_023670, intron 6 of 14)
chr7	52898535	14.268	0.023	Mamstr	intron (NM_172418, intron 5 of 9)
chr7	52898486	6.399	0.094	Mamstr	intron (NM_172418, intron 5 of 9)
chr7	52898542	10.250	0.099	Mamstr	intron (NM_172418, intron 5 of 9)
chr10	53760818	-15.637	0.086	Man1a	intron (NM_008548, intron 2 of 12)
chr10	53760389	-13.721	0.107	Man1a	intron (NM_008548, intron 2 of 12)
chr10	53760117	-11.834	0.142	Man1a	intron (NM_008548, intron 2 of 12)
chr10	53760812	-12.548	0.185	Man1a	intron (NM_008548, intron 2 of 12)
chr17	64952562	-14.961	0.151	Man2a1	intron (NM_008549, intron 1 of 21)
chr11	110434230	-12.893	0.061	Map2k6	Intergenic
chr11	110434267	-12.321	0.063	Map2k6	Intergenic
chr11	110398659	-13.206	0.106	Map2k6	Intergenic
chr11	110434295	-10.283	0.112	Map2k6	Intergenic
chr11	110434232	-10.222	0.131	Map2k6	Intergenic
chr11	110398765	-9.365	0.172	Map2k6	Intergenic
chr4	32178395	13.509	0.06	Map3k7	MTD LTR MaLR
chr17	81155320	-22.055	0.016	Map4k3	Intergenic
chr4	125914745	-19.437	0.056	Map7d1	ID4 SINE ID
chr5	103589414	-19.542	0.018	Mapk10	intron (NM_009158, intron 2 of 13)
chr18	24036376	-15.481	0.12	Mapre2	intron (NM_001162941, intron 5 of 7)
chr18	24036446	-13.407	0.17	Mapre2	exon (NM_153058, exon 5 of 7)
chr11	104154767	-16.547	0.103	Mapt	intron (NM_001038609, intron 4 of 11)
chr11	104166685	-15.441	0.106	Mapt	intron (NM_001038609, intron 6 of 11)
chr11	104166743	-9.474	0.138	Mapt	intron (NM_001038609, intron 6 of 11)
chr11	104154753	-12.882	0.155	Mapt	intron (NM_001038609, intron 4 of 11)
chr18	57083594	-11.295	0.033	March3	intron (NM_177115, intron 1 of 4)
chr8	112475922	-12.551	0.1	Marveld3	TTS (NM_028584)
chr8	112475991	-9.628	0.18	Marveld3	TTS (NM_028584)
chr8	112475954	-10.000	0.185	Marveld3	TTS (NM_028584)
chr13	103911354	21.357	0.02	Mast4	intron (NM_175171, intron 3 of 28)
chr12	78160379	-13.866	0.018	Max	Intergenic
chr12	78160362	-7.177	0.043	Max	Intergenic
chr3	60278002	-17.241	0.049	Mbnl1	intron (NM_001253713, intron 2 of 9)
chr3	60278299	-13.111	0.094	Mbnl1	intron (NM_001253713, intron 2 of 9)
chr3	60278245	-9.984	0.196	Mbnl1	intron (NM_001253713, intron 2 of 9)
chr14	120767011	12.850	0.111	Mbnl2	intron (NM_175341, intron 2 of 8)
chr8	122088089	25.010	0.001	Mbtps1	intron (NM_175185, intron 4 of 4)
chr18	68496817	-5.780	0.111	Mc5r	promoter-TSS (NM_013596)
chr9	43989817	-9.519	0.09	Mcam	intron (NM_007619, intron 2 of 15)
chr9	43989839	-8.497	0.15	Mcam	intron (NM_007619, intron 2 of 15)
chr18	44822405	-6.834	0.096	Mcc	promoter-TSS (NM_001085374)
chr3	95455334	-10.753	0.065	Mcl1	Intergenic
chr3	95455356	-10.561	0.116	Mcl1	Intergenic

chr10	117113780	-15.368	0.031	Mdm2	intron (NM_027468, intron 7 of 8)
chr10	117113941	-12.709	0.043	Mdm2	intron (NM_027468, intron 7 of 8)
chr10	117113794	-11.535	0.053	Mdm2	intron (NM_027468, intron 7 of 8)
chr10	117113226	-9.261	0.144	Mdm2	intron (NM_027468, intron 7 of 8)
chr10	117113102	-8.265	0.162	Mdm2	exon (NM_027468, exon 7 of 9)
chr10	117113956	-10.046	0.166	Mdm2	intron (NM_027468, intron 7 of 8)
chr10	117113683	-10.434	0.182	Mdm2	intron (NM_027468, intron 7 of 8)
chr3	30356967	-15.992	0.092	Mecom	intron (NM_021442, intron 1 of 2)
chr3	30356958	-11.487	0.183	Mecom	intron (NM_021442, intron 1 of 2)
chr11	18767721	-14.358	0.075	Meis1	Intergenic
chr11	18767661	-11.559	0.182	Meis1	Intergenic
chr2	115887667	-18.895	0.011	Meis2	intron (NM_001159568, intron 2 of 11)
chr2	115887638	-13.509	0.033	Meis2	intron (NM_001159568, intron 2 of 11)
chr2	115887557	-8.000	0.07	Meis2	intron (NM_001159568, intron 2 of 11)
chr2	115887945	-5.387	0.082	Meis2	intron (NM_001159568, intron 2 of 11)
chr2	115887611	-7.883	0.094	Meis2	intron (NM_001159568, intron 2 of 11)
chr2	115887873	-7.489	0.194	Meis2	intron (NM_001159568, intron 2 of 11)
chr2	115887972	-5.122	0.194	Meis2	CpG
chr6	30688683	-15.773	0.099	Mest	intron (NM_008590, intron 1 of 11)
chr2	70893044	-14.342	0.012	Mettl8	promoter-TSS (NM_001165982)
chr2	70893020	-7.215	0.105	Mettl8	promoter-TSS (NM_001165982)
chr19	45871047	9.605	0.052	Mgea5	intron (NM_145703, intron 2 of 9)
chr19	45871040	10.820	0.062	Mgea5	intron (NM_145703, intron 2 of 9)
chr6	88725404	-23.825	0.019	Mgll	intron (NM_011844, intron 3 of 7)
chr6	88725401	-21.615	0.029	Mgll	intron (NM_011844, intron 3 of 7)
chr1	169304759	18.087	0.093	Mgst3	intron (NM_025569, intron 4 of 5)
chr1	169304784	13.049	0.157	Mgst3	intron (NM_025569, intron 4 of 5)
chr6	121079703	-11.849	0.085	Mical3	intron (NM_001270475, intron 1 of 31)
chr6	121079590	-7.449	0.197	Mical3	intron (NM_001270475, intron 1 of 31)
chr5	140172217	-17.951	0.026	Micall2	Intergenic
chr5	140172299	-14.029	0.198	Micall2	Intergenic
chr10	59249244	14.816	0.036	Micu1	intron (NM_144822, intron 6 of 11)
chr10	59249425	16.301	0.049	Micu1	intron (NM_144822, intron 6 of 11)
chr8	41406942	16.132	0.018	Micu3	intron (NM_030110, intron 1 of 14)
chr8	41407046	16.690	0.042	Micu3	intron (NM_030110, intron 1 of 14)
chr8	41406944	14.596	0.044	Micu3	intron (NM_030110, intron 1 of 14)
chr8	41407049	15.607	0.082	Micu3	intron (NM_030110, intron 1 of 14)
chrX	166417270	24.609	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166440873	23.363	0.000	Mid1	Intergenic
chrX	166438684	-11.199	0.000	Mid1	Intergenic
chrX	166427567	-14.739	0.000	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166445032	-20.405	0.000	Mid1	Intergenic
chrX	166440879	20.242	0.000	Mid1	Intergenic
chrX	166417260	21.793	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166417256	21.885	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166417253	22.318	0.000	Mid1	Intron (NM_010797 4 of 9)

chrX	166427536	-17.299	0.000	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166417266	20.651	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166417010	21.010	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166417000	21.553	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166426612	-27.636	0.000	Mid1	intron (NM_183151, intron 9 of 9)
chrX	166417232	18.941	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166417185	18.197	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166417136	15.476	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166443349	15.600	0.000	Mid1	Intergenic
chrX	166417225	17.584	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166417213	15.797	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166441665	-16.399	0.000	Mid1	Intergenic
chrX	166416621	18.613	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166417315	18.028	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166425203	20.172	0.000	Mid1	CpG
chrX	166427373	-20.121	0.000	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166443368	10.923	0.000	Mid1	Intergenic
chrX	166417340	17.427	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166422217	-9.168	0.000	Mid1	intron (NM_010797, intron 6 of 9)
chrX	166416645	17.303	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166440898	13.475	0.000	Mid1	Intergenic
chrX	166425197	19.455	0.000	Mid1	CpG
chrX	166417102	13.531	0.000	Mid1	Intron (NM_010797 4 of 9)
chrX	166417467	20.456	0.001	Mid1	Intron (NM_010797 4 of 9)
chrX	166417350	15.105	0.002	Mid1	Intron (NM_010797 4 of 9)
chrX	166417210	12.865	0.002	Mid1	Intron (NM_010797 4 of 9)
chrX	166417309	14.225	0.002	Mid1	Intron (NM_010797 4 of 9)
chrX	166417808	16.423	0.003	Mid1	Intron (NM_010797 4 of 9)
chrX	166417817	15.398	0.003	Mid1	Intron (NM_010797 4 of 9)
chrX	166443343	12.624	0.003	Mid1	Intergenic
chrX	166444809	12.493	0.003	Mid1	Intergenic
chrX	166418508	9.939	0.004	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166416709	16.027	0.004	Mid1	Intron (NM_010797 4 of 9)
chrX	166425100	20.395	0.006	Mid1	CpG
chrX	166421976	10.457	0.007	Mid1	exon (NM_010797, exon 6 of 10)
chrX	166418087	10.912	0.007	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166416628	14.235	0.007	Mid1	Intron (NM_010797, intron 4 of 9)
chrX	166416503	13.212	0.009	Mid1	Intron (NM_010797, intron 4 of 9)
chrX	166416722	14.704	0.012	Mid1	Intron (NM_010797, intron 4 of 9)
chrX	166424805	21.115	0.012	Mid1	CpG
chrX	166424620	18.292	0.013	Mid1	intron (NM_010797, intron 8 of 9)
chrX	166417970	11.956	0.013	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166419899	10.207	0.013	Mid1	exon (NM_010797, exon 5 of 10)
chrX	166416485	13.872	0.014	Mid1	Intron (NM_010797, 4 of 9)
chrX	166417346	11.931	0.014	Mid1	Intron (NM_010797, 4 of 9)
chrX	166422944	8.538	0.014	Mid1	exon (NM_010797, exon 7 of 10)

chrX	166425234	16.408	0.016	Mid1	CpG
chrX	166421255	8.939	0.017	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166417752	15.156	0.018	Mid1	Intron (NM_010797 4 of 9)
chrX	166417900	11.281	0.018	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166421313	12.067	0.019	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166416828	19.195	0.02	Mid1	Intron (NM_010797, intron 4 of 9)
chrX	166419931	9.709	0.021	Mid1	exon (NM_010797, exon 5 of 10)
chrX	166421197	5.667	0.021	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166421234	6.680	0.022	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166427992	10.316	0.022	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166428120	9.159	0.022	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166442831	6.810	0.024	Mid1	Intergenic
chrX	166428186	13.550	0.027	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166424980	16.738	0.027	Mid1	CpG
chrX	166422977	7.692	0.027	Mid1	exon (NM_010797, exon 7 of 10)
chrX	166416931	17.720	0.027	Mid1	Intron (NM_010797, intron 4 of 9)
chrX	166444934	12.744	0.027	Mid1	Intergenic
chrX	166418492	6.969	0.028	Mid1	intron (NM__010797, intron 4 of 9)
chrX	166424840	16.616	0.029	Mid1	CpG
chrX	166424813	17.618	0.029	Mid1	CpG
chrX	166443025	8.904	0.03	Mid1	Intergenic
chrX	166419893	8.856	0.03	Mid1	exon (NM_010797, exon 5 of 10)
chrX	166419395	-7.603	0.03	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166428195	13.441	0.031	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166446717	16.842	0.033	Mid1	Intergenic
chrX	166424826	15.970	0.033	Mid1	CpG
chrX	166417787	12.635	0.036	Mid1	Intron (NM_010797, intron 4 of 9)
chrX	166416812	14.465	0.036	Mid1	Intron (NM_010797, intron 4 of 9)
chrX	166445879	-7.101	0.036	Mid1	Intergenic
chrX	166427753	-9.623	0.036	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166428100	9.580	0.038	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166418049	10.059	0.039	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166428147	10.136	0.04	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166422857	6.183	0.043	Mid1	CpG
chrX	166422691	5.132	0.045	Mid1	intron (NM_010797, intron 6 of 9)
chrX	166428106	8.292	0.045	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166422320	6.587	0.048	Mid1	intron (NM_010797, intron 6 of 9)
chrX	166443409	13.950	0.048	Mid1	Intergenic
chrX	166422355	7.983	0.049	Mid1	intron (NM_010797, intron 6 of 9)
chrX	166424984	14.422	0.05	Mid1	CpG
chrX	166418312	5.778	0.053	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166421293	7.271	0.054	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166419908	8.147	0.055	Mid1	exon (NM_010797, exon 5 of 10)
chrX	166419927	7.427	0.058	Mid1	exon (NM_010797, exon 5 of 10)
chrX	166424811	-6.730	0.059	Mid1	CpG
chrX	166443375	11.310	0.061	Mid1	Intergenic



chrX	166421242	6.774	0.062	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166425119	11.502	0.062	Mid1	CpG
chrX	166428214	13.098	0.064	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166425255	-7.163	0.064	Mid1	CpG
chrX	166417427	10.272	0.066	Mid1	Intron (NM_010797 4 of 9)
chrX	166418487	5.861	0.066	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166428153	9.946	0.068	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166425352	10.417	0.071	Mid1	CpG
chrX	166424685	14.208	0.072	Mid1	intron (NM_010797, intron 8 of 9)
chrX	166416588	9.129	0.072	Mid1	Intron (NM_010797 4 of 9)
chrX	166424584	11.255	0.072	Mid1	intron (NM_010797, intron 8 of 9)
chrX	166426624	-6.526	0.073	Mid1	intron (NM_010797, intron 9 of 9)
chrX	166424842	12.810	0.079	Mid1	CpG
chrX	166419668	7.921	0.079	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166426834	-8.838	0.081	Mid1	exon (NM_010797, exon 10 of 10)
chrX	166428050	7.035	0.085	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166428172	10.073	0.086	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166419771	5.370	0.087	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166424010	-9.340	0.087	Mid1	exon (NM_010797, exon 8 of 10)
chrX	166421604	7.687	0.092	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166421599	8.477	0.095	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166425228	10.967	0.096	Mid1	CpG
chrX	166425112	10.861	0.096	Mid1	CpG
chrX	166428001	7.242	0.098	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166440905	7.056	0.098	Mid1	Intergenic
chrX	166425097	13.894	0.099	Mid1	CpG
chrX	166445429	6.934	0.1	Mid1	Intergenic
chrX	166428095	6.801	0.111	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166417729	10.831	0.111	Mid1	promoter-TSS (NR_029457)
chrX	166427973	6.726	0.118	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166416383	7.973	0.122	Mid1	Intron (NM_010797 4 of 9)
chrX	166443013	6.863	0.122	Mid1	Intergenic
chrX	166417402	7.664	0.128	Mid1	Intron (NM_010797 4 of 9)
chrX	166424639	10.796	0.13	Mid1	intron (NM_010797, intron 8 of 9)
chrX	166421759	5.964	0.131	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166424692	11.514	0.133	Mid1	intron (NM_010797, intron 8 of 9)
chrX	166419884	5.912	0.146	Mid1	exon (NM_010797, exon 5 of 10)
chrX	166416554	7.260	0.147	Mid1	Intron (NM_010797 4 of 9)
chrX	166421346	6.769	0.167	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166421338	6.464	0.169	Mid1	intron (NM_010797, intron 5 of 9)
chrX	166428059	5.225	0.171	Mid1	3' UTR (NM_010797, exon 10 of 10)
chrX	166418837	6.746	0.171	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166426824	-7.008	0.18	Mid1	exon (NM_010797, exon 10 of 10)
chrX	166419809	6.263	0.182	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166419008	7.738	0.183	Mid1	intron (NM_010797, intron 4 of 9)
chrX	166421746	5.003	0.185	Mid1	intron (NM_010797, intron 5 of 9)

chrX	166416412	6.386	0.192	Mid1	Intron (NM_010797 4 of 9)
chr11	87565460	12.128	0.073	Mir142	Intergenic
chr18	69312930	18.374	0.036	Mir145b	Intergenic
chr18	69312915	12.261	0.115	Mir145b	Intergenic
chr16	84705257	-14.583	0.1	Mir155	Intergenic
chr16	84705259	-14.327	0.111	Mir155	Intergenic
chr14	115348129	-13.740	0.099	Mir17	Intergenic
chr14	115348146	-12.725	0.131	Mir17	Intergenic
chr8	86716266	-25.094	0.033	Mir181c	Intergenic
chr8	131012812	-6.132	0.184	Mir1903	intron (NM_008737, intron 12 of 16)
chr10	44100549	-19.388	0.052	Mir1929	Intergenic
chr10	44100546	-16.393	0.091	Mir1929	Intergenic
chr10	44100557	-13.358	0.126	Mir1929	Intergenic
chr10	44100362	-11.382	0.148	Mir1929	Intergenic
chr3	138213953	-15.476	0.068	Mir1956	exon (NM_007917, exon 6 of 8)
chr3	138213938	-14.418	0.108	Mir1956	exon (NM_007917, exon 6 of 8)
chr3	138213449	-14.773	0.108	Mir1956	intron (NM_007917, intron 5 of 7)
chr3	138213623	-11.941	0.179	Mir1956	intron (NM_007917, intron 5 of 7)
chr3	138213949	-11.792	0.191	Mir1956	exon (NM_007917, exon 6 of 8)
chr7	142771936	-18.836	0.025	Mir1962	intron (NM_011212, intron 1 of 20)
chr7	142771925	-14.259	0.08	Mir1962	intron (NM_011212, intron 1 of 20)
chr1	186651344	-19.442	0.011	Mir1981	intron (NM_133684, intron 4 of 7)
chr1	186651435	-13.500	0.068	Mir1981	intron (NM_133684, intron 4 of 7)
chr1	186651354	-13.868	0.133	Mir1981	intron (NM_133684, intron 4 of 7)
chr1	186651432	-10.576	0.154	Mir1981	intron (NM_133684, intron 4 of 7)
chr1	186651430	-7.994	0.194	Mir1981	intron (NM_133684, intron 4 of 7)
chr18	10866401	12.386	0.135	Mir1a-2	Intergenic
chr18	10866329	15.016	0.141	Mir1a-2	Intergenic
chr18	10866462	11.310	0.168	Mir1a-2	Intergenic
chr11	86407229	17.253	0.095	Mir21	intron (NM_029478, intron 10 of 11)
chr11	86407208	12.072	0.185	Mir21	intron (NM_029478, intron 10 of 11)
chr11	51930157	-19.635	0.044	Mir3061	intron (NM_019411, intron 2 of 6)
chr11	51930153	-16.902	0.08	Mir3061	intron (NM_019411, intron 2 of 6)
chr8	86746656	-14.641	0.095	Mir3074-2	intron (NM_172503, intron 10 of 13)
chr8	86746705	-12.585	0.152	Mir3074-2	intron (NM_172503, intron 10 of 13)
chr16	44557534	-9.895	0.116	Mir3081	TTS (NR_037242)
chr8	111461493	-11.852	0.154	Mir3108	TTS (NR_037295)
chr8	111461236	-11.815	0.158	Mir3108	TTS (NR_037295)
chr1	108304569	14.957	0.133	Mir3473f	Intergenic
chr1	108304606	14.129	0.151	Mir3473f	Intergenic
chr1	34466972	-9.723	0.106	Mir5103	Intergenic
chr1	34466960	-8.502	0.175	Mir5103	Intergenic
chr19	58001824	13.542	0.039	Mir5623	intron (NM_181415, intron 26 of 28)
chr19	58001915	17.496	0.071	Mir5623	intron (NM_181415, intron 26 of 28)
chr1	39234769	-16.658	0.036	Mir6349	Intergenic
chr1	39236649	-7.317	0.146	Mir6349	Intergenic

chr1	39236982	-13.102	0.178	Mir6349	Intergenic
chr1	39236711	-8.269	0.196	Mir6349	Intergenic
chr1	77275921	16.265	0.053	Mir6352	Intergenic
chr1	77501867	-11.817	0.067	Mir6352	intron (NM_007936, intron 3 of 17)
chr18	76331931	19.873	0.046	Mir6358	Intergenic
chr18	76331924	19.013	0.066	Mir6358	Intergenic
chr2	166400924	-14.723	0.099	Mir6364	intron (NM_177782, intron 32 of 39)
chr2	166400840	-11.551	0.189	Mir6364	intron (NM_177782, intron 32 of 39)
chr6	102730933	7.745	0.036	Mir6373	Intergenic
chr10	75465354	-19.666	0.014	Mir6409	intron (NM_198635, intron 11 of 13)
chr17	30399116	14.651	0.035	Mir6412	intron (NM_172618, intron 9 of 11)
chr2	17429356	18.899	0.037	Mir6419	intron (NM_028757, intron 4 of 6)
chr5	24096708	-19.300	0.04	Mir671	intron (NM_133913, intron 3 of 3)
chr5	24096734	-17.949	0.077	Mir671	intron (NM_133913, intron 3 of 3)
chr14	73575766	-21.348	0.015	Mir687	intron (NR_033185, intron 13 of 15)
chr14	73575788	-16.140	0.049	Mir687	intron (NR_033185, intron 13 of 15)
chr11	59997810	-20.143	0.049	Mir6921	intron (NM_001037764, intron 1 of 4)
chr11	59997707	-13.581	0.177	Mir6921	intron (NM_001037764, intron 1 of 4)
chr11	120172736	-11.924	0.068	Mir6935	Intergenic
chr11	120172697	-14.274	0.087	Mir6935	Intergenic
chr12	86598141	-23.946	0.022	Mir6938	intron (NM_175337, intron 5 of 11)
chr12	86598294	-12.719	0.053	Mir6938	intron (NM_175337, intron 5 of 11)
chr19	47413275	19.186	0.046	Mir6995	intron (NM_001164717, intron 6 of 13)
chr19	47413185	9.206	0.185	Mir6995	intron (NM_001164717, intron 6 of 13)
chr5	111409798	-9.376	0.107	Mir701	intron (NM_001267622, intron 2 of 23)
chr5	111409901	-10.404	0.194	Mir701	intron (NM_001267622, intron 2 of 23)
chr6	82995100	-13.607	0.115	Mir7040	intron (NM_013586, intron 4 of 13)
chr6	82995071	-12.489	0.126	Mir7040	intron (NM_013586, intron 4 of 13)
chr6	94573262	11.159	0.166	Mir7041	intron (NM_008377, intron 7 of 18)
chr6	125048252	-12.387	0.192	Mir7045	intron (NM_145979, intron 2 of 38)
chr7	25729240	-11.038	0.087	Mir7046	CpG
chr7	25729237	-8.952	0.129	Mir7046	CpG
chr7	26002508	13.327	0.074	Mir7048	TTS (NR_106015)
chr9	109811587	8.491	0.018	Mir7089	Intergenic
chr13	62861544	11.100	0.088	Mir713	promoter-TSS (NR_030493)
chr8	73322456	-9.875	0.133	Mir7240	TTS (NR_106099)
chr8	73322383	-5.069	0.165	Mir7240	TTS (NR_106099)
chr8	73322378	-5.300	0.188	Mir7240	TTS (NR_106099)
chr14	80138108	-16.839	0.039	Mir759	promoter-TSS (NR_030436)
chr14	80138083	-12.353	0.136	Mir759	promoter-TSS (NR_030436)
chr16	21256109	-10.053	0.034	Mir7680	promoter-TSS (NR_106145)
chr16	21256313	-11.788	0.153	Mir7680	promoter-TSS (NR_106145)
chr4	36236379	9.073	0.047	Mir876	intron (NM_001165999, intron 3 of 7)
chr6	97827488	14.322	0.044	Mitf	intron (NM_001113198, intron 1 of 9)
chr6	97827640	17.794	0.075	Mitf	intron (NM_001113198, intron 1 of 9)
chr6	97827643	12.617	0.134	Mitf	intron (NM_001113198, intron 1 of 9)

chr16	13183623	-17.293	0.04	Mkl2	Intergenic
chr5	115605450	-16.308	0.08	Mlec	intron (NM_175403, intron 1 of 4)
chr5	115605547	-12.592	0.14	Mlec	intron (NM_175403, intron 1 of 4)
chr5	115605504	-9.887	0.152	Mlec	intron (NM_175403, intron 1 of 4)
chr17	13869215	9.962	0.148	Mllt4	intron (NM_022311, intron 1 of 2)
chr14	10439516	-14.389	0.066	Mnd1-ps	intron (NM_010210, intron 7 of 8)
chr9	107791274	14.498	0.02	Mon1a	intron (NM_028369, intron 1 of 5)
chr16	48431515	12.858	0.141	Morc1	intron (NM_010816, intron 1 of 26)
chr4	154524130	-9.623	0.144	Morn1	Intergenic
chr4	154524101	-8.197	0.185	Morn1	Intergenic
chr4	154524081	-6.150	0.188	Morn1	Intergenic
chr8	73282427	-22.028	0.009	Mpv17l2	TTS (NM_183170)
chr8	73282424	-15.312	0.063	Mpv17l2	TTS (NM_183170)
chr1	167585333	-16.987	0.065	Mpzl1	intron (NM_001038846, intron 5 of 5)
chr1	167585199	-10.198	0.08	Mpzl1	intron (NM_001038846, intron 5 of 5)
chr17	13072969	-13.615	0.054	Mrgprh	Intergenic
chr17	13072931	-5.475	0.105	Mrgprh	Intergenic
chr17	13072813	-9.247	0.171	Mrgprh	Intergenic
chr17	13072908	-7.424	0.199	Mrgprh	Intergenic
chr15	73906396	-10.324	0.043	Mroh5	Intergenic
chr15	73906292	-15.853	0.057	Mroh5	Intergenic
chr15	73906804	-11.348	0.118	Mroh5	Intergenic
chr15	73906416	-7.331	0.185	Mroh5	Intergenic
chr15	73906797	-9.284	0.194	Mroh5	Intergenic
chr14	58446673	-17.997	0.044	Mrp63	3' UTR (NM_026401, exon 2 of 2)
chr9	37293071	-16.452	0.044	Msantd2	Intergenic
chr1	14696325	-20.206	0.039	Msc	Intergenic
chr11	88492090	9.371	0.048	Msi2	intron (NM_054043, intron 5 of 13)
chr11	88492066	6.388	0.142	Msi2	intron (NM_054043, intron 5 of 13)
chr10	120333265	21.011	0.034	Msrp3	intron (NM_177092, intron 1 of 6)
chr10	120333225	19.058	0.073	Msrp3	intron (NM_177092, intron 1 of 6)
chr10	120333244	16.376	0.079	Msrp3	intron (NM_177092, intron 1 of 6)
chr10	120333314	13.124	0.09	Msrp3	intron (NM_177092, intron 1 of 6)
chr10	120333236	15.990	0.112	Msrp3	intron (NM_177092, intron 1 of 6)
chr4	147420715	-19.158	0.04	Mthfr	intron (NM_001161798, intron 4 of 11)
chr8	42239203	21.289	0.031	Mtus1	Intergenic
chr8	42239187	14.170	0.086	Mtus1	Intergenic
chr8	42139978	13.319	0.129	Mtus1	exon (NM_001005864, exon 1 of 12)
chr8	42139982	11.634	0.189	Mtus1	exon (NM_001005864, exon 1 of 12)
chr2	74939601	-8.789	0.187	Mtx2	Intergenic
chr4	60187890	-8.019	0.034	Mup15	Intergenic
chr4	61685061	14.626	0.028	Mup20	Intergenic
chr2	33743685	10.899	0.159	Mvb12b	promoter-TSS (NM_175184)
chr13	55429433	-14.642	0.083	Mxd3	intron (NM_016662, intron 4 of 5)
chr10	20821839	12.798	0.138	Myb	Intergenic
chr15	61831575	-16.154	0.018	Myc	Intergenic

chr15	61821304	-18.118	0.04	Myc	exon (NM_010849, exon 3 of 3)
chr15	61821436	-11.859	0.149	Myc	exon (NM_010849, exon 3 of 3)
chr11	94387947	14.390	0.043	Mycbpap	Intergenic
chr11	104431975	-12.134	0.007	Myl4	intron (NM_010858, intron 2 of 8)
chr13	45487430	-14.634	0.042	Myliip	intron (NM_153789, intron 2 of 6)
chr13	45487425	-11.379	0.122	Myliip	intron (NM_153789, intron 2 of 6)
chr13	45487041	-14.874	0.177	Myliip	intron (NM_153789, intron 2 of 6)
chr13	45487087	-11.905	0.193	Myliip	intron (NM_153789, intron 2 of 6)
chr16	34746355	10.506	0.051	Mylk	Intergenic
chr16	34746115	11.123	0.173	Mylk	Intergenic
chr11	80575921	6.815	0.043	Myo1d	intron (NM_177390, intron 1 of 21)
chr5	114749934	13.999	0.073	Myo1h	Intergenic
chr5	114749971	10.205	0.102	Myo1h	Intergenic
chr17	71438861	-14.883	0.056	Myom1	intron (NM_001083934, intron 19 of 36)
chr17	71438514	-5.491	0.185	Myom1	intron (NM_001083934, intron 19 of 36)
chr18	60756660	-13.955	0.16	Myoz3	intron (NM_177340, intron 2 of 2)
chr18	60756650	-12.326	0.186	Myoz3	intron (NM_177340, intron 2 of 2)
chr10	62640493	-20.394	0.034	Mypn	intron (NM_182992, intron 2 of 19)
chr10	62623635	12.757	0.068	Mypn	intron (NM_182992, intron 6 of 19)
chr10	62640384	-13.492	0.119	Mypn	intron (NM_182992, intron 2 of 19)
chr10	62623824	11.263	0.171	Mypn	intron (NM_182992, intron 6 of 19)
chr10	62623730	-8.333	0.199	Mypn	intron (NM_182992, intron 6 of 19)
chr9	71454574	-15.659	0.018	Myzap	Intergenic
chr5	97820881	-14.738	0.036	Naa11	promoter-TSS (NR_045981)
chr1	51651786	15.467	0.086	Nabp1	Intergenic
chr1	51651897	7.899	0.113	Nabp1	Intergenic
chr11	101995722	14.120	0.095	Nags	Intergenic
chr11	101995612	11.867	0.152	Nags	Intergenic
chr6	58871895	15.369	0.009	Nap115	Intergenic
chr7	56247994	-11.875	0.046	Nav2	intron (NM_001111016, intron 2 of 38)
chr7	56247542	-14.770	0.052	Nav2	intron (NM_001111016, intron 2 of 38)
chr15	37720396	-15.836	0.115	Ncald	intron (NM_134094, intron 1 of 6)
chr15	37720725	-8.108	0.122	Ncald	intron (NM_134094, intron 1 of 6)
chr15	37720495	-11.776	0.179	Ncald	intron (NM_134094, intron 1 of 6)
chr15	37720204	-10.285	0.189	Ncald	intron (NM_134094, intron 1 of 6)
chr1	43531077	-12.849	0.061	Nck2	intron (NM_010879, intron 1 of 4)
chr1	43531101	-11.653	0.1	Nck2	intron (NM_010879, intron 1 of 4)
chr1	43362960	14.545	0.107	Nck2	Intergenic
chr1	43362977	12.512	0.156	Nck2	Intergenic
chr15	99293815	-23.674	0.018	Nckap5l	Intergenic
chr15	99293838	-12.456	0.126	Nckap5l	Intergenic
chr15	99293884	-9.240	0.194	Nckap5l	Intergenic
chr1	13418154	12.943	0.074	Ncoa2	Intergenic
chr1	13418146	11.106	0.124	Ncoa2	Intergenic
chr1	13418159	8.051	0.194	Ncoa2	Intergenic
chr5	125634265	7.857	0.105	Ncor2	intron (NM_001253904, intron 1 of 47)

chr5	125657204	7.716	0.143	Ncor2	intron (NM_001253904, intron 1 of 47)
chr5	125657634	12.095	0.169	Ncor2	MIR SINE MIR
chr5	125634155	7.500	0.197	Ncor2	intron (NM_001253904, intron 1 of 47)
chr18	60888953	-19.152	0.036	Ndst1	Intergenic
chr3	123464589	10.035	0.086	Ndst3	Intergenic
chr3	123464632	12.811	0.107	Ndst3	Intergenic
chr6	126799817	13.913	0.107	Ndufa9	promoter-TSS (NM_025358)
chr2	119467097	10.370	0.08	Ndufaf1	intron (NM_001042652, intron 7 of 9)
chr16	37634782	-15.291	0.03	Ndufb4	Intergenic
chr16	37634856	-11.243	0.103	Ndufb4	Intergenic
chr16	37634731	-8.031	0.175	Ndufb4	Intergenic
chr19	5843759	-10.606	0.067	Neat1	non-coding (NR_003513, exon 1 of 1)
chr19	5843955	-13.717	0.144	Neat1	non-coding (NR_003513, exon 1 of 1)
chr2	17774781	16.229	0.094	Nebi	Intergenic
chr9	72488692	12.689	0.054	Nedd4	Intergenic
chr9	72541304	12.096	0.097	Nedd4	intron (NM_010890, intron 6 of 28)
chr9	72541034	12.284	0.106	Nedd4	intron (NM_010890, intron 6 of 28)
chr9	72488702	8.916	0.159	Nedd4	Intergenic
chr9	72488665	8.915	0.189	Nedd4	Intergenic
chr1	193663585	18.655	0.04	Nek2	Intergenic
chr1	193663543	13.814	0.106	Nek2	Intergenic
chr1	193663277	-10.716	0.193	Nek2	Intergenic
chr1	140515256	-10.800	0.031	Nek7	intron (NM_021605, intron 1 of 9)
chr9	58837243	-14.755	0.095	Neo1	intron (NM_001042752, intron 2 of 27)
chr9	58837240	-11.518	0.184	Neo1	intron (NM_001042752, intron 2 of 27)
chr3	87778635	14.376	0.084	Nes	intron (NM_016701, intron 2 of 3)
chr3	87778073	17.516	0.087	Nes	intron (NM_016701, intron 2 of 3)
chr3	87778541	13.290	0.093	Nes	intron (NM_016701, intron 2 of 3)
chr3	87778921	14.232	0.179	Nes	intron (NM_016701, intron 3 of 3)
chr3	87778006	-14.268	0.184	Nes	intron (NM_016701, intron 2 of 3)
chr18	86454089	-14.799	0.075	Neto1	Intergenic
chr18	86454112	-13.206	0.077	Neto1	Intergenic
chr18	86454152	-9.472	0.192	Neto1	Intergenic
chr6	55629630	-13.968	0.098	Neurod6	exon (NM_009717, exon 2 of 2)
chr6	55629342	-9.754	0.135	Neurod6	exon (NM_009717, exon 2 of 2)
chr6	55629340	-9.277	0.158	Neurod6	exon (NM_009717, exon 2 of 2)
chr6	55629328	-8.947	0.176	Neurod6	exon (NM_009717, exon 2 of 2)
chr11	4706313	13.895	0.054	Nf2	exon (NM_010898, exon 6 of 16)
chr11	4706641	13.583	0.107	Nf2	intron (NM_001252250, intron 5 of 16)
chr11	4706269	14.900	0.111	Nf2	exon (NM_010898, exon 6 of 16)
chr15	82885892	-16.355	0.105	Nfam1	Intergenic
chr15	82885905	-14.118	0.17	Nfam1	Intergenic
chr15	103088648	-10.689	0.049	Nfe2	Intergenic
chr15	103088657	-9.489	0.089	Nfe2	Intergenic
chr15	103088651	-7.113	0.162	Nfe2	Intergenic
chr4	82184801	-16.714	0.009	Nfib	Intergenic

chr4	82265548	-19.326	0.048	Nfib	tRNA-His-CAY_tRNA tRNA
chr4	82046518	-16.340	0.079	Nfib	intron (NM_008687, intron 2 of 8)
chr4	82184769	-8.549	0.159	Nfib	Intergenic
chr4	82184829	-11.244	0.165	Nfib	Intergenic
chr14	20570151	-20.390	0.057	Nid2	promoter-TSS (NM_008695)
chr12	71180240	-12.576	0.044	Nin	intron (NM_001286080, intron 4 of 29)
chr12	71180232	-12.697	0.05	Nin	intron (NM_001286080, intron 4 of 29)
chr12	71176814	-11.184	0.092	Nin	intron (NM_001286080, intron 5 of 29)
chr12	71176811	-11.142	0.096	Nin	intron (NM_001286080, intron 5 of 29)
chr4	53093540	-14.666	0.073	Nipsnap3b	intron (NM_013454, intron 17 of 49)
chr4	53093532	-6.283	0.194	Nipsnap3b	intron (NM_013454, intron 17 of 49)
chr7	139788577	-11.141	0.056	Nkx1-2	3' UTR (NM_009123, exon 2 of 2)
chr7	139788381	-13.393	0.111	Nkx1-2	3' UTR (NM_009123, exon 2 of 2)
chr7	139788278	15.808	0.126	Nkx1-2	3' UTR (NM_009123, exon 2 of 2)
chr7	139788607	-6.242	0.129	Nkx1-2	3' UTR (NM_009123, exon 2 of 2)
chr7	139788535	-8.969	0.184	Nkx1-2	3' UTR (NM_009123, exon 2 of 2)
chr19	43692910	-15.940	0.097	Nkx2-3	Intergenic
chr3	26129259	-17.529	0.043	Nlgn1	intron (NM_138666, intron 1 of 7)
chr3	26129152	-11.944	0.135	Nlgn1	intron (NM_138666, intron 1 of 7)
chr11	107126684	-14.091	0.105	Nol11	intron (NM_145823, intron 5 of 9)
chr11	107126663	-12.299	0.155	Nol11	intron (NM_145823, intron 5 of 9)
chr2	68886430	-14.242	0.111	Nostrin	intron (NM_172856, intron 5 of 9)
chr2	68886222	-10.437	0.189	Nostrin	intron (NM_172856, intron 5 of 9)
chr18	12392234	11.593	0.124	Npc1	intron (NM_008720, intron 1 of 24)
chr18	12392723	8.194	0.18	Npc1	intron (NM_008720, intron 1 of 24)
chr14	71082045	-14.388	0.029	Npm2	intron (NM_023045, intron 18 of 27)
chr11	98632921	16.582	0.049	Nr1d1	intron (NM_145434, intron 2 of 7)
chr11	98632645	-17.252	0.08	Nr1d1	exon (NM_145434, exon 4 of 8)
chr11	98632586	-10.806	0.15	Nr1d1	exon (NM_145434, exon 4 of 8)
chr11	98632164	-12.500	0.152	Nr1d1	intron (NM_145434, intron 4 of 7)
chr11	98632552	-9.893	0.166	Nr1d1	exon (NM_145434, exon 4 of 8)
chr11	98632582	-10.877	0.174	Nr1d1	exon (NM_145434, exon 4 of 8)
chr7	78274203	12.058	0.115	Nr2f2	Intergenic
chr7	78274126	13.333	0.2	Nr2f2	Intergenic
chr2	56970304	-6.612	0.032	Nr4a2	intron (NM_001139509, intron 1 of 7)
chr16	76319050	11.875	0.092	Nrip1	intron (NM_173440, intron 3 of 3)
chr16	76319016	9.397	0.156	Nrip1	intron (NM_173440, intron 3 of 3)
chr16	76319053	8.140	0.162	Nrip1	intron (NM_173440, intron 3 of 3)
chr16	32165955	-19.826	0.06	Nrros	promoter-TSS (NM_146069)
chr19	6421306	-16.154	0.119	Nrxn2	intron (NM_020253, intron 1 of 22)
chr19	6421354	-14.444	0.127	Nrxn2	intron (NM_020253, intron 1 of 22)
chr13	69762578	20.451	0.042	Nsun2	intron (NM_145354, intron 9 of 18)
chr19	47043650	-11.337	0.034	Nt5c2	intron (NM_001164363, intron 1 of 17)
chr6	126059015	-7.783	0.084	Ntf3	intron (NM_008742, intron 1 of 1)
chr6	126059202	-9.532	0.162	Ntf3	intron (NM_008742, intron 1 of 1)
chr10	93105491	14.843	0.052	Ntn4	intron (NM_021320, intron 1 of 9)

chr10	93105458	12.455	0.159	Ntn4	intron (NM_021320, intron 1 of 9)
chr13	58911380	20.179	0.037	Ntrk2	intron (NM_001025074, intron 2 of 17)
chr13	58911374	18.206	0.039	Ntrk2	intron (NM_001025074, intron 2 of 17)
chr13	58911367	11.035	0.184	Ntrk2	intron (NM_001025074, intron 2 of 17)
chr10	83901262	-16.836	0.041	Nuak1	intron (NM_001004363, intron 1 of 6)
chr10	83901707	-10.969	0.123	Nuak1	intron (NM_001004363, intron 1 of 6)
chr10	83901898	-8.123	0.135	Nuak1	intron (NM_001004363, intron 1 of 6)
chr10	117228622	13.057	0.025	Nup107	intron (NM_134010, intron 1 of 27)
chr10	117228652	11.827	0.036	Nup107	intron (NM_134010, intron 1 of 27)
chr8	75189460	24.639	0.023	Nwd1	intron (NM_176940, intron 4 of 18)
chr8	75189264	9.715	0.143	Nwd1	intron (NM_176940, intron 4 of 18)
chr13	39919337	18.795	0.031	Ofcc1	Intergenic
chr13	40557379	-15.934	0.1	Ofcc1	Intergenic
chr13	40557326	-14.986	0.133	Ofcc1	Intergenic
chr13	39919061	8.599	0.169	Ofcc1	Intergenic
chr2	72988758	20.468	0.055	Ola1	intron (NM_030091, intron 5 of 7)
chr1	172574266	15.385	0.004	Olfml2b	promoter-TSS (NM_177068)
chr3	97295561	18.818	0.08	Olf1402	Intergenic
chr3	97295625	12.586	0.152	Olf1402	Intergenic
chr9	39419905	-27.200	0.006	Olf148	Intergenic
chr8	74559546	5.806	0.135	Olf372	Intergenic
chr8	74559351	-5.489	0.18	Olf372	Intergenic
chr8	74559291	-5.002	0.196	Olf372	Intergenic
chr17	38133286	-15.708	0.061	Olf761	Intergenic
chr17	38133232	-10.614	0.113	Olf761	Intergenic
chr10	129530224	-18.828	0.03	Olf822	Intergenic
chr10	19124130	26.659	0.006	Olig3	Intergenic
chr6	129457190	-14.373	0.119	Olr1	promoter-TSS (NM_138648)
chr9	74708307	-16.270	0.073	Onecut1	Intergenic
chr9	74708261	-8.670	0.123	Onecut1	Intergenic
chr19	41148357	-19.865	0.045	Opalin	intron (NM_153520, intron 1 of 5)
chr1	177620913	-14.522	0.107	Opn3	intron (NM_010098, intron 1 of 3)
chr18	13018360	-11.432	0.07	Osbpl1a	intron (NM_001252489, intron 2 of 14)
chr18	13018428	-12.013	0.183	Osbpl1a	intron (NM_001252489, intron 2 of 14)
chr18	13018437	-10.035	0.186	Osbpl1a	intron (NM_001252489, intron 2 of 14)
chr6	50409325	-13.805	0.092	Osbpl3	Intergenic
chr6	50409238	-7.119	0.136	Osbpl3	Intergenic
chr6	50409159	-12.407	0.183	Osbpl3	Intergenic
chr1	94543751	-11.237	0.107	Otos	intron (NM_153114, intron 1 of 4)
chr1	94543853	-16.133	0.111	Otos	intron (NM_153114, intron 1 of 4)
chr19	7241335	-19.071	0.036	Otub1	intron (NM_134147, intron 3 of 10)
chr19	7241303	-12.337	0.147	Otub1	intron (NM_134147, intron 3 of 10)
chr19	7241348	-10.505	0.174	Otub1	intron (NM_134147, intron 3 of 10)
chr19	7241346	-10.730	0.179	Otub1	intron (NM_134147, intron 3 of 10)
chr11	21908611	-8.713	0.126	Otx1	intron (NM_001252515, intron 23 of 24)
chr11	21908592	-8.639	0.141	Otx1	intron (NM_001252515, intron 23 of 24)



chr11	21908596	-7.340	0.191	Otx1	intron (NM_001252515, intron 23 of 24)
chr14	54949316	-19.122	0.074	Oxa1l	Intergenic
chr14	54949275	-13.709	0.191	Oxa1l	Intergenic
chr15	41280820	-13.831	0.066	Oxr1	intron (NM_001130166, intron 1 of 16)
chr15	41280655	-15.954	0.098	Oxr1	intron (NM_001130166, intron 1 of 16)
chr15	41280787	-11.976	0.157	Oxr1	intron (NM_001130166, intron 1 of 16)
chr11	53936308	-16.942	0.053	P4ha2	intron (NM_001136076, intron 9 of 15)
chr11	53936352	-9.737	0.192	P4ha2	intron (NM_001136076, intron 9 of 15)
chr2	118485468	-11.647	0.191	Pak6	Intergenic
chr12	107057154	-15.821	0.029	Papola	intron (NM_011112, intron 14 of 21)
chr12	107057015	-9.397	0.068	Papola	exon (NM_011112, exon 14 of 22)
chr12	107057179	-13.624	0.08	Papola	intron (NM_011112, intron 14 of 21)
chr2	167937846	-8.036	0.156	Pard6b	Intergenic
chr7	119572348	-10.298	0.168	Parva	intron (NM_020606, intron 1 of 12)
chr2	24298965	-14.537	0.054	Pax8	intron (NM_011040, intron 3 of 11)
chr2	24316324	14.697	0.129	Pax8	intron (NM_011040, intron 2 of 11)
chr2	24316218	9.921	0.147	Pax8	intron (NM_011040, intron 2 of 11)
chr1	170238824	-10.659	0.09	Pbx1	intron (NM_008783, intron 2 of 7)
chr1	170238751	-9.945	0.154	Pbx1	intron (NM_008783, intron 2 of 7)
chr5	58290526	-20.649	0.02	Pcdh7	intron (NM_001122758, intron 1 of 2)
chr18	37120367	-13.310	0.056	Pcdha5	exon (NM_009959, exon 1 of 4)
chr18	37120812	-17.313	0.069	Pcdha5	exon (NM_009959, exon 1 of 4)
chr18	37120663	-11.142	0.1	Pcdha5	exon (NM_009959, exon 1 of 4)
chr18	37139923	-14.347	0.043	Pcdha7	CpG
chr18	37139894	-13.293	0.167	Pcdha7	CpG
chr18	37152709	-21.467	0.033	Pcdha8	exon (NM_201243, exon 1 of 4)
chr18	37152252	-14.789	0.146	Pcdha8	exon (NM_201243, exon 1 of 4)
chr18	37152394	-8.452	0.159	Pcdha8	exon (NM_201243, exon 1 of 4)
chr18	37152408	-9.193	0.165	Pcdha8	exon (NM_201243, exon 1 of 4)
chr18	37152524	-8.590	0.167	Pcdha8	exon (NM_201243, exon 1 of 4)
chr18	37152417	-9.931	0.171	Pcdha8	exon (NM_201243, exon 1 of 4)
chr18	37152702	-10.965	0.175	Pcdha8	exon (NM_201243, exon 1 of 4)
chr18	37927758	-25.523	0.033	Pcdhga12	exon (NM_033595, exon 1 of 4)
chr18	37944474	-9.756	0.126	Pcdhga12	intron (NM_033595, intron 1 of 3)
chr18	37944506	-9.819	0.143	Pcdhga12	intron (NM_033595, intron 1 of 3)
chr18	37890259	-24.778	0.019	Pcdhgb5	promoter-TSS (NM_033577)
chr18	37979932	-16.688	0.038	Pcdhgc5	exon (NM_033583, exon 1 of 4)
chr18	37979970	-11.800	0.115	Pcdhgc5	exon (NM_033583, exon 1 of 4)
chr16	56030875	-13.407	0.102	Pcnp	Intergenic
chr16	56030658	-11.641	0.109	Pcnp	promoter-TSS (NM_001024622)
chr16	56030789	-8.990	0.17	Pcnp	promoter-TSS (NM_001024622)
chr16	56030635	-9.420	0.184	Pcnp	promoter-TSS (NM_001024622)
chr13	75365565	17.484	0.085	Pcsk1	Intergenic
chr13	75365567	13.147	0.183	Pcsk1	Intergenic
chr7	73100886	-17.288	0.07	Pcsk6	intron (NM_011048, intron 7 of 21)
chr7	73100958	-13.352	0.156	Pcsk6	intron (NM_011048, intron 7 of 21)

chr16	32434317	-17.077	0.061	Pcyl1a	intron (NM_001163160, intron 1 of 8)
chr16	32434396	-9.980	0.096	Pcyl1a	intron (NM_001163160, intron 1 of 8)
chr16	32434293	-9.504	0.126	Pcyl1a	intron (NM_001163160, intron 1 of 8)
chr19	53899539	-16.741	0.028	Pdcd4	intron (NM_001170847, intron 5 of 13)
chr19	53899554	-12.711	0.076	Pdcd4	intron (NM_001170847, intron 5 of 13)
chr19	53899522	-10.243	0.148	Pdcd4	intron (NM_001170847, intron 5 of 13)
chr19	53899585	-8.794	0.167	Pdcd4	intron (NM_001170847, intron 5 of 13)
chr17	8992047	23.517	0.052	Pde10a	Intergenic
chr17	8992027	12.770	0.184	Pde10a	Intergenic
chr6	56426645	-9.409	0.117	Pde1c	Intergenic
chr6	56426760	-11.313	0.166	Pde1c	Intergenic
chr9	20971967	15.779	0.128	Pde4a	intron (NM_183408, intron 1 of 14)
chr9	20971995	13.537	0.18	Pde4a	intron (NM_183408, intron 1 of 14)
chr4	102243633	21.000	0.034	Pde4b	intron (NM_001177980, intron 1 of 9)
chr4	102243639	15.899	0.128	Pde4b	intron (NM_001177980, intron 1 of 9)
chr19	38236497	-10.932	0.13	Pde6c	exon (NM_033614, exon 12 of 22)
chr19	38236832	-6.914	0.165	Pde6c	exon (NM_033614, exon 13 of 22)
chr7	88309214	13.997	0.15	Pde8a	exon (NM_001004184, exon 13 of 18)
chr7	88309271	12.509	0.182	Pde8a	exon (NM_001004184, exon 13 of 18)
chr13	95985572	16.215	0.024	Pde8b	intron (NM_001170669, intron 1 of 18)
chr7	126656867	10.133	0.066	Pdilt	intron (NM_027943, intron 3 of 11)
chr7	126656987	9.063	0.185	Pdilt	intron (NM_027943, intron 3 of 11)
chr2	71705652	-11.707	0.084	Pdk1	Intergenic
chr2	71705628	-12.237	0.107	Pdk1	Intergenic
chr2	129575714	-18.679	0.031	Pdyn	Intergenic
chr15	92427608	16.286	0.029	Pdzrn4	promoter-TSS (NM_001164594)
chr15	92427610	17.069	0.042	Pdzrn4	promoter-TSS (NM_001164594)
chr15	92427602	11.609	0.066	Pdzrn4	promoter-TSS (NM_001164594)
chr15	92228213	-13.372	0.076	Pdzrn4	intron (NM_001164593, intron 1 of 9)
chr15	92427583	6.941	0.168	Pdzrn4	promoter-TSS (NM_001164594)
chr15	92427590	9.874	0.178	Pdzrn4	promoter-TSS (NM_001164594)
chr5	77897768	-14.759	0.101	Pea15b	Intergenic
chr5	77897591	-14.189	0.128	Pea15b	Intergenic
chr5	77897751	-13.309	0.141	Pea15b	Intergenic
chr5	117732654	-16.559	0.033	Pebp1	TTS (NM_018858)
chr14	48753725	-13.953	0.045	Peli2	intron (NM_033602, intron 1 of 5)
chr14	48753723	-11.545	0.107	Peli2	intron (NM_033602, intron 1 of 5)
chr17	46851001	12.000	0.039	Pex6	exon (NM_145488, exon 2 of 17)
chr17	46850957	10.868	0.043	Pex6	exon (NM_145488, exon 2 of 17)
chr17	46850800	10.856	0.197	Pex6	intron (NM_145488, intron 1 of 16)
chr8	126894510	-18.343	0.039	Pgbd5	exon (NM_171824, exon 7 of 7)
chr8	126894522	-12.957	0.143	Pgbd5	exon (NM_171824, exon 7 of 7)
chrX	103384986	10.897	0.035	Pgk1	intron (NM_008828, intron 1 of 10)
chr3	40959108	-15.455	0.031	Pgrmc2	Intergenic
chr13	43023303	-17.512	0.111	Phactr1	intron (NM_001005740, intron 1 of 12)
chr13	43023529	-11.131	0.169	Phactr1	intron (NM_001005740, intron 1 of 12)

chr13	43023513	-10.784	0.196	Phactr1	intron (NM_001005740, intron 1 of 12)
chr4	131954011	9.559	0.171	Phactr4	intron (NM_001161797, intron 2 of 12)
chr11	95529015	-14.403	0.054	Phb	intron (NM_008831, intron 1 of 6)
chr11	95529114	-15.748	0.06	Phb	intron (NM_008831, intron 1 of 6)
chr11	95529106	-11.774	0.121	Phb	intron (NM_008831, intron 1 of 6)
chr6	122319679	16.194	0.042	Phc1	Intergenic
chr6	122319666	9.480	0.09	Phc1	Intergenic
chr10	110942333	-10.689	0.159	Phlda1	Intergenic
chr10	110942377	-11.384	0.182	Phlda1	promoter-TSS (NM_009344)
chr10	110942600	-8.518	0.195	Phlda1	promoter-TSS (NM_009344)
chr11	68231427	-12.313	0.102	Pik3r5	Intergenic
chr11	68231522	-10.251	0.155	Pik3r5	Intergenic
chr2	18914012	-9.866	0.029	Pip4k2a	intron (NM_008845, intron 1 of 9)
chr11	77723177	9.025	0.063	Pipox	Intergenic
chr11	77723279	17.821	0.069	Pipox	Intergenic
chr11	77723286	9.141	0.171	Pipox	Intergenic
chr5	33084952	17.978	0.031	Pisd	intron (NM_177298, intron 3 of 7)
chr5	33084377	17.356	0.083	Pisd	intron (NM_177298, intron 3 of 7)
chr8	112138113	-14.716	0.023	Pkd1l3	promoter-TSS (NM_181544)
chr8	112138350	-9.093	0.056	Pkd1l3	promoter-TSS (NM_181544)
chr8	112138378	-7.825	0.107	Pkd1l3	promoter-TSS (NM_181544)
chr8	112138263	-5.349	0.115	Pkd1l3	promoter-TSS (NM_181544)
chr8	112138695	-13.693	0.119	Pkd1l3	exon (NM_181544, exon 1 of 32)
chr8	112138180	-6.246	0.139	Pkd1l3	promoter-TSS (NM_181544)
chr8	112138489	-10.484	0.141	Pkd1l3	promoter-TSS (NM_181544)
chr8	112138342	-5.536	0.159	Pkd1l3	promoter-TSS (NM_181544)
chr8	112138259	-5.780	0.171	Pkd1l3	promoter-TSS (NM_181544)
chr8	112138034	-11.814	0.184	Pkd1l3	promoter-TSS (NM_181544)
chr17	83575993	12.325	0.108	Pkdcc	Intergenic
chr3	7010741	-19.023	0.075	Pkia	Intergenic
chr16	38442071	-16.062	0.097	Pla1a	Intergenic
chr16	38442124	-13.046	0.159	Pla1a	Intergenic
chr1	150977038	-13.966	0.054	Pla2g4a	Intergenic
chr1	151794325	-14.973	0.1	Pla2g4a	intron (NM_008869, intron 1 of 17)
chr1	151794340	-13.257	0.152	Pla2g4a	intron (NM_008869, intron 1 of 17)
chr17	43696035	10.526	0.028	Pla2g7	Intergenic
chr1	178154076	-14.544	0.152	Pld5	intron (NM_176916, intron 1 of 9)
chr1	178154221	-12.592	0.163	Pld5	intron (NM_176916, intron 1 of 9)
chr12	77637028	15.674	0.095	Plekhg3	intron (NM_153804, intron 1 of 18)
chr12	77637014	12.727	0.177	Plekhg3	intron (NM_153804, intron 1 of 18)
chr12	80136516	25.979	0.017	Plekhh1	intron (NM_181073, intron 1 of 28)
chr12	80129654	13.647	0.039	Plekhh1	promoter-TSS (NM_181073)
chr12	80129651	14.660	0.069	Plekhh1	promoter-TSS (NM_181073)
chr17	12571013	-7.931	0.135	Plg	promoter-TSS (NM_008877)
chr17	12571003	-5.946	0.189	Plg	promoter-TSS (NM_008877)
chr13	111187949	-18.978	0.052	Plk2	exon (NM_152804, exon 7 of 14)

chr13	111187926	-19.519	0.08	Plk2	exon (NM_152804, exon 7 of 14)
chr13	111187712	-12.057	0.164	Plk2	exon (NM_152804, exon 6 of 14)
chr6	32589113	-10.282	0.128	Plxna4	Intergenic
chr1	133693685	-18.666	0.033	Pm20d1	promoter-TSS (NM_178079)
chr18	66563385	-9.269	0.128	Pmaip1	Intergenic
chr1	168360452	-20.669	0.032	Pogk	Intergenic
chr1	168360370	-6.637	0.16	Pogk	Intergenic
chr18	70705092	19.210	0.074	Poli	Intergenic
chr18	70705094	18.068	0.096	Poli	Intergenic
chr18	70705084	15.753	0.14	Poli	Intergenic
chr14	70842484	16.523	0.039	Polr3d	promoter-TSS (NR_029802)
chr8	28548703	-11.458	0.196	Poteg	Intergenic
chr13	113550026	13.064	0.038	Ppap2a	Intergenic
chr4	104876484	-15.129	0.097	Ppap2b	intron (NM_080555, intron 2 of 5)
chr4	104876528	-13.418	0.107	Ppap2b	intron (NM_080555, intron 2 of 5)
chr4	104876550	-11.720	0.164	Ppap2b	intron (NM_080555, intron 2 of 5)
chr5	92668498	-20.105	0.067	Ppef2	intron (NM_011148, intron 9 of 15)
chr7	151713868	-15.617	0.053	Ppfia1	intron (NM_001033319, intron 2 of 30)
chr16	5137404	10.984	0.087	Ppl	Intergenic
chr16	5137282	11.984	0.1	Ppl	Intergenic
chr16	5137216	8.688	0.176	Ppl	Intergenic
chr17	85358915	18.123	0.041	Ppm1b	intron (NM_011151, intron 1 of 5)
chr17	85358917	10.151	0.182	Ppm1b	intron (NM_011151, intron 1 of 5)
chr7	4454835	12.629	0.09	Ppp1r12c	Intergenic
chr10	6938616	-10.930	0.075	Ppp1r14c	intron (NM_133485, intron 1 of 3)
chr10	6938648	-8.332	0.155	Ppp1r14c	L1MB3 LINE L1
chr2	158495367	16.032	0.071	Ppp1r16b	intron (NM_001159662, intron 1 of 10)
chr2	158495223	13.012	0.137	Ppp1r16b	intron (NM_001159662, intron 1 of 10)
chr17	36008186	-10.899	0.085	Ppp1r18	intron (NM_001146710, intron 2 of 3)
chr17	36008178	-9.226	0.135	Ppp1r18	intron (NM_001146710, intron 2 of 3)
chr19	36842624	-15.320	0.086	Ppp1r3c	Intergenic
chr19	36842703	-12.887	0.12	Ppp1r3c	Intergenic
chr2	178146678	14.806	0.048	Ppp1r3d	3' UTR (NM_001085501, exon 1 of 1)
chr2	178146669	8.821	0.124	Ppp1r3d	3' UTR (NM_001085501, exon 1 of 1)
chr2	178146673	8.783	0.136	Ppp1r3d	3' UTR (NM_001085501, exon 1 of 1)
chr1	193263151	-14.977	0.083	Ppp2r5a	Intergenic
chr19	6235461	-7.156	0.095	Ppp2r5b	intron (NM_198168, intron 1 of 13)
chr17	46839642	-13.429	0.055	Ppp2r5d	intron (NM_009358, intron 1 of 14)
chr17	46839721	-9.163	0.196	Ppp2r5d	intron (NM_009358, intron 1 of 14)
chr18	80493409	9.809	0.107	Pqlc1	intron (NM_001190373, intron 3 of 3)
chr18	80493411	8.874	0.122	Pqlc1	intron (NM_001190373, intron 3 of 3)
chr10	44142041	-19.399	0.019	Prdm1	Intergenic
chr1	13091040	12.051	0.082	Prdm14	Intergenic
chr1	13091105	9.996	0.103	Prdm14	Intergenic
chr1	13091114	6.152	0.18	Prdm14	Intergenic
chr1	13091083	7.268	0.186	Prdm14	Intergenic

chr10	60762622	16.765	0.096	Prf1	intron (NM_011073, intron 1 of 2)
chr10	60762702	12.412	0.127	Prf1	exon (NM_011073, exon 2 of 3)
chr10	60762740	13.295	0.176	Prf1	exon (NM_011073, exon 2 of 3)
chr15	93582483	-19.939	0.021	Prickle1	Intergenic
chr15	93582443	-18.681	0.046	Prickle1	Intergenic
chr15	93582558	-14.948	0.053	Prickle1	Intergenic
chr15	93582438	-16.420	0.097	Prickle1	Intergenic
chr15	93582486	-10.793	0.169	Prickle1	Intergenic
chr8	86498019	13.773	0.111	Prkaca	intron (NM_008854, intron 1 of 9)
chr8	86498200	13.958	0.149	Prkaca	intron (NM_008854, intron 1 of 9)
chr3	146398789	-9.082	0.146	Prkacb	intron (NM_011100, intron 9 of 9)
chr3	146398044	-10.855	0.153	Prkacb	intron (NM_011100, intron 9 of 9)
chr5	24590739	-17.007	0.043	Prkag2	intron (NM_145401, intron 1 of 15)
chr5	24590768	-15.031	0.05	Prkag2	intron (NM_145401, intron 1 of 15)
chr5	24590639	-14.120	0.126	Prkag2	intron (NM_145401, intron 1 of 15)
chr12	32808957	-12.979	0.073	Prkar2b	Intergenic
chr17	86614297	17.598	0.053	Prkce	intron (NM_011104, intron 1 of 14)
chr17	86614274	13.536	0.122	Prkce	intron (NM_011104, intron 1 of 14)
chr17	86614272	13.399	0.134	Prkce	intron (NM_011104, intron 1 of 14)
chr2	11115021	-10.018	0.062	Prkcq	intron (NM_008859, intron 1 of 17)
chr2	11115014	-8.546	0.154	Prkcq	intron (NM_008859, intron 1 of 17)
chr7	17443679	9.462	0.09	Prkd2	intron (NM_178900, intron 13 of 17)
chr6	87565747	-14.008	0.103	Prokr1	Intergenic
chr6	87565838	-14.530	0.119	Prokr1	Intergenic
chr6	87565734	-11.068	0.167	Prokr1	Intergenic
chr6	87565775	-11.708	0.189	Prokr1	Intergenic
chr16	62854702	-7.659	0.056	Pros1	intron (NM_011173, intron 1 of 14)
chr16	62854974	-11.407	0.103	Pros1	intron (NM_011173, intron 1 of 14)
chr16	62854874	-7.051	0.145	Pros1	intron (NM_011173, intron 1 of 14)
chr16	62854630	-5.118	0.194	Pros1	intron (NM_011173, intron 1 of 14)
chr13	34965557	-18.037	0.036	Prpf4b	Intergenic
chr13	34965484	-14.570	0.064	Prpf4b	Intergenic
chr15	84500380	-17.974	0.048	Prr5	Intergenic
chr15	84500393	-12.174	0.182	Prr5	Intergenic
chr17	35298395	-22.148	0.036	Prrc2a	exon (NM_001199044, exon 6 of 31)
chr17	35298386	-19.444	0.06	Prrc2a	exon (NM_001199044, exon 6 of 31)
chr17	35298397	-13.757	0.139	Prrc2a	exon (NM_001199044, exon 6 of 31)
chr17	35298373	-15.137	0.175	Prrc2a	exon (NM_001199044, exon 6 of 31)
chr8	98123758	18.265	0.089	Prss54	Intergenic
chr8	98123729	14.155	0.117	Prss54	Intergenic
chr9	72699945	11.671	0.095	Prtg	intron (NM_175485, intron 8 of 19)
chr9	72699996	12.432	0.1	Prtg	intron (NM_175485, intron 8 of 19)
chr19	17200097	-12.305	0.108	Prune2	exon (NM_181348, exon 9 of 20)
chr10	59743148	-14.029	0.096	Psap	intron (NM_001146123, intron 1 of 13)
chr10	59743001	-12.159	0.127	Psap	intron (NM_001146123, intron 1 of 13)
chr5	36506510	-16.530	0.035	Psapl1	intron (NM_030889, intron 2 of 26)

chr8	110209154	-13.231	0.095	Psm7	Intergenic
chr8	110209039	-11.795	0.138	Psm7	Intergenic
chr8	110209052	-11.068	0.149	Psm7	Intergenic
chr5	123718551	12.254	0.043	Psm9	Intergenic
chr9	55922549	6.486	0.075	Pstip1	Intergenic
chr11	121709028	-7.759	0.035	Ptch3	Intergenic
chr8	86192928	-5.927	0.196	Ptger1	TTS (NM_177262)
chr8	86192849	-7.591	0.199	Ptger1	TTS (NM_177262)
chr15	5190248	-17.565	0.033	Ptger4	intron (NM_001136079, intron 2 of 2)
chr4	59003723	14.461	0.084	Ptgr1	Intergenic
chr4	59003775	9.421	0.159	Ptgr1	Intergenic
chr1	152012823	-8.021	0.175	Ptgs2	Intergenic
chr1	152012727	-5.136	0.177	Ptgs2	Intergenic
chr1	152012110	-9.194	0.194	Ptgs2	Intergenic
chr14	66884471	-23.808	0.025	Ptk2b	intron (NM_001162365, intron 1 of 30)
chr14	66884522	-14.469	0.04	Ptk2b	intron (NM_001162365, intron 1 of 30)
chr14	66884698	-13.227	0.112	Ptk2b	intron (NM_001162365, intron 1 of 30)
chr7	52123407	12.156	0.096	Ptov1	intron (NM_133949, intron 1 of 11)
chr7	52123432	8.358	0.17	Ptov1	intron (NM_133949, intron 1 of 11)
chr7	52123266	8.214	0.171	Ptov1	intron (NM_133949, intron 1 of 11)
chr4	57333714	-8.730	0.01	Ptpn3	Intergenic
chr4	57333767	-5.527	0.1	Ptpn3	Intergenic
chr4	57333908	-8.351	0.197	Ptpn3	Intergenic
chr4	131382119	-14.640	0.031	Ptpru	intron (NM_001083119, intron 1 of 30)
chr18	36444323	-21.929	0.031	Pura	intron (NM_008989, intron 1 of 1)
chr18	36444107	-15.217	0.064	Pura	intron (NM_008989, intron 1 of 1)
chr18	36444118	-16.801	0.065	Pura	intron (NM_008989, intron 1 of 1)
chr5	111215571	-16.558	0.09	Pus1	intron (NM_009469, intron 26 of 27)
chr5	111215739	-12.099	0.097	Pus1	intron (NM_009469, intron 26 of 27)
chr5	111215728	-9.537	0.18	Pus1	intron (NM_009469, intron 26 of 27)
chr15	94348602	-18.571	0.027	Pus7l	Intergenic
chr15	94349108	-15.904	0.053	Pus7l	Intergenic
chr15	94349129	-13.967	0.075	Pus7l	Intergenic
chr15	94348535	-12.254	0.108	Pus7l	Intergenic
chr15	94348594	-11.825	0.119	Pus7l	Intergenic
chr15	94349040	-9.901	0.179	Pus7l	Intergenic
chr15	94348983	-13.586	0.187	Pus7l	Intergenic
chr14	8932273	17.784	0.031	Pxk	intron (NM_178279, intron 1 of 18)
chr14	8932540	16.211	0.059	Pxk	intron (NM_178279, intron 1 of 18)
chr14	8932407	15.709	0.081	Pxk	intron (NM_178279, intron 1 of 18)
chr14	8932450	11.651	0.134	Pxk	intron (NM_178279, intron 1 of 18)
chr6	128493720	-13.920	0.028	Pzp	intron (NM_001001179, intron 31 of 35)
chr6	128493602	-9.970	0.129	Pzp	intron (NM_001001179, intron 31 of 35)
chr17	26148695	-16.578	0.033	Rab11fip3	intron (NM_001162868, intron 5 of 13)
chr11	79382315	8.081	0.031	Rab11fip4	intron (NM_010897, intron 55 of 57)
chr1	162231531	-17.562	0.038	Rabgap1l	intron (NM_001038621, intron 2 of 8)

chr1	162231521	-16.260	0.049	Rabgap11	intron (NM_001038621, intron 2 of 8)
chr1	162721974	-5.016	0.096	Rabgap11	intron (NM_013862, intron 1 of 20)
chr1	162721680	-8.570	0.124	Rabgap11	intron (NM_013862, intron 1 of 20)
chr1	162721932	-12.135	0.127	Rabgap11	intron (NM_013862, intron 1 of 20)
chr14	56342365	15.019	0.018	Rabgga	Intergenic
chr15	10431019	12.823	0.055	Rad1	Intergenic
chr6	112726972	-10.873	0.041	Rad18	intron (NM_080448, intron 6 of 21)
chr4	55244759	10.996	0.1	Rad23b	Intergenic
chr6	119837091	-13.775	0.119	Rad52	Intergenic
chr15	10617507	11.715	0.084	Rai14	intron (NM_001166408, intron 2 of 17)
chr15	10617497	12.688	0.086	Rai14	intron (NM_001166408, intron 2 of 17)
chr11	74334990	-11.944	0.159	Rap1gap2	MER113 DNA MER1_type
chr3	78829321	-19.351	0.025	Rapgef2	Intergenic
chr11	98700127	-15.904	0.103	Rapgef11	intron (NM_001080925, intron 1 of 14)
chr11	98700125	-15.432	0.118	Rapgef11	intron (NM_001080925, intron 1 of 14)
chr15	102071452	-16.520	0.048	Rarg	intron (NM_011244, intron 5 of 9)
chr15	102071436	-14.886	0.099	Rarg	intron (NM_011244, intron 5 of 9)
chr15	102071510	-11.302	0.149	Rarg	exon (NM_001042727, exon 3 of 8)
chr2	131822258	-17.377	0.02	Rassf2	intron (NM_175445, intron 10 of 10)
chr2	131865606	-11.148	0.163	Rassf2	Intergenic
chr2	131865604	-9.821	0.196	Rassf2	Intergenic
chr10	120873100	9.158	0.147	Rassf3	intron (NM_138956, intron 1 of 4)
chr15	77174096	17.463	0.042	Rbfox2	Intergenic
chr15	77174162	12.063	0.158	Rbfox2	Intergenic
chr11	118753011	-23.381	0.018	Rbfox3	intron (NM_001285437, intron 1 of 13)
chr11	118753118	-11.395	0.171	Rbfox3	intron (NM_001285437, intron 1 of 13)
chr13	46512924	-25.613	0.01	Rbm24	promoter-TSS (NM_001081425)
chr13	46512875	-11.275	0.19	Rbm24	promoter-TSS (NM_001081425)
chr12	84961743	18.929	0.024	Rbm25	Intergenic
chr12	84961914	15.118	0.13	Rbm25	CpG
chr6	29113362	10.202	0.095	Rbm28	intron (NM_133925, intron 1 of 18)
chr6	29113330	10.120	0.116	Rbm28	RMER6A LTR ERVK
chr2	60641101	-14.583	0.043	Rbms1	intron (NM_020296, intron 2 of 13)
chr2	60641069	-14.632	0.05	Rbms1	intron (NM_020296, intron 2 of 13)
chr19	38198299	14.552	0.035	Rbp4	intron (NM_001159487, intron 4 of 5)
chr19	38198484	12.081	0.188	Rbp4	intron (NM_001159487, intron 4 of 5)
chr8	35098500	15.811	0.041	Rbpms	Intergenic
chr17	44134745	24.592	0.024	Rcan2	intron (NM_030598, intron 1 of 3)
chr17	44134727	19.177	0.065	Rcan2	intron (NM_030598, intron 1 of 3)
chr17	44134687	14.332	0.123	Rcan2	intron (NM_030598, intron 1 of 3)
chr14	73507031	-18.527	0.027	Rcbtb2	Intergenic
chr12	10447012	13.544	0.074	Rdh14	Intergenic
chr12	10447037	12.368	0.104	Rdh14	Intergenic
chr10	66567313	-18.615	0.007	Reep3	Intergenic
chr10	66484381	-12.677	0.044	Reep3	intron (NM_001204915, intron 6 of 8)
chr10	66567323	-13.990	0.049	Reep3	Intergenic

chr10	66567395	-9.788	0.107	Reep3	Intergenic
chr10	66484624	-15.907	0.111	Reep3	exon (NM_178606, exon 6 of 8)
chr10	66567327	-9.587	0.127	Reep3	Intergenic
chrX	159079864	-16.367	0.038	Reps2	intron (NM_178256, intron 1 of 17)
chr4	149688842	-13.735	0.132	Rere	intron (NM_001085492, intron 1 of 22)
chr4	149688851	-14.286	0.135	Rere	intron (NM_001085492, intron 1 of 22)
chr1	38188405	-17.545	0.088	Rev1	Intergenic
chr1	38187742	-11.933	0.155	Rev1	Intergenic
chr1	38188384	-11.536	0.171	Rev1	Intergenic
chr1	38187640	-8.585	0.199	Rev1	Intergenic
chr1	39818225	-10.844	0.057	Rfx8	Intergenic
chr1	39818229	-6.034	0.178	Rfx8	Intergenic
chr12	83719280	-11.582	0.104	Rgs6	intron (NM_001282061, intron 1 of 16)
chr12	83719056	-8.075	0.124	Rgs6	intron (NM_001282061, intron 1 of 16)
chr13	105842170	-14.364	0.078	Rgs7bp	intron (NM_029879, intron 2 of 5)
chr13	105838929	-15.481	0.08	Rgs7bp	intron (NM_029879, intron 2 of 5)
chr13	105842074	-10.716	0.142	Rgs7bp	intron (NM_029879, intron 2 of 5)
chr13	105842337	-13.388	0.157	Rgs7bp	intron (NM_029879, intron 2 of 5)
chr13	105842754	-12.294	0.176	Rgs7bp	intron (NM_029879, intron 2 of 5)
chr1	155506949	17.586	0.096	Rgs8	intron (NM_026380, intron 1 of 6)
chr1	155506960	16.345	0.101	Rgs8	intron (NM_026380, intron 1 of 6)
chr2	119094844	-14.635	0.032	Rhov	TTS (NM_145530)
chr10	84371891	-20.625	0.031	Ric8b	Intergenic
chr6	122420550	-13.520	0.031	Rimklb	intron (NM_027664, intron 2 of 5)
chr6	47623081	-7.361	0.028	Rn4.5s	promoter-TSS (NR_002841).5
chr6	47631809	-7.043	0.033	Rn4.5s	promoter-TSS (NR_002841).8
chr6	47718333	-7.850	0.039	Rn4.5s	CpG
chr6	47631815	-8.433	0.043	Rn4.5s	promoter-TSS (NR_002841).8
chr6	47718329	-8.303	0.043	Rn4.5s	CpG
chr6	47627292	-11.822	0.05	Rn4.5s	promoter-TSS (NR_002841).7
chr6	47627309	-10.141	0.05	Rn4.5s	promoter-TSS (NR_002841).7
chr6	47623085	-6.123	0.065	Rn4.5s	promoter-TSS (NR_002841).5
chr6	47703548	-6.838	0.078	Rn4.5s	promoter-TSS (NR_002841).6
chr6	47703593	-11.083	0.092	Rn4.5s	promoter-TSS (NR_002841).6
chr6	47694973	-5.097	0.094	Rn4.5s	promoter-TSS (NR_002841).10
chr6	47718348	-5.378	0.106	Rn4.5s	CpG
chr6	47631826	-5.859	0.111	Rn4.5s	promoter-TSS (NR_002841).8
chr6	47694526	-6.319	0.122	Rn4.5s	promoter-TSS (NR_002841).10
chr6	47703532	-5.961	0.125	Rn4.5s	promoter-TSS (NR_002841).6
chr6	47694538	-5.664	0.134	Rn4.5s	promoter-TSS (NR_002841).10
chr6	47703601	-9.231	0.134	Rn4.5s	promoter-TSS (NR_002841).6
chr6	47718358	-5.015	0.135	Rn4.5s	CpG
chr6	47623275	10.406	0.137	Rn4.5s	promoter-TSS (NR_002841).5
chr6	47627798	-6.764	0.147	Rn4.5s	RMER12B LTR ERVK
chr6	47623372	-7.182	0.152	Rn4.5s	promoter-TSS (NR_002841).5
chr6	47627007	-5.083	0.158	Rn4.5s	promoter-TSS (NR_002841).7



chr6	47623140	-5.185	0.159	Rn4.5s	promoter-TSS (NR_002841).5
chr6	47627780	-11.022	0.16	Rn4.5s	RMER12B LTR ERVK
chr6	47718320	-5.742	0.171	Rn4.5s	CpG
chr6	47718167	8.333	0.177	Rn4.5s	CpG
chr6	47703846	-9.737	0.185	Rn4.5s	promoter-TSS (NR_002841).6
chr6	47627919	-12.279	0.196	Rn4.5s	RMER12B LTR ERVK
chr6	47718214	-8.236	0.196	Rn4.5s	CpG
chr6	47703561	-5.290	0.2	Rn4.5s	promoter-TSS (NR_002841).6
chr2	50996213	-18.287	0.063	Rnd3	intron (NM_028810, intron 2 of 4)
chr2	50996219	-14.618	0.148	Rnd3	intron (NM_028810, intron 2 of 4)
chr7	117959601	-15.750	0.043	Rnf141	TTS (NM_025999)
chr7	117959583	-16.181	0.053	Rnf141	TTS (NM_025999)
chr7	117959686	-6.301	0.13	Rnf141	TTS (NM_025999)
chr7	117959638	-11.197	0.141	Rnf141	TTS (NM_025999)
chr11	116274887	-14.707	0.079	Rnf157	promoter-TSS (NM_027258)
chr11	116274924	-9.746	0.197	Rnf157	promoter-TSS (NM_027258)
chr13	106082691	10.251	0.145	Rnf180	intron (NM_027934, intron 1 of 7)
chr13	106082743	8.910	0.158	Rnf180	intron (NM_027934, intron 1 of 7)
chr15	36304295	-12.843	0.068	Rnf19a	Intergenic
chr15	36304324	-9.420	0.166	Rnf19a	Intergenic
chr4	117145725	-15.851	0.049	Rnf220	intron (NM_025739, intron 2 of 14)
chr4	117100507	12.344	0.067	Rnf220	intron (NM_025739, intron 2 of 14)
chr4	117100588	10.066	0.104	Rnf220	intron (NM_025739, intron 2 of 14)
chr4	117100562	11.362	0.126	Rnf220	intron (NM_025739, intron 2 of 14)
chr4	117100510	8.658	0.194	Rnf220	intron (NM_025739, intron 2 of 14)
chr4	155500971	13.549	0.04	Rnf223	3' UTR (NM_177205, exon 10 of 10)
chr5	34670379	-12.518	0.094	Rnf4	Intergenic
chr5	34670200	-9.573	0.127	Rnf4	Intergenic
chr11	87478802	13.793	0.034	Rnf43	intron (NM_172448, intron 2 of 9)
chr11	87478838	13.819	0.053	Rnf43	intron (NM_172448, intron 2 of 9)
chr11	87478773	9.149	0.184	Rnf43	intron (NM_172448, intron 2 of 9)
chr16	72699870	15.686	0.053	Robo1	intron (NM_019413, intron 1 of 28)
chr16	72699885	11.735	0.134	Robo1	intron (NM_019413, intron 1 of 28)
chr15	97337815	-14.353	0.027	Rpap3	Intergenic
chr15	97337818	-12.599	0.039	Rpap3	Intergenic
chr15	97337832	-12.650	0.045	Rpap3	Intergenic
chr15	97337838	-8.173	0.167	Rpap3	Intergenic
chr1	72811765	15.282	0.088	Rpl37a	Intergenic
chr5	121656142	-21.052	0.046	Rpl6	intron (NM_011290, intron 3 of 6)
chr1	16093537	10.112	0.196	Rpl7	intron (NM_011291, intron 2 of 6)
chr1	16093342	11.437	0.198	Rpl7	exon (NM_011291, exon 3 of 7)
chr2	53935945	-11.533	0.09	Rprm	TTS (NM_023396)
chr2	53935949	-9.586	0.131	Rprm	TTS (NM_023396)
chr7	29133962	-14.211	0.049	Rps16	Intergenic
chr13	91079388	10.660	0.12	Rps23	intron (NM_025770, intron 5 of 7)
chr3	90002146	13.617	0.032	Rps27rt	intron (NM_029937, intron 33 of 39)

chr3	90002099	13.078	0.035	Rps27rt	exon (NM_029937, exon 33 of 40)
chr3	90002104	8.423	0.085	Rps27rt	exon (NM_029937, exon 33 of 40)
chr12	70259707	-5.042	0.092	Rps29	exon (NM_009093, exon 2 of 3)
chr7	13495928	-5.951	0.159	Rps5	Intergenic
chr7	13495692	-7.240	0.183	Rps5	Intergenic
chr12	29318070	6.689	0.066	Rps7	intron (NM_011300, intron 5 of 6)
chr12	29318309	5.487	0.186	Rps7	B1_Mur4 SINE Alu
chr4	123810198	13.189	0.007	Rragc	Intergenic
chr4	33083081	8.254	0.033	Rragd	intron (NM_027491, intron 2 of 6)
chr4	33073591	-7.822	0.117	Rragd	intron (NM_027491, intron 1 of 6)
chr4	33073503	-7.424	0.133	Rragd	intron (NM_027491, intron 1 of 6)
chr4	33083042	5.968	0.143	Rragd	exon (NM_027491, exon 2 of 7)
chr4	33083034	5.155	0.155	Rragd	exon (NM_027491, exon 2 of 7)
chr7	121202481	-12.551	0.102	Rras2	exon (NM_025846, exon 3 of 6)
chr7	121202452	-12.747	0.104	Rras2	exon (NM_025846, exon 3 of 6)
chr7	121202437	-12.888	0.116	Rras2	intron (NM_025846, intron 3 of 5)
chr7	109537919	11.891	0.093	Rrm1	intron (NM_009287, intron 3 of 11)
chr7	109537953	12.031	0.095	Rrm1	intron (NM_009287, intron 3 of 11)
chr12	25397595	10.143	0.061	Rrm2	exon (NM_009104, exon 8 of 10)
chr12	25397612	8.756	0.095	Rrm2	exon (NM_009104, exon 8 of 10)
chr12	25397510	9.275	0.18	Rrm2	intron (NM_009104, intron 7 of 9)
chr11	75068156	-14.325	0.074	Rtn4r1	intron (NM_177708, intron 1 of 1)
chr11	75068506	-12.430	0.157	Rtn4r1	intron (NM_177708, intron 1 of 1)
chr11	75068113	-12.588	0.168	Rtn4r1	intron (NM_177708, intron 1 of 1)
chr5	150858708	10.840	0.133	Rxfp2	intron (NM_080468, intron 10 of 17)
chr5	150918154	-12.576	0.2	Rxfp2	Intergenic
chr9	102762693	-9.037	0.116	Ryk	intron (NM_001284258, intron 1 of 13)
chr9	102762550	-9.464	0.2	Ryk	intron (NM_001284258, intron 1 of 13)
chr17	35167316	-11.522	0.127	Sapcd1	intron (NM_001146215, intron 20 of 24)
chr2	25225792	5.951	0.08	Sapcd2	Intergenic
chr2	25225780	10.311	0.089	Sapcd2	Intergenic
chr15	96337981	-8.278	0.139	Scaf11	Intergenic
chr15	96337992	-8.965	0.164	Scaf11	Intergenic
chr5	92928584	-15.934	0.126	Scarb2	intron (NM_007644, intron 1 of 11)
chr5	92928618	-13.521	0.169	Scarb2	intron (NM_007644, intron 1 of 11)
chr18	74899233	-12.565	0.161	Scarna17	intron (NM_201600, intron 32 of 38)
chr18	74899157	-8.013	0.169	Scarna17	intron (NM_201600, intron 32 of 38)
chr14	103955935	-24.506	0.009	Scel	intron (NM_022886, intron 8 of 30)
chr14	103940379	-18.236	0.015	Scel	intron (NM_022886, intron 6 of 30)
chr14	103940264	-14.899	0.109	Scel	B3 SINE B2
chr14	103940349	-11.880	0.113	Scel	intron (NM_022886, intron 6 of 30)
chr14	103940304	-10.656	0.18	Scel	intron (NM_022886, intron 6 of 30)
chr14	103940298	-10.972	0.181	Scel	intron (NM_022886, intron 6 of 30)
chr3	68375983	-9.474	0.009	Schip1	promoter-TSS (NM_013928)
chr3	68375950	-14.127	0.147	Schip1	promoter-TSS (NM_013928)
chr4	120042307	16.118	0.071	Scmh1	Intergenic

chr7	31909678	-17.341	0.095	Scn1b	RSINE1 SINE B4
chr7	31909745	-9.854	0.162	Scn1b	intron (NM_011322, intron 2 of 5)
chr9	119481130	13.099	0.039	Scn5a	intron (NM_021544, intron 1 of 27)
chr15	100782453	-20.258	0.04	Scn8a	intron (NM_001077499, intron 2 of 26)
chr8	59910012	-12.579	0.108	Scrg1	Intergenic
chr8	59910253	-10.544	0.119	Scrg1	Intergenic
chr8	59910249	-8.214	0.159	Scrg1	Intergenic
chr6	54516771	-6.141	0.055	Scrn1	promoter-TSS (NM_027268)
chr6	54516697	-6.102	0.192	Scrn1	promoter-TSS (NM_027268)
chr11	96884873	10.088	0.182	Scrn2	3' UTR (NM_031183, exon 2 of 2)
chr2	164267627	10.784	0.11	Sdc4	intron (NM_011521, intron 1 of 4)
chr2	164267709	10.124	0.137	Sdc4	intron (NM_011521, intron 1 of 4)
chr1	173079569	-14.405	0.051	Sdhc	intron (NM_025321, intron 1 of 5)
chr5	141673931	10.088	0.166	Sdk1	Intergenic
chr11	113833280	-9.045	0.135	Sdk2	intron (NM_172800, intron 1 of 44)
chr11	113833260	-10.296	0.157	Sdk2	intron (NM_172800, intron 1 of 44)
chr11	113833285	-8.202	0.168	Sdk2	intron (NM_172800, intron 1 of 44)
chr6	113698825	-15.459	0.086	Sec13	exon (NM_009723, exon 22 of 22)
chr6	113698820	-13.556	0.124	Sec13	exon (NM_009723, exon 22 of 22)
chr6	113698833	-10.849	0.148	Sec13	exon (NM_009723, exon 22 of 22)
chr11	116978112	-11.602	0.059	Sec14I1	intron (NM_001166507, intron 1 of 16)
chr11	116978635	-17.924	0.065	Sec14I1	intron (NM_001166507, intron 2 of 16)
chr11	116978079	-11.944	0.098	Sec14I1	intron (NM_001166507, intron 1 of 16)
chr4	47610603	-20.204	0.044	Sec61b	Intergenic
chr4	47610595	-15.401	0.076	Sec61b	Intergenic
chr4	47610610	-15.056	0.099	Sec61b	Intergenic
chr13	51903396	-24.347	0.016	Sema4d	Intergenic
chr13	51903402	-21.860	0.022	Sema4d	Intergenic
chr16	35604425	13.043	0.092	Sema5b	intron (NM_013661, intron 1 of 21)
chr9	57787098	-18.043	0.044	Sema7a	promoter-TSS (NM_011352)
chr11	53330915	-13.031	0.061	Sept8	Intergenic
chr11	53330904	-12.138	0.102	Sept8	Intergenic
chr13	100877512	13.934	0.026	Serf1	promoter-TSS (NM_011353)
chr14	76969363	-10.312	0.081	Serp2	Intergenic
chr14	76969138	-11.249	0.115	Serp2	Intergenic
chr14	76969055	-7.058	0.152	Serp2	Intergenic
chr14	76969324	-7.074	0.164	Serp2	Intergenic
chr14	76969259	-8.002	0.165	Serp2	Intergenic
chr13	33854686	-10.885	0.114	Serpib6e	Intergenic
chr13	33854977	-11.828	0.134	Serpib6e	Intergenic
chr13	33854665	-9.672	0.152	Serpib6e	Intergenic
chr13	33854898	-8.949	0.198	Serpib6e	Intergenic
chr10	41531286	-5.733	0.061	Sesn1	intron (NM_001162908, intron 1 of 9)
chr19	6370428	-14.665	0.066	Sf1	intron (NM_011750, intron 3 of 12)
chr19	6370153	-12.193	0.083	Sf1	intron (NM_011750, intron 3 of 12)
chr19	6370115	-11.826	0.138	Sf1	intron (NM_011750, intron 3 of 12)

chr11	3081094	-7.897	0.168	Sfi1	B1_Mus1 SINE Alu
chr6	85236510	-10.106	0.116	Sfxn5	intron (NM_178639, intron 6 of 13)
chr4	102535939	18.895	0.046	Sgip1	intron (NM_001285852, intron 4 of 25)
chr10	21611677	-18.951	0.085	Sgk1	intron (NM_001161845, intron 1 of 13)
chr10	21717262	-12.273	0.135	Sgk1	intron (NM_001161847, intron 9 of 11)
chr10	21611687	-14.001	0.163	Sgk1	intron (NM_001161845, intron 1 of 13)
chr3	131038087	-16.274	0.053	Sgms2	intron (NM_028943, intron 3 of 5)
chr3	131038275	-11.821	0.106	Sgms2	intron (NM_028943, intron 3 of 5)
chr3	131038245	-9.515	0.141	Sgms2	intron (NM_028943, intron 3 of 5)
chr3	131038070	-11.329	0.179	Sgms2	intron (NM_028943, intron 3 of 5)
chr14	41602670	-20.863	0.052	Sh2d4b	Intergenic
chr4	137807319	20.467	0.076	Sh2d5	intron (NM_001099631, intron 1 of 9)
chr14	32241932	-13.821	0.124	Sh3bp5	intron (NM_011894, intron 2 of 8)
chr14	32241894	-13.293	0.196	Sh3bp5	intron (NM_011894, intron 2 of 8)
chr14	32241938	-11.904	0.197	Sh3bp5	intron (NM_011894, intron 2 of 8)
chr10	58274646	-13.216	0.06	Sh3rf3	Intergenic
chr10	58274260	-7.167	0.122	Sh3rf3	Intergenic
chr10	58274582	-10.449	0.164	Sh3rf3	Intergenic
chr5	36083150	10.157	0.119	Sh3tc1	Intergenic
chr5	36083217	9.454	0.171	Sh3tc1	Intergenic
chr7	151360260	-15.368	0.134	Shank2	Intergenic
chr7	151480346	-12.665	0.143	Shank2	intron (NM_001113373, intron 7 of 15)
chr7	151480382	-8.990	0.182	Shank2	intron (NM_001113373, intron 7 of 15)
chr7	151360145	-10.895	0.188	Shank2	Intergenic
chr15	76180446	-5.145	0.05	Sharpin	intron (NM_025340, intron 2 of 8)
chr7	4794082	-11.293	0.116	Shisa7	intron (NM_172737, intron 1 of 5)
chr7	4794090	-11.413	0.125	Shisa7	intron (NM_172737, intron 1 of 5)
chrX	149202884	20.879	0.058	Shroom2	intron (NM_172441, intron 1 of 9)
chr8	89292322	-19.242	0.012	Siah1a	Intergenic
chr8	89292379	-14.553	0.105	Siah1a	L2 LINE L2
chr8	89292357	-10.746	0.195	Siah1a	Intergenic
chr17	31953604	11.234	0.031	Sik1	Intergenic
chr17	31909193	18.420	0.035	Sik1	Intergenic
chr17	31909170	11.214	0.145	Sik1	Intergenic
chr17	31909380	10.373	0.15	Sik1	Intergenic
chr18	35657775	-14.698	0.1	Sil1	intron (NM_030749, intron 1 of 9)
chr7	30304685	-20.681	0.019	Sipa1l3	Intergenic
chr7	30325705	-5.660	0.031	Sipa1l3	Intergenic
chr17	86089237	-9.444	0.111	Six2	Intergenic
chr17	86089195	-10.144	0.169	Six2	Intergenic
chr17	86011052	-14.943	0.049	Six3os1	non-coding (NR_015386, exon 3 of 3)
chr17	86011042	-11.891	0.103	Six3os1	non-coding (NR_015386, exon 3 of 3)
chr17	86007340	-5.358	0.108	Six3os1	intron (NR_015387, intron 3 of 3)
chr17	86007981	-7.010	0.159	Six3os1	TTS (NR_015386)
chr15	66657140	-10.650	0.098	Sla	intron (NM_009192, intron 1 of 8)
chr15	66657121	-12.153	0.108	Sla	intron (NM_009192, intron 1 of 8)

chr14	104128524	9.307	0.115	Slain1os	Intergenic
chr14	104128112	6.802	0.19	Slain1os	Intergenic
chr1	173718836	-13.359	0.078	Slamf1	intron (NM_013730, intron 4 of 6)
chr1	173718959	-17.722	0.121	Slamf1	intron (NM_013730, intron 4 of 6)
chr8	81101786	14.408	0.127	Slc10a7	intron (NM_001282108, intron 4 of 9)
chr8	81101727	12.602	0.194	Slc10a7	intron (NM_001282108, intron 4 of 9)
chr3	104441778	-8.963	0.043	Slc16a1	promoter-TSS (NM_009196)
chr3	104441739	-5.095	0.2	Slc16a1	promoter-TSS (NM_009196)
chr10	39848512	-10.399	0.073	Slc16a10	intron (NM_028247, intron 1 of 2)
chr10	39848542	-8.581	0.111	Slc16a10	intron (NM_028247, intron 1 of 2)
chr10	39848620	-9.108	0.137	Slc16a10	intron (NM_028247, intron 1 of 2)
chr2	102497375	-8.786	0.061	Slc1a2	Intergenic
chr2	102497442	-6.201	0.137	Slc1a2	Intergenic
chr7	150667901	-14.775	0.112	Slc22a18	intron (NM_001042760, intron 5 of 10)
chr12	103366119	-9.660	0.061	Slc24a4	Intergenic
chr8	72718518	24.288	0.015	Slc25a42	intron (NM_001007570, intron 1 of 7)
chr8	72718657	16.305	0.031	Slc25a42	intron (NM_001007570, intron 1 of 7)
chr4	45440598	12.207	0.031	Slc25a51	MIRc SINE MIR
chr4	45440495	11.531	0.041	Slc25a51	intron (NM_001033306, intron 5 of 5)
chr4	45405784	-7.833	0.084	Slc25a51	Intergenic
chr4	45405230	-16.667	0.129	Slc25a51	B3 SINE B2
chr4	14474220	14.882	0.044	Slc26a7	intron (NM_145947, intron 7 of 18)
chr4	14474226	17.128	0.1	Slc26a7	intron (NM_145947, intron 7 of 18)
chr4	14474137	9.856	0.173	Slc26a7	intron (NM_145947, intron 7 of 18)
chr18	58641347	-19.027	0.042	Slc27a6	Intergenic
chr18	58759075	17.059	0.047	Slc27a6	intron (NM_001081072, intron 5 of 9)
chr4	118761370	11.262	0.045	Slc2a1	Intergenic
chr4	149513389	-19.190	0.028	Slc2a7	intron (NM_019741, intron 7 of 13)
chr4	149513383	-11.491	0.162	Slc2a7	intron (NM_019741, intron 7 of 13)
chr5	38813826	13.548	0.085	Slc2a9	intron (NM_001012363, intron 5 of 11)
chr5	38813841	9.711	0.105	Slc2a9	intron (NM_001012363, intron 5 of 11)
chr17	31431556	-22.078	0.05	Slc37a1	promoter-TSS (NM_153062)
chr6	39269364	12.540	0.088	Slc37a3	Intergenic
chr6	39269370	8.442	0.197	Slc37a3	Intergenic
chr15	96628258	-13.730	0.044	Slc38a2	Intergenic
chr15	96589925	16.808	0.108	Slc38a2	Intergenic
chr15	96628123	-10.727	0.194	Slc38a2	Intergenic
chr15	96886170	21.993	0.042	Slc38a4	(CA)n Simple_repeat Simple_repeat
chr15	96886168	18.132	0.084	Slc38a4	(CA)n Simple_repeat Simple_repeat
chr15	96886180	18.078	0.099	Slc38a4	(CA)n Simple_repeat Simple_repeat
chr15	96886242	17.647	0.101	Slc38a4	intron (NM_027052, intron 1 of 15)
chr15	96886250	15.165	0.129	Slc38a4	intron (NM_027052, intron 1 of 15)
chr15	96886308	13.807	0.136	Slc38a4	promoter-TSS (NM_027052)
chr15	96886130	13.129	0.167	Slc38a4	intron (NM_027052, intron 1 of 15)
chr15	96886287	13.506	0.168	Slc38a4	promoter-TSS (NM_027052)
chr15	96886108	12.593	0.178	Slc38a4	intron (NM_027052, intron 1 of 15)

chr15	96886126	12.092	0.184	Slc38a4	intron (NM_027052, intron 1 of 15)
chr15	96886150	11.805	0.192	Slc38a4	intron (NM_027052, intron 1 of 15)
chr15	96886142	11.564	0.2	Slc38a4	intron (NM_027052, intron 1 of 15)
chr8	98377637	-6.207	0.068	Slc38a7	promoter-TSS (NM_172758)
chr3	31207337	-12.290	0.164	Slc7a14	intron (NM_172861, intron 1 of 7)
chr14	55034290	10.452	0.046	Slc7a7	intron (NM_011405, intron 2 of 11)
chr14	55034313	19.043	0.065	Slc7a7	intron (NM_011405, intron 2 of 11)
chr14	55034271	9.555	0.103	Slc7a7	intron (NM_011405, intron 2 of 11)
chr14	55034048	8.970	0.135	Slc7a7	intron (NM_011405, intron 2 of 11)
chr9	94575264	-10.398	0.033	Slc9a9	intron (NM_177909, intron 1 of 15)
chr11	82805031	-5.787	0.183	Slfn9	intron (NM_172796, intron 1 of 4)
chr19	47637051	-19.412	0.043	Slk	Intergenic
chr14	27345689	-13.658	0.087	Slmap	intron (NM_032008, intron 1 of 22)
chr14	27345668	-10.164	0.11	Slmap	intron (NM_032008, intron 1 of 22)
chr9	70391872	-12.229	0.072	Sltm	intron (NM_025690, intron 2 of 20)
chr9	70391936	-7.131	0.122	Sltm	intron (NM_025690, intron 2 of 20)
chr8	81886426	-15.782	0.101	Smad1	intron (NM_008539, intron 2 of 6)
chr8	81886404	-12.446	0.175	Smad1	intron (NM_008539, intron 2 of 6)
chr9	63589767	-19.122	0.043	Smad3	intron (NM_016769, intron 1 of 8)
chr9	63589961	-18.064	0.081	Smad3	intron (NM_016769, intron 1 of 8)
chr9	63589762	-12.573	0.183	Smad3	intron (NM_016769, intron 1 of 8)
chr18	73825299	-17.463	0.1	Smad4	intron (NM_008540, intron 4 of 11)
chr18	73825291	-15.922	0.104	Smad4	intron (NM_008540, intron 4 of 11)
chr18	73825196	-12.151	0.187	Smad4	intron (NM_008540, intron 4 of 11)
chr18	73825186	-12.645	0.187	Smad4	intron (NM_008540, intron 4 of 11)
chr15	99529285	-22.668	0.053	Smarcd1	exon (NM_009597, exon 11 of 12)
chr15	99529302	-16.492	0.103	Smarcd1	exon (NM_009597, exon 11 of 12)
chr15	99529473	-12.450	0.161	Smarcd1	exon (NM_009597, exon 12 of 12)
chr6	146783138	17.734	0.033	Smco2	Intergenic
chr15	91730957	-15.339	0.073	Smgc	intron (NM_207243, intron 28 of 43)
chr15	91730889	-12.897	0.142	Smgc	exon (NM_207243, exon 28 of 44)
chr15	91730868	-11.273	0.146	Smgc	exon (NM_207243, exon 28 of 44)
chr19	53489933	-27.936	0.016	Smndc1	Intergenic
chr19	53489186	-10.246	0.094	Smndc1	Intergenic
chr19	53489286	-10.426	0.095	Smndc1	Intergenic
chr19	53489970	-12.514	0.199	Smndc1	Intergenic
chr1	191744361	-11.311	0.115	Smyd2	intron (NM_026796, intron 1 of 11)
chr1	191744683	-16.137	0.118	Smyd2	intron (NM_026796, intron 1 of 11)
chr6	28433001	11.920	0.049	Snd1	intron (NM_019776, intron 1 of 23)
chr9	88416384	6.296	0.096	Shhg5	intron (NR_040721, intron 4 of 4)
chr2	26494966	12.189	0.129	Snora17	promoter-TSS (NR_028571)
chr2	26494887	6.741	0.188	Snora17	promoter-TSS (NR_028571)
chr11	106373230	12.942	0.022	Snord104	exon (NM_198292, exon 10 of 12)
chr7	67031315	-11.467	0.005	Snord116l2	Intergenic
chr2	166927132	-14.336	0.097	Snord12	3' UTR (NM_008420, exon 2 of 2)
chr2	166927372	-14.281	0.149	Snord12	3' UTR (NM_008420, exon 2 of 2)

chr15	79912120	8.962	0.148	Snord43	exon (NM_013762, exon 3 of 10)
chr15	79912343	5.122	0.193	Snord43	TTS (NR_028281)
chr11	83109700	-15.303	0.069	Snord7	exon (NM_134025, exon 4 of 4)
chr11	83109879	-11.093	0.151	Snord7	exon (NM_134025, exon 4 of 4)
chr11	96530046	16.075	0.032	Snx11	intron (NM_001033186, intron 4 of 12)
chr13	114396546	-15.179	0.076	Snx18	intron (NM_130796, intron 1 of 1)
chr13	114396395	-17.157	0.084	Snx18	intron (NM_130796, intron 1 of 1)
chr13	114396610	-12.077	0.158	Snx18	intron (NM_130796, intron 1 of 1)
chr13	114396622	-11.426	0.158	Snx18	intron (NM_130796, intron 1 of 1)
chr15	36457157	-16.823	0.031	Snx31	intron (NM_025712, intron 9 of 13)
chr15	36457159	-13.831	0.095	Snx31	intron (NM_025712, intron 9 of 13)
chr17	66788953	-18.602	0.031	Soga2	intron (NM_172963, intron 1 of 13)
chr17	66788391	-11.370	0.095	Soga2	intron (NM_172963, intron 1 of 13)
chr17	66788836	-11.459	0.196	Soga2	intron (NM_172963, intron 1 of 13)
chr8	46682178	-15.945	0.043	Sorbs2	intron (NM_172752, intron 1 of 22)
chr8	46682217	-13.003	0.1	Sorbs2	intron (NM_172752, intron 1 of 22)
chr17	80884144	15.152	0.028	Sos1	Intergenic
chr17	80884718	8.342	0.088	Sos1	Intergenic
chr12	70798046	10.229	0.197	Sos2	intron (NM_145443, intron 9 of 9)
chr5	93412894	-10.924	0.046	Sowahb	Intergenic
chr5	93412987	-17.252	0.117	Sowahb	Intergenic
chr1	4480807	-14.183	0.022	Sox17	TTS (NM_011441)
chr1	4480693	-10.322	0.135	Sox17	TTS (NM_011441)
chr6	144006053	-24.099	0.017	Sox5	intron (NM_001243163, intron 3 of 13)
chr6	144006005	-13.647	0.118	Sox5	intron (NM_001243163, intron 3 of 13)
chr6	144702242	-13.598	0.046	Sox5os3	Intergenic
chr6	144771560	-10.687	0.082	Sox5os3	Intergenic
chr6	144702670	-16.477	0.095	Sox5os3	Intergenic
chr6	144771267	-11.447	0.138	Sox5os3	Intergenic
chr6	144771524	-8.313	0.154	Sox5os3	Intergenic
chr17	25705352	19.643	0.049	Sox8	intron (NM_011447, intron 2 of 2)
chr17	25705368	11.338	0.097	Sox8	intron (NM_011447, intron 2 of 2)
chr2	72892279	-11.708	0.149	Sp3	Intergenic
chr2	72892459	-6.825	0.154	Sp3	Intergenic
chr2	72892301	-9.982	0.19	Sp3	Intergenic
chr12	119611997	-19.060	0.061	Sp4	Intergenic
chr12	119611953	-15.220	0.123	Sp4	Intergenic
chr12	119538270	15.582	0.131	Sp4	exon (NM_009239, exon 3 of 6)
chr3	26539076	-24.842	0.026	Spata16	intron (NM_027583, intron 1 of 9)
chr5	74077632	-5.313	0.149	Spata18	Intergenic
chr11	103084799	-13.251	0.103	Spata32	intron (NM_016896, intron 14 of 15)
chr11	103084834	-11.262	0.111	Spata32	intron (NM_016896, intron 14 of 15)
chr11	103084850	-12.337	0.112	Spata32	intron (NM_016896, intron 14 of 15)
chr10	74721884	-17.196	0.017	Specc1l	exon (NM_153406, exon 7 of 16)
chr10	74721892	-13.026	0.134	Specc1l	intron (NM_001145826, intron 10 of 18)
chr5	15137804	-11.949	0.022	Speer4d	Intergenic

chr5	15137293	-8.741	0.088	Speer4d	Intergenic
chr7	134281233	-25.581	0.012	Spn	promoter-TSS (NM_009259)
chr11	72363755	-20.905	0.046	Spns3	promoter-TSS (NM_029932)
chr2	116874041	-10.761	0.073	Spred1	Intergenic
chr2	116874193	-9.860	0.17	Spred1	Intergenic
chr11	19879627	-19.195	0.024	Spred2	intron (NM_033523, intron 1 of 5)
chr11	19613359	18.619	0.076	Spred2	Intergenic
chr11	19613352	16.759	0.086	Spred2	Intergenic
chr11	19879639	-11.522	0.131	Spred2	intron (NM_033523, intron 1 of 5)
chr11	19862785	-12.603	0.135	Spred2	intron (NM_033523, intron 1 of 5)
chr11	19879596	-9.540	0.165	Spred2	intron (NM_033523, intron 1 of 5)
chr11	19862793	-11.083	0.197	Spred2	intron (NM_033523, intron 1 of 5)
chr19	4720342	-20.447	0.015	Sptbn2	intron (NM_021287, intron 2 of 36)
chr19	4720339	-18.060	0.033	Sptbn2	intron (NM_021287, intron 2 of 36)
chr19	4720384	-15.172	0.039	Sptbn2	intron (NM_021287, intron 2 of 36)
chr19	4720352	-13.910	0.053	Sptbn2	intron (NM_021287, intron 2 of 36)
chr19	4720470	6.212	0.194	Sptbn2	intron (NM_021287, intron 2 of 36)
chr13	53441914	11.987	0.033	Sptlc1	intron (NM_009269, intron 8 of 14)
chr12	88728167	-6.796	0.043	Sptlc2	intron (NM_011479, intron 1 of 11)
chr2	157306267	-19.061	0.059	Src	Intergenic
chr2	157306275	-15.928	0.119	Src	Intergenic
chr15	81980024	21.841	0.045	Sreb2	intron (NM_033218, intron 1 of 18)
chr1	133398331	-15.120	0.02	Srgap2	intron (NM_001081011, intron 2 of 22)
chr17	28757662	-17.373	0.033	Srp1	intron (NM_016795, intron 2 of 15)
chr17	28757797	-17.686	0.049	Srp1	intron (NM_016795, intron 2 of 15)
chr11	87840920	9.808	0.125	Srsf1	Intergenic
chr11	87840959	8.957	0.163	Srsf1	Intergenic
chr2	151938803	-11.550	0.122	Srxn1	Intergenic
chr2	151938855	-8.574	0.199	Srxn1	Intergenic
chr18	14815961	-16.641	0.1	Ss18	intron (NM_009280, intron 3 of 10)
chr18	14815679	-11.254	0.115	Ss18	intron (NM_009280, intron 3 of 10)
chr18	14815500	-11.997	0.155	Ss18	intron (NM_009280, intron 3 of 10)
chr6	40422746	12.955	0.065	Ssbp1	intron (NM_001286664, intron 1 of 5)
chr6	40422210	7.887	0.162	Ssbp1	intron (NM_001286664, intron 1 of 5)
chr6	40422115	11.025	0.184	Ssbp1	exon (NM_028358, exon 2 of 6)
chr15	66934399	15.065	0.074	St3gal1	TTS (NM_009177)
chr15	66934396	13.488	0.111	St3gal1	TTS (NM_009177)
chr15	66934681	10.795	0.184	St3gal1	3' UTR (NM_009177, exon 9 of 9)
chr3	153352832	21.146	0.048	St6galnac3	intron (NM_011372, intron 1 of 4)
chr3	153352926	14.657	0.107	St6galnac3	intron (NM_011372, intron 1 of 4)
chr3	153175132	-10.093	0.192	St6galnac3	intron (NM_011372, intron 1 of 4)
chr3	153175121	-12.289	0.192	St6galnac3	intron (NM_011372, intron 1 of 4)
chr3	153175106	-10.778	0.192	St6galnac3	intron (NM_011372, intron 1 of 4)
chr7	108469356	10.959	0.024	Stard10	promoter-TSS (NM_019990)
chr5	151977203	13.779	0.075	Stard13	intron (NM_146258, intron 1 of 13)
chr5	151977211	12.685	0.104	Stard13	intron (NM_146258, intron 1 of 13)



chr5	151977324	11.573	0.189	Stard13	intron (NM_146258, intron 1 of 13)
chr13	19457852	-17.331	0.073	Stard3nl	intron (NM_024270, intron 7 of 8)
chr13	19457605	-12.619	0.136	Stard3nl	intron (NM_024270, intron 7 of 8)
chr7	90808951	-21.091	0.017	Stard5	intron (NM_010551, intron 12 of 18)
chr7	90808949	-15.492	0.053	Stard5	intron (NM_010551, intron 12 of 18)
chr11	100732045	-17.821	0.083	Stat5a	intron (NM_011488, intron 6 of 19)
chr11	31271740	19.288	0.071	Stc2	CpG
chr11	31271728	14.393	0.136	Stc2	CpG
chr1	95529556	-12.987	0.058	Stk25	intron (NM_021537, intron 2 of 11)
chr1	95529543	-9.091	0.194	Stk25	intron (NM_021537, intron 2 of 11)
chr8	48372692	6.545	0.189	Stox2	intron (NM_175162, intron 1 of 4)
chr12	52800934	21.723	0.04	Strn3	intron (NM_021710, intron 1 of 5)
chr12	52835985	-18.526	0.067	Strn3	intron (NM_021710, intron 5 of 5)
chr12	52835954	-16.045	0.082	Strn3	intron (NM_021710, intron 5 of 5)
chr12	52835781	-15.445	0.11	Strn3	intron (NM_021710, intron 5 of 5)
chr14	79986739	9.331	0.065	Sugt1	promoter-TSS (NM_026474)
chr14	79986625	9.850	0.096	Sugt1	promoter-TSS (NM_026474)
chr14	79986683	11.294	0.104	Sugt1	promoter-TSS (NM_026474)
chr14	79986486	12.086	0.131	Sugt1	Intergenic
chr14	79986462	12.085	0.16	Sugt1	Intergenic
chr4	59451722	8.071	0.067	Susd1	promoter-TSS (NM_001163288)
chr4	59451654	9.140	0.081	Susd1	promoter-TSS (NM_001163288)
chr7	82230618	-14.563	0.053	Sv2b	Intergenic
chr7	82230596	-8.667	0.167	Sv2b	Intergenic
chr13	96939349	11.924	0.116	Sv2c	Intergenic
chr13	96939338	10.441	0.14	Sv2c	Intergenic
chr3	102750789	14.775	0.106	Sycp1	intron (NM_201619, intron 8 of 10)
chr10	78055156	-15.558	0.023	Syde1	promoter-TSS (NM_027875)
chr10	78055165	-12.841	0.071	Syde1	promoter-TSS (NM_027875)
chr4	134550969	-17.060	0.094	Syf2	Intergenic
chr4	134550981	-12.541	0.183	Syf2	Intergenic
chr10	5352494	-16.643	0.036	Syne1	intron (NM_007956, intron 7 of 8)
chr10	5352967	-11.557	0.099	Syne1	intron (NM_007956, intron 7 of 8)
chr10	5352526	-10.747	0.197	Syne1	intron (NM_007956, intron 7 of 8)
chr12	106239415	-18.894	0.05	Syne3	intron (NM_172500, intron 1 of 16)
chr12	106239275	-14.203	0.067	Syne3	intron (NM_172500, intron 1 of 16)
chr12	106239236	-13.224	0.087	Syne3	intron (NM_172500, intron 1 of 16)
chr10	23669900	-13.367	0.05	Taar3	exon (NM_001008429, exon 1 of 1)
chr10	23669794	-11.719	0.094	Taar3	exon (NM_001008429, exon 1 of 1)
chr10	23669938	-8.452	0.187	Taar3	exon (NM_001008429, exon 1 of 1)
chr10	23669590	-8.288	0.189	Taar3	exon (NM_001008429, exon 1 of 1)
chr8	109251703	11.378	0.134	Tango6	intron (NM_173037, intron 11 of 17)
chr5	117604950	-15.833	0.036	Taok3	intron (NM_001081308, intron 1 of 19)
chr17	34341191	15.422	0.122	Tap2	promoter-TSS (NM_011530)
chr17	34341132	-11.177	0.19	Tap2	promoter-TSS (NM_011530)
chr8	112506397	8.972	0.131	Tat	Intergenic

chr8	112506187	-7.239	0.141	Tat	Intergenic
chr5	64620925	17.955	0.045	Tbc1d1	intron (NM_019636, intron 2 of 19)
chr9	90157927	11.432	0.144	Tbc1d2b	intron (NM_194334, intron 1 of 12)
chr9	90157079	11.194	0.197	Tbc1d2b	intron (NM_194334, intron 1 of 12)
chr10	120704740	-9.502	0.079	Tbc1d30	intron (NM_029057, intron 11 of 11)
chr10	120704821	-9.544	0.179	Tbc1d30	intron (NM_029057, intron 11 of 11)
chr14	101909893	-6.349	0.135	Tbc1d4	intron (NM_001081278, intron 1 of 18)
chr17	51155946	18.059	0.024	Tbc1d5	intron (NM_028162, intron 3 of 21)
chr16	18585665	17.287	0.018	Tbx1	intron (NM_001285476, intron 1 of 6)
chr16	18585785	9.533	0.122	Tbx1	intron (NM_001285476, intron 1 of 6)
chr16	18585706	11.253	0.123	Tbx1	intron (NM_001285476, intron 1 of 6)
chr16	18585584	14.462	0.143	Tbx1	intron (NM_001285476, intron 1 of 6)
chr2	151968403	-17.681	0.028	Tcf15	promoter-TSS (NM_009328)
chr2	151968416	-13.990	0.075	Tcf15	promoter-TSS (NM_009328)
chr2	151968424	-10.047	0.182	Tcf15	promoter-TSS (NM_009328)
chr19	55824858	-12.500	0.107	Tcf712	intron (NM_001142923, intron 3 of 11)
chr19	55824845	-12.504	0.13	Tcf712	intron (NM_001142923, intron 3 of 11)
chr19	55824881	-10.230	0.144	Tcf712	intron (NM_001142923, intron 3 of 11)
chr19	55824767	-11.874	0.149	Tcf712	intron (NM_001142923, intron 3 of 11)
chr19	56002333	-8.508	0.167	Tcf712	intron (NM_001142924, intron 11 of 11)
chr19	3906559	10.272	0.14	Tcird1	5' UTR (NM_001167784, exon 1 of 20)
chr19	3906585	9.989	0.164	Tcird1	5' UTR (NM_001167784, exon 1 of 20)
chr19	3906583	10.259	0.17	Tcird1	5' UTR (NM_001167784, exon 1 of 20)
chr8	13988832	-18.906	0.064	Tdrp	Intergenic
chr8	13971683	-11.030	0.083	Tdrp	intron (NM_173744, intron 1 of 2)
chr8	13988828	-16.576	0.096	Tdrp	Intergenic
chr8	13971745	-8.529	0.157	Tdrp	intron (NM_173744, intron 1 of 2)
chr15	81632441	-12.747	0.13	Tef	promoter-TSS (NM_153484)
chr15	81632531	-10.465	0.17	Tef	promoter-TSS (NM_153484)
chr8	50498014	13.194	0.048	Tenm3	Intergenic
chr13	73764318	-5.878	0.089	Tert	promoter-TSS (NM_009354)
chr3	133421065	-14.984	0.046	Tet2	Intergenic
chr3	133421249	-12.284	0.068	Tet2	Intergenic
chr3	133421291	-9.747	0.164	Tet2	Intergenic
chr4	48420413	-14.997	0.084	Tex10	intron (NM_001281977, intron 11 of 16)
chr4	48420367	-11.137	0.095	Tex10	B1_Mus1 SINE Alu
chr7	140608355	13.896	0.04	Tex36	Intergenic
chr2	84314237	-19.245	0.052	Tfpi	promoter-TSS (NM_011576)
chr2	84314249	-10.759	0.185	Tfpi	promoter-TSS (NM_011576)
chr6	86184098	13.695	0.134	Tgfa	intron (NM_031199, intron 2 of 5)
chr6	86184196	12.838	0.176	Tgfa	intron (NM_031199, intron 2 of 5)
chr17	71222778	15.241	0.025	Tgif1	Intergenic
chr17	71203114	-15.315	0.096	Tgif1	promoter-TSS (NM_001164074)
chr17	71222987	9.102	0.115	Tgif1	Intergenic
chr17	71222740	8.586	0.119	Tgif1	Intergenic
chr17	71203137	-9.472	0.167	Tgif1	promoter-TSS (NM_001164074)

chr17	71203222	-12.314	0.195	Tgif1	promoter-TSS (NM_001164074)
chr10	28246362	-25.809	0.018	Themis	intron (NM_008983, intron 13 of 31)
chr14	14792857	-6.410	0.018	Thoc7	intron (NM_001285780, intron 1 of 8)
chr17	81463641	-11.222	0.051	Thumpd2	intron (NM_028138, intron 1 of 9)
chr16	89874024	22.904	0.002	Tiam1	intron (NM_001145886, intron 6 of 27)
chr18	46712994	-11.193	0.103	Ticam2	Intergenic
chr18	46712996	-11.967	0.11	Ticam2	Intergenic
chr3	84408070	-9.210	0.032	Tigd4	Intergenic
chr14	33006821	-17.741	0.032	Timm23	intron (NM_016897, intron 3 of 6)
chr7	72516669	-9.109	0.073	Tjp1	promoter-TSS (NM_001163574)
chr7	72516602	-5.871	0.196	Tjp1	promoter-TSS (NM_001163574)
chr19	14738307	-11.694	0.073	Tle4	Intergenic
chr19	14738079	-10.961	0.136	Tle4	Intergenic
chr11	33096861	13.351	0.045	Tlx3	Intergenic
chr3	57109578	-9.480	0.19	Tm4sf1	Intergenic
chr6	116123848	-12.821	0.155	Tmcc1	CpG
chr10	94009563	14.597	0.029	Tmcc3	intron (NM_172051, intron 1 of 3)
chr10	93983887	11.724	0.137	Tmcc3	intron (NM_172051, intron 1 of 3)
chr10	94037772	11.603	0.145	Tmcc3	promoter-TSS (NM_001168684)
chr10	94037674	8.887	0.186	Tmcc3	promoter-TSS (NM_001168684)
chr10	94009470	9.563	0.192	Tmcc3	intron (NM_172051, intron 1 of 3)
chr12	86731094	13.784	0.032	Tmed10	Intergenic
chr12	86731097	9.110	0.142	Tmed10	Intergenic
chr9	107371712	-10.518	0.139	Tmem115	intron (NM_001174047, intron 3 of 38)
chr4	118252269	14.363	0.048	Tmem125	intron (NM_026789, intron 15 of 21)
chr5	38652191	-12.024	0.078	Tmem128	intron (NM_025480, intron 1 of 4)
chr5	38652159	-11.105	0.116	Tmem128	intron (NM_025480, intron 1 of 4)
chr1	37098227	6.252	0.182	Tmem131	Intergenic
chr1	37098284	6.667	0.187	Tmem131	Intergenic
chr7	96317226	-6.093	0.082	Tmem135	intron (NM_028343, intron 6 of 14)
chr3	79650645	5.316	0.116	Tmem144	Intergenic
chr3	79650744	5.250	0.173	Tmem144	Intergenic
chr17	81341407	-18.027	0.04	Tmem178	Intergenic
chr17	81341416	-15.493	0.071	Tmem178	Intergenic
chr17	81340739	-14.557	0.099	Tmem178	Intergenic
chr17	81341411	-13.575	0.108	Tmem178	Intergenic
chr17	81340727	-14.208	0.111	Tmem178	Intergenic
chr17	81341626	-11.127	0.18	Tmem178	Intergenic
chr17	81340967	-9.952	0.189	Tmem178	Intergenic
chr17	6452040	-13.783	0.04	Tmem181b-ps	Intergenic
chr17	6492330	-9.485	0.074	Tmem181b-ps	Intergenic
chr17	6452005	-12.018	0.077	Tmem181b-ps	Intergenic
chr17	6492349	-6.962	0.155	Tmem181b-ps	Intergenic
chr17	6452022	-9.142	0.159	Tmem181b-ps	Intergenic
chr16	26519837	-15.002	0.045	Tmem207	intron (NM_001101640, intron 2 of 4)
chr5	113638150	12.877	0.172	Tmem211	Intergenic

chr5	9099931	-8.654	0.176	Tmem243	promoter-TSS (NM_001081029)
chr5	9099996	-7.938	0.191	Tmem243	promoter-TSS (NM_001081029)
chr14	49156816	-19.768	0.009	Tmem260	Intergenic
chr14	49156984	-13.393	0.155	Tmem260	Intergenic
chr12	74618650	-6.283	0.137	Tmem30b	Intergenic
chr9	122915173	7.710	0.129	Tmem42	intron (NM_010620, intron 26 of 34)
chr4	116228990	-6.785	0.132	Tmem69	promoter-TSS (NM_177670)
chr16	97892374	-18.408	0.05	Tmprss2	Intergenic
chr16	97892417	-10.714	0.181	Tmprss2	Intergenic
chr6	72939272	-18.289	0.045	Tmsb10	Intergenic
chr18	50190361	-15.082	0.028	Tnfaip8	intron (NM_001177759, intron 1 of 1)
chr18	50190855	-10.817	0.152	Tnfaip8	intron (NM_001177759, intron 1 of 1)
chr18	50190266	-6.362	0.187	Tnfaip8	intron (NM_001177759, intron 1 of 1)
chr1	107677962	-16.983	0.069	Tnfrsf11a	intron (NM_009399, intron 1 of 9)
chr1	107677861	-12.850	0.073	Tnfrsf11a	intron (NM_009399, intron 1 of 9)
chr1	107677940	-9.075	0.18	Tnfrsf11a	intron (NM_009399, intron 1 of 9)
chr7	4474398	15.545	0.06	Tnni3	promoter-TSS (NM_009406)
chr7	4474487	8.818	0.17	Tnni3	promoter-TSS (NM_009406)
chr7	4474235	8.764	0.199	Tnni3	promoter-TSS (NM_009406)
chr6	29582037	9.954	0.15	Tnpo3	Intergenic
chr6	29582186	7.324	0.187	Tnpo3	Intergenic
chr15	80540782	9.631	0.117	Tnrc6b	promoter-TSS (NM_144812)
chr15	80540778	7.246	0.186	Tnrc6b	promoter-TSS (NM_144812)
chr11	94050968	12.377	0.046	Tob1	Intergenic
chr4	6702613	8.412	0.123	Tox	intron (NM_145711, intron 3 of 8)
chr8	107979425	-9.324	0.124	Tppp3	intron (NM_001033371, intron 7 of 10)
chr8	107979429	-6.168	0.2	Tppp3	intron (NM_001033371, intron 7 of 10)
chr6	88927601	-13.431	0.17	Tpra1	Intergenic
chr6	88927586	-8.255	0.17	Tpra1	Intergenic
chr2	34820996	13.473	0.034	Traf1	Intergenic
chr1	13564618	-9.225	0.099	Tram1	intron (NM_028173, intron 6 of 10)
chr1	13564257	-10.019	0.124	Tram1	intron (NM_028173, intron 6 of 10)
chr1	13564280	-9.006	0.148	Tram1	intron (NM_028173, intron 6 of 10)
chr4	125951100	-14.196	0.084	Trappc3	intron (NM_013718, intron 3 of 4)
chr4	125951058	-12.798	0.13	Trappc3	intron (NM_013718, intron 3 of 4)
chr4	125951138	-13.069	0.131	Trappc3	exon (NM_013718, exon 4 of 5)
chr4	125951071	-9.780	0.182	Trappc3	intron (NM_013718, intron 3 of 4)
chr15	72865231	-17.109	0.113	Trappc9	intron (NM_001164643, intron 4 of 8)
chr17	47280502	15.259	0.107	Trerf1	intron (NM_001097623, intron 3 of 19)
chr17	47280398	10.939	0.146	Trerf1	intron (NM_001097623, intron 3 of 19)
chr19	46553874	-26.612	0.026	Trim8	intron (NM_001025391, intron 10 of 11)
chr19	46553911	-17.405	0.092	Trim8	intron (NM_001025391, intron 10 of 11)
chr2	93007361	-22.349	0.027	Trp53i11	Intergenic
chr2	93010507	-15.034	0.098	Trp53i11	Intergenic
chr2	93007437	-12.249	0.103	Trp53i11	Intergenic
chr2	93010601	-12.150	0.191	Trp53i11	Intergenic

chr3	53963148	-18.674	0.033	Trpc4	intron (NR_046161, intron 1 of 10)
chr11	62390224	-18.608	0.033	Trpv2	intron (NM_011706, intron 2 of 15)
chr11	62390218	-17.662	0.058	Trpv2	intron (NM_011706, intron 2 of 15)
chr10	115246200	-10.188	0.127	Tspan8	Intergenic
chr10	115246443	-11.111	0.156	Tspan8	Intergenic
chr10	115246484	-6.477	0.168	Tspan8	Intergenic
chr6	128083681	-11.447	0.095	Tspan9	intron (NM_175414, intron 1 of 8)
chr6	128083700	-11.118	0.149	Tspan9	intron (NM_175414, intron 1 of 8)
chr6	128083815	-12.471	0.17	Tspan9	intron (NM_175414, intron 1 of 8)
chr17	46622224	-12.775	0.038	Ttbk1	intron (NM_001162864, intron 1 of 14)
chr17	46622212	-8.384	0.163	Ttbk1	intron (NM_001162864, intron 1 of 14)
chr11	62095889	-12.505	0.069	Ttc19	promoter-TSS (NM_027198)
chr17	87704314	15.949	0.046	Ttc7	intron (NM_028639, intron 3 of 19)
chr12	101743637	-10.407	0.046	Ttc7b	intron (NM_001033213, intron 1 of 19)
chr12	101766342	14.866	0.06	Ttc7b	Intergenic
chr12	101766359	12.600	0.126	Ttc7b	Intergenic
chr5	73154593	-13.467	0.049	Txk	intron (NM_001113464, intron 14 of 17)
chr5	73154513	-10.073	0.149	Txk	intron (NM_001113464, intron 14 of 17)
chr5	30398471	14.431	0.059	Tyms	intron (NM_021288, intron 1 of 6)
chr7	31194788	10.433	0.102	Tyrobp	Intergenic
chr7	31194725	13.145	0.123	Tyrobp	Intergenic
chr5	86609873	-31.255	0.012	Uba6	Intergenic
chr5	86609931	-12.323	0.165	Uba6	Intergenic
chr5	86609882	-13.707	0.2	Uba6	Intergenic
chr14	19906567	12.181	0.068	Ube2e2	Intergenic
chr6	30162380	19.240	0.055	Ube2h	3' UTR (NM_001169576, exon 5 of 5)
chr6	30162393	14.640	0.143	Ube2h	3' UTR (NM_001169576, exon 5 of 5)
chr5	149371084	-27.870	0.019	Ubl3	Intergenic
chr5	149371060	-18.517	0.088	Ubl3	Intergenic
chr5	65853512	-17.045	0.039	Ugdh	intron (NM_133697, intron 2 of 4)
chr5	87316006	-19.161	0.04	Ugt2b34	Intergenic
chr17	27994439	6.383	0.043	Uhrf1bp1	intron (NM_001080769, intron 1 of 20)
chr11	61656400	12.416	0.1	Ulk2	intron (NM_013881, intron 3 of 26)
chr5	115577393	-12.591	0.067	Unc119b	exon (NM_175352, exon 3 of 5)
chr5	115577387	-12.405	0.1	Unc119b	exon (NM_175352, exon 3 of 5)
chr5	115577390	-11.961	0.112	Unc119b	exon (NM_175352, exon 3 of 5)
chr1	66515815	-13.229	0.088	Unc80	intron (NM_175510, intron 1 of 64)
chr1	66515741	-14.003	0.102	Unc80	intron (NM_175510, intron 1 of 64)
chr1	66514111	-13.619	0.107	Unc80	promoter-TSS (NM_175510)
chr3	146261610	-16.003	0.109	Uox	intron (NM_009474, intron 1 of 7)
chr3	146261384	-11.256	0.162	Uox	intron (NM_009474, intron 1 of 7)
chr2	58517841	-15.811	0.072	Upp2	Intergenic
chr7	53491361	11.960	0.067	Ush1c	intron (NM_001163733, intron 1 of 26)
chr7	53491425	9.391	0.16	Ush1c	intron (NM_001163733, intron 1 of 26)
chr7	53491305	7.543	0.189	Ush1c	intron (NM_001163733, intron 1 of 26)
chr4	98570012	11.929	0.127	Usp1	Intergenic

chr16	87454798	15.686	0.07	Usp16	promoter-TSS (NM_024258)
chr16	87454791	14.491	0.122	Usp16	promoter-TSS (NM_024258)
chr16	87454326	9.323	0.175	Usp16	promoter-TSS (NM_024258)
chr4	105872678	20.915	0.043	Usp24	Intergenic
chr4	105872668	16.841	0.073	Usp24	Intergenic
chr4	105872751	13.867	0.09	Usp24	Intergenic
chr4	105872673	13.505	0.166	Usp24	Intergenic
chr16	77027348	-13.097	0.121	Usp25	intron (NM_013918, intron 1 of 23)
chr16	77027298	-12.739	0.128	Usp25	intron (NM_013918, intron 1 of 23)
chr11	23207805	-7.240	0.136	Usp34	intron (NM_001190401, intron 1 of 79)
chr16	8731820	-19.682	0.044	Usp7	intron (NM_001003918, intron 1 of 30)
chr16	8731956	-11.275	0.062	Usp7	intron (NM_001003918, intron 1 of 30)
chr10	12580309	8.729	0.122	Utrn	intron (NM_011682, intron 1 of 73)
chr10	12580339	7.428	0.165	Utrn	intron (NM_011682, intron 1 of 73)
chr5	33721776	5.814	0.044	Uvssa	intron (NM_001081101, intron 1 of 13)
chr5	33721859	12.172	0.066	Uvssa	intron (NM_001081101, intron 1 of 13)
chr5	33721857	10.498	0.149	Uvssa	intron (NM_001081101, intron 1 of 13)
chr4	150432944	-13.286	0.165	Vamp3	promoter-TSS (NM_009498)
chr1	173958614	9.085	0.096	Vangl2	Intergenic
chr1	173958525	12.071	0.137	Vangl2	Intergenic
chr3	109300161	-14.442	0.149	Vav3	intron (NM_020505, intron 4 of 26)
chr3	109300197	-13.351	0.17	Vav3	intron (NM_020505, intron 4 of 26)
chr11	52151302	19.778	0.044	Vdac1	Intergenic
chr11	52151091	12.332	0.111	Vdac1	Intergenic
chr11	52151166	8.970	0.194	Vdac1	Intergenic
chr11	52151184	11.159	0.195	Vdac1	Intergenic
chr4	144733396	-15.829	0.029	Vps13d	intron (NM_001276502, intron 21 of 68)
chr4	144733894	-10.796	0.096	Vps13d	intron (NM_001276502, intron 21 of 68)
chr9	26835719	-18.712	0.059	Vps26b	intron (NM_178027, intron 1 of 5)
chr5	147214092	14.424	0.123	Wasf3	intron (NM_145155, intron 1 of 9)
chr19	46681492	-6.547	0.114	Wbp1l	intron (NM_001177812, intron 2 of 4)
chr19	46681596	-8.671	0.136	Wbp1l	intron (NM_001177812, intron 2 of 4)
chr19	46681404	-7.089	0.158	Wbp1l	intron (NM_001177812, intron 2 of 4)
chr19	46681594	-6.856	0.169	Wbp1l	intron (NM_001177812, intron 2 of 4)
chr5	102520236	-12.808	0.018	Wdfy3	Intergenic
chr5	102520196	-8.217	0.137	Wdfy3	Intergenic
chr18	64023542	-16.817	0.028	Wdr7	intron (NM_001014981, intron 20 of 27)
chr18	64023532	-7.785	0.134	Wdr7	intron (NM_001014981, intron 20 of 27)
chr15	7917655	12.997	0.022	Wdr70	intron (NM_001081402, intron 10 of 17)
chr2	59841791	7.720	0.044	Wdsub1	intron (NM_001001182, intron 3 of 35)
chr2	59841795	5.997	0.111	Wdsub1	intron (NM_001001182, intron 3 of 35)
chr10	120484634	17.976	0.053	Wif1	MER91A DNA Tip100
chr10	120484444	12.033	0.06	Wif1	intron (NM_011915, intron 2 of 9)
chr2	73389266	-10.965	0.053	Wipf1	Intergenic
chr2	73389271	-9.964	0.062	Wipf1	Intergenic

chr13	49240690	-14.741	0.103	Wnk2	intron (NM_029361, intron 2 of 27)
chr13	49240678	-13.881	0.139	Wnk2	intron (NM_029361, intron 2 of 27)
chr1	74842243	-27.429	0.018	Wnt10a	intron (NM_009518, intron 2 of 3)
chr11	103670837	-14.334	0.087	Wnt3	intron (NM_009521, intron 2 of 4)
chr11	103670890	-13.512	0.16	Wnt3	intron (NM_009521, intron 2 of 4)
chr11	103670830	-10.731	0.182	Wnt3	intron (NM_009521, intron 2 of 4)
chr11	35859120	-10.904	0.123	Wwc1	intron (NM_011856, intron 23 of 28)
chr11	35859124	-10.975	0.186	Wwc1	intron (NM_011856, intron 23 of 28)
chr8	117532576	-19.791	0.033	Wwox	intron (NM_019573, intron 8 of 8)
chr8	117374432	21.630	0.048	Wwox	intron (NM_019573, intron 8 of 8)
chr8	117532628	-11.783	0.128	Wwox	intron (NM_019573, intron 8 of 8)
chr8	117374579	11.179	0.179	Wwox	intron (NM_019573, intron 8 of 8)
chr11	5399073	-20.017	0.042	Xbp1	Intergenic
chr11	5398027	8.796	0.089	Xbp1	Intergenic
chr11	5399210	-11.457	0.169	Xbp1	Intergenic
chr2	67353708	-14.737	0.163	Xirp2	exon (NM_001083919, exon 7 of 9)
chr1	3601517	15.503	0.035	Xkr4	intron (NM_001011874, intron 1 of 2)
chr8	18950112	-12.366	0.194	Xkr5	5' UTR (NM_001286469, exon 1 of 7)
chr8	18950368	-6.155	0.194	Xkr5	5' UTR (NM_001286469, exon 1 of 7)
chr4	132262993	-18.551	0.053	Xkr8	exon (NM_010166, exon 14 of 18)
chr4	132262947	-12.708	0.129	Xkr8	exon (NM_010166, exon 14 of 18)
chr6	91459675	16.577	0.032	Xpc	intron (NM_009531, intron 2 of 15)
chr6	91459673	14.306	0.093	Xpc	intron (NM_009531, intron 2 of 15)
chr1	157259908	10.454	0.181	Xpr1	intron (NM_011273, intron 1 of 14)
chr15	36636157	-19.145	0.08	Ywhaz	Intergenic
chr6	38255017	-7.778	0.021	Zc3hav1l	Intergenic
chr8	111223825	9.651	0.028	Zfhx3	Intergenic
chr8	111223764	9.459	0.117	Zfhx3	Intergenic
chr8	111222749	-8.114	0.124	Zfhx3	Intergenic
chr8	111222753	-13.358	0.131	Zfhx3	Intergenic
chr8	111223797	6.618	0.173	Zfhx3	Intergenic
chr8	111222710	-11.919	0.181	Zfhx3	Intergenic
chr8	111223931	5.742	0.196	Zfhx3	Intergenic
chr2	170018840	13.907	0.043	Zfp217	Intergenic
chr2	170018873	12.631	0.09	Zfp217	Intergenic
chr2	170018897	10.410	0.171	Zfp217	Intergenic
chr18	82874731	-13.589	0.031	Zfp236	Intergenic
chr18	82874817	-12.068	0.096	Zfp236	Intergenic
chr15	76703154	-18.549	0.044	Zfp251	Intergenic
chr5	106359263	-22.367	0.058	Zfp326	Intergenic
chr5	106246810	13.909	0.106	Zfp326	Intergenic
chr5	106246791	14.096	0.108	Zfp326	Intergenic
chr5	106246679	12.946	0.119	Zfp326	Intergenic
chr5	106246692	14.765	0.126	Zfp326	Intergenic
chr4	128517444	-14.346	0.126	Zfp362	Intergenic
chr4	128517398	-14.958	0.131	Zfp362	Intergenic

chr13	65359752	-10.220	0.123	Zfp369	Intergenic
chr13	65359748	-11.341	0.127	Zfp369	Intergenic
chr13	65359963	-10.600	0.146	Zfp369	Intergenic
chr12	80928215	-16.825	0.05	Zfp3611	Intergenic
chr12	80928697	-13.054	0.108	Zfp3611	Intergenic
chr12	80928165	-8.867	0.128	Zfp3611	Intergenic
chr12	80928202	-10.996	0.132	Zfp3611	Intergenic
chr2	77653285	-15.912	0.039	Zfp385b	intron (NM_178723, intron 1 of 9)
chr2	77653447	-12.466	0.062	Zfp385b	intron (NM_178723, intron 1 of 9)
chr2	77653647	-11.825	0.122	Zfp385b	intron (NM_178723, intron 1 of 9)
chr2	77653294	-11.118	0.134	Zfp385b	intron (NM_178723, intron 1 of 9)
chr2	77653327	-10.613	0.158	Zfp385b	intron (NM_178723, intron 1 of 9)
chr2	77653129	-8.931	0.194	Zfp385b	intron (NM_178723, intron 1 of 9)
chr14	65995483	24.043	0.026	Zfp395	intron (NM_199029, intron 1 of 9)
chr14	65970421	-12.413	0.098	Zfp395	Intergenic
chr14	65995150	15.397	0.105	Zfp395	intron (NM_199029, intron 1 of 9)
chr14	65970414	-11.429	0.11	Zfp395	Intergenic
chr18	65670592	-19.289	0.066	Zfp532	Intergenic
chr18	65670656	-13.728	0.136	Zfp532	Intergenic
chr7	38475519	12.856	0.095	Zfp536	intron (NM_172385, intron 2 of 5)
chr7	38475494	12.384	0.095	Zfp536	intron (NM_172385, intron 2 of 5)
chr7	38475373	10.662	0.172	Zfp536	intron (NM_172385, intron 2 of 5)
chr7	38475505	8.016	0.197	Zfp536	intron (NM_172385, intron 2 of 5)
chr9	20189406	5.483	0.078	Zfp560	CpG
chr4	62483874	-14.281	0.078	Zfp618	Intergenic
chr4	62483995	-9.696	0.184	Zfp618	Intergenic
chr11	95640396	18.245	0.021	Zfp652	Intergenic
chr11	95640412	19.316	0.039	Zfp652	Intergenic
chr3	94831875	-13.429	0.077	Zfp687	Intergenic
chr3	94831822	-7.814	0.124	Zfp687	Intergenic
chr3	9563654	21.842	0.027	Zfp704	intron (NM_133218, intron 2 of 8)
chr15	36890048	-16.376	0.058	Zfp706	Intergenic
chr15	36972939	15.571	0.064	Zfp706	Intergenic
chr15	36890007	-13.633	0.125	Zfp706	Intergenic
chr15	36941756	9.030	0.134	Zfp706	L2c LINE L2
chr15	36890026	-11.667	0.164	Zfp706	Intergenic
chr15	36941712	7.650	0.176	Zfp706	L2c LINE L2
chr15	36890143	-10.955	0.186	Zfp706	Intergenic
chr2	114026004	-9.632	0.077	Zfp770	intron (NM_175466, intron 1 of 1)
chr2	114026134	-10.849	0.167	Zfp770	intron (NM_175466, intron 1 of 1)
chr7	7089299	-8.495	0.031	Zfp773	exon (NM_029584, exon 1 of 4)
chr7	7089297	-5.402	0.133	Zfp773	exon (NM_029584, exon 1 of 4)
chr12	112092212	-18.233	0.031	Zfp839	intron (NM_001199785, intron 1 of 6)
chr8	74433184	-14.705	0.034	Zfp882	intron (NM_001166645, intron 1 of 2)
chr17	22289162	-10.711	0.113	Zfp947	L1M4 LINE L1
chr17	22289020	-11.376	0.177	Zfp947	L1M4 LINE L1



chr12	84932904	-8.128	0.107	Zfyve1	intron (NM_183154, intron 2 of 11)
chr12	84932844	-8.204	0.109	Zfyve1	intron (NM_183154, intron 2 of 11)
chrX	55292909	-21.397	0.067	Zic3	Intergenic
chr13	9796075	-21.056	0.047	Zmynd11	Intergenic
chr2	165687202	9.591	0.163	Zmynd8	CpG
chr17	56677283	21.935	0.042	Znrf4	Intergenic
chr11	22864433	-20.197	0.036	Zrsr1	intron (NM_144514, intron 1 of 2)
chr13	108637826	-17.321	0.026	Zswim6	intron (NM_145456, intron 2 of 14)
chr13	108637813	-10.608	0.147	Zswim6	intron (NM_145456, intron 2 of 14)
chr13	108637817	-8.837	0.161	Zswim6	intron (NM_145456, intron 2 of 14)
chr13	108637831	-8.297	0.172	Zswim6	intron (NM_145456, intron 2 of 14)

In this Issue, Richetto et al. identify large-scale epigenetic changes in offspring of mice who were infected during pregnancy. These abnormalities affect gene expression in adulthood and likely contribute to behavioral deficits as seen in neurodevelopmental disorders, such as schizophrenia and autism.

## Bedgraph files

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