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Genome-wide DNA methylation profiling of the regenerative MRL/MpJ mouse and two normal strains.

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ABSTRACT

Aims

We aimed to identify the pivotal differences in the DNA methylation profiles between the regeneration capable MRL/MpJ mouse and reference mouse strains.

Materials and Methods

Global DNA methylation profiling was performed in ear pinnae, bone marrow, spleen, liver, heart from uninjured adult females of the MRL/MpJ and C57BL/6J and BALB/c.

Results and conclusion

A number of differentially methylated regions distinguishing between the MRL/MpJ mouse and both references were identified. In the ear pinnae, the differentially methylated regions were enriched in genes associated with development, inflammation and apoptosis, and in binding sites of transcriptional modulator Smad1. Several differentially methylated regions overlapped previously mapped quantitative trait loci of regenerative capability. The results suggest a potential epigenetic determinants of regenerative phenomenon.

Key words: MRL/MpJ, regeneration, wound healing, DNA methylation, epigenetics, MeDIP-chip, micrzoarray

INTRODUCTION

The regeneration phenomena such as scarless skin wound healing [1] and perfect heart *repair [2], and spinal cord regeneration [3] have been observed in mammals in embryonic and neonatal periods. Regenerative abilities in mammals are known to decline along with development but the adult mouse of the MRL/MpJ mouse appears to be a remarkable exception to this common rule. The first report on the MRL/MpJ enhanced capacity for regeneration pertained the closure of the punches in the ear pinnae [4], which are used for permanent animal marking, which is to say the holes remain for life in most laboratory murine strains. The discovery was followed by a number of studies showing enhanced regenerative responses in different organs and tissues [5-16]. It is important to notice that the ear hole closure in the MRL/MpJ mouse is not a typical example of cutaneous full-thickness wound healing but it involves the restoration of tissue architecture, which is associated with vascularisation, the regrowth of peripheral nerves and muscles, the emergence of sebaceous glands and hair follicles, as well as cartilage formation [4, 16]. The ability to close punches in the ear pinnae in the MRL/MpJ mouse was connected with several molecular features commonly observed in classical models of regeneration, i.e. in the amphibians. In particular, the regeneration process in the MRL/MpJ mouse is driven by the formation of blastema-like structure [4] and the fibroblast-like cells in the MRL/MpJ mouse show a higher accumulation in the G_2 phase of the cell cycle [17]. Another important feature is that the wound edges are remodelled by an increased activity of matrix metalloproteinases (MMPs) [18]. What is more, the adult MRL/MpJ mouse seems to retain some characteristics of embryonic metabolism with increased aerobic glycolysis and expression of stem cell transcription markers [19, 20].

The formation of blastema-like structure, is a key feature of ear hole regeneration in the MRL/MpJ mouse and it is uncommon in other laboratory murine strains [21]. The robust cell proliferation and differentiation is a hallmark of regeneration, as well as, organism development. Therefore we assumed that the mechanisms that control cell fate decision in development is very likely to play a role in regeneration. One of them is DNA methylation, an epigenetic mechanism that consists in addition of a methyl group to cytosine residues within CpG dinucleotides. The global DNA demethylation occurs shortly after fertilization and it is followed by gradual gain in DNA methylation during subsequent cell divisions and specialisation. The classical mode of action of DNA methylation assumes that DNA methylation affects gene expression through the inhibition of transcription factor binding, therefore high DNA methylation levels within the promoter regions result in decreased gene expression. A methylated cytosine serves as a docking site for chromatin remodelling complexes, which perform chromatin condensation. However, the results of genome-wide DNA methylation profiling show that the nature of DNA methylation-mediated regulation is far more complex, since the majority of tissue specific DNA methylation occurs outside of the promoter regions [22].

In our previous works we have attempted to investigate links between regenerative potential and DNA methylation profiles in three different mammalian models of regeneration: foetal skin [23], neonatal hearts [24], and the adult mouse of the MRL/MpJ strain [25]. In the last study listed, we analysed the DNA methylation profiles in the hearts, livers, and spleens of 5-week-old male mice of C57BL/6J and MRL/MpJ mouse strains [25]. As the result, we observed an increased number of hypomethylated regions in the vicinity of homeotic genes' promoters in the MRL/MpJ mouse. Although that result is very interesting, it may reflect predominantly the inter-strain differences. What is more, the examined tissue samples were obtained from relatively young 5-week-old animals. In order to narrow down the number of inter-strain differences and to exclude the possible impact of juvenile age, in the current study, we included an additional reference strain, the BALB/c, which does not close ear punches as the C57BL/6J, and we performed genome-wide DNA methylation profiling for 8-week-old females. We used females as a more suitable model because the regenerative abilities are less pronounced in males of the MRL/MpJ mouse [26]. The selected tissues were the ear pinnae, where the capacity for regeneration is markedly manifested in the MRL/MpJ, the heart where enhanced healing after cryoinjury has been reported [5, 27], the liver owing to its importance in metabolism, production of many plasma proteins including coagulation factors and intrinsic capacity for regeneration, the spleen and the bone marrow by reason of their roles immune system.

Ear pinnae hole closure in the MRL/MpJ mouse is an established model of epimorphic regeneration in adult mammals. For the first time, we present the methylome profiling of this organ and discuss the epigenetic basis of its regenerative potential.

MATERIALS AND METHODS

Animals, sample collection and processing

The tissue samples, ears, hearts, livers, spleens, bone marrow, were collected from adult, 2-month-old, females of the MRL/MpJ, C67BL/6J and BLAB/c mice, three of each strain. The tissues of MRL/MpJ and C67BL/6J mice were purchased from the Jackson Laboratories (Bar Harbor, USA), while those of BALB/c mice from the Tri-City Academic Laboratory Animal Centre - Research & Services Centre. The tissues were collected in RNALater reagent (Qiagen cat. no. 76104) and transported on dry ice. Tissues were disrupted with mortar and pestle in liquid nitrogen, and divided into two portions, one used for DNA and another for RNA extraction. DNA isolation was performed with DNeasy Blood and Tissues Kit (Qiagen, cat. no. 69504) with RNase A treatment (Qiagen, cat. no. 19101). RNA was extracted with RNeasy Mini Kit (Qiagen, cat. no. 74104) with on-column DNA digestion with RNase Free DNase Set Kit (Qiagen, cat. no. 79254).

MeDIP-chip

Methylated DNA immunoprecipitation (MeDIP) was carried out for pooled samples from three mice for each strain and tissue following microarray analysis using Mouse DNA Methylation 3x720K CpG Island Plus RefSeq Promoter Arrays (Roche, NimbleGen). The method is described in details in a previous paper [25]. Raw data was quantile normalized with background correction separately for each channel, following computing biweighted $\log_2$ ratios, determining KS Scores (with 750 bp sliding window and 500 bp spacing between nearby probes) and mapping DNA probes to genes and CpG islands with NimbleScan v. 2.6 (Roche, NimbleGen). The genomic coordinates of genes and CpG islands were mapped to mm9 genome (NCBI37/mm9 build). The data files have been deposited in Gene Expression Omnibus Database under accession number GSE89518 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89518). Gene expression profiles from the corresponding tissues were downloaded from Gene Expression Omnibus Database (GSE64624) as they were reported in a previous study focused on transcriptomic analysis of the MRL/MpJ mouse [20].

Identification of the differentially methylated regions

A region was considered as differentially methylated (DMR) if it was delineated by at least three consecutive probes displaying at least a two-fold and not less than 1.0 ($\Delta KS \geq 1.0$) difference in KS score between any two contrasted samples. The obtained DMRs were classified into the following groups: *proximal* situated from +500 bp up to -100 bp from the transcription start site, *distal* located from +5000 bp to +500 bp from the transcription start site, *intragenic* associated with a CpG island located within a primary transcript, and *intergenic* located within a CpG island located over 5000 bp upstream and over 500 bp downstream of any of primary transcripts in the analysis.

Bioinformatics tools

Gene ontology analysis was performed on the differentially methylated genes with ClueGO [28] using right-sided hypergeometric test with Benjamini-Hochberg correction. Transcription factors targeting the promoter regions of genes annotated to DMRs were predicted with iRegulon [29] using a 500 bp interval flanking transcription start sites. Principal component analysis (PCA) was carried out in R environment by performing multidimentional scaling with *cmdscale* function on the matrix of distance *dist* calculated for transposed matrix of KS Scores citation.

MDRE-qPCR

The methylation status of selected DMRs was examined using CpG methylation dependent restriction enzyme digestion with McrBC (New England Biolabs, cat. no. M0272S) for digestion of sample portion within the examined locus and TaqI (Thermoscientific, cat. no. K1451) for digestion of control sample portion outside of examined locus [30]. Approximately 100 ng of DNA was used for digestion and 4 ng of digested DNA was used for subsequent quantitative PCR reaction with FastStart Essential DNA Green Master (Roche, cat. no. 06402712001) on a LightCycler 96 (Roche). The results were presented as McrBC to TaqI ratio. The results were analysed using one-way ANOVA with *post hoc* Tukey’s multiple comparison test. The PCR primers are listed in Supplemental File 1.

RESULTS

Global DNA methylation profiles and differentially methylated regions

We used methylated DNA immunoprecipitation followed by microarray analysis (MeDIP-chip) to identify genomic regions that are marked with different DNA methylation levels between the MRL/MpJ mouse, which is able to close hole punches in the ear auricles, and two reference strains, the C57BL/6J and BALB/c, normal laboratory mice in which such holes remain for life. In our analysis we examined a selection of organs, which included hearts, livers, spleens, bone marrows and ear pinnae, that were obtained from uninjured adult females. The microarray we applied covers few intergenic regions but most known murine genes: 15,980 CpG islands and 20,404 promoter regions associated to 22,881 transcripts. As indicated by Principal Component Analysis, the DNA methylation profiles of the three strains exhibited high similarity for each organ type, except the liver, with little inter-strain differences, and were highly variable between different organs (Figure 1).

Further analysis was concentrated on the characterization of the most significant differences in DNA methylation profiles between the MRL/MpJ and the reference strains. A genomic region was considered as differentially methylated (differentially methylated region - DMR) characteristic for the MRL/MpJ mouse, if it was significantly more/less enriched for the MRL/MpJ mouse than for both the reference strains; thereafter referred as hyper- and hypomethylated, respectively (detailed criteria of DMR are given in Materials an Methods). Different numbers of DMRs were found for each of examined tissues (Table 1), with the highest number in bone marrow and the smallest in the ear. The majority of DMRs in all tissues were between 250-750 bp in length and they were located between 5000 bp and 500 bp upstream of transcription start sites, that reflected the promoter structure and the microarray design.

Genes differentially methylated in heart, liver, ear, spleen, and bone marrow

Among all DMRs, a group of 10 were common for all tissues, including 5 genes and 5 intergenic CpG islands (Table 2a). The five genes, *Akr1e1*, *Rbp7, Msgn1*, *Cpsf6*, and *Cops3,* are not associated with a single functional category. Two of them *Rbp7* and *Akr1e1* show not only differences in promoter methylation but also in expression (Table 2b). The *Rbp7* gene encoding a retinol binding protein belongs to a group of retinol metabolism genes differentially expressed in the MRL/MpJ mouse [20].

Gene ontology analysis

The results of ontology analyses for the genes connected with the DMRs found in five tissues under the study are presented in Figure 2. We decided to focus on the results obtained for the ear auricle because the manifestation of increased regeneration capacity in the MRL/MpJ mouse is the most spectacular in this organ and we were able to find potential associations between the genes differentially methylated genes in the ear pinnae and regeneration. In the ear auricle, we identified 81 DMRs, out of which 36 were hypomethylated (lower enrichment) and 45 were hypermethylated (higher enrichment) in the MRL/MpJ comparing to the two control strains. These 81 DRMs were associated with 73 genes and 6 intergenic CpG islands.

An ontology analysis for the differentially methylated regions showed a significant enrichment for the genes related to three major biological processes: apoptosis (i.e. "*positive regulation of neuron apoptotic process"*), inflammation (i.e. "*cellular response to molecule of bacterial origin*") and development (i.e. "*anterior/posterior pattern formation*", Figure 3, Table 3). The complete list of gene ontology terms for all tissues is listed in Supplemental File 2. The DNA methylation levels of selected genes were verified using methylation dependent restriction enzyme digestion followed by qPCR (Figure 4).

Transcription factors regulating genes associated with DMRs in the ear pinnae tissue

The genes that are differentially methylated may be regulated by a common transcription factor. We performed a computer prediction to analyse if the promoter regions of genes located in the vicinity of DMRs shared a DNA sequence motif, which could be targeted by a common transcription factor (Two other highly enriched transcription factors found in this prediction were Tal1, an erythroid differentiation factor and Foxa3, a pioneer factor involved chromatin opening for other regulators.

). We found that 39 out of 73 differentially methylated genes had a putative Smad1 binding site at their promoter regions. Two other highly enriched transcription factors found in this prediction were Tal1, an erythroid differentiation factor and Foxa3, a pioneer factor involved chromatin opening for other regulators.

DMRs and quantitative trait loci (QTL) in the ear pinnae tissue

The ear hole closure phenotype is a multigenic trait, which was connected with a number of QTLs (quantitative trait loci) in many different studies and strain crosses (MRL/MpJ x C57BL/6, MRL/MpJ x CAST/Ei, MRL/MpJ x SJL/J). Therefore genes associated with DMRs located within intervals of QTLs are especially interesting in the context of regeneration. The heal loci were matched with corresponding DMRs and listed in Table 5.

DMRs and gene expression

The presence of DMR within a promoter region may indicate potential differences in its regulation. We compared gene expression [20] and DMRs in the MRL/MpJ and two reference strains.

In order to obtain gene expression and DNA methylation profiles representing exactly the same tissues, we homogenized tissue samples and divided them into two portions, one used for DNA, the other for RNA extraction. The transcriptome profiling was performed using a microarray interrogating 24,200 genes, which is to say, most known protein coding genes in the mouse that correspond to a selection of 44,170 transcripts. The differentially expressed gene (DEGs) selected on the base of at least a two-fold differences in expression between the MRL/MpJ and both reference strains were listed in (Table 6).

DISCUSSION

In this study we performed global DNA methylation profiling in the tissues of the MRL/MpJ mouse, which is a model of mammalian regeneration, and two control strains, the C57BL/6J and BALB/c mice. Two reference strains were used in order to single out the most distinctive traits of DNA methylation profiles in the MRL/MpJ strain.

Genes related to apoptosis

In the ear pinnae, among the genes showing differential methylation in the MRL/MpJ mouse those related to apoptosis formed the most numerous group consisting of 20 members (Table 3). Robust apoptosis is observed in a several regeneration studies [31-33]. Apoptosis allows to control the number of cells in the area of injury, to remove the excess of cells and to remodel wound margins.

We observed a lower DNA methylation level in the promoter region of *Bcl2l11* (Figure 4). *Bcl2l11* (*Bim*) is a member of Bcl2 family of proteins involved in the regulation of apoptosis. The expression of *Bcl2l11* and that of *Bax* and *Bid*, the other members of the Bcl2 family, was reported to fall between the day 5 and 14 post injury in the blastema-like structure of the MRL/MpJ mouse[34].

Another gene from this group was *Ghrhr*, which had a lower level of DNA methylation in the promoter region (Figure 4). *Ghrhr* encodes a receptor of growth hormone releasing hormone (Ghrh). Ghrh stimulates the growth hormone synthesis and release in the pituitary gland, but it also plays an important role in peripheral organs[35]. Both mouse embryonic fibroblasts (MEFs) and wound associated fibroblasts express *Ghrhr*. The Ghrh stimulation induces the expression of α-Smooth Muscle Actin (αSMA) in fibroblasts and promotes cell migration. In addition, Ghrh and its agonist JI-38 accelerate dorsal skin wound closure [36].

Ankrd1 showed an increased DNA methylation level in the MRL/MpJ mouse. *Ankrd1* is strongly induced after excisional dorsal skin injury, reaching a maximum at 15 and 24 h post wounding, and remaining elevated for at least two weeks. *Ankrd1* contributes to wound healing by promoting angiogenesis [37]. *Ankrd1* regulates expression of several matrix metalloproteinases (MMPs), including MMP-9 and MMP-10 [38]. Wound closure and contraction is delayed in *Ankrd1*$^{-/-}$ mice at excisional dorsal skin model injury by affecting fibroblast migration[39].

A member of the group of genes related to apoptosis was *Gas2l2*, which had decreased level of DNA methylation in the MRL/MpJ mouse. *Gas2l2* encodes a protein regulating activity of adenosine receptor A_{2A} (*Adora2a*), which is responsible for increased cAMP concertation [40]. A_{2A} receptor plays a role in regulating inflammation[41]. Its activity results in a decreased production of

Tnf by macrophages and an increase in proangiogenic factors expression [42]. Pharmacological inhibition of this receptor or the knockout of *Adora2a* gene results in a decrease in scar size [43, 44].

Genes related to development

A number of genes related to anterior/posterior pattern formation were located in the proximity of DMRs in the ear auricle, which included homeotic genes *En1* and *Msgn1*, chromatin modifying genes *Yeats4*, *Ring1,* and *Mcrs1*, and *Ski,* a proto-oncogene (Table 3).

En1 (engrailed homeobox 1) and *Msgn1* (mesogenin 1), hypomethylated in the MRL/MpJ mouse, are the genes expressed during somite differentiation [45, 46]. In particular, *En1*-expressing cells give rise to dorsal dermis, epaxial muscle and interscapular brown fat[45]. This transient expression of *En1* defines also one of fibroblasts population exhibiting a unique gene expression profile found in murine skin. The population of *En1*-originated fibroblasts is low (1%) during murine embryonic development and it gradually increases with time, reaching 43% at the postnatal day 1 and 75% at that of 30, when its proportion stabilises. *En1*-originated fibroblasts play a crucial role in the secretion of extracellular matrix proteins, and therefore they are involved in wound repair process. In particular, the *En1*-originated fibroblast population have a surface marker Cd26, which is dipeptidyl-peptidase 4 (*Dpp4*). The inhibition of Cd26 with diprotin A though delayed wound healing, reduced the scar size [47]. A number of genes hypomethylated in the ear auricle of the MRL/MpJ mouse have putative En1 binding sites within their promoter regions, including *Gas2l2*, *Gjb4*, *and Hsd17b1*. What is more, it is located within one of heal loci identified for the strain (Table 5).

An increased DNA methylation was observed in the distal promoter regions of the *Ski* proto-oncogene in the MRL/MpJ mouse (Figure 4). The *Ski* gene is expressed in a number of tissues. The role of the *Ski* gene in wound healing was examined in skin wound healing in rats, where it is expressed in a vast majority of cells that contribute to this process [48]. *Ski* increases the proliferation rate of the rat fibroblasts [49]. Ectopic expression of *Ski* results in faster reepithelization and the formation of granulation tissue. Besides, a decreased macrophage migration is observed, as well as, Il6 and Tnf production in addition to a decrease in scar size [50]. *Ski* affects wound healing through the regulation of Smad3 and collagen type I formation [49]. *Ski* is regulated by *Pparδ* (peroxisome proliferator-activated receptor delta), a transcription factor involved in cell differentiation [51, 52]. Most of this effects are the results of affecting fibroblast behaviour in the wound margin. The role of *Ski* in mice has not been examined in the context of wound healing.

Genes related to inflammation

The third group of genes that were significantly enriched among those located in the vicinity of DMRs was involved in cellular response to molecules of bacterial origin, which may play a role in the regulation of inflammatory response (Table 3). This group included *Fcgr2b*, encoding an immunoglobulin receptor, *Ticam2*, encoding toll/interleukin-1 receptor domain-containing protein, *Ikbkg*, involved in modification of NF-kB signalling. Their overrepresentation may suggest the epigenetic background of differences observed in the inflammatory phase of wound healing in the MRL/MpJ mouse. *Ticam2* involved in Toll-like receptor signalling displays increased methylation and decreased expression in the MRL/MpJ mouse. Toll-like receptors interact with endogenous ligands released following inflammation, but also tissue injury, to induce expression of various cytokines, thus playing an important role in tissue regeneration[53].

DMRs and master regulators

We found that the genes located close to DMRs show enriched number of sequence motifs recognized by Smad1 transcription factor, a mediator of Tgfβ/Bmp signalling. Smad1 may be activated by Tgfb1 and Tgfb3, known as critical regulators of wound healing [54]. Although Smad1 overexpression in keratinocytes decreases their proliferation and migration and increases apoptosis, thus resulting in delayed healing of dorsal skin wounds [55], it is worth to examine the role of Tgfβ signalling in the MRL/MpJ mouse during ear closure, since its splenocytes express Tgfβ1 at high levels [56].

DMRs located within QTL intervals

Some of the genes with different DNA methylation levels that we identified in the ear pinnae are located within the quantitative trait loci (QTL) intervals; this list includes several genes described above such as *Ski*, *Ticam2*, *Gas2l2*, *and Ghrhr*. However, other genes with less obvious, but potential, role in wound healing could be found within the intervals; for example the gene of inverted formin 2 (*Inf2*) which accelerates actin filament formation and is required in extracellular matrix remodelling performed by fibroblasts[57]; *Gjb4,* encoding connexion 30.3 required for skin homeostasis, the mutations of which are associated with the presence of localised demarcated hyperkeratotic (thickened) skin lesions in humans[58, 59]; *Kcnab2* which was shown to be differentially methylated in keloids[60]; and that of Kifc3 which is required for axon growth during regeneration[61].

DMRs and differential gene expression

As a rule, increased DNA methylation in a promoter region is associated with decreased gene expression. However, we selected few inverse correlations between DNA methylation and gene expression. E. g., in the ear pinnae, out of eight genes displaying differential methylation and expression, only four showed inverse correlations between DNA methylation and expression levels (Table 6). However, we should accentuate that we investigated only the top-ranked differences in gene expression and DNA methylation, and two reference strains were used in the comparison.

Therefore we singled out a small number of the most distinctive DMRs connected with changes in gene expression levels in the MRL/MpJ mouse. This narrow selection does not reflect global correlation between DNA methylation and gene expression in the examined tissues. It is also worth stressing that DNA methylation is only one of mechanisms involved in transcriptional repression and gene expression also requires induction.

CONCLUSIONS

Although ear hole closure in the MRL/MpJ mouse is a recognized mammalian regeneration model, the epigenetic aspects of this phenomenon remain unknown. Here we present genome-wide DNA methylation profiles of the ear pinnae, which can serve as a starting point for exploiting this epigenetic mechanism in regulating ear hole closure model of injury.

The analysis of DNA methylation profiles identified a short list of DMRs in the ear pinnae, which distinguishes the MRL/MpJ mouse, the strain exhibiting enhanced regenerative abilities, from the normal reference strains C57BL/6J and BALB/c mice. The genes associated with the DMRs in the ear pinnae are involved in molecular processes critical for wound healing. What is more, many of them are located in the QTL intervals of the ear healing trait. The predominant part of differentially methylated genes are not differentially expressed in uninjured tissues, we examined. However, it should be taken into consideration that the differences in DNA methylation are possible to impact gene expression following injury.

SUMMARY POINTS

- Adult mice of the MRL/MpJ strain are known for enhanced regenerative capacity in different tissues
- Ear-pinnae hole closure is a particular manifestation of the regenerative abilities in the MRL/MpJ mouse
- The study interrogates the epigenetic basis of the regeneration potential in the MRL/MpJ mouse.
- Methylome profiling was performed in ear pinnae, bone marrow, spleen, liver and heart of the MRL/MpJ mouse and two reference strains C567BL/6 and BALB/c using MeDIP and microarray analysis
- A number of DMRs distinguishing the MRL/MpJ mouse from the references were identified in ear pinnae and other examined tissues
- The genes located in the vicinity of DMRs are related to development, inflammation, and apoptosis.
- The promoter regions of genes located in the vicinity of DMRs in the ear pinnae are enriched in Smad1 transcription factor binding sites.
- Many genes located in the vicinity of DMRs in the ear pinnae are located within QTL intervals of ear hole closure loci.
- The results indicate potential epigenetic determinants of the regenerative phenomenon of the MRL/MpJ mouse.

Competing financial interests

The authors declare no conflict of interests.

Ethical Statement

The ethical approval for the collection of murine samples no. 12/2014 was issued by the Local Ethics Commission for Experimentation on Animals at the Medical University of Gdansk, Poland.

Authors' Contributions

BG - tissue processing and DNA extraction, the analysis design and microarray data analysis, qPCR verification of microarray results, manuscript preparation, AR – cDNA labelling, microarray experiments and data processing; PM – preliminary microarray data analysis, PS – concept and design of the study; manuscript revising.

References:

1. Yates CC, Hebda P, Wells A. Skin wound healing and scarring: fetal wounds and regenerative restitution. *Birth defects research. Part C, Embryo today : reviews* 96(4), 325-333 (2012).
2. Porrello ER, Olson EN. A neonatal blueprint for cardiac regeneration. *Stem cell research* doi:10.1016/j.scr.2014.06.003 (2014).
3. Saunders NR, Kitchener P, Knott GW, Nicholls JG, Potter A, Smith TJ. Development of walking, swimming and neuronal connections after complete spinal cord transection in the neonatal opossum, Monodelphis domestica. *The Journal of neuroscience : the official journal of the Society for Neuroscience* 18(1), 339-355 (1998).
4. Clark LD, Clark RK, Heber-Katz E. A new murine model for mammalian wound repair and regeneration. *Clinical immunology and immunopathology* 88(1), 35-45 (1998).
5. Leferovich JM, Bedelbaeva K, Samulewicz S *et al*. Heart regeneration in adult MRL mice. *Proceedings of the National Academy of Sciences of the United States of America* 98(17), 9830-9835 (2001).
6. Gourevitch DL, Clark L, Bedelbaeva K, Leferovich J, Heber-Katz E. Dynamic changes after murine digit amputation: the MRL mouse digit shows waves of tissue remodeling, growth, and apoptosis. *Wound repair and regeneration : official publication of the Wound Healing Society [and] the European Tissue Repair Society* 17(3), 447-455 (2009).
7. Ueno M, Lyons BL, Burzenski LM *et al*. Accelerated wound healing of alkali-burned corneas in MRL mice is associated with a reduced inflammatory signature. *Investigative ophthalmology & visual science* 46(11), 4097-4106 (2005).
8. Chadwick RB, Bu L, Yu H *et al*. Digit tip regrowth and differential gene expression in MRL/Mpj, DBA/2, and C57BL/6 mice. *Wound repair and regeneration : official publication of the Wound Healing Society [and] the European Tissue Repair Society* 15(2), 275-284 (2007).
9. Turner NJ, Johnson SA, Badylak SF. A histomorphologic study of the normal healing response following digit amputation in C57bl/6 and MRL/MpJ mice. *Archives of histology and cytology* 73(2), 103-111 (2010).
10. Kostyk SK, Popovich PG, Stokes BT, Wei P, Jakeman LB. Robust axonal growth and a blunted macrophage response are associated with impaired functional recovery after spinal cord injury in the MRL/MpJ mouse. *Neuroscience* 156(3), 498-514 (2008).
11. Thuret S, Thallmair M, Horky LL, Gage FH. Enhanced functional recovery in MRL/MpJ mice after spinal cord dorsal hemisection. *PloS one* 7(2), e30904 (2012).
12. Xia H, Krebs MP, Kaushal S, Scott EW. Enhanced retinal pigment epithelium regeneration after injury in MRL/MpJ mice. *Experimental eye research* 93(6), 862-872 (2011).
13. Tucker B, Klassen H, Yang L, Chen DF, Young MJ. Elevated MMP Expression in the MRL Mouse Retina Creates a Permissive Environment for Retinal Regeneration. *Investigative ophthalmology & visual science* 49(4), 1686-1695 (2008).
14. Lalley AL, Dyment NA, Kazemi N *et al*. Improved biomechanical and biological outcomes in the MRL/MpJ murine strain following a full-length patellar tendon injury. *Journal of orthopaedic research : official publication of the Orthopaedic Research Society* doi:10.1002/jor.22928 (2015).
15. Fitzgerald J, Rich C, Burkhardt D, Allen J, Herzka AS, Little CB. Evidence for articular cartilage regeneration in MRL/MpJ mice. *Osteoarthritis and cartilage / OARS, Osteoarthritis Research Society* 16(11), 1319-1326 (2008).
16. Buckley G, Metcalfe AD, Ferguson MW. Peripheral nerve regeneration in the MRL/MpJ ear wound model. *Journal of anatomy* 218(2), 163-172 (2011).
17. Bedelbaeva K, Snyder A, Gourevitch D *et al*. Lack of p21 expression links cell cycle control and appendage regeneration in mice. *Proceedings of the National Academy of Sciences of the United States of America* 107(13), 5845-5850 (2010).

18. Gourevitch D, Clark L, Chen P, Seitz A, Samulewicz SJ, Heber-Katz E. Matrix metalloproteinase activity correlates with blastema formation in the regenerating MRL mouse ear hole model. *Developmental dynamics : an official publication of the American Association of Anatomists* 226(2), 377-387 (2003).
19. Naviaux RK, Le TP, Bedelbaeva K *et al*. Retained features of embryonic metabolism in the adult MRL mouse. *Molecular genetics and metabolism* 96(3), 133-144 (2009).
20. Podolak-Popinigis J, Gornikiewicz B, Ronowicz A, Sachadyn P. Transcriptome profiling reveals distinctive traits of retinol metabolism and neonatal parallels in the MRL/MpJ mouse. *BMC genomics* 16 926 (2015).
21. Li X, Gu W, Masinde G *et al*. Genetic control of the rate of wound healing in mice. *Heredity* 86(Pt 6), 668-674 (2001).
22. Koh KP, Rao A. DNA methylation and methylcytosine oxidation in cell fate decisions. *Current opinion in cell biology* 25(2), 152-161 (2013).
23. Podolak-Popinigis J, Ronowicz A, Dmochowska M, Jakubiak A, Sachadyn P. The methylome and transcriptome of fetal skin: implications for scarless healing. *Epigenomics* 8(10), 1331-1345 (2016).
24. Gornikiewicz B, Ronowicz A, Krzeminski M, Sachadyn P. Changes in gene methylation patterns in neonatal murine hearts: Implications for the regenerative potential. *BMC genomics* 17 231 (2016).
25. Gornikiewicz B, Ronowicz A, Podolak J, Madanecki P, Stanislawska-Sachadyn A, Sachadyn P. Epigenetic basis of regeneration: analysis of genomic DNA methylation profiles in the MRL/MpJ mouse. *DNA research : an international journal for rapid publication of reports on genes and genomes* 20(6), 605-621 (2013).
26. Blankenhorn EP, Troutman S, Clark LD, Zhang XM, Chen P, Heber-Katz E. Sexually dimorphic genes regulate healing and regeneration in MRL mice. *Mammalian genome : official journal of the International Mammalian Genome Society* 14(4), 250-260 (2003).
27. Naseem RH, Meeson AP, Michael Dimaio J *et al*. Reparative myocardial mechanisms in adult C57BL/6 and MRL mice following injury. *Physiological genomics* 30(1), 44-52 (2007).
28. Bindea G, Mlecnik B, Hackl H *et al*. ClueGO: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks. *Bioinformatics (Oxford, England)* 25(8), 1091-1093 (2009).
29. Janky R, Verfaillie A, Imrichova H *et al*. iRegulon: from a gene list to a gene regulatory network using large motif and track collections. *PLoS computational biology* 10(7), e1003731 (2014).
30. Krygier M, Podolak-Popinigis J, Limon J, Sachadyn P, Stanislawska-Sachadyn A. A simple modification to improve the accuracy of methylation-sensitive restriction enzyme quantitative polymerase chain reaction. *Analytical biochemistry* 500 88-90 (2016).
31. Tseng AS, Adams DS, Qiu D, Koustubhan P, Levin M. Apoptosis is required during early stages of tail regeneration in Xenopus laevis. *Developmental biology* 301(1), 62-69 (2007).
32. Bergmann A, Steller H. Apoptosis, stem cells, and tissue regeneration. *Science signaling* 3(145), re8 (2010).
33. Li F, Huang Q, Chen J *et al*. Apoptotic cells activate the "phoenix rising" pathway to promote wound healing and tissue regeneration. *Science signaling* 3(110), ra13 (2010).
34. Metcalfe AD, Willis H, Beare A, Ferguson MW. Characterizing regeneration in the vertebrate ear. *Journal of anatomy* 209(4), 439-446 (2006).
35. Granata R. Peripheral activities of growth hormone-releasing hormone. *Journal of endocrinological investigation* doi:10.1007/s40618-016-0440-x (2016).
36. Dioufa N, Schally AV, Chatzistamou I *et al*. Acceleration of wound healing by growth hormone-releasing hormone and its agonists. *Proceedings of the National Academy of Sciences of the United States of America* 107(43), 18611-18615 (2010).

37. Shi Y, Reitmaier B, Regenbogen J *et al*. CARP, a cardiac ankyrin repeat protein, is up-regulated during wound healing and induces angiogenesis in experimental granulation tissue. *The American journal of pathology* 166(1), 303-312 (2005).
38. Almodovar-Garcia K, Kwon M, Samaras SE, Davidson JM. ANKRD1 acts as a transcriptional repressor of MMP13 via the AP-1 site. *Molecular and cellular biology* 34(8), 1500-1511 (2014).
39. Samaras SE, Almodovar-Garcia K, Wu N, Yu F, Davidson JM. Global deletion of Ankrd1 results in a wound-healing phenotype associated with dermal fibroblast dysfunction. *The American journal of pathology* 185(1), 96-109 (2015).
40. Wu YC, Lai HL, Chang WC, Lin JT, Liu YJ, Chern Y. A novel Galphas-binding protein, Gas-2 like 2, facilitates the signaling of the A2A adenosine receptor. *Biochimica et biophysica acta* 1833(12), 3145-3154 (2013).
41. Arasa J, Martos P, Terencio MC, Valcuende-Cavero F, Montesinos MC. Topical application of the adenosine A2A receptor agonist CGS-21680 prevents phorbol-induced epidermal hyperplasia and inflammation in mice. *Experimental dermatology* 23(8), 555-560 (2014).
42. Macedo L, Pinhal-Enfield G, Alshits V, Elson G, Cronstein BN, Leibovich SJ. Wound healing is impaired in MyD88-deficient mice: a role for MyD88 in the regulation of wound healing by adenosine A2A receptors. *The American journal of pathology* 171(6), 1774-1788 (2007).
43. Perez-Aso M, Chiriboga L, Cronstein BN. Pharmacological blockade of adenosine A2A receptors diminishes scarring. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology* 26(10), 4254-4263 (2012).
44. Hu X, Ran H, Dechang W, Yibing W, Yongqiang F, Qiang L. Absence of the adenosine A(2A) receptor attenuates hypertrophic scarring in mice. *Journal of burn care & research : official publication of the American Burn Association* 34(3), e161-167 (2013).
45. Atit R, Sgaier SK, Mohamed OA *et al*. Beta-catenin activation is necessary and sufficient to specify the dorsal dermal fate in the mouse. *Developmental biology* 296(1), 164-176 (2006).
46. Chalamalasetty RB, Garriock RJ, Dunty WC, Jr. *et al*. Mesogenin 1 is a master regulator of paraxial presomitic mesoderm differentiation. *Development (Cambridge, England)* 141(22), 4285-4297 (2014).
47. Rinkevich Y, Walmsley GG, Hu MS *et al*. Skin fibrosis. Identification and isolation of a dermal lineage with intrinsic fibrogenic potential. *Science (New York, N.Y.)* 348(6232), aaa2151 (2015).
48. Liu X, Zhang E, Li P *et al*. Expression and possible mechanism of c-ski, a novel tissue repair-related gene during normal and radiation-impaired wound healing. *Wound repair and regeneration : official publication of the Wound Healing Society [and] the European Tissue Repair Society* 14(2), 162-171 (2006).
49. Liu X, Li P, Chen XY, Zhou YG. c-Ski promotes skin fibroblast proliferation but decreases type I collagen: implications for wound healing and scar formation. *Clinical and experimental dermatology* 35(4), 417-424 (2010).
50. Li P, Liu P, Xiong RP *et al*. Ski, a modulator of wound healing and scar formation in the rat skin and rabbit ear. *The Journal of pathology* 223(5), 659-671 (2011).
51. Li J, Li P, Zhang Y *et al*. Upregulation of ski in fibroblast is implicated in the peroxisome proliferator--activated receptor delta-mediated wound healing. *Cellular physiology and biochemistry : international journal of experimental cellular physiology, biochemistry, and pharmacology* 30(4), 1059-1071 (2012).
52. Giordano Attianese GM, Desvergne B. Integrative and systemic approaches for evaluating PPARbeta/delta (PPARD) function. *Nuclear receptor signaling* 13 e001 (2015).
53. Zhang Z, Schluesener HJ. Mammalian toll-like receptors: from endogenous ligands to tissue regeneration. *Cellular and molecular life sciences : CMLS* 63(24), 2901-2907 (2006).

54. Shah M, Foreman DM, Ferguson MW. Neutralisation of TGF-beta 1 and TGF-beta 2 or exogenous addition of TGF-beta 3 to cutaneous rat wounds reduces scarring. *Journal of cell science* 108 (Pt 3) 985-1002 (1995).
55. Lewis CJ, Mardaryev AN, Poterlowicz K *et al*. Bone morphogenetic protein signaling suppresses wound-induced skin repair by inhibiting keratinocyte proliferation and migration. *The Journal of investigative dermatology* 134(3), 827-837 (2014).
56. Kench JA, Russell DM, Fadok VA *et al*. Aberrant wound healing and TGF-beta production in the autoimmune-prone MRL/+ mouse. *Clinical immunology (Orlando, Fla.)* 92(3), 300-310 (1999).
57. Skau CT, Plotnikov SV, Doyle AD, Waterman CM. Inverted formin 2 in focal adhesions promotes dorsal stress fiber and fibrillar adhesion formation to drive extracellular matrix assembly. *Proceedings of the National Academy of Sciences of the United States of America* 112(19), E2447-2456 (2015).
58. Kokotas H, Papagiannaki K, Grigoriadou M, Petersen MB, Katsarou A. Erythrokeratodermia variabilis: report of two cases and a novel missense variant in GJB4 encoding connexin 30.3. *European journal of dermatology : EJD* 22(2), 182-186 (2012).
59. Xu J, Nicholson BJ. The role of connexins in ear and skin physiology - functional insights from disease-associated mutations. *Biochimica et biophysica acta* 1828(1), 167-178 (2013).
60. Garcia-Rodriguez L, Jones L, Chen KM, Datta I, Divine G, Worsham MJ. Causal network analysis of head and neck keloid tissue identifies potential master regulators. *The Laryngoscope* doi:10.1002/lary.25958 (2016).
61. Gumy LF, Chew DJ, Tortosa E *et al*. The kinesin-2 family member KIF3C regulates microtubule dynamics and is required for axon growth and regeneration. *The Journal of neuroscience : the official journal of the Society for Neuroscience* 33(28), 11329-11345 (2013).
62. Cheverud JM, Lawson HA, Funk R, Zhou J, Blankenhorn EP, Heber-Katz E. Healing quantitative trait loci in a combined cross analysis using related mouse strain crosses. *Heredity* 108(4), 441-446 (2012).
63. Mcbrearty BA, Clark LD, Zhang XM, Blankenhorn EP, Heber-Katz E. Genetic analysis of a mammalian wound-healing trait. *Proceedings of the National Academy of Sciences of the United States of America* 95(20), 11792-11797 (1998).
64. Masinde GL, Li X, Gu W, Davidson H, Mohan S, Baylink DJ. Identification of wound healing/regeneration quantitative trait loci (QTL) at multiple time points that explain seventy percent of variance in (MRL/MpJ and SJL/J) mice F2 population. *Genome research* 11(12), 2027-2033 (2001).

Table 1 Size and position distributions of DMRs.

		Ear	Bone Marrow	Liver	Heart	Spleen	Common
DNA methylation level	Hypometylated	**36**	72	46	75	114	2
	Hypermethylated	**45**	209	122	116	57	8
Genes	Hypometylated	**34**	56	44	69	92	2
	Hypermethylated	**40**	198	114	107	38	3
Size	<250	**6**	23	12	11	14	-
	250-500	**20**	91	51	48	46	-
	500-750	**24**	84	59	51	47	6
	>750	**31**	83	46	50	64	4
Position from TSS	-5000 to -500 bp	**48**	130	84	91	96	3
	-500 to +100 bp	**20**	90	51	41	41	2
	Intragenic	**7**	38	24	16	18	-
	Intergenic CGI	**6**	23	9	12	16	5

Table 2 DMRs characteristic of the MRL/MpJ mouse common for all examined tissues.

A. Genomic coordinates and methylation levels in the DMRs

				Bone marrow			Liver			Ear			Heart			Spleen		
Gene	**Chr**	**Start**	**End**	**B6**	**Bc**	**M**	**B6**	**Bc**	**M**	**B6**	**Bc**	**M**	**B6**	**Bc**	**M**	**B6**	**Bc**	**M**
Rbp7	chr4	148830650	148831853	1.7	1.8	0.5	3.2	1.8	0.5	2.5	1.9	0.5	2.4	2.0	0.3	2.4	2.5	0.4
CGI(*Trim43a*)	chr9	88494209	88494858	0.2	0.0	1.8	0.5	0.0	1.7	0.1	0.0	1.4	0.4	0.0	1.7	0.1	0.0	1.2
CGI(*Trim43c*)	chr9	88753512	88754171	0.0	0.0	1.8	0.2	0.0	1.7	0.1	0.0	1.3	0.2	0.0	1.9	0.1	0.0	1.3
CGI(*Trim43b*)	chr9	88961199	88961948	0.3	0.0	2.2	0.7	0.0	1.8	0.5	0.0	1.7	0.5	0.0	2.3	0.2	0.0	1.9
CG I(*Rasa2*)	chr9	96437157	96437816	1.1	1.2	4.3	0.9	0.8	4.7	0.2	0.5	3.9	0.7	0.7	4.1	1.0	1.8	4.1
Cpsf6	chr10	116814283	116815261	0.5	0.3	2.9	0.5	0.1	1.6	0.2	0.1	1.2	0.5	0.2	2.2	0.1	0.2	1.6
Cops3	chr11	59654752	59655702	0.2	0.7	3.1	0.9	0.6	2.7	0.3	0.4	1.5	0.4	0.5	3.0	0.5	0.5	1.9
Msgn1	chr12	11218036	11218673	2.3	2.4	0.2	2.0	1.8	0.3	1.3	1.6	0.0	2.2	2.0	0.8	1.7	1.5	0.1
Akr1e1	chr13	4607703	4608482	0.0	0.0	3.5	0.0	0.0	2.4	0.0	0.0	3.1	0.0	0.0	2.4	0.0	0.0	2.7
CGI(*Pdcd2*)	chr17	15673304	15673974	0.1	0.2	1.7	0.1	0.2	1.9	0.1	0.2	2.1	0.3	0.1	2.1	0.1	0.1	2.0
			SCALE	0.0	1.0	2.0	3.0	4.0	5.0									

If DMR was located within intergenic CGI the name of the closest gene was given in the brackets. B6 –C57BL/6J, Bc – BALB/c, M – MRL/MpJ.

The genomic coordinates were mapped to mm9 genome (NCBI37/mm9 build).

B. Expression and functions of differentially methylated genes

			Gene expression fold difference (microarray data)									
			Bone marrow		Liver		Ear		Heart		Spleen	
Gene symbol	**Full name**	**Function**	**M/Bc**	**M/B6**	**M/Bc**	**M/B6**	**M/Bc**	**M/B6**	**M/Bc**	**M/B6**	**M/Bc**	**M/B6**
Akr1e1	aldo-keto reductase family 1	reduces 1,5-anhydro-D-glucitol, a monosaccharide decreased in hyperglycemia	**0.25**	**0.19**	**0.18**	**0.15**	**0.18**	**0.14**	**0.41**	0.26	0.13	0.13
Cops3	COP9 signalosome subunit 3	COP9 signalosome complex regulates protein degradation	**1.51**	**1.07**	**1.11**	**0.76**	**0.72**	**0.83**	**1.21**	0.96	0.66	0.65
Cpsf6	cleavage and polyadenylation specific factor 6	mRNA cleavage and polyadenylation	**0.85**	**0.78**	**2.03**	**0.84**	**0.68**	**1.23**	**0.85**	0.66	0.57	0.61
Msgn1	mesogenin 1	homeotic gene involved in mesoderm specification	**0.69**	**1.22**	**0.80**	**0.79**	**0.99**	**0.75**	**1.87**	1.19	0.25	0.76
Rbp7	retinol binding protein 7	a carrier involved in retinol transport	**1.26**	**1.60**	**5.75**	**2.75**	**2.94**	**5.01**	**5.06**	2.45	1.20	0.64
		SCALE	**0.25**	**0.50**	**0.66**	**1.00**	**1.50**	**2.00**	**4.00**			

B6 –C57BL/6J, Bc – BALB/c, M – MRL/MpJ.

Table 3 Genes located in the vicinity of DMRs characteristic for MRL/MpJ mouse in the ear pinnae and associated with functional categories.

Functional cluster	-log(BH)	Genes	Hypomethylated	Hypermethylated
positive regulation of neuron apoptotic process	1.92	20	*Bcl2l11, Fcgr2b, Gas2l2, Ghrhr, Hsd17b1, Kcnab2, Kifc3, Mid1, Nos1ap, Osbpl7, Tnf*	*Akr1e1, Ankrd1, Cnga3, Cops3, Cyp2d22, Npc1l1, Pcsk9, Ticam2, Vapb*
microtubule binding	1.91	10	*Bcl2l11, Gas2l2, Inf2, Kifc3, Tnf*	*Ankrd1, Npc1l1, Pxk, Tnnt2, Vapb*
anterior/posterior pattern specification	1.82	8	*Bcl2l11, En1, Mcrs1, Msgn1, Ring1*	*Cnga3, Ski, Yeats4*
hexosaminidase activity	1.87	3	*Naga*	*4931440L10Rik, Maneal*
leukocyte homeostasis	1.93	3	*Bcl2l11, Fcgr2b*	*Ikbkg*
cellular response to molecule of bacterial origin	1.81	8	*Fcgr2b, Osbpl7, Tnf*	*Akr1e1, Ankrd1, Ikbkg, Pcsk9, Ticam2*
negative regulation of protein complex disassembly	1.99	6	*Gas2l2, Mid1, Osbpl7, Tnf*	*Akr1e1, Pcsk9*
oxidoreductase activity	1.74	3	*Hsd17b1, Kcnab2*	*Akr1e1*
regulation of neuron death	1.70	7	*Bcl2l11, Kcnab2, Nos1ap, Tnf*	*Cnga3, Htra4, Pcsk9*
response to insulin	1.59	3	*Ghrhr, Prlh*	*Pcsk9*

BH is a p-value of the term after Benjamini-Hochberg correction. The categories discussed in the text are bolded. The genes showing increased DNA methylation and decreased expression in the MRL/MpJ mouse are distinguished by red font.

Table 4 Transcription factors predicted to target the promoter regions associated with the DMRs in the ear pinnae of the MRL/MpJ mouse.

Transcription factor	NES	Genes	Motifs	Hypomethylated	Hypermethylated
Smad1	4.82	39	9	*BC018465, Bcl2l11, Bsnd, Cyp4f14, En1, Fcgr2b, Gas2l2, Ghrhr, H1foo, Hsd17b1, Kifc3, Mid1, Msgn1, Optc, Prlh, Rbp7, Rya3, Slc28a1, Tmem40, Tnf, Trfr2, Zc3h12d*	*Ankrd1, Arl1, Cnga3, Cops3, Eif1b, Fam18b, Gjb4, Gm7120, Inf2, Mcm8, Nos1ap, Npc1l1, Pibf1, Pxk, Tnnt2, Tpd52, Zfp428*
Tal1	4.79	30	18	*BC018465, Bcl2l11, Bsnd, Cyp4f14, Fcgr2b, Gas2l2, Ghrhr, Hsd17b1, Inf2, Kifc3, Mid1, Msgn1, Optc, Prlh, Rbp7, Tmem40, Tnf, Uox, Zc3h12d*	*4931440L10Rik, Ankrd1, Gjb4, Gm5148, Gpr50, Inf2, Krtap14, Nos1ap, Npc1l1, Tnnt2, Tpd52, Tpd52, Uox, Zfp428*
Foxa3	4.20	16	7	*Bcl2l11, Bsnd, En1, Gas2l2, Ghrhr, Kcnab2, Mid1, Msgn1, Optc, Uox*	*Ankrd1, Gjb4, Ikbkg, Tpd52, Tpd52, Uox, Vapb, Zfp428*
Meis1	4.19	38	5	*BC018465, Bsnd, Cyp4f14, En1, Fcgr2b, Gas2l2, Ghrhr, Hsd17b1, Kifc3, Mid1, Msgn1, Optc, Osbpl7, Prlh, Rya3, Slc28a1, Tmem40, Tnf, Uox, Zc3h12d*	*4931440L10Rik, Ankrd1, Arl1, Cnga3, D030016E14Rik, Fam18b, Gjb4, Gm5148, Gpr50, Ikbkg, Inf2, Krtap14, Nos1ap, Npc1l1, Pxk, Tbrg1, Tnnt2, Tpd52, Uox*
Smap2	4.11	16	3	*BC018465, Bsnd, Cyp4f14, Gas2l2, Hsd17b1, Kifc3, Mid1, Msgn1, Optc, Slc28a1, Tmem40*	*Gjb4, Pibf1, Pxk, Tnnt2, Tpd52*
En1	3.83	29	9	*Bsnd, Cyp4f14, En1, Gas2l2, Hsd17b1, Kcnab2, Kifc3, Mcrs1, Mid1, Msgn1, Osbpl7, Rbp7, Uox*	*4931440L10Rik, Ankrd1, Cnga3, Cops3, Cpsf6, Eif1b, Krtap14, Nos1ap, Npc1l1, Pcsk9, Pibf1, Tbrg1, Tnnt2, Tpd52, Uox, Vapb, Zfp428*
Tbx5	3.65	15	3	*BC018465, Bsnd, Cyp4f14, Mid1, Msgn1, Prlh, Rya3*	*Ankrd1, Cops3, Cpsf6, Fam18b, Gjb4, Gpr50, Nos1ap, Tpd52*
Jazf1	3.45	27	2	*BC018465, Bcl2l11, Cyp4f14, En1, Fcgr2b, Ghrhr, Hsd17b1, Mid1, Msgn1, Optc, Prlh, Ring1, Tnf, Trfr2, Zc3h12d*	*Cnga3, Cpsf6, Fam18b, Gjb4, Gpr50, Htra4, Krtap14, Nos1ap, Npc1l1, Pibf1, Tnnt2, Tpd52*
Nfia	3.41	9	2	*BC018465, Cyp4f14, En1, Kifc3, Optc, Tmem40*	*Gjb4, Ikbkg, Krtap14*
Neurod1	3.40	10	2	*En1, Kcnab2, Mid1, Optc, Rbp7, Tnf, Uox*	*4931440L10Rik, Gjb4, Tnnt2, Uox*
Gata5	3.39	25	4	*BC018465, Bcl2l11, Bsnd, Cyp4f14, En1, Ghrhr, Hsd17b1, Mid1, Msgn1, Optc, Osbpl7, Prlh, Zc3h12d*	*4931440L10Rik, Ankrd1, Cnga3, Fam105b, Gjb4, Gpr50, Krtap14, Nos1ap, Npc1l1, Rgs4, Tnnt2, Tpd52*
Six2	3.19	13	4	*Bsnd, En1, Hsd17b1, Kifc3, Mid1, Msgn1*	*Ankrd1, Cnga3, Gjb4, Nos1ap, Tpd52, Vapb, Zfp428*
Gbx2	3.01	7	1	*Kifc3, Msgn1, Optc, Slc28a1, Uox*	*Ankrd1, Rgs4, Uox*

NES – normalised enrichment score. Motifs – number of motifs associated with the given transcription factor. The genes showing decreased DNA methylation and enhanced expression in the MRL/MpJ mouse are distinguished by green font.

Table 5 Genes associated with DMRs in the ear pinnae and located within QTL intervals.

Gene	chr	cM	MeDIP			Cheverud et al., 2012 [62]	McBrearty et al., 1998 [63]	Masinde et al., 2001 [64]	Blankenhorn et al., 2003 [26]
			B6	**Bc**	**M**				
Prlh	1	45.81	1.9	2.9	0.6			Sth1	
En1	1	52.74	1.8	2.1	0.7			Sth1	
Ren2	1	57.91	2.1	2.5	0.8			Sth1	
Optc	1	58.02	3.6	3.7	1.6			Sth1	
4931440L10Rik	1	58.24	1.3	1.0	2.6			Sth1	
Tnnt2	1	59.32	1.0	0.9	2.9			Sth1	
Uox	3	72.09	2.0	2.0	0.8			Sth2	
Uox	3	72.09	0.3	0.2	2.0			Sth2	
Pcsk9	4	49.67	0.9	1.1	2.4			Sth4	
Bsnd	4	49.67	2.5	1.9	0.7			Sth4	
Maneal	4	57.92	0.7	0.6	2.6			Sth4	
Gjb4	4	61.51	1.9	1.5	5.1	Heal8		Sth4	
Rbp7	4	79.40	2.5	1.9	0.5	Heal8			Heal8
Kcnab2	4	83.08	2.3	2.4	1.1	Heal8			Heal8
Ski	4	86.17	0.1	0.4	1.6	Heal8			Heal8
Ghrhr	6	27.38	2.0	1.9	0.8			Sth5	
Tmem40	6	53.68	2.5	2.3	1.0			Sth5	
H1foo	6	53.72	1.9	1.9	0.7			Sth5	
Slc28a1	7	45.71	1.5	1.8	0.5			Sth6	Heal6
Lonrf1	8	23.05	0.6	0.7	1.8		Heal1		
D030016E14Rik	8	26.86	0.6	0.0	2.1		Heal1		
Tm6sf2	8	34.15	1.3	1.4	0.2		Heal1		
Kifc3	8	47.12	2.3	2.8	1.1	Heal1	Heal1		
Gm8884	9	26.42	3.5	2.6	1.0			Sth8	
Eif1b	9	71.67	0.7	0.6	2.0	Sth9b			
Gas2l2	11	50.33	2.9	3.2	1.3	Heal10			
Gas2l2	11	50.33	1.9	1.8	0.6	Heal10			
Osbpl7	11	60.75	1.9	2.1	0.7	Heal10			Heal10
Hsd17b1	11	64.17	1.8	1.7	0.6	Heal10			
Inf2	12	61.20	0.7	0.7	1.9		Heal5		Heal5
Btbd6	12	61.50	2.5	2.1	0.9		Heal5		Heal5
Akr1e1	13	2.57	0.0	0.0	3.1		Heal2		
Gm7120	13	67.25	1.7	1.3	3.7		Heal3		
Naga	15	38.56	2.7	2.0	1.0		Heal4		Heal4
Cyp2d22	15	38.57	0.4	0.9	2.3		Heal4		Heal4
Ticam2	18	24.65	0.6	0.4	3.7	Heal9			

MeDIP – methylation score, chr – chromosome, cM – centimorgan, B6 –C57BL/6J, Bc – BALB/c, M – MRL/MpJ

Table 6 DMR associated genes showing at least a twofold difference in expression level.

		MeDIP			mRNA			
Tissue	**Gene**	**B6**	**Bc**	**M**	**B6**	**Bc**	**M**	**DMR localisation**
Bone marrow	***2610109H07Rik***	0.9	0.7	2.1	260	854	128	distal
	Akr1e1	0.0	0.0	3.5	533	432	91	proximal
	Cd72	1.0	1.8	3.8	7919	9353	3919	distal
	Fcamr	0.7	1.2	2.4	140	160	20	proximal
	Gm16515	0.6	0.7	2.0	2550	2077	6913	distal
	Gpr132	1.1	1.1	3.2	461	353	119	distal
	H2-Aa	1.7	1.9	0.4	103	98	38	distal
	Nlrp3	2.2	2.0	0.7	1162	1630	569	proximal
	Ntm	0.3	0.9	2.0	95	119	580	proximal
	Phlda3	1.8	1.8	0.4	89	145	341	Distal
	Plscr4	0.5	0.2	2.2	84	102	38	Distal
	Spata16	3.1	3.4	0.3	21	28	74	Distal
	Ticam2	0.6	0.4	2.1	1033	1323	174	Proximal
	Tnni1	1.3	1.3	2.7	532	276	1387	Distal
Liver	***2510049J12Rik***	0.7	0.1	2.0	135	172	40	Distal
	Akr1e1	0.0	0.0	2.4	4470	3786	673	Proximal
	Gpr56	0.2	0.9	2.2	1050	1028	3605	Proximal
	Slc1a2	0.6	0.5	1.6	6574	4546	1438	Distal
	Ttc39a	2.4	2.2	0.8	219	335	3205	Distal
Ears	***Akr1e1***	0.0	0.0	3.1	918	691	129	Proximal
	***Bpifb5* (BC018465)**	2.4	2.5	1.0	27	24	86	Distal
	Fcgr2b	1.7	2.2	0.4	146	99	43	Proximal
	Krtap14	1.2	1.2	3.1	56	6	5171	intragenic
	Optc	3.6	3.7	1.6	161	159	57	intragenic
	Rbp7	2.5	1.9	0.5	166	267	805	distal
	Ticam2	0.6	0.4	3.7	120	136	49	proximal
	Zfp428	1.0	0.8	3.1	42	47	95	distal
Heart	***3110035E14Rik***	3.2	2.4	0.5	21	57	133	proximal
	Acaa1b	1.2	1.2	2.5	146	242	602	proximal
	Agr2	2.4	1.9	0.8	26	25	68	proximal
	Akr1e1	0.0	0.0	2.4	1951	1216	501	proximal
	Alox5	1.0	1.0	2.3	2453	1422	432	proximal
	Capg	0.7	1.0	2.0	2030	4190	536	proximal
	Fcgr2b	3.3	2.4	0.6	48	115	16	proximal
	Lnx1	1.9	1.6	0.5	1916	2027	876	distal
	Metapl1	0.7	0.8	1.9	2528	2283	710	distal
	Rbp7	2.4	2.0	0.3	2367	1144	6062	distal
	Tmem179	1.2	1.5	3.1	2035	1711	538	proximal
Spleen	***Akr1e1***	0.0	0.0	2.7	538	536	72	proximal
	Capg	2.3	2.6	1.2	12070	13476	4015	distal
	Cldn13	3.2	3.4	1.4	4588	4633	1126	proximal
	Cnga3	0.7	1.0	2.3	41	46	13	distal
	D030028A08Rik	1.8	1.8	0.6	470	549	151	distal
	Maneal	0.8	0.8	2.6	69	72	28	distal
	Nbl1	2.6	3.1	1.5	387	415	840	proximal
	Nmral1	0.6	0.0	1.7	76	86	34	proximal
	Nos1ap	1.0	1.2	3.3	568	526	1235	distal
	Serpina3n	0.2	0.2	1.5	3329	3102	6661	distal

MeDIP SCALE 0.0 1.0 2.0 3.0 4.0 5.0

The genes displaying inversely correlated DNA methylation and gene expression levels are marked with red and green colour if they are hyper- or hypo- methylated in MRL/MpJ mouse. MeDIP – DNA methylation score, mRNA – level of gene expression – normalized signal value, B6 –C57BL/6J, Bc – BALB/c, M – MRL/MpJ.

Figure Legends

Figure 1 Principal Component Analysis of DNA methylation profiles.

Figure 2 Ontology analyses for genes associated with DMRs in the tissues of the MRL/MpJ mouse.

The results are presented as –log(BH); Benjamini-Hochberg corrected p-value. The significance of p=0.05 corresponds to –log(BH) = 1.3.

Figure 3 Ontology network for the genes associated with DMRs in the ear pinnae of the MRL/MpJ mouse.

Ontological terms associated with the genes located close to the DMRs in the ears are presented by nodes. Gene set enrichment was performed with ClueGO.

Figure 4 Verification of the DMRs by MDRE-qPCR in the ear pinnae.

The methylation level is shown as 1-McrBC/TaqI ratio. The verified genes belong to *anterior/posterior pattern formation* (*Ski, Bcl2l11*), positive regulation of neuron apoptotic process (*Bcl2l11, Cyp2d22, Ghrhr, Ticam2*), or showed big differences in MeDIP score (*Krtap14, Gjb4, Gm8884*). Statistical significance was calculated with one-way ANOVA with *post hoc* Tukey's multiple comparison test; *p-value<0.05; **p-value<0.01; ***p-value<0.001.

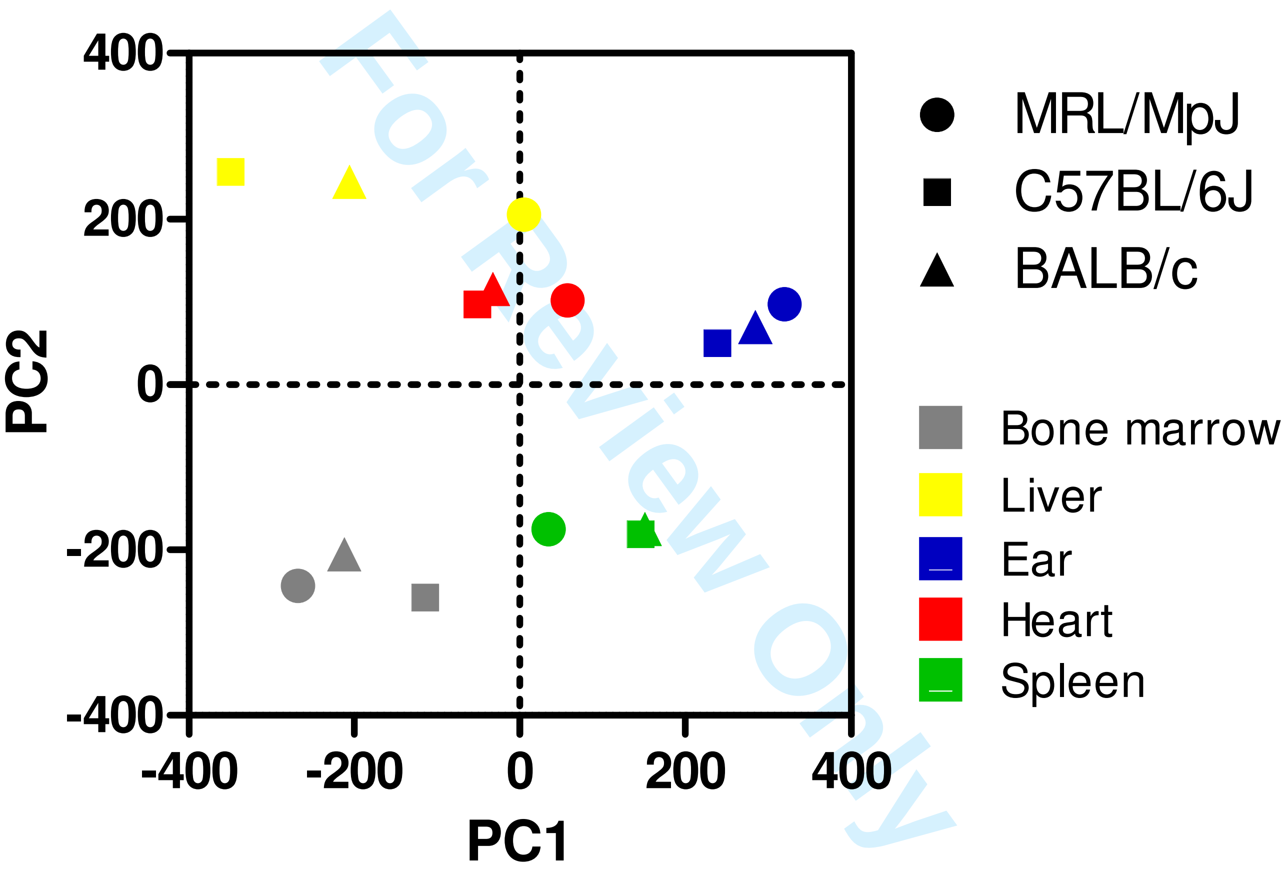
400
200
0
-200
-400
PC2
-400
-200
0
200
400
PC1
● MRL/MpJ
■ C57BL/6J
▲ BALB/c
Bone marrow
Liver
Ear
Heart
Spleen

Figure 1

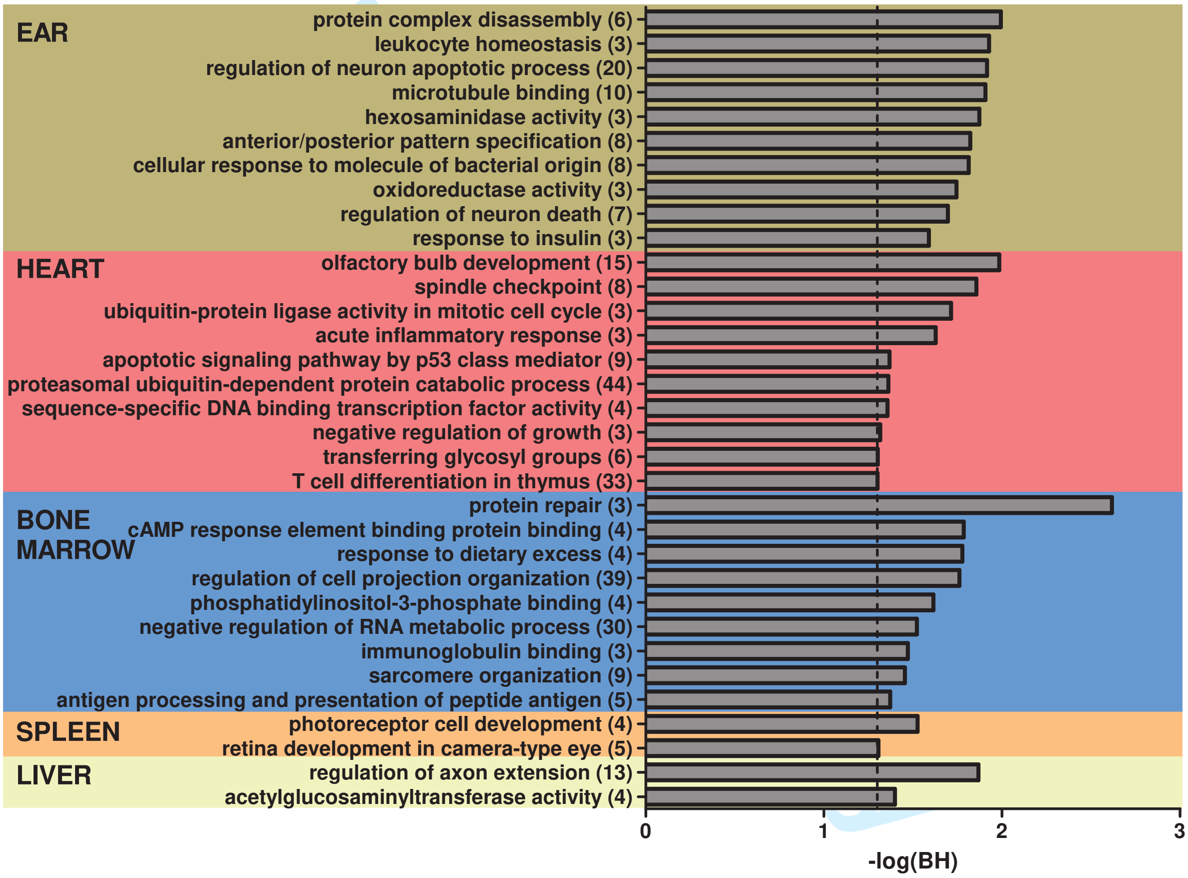
EAR
protein complex disassembly (6)
leukocyte homeostasis (3)
regulation of neuron apoptotic process (20)
microtubule binding (10)
hexosaminidase activity (3)
anterior/posterior pattern specification (8)
cellular response to molecule of bacterial origin (8)
oxidoreductase activity (3)
regulation of neuron death (7)
response to insulin (3)
HEART
olfactory bulb development (15)
spindle checkpoint (8)
ubiquitin-protein ligase activity in mitotic cell cycle (3)
acute inflammatory response (3)
apoptotic signaling pathway by p53 class mediator (9)
proteasomal ubiquitin-dependent protein catabolic process (44)
sequence-specific DNA binding transcription factor activity (4)
negative regulation of growth (3)
transferring glycosyl groups (6)
T cell differentiation in thymus (33)
BONE MARROW
protein repair (3)
cAMP response element binding protein binding (4)
response to dietary excess (4)
regulation of cell projection organization (39)
phosphatidylinositol-3-phosphate binding (4)
negative regulation of RNA metabolic process (30)
immunoglobulin binding (3)
sarcomere organization (9)
antigen processing and presentation of peptide antigen (5)
SPLEEN
photoreceptor cell development (4)
retina development in camera-type eye (5)
LIVER
regulation of axon extension (13)
acetylglucosaminyltransferase activity (4)
0
1
2
3
-log(BH)

Figure 2

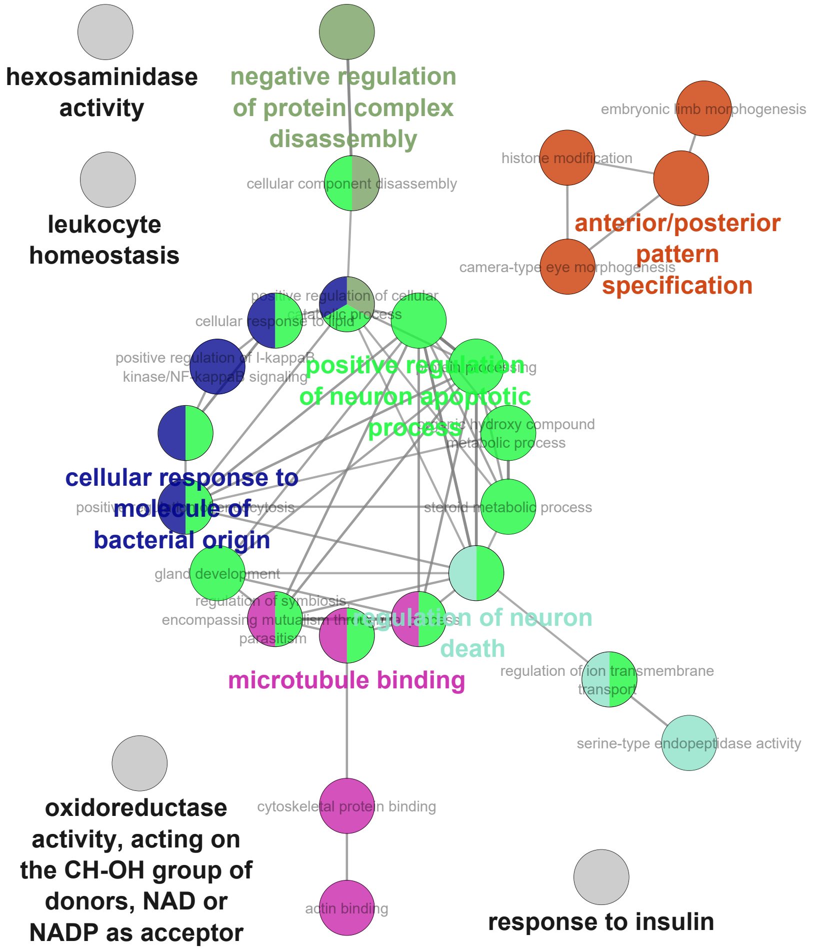
hexosaminidase activity
negative regulation of protein complex disassembly
embryonic limb morphogenesis
histone modification
leukocyte homeostasis
cellular component disassembly
anterior/posterior pattern specification
camera-type eye morphogenesis
positive regulation of cellular catabolic process
cellular response to lipid
positive regulation of I-kappaB kinase/NF-kappaB signaling
positive regulation of neuron apoptotic process
protein processing
organic hydroxy compound metabolic process
cellular response to molecule of bacterial origin
positive regulation of endocytosis
steroid metabolic process
gland development
regulation of symbiosis, encompassing mutualism through parasitism
regulation of neuron death
microtubule binding
regulation of ion transmembrane transport
serine-type endopeptidase activity
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
cytoskeletal protein binding
actin binding
response to insulin

Figure 3

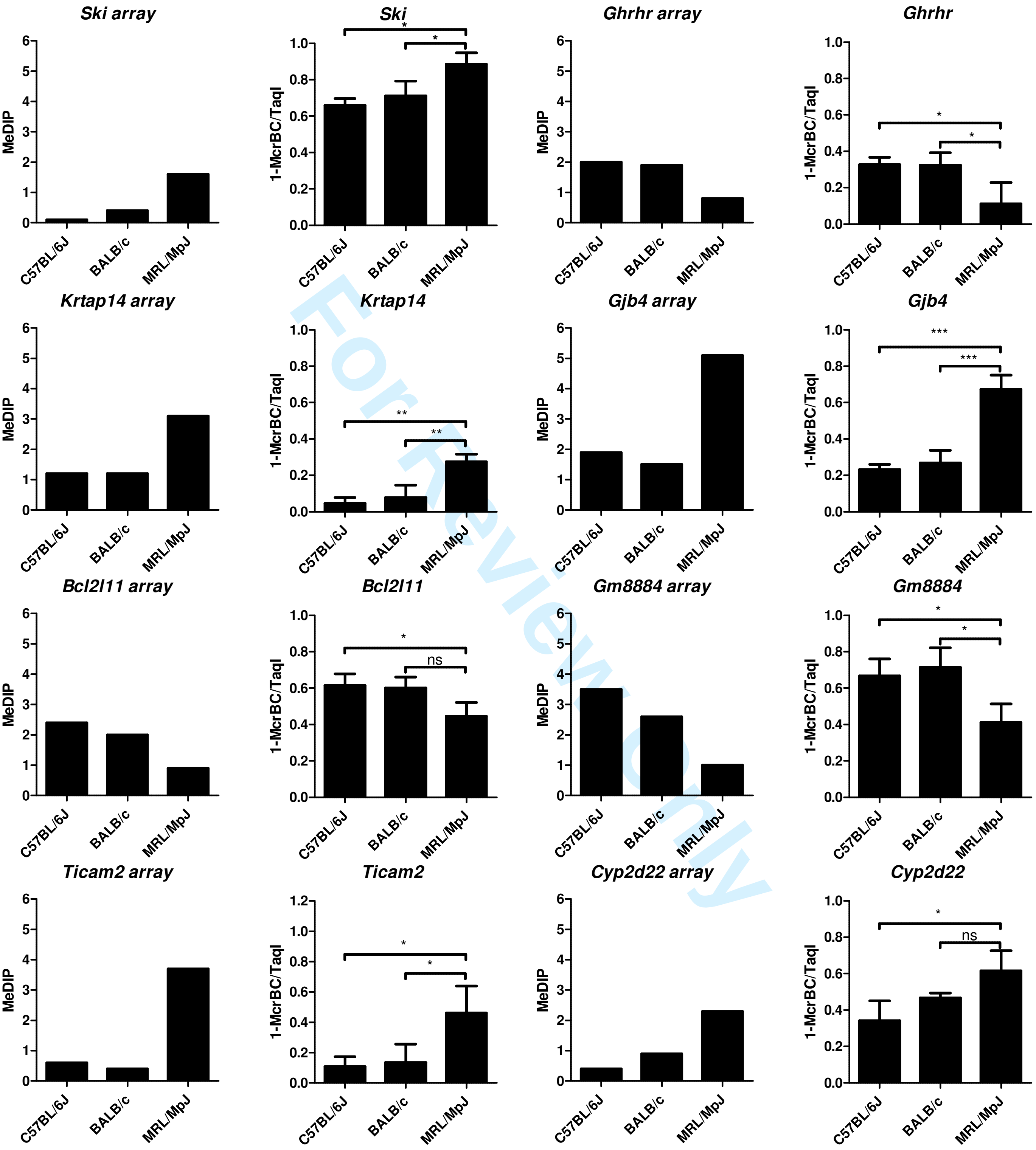
Ski array
MeDIP
Ski
1-McrBC/TaqI
*
*
Ghrhr array
MeDIP
Ghrhr
1-McrBC/TaqI
*
*
Krtap14 array
MeDIP
Krtap14
1-McrBC/TaqI
**
**
Gjb4 array
MeDIP
Gjb4
1-McrBC/TaqI
***
***
Bcl2l11 array
MeDIP
Bcl2l11
1-McrBC/TaqI
*
ns
Gm8884 array
MeDIP
Gm8884
1-McrBC/TaqI
*
*
Ticam2 array
MeDIP
Ticam2
1-McrBC/TaqI
*
*
Cyp2d22 array
MeDIP
Cyp2d22
1-McrBC/TaqI
*
ns
0
1
2
3
4
5
6
0.0
0.2
0.4
0.6
0.8
1.0
1.2
C57BL/6J
BALB/c
MRL/MpJ

Figure 4

TableS1. Primer sequences used for validation of DMRs.

Gene	Forward	Reverse	L [bp]
Ski	CAACATCTGTCTACTGGACC	CAGCCTGAGAATCACAGAG	150
Ghrhr	TGCCCTGTCTGTGTTCTC	ACCCAGCTGAATATTGAACG	161
Krtap14	ACAGCACGGCTCTTAACACA	ATCCAGCTTTTACCGCCCAA	154
Gjb4	TCCCTTTGGGAAGCTAAGT	TAAGTGAGGAACAAAAGCTGC	173
Bcl2l11	GGATTCACTTGAGAAGCTAGAC	AGGCTGGCAGTAAGTAGGA	161
Gm8884	GAGGCTGTAGACGGCGAATAG	CGCTGGTGTTTCCCTAGTGC	75
Ticam2	GGAGGCACTGTTCTGATG	TCAGTGCGAGAGGAAGAT	155
Cyp2d22	GACGCTAACTGCCACATTCC	GCACAGTTCGCAAGTTCACG	241

Differentially methylated regions found in ear.

ACC	Name	chr	start	end	BEarS	BcEarS	MEarS	feature DI
NR_026896	4931440L1	chr1	1.36E+08	1.36E+08	1.3	1.0	2.6	transcriptic
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	3.1	transcriptic
NM_01346	Ankrd1	chr19	36195732	36195982	0.6	0.5	1.9	transcriptic
NM_02585	Arl1	chr10	88191503	88192282	0.2	0.0	1.3	transcriptic
NM_02984	Arsk	chr13	76237743	76238342	0.6	0.5	1.7	transcriptic
NM_14489	BC018465	chr2	1.54E+08	1.54E+08	2.4	2.5	1.0	transcriptic
NM_20768	Bcl2l11	chr2	1.28E+08	1.28E+08	2.4	2.0	0.9	transcriptic
NM_08045	Bsnd	chr4	1.06E+08	1.06E+08	2.5	1.9	0.7	transcriptic
NM_00114	Btbd6	chr12	1.14E+08	1.14E+08	2.5	2.1	0.9	transcriptic
NM_00991	Cnga3	chr1	37273757	37273996	0.8	0.5	1.8	transcriptic
NM_01199	Cops3	chr11	59654752	59655702	0.3	0.4	1.5	transcriptic
NM_00101	Cpsf6	chr10	1.17E+08	1.17E+08	0.2	0.1	1.2	transcriptic
NM_01982	Cyp2d22	chr15	82208073	82209452	0.4	0.9	2.3	transcriptic
NM_02243	Cyp4f14	chr17	33056077	33056731	1.4	1.6	0.3	transcriptic
NM_17724	D030016E1	chr8	48621288	48621749	0.6	0.0	2.1	transcriptic
NM_02689	Eif1b	chr9	1.2E+08	1.2E+08	0.7	0.6	2.0	transcriptic
NM_01013	En1	chr1	1.23E+08	1.23E+08	1.8	2.1	0.7	Primary Tra
NM_00101	Fam105b	chr15	27562080	27562932	0.6	0.6	1.7	transcriptic
NM_02621	Fam18b	chr11	62690533	62691505	1.0	0.4	2.4	transcriptic
NM_00107	Fcgr2b	chr1	1.73E+08	1.73E+08	1.7	2.2	0.4	transcriptic
NM_00101	Gas2l2	chr11	83242222	83242886	2.9	3.2	1.3	transcriptic
NM_00101	Gas2l2	chr11	83243442	83243878	1.9	1.8	0.6	transcriptic
NM_00100	Ghrhr	chr6	55326006	55326575	2.0	1.9	0.8	transcriptic
NM_00812	Gjb4	chr4	1.27E+08	1.27E+08	1.9	1.5	5.1	transcriptic
NM_19865	Gm5148	chr3	37624779	37626218	1.1	0.4	2.4	transcriptic
NM_00103	Gm7120	chr13	1.2E+08	1.2E+08	1.7	1.3	3.7	transcriptic
NR_026561	Gm8884	chr9	48261250	48261792	3.5	2.6	1.0	transcriptic
NM_01034	Gpr50	chrX	68914681	68916559	1.1	1.1	2.5	transcriptic
NM_13831	H1foo	chr6	1.16E+08	1.16E+08	1.9	1.9	0.7	transcriptic
NM_01047	Hsd17b1	chr11	1.01E+08	1.01E+08	1.8	1.7	0.6	transcriptic
NM_00108	Htra4	chr8	26150844	26151187	0.3	0.6	1.7	transcriptic
NM_17859	Ikbkg	chrX	71673409	71673878	1.1	1.2	2.8	transcriptic
NM_19841	Inf2	chr12	1.14E+08	1.14E+08	0.7	0.7	1.9	transcriptic
NM_01059	Kcnab2	chr4	1.52E+08	1.52E+08	2.3	2.4	1.1	transcriptic
NM_00114	Kifc3	chr8	97637777	97638027	2.3	2.8	1.1	transcriptic
NM_01370	Krtap14	chr16	88825671	88826015	1.2	1.2	3.1	transcriptic
NM_00108	Lonrf1	chr8	37313285	37313736	0.6	0.7	1.8	transcriptic
NM_00100	Maneal	chr4	1.25E+08	1.25E+08	0.7	0.6	2.6	transcriptic
NM_02567	Mcm8	chr2	1.33E+08	1.33E+08	1.0	0.7	2.2	transcriptic
NM_01676	Mcrs1	chr15	99081644	99081893	1.1	1.3	0.0	transcriptic
NM_18315	Mid1	chrX	1.66E+08	1.66E+08	2.5	2.7	0.7	Primary Tra
NM_01954	Msgn1	chr12	11218036	11218673	1.3	1.6	0.0	transcriptic
NM_00866	Naga	chr15	82169679	82170243	2.7	2.0	1.0	transcriptic
NM_02752	Nos1ap	chr1	1.72E+08	1.72E+08	1.2	1.0	3.1	transcriptic
NM_20724	Npc1l1	chr11	6132442	6132686	1.0	0.8	2.2	transcriptic
NM_05407	Optc	chr1	1.36E+08	1.36E+08	3.6	3.7	1.6	transcriptic
NM_00108	Osbpl7	chr11	96909374	96910572	1.9	2.1	0.7	transcriptic
NM_15356	Pcsk9	chr4	1.06E+08	1.06E+08	0.9	1.1	2.4	transcriptic

NM_02932	Pibf1	chr14	99495716	99496140	1.9	1.3	4.3	transcriptic
NM_02614	Ppil4	chr10	7509779	7510958	0.3	0.1	1.4	transcriptic
NM_00110	Prlh	chr1	92848564	92849198	1.9	2.9	0.6	transcriptic
NM_14545	Pxk	chr14	8928640	8929546	0.2	0.1	1.6	transcriptic
NM_02202	Rbp7	chr4	1.49E+08	1.49E+08	2.5	1.9	0.5	transcriptic
NM_03119	Ren2	chr1	1.35E+08	1.35E+08	2.1	2.5	0.8	transcriptic
NM_00906	Rgs4	chr1	1.72E+08	1.72E+08	0.3	0.0	3.1	transcriptic
NM_00906	Ring1	chr17	34161008	34161337	2.4	2.0	0.9	transcriptic
NM_19435	Rya3	chr2	1.54E+08	1.54E+08	2.8	2.3	1.1	transcriptic
NA	chr1:13868	chr1	1.39E+08	1.39E+08	2.9	2.3	1.0	CpG Island
NA	chr17:1567	chr17	15673304	15673974	0.1	0.2	2.1	CpG Island
NA	chr9:88494	chr9	88494209	88494858	0.1	0.0	1.4	CpG Island
NA	chr9:88753	chr9	88753512	88754171	0.1	0.0	1.3	CpG Island
NA	chr9:88961	chr9	88961199	88961948	0.5	0.0	1.7	CpG Island
NA	chr9:96437	chr9	96437157	96437816	0.2	0.5	3.9	CpG Island
NM_01138	Ski	chr4	1.55E+08	1.55E+08	0.1	0.4	1.6	transcriptic
NM_00100	Slc28a1	chr7	88257446	88257775	1.5	1.8	0.5	transcriptic
NM_02528	Tbrg1	chr9	37467057	37467817	0.2	0.5	2.0	transcriptic
NM_17339	Ticam2	chr18	46733459	46734858	0.6	0.4	3.7	transcriptic
NM_18154	Tm6sf2	chr8	72596793	72597242	1.3	1.4	0.2	transcriptic
NM_14480	Tmem40	chr6	1.16E+08	1.16E+08	2.5	2.3	1.0	transcriptic
NM_01369	Tnf	chr17	35338904	35339578	2.0	2.6	0.6	transcriptic
NM_00113	Tnnt2	chr1	1.38E+08	1.38E+08	1.0	0.9	2.9	transcriptic
NM_00102	Tpd52	chr3	8966192	8966468	0.9	1.0	2.1	transcriptic
NM_01579	Trfr2	chr5	1.38E+08	1.38E+08	1.6	1.7	0.3	transcriptic
NM_00947	Uox	chr3	1.46E+08	1.46E+08	2.0	2.0	0.8	transcriptic
NM_00947	Uox	chr3	1.46E+08	1.46E+08	0.3	0.2	2.0	transcriptic
NM_01980	Vapb	chr2	1.74E+08	1.74E+08	0.3	0.7	1.9	transcriptic
NM_02657	Yeats4	chr10	1.17E+08	1.17E+08	0.7	0.4	1.8	transcriptic
NM_17278	Zc3h12d	chr10	7587001	7587665	1.7	1.5	0.5	Primary Tra
NM_02770	Zdhhc11	chr13	74098871	74100310	2.3	2.0	1.0	transcriptic
NM_14618	Zfp428	chr7	25290998	25291276	1.0	0.8	3.1	transcriptic
NM_00100	Zscan22	chr7	13482077	13482326	1.3	1.2	0.1	transcriptic

orientatior	descriptior	DISSTRIBU	gene_id
-	RIKEN cDN,	PROXIMAL	71001
-	aldo-keto r	PROXIMAL	56043
-	ankyrin rep	DISTAL	107765
+	ADP-ribosy	DISTAL	104303
-	arylsulfatas	DISTAL	77041
+	cDNA sequ	DISTAL	228802
+	BCL2-like 1	DISTAL	12125
-	Bartter syn	DISTAL	140475
+	BTB (POZ) (	DISTAL	399566
+	cyclic nucle	DISTAL	12790
-	COP9 (cons	DISTAL	26572
-	cleavage ar	PROXIMAL	432508
-	cytochrome	DISTAL	56448
-	cytochrome	DISTAL	64385
-	RIKEN cDN,	DISTAL	320714
+	eukaryotic	DISTAL	68969
+	engrailed 1	INTRAGENI	13798
-	family with	DISTAL	432940
+	family with	DISTAL	67510
-	Fc receptor	PROXIMAL	14130
-	growth arre	PROXIMAL	237891
-	growth arre	PROXIMAL	237891
+	growth hor	PROXIMAL	14602
-	gap junctio	PROXIMAL	14621
-	predicted g	DISTAL	381438
+	predicted g	PROXIMAL	633640
+	predicted g	DISTAL	667933
+	G-protein-c	PROXIMAL	14765
+	H1 histone	DISTAL	171506
+	hydroxyste	DISTAL	15485
-	HtrA serine	DISTAL	330723
+	inhibitor of	DISTAL	16151
+	inverted fo	DISTAL	70435
-	potassium	DISTAL	16498
-	kinesin fam	DISTAL	16582
-	keratin asso	INTRAGENI	23927
-	LON peptid	DISTAL	244421
-	mannosida	DISTAL	215090
+	minichrom	DISTAL	66634
-	microspher	INTRAGENI	51812
+	midline 1	INTRAGENI	17318
-	mesogenin	DISTAL	56184
-	N-acetyl ga	PROXIMAL	17939
-	nitric oxide	DISTAL	70729
-	NPC1-like 1	DISTAL	237636
-	opticin	INTRAGENI	269120
+	oxysterol b	DISTAL	71240
-	proprotein	PROXIMAL	100102

+	progestero	DISTAL	52023
+	peptidylpr	DISTAL	67418
+	prolactin r	PROXIMAL	623503
+	PX domain	DISTAL	218699
-	retinol bin	DISTAL	63954
+	renin 2 tan	PROXIMAL	19702
-	regulator o	DISTAL	19736
-	ring finger	INTRAGENI	19763
+	antimicrob	DISTAL	378700
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
-	ski sarcom	DISTAL	20481
+	solute carri	DISTAL	434203
-	transformi	DISTAL	21376
-	toll-like rec	PROXIMAL	225471
+	transmem	PROXIMAL	107770
-	transmem	DISTAL	94346
-	tumor necr	PROXIMAL	21926
+	troponin T	DISTAL	21956
-	tumor prot	DISTAL	21985
+	transferrin	PROXIMAL	50765
+	urate oxid	DISTAL	22262
+	urate oxid	PROXIMAL	22262
+	vesicle-ass	DISTAL	56491
-	YEATS dom	PROXIMAL	64050
+	zinc finger	INTRAGENI	237256
+	zinc finger,	DISTAL	71164
+	zinc finger	DISTAL	232969
+	zinc finger	DISTAL	232878

Differentially methylated regions found in ear connected with 2 fold in gene expression level.

ACC	Name	chr	start	end	BEarS	BcEarS	MEarS	feature DI :
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	3.1	transcriptic
NM_14489	BC018465	chr2	1.54E+08	1.54E+08	2.4	2.5	1.0	transcriptic
NM_00107	Fcgr2b	chr1	1.73E+08	1.73E+08	1.7	2.2	0.4	transcriptic
NM_01370	Krtap14	chr16	88825671	88826015	1.2	1.2	3.1	transcriptic
NM_05407	Optc	chr1	1.36E+08	1.36E+08	3.6	3.7	1.6	transcriptic
NM_05407	Optc	chr1	1.36E+08	1.36E+08	3.6	3.7	1.6	transcriptic
NM_02202	Rbp7	chr4	1.49E+08	1.49E+08	2.5	1.9	0.5	transcriptic
NM_17339	Ticam2	chr18	46733459	46734858	0.6	0.4	3.7	transcriptic
NM_14618	Zfp428	chr7	25290998	25291276	1.0	0.8	3.1	transcriptic

orientatior	descriptior	DISSTRIBU	gene_id	transcript_	BEarS	SE_EXPRS	BcEarS	SE_EXPRS
-	aldo-keto r	PROXIMAL	56043	BC012692	917.5759	0.9781	690.7206	0.9668
+	cDNA sequ	DISTAL	228802	BC018465	27.4916	0.7271	23.9458	0.7147
-	Fc receptor	PROXIMAL	14130	AK080885	145.5439	0.8715	99.1748	0.8598
-	keratin ass	INTRAGENI	23927	BC104262	56.4528	0.7807	6.4112	0.4649
-	opticin	INTRAGENI	269120	AK153750	187.7414	0.8613	164.1239	0.8619
-	opticin	INTRAGENI	269120	BC115928	160.6912	0.9008	158.5352	0.9006
-	retinol binc	DISTAL	63954	BC028432	165.7552	0.8881	266.807	0.9206
-	toll-like rec	PROXIMAL	225471	BC099933	119.5264	0.8871	136.4732	0.9029
+	zinc finger	DISTAL	232969	AK080517	42.386	0.7461	47.3414	0.7683

MEarS	SE_EXPRS
129.4592	0.8959
86.4612	0.832
43.1654	0.7668
5170.603	0.9548
26.6872	0.6691
56.7962	0.7424
805.4846	0.9613
48.7694	0.7485
94.7677	0.8569

Gene ontology analysis for ear.

GOTerm	Nr. Genes	Term PVal	Associated	Genes in cl	Nr. Genes i	-log(P-value)
negative re	3	0.010148	[Gas2l2, M	Akr1e1|Ga	6	1.993614
leukocyte	3	0.011834	[Bcl2l11, F	Bcl2l11|Fc	3	1.926853
positive reg	3	0.012147	[Bcl2l11, P	Akr1e1|An	20	1.915519
microtubul	4	0.012383	[Bcl2l11, G	Ankrd1|Bc	10	1.90717
hexosamin	3	0.013399	[4931440L	4931440L1	3	1.872913
anterior/p	4	0.015072	[En1, Msgn	Bcl2l11|Cn	8	1.821818
cellular res	4	0.015362	[Ankrd1, F	Akr1e1|An	8	1.813542
oxidoreduc	3	0.017999	[Akr1e1, H	Akr1e1|Hs	3	1.74475
regulation	4	0.020139	[Bcl2l11, N	Bcl2l11|Cn	7	1.695953
response t	3	0.025752	[Ghrhr, Pcs	Ghrhr|Pcs	3	1.589196

Transcription factor identification for ear.

Interval	TF	NES	Targets	Motifs
500bp	Smad1	4.823	33	9
500bp	Tal1	4.791	37	19
500bp	Foxa3	4.201	16	7
500bp	Smap2	4.112	27	4
500bp	Msc	3.934	32	4
500bp	En1	3.83	29	9
500bp	Tbx5	3.646	12	2
500bp	Tfap2a	3.489	31	3
500bp	Jazf1	3.445	27	2
500bp	Nifa	3.408	9	2
500bp	NeuroD1	3.396	10	2
500bp	Nkx2-5	3.203	5	1
500bp	Six2	3.192	13	4
500bp	Gbx2	3.015	7	1

Promoter sequence motifs

# Rank	Motif id	AUC	NES	ClusterCod	Transcripti	Target genes
1	transfac_p	0.090821	4.82278	M1	Smad1	Kifc3,Tpd52,Optc,Tnnt2,Gas2l2,Gj
2	transfac_p	0.090365	4.79098	M2	Tal1	Optc,Tnnt2,Mid1,Krtap14,Cyp4f14
3	homer-M0	0.085689	4.46435	M2	Neurod1,T	Optc,Tnnt2,Krtap14,4931440L10R
4	homer-M0	0.081923	4.2013	M3	Foxa3,Foxa	Tpd52,Zfp428,Gjb4,Uox,Mid1,Bcl2
5	tfdimers-M	0.081737	4.1883	M2	Meis1,Nr1	Ankrd1,Cyp4f14,BC018465,Bsnd,4
6	hdpi-SMAP	0.08064	4.1117	M4	Smap2	Cyp4f14,Gas2l2,Gjb4,BC018465,H
7	transfac_p	0.078467	3.95994	M2	Myf6,Tcf3,	Tnnt2,Ankrd1,Optc,Cyp4f14,BC01
8	taipale-AA	0.078095	3.93392	M5	Msc	Tnnt2,Ankrd1,BC018465,Gpr50,Cy
9	homer-M0	0.077391	3.88478	M2	Atoh1,Ascl	Tnnt2,Optc,Ankrd1,Cyp4f14,Krtap
10	tfdimers-M	0.076605	3.82986	M6	Pbx1	Krtap14,Npc1l1,Tpd52,En1,Mid1,V
11	hdpi-TRIM	0.076294	3.80818	M4	Trim21	Cyp4f14,Gjb4,Gas2l2,BC018465,Tr
12	tfdimers-M	0.075943	3.78361	M5	Tfap4,Pdx1	Msgn1,Gpr50,Zc3h12d,Uox,BC018
13	hdpi-NAP1	0.075901	3.78072	M4	Gm4204,N	Cyp4f14,BC018465,Pibf1,Gas2l2,G
14	transfac_p	0.075301	3.73881	M2	Tcf3,Myc,M	Nos1ap,Ankrd1,Hsd17b1,Gjb4,Mic
15	transfac_p	0.074266	3.66654	M2	Tal1,Tcf4,T	Optc,Krtap14,4931440L10Rik,Tnnt
16	transfac_p	0.073977	3.64631	M7	Tbx5	Msgn1,Mid1,Gpr50,Cyp4f14,Bsnd,
17	tfdimers-M	0.073749	3.63041	M6	Pou3f2,Pd	Kifc3,Krtap14,Mid1,Tpd52,En1,Cn
18	jaspar-MA	0.072921	3.5726	M2	Tcf3,Tal1,T	Optc,Tnnt2,BC018465,Tpd52,Cyp4

19	transfac_p	0.072363	3.53358	M3	Foxa3,Foxa	Tpd52,Mid1,Gjb4,Zfp428,Uox,Bcl2
20	jaspar-CN0	0.071742	3.49022	M8		Ankrd1,Tpd52,Slc28a1,Gm5148,T
21	yetfasco-6	0.071721	3.48877	M9		Gjb4,Tpd52,BC018465,Cyp4f14,N
22	encode-U	0.071576	3.47866	M1		Optc,Tnnt2,Cops3,Pibf1,Zc3h12d,
23	tfdimers-M	0.071556	3.47721	M2	Yy1,Tcf3,Zf	Krtap14,Tpd52,Cyp4f14,Optc,Gas2
24	transfac_p	0.071411	3.46709	M3	Pou2f1,Po	Zfp428,Kcnab2,Ankrd1,Optc,Mid1,
25	transfac_p	0.071245	3.45553	M3	Pou2f1,Po	Zfp428,Msgn1,Kcnab2,Ankrd1,Bsn
26	transfac_p	0.071204	3.45264	M2	Tcf3,Myf6,	Gpr50,Gjb4,Tpd52,BC018465,Cyp
27	tfdimers-M	0.071183	3.4512	M2	Yy1,Mafa,	Tnnt2,Optc,Krtap14,Gjb4,Cyp4f14,
28	taipale-RT	0.071121	3.44686	M3	Foxp3,Foxj	Bcl2l11,Gas2l2,En1,Mid1,Uox,Vap
29	yetfasco-1	0.0711	3.44541	M10	Jazf1,Foxn	Pibf1,Tnf,En1,Krtap14,Prlh,Fcgr2b,
30	jaspar-MA	0.071059	3.44252	M3	Foxa2,Foxa	Gjb4,Uox,Ankrd1,Mid1,Ghrhr,Tpd
31	swissregul	0.071059	3.44252	M3	Foxa2,Foxa	Gjb4,Uox,Ankrd1,Mid1,Ghrhr,Tpd
32	transfac_p	0.070873	3.42952	M2	Tal1,Tcf3,T	Krtap14,Tpd52,Optc,BC018465,Tn
33	tfdimers-M	0.070562	3.40784	M2	Srebf2,Nr3	Tnnt2,Gpr50,Optc,Tmem40,Nos1a
34	transfac_p	0.070562	3.40784	M11		Tmem40,Kifc3,Gjb4,Krtap14,Ikbkg
35	tfdimers-M	0.070397	3.39627	M12	Neurod1,El	En1,Mid1,4931440L10Rik,Gjb4,Op
36	transfac_p	0.070376	3.39483	M1		Osbpl7,Ghrhr,Npc1l1,Tpd52,Rgs4,
37	tfdimers-M	0.069507	3.33413	M2	Nr3c1,Pgr,	Tnnt2,Ankrd1,Optc,Tmem40
38	taipale-AA	0.069362	3.32401	M5	Myf6,Msc	Ankrd1,BC018465,Gpr50,Npc1l1,T
39	transfac_p	0.069073	3.30378	M2	Tcf3,Myod	Tnnt2,Optc,Gjb4,Tpd52,Ankrd1,Cy
40	yetfasco-2	0.068907	3.29221	M1	Gata2,Gata	Cyp4f14,BC018465,Fcgr2b,Gas2l2,
41	homer-M0	0.068866	3.28932	M2	Olig2,Tal1,	Optc,Tnnt2,Krtap14,Zc3h12d,Uox,
42	tfdimers-M	0.068804	3.28499	M6	Yy1,Pax7,V	Mid1,Npc1l1,Krtap14,Kifc3,Tpd52,
43	transfac_p	0.068659	3.27487	M6	Hnf1b,Hm	Mid1,Npc1l1,En1,Gas2l2,Msgn1,A
44	encode-U	0.067976	3.22717	M4		Pibf1,Cyp4f14,Ghrhr,Gm7120,Tme
45	elemento-	0.067955	3.22573	M13		Pibf1,Slc28a1,Trfr2,H1foo,BC0184
46	transfac_p	0.067624	3.2026	M14	Nkx2-5	Msgn1,Cops3,Fam18b,BC018465,
47	transfac_p	0.067583	3.19971	M2	Tcf3,Tal1,T	Optc,Tnnt2,Krtap14,Ankrd1,Tpd52
48	homer-M0	0.067479	3.19249	M15	Six2	Ankrd1,Gjb4,Tpd52,Vapb,Bsnd,Kif
49	transfac_p	0.06721	3.1737	M1	Tfcp2,Tfcp	Gas2l2,Slc28a1,Mid1,BC018465,Cy
50	transfac_p	0.067107	3.16647	M15		Msgn1,Tpd52,Nos1ap,Mid1,En1,Z
51	transfac_p	0.066983	3.1578	M1	Gata5,Gata	Gpr50,Bsnd,4931440L10Rik,Gjb4,
52	yetfasco-8	0.066983	3.1578	M1	Gata5,Gata	Gpr50,Bsnd,4931440L10Rik,Gjb4,
53	transfac_p	0.066858	3.14913	M2	Myf6,Tcf3,	Ankrd1,Tnnt2,Gpr50,Gjb4,Npc1l1,
54	transfac_p	0.066589	3.13034	M11	Nfia,Nf1,Yy	BC018465,Optc,Cyp4f14
55	jaspar-MA	0.0663	3.11011	M1	Gata5,Gata	Gpr50,4931440L10Rik,Bsnd,Gjb4,
56	taipale-NT	0.066176	3.10143	M15	Dmbx1,Gsc	Tpd52,En1,Zfp428,Cnga3,Ankrd1,
57	homer-M0	0.066072	3.09421	M10	Jazf1,Foxn	En1,Htra4,Tnf,Prlh,Optc,BC018465
58	tfdimers-M	0.065865	3.07975	M9	Tfap2a,Ne	Cyp4f14,Fcgr2b,Tnnt2,Ankrd1,Opt
59	tfdimers-M	0.065845	3.07831	M6	Crx,Jun,Fos	Npc1l1,Msgn1,Kifc3,Tpd52,Cnga3,
60	taipale-NN	0.06572	3.06964	M15	Gsc,Gsc2	Tpd52,En1,Kifc3,Zfp428,Ankrd1,Cr
61	homer-M0	0.065638	3.06386	M6	Pax4,Shox	Mcrs1,Npc1l1,Krtap14,Mid1,Msgn
62	swissregul	0.065534	3.05663	M1	Smad2,Sm	Gas2l2,Bsnd,Pibf1,Prlh,Gjb4,Rya3,
63	transfac_p	0.065513	3.05518	M6	Lhx5,Alx1,	Krtap14,Msgn1,En1,Mid1,Npc1l1,
64	hdpi-PKNO	0.06541	3.04796	M5	Pknox2	Prlh,Ankrd1,En1,Gpr50,Gas2l2,Slc
65	transfac_p	0.065286	3.03929	M2	Myod1,Tcf	Tnnt2,Gjb4,Tpd52,Bsnd,Ankrd1,Cy
66	transfac_p	0.065265	3.03784	M9		Tnnt2,Gjb4,Bsnd,Optc,Mid1,Cnga
67	taipale-AG	0.065244	3.0364	M7	Tbx4,Eome	Bsnd,Prlh,Nos1ap,Gjb4,Cyp4f14,T
68	transfac_p	0.065244	3.0364	M6	Lhx5,Otp,A	Krtap14,Mid1,En1,Npc1l1,Mcrs1,

69	jaspar-CN0	0.065141	3.02917	M12		Mid1,4931440L10Rik,Optc,Uox,Tn
70	jaspar-CN0	0.064934	3.01472	M16	Gbx2	Msgn1,Ankrd1,Kifc3,Uox,Slc28a1,F
71	transfac_pı	0.064934	3.01472	M6	Lhx5,Otp,Ll	En1,Krtap14,Mid1,Msgn1,Npc1l1,N

4,Tmem40,Cyp4f14,Prlh,Slc28a1
,Gas2l2,Zc3h12d,Tpd52,Nos1ap,4931440L10Rik,Kifc3,Gjb4
ik,Tpd52,Ankrd1,Cyp4f14,Zc3h12d,Mid1,Gas2l2,Kifc3,Fcgr2b,Gjb4,BC018465,Tnf
l11,En1,Ikbkg,Ghrhr,Ankrd1
931440L10Rik,Fcgr2b,Osbpl7,Tnnt2,Optc,Mid1,Tmem40,Kifc3,Cnga3,Krtap14,Ghrhr,Gas2l2,Tbrg1,Tpd52
sd17b1,Slc28a1,Tnnt2,Pibf1,Bsnd,Optc,Tmem40,Mid1
465,Gpr50,Fcgr2b,Tpd52,Zc3h12d,4931440L10Rik,Bsnd
p4f14,Gjb4,Tpd52
14,Tpd52,Zc3h12d,4931440L10Rik,Mid1,BC018465,Msgn1,Gas2l2,Fcgr2b,Zfp428,Tnf,Gjb4,Kifc3
apb,Cnga3
nt2,Hsd17b1,Tmem40,Optc,Pibf1,Bsnd,Slc28a1,Kifc3,Msgn1,Mid1
465,Npc1l1
jb4,Tmem40,Pxk,Tpd52,Hsd17b1,Optc,Mid1,Slc28a1,Kifc3,Msgn1
1,Tnnt2,Tpd52
2,Tpd52,Ankrd1,Zc3h12d,BC018465,Uox,Cyp4f14,Gpr50
Prlh,Rya3
a3,Vapb
f14,Uox,Krtap14,Ankrd1,4931440L10Rik

l11,Ikbkg,En1,Ghrhr
nt2,BC018465,Mid1,Btbd6,Pibf1
s1ap,Bsnd,Pibf1,Gas2l2,Ghrhr,Npc1l1,Hsd17b1,Tnnt2,Pxk,En1,Optc,Rya3,Ankrd1,H1foo,Fcgr2b,Cnga3,P
as2l2,Hsd17b1
l2,Tnnt2,Zfp428,Uox,Ankrd1,Fcgr2b,Tnf,Nos1ap,Mid1,4931440L10Rik,Inf2,Ghrhr
,Msgn1,Bsnd
d,Optc
f14,Tnnt2
,Mid1,Gas2l2,Gpr50,Zfp428,Tnf,Tpd52,Nos1ap,BC018465,4931440L10Rik,Kifc3
,Ankrd1,Gjb4
Bcl2l11,Hsd17b1,Cpsf6,BC018465,Cyp4f14,Cnga3,Tnnt2,Tpd52,Gjb4,Htra4,Npc1l1,Optc,Gpr50,Ring1,No
2,Bcl2l11
2,Bcl2l11
nt2,4931440L10Rik,Ankrd1,Zc3h12d,Gjb4,Cyp4f14,Uox,Gpr50,Fcgr2b
p,Bsnd,Cyp4f14,Msgn1,Gas2l2,Prlh,Rbp7,4931440L10Rik,Zc3h12d,Ghrhr,Gm5148
,En1
tc,Kcnab2
BC018465,Mid1,Krtap14,Nos1ap,Ankrd1,Cnga3,Optc,En1,Bsnd,Cyp4f14,Hsd17b1,Zc3h12d,Bcl2l11,Prlh,F

nnt2,Tnf,Gjb4,Cyp4f14
p4f14,Msgn1,Nos1ap,Zc3h12d
Bsnd,Gjb4,Ghrhr,Kifc3,Optc
Cyp4f14,Tpd52,4931440L10Rik,Tnf,Prlh,Mid1,Gas2l2,Ankrd1
Msgn1
nkrd1,Kifc3,Kcnab2,Tpd52,Eif1b,Uox,Tnnt2,Tbrg1,4931440L10Rik,Cyp4f14,Nos1ap,Hsd17b1,Bsnd,Osbpl
m40,Fcgr2b,Tnf,Npc1l1,En1,Kifc3,Gjb4,Bsnd,Pxk,Tpd52,Nos1ap,Msgn1,Slc28a1,Eif1b,Prlh,Rbp7,Trfr2,BC
5,Gas2l2,Fcgr2b
psf6
,BC018465,Kifc3,Cyp4f14,Gas2l2,Bsnd,Tnf,Uox,Tmem40
3
p4f14,Hsd17b1
p428,Hsd17b1
sgn1
sgn1
Cyp4f14,Bsnd,Tnf,Optc,4931440L10Rik,BC018465,Nos1ap,Tpd52,Kifc3

sgn1
ifc3,Mid1

c,Inf2,Kifc3,Tpd52,Bsnd,Gas2l2
Rbp7,En1
ga3
1,En1
Tnnt2,BC018465,Kifc3
crs1
28a1,Tnnt2,Ghrhr,Bsnd,Osbpl7,Krtap14,Mid1,Fam18b,Msgn1,Gm5148,Optc,4931440L10Rik,Kifc3,D0300
p4f14,Gpr50,Optc,BC018465,Bcl2l11
,Cyp4f14,Nos1ap,Npc1l1,Prlh,En1,Pxk,BC018465,Hsd17b1,Bcl2l11,Slc28a1,Gas2l2
d52,Msgn1,Ankrd1,Gpr50,BC018465
sgn1

nt2,Tnf,Rbp7
Rgs4,Optc
Mcrs1,Kifc3,Pibf1,Vapb,Uox,Hsd17b1,Tpd52,Osbpl7,Zfp428,Cops3,Cnga3

,Pxk,Arl1,Rya3,Nos1ap,Ikbkg

rlh,Slc28a1,Mcm8,Fam18b,Arl1,Zfp428,Bcl2l11,Zc3h12d

s1ap,Fam18b,Zc3h12d,Mid1,Msgn1,Trfr2,Ghrhr

am105b,Tnnt2

,Cpsf6,Pcsk9,Mcrs1
018465,Gas2l2

16E14Rik,Inf2,Tmem40,Tpd52,Tnf,Hsd17b1,Zc3h12d,Rya3,Pxk,Uox,BC018465

Differentially methylated regions found in bone marrow.

ACC	Name	chr	start	end	BBMrS	BcBMrS	MBMrS	feature DI
NM_00856	Mcm3	chr1	20812464	20813030	2.3	1.9	0.4	transcriptic
NM_00108	Phf3	chr1	30921358	30921601	2.4	1.8	0.8	transcriptic
NM_00114	Rfx8	chr1	39777740	39778705	2.5	2.0	0.7	transcriptic
NM_17520	Als2cr11	chr1	59152105	59152564	2.6	2.7	0.9	transcriptic
NM_17764	1110028C1	chr1	66865360	66865784	0.2	0.0	1.9	transcriptic
NM_17556	Tmem169	chr1	72328106	72328782	0.2	0.5	1.6	transcriptic
NM_02735	Psmd1	chr1	87959655	87960216	0.6	0.8	2.0	transcriptic
NM_00115	Rab17	chr1	92863513	92863957	2.2	2.3	0.7	transcriptic
NM_00115	Rab17	chr1	92864208	92864467	4.3	4.8	1.9	transcriptic
NM_01947	Hes6	chr1	93309982	93310506	0.7	0.8	2.2	transcriptic
NM_17888	D2hgdh	chr1	95721562	95721811	0.5	0.7	1.9	transcriptic
NM_17760	AA986860	chr1	1.33E+08	1.33E+08	1.9	1.5	0.2	transcriptic
NM_14496	Fcamr	chr1	1.33E+08	1.33E+08	0.7	1.2	2.4	transcriptic
NM_17708	Ptpn7	chr1	1.37E+08	1.37E+08	2.3	3.0	0.7	transcriptic
NM_15377	Ipo9	chr1	1.37E+08	1.37E+08	0.3	0.5	1.7	transcriptic
NM_01375	Phlda3	chr1	1.38E+08	1.38E+08	1.8	1.8	0.4	transcriptic
NM_02146	Tnni1	chr1	1.38E+08	1.38E+08	1.3	1.3	2.7	transcriptic
NM_00113	Tnnt2	chr1	1.38E+08	1.38E+08	0.8	1.3	2.7	transcriptic
NA	chr1:13868	chr1	1.39E+08	1.39E+08	2.8	2.4	1.0	CpG Islands
NA	chr1:17218	chr1	1.72E+08	1.72E+08	2.1	2.0	0.3	CpG Islands
NM_02752	Nos1ap	chr1	1.72E+08	1.72E+08	0.6	0.8	2.0	transcriptic
NM_01018	Fcgr3	chr1	1.73E+08	1.73E+08	0.1	0.2	1.6	transcriptic
NA	chr1:1730	chr1	1.73E+08	1.73E+08	0.4	0.7	2.4	CpG Islands
NA	chr1:1730	chr1	1.73E+08	1.73E+08	0.0	0.0	1.2	CpG Islands
NA	chr1:1730	chr1	1.73E+08	1.73E+08	0.3	0.5	2.0	CpG Islands
NA	chr1:1730	chr1	1.73E+08	1.73E+08	0.1	0.3	1.7	CpG Islands
NM_17284	Dnahc14	chr1	1.84E+08	1.84E+08	0.6	0.9	1.9	transcriptic
NM_01205	Srp9	chr1	1.84E+08	1.84E+08	2.1	1.9	0.6	transcriptic
NM_02614	Ppil4	chr10	7509779	7510958	0.4	0.1	2.9	transcriptic
NM_00108	Rhobtb1	chr10	68672744	68673415	0.5	1.3	3.0	transcriptic
NM_15359	BC030307	chr10	86173773	86174202	3.1	2.1	1.0	transcriptic
NM_02585	Arl1	chr10	88191503	88192282	0.9	0.2	2.1	transcriptic
NM_01162	Nr2c1	chr10	93608519	93609667	0.1	0.2	1.8	transcriptic
NM_00101	Cpsf6	chr10	1.17E+08	1.17E+08	0.5	0.3	2.9	transcriptic
NM_17709	Msrb3	chr10	1.2E+08	1.2E+08	1.1	1.4	3.0	transcriptic
NM_02945	Hormad2	chr11	4340369	4340918	4.2	3.9	1.3	transcriptic
NM_00834	Igfbp1	chr11	7095925	7096554	0.6	0.5	2.3	transcriptic
NM_01141	Slit3	chr11	34933219	34933808	0.3	0.3	2.2	transcriptic
NM_17225	Slc36a3	chr11	54964486	54964925	1.0	0.8	3.0	transcriptic
NM_02448	Sh3bp5l	chr11	58144296	58144755	0.6	1.1	2.4	transcriptic
NM_13929	Wnt9a	chr11	59119196	59120270	0.0	0.2	1.4	transcriptic
NM_17841	Zfp867	chr11	59286649	59287108	1.7	1.7	0.6	transcriptic
NM_14582	Nlrp3	chr11	59355460	59356014	2.2	2.0	0.7	transcriptic
NM_01199	Cops3	chr11	59654752	59655702	0.2	0.7	3.1	transcriptic
NM_17294	Alkbh5	chr11	60348856	60349643	0.3	0.4	1.6	transcriptic
NM_17345	Tmem11	chr11	60694485	60695215	0.8	0.9	2.1	transcriptic
NM_02529	Gm16515	chr11	60728623	60729532	0.6	0.7	2.0	transcriptic
NA	chr11:6237	chr11	62374031	62374707	1.1	0.7	2.2	CpG Islands

NM_02621	Fam18b	chr11	62690533	62691505	1.7	1.2	4.2	transcriptic
NM_15310	Kif1c	chr11	70514177	70514731	0.4	1.1	2.3	transcriptic
NM_17771	Ssh2	chr11	77029808	77030142	0.6	0.8	2.0	transcriptic
NM_02953	Tmem98	chr11	80624209	80624682	2.3	2.6	1.1	transcriptic
NM_00774	Col1a1	chr11	94797728	94798282	0.8	1.4	3.1	transcriptic
NM_17226	Ppp1r9b	chr11	94850167	94850416	2.0	2.6	1.0	transcriptic
NM_02702	Lrrc46	chr11	96904513	96905667	1.3	1.0	3.6	transcriptic
NM_02695	Cdk12	chr11	98061783	98062167	0.8	1.0	2.1	transcriptic
NM_00847	Krt19	chr11	1E+08	1E+08	0.4	0.9	1.9	transcriptic
NM_02891	Ttc25	chr11	1E+08	1E+08	0.3	0.1	1.4	transcriptic
NM_00102	Cant1	chr11	1.18E+08	1.18E+08	1.4	2.0	4.0	transcriptic
NM_15354	Lrrc45	chr11	1.21E+08	1.21E+08	0.9	1.5	3.0	transcriptic
NM_01954	Msgn1	chr12	11218036	11218673	2.3	2.4	0.2	transcriptic
NM_02975	Fam49a	chr12	12268597	12269359	0.2	0.5	1.6	transcriptic
NA	chr12:1995	chr12	19960055	19960294	0.9	0.8	2.1	CpG Island
NM_01178	Agr2	chr12	36718163	36719728	2.8	2.5	1.3	transcriptic
NM_17780	Prpf39	chr12	66135284	66136843	2.2	1.6	0.3	transcriptic
NM_01138	Six4	chr12	74214356	74215132	0.4	0.8	1.9	transcriptic
NM_02844	Trip11	chr12	1.03E+08	1.03E+08	1.1	1.2	2.3	transcriptic
NM_17336	Eif5	chr12	1.13E+08	1.13E+08	0.2	0.1	1.2	transcriptic
NM_00102	Klc1	chr12	1.13E+08	1.13E+08	0.7	1.1	2.7	transcriptic
NM_00112	BC048943	chr12	1.13E+08	1.13E+08	1.6	1.6	3.3	transcriptic
NM_00108	Aspg	chr12	1.13E+08	1.13E+08	0.4	1.2	2.4	transcriptic
NM_01992	Gpr132	chr12	1.14E+08	1.14E+08	1.1	1.1	3.2	transcriptic
NM_05408	Mta1	chr12	1.14E+08	1.14E+08	0.3	0.6	1.6	transcriptic
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	3.5	transcriptic
NM_02684	Ubqln1	chr13	58286170	58287146	0.4	0.7	1.8	transcriptic
NM_02815	1700013B1	chr13	59807705	59808667	2.7	2.3	0.9	transcriptic
NM_00100	Zfp58	chr13	67600723	67600995	0.2	0.5	2.0	transcriptic
NM_17205	Adamts16	chr13	70981966	70982210	2.2	2.3	0.8	transcriptic
NM_00103	Lrrc14b	chr13	74501428	74501873	0.7	0.8	1.8	transcriptic
NM_02288	Bhmt2	chr13	94446559	94446913	1.0	1.2	2.6	transcriptic
NM_00114	Fam169a	chr13	97837059	97837582	1.9	2.5	0.7	transcriptic
NM_00103	Gm7120	chr13	1.2E+08	1.2E+08	1.0	1.0	2.1	transcriptic
NM_02593	Rpp14	chr14	8912866	8913290	0.0	0.2	1.3	transcriptic
NM_00103	Defb47	chr14	63613985	63614658	2.1	1.8	0.4	transcriptic
NM_14624	Rp1l1	chr14	64609950	64610499	0.2	0.5	1.6	transcriptic
NM_02632	Msra	chr14	65075018	65075757	0.3	0.5	1.6	transcriptic
NM_01351	Epb4.9	chr14	71029234	71030178	1.3	0.9	3.2	transcriptic
NM_00976	Klf5	chr14	99695156	99695610	2.6	2.0	0.6	transcriptic
NA	chr14:1212	chr14	1.21E+08	1.21E+08	0.6	0.9	2.1	CpG Island
NM_14452	Zfp622	chr15	25911170	25911834	0.1	0.0	1.9	transcriptic
NM_00101	Fam105b	chr15	27560776	27561139	1.0	1.0	2.2	transcriptic
NM_18131	Kcns2	chr15	34765879	34766535	0.4	0.5	1.7	transcriptic
NM_05327	Rims2	chr15	39028733	39028967	0.0	0.1	1.3	transcriptic
NM_17722	Samd12	chr15	53733253	53734732	0.0	0.1	1.4	transcriptic
NM_17775	Klhl38	chr15	58155984	58156510	0.9	1.0	2.1	transcriptic
NM_02050	Tob2	chr15	81690041	81691672	0.0	0.0	1.3	transcriptic
NM_17826	Cenpm	chr15	82075636	82076139	0.6	0.7	2.3	transcriptic
NM_01188	Sept3	chr15	82104802	82106136	0.5	0.5	2.1	transcriptic

NM_02691	1500032L2	chr15	82174923	82175984	1.5	1.4	3.3	transcriptic
NM_00111	Tcf20	chr15	82744624	82745070	3.7	2.9	1.2	transcriptic
NM_17523	5830427D(	chr15	98592518	98593066	1.0	1.3	2.6	transcriptic
NM_01066	Krt86	chr15	1.01E+08	1.01E+08	0.0	0.2	2.4	Primary Tra
NM_17771	4732456N1	chr15	1.01E+08	1.01E+08	0.8	1.1	2.4	transcriptic
NM_02639	Nmral1	chr16	4719145	4719399	1.1	0.0	2.4	transcriptic
NM_00112	Atp13a3	chr16	30388001	30388435	0.4	0.6	1.6	transcriptic
NM_00846	Kpna1	chr16	35983895	35984159	0.8	0.9	2.4	transcriptic
NM_17251	Abhd10	chr16	45744899	45745784	0.7	0.7	2.2	transcriptic
NM_02388	Retnlb	chr16	48816628	48817705	2.9	2.5	0.8	transcriptic
NM_01391	Usp25	chr16	77013178	77013802	0.4	0.5	1.7	transcriptic
NM_00938	Tiam1	chr16	89960639	89961959	2.5	2.6	0.9	transcriptic
NA	chr17:1567	chr17	15673304	15673974	0.1	0.2	1.7	CpG Island:
NM_01375	Sepx1	chr17	24873427	24874176	0.0	0.2	1.3	transcriptic
NA	chr17:2765	chr17	27657529	27658168	0.1	0.8	1.9	CpG Island:
NM_01022	Fkbp5	chr17	28623140	28623384	0.5	0.3	1.5	transcriptic
NM_01083	Sik1	chr17	31991950	31992389	1.4	1.4	3.0	transcriptic
NA	chr17:3306	chr17	33061503	33062137	0.7	1.4	3.5	CpG Island:
NM_01038	H2-DMb1	chr17	34288861	34289150	2.1	3.4	0.8	transcriptic
NM_01153	Tap2	chr17	34338563	34340817	1.0	1.4	3.0	transcriptic
NM_01037	H2-Aa	chr17	34426788	34427047	1.7	1.9	0.4	transcriptic
NM_01089	Neu1	chr17	35066182	35066458	0.8	0.9	2.0	transcriptic
NM_14894	Ly6g5c	chr17	35245006	35245255	1.4	1.3	3.1	transcriptic
NM_01039	H2-Q1	chr17	35456143	35456412	0.0	0.2	1.2	transcriptic
NM_14607	Trim31	chr17	37034587	37035831	0.6	0.8	2.6	transcriptic
NM_02316	Znrd1	chr17	37094580	37094946	0.1	0.4	1.9	transcriptic
NM_14647	Olfr90	chr17	37222990	37223631	3.6	2.4	0.8	transcriptic
NA	chr17:3998	chr17	39985220	39985574	0.7	0.6	1.8	CpG Island:
NM_13377	Gpr110	chr17	43405385	43406682	2.1	1.9	0.9	transcriptic
NM_00100	Tmem232	chr17	65889800	65890438	0.7	0.6	1.8	transcriptic
NM_00115	Cox7a2l	chr17	83914575	83915024	3.2	3.1	1.4	transcriptic
NM_02532	Haao	chr17	84245404	84246965	0.1	0.7	1.9	transcriptic
NM_17339	Ticam2	chr18	46733459	46734858	0.6	0.4	2.1	transcriptic
NM_02145	Pmaip1	chr18	66616720	66617155	0.6	0.8	2.0	transcriptic
NM_01697	Mc4r	chr18	67019389	67019838	0.3	0.5	1.8	transcriptic
NM_02128	Spnb3	chr19	4711562	4712113	0.4	1.0	2.1	transcriptic
NM_00795	Esrra	chr19	6995766	6996010	0.0	0.2	1.2	transcriptic
NM_14487	Uhrf2	chr19	30103567	30104129	3.1	1.8	0.8	transcriptic
NM_00104	Dntt	chr19	41102251	41102580	0.9	0.5	2.5	transcriptic
NM_00104	Dntt	chr19	41103603	41103937	0.2	0.2	1.5	transcriptic
NM_00110	Gm6813	chr19	45953657	45953916	0.8	1.0	2.2	transcriptic
NM_00770	Elovl3	chr19	46206175	46207124	0.2	0.3	1.4	transcriptic
NM_00108	Calhm1	chr19	47220974	47221648	0.8	0.9	3.5	transcriptic
NM_00896	Pter	chr2	12844076	12844325	3.7	3.5	1.4	transcriptic
NM_17059	Mettl11a	chr2	30663012	30663361	0.1	0.7	1.9	transcriptic
NM_01940	Nmi	chr2	51831185	51831734	0.2	0.3	1.6	transcriptic
NM_00111	Acvr1c	chr2	58209935	58210199	0.6	1.1	2.3	transcriptic
NM_02563	Metapl1	chr2	71290205	71290560	0.9	0.9	2.5	transcriptic
NM_02823	Ttc30b	chr2	75775796	75777551	0.7	0.7	2.0	transcriptic
NM_03018	Ttc30a1	chr2	75819405	75820054	0.3	0.7	1.7	transcriptic

NM_00902	Rapsn	chr2	90874151	90875165	2.9	2.9	1.0	transcriptic
NM_17267	Gyltl1b	chr2	92212550	92214079	0.3	0.9	2.0	transcriptic
NM_13831	Bmf	chr2	1.18E+08	1.18E+08	0.2	0.3	1.7	transcriptic
NM_17059	Disp2	chr2	1.19E+08	1.19E+08	1.4	1.1	3.5	transcriptic
NM_00104	Bahd1	chr2	1.19E+08	1.19E+08	0.2	0.2	1.5	transcriptic
NM_00922	Snrpb	chr2	1.3E+08	1.3E+08	0.5	0.7	1.9	transcriptic
NM_02996	9230104L0	chr2	1.49E+08	1.49E+08	0.1	0.6	1.6	transcriptic
NM_02852	1700058C1	chr2	1.54E+08	1.54E+08	1.5	1.5	0.2	transcriptic
NM_14489	BC018465	chr2	1.54E+08	1.54E+08	2.5	2.7	1.1	transcriptic
NM_00104	Dlgap4	chr2	1.57E+08	1.57E+08	1.1	1.6	3.2	transcriptic
NM_17211	Myl9	chr2	1.57E+08	1.57E+08	0.8	0.9	2.1	transcriptic
NM_00103	4922505G1	chr2	1.57E+08	1.57E+08	2.4	1.5	0.5	transcriptic
NM_02696	Manbal	chr2	1.57E+08	1.57E+08	3.0	2.3	0.8	transcriptic
NM_02696	Manbal	chr2	1.57E+08	1.57E+08	0.7	0.3	1.8	transcriptic
NM_02156	Jph2	chr2	1.63E+08	1.63E+08	0.8	0.9	1.9	Primary Tra
NM_05405	Slc13a3	chr2	1.65E+08	1.65E+08	1.1	1.4	2.8	transcriptic
NM_00103	Gcnt7	chr2	1.72E+08	1.72E+08	0.2	0.7	1.9	transcriptic
NM_02058	Th1l	chr2	1.74E+08	1.74E+08	0.7	0.8	2.3	transcriptic
NM_17772	Lsm14b	chr2	1.8E+08	1.8E+08	0.2	0.7	1.7	transcriptic
NM_19816	Gmeb2	chr2	1.81E+08	1.81E+08	0.1	0.2	1.6	transcriptic
NM_13321	Zfp704	chr3	9450805	9452089	2.1	1.8	0.7	Primary Tra
NM_02915	Spata16	chr3	26535189	26535925	3.1	3.4	0.3	transcriptic
NM_00111	Fxr1	chr3	33917468	33917962	0.4	0.2	1.5	transcriptic
NM_00982	Ccna2	chr3	36472717	36473089	0.0	0.0	1.4	transcriptic
NM_19865	Gm5148	chr3	37624779	37626218	0.6	0.7	2.7	transcriptic
NA	chr3:38383	chr3	38383420	38384254	0.9	1.4	2.9	CpG Islands
NM_13378	Nmd3	chr3	69523082	69523736	2.5	2.3	0.7	transcriptic
NM_18181	Rxfp4	chr3	88458795	88459034	1.6	1.7	0.3	transcriptic
NM_01043	Hipk1	chr3	1.04E+08	1.04E+08	0.1	0.5	1.6	transcriptic
NM_00861	Mov10	chr3	1.05E+08	1.05E+08	0.0	0.6	1.7	transcriptic
NM_02748	5730508BC	chr3	1.28E+08	1.28E+08	0.9	0.4	2.3	transcriptic
NM_01675	H2afz	chr3	1.38E+08	1.38E+08	0.8	0.8	2.5	transcriptic
NM_00756	Bmpr1b	chr3	1.42E+08	1.42E+08	4.0	4.0	1.9	transcriptic
NM_00752	Bach2	chr4	32325778	32326059	0.8	0.8	2.0	transcriptic
NM_00103	Gm136	chr4	34704589	34705258	2.3	2.5	0.6	transcriptic
NM_00111	Cd72	chr4	43469602	43470408	1.0	1.8	3.8	transcriptic
NM_01349	Creb3	chr4	43573457	43574034	0.8	1.2	2.7	transcriptic
NM_01079	Melk	chr4	44313278	44313627	0.4	0.5	1.6	transcriptic
NM_01999	Alg2	chr4	47488672	47489525	3.4	2.1	1.0	transcriptic
NM_14490	6330416G1	chr4	63220654	63220983	0.6	0.5	1.6	transcriptic
NM_14490	Sgip1	chr4	1.02E+08	1.02E+08	0.6	0.8	1.9	transcriptic
NM_15356	Pcsk9	chr4	1.06E+08	1.06E+08	1.2	1.6	3.1	transcriptic
NM_00100	Zfp69	chr4	1.21E+08	1.21E+08	0.4	0.4	1.8	transcriptic
NM_00100	Maneal	chr4	1.25E+08	1.25E+08	1.3	1.2	2.6	transcriptic
NM_02703	Hmgb4	chr4	1.28E+08	1.28E+08	0.5	1.1	2.6	transcriptic
NM_02599	Nkain1	chr4	1.3E+08	1.3E+08	1.3	1.2	3.1	transcriptic
NM_00113	Catsper4	chr4	1.34E+08	1.34E+08	1.2	1.1	2.9	transcriptic
NM_02366	D4Wsu53e	chr4	1.34E+08	1.34E+08	0.0	0.1	1.2	transcriptic
NM_17825	Il22ra1	chr4	1.35E+08	1.35E+08	0.7	1.1	2.3	transcriptic
NM_13387	Kdm1a	chr4	1.36E+08	1.36E+08	0.7	0.8	1.9	transcriptic

NM_00854	Mfap2	chr4	1.41E+08	1.41E+08	2.3	2.4	1.1	transcriptic
NM_03137	Pramel1	chr4	1.43E+08	1.43E+08	3.2	3.1	1.5	transcriptic
NM_00108	Aadacl3	chr4	1.44E+08	1.44E+08	0.5	0.6	1.8	transcriptic
NM_01024	Fv1	chr4	1.47E+08	1.47E+08	2.4	2.1	0.5	transcriptic
NM_02742	2610109H	chr4	1.48E+08	1.48E+08	0.9	0.7	2.1	transcriptic
NM_00103	Angptl7	chr4	1.48E+08	1.48E+08	1.8	1.8	0.8	transcriptic
NM_00100	Tardbp	chr4	1.48E+08	1.48E+08	3.1	2.7	1.2	transcriptic
NM_02202	Rbp7	chr4	1.49E+08	1.49E+08	1.7	1.8	0.5	transcriptic
NM_02305	Clstn1	chr4	1.49E+08	1.49E+08	0.6	1.1	2.3	transcriptic
NM_01974	Slc2a5	chr4	1.49E+08	1.49E+08	0.5	1.2	2.7	transcriptic
NM_20768	Espn	chr4	1.52E+08	1.52E+08	0.6	1.1	2.2	transcriptic
NM_15342	Nphp4	chr4	1.52E+08	1.52E+08	0.5	0.7	2.7	transcriptic
NM_01138	Ski	chr4	1.55E+08	1.55E+08	0.4	0.5	2.2	transcriptic
NM_03187	Tas1r3	chr4	1.55E+08	1.55E+08	0.8	0.8	2.3	transcriptic
NM_14555	9430015G1	chr4	1.55E+08	1.55E+08	0.4	0.3	2.2	transcriptic
NM_00108	Mll3	chr5	25004029	25004691	0.4	1.0	2.2	transcriptic
NM_14514	Gtpbp6	chr5	1.11E+08	1.11E+08	0.8	0.9	2.2	Primary Tra
NM_14520	Oasl1	chr5	1.15E+08	1.15E+08	0.9	0.8	2.4	transcriptic
NM_00103	Vgf	chr5	1.38E+08	1.38E+08	1.2	1.4	3.0	transcriptic
NM_14491	Mepce	chr5	1.38E+08	1.38E+08	0.0	0.1	1.2	transcriptic
NM_00108	Trrap	chr5	1.46E+08	1.46E+08	2.0	1.7	0.4	transcriptic
NM_02700	Rfc3	chr5	1.52E+08	1.52E+08	0.7	0.5	1.7	transcriptic
NR_01534	Hoxa11as	chr6	52193035	52193284	0.1	0.2	1.5	transcriptic
NM_00116	Smyd1	chr6	71211535	71211909	3.0	2.3	0.8	transcriptic
NM_02354	Ino80b	chr6	83074812	83075241	0.6	0.9	1.9	transcriptic
NM_05320	Foxp1	chr6	99113652	99114001	3.6	2.9	1.3	transcriptic
NM_00110	2510049J1	chr6	1.16E+08	1.16E+08	1.4	1.1	0.1	transcriptic
NM_02658	D6Wsu116	chr6	1.16E+08	1.16E+08	2.7	2.3	1.0	transcriptic
NM_02170	Cxcl12	chr6	1.17E+08	1.17E+08	0.3	1.0	2.4	transcriptic
NM_17552	Leng9	chr7	4103135	4103487	0.4	0.8	2.0	transcriptic
NM_01176	Zim1	chr7	6651662	6652106	0.0	0.0	1.5	transcriptic
NM_01133	Clcn4-2	chr7	7253199	7253628	3.3	3.3	1.5	transcriptic
NM_00771	Ckm	chr7	19994706	19995055	1.4	1.6	0.3	transcriptic
NM_18278	Lypd4	chr7	25654065	25654794	1.5	1.7	3.7	transcriptic
NA	chr7:30928	chr7	30928705	30929145	0.6	0.3	1.7	CpG Islands
NM_00876	Fxyd5	chr7	31829646	31830275	0.8	1.4	2.7	transcriptic
NM_01132	Scn1b	chr7	31912858	31914178	0.8	0.9	2.3	transcriptic
NM_17486	Klk15	chr7	51188879	51189531	1.7	1.3	3.9	transcriptic
NM_00101	Izumo1	chr7	52875829	52876398	1.8	2.0	4.6	transcriptic
NA	chr7:74948	chr7	74948300	74948975	0.1	0.2	1.6	CpG Islands
NM_01055	Il16	chr7	90883272	90883721	3.6	3.3	1.5	transcriptic
NM_02824	Prcp	chr7	1E+08	1E+08	0.6	0.6	2.7	transcriptic
NM_18185	Trim66	chr7	1.17E+08	1.17E+08	0.7	0.8	2.0	transcriptic
NM_00947	Umod	chr7	1.27E+08	1.27E+08	1.2	1.3	3.1	transcriptic
NM_02530	Lcmt1	chr7	1.31E+08	1.31E+08	1.6	2.1	0.4	transcriptic
NM_18328	Tcerg1l	chr7	1.46E+08	1.46E+08	0.1	0.4	1.7	transcriptic
NM_01150	Stxbp2	chr8	3629320	3629942	1.3	1.4	3.0	transcriptic
NM_17708	Zmat4	chr8	24779815	24780851	0.9	1.1	2.3	transcriptic
NM_00103	Ccdc110	chr8	47020449	47020693	0.1	0.4	1.4	transcriptic
NM_00100	Crtc1	chr8	72964805	72965279	2.0	2.2	0.8	transcriptic

NM_01059	Jund	chr8	73220847	73221777	0.3	0.7	1.8	transcriptic
NM_14562	Zfp709	chr8	74404951	74405378	0.2	0.2	1.5	transcriptic
NA	chr8:74432	chr8	74432347	74432981	0.0	0.3	1.8	CpG Island
NR_02688	4930488L2	chr8	96339711	96339955	0.7	1.2	2.6	transcriptic
NM_00104	Ccdc135	chr8	97576064	97576626	3.1	2.4	0.9	transcriptic
NM_02853	Tepp	chr8	97844191	97844840	0.1	0.3	1.5	Primary Tra
NM_00917	St3gal2	chr8	1.13E+08	1.13E+08	1.1	1.1	2.4	transcriptic
NM_00917	St3gal2	chr8	1.13E+08	1.13E+08	0.7	0.4	1.7	Primary Tra
NM_02968	Pkd1l2	chr8	1.2E+08	1.2E+08	2.1	2.8	0.5	transcriptic
NM_02968	Pkd1l2	chr8	1.2E+08	1.2E+08	1.7	1.5	0.5	transcriptic
NM_14560	Chmp1a	chr8	1.26E+08	1.26E+08	0.9	0.9	2.1	transcriptic
NM_05407	Afg3l1	chr8	1.26E+08	1.26E+08	1.8	1.6	0.1	transcriptic
NM_01687	Eif3g	chr9	20705450	20705821	0.7	0.7	2.0	transcriptic
NM_17229	Ntm	chr9	29769978	29770629	0.3	0.9	2.0	transcriptic
NM_02887	Snx19	chr9	30233402	30234760	0.5	0.6	1.8	transcriptic
NM_02528	Tbrg1	chr9	37467057	37467817	0.3	0.5	1.7	transcriptic
NM_14641	Olfr877	chr9	37661972	37662731	3.0	1.8	0.2	transcriptic
NM_14685	Olfr982	chr9	39881443	39882282	2.5	1.5	0.5	transcriptic
NM_14561	Etfa	chr9	55361668	55362512	0.5	0.5	1.6	transcriptic
NA	chr9:63775	chr9	63775218	63775860	0.4	1.5	3.5	CpG Island
NA	chr9:88494	chr9	88494209	88494858	0.2	0.0	1.8	CpG Island
NA	chr9:88753	chr9	88753512	88754171	0.0	0.0	1.8	CpG Island
NA	chr9:88961	chr9	88961199	88961948	0.3	0.0	2.2	CpG Island
NM_17871	Plscr4	chr9	92351355	92351705	0.5	0.2	2.2	transcriptic
NA	chr9:96437	chr9	96437157	96437816	1.1	1.2	4.3	CpG Island
NM_02231	Clstn2	chr9	97932848	97933502	0.4	1.1	2.2	transcriptic
NM_02156	Pcbp4	chr9	1.06E+08	1.06E+08	0.3	0.7	1.9	transcriptic
NM_17711	Dlec1	chr9	1.19E+08	1.19E+08	2.4	2.5	1.2	transcriptic
NM_01188	Scn11a	chr9	1.2E+08	1.2E+08	2.0	2.1	0.9	transcriptic
NM_15328	Csrnp1	chr9	1.2E+08	1.2E+08	0.6	1.1	2.4	transcriptic
NA	chr9:12048	chr9	1.2E+08	1.2E+08	0.1	0.0	1.3	CpG Island
NM_21113	Pcyt1b	chrX	90920589	90921128	0.0	0.5	1.6	transcriptic
NM_02656	Apool	chrX	1.09E+08	1.09E+08	0.7	0.9	2.0	transcriptic

orientatior	descriptior	DISSTRIBU	gene_id
-	minichrom	DISTAL	17215
-	PHD finger	DISTAL	213109
-	regulatory	PROXIMAL	619289
-	amyotroph	PROXIMAL	73463
-	RIKEN cDN	DISTAL	68691
+	transmemb	DISTAL	271711
+	proteasom	DISTAL	70247
-	RAB17, me	INTRAGENI	19329
-	RAB17, me	PROXIMAL	19329
-	hairy and e	PROXIMAL	55927
+	D-2-hydrox	PROXIMAL	98314
+	expressed :	DISTAL	212439
+	Fc receptor	PROXIMAL	64435
+	protein tyr	DISTAL	320139
-	importin 9	INTRAGENI	226432
+	pleckstrin h	DISTAL	27280
+	troponin I,	DISTAL	21952
+	troponin T:	DISTAL	21956
.	0	INTERGENI	0
.	0	INTERGENI	0
-	nitric oxide	INTRAGENI	70729
-	Fc receptor	DISTAL	14131
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
+	dynein, axc	DISTAL	240960
+	signal reco	DISTAL	27058
+	peptidylprc	DISTAL	67418
+	Rho-relate	DISTAL	69288
+	cDNA sequ	DISTAL	103220
+	ADP-ribosy	DISTAL	104303
+	nuclear rec	DISTAL	22025
-	cleavage ar	PROXIMAL	432508
-	methionine	DISTAL	320183
-	HORMA do	INTRAGENI	75828
+	insulin-like	DISTAL	16006
+	slit homolo	DISTAL	20564
-	solute carri	INTRAGENI	215332
+	SH3 bindin	PROXIMAL	79566
+	wingless-ty	PROXIMAL	216795
-	zinc finger	DISTAL	237775
+	NLR family,	PROXIMAL	216799
-	COP9 (cons	DISTAL	26572
+	alkB, alkyla	DISTAL	268420
-	transmemb	DISTAL	216821
-	predicted g	DISTAL	24083
.	0	INTERGENI	0

+	family with	DISTAL	67510
+	kinesin fam	INTRAGENI	16562
+	slingshot h	PROXIMAL	237860
+	transmemb	INTRAGENI	103743
+	collagen, ty	INTRAGENI	12842
+	protein pho	DISTAL	217124
-	leucine rich	DISTAL	69297
+	cyclin-depe	DISTAL	69131
-	keratin 19	PROXIMAL	16669
+	tetratricop	DISTAL	74407
-	calcium act	PROXIMAL	76025
+	leucine rich	DISTAL	217366
-	mesogenin	DISTAL	56184
+	family with	PROXIMAL	76820
.	0	INTERGENI	0
+	anterior gra	PROXIMAL	23795
+	PRP39 pre-	PROXIMAL	328110
-	sine oculis-	PROXIMAL	20474
-	thyroid hor	DISTAL	109181
+	eukaryotic	PROXIMAL	217869
+	kinesin ligh	DISTAL	16593
-	cDNA sequ	DISTAL	217874
+	asparagina	PROXIMAL	104816
-	G protein-c	DISTAL	56696
+	metastasis	INTRAGENI	116870
-	aldo-keto r	PROXIMAL	56043
-	ubiquilin 1	DISTAL	56085
-	RIKEN cDNA	PROXIMAL	72219
-	zinc finger	INTRAGENI	238693
-	a disintegri	DISTAL	271127
-	leucine rich	PROXIMAL	432779
-	betaine-ho	DISTAL	64918
+	family with	PROXIMAL	320557
+	predicted g	PROXIMAL	633640
+	ribonucleas	PROXIMAL	67053
+	defensin be	DISTAL	654465
+	retinitis pig	DISTAL	271209
-	methionine	PROXIMAL	110265
-	erythrocyte	PROXIMAL	13829
+	Kruppel-lik	DISTAL	12224
.	0	INTERGENI	0
+	zinc finger	DISTAL	52521
-	family with	PROXIMAL	432940
+	K+ voltage-	DISTAL	16539
+	regulating s	DISTAL	116838
-	sterile alph	PROXIMAL	320679
-	kelch-like 3	PROXIMAL	268807
-	transducer	DISTAL	57259
-	centromere	PROXIMAL	66570
+	septin 3	PROXIMAL	24050

+	RIKEN cDN	PROXIMAL	69029
-	transcriptic	DISTAL	21411
-	0	PROXIMAL	0
+	keratin 86	INTRAGENI	16679
-	RIKEN cDN	DISTAL	239673
-	NmrA-like f	PROXIMAL	67824
-	ATPase typ	INTRAGENI	224088
+	karyopheri	INTRAGENI	16646
-	abhydrolas	DISTAL	213012
+	resistin like	PROXIMAL	57263
+	ubiquitin s	DISTAL	30940
-	T-cell lymp	PROXIMAL	21844
.	0	INTERGENI	0
+	selenoprot	PROXIMAL	27361
.	0	INTERGENI	0
-	FK506 bind	PROXIMAL	14229
-	salt inducib	INTRAGENI	17691
.	0	INTERGENI	0
+	histocomp	DISTAL	14999
+	transporte	DISTAL	21355
-	histocomp	DISTAL	14960
+	neuraminic	DISTAL	18010
+	lymphocyt	PROXIMAL	114652
+	histocomp	DISTAL	15006
+	tripartite m	PROXIMAL	224762
-	zinc ribbon	INTRAGENI	66136
-	olfactory re	PROXIMAL	258469
.	0	INTERGENI	0
+	G protein-c	DISTAL	77596
-	transmemb	PROXIMAL	381107
-	cytochrom	DISTAL	20463
-	3-hydroxya	PROXIMAL	107766
-	toll-like rec	PROXIMAL	225471
+	phorbol-12	DISTAL	58801
-	melanocor	INTRAGENI	17202
+	spectrin be	INTRAGENI	20743
-	estrogen re	INTRAGENI	26379
+	ubiquitin-li	DISTAL	109113
+	deoxynucle	DISTAL	21673
+	deoxynucle	PROXIMAL	21673
-	predicted g	DISTAL	627939
+	elongation	PROXIMAL	12686
-	calcium ho	DISTAL	546729
+	phosphotri	DISTAL	19212
+	methyltran	PROXIMAL	66617
-	N-myc (anc	DISTAL	64685
-	activin A re	PROXIMAL	269275
+	methionine	DISTAL	66559
-	tetratricop	PROXIMAL	72421
-	tetratricop	PROXIMAL	78802

+	receptor-a	DISTAL	19400
-	glycosyltra	DISTAL	228366
-	BCL2 modi	DISTAL	171543
+	dispatched	INTRAGENI	214240
+	bromo adj	PROXIMAL	228536
-	small nucle	PROXIMAL	20638
-	RIKEN cDN	PROXIMAL	77705
+	RIKEN cDN	DISTAL	73388
+	cDNA sequ	PROXIMAL	228802
+	discs, large	PROXIMAL	228836
+	myosin, lig	DISTAL	98932
-	RIKEN cDN	DISTAL	629499
+	mannosida	DISTAL	69161
+	mannosida	PROXIMAL	69161
-	junctophili	INTRAGENI	59091
-	solute carri	PROXIMAL	114644
-	glucosamin	DISTAL	654821
+	TH1-like h	PROXIMAL	57314
+	LSM14 hon	DISTAL	241846
-	glucocortic	INTRAGENI	229004
-	zinc finger	INTRAGENI	170753
+	spermatog	DISTAL	70862
+	fragile X m	DISTAL	14359
-	cyclin A2	DISTAL	12428
-	predicted g	DISTAL	381438
.	0	INTERGENI	0
+	NMD3 hon	DISTAL	97112
-	relaxin fam	DISTAL	242093
-	homeodon	PROXIMAL	15257
-	Moloney le	PROXIMAL	17454
-	RIKEN cDN	PROXIMAL	70617
+	H2A histon	INTRAGENI	51788
-	bone morp	INTRAGENI	12167
+	BTB and C	PROXIMAL	12014
-	predicted g	DISTAL	214568
-	CD72 antig	DISTAL	12517
+	cAMP resp	DISTAL	12913
+	maternal e	PROXIMAL	17279
-	asparagine	DISTAL	56737
+	RIKEN cDN	PROXIMAL	230279
+	SH3-domai	PROXIMAL	73094
-	proprotein	PROXIMAL	100102
-	zinc finger	PROXIMAL	381549
-	mannosida	DISTAL	215090
-	high-mobili	DISTAL	69317
+	Na+/K+ tra	PROXIMAL	67149
-	cation char	DISTAL	329954
+	DNA segme	DISTAL	27981
+	interleukin	DISTAL	230828
-	lysine (K)-s	PROXIMAL	99982

+	microfibrill	PROXIMAL	17150
+	preferentia	PROXIMAL	83491
-	arylacetam	PROXIMAL	230883
+	Friend viru	INTRAGENI	14349
-	RIKEN cDN	DISTAL	70433
-	angiopoieti	PROXIMAL	654812
-	TAR DNA b	DISTAL	230908
-	retinol bin	DISTAL	63954
+	calsynteni	INTRAGENI	65945
+	solute carri	DISTAL	56485
-	espin	DISTAL	56226
+	nephronop	INTRAGENI	260305
-	ski sarcom	DISTAL	20481
-	taste recep	PROXIMAL	83771
+	RIKEN cDN	DISTAL	230996
-	myeloid/ly	PROXIMAL	231051
-	GTP bindin	INTRAGENI	107999
+	2'-5' oligoa	DISTAL	231655
+	VGF nerve	DISTAL	381677
-	methylpho	INTRAGENI	231803
+	transforma	DISTAL	100683
-	replication	INTRAGENI	69263
+	HOXA11 ar	DISTAL	15397
-	SET and M	INTRAGENI	12180
-	INO80 com	PROXIMAL	70020
-	forkhead b	DISTAL	108655
-	RIKEN cDN	DISTAL	70291
+	DNA segm	DISTAL	28006
+	chemokine	DISTAL	20315
-	leukocyte r	DISTAL	243813
-	zinc finger,	DISTAL	22776
-	chloride ch	DISTAL	12727
+	creatine ki	DISTAL	12715
-	Ly6/Plaur c	PROXIMAL	232973
.	0	INTERGENI	0
-	FXYD dom	DISTAL	18301
-	sodium ch	DISTAL	20266
+	kallikrein r	PROXIMAL	317652
+	izumo sper	DISTAL	73456
.	0	INTERGENI	0
-	interleukin	INTRAGENI	16170
+	prolylcarb	DISTAL	72461
-	tripartite	DISTAL	330627
-	uromoduli	DISTAL	22242
+	leucine car	DISTAL	30949
-	transcripti	INTRAGENI	70571
+	syntaxin bi	DISTAL	20911
+	zinc finger,	PROXIMAL	320158
+	coiled-coil	INTRAGENI	212392
-	CREB regul	DISTAL	382056

+	Jun proto-	PROXIMAL	16478
+	zinc finger	DISTAL	236193
.	0	INTERGENI	0
-	RIKEN cDN	DISTAL	75809
+	coiled-coil	DISTAL	330830
+	testis, pros	INTRAGENI	73407
+	ST3 beta-g	INTRAGENI	20444
+	ST3 beta-g	INTRAGENI	20444
-	polycystic	PROXIMAL	76645
-	polycystic	DISTAL	76645
-	chromatin	DISTAL	234852
+	AFG3(ATPa	DISTAL	114896
-	eukaryotic	DISTAL	53356
-	neurotrimi	PROXIMAL	235106
+	sorting nex	PROXIMAL	102607
-	transformi	DISTAL	21376
+	olfactory r	PROXIMAL	258412
+	olfactory r	PROXIMAL	258853
-	electron tr	DISTAL	110842
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
+	phospholip	DISTAL	235527
.	0	INTERGENI	0
-	calsynteni	PROXIMAL	64085
+	poly(rC) bi	PROXIMAL	59092
+	deleted in	DISTAL	320256
-	sodium ch	PROXIMAL	24046
-	cysteine-se	DISTAL	215418
.	0	INTERGENI	0
+	phosphate	INTRAGENI	236899
+	apolipopro	PROXIMAL	68117

Differentially methylated regions found in bone marrow connected with 2 fold in gene expression lev

ACC	Name	chr	start	end	BBMrS	BcBMrS	MBMrS	feature DI
NM_02742	2610109H	chr4	1.48E+08	1.48E+08	0.9	0.7	2.1	transcriptic
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	3.5	transcriptic
NM_00111	Cd72	chr4	43469602	43470408	1.0	1.8	3.8	transcriptic
NM_14496	Fcamr	chr1	1.33E+08	1.33E+08	0.7	1.2	2.4	transcriptic
NM_14496	Fcamr	chr1	1.33E+08	1.33E+08	0.7	1.2	2.4	transcriptic
NM_02529	Gm16515	chr11	60728623	60729532	0.6	0.7	2.0	transcriptic
NM_01992	Gpr132	chr12	1.14E+08	1.14E+08	1.1	1.1	3.2	transcriptic
NM_01037	H2-Aa	chr17	34426788	34427047	1.7	1.9	0.4	transcriptic
NM_14582	Nlrp3	chr11	59355460	59356014	2.2	2.0	0.7	transcriptic
NM_17229	Ntm	chr9	29769978	29770629	0.3	0.9	2.0	transcriptic
NM_01375	Phlda3	chr1	1.38E+08	1.38E+08	1.8	1.8	0.4	transcriptic
NM_17871	Plscr4	chr9	92351355	92351705	0.5	0.2	2.2	transcriptic
NM_02915	Spata16	chr3	26535189	26535925	3.1	3.4	0.3	transcriptic
NM_17339	Ticam2	chr18	46733459	46734858	0.6	0.4	2.1	transcriptic
NM_02146	Tnni1	chr1	1.38E+08	1.38E+08	1.3	1.3	2.7	transcriptic

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orientatior	descriptior	DISSTRIBU	gene_id	transcript_	BBMrS	SE_EXPRS	BcBMrS	SE_EXPRS
-	RIKEN cDN.	DISTAL	70433	BC060239	260.14	0.8844	853.6348	0.8143
-	aldo-keto r	PROXIMAL	56043	BC012692	533.4892	0.9742	432.1439	0.9533
-	CD72 antig	DISTAL	12517	NM_0011	7919.253	0.9929	9352.71	0.9871
+	Fc receptor	PROXIMAL	64435	BC110549	139.5055	0.8601	159.7416	0.8754
+	Fc receptor	PROXIMAL	64435	BC110550	128.2052	0.8794	198.2844	0.901
-	predicted g	DISTAL	24083	BC034332	2550.147	0.9874	2077.093	0.9707
-	G protein-c	DISTAL	56696	BC120522	461.2466	0.944	352.7706	0.9062
-	histocompa	DISTAL	14960	AK170844	102.7279	0.836	98.2533	0.7597
+	NLR family,	PROXIMAL	216799	BC116175	1161.682	0.9414	1629.876	0.9337
-	neurotrimi	PROXIMAL	235106	BC023307	95.2075	0.7797	119.2547	0.8144
+	pleckstrin h	DISTAL	27280	BC023408	88.7977	0.8097	144.7443	0.7721
+	phospholip	DISTAL	235527	BC052067	84.3819	0.8247	102.4358	0.8353
+	spermatog	DISTAL	70862	BC100443	21.4787	0.5404	27.9147	0.6601
-	toll-like rec	PROXIMAL	225471	BC099933	1033.388	0.9509	1323.4	0.9582
+	troponin I,	DISTAL	21952	BC023170	532.1472	0.9527	276.4404	0.9141

MBMrS	**SE_EXPRS**
127.8866	0.8354
91.0222	0.848
3918.866	0.9779
20.4445	0.6222
29.1175	0.6426
6912.885	0.9825
119.1599	0.8743
37.9203	0.7114
568.9492	0.9394
579.6068	0.8485
340.5161	0.912
37.7412	0.6729
73.9808	0.8221
173.7285	0.9043
1387.449	0.9413

Gene ontology analysis for bone marrow.

GOTerm	Nr. Genes	Term PVal	Associated	Group Gen	Nr. Genes	-log(P-value)
protein rep	3	0.002417	[Msra, Msr	Msra|Msr	3	2.616761
cAMP resp	3	0.016402	[Creb3, Crt	Creb3|Crtc	4	1.785109
response t	4	0.016682	[Acvr1c, M	Acvr1c|Mc	4	1.777759
regulation	16	0.017355	[Adamts16	Adamts16|	39	1.760586
phosphatid	4	0.02425	[Fam21, Jp	Fam21|Jph	4	1.61528
negative re	25	0.030079	[Bach2, Ba	Bach2|Bah	30	1.521731
immunogl	3	0.033783	[Fcamr, Fc	Fcamr|Fcg	3	1.471307
sarcomere	4	0.035096	[Foxp1, Krt	Adamts16|	9	1.454743
antigen pr	5	0.042434	[Fcgr3, H2-	Fcgr3|H2-	5	1.372284

Transcription factor identification for bone marrow.

TF	NES	Targets	Motifs
Srf	4.234	70	7
Eif5a2	4.133	31	2
Yy1	4.018	44	3
Mef2d	3.891	19	3
Ssxa1	3.669	14	2
Msx3	3.478	10	1
Gm9897	3.475	17	1
Snai1	3.402	74	6
Pdx1	3.303	34	4
Meis3	3.284	21	2
Hsf1	3.072	15	1
Rela	3.043	13	1

Promoter sequence motifs

# Rank	Motif id	AUC	NES	ClusterCod	Transcripti	Target genes
1	transfac_p	0.045426	4.23369	M1	Srf	Myl9,Jph2,Ckm,Smyd1,Espn,Zmat
2	tiffin-TIFD	0.044759	4.13255	M2		Tcf20,Six4,Snx19,Arl1,Hmgb4,Mll3
3	encode-U	0.044001	4.01762	M3		Bmpr1b,Vgf,Il16,Tnnt2,Klf5,Krt86,
4	jaspar-PF0	0.043164	3.89074	M4		BC048943,Tnni1,Jph2,Tnnt2,Trim6
5	transfac_p	0.042035	3.71972	M1	Srf	Myl9,Msrb3,Krt19,Col1a1,Ckm,Jp
6	hdpi-SSX3	0.041702	3.66915	M5	Ssxa1,Gm2	Ntm,Kcns2,Uhrf2,Six4,Espn,Cops3,
7	elemento-	0.041046	3.56985	M6		Bahd1,Cdk12,Six4,Trim31,Crtc1,Ar
8	jaspar-MA	0.040786	3.53032	M1	Srf	Myl9,Tnnt2,Krt19,Msrb3,Ckm,Smy
9	flyfactorsu	0.04044	3.47791	M7	Msx3,Msx	Krt86,Foxp1,Tcf20,Espn,Msgn1,Bm
10	encode-U	0.040434	3.47699	M8		BC018465,Scn11a,Klhl38,Zmat4,Kl
11	transfac_p	0.040422	3.47515	M9	Mterf,Gm9	Tiam1,Foxp1,H2-Aa,Rxfp4,Msrb3,
12	tiffin-TIFD	0.040343	3.4632	M8		Cdk12,Trim66,Pcbp4,Ppp1r9b,Jph
13	hdpi-DAZA	0.0403	3.45676	M5	Dazap1	Ntm,Kcns2,Six4,Uhrf2,Foxp1,Mcm
14	transfac_p	0.039936	3.4016	M10	Snai1,Tcf3,	Ssh2,Il16,Rapsn,Tnnt2,Pcyt1b,Smy
15	yetfasco-1	0.039578	3.34735	M11		Sgip1,Rims2,Lypd4,Bmf,H2afz,Ssh
16	taipale-TG	0.039518	3.33816	M10	Meis3,Tgif	Il16,Klhl38,Tiam1,Kcns2,Ssh2,Tnnt
17	factorbook	0.039324	3.30873	M1	Srf	Myl9,Jph2,Ckm,Vgf,Smyd1,Tnnt2,
18	transfac_p	0.039287	3.30322	M12	Pdx1	Msgn1,Scn11a,Clstn2,Vgf,Hormad

19	hdpi-MEIS	0.03916	3.28391	M13	Meis3	Smyd1,Six4,Tnnt2,Rapsn,Il16,Kcns
20	tfdimers-M	0.039105	3.27563	M3	Yy1,Mycs,	Tnnt2,Il16,Klhl38,Angptl7,Rapsn,A
21	taipale-TG	0.038996	3.25908	M10	Gm7148	Il16,Kcns2,Ssh2,Tiam1,Klhl38,Trim
22	hdpi-EIF5A	0.038662	3.20852	M2	Eif5a2	Trim66,Klf5,Espn,Tcf20,Krt19,Klhl
23	tiffin-TIFD	0.038553	3.19197	M14		Tnnt2,Rp1l1,Phf3,Six4,Spnb3,AA9
24	encode-U	0.038529	3.18829	M10		1700058C13Rik,Gm5148,Zmat4,H
25	transfac_p	0.038474	3.18001	M1	Srf	Myl9,Smyd1,Ckm,Msrb3,Zmat4,Jp
26	transfac_p	0.038462	3.17817	M1	Srf	Myl9,Vgf,Ckm,Msrb3,Tnnt2,Zmat4
27	transfac_p	0.038426	3.17266	M12	Nkx2-5	Foxp1,Msgn1,Alkbh5,Zmat4,Lsm1
28	tfdimers-M	0.03828	3.15059	M3	Yy1,Mycs	Klhl38,Smyd1,Tiam1,Ssh2,Trim66,
29	hdpi-TRIP1	0.038183	3.13588	M12	Trip10	Hes6,Fkbp5,Lsm14b,Ntm,1110028
30	tfdimers-M	0.038171	3.13404	M10	Meis1,Hic1	Tnnt2,Mll3,Smyd1,Rapsn,Ssh2,Tri
31	jaspar-PF0	0.038122	3.12669	M1	Srf	Myl9,Ckm,Msgn1,Zmat4,Tnnt2,Ca
32	encode-U	0.037837	3.08347	M13		Csrnp1,Bmpr1b,Tepp,Col1a1,Cats
33	taipale-TT	0.037764	3.07244	M15	Hsf1,Hsf2,	1110028C15Rik,Ubqln1,H2afz,BC0
34	homer-M0	0.03757	3.04302	M16	Rela,Rel,Re	Espn,Ntm,Msrb3,Bahd1,Msra,111
35	hdpi-ZDHH	0.037546	3.03934	M12	Zdhhc15	Tcf20,Lsm14b,Rims2,Smyd1,Ccna2
36	yetfasco-1	0.037443	3.02371	M10	Cnot4	Tcf20,Pter,Gm5148,Nos1ap,Tnnt2,
37	swissregul	0.037382	3.01451	M4	Mef2d,Me	Tcf20,BC048943,Hmgb4,Smyd1,Kl
38	homer-M0	0.037352	3.00992	M4	Mef2c,Mef	BC048943,Tcf20,Klhl38,Jph2,Tnni1

4,Tnnt2,Msrb3,Spnb3,Il16,Kcns2,Bmpr1b,Retnlb,Fkbp5,Vgf,Col1a1
,Ubqln1,Rfc3,Angptl7,Vgf,Trim66,Ccna2,Cd72,Ntm,Sik1,Kcns2,Csrnp1,Ppp1r9b,Bmf,Tmem232,Tmem11,
3C048943,Agr2,Tnni1,Col1a1,1700058C13Rik,Stxbp2,Il22ra1,BC018465,Msgn1
6,Msra,Igfbp1,Lrrc14b,Fam169a,1110028C15Rik,Hmgb4,Klhl38,Ubqln1,Phf3,Agr2
2,Spnb3,Gmeb2,Tnnt2,Il16,Smyd1,Bmpr1b,Lsm14b,Fkbp5,Mov10
,Klhl38,Bmpr1b,1110028C15Rik,Mcm3,4930488L21Rik,Ino80b,Foxp1
l1,Vgf,Mc4r,Nos1ap,Rims2,Sgip1,Ttc30b,Ssh2,Lcmt1
d1,Vgf,Jph2,Bmpr1b,Cant1,Wnt9a,Lsm14b,Spnb3,Ly6g5c
pr1b,Alkbh5,Zmat4,Elovl3,Rp1l1
f5,Oasl1,Pcyt1b,Umod,Il16,Angptl7,Tnni1,Smyd1,Gyltl1b,Olfr90,Nos1ap,Krt19,Jph2,Rhobtb1,H2-Aa,Klk1
Mov10,Elovl3,Olfr90,BC018465,Haao,Hmgb4,Sh3bp5l,Rfx8,Dlgap4,Kpna1,Zmat4,Manbal
2,Tob2,Sgip1,Rhobtb1,Kcns2,Nphp4,2610109H07Rik,H2afz,Tbrg1,Msgn1,H2-Aa,Vgf,Calhm1,Apool,Zmat4
3,Cops3,Bmpr1b,Gpr110,4930488L21Rik,1110028C15Rik,Klhl38,Ino80b,Espn
d1,Krt19,Pkd1l2,Trim66,Stxbp2,Bmpr1b,Tas1r3,Gyltl1b,Aadacl3,Tiam1
2,Fam105b,Rfc3,D4Wsu53e,Sik1,Manbal,Cxcl12,Usp25,Zfp622,Nphp4,Kdm1a,Ubqln1,Dlgap4,Tob2,Eif5,T
2,Klf5,Trim66,Espn,Smyd1,Hipk1,Foxp1,Csrnp1
Zmat4,Msrb3,Msgn1,Spnb3,Espn,Fkbp5,Als2cr11,Kcns2,Bmpr1b,Col1a1,Il16
2,Six4,Rims2,Myl9,Foxp1,Zfp622,Csrnp1,Ntm,Wnt9a,Angptl7,Smyd1,Pcbp4,Lsm14b

2,Mll3,Msgn1,Srp9,Hmgb4,BC018465,Ckm
gr2,Tcf20,Igfbp1,BC030307,Nkain1,Tnni1,Espn,BC018465,Trim66,Pcyt1b
66,Tnnt2,Smyd1,Foxp1,Klf5,Espn,Csrnp1,Hipk1
38,Cd72,Catsper4,Il16,Clstn2,Mfap2
36860,Zfp704,Msgn1,Agr2,Pcyt1b,Angptl7
mgb4,Smyd1,BC018465,Klf5,Foxp1,Kpna1,Gpr110,Aadacl3,Olfr90,Tnnt2,Trim31,Mcm3,Rxfp4,Calhm1,Ptp
h2,Tnnt2,Vgf,Bmpr1b,Kcns2,Col1a1,Cant1,Spnb3,Retnlb,Gm5148,Ubqln1,Tnni1,Krt19,Als2cr11,Fkbp5,BC
,Jph2,Fkbp5,Col1a1,Krt19,Gm5148,Als2cr11,Gmeb2,Smyd1,Msgn1,Spnb3,Lsm14b,Bmpr1b,Espn,Il16,Kcn
4b,Krt86,Myl9,Krt19,Gmeb2,Bmpr1b,Wnt9a,Espn,Tcf20
Tnnt2,BC030307,Angptl7,Msgn1,Scn11a,Pcyt1b,Fcamr,Rapsn,Bmpr1b,Il22ra1,Apool,Bmf,Il16,Gm136,H2-
C15Rik,Krt19,Zmat4,Pcyt1b,Espn,Rhobtb1,Rims2
n66,Ntm,Scn11a,Bmf,Angptl7,Pcyt1b,Il22ra1,Gyltl1b,Il16,Msgn1,Tiam1,Uhrf2,Calhm1,BC018465,Klhl38,
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18465,Acvr1c,Izumo1,Als2cr11,Sept3,Pcsk9,Plscr4,Ticam2,D4Wsu53e,Aadacl3,Alkbh5,Il22ra1
0028C15Rik,Zfp704,Fcamr,Six4,Klhl38,Pter,4930488L21Rik,H2-Aa
2,Klhl38,Foxp1,1110028C15Rik,Six4,Col1a1,Usp25,Wnt9a
,Alg2,Tnni1,Espn,4732456N10Rik,2610109H07Rik,Pcyt1b
hl38,Uhrf2,Lsm14b,Lrrc14b,Tnni1,Msra,Phf3,Tnnt2,Agr2,Fam169a
,Tnnt2,1110028C15Rik,Smyd1,Lrrc14b,Lsm14b,Trim66,Fam169a,Uhrf2

Espn,Fkbp5,Prpf39

5,Bmpr1b,Fxyd5,Ntm,Tiam1,Olfr877,Gpr110,Lypd4,Calhm1,1110028C15Rik,2510049J12Rik,4732456N10

4,Bach2,Aadacl3,Esrra

Tmem11,2610109H07Rik,Pcyt1b,Trip11

on7,Il22ra1,Cpsf6,Angptl7,Ssh2,2510049J12Rik,Pkd1l2,St3gal2,Ttc25,Lcmt1,Spnb3
C030307,Il16,Espn,Hmgb4,Six4,Tepp,Lsm14b,Hes6,Gmeb2,Ttc25,Lcmt1,Mov10,4922505G16Rik,Igfbp1,B
ns2,Acvr1c,Lcmt1,Tas1r3,Mov10,Pcyt1b,Cant1,Six4,Nos1ap,2610109H07Rik,Tepp,BC018465,Krt86,Slit3

-Aa,Rhobtb1,Mll3,Kcns2,Slc36a3,Pkd1l2,Sgip1,Klf5,Catsper4,Rp1l1,Csrnp1,Aadacl3

Kcns2,Tnni1,BC030307,Six4,H2-Aa,Srp9,Hmgb4,Phlda3,Oasl1,Apool,Bmpr1b,Catsper4,Espn,Slc13a3,Lrrc1

Rik,Agr2,AA986860,Fam49a,Tnnt2,Pkd1l2,BC030307,Kcns2,Lsm14b,Rapsn mf,Msgn1,Msra,Prpf39,Izumo1,Pcyt1b,2610109H07Rik,Mepce,Tmem11,Uhrf2,Ppp1r9b,Dntt,Apool,Kpna

L4b,Pkd1l2,Fkbp5,Mfap2,Lcmt1,Rhobtb1,Umod,Hes6,Tcf20,Tbrg1,Klf5,Tmem232,Rp1l1

a1,Ino80b,Acvr1c,Cox7a2l,Rbp7,Hormad2,Nos1ap,Umod,BC018465,Tcf20,Aadacl3,Usp25,4930488L21Ri

,Snrpb,Gm16515,Rims2,Sept3

Differentially methylated regions found in liver.

ACC	Name	chr	start	end	BLivS	BcLivS	MLivS	feature DI
NM_00991	Cnga3	chr1	37273757	37273996	0.7	0.5	1.7	transcripti
NM_01979	Tmeff2	chr1	50982423	50983087	0.6	0.5	1.8	transcripti
NM_05301	Mlph	chr1	92811145	92811789	1.8	1.5	0.5	transcripti
NM_00110	Prlh	chr1	92848564	92849198	3.8	3.6	1.8	transcripti
NM_17888	D2hgdh	chr1	95721562	95721811	0.0	0.0	1.0	transcripti
NM_00115	Serpinb8	chr1	1.09E+08	1.09E+08	0.3	0.3	1.4	transcripti
NM_21361	Atp2b4	chr1	1.36E+08	1.36E+08	0.7	0.7	1.9	transcripti
NR_02689	4931440L1	chr1	1.36E+08	1.36E+08	1.7	1.6	3.6	transcripti
NM_17708	Ptpn7	chr1	1.37E+08	1.37E+08	2.7	3.6	1.1	transcripti
NM_13366	Lad1	chr1	1.38E+08	1.38E+08	2.3	1.9	0.9	transcripti
NM_00906	Rgs4	chr1	1.72E+08	1.72E+08	0.0	0.0	1.4	transcripti
NM_01200	Sh2d1b1	chr1	1.72E+08	1.72E+08	0.7	0.3	1.9	transcripti
NM_00102	Fcrlb	chr1	1.73E+08	1.73E+08	0.5	1.1	2.2	transcripti
NM_14665	Olfr418-ps	chr1	1.75E+08	1.75E+08	0.6	1.1	2.2	transcripti
NM_17278	Zc3h12d	chr10	7587001	7587665	4.2	2.3	0.6	Primary Tr
NM_02966	1700027D	chr10	76023854	76024088	0.7	0.9	1.9	transcripti
NM_17499	Gm4792	chr10	93761597	93763163	0.9	0.7	2.5	transcripti
NM_02860	Glipr1	chr10	1.11E+08	1.11E+08	0.9	1.0	2.2	transcripti
NM_00101	Cpsf6	chr10	1.17E+08	1.17E+08	0.5	0.1	1.6	transcripti
NM_02802	D10Ertd61	chr10	1.27E+08	1.27E+08	1.4	1.5	3.3	transcripti
NM_02381	Ankrd36	chr11	5467066	5467900	0.6	0.8	2.3	transcripti
NM_00834	Igfbp1	chr11	7098112	7098566	2.3	2.4	0.7	transcripti
NM_01141	Slit3	chr11	34933219	34933808	0.4	0.1	2.0	transcripti
NM_14650	Olfr319	chr11	58515470	58515919	0.7	0.9	2.1	transcripti
NM_14653	Olfr313	chr11	58630713	58631267	1.8	1.8	4.5	transcripti
NM_01199	Cops3	chr11	59654752	59655702	0.9	0.6	2.7	transcripti
NM_14641	Olfr463	chr11	87709058	87709487	1.2	0.8	2.5	transcripti
NM_00110	Gm11545	chr11	94625051	94625306	0.1	0.1	1.5	transcripti
NM_17226	Ppp1r9b	chr11	94854043	94854312	0.6	0.6	1.8	Primary Tr
NM_01005	Dlx3	chr11	94982160	94982394	0.8	1.0	2.5	transcripti
NM_17806	Thra	chr11	98601916	98602155	0.4	0.3	1.6	transcripti
NR_00336	BC018473	chr11	1.17E+08	1.17E+08	2.4	2.2	1.0	transcripti
NM_01954	Msgn1	chr12	11218036	11218673	2.0	1.8	0.3	transcripti
NM_13405	Adi1	chr12	29357759	29358225	1.5	1.6	3.5	transcripti
NM_17780	Prpf39	chr12	66135284	66136843	2.6	1.5	0.4	transcripti
NM_00108	Galntl1	chr12	81618420	81618689	1.1	1.2	2.5	transcripti
NM_01138	Slc10a1	chr12	82068540	82068884	1.9	1.8	0.5	transcripti
NM_00102	Klc1	chr12	1.13E+08	1.13E+08	0.9	0.4	2.1	transcripti
NM_02905	Tdrd9	chr12	1.13E+08	1.13E+08	2.9	3.1	1.2	transcripti
NM_00108	Aspg	chr12	1.13E+08	1.13E+08	0.3	0.1	1.6	transcripti
NM_17891	Pld4	chr12	1.14E+08	1.14E+08	0.0	0.0	1.2	transcripti
NM_02938	Tex22	chr12	1.14E+08	1.14E+08	0.1	0.0	1.4	transcripti
NM_05408	Mta1	chr12	1.14E+08	1.14E+08	3.0	2.8	1.2	transcripti
NM_00776	Crip1	chr12	1.14E+08	1.14E+08	0.7	0.7	1.8	transcripti
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	2.4	transcripti
NM_14597	Tifab	chr13	56281547	56282296	1.3	0.9	2.9	transcripti
NM_01092	Nkx2-6	chr14	69789892	69790521	0.8	0.8	2.8	transcripti
NM_14452	Zfp622	chr15	25911170	25911834	0.1	0.2	1.4	transcripti

NM_18131	Kcns2	chr15	34765879	34766535	1.0	0.6	2.2	transcriptic
NM_17722	Samd12	chr15	53733253	53734732	0.1	0.1	2.3	transcriptic
NM_01041	Hemt1	chr15	74646545	74647194	1.2	1.4	3.2	transcriptic
NM_19811	Lrrc24	chr15	76546035	76546284	0.0	0.2	1.3	Primary Tra
NM_02050	Tob2	chr15	81690041	81691672	0.0	0.0	1.5	transcriptic
NM_14547	Cerk	chr15	86016337	86016691	0.6	1.0	2.4	transcriptic
NM_01066	Krt86	chr15	1.01E+08	1.01E+08	0.3	0.3	1.6	Primary Tra
NM_02639	Nmral1	chr16	4719145	4719399	0.8	0.0	1.9	transcriptic
NM_13930	Mylk	chr16	34783704	34785547	0.8	1.2	2.7	transcriptic
NM_02388	Retnlb	chr16	48816628	48817705	1.8	1.8	0.5	transcriptic
NM_00115	Cep97	chr16	55937543	55937892	0.8	0.4	2.0	transcriptic
NM_02548	Senp7	chr16	56074335	56074999	0.3	0.6	1.7	transcriptic
NA	chr17:1567	chr17	15673304	15673974	0.1	0.2	1.9	CpG Island
NM_01991	Dcpp1	chr17	24016219	24016906	0.5	0.6	1.6	transcriptic
NM_00103	Dcpp2	chr17	24034335	24034999	0.2	0.4	1.7	transcriptic
NM_00107	Dcpp3	chr17	24053069	24053428	0.5	0.4	1.6	transcriptic
NM_02878	Unkl	chr17	25359128	25360271	0.4	1.0	2.3	transcriptic
NA	chr17:3306	chr17	33061503	33062137	0.7	0.7	1.9	CpG Island
NM_01092	Notch4	chr17	34701110	34701969	0.8	1.3	2.6	transcriptic
NM_01039	H2-Q1	chr17	35456143	35456412	0.1	0.1	1.4	transcriptic
NM_17759	Mkx	chr18	7002235	7002789	0.0	0.0	1.3	Primary Tra
NM_00104	Gypc	chr18	32720257	32720503	0.9	0.4	2.0	transcriptic
NM_17339	Ticam2	chr18	46733459	46734858	0.3	0.5	3.9	transcriptic
NM_02128	Spnb3	chr19	4710534	4711211	2.1	1.8	0.7	transcriptic
NM_13368	4930579J0	chr19	10559994	10560352	0.7	0.7	2.0	transcriptic
NM_00113	Gcnt1	chr19	17413852	17414814	1.1	1.1	2.6	transcriptic
NM_17764	D030056L2	chr19	18786228	18786679	2.2	1.9	0.5	transcriptic
NM_00103	Trpm3	chr19	22211573	22212797	3.0	3.3	1.2	transcriptic
NM_01574	Slit1	chr19	41819375	41820023	0.4	0.6	2.0	transcriptic
NM_00114	Golga7b	chr19	42321408	42321857	0.2	0.1	1.3	transcriptic
NM_14612	Cacnb4	chr2	52416410	52416964	0.6	0.5	1.9	transcriptic
NM_19922	Rtn4rl2	chr2	84729055	84729600	0.3	0.3	1.3	transcriptic
NM_00865	Mybpc3	chr2	90955319	90956078	2.0	1.8	0.7	transcriptic
NM_18322	Accs	chr2	93692338	93692917	0.7	0.5	2.0	transcriptic
NM_00107	Slc1a2	chr2	1.03E+08	1.03E+08	0.6	0.5	1.6	transcriptic
NM_17760	Ccdc73	chr2	1.05E+08	1.05E+08	1.1	0.5	2.5	transcriptic
NM_02884	Aven	chr2	1.12E+08	1.12E+08	1.8	2.4	0.5	transcriptic
NM_00916	Scg5	chr2	1.14E+08	1.14E+08	1.1	0.8	2.5	transcriptic
NM_02872	Rin2	chr2	1.46E+08	1.46E+08	2.7	2.3	0.4	transcriptic
NM_03013	8030411F2	chr2	1.49E+08	1.49E+08	0.5	0.5	1.6	transcriptic
NM_19435	Rya3	chr2	1.54E+08	1.54E+08	3.0	3.1	1.4	transcriptic
NM_00895	Psp	chr2	1.54E+08	1.54E+08	1.2	0.6	2.9	transcriptic
NM_00103	4922505G1	chr2	1.57E+08	1.57E+08	2.6	1.4	0.3	transcriptic
NM_02696	Manbal	chr2	1.57E+08	1.57E+08	3.0	2.4	0.8	transcriptic
NM_00930	Svs5	chr2	1.64E+08	1.64E+08	0.8	0.6	1.9	transcriptic
NM_00108	Ctcfl	chr2	1.73E+08	1.73E+08	2.1	1.9	0.8	transcriptic
NM_02915	Spata16	chr3	26535189	26535925	2.9	2.4	0.4	transcriptic
NM_01939	Exosc9	chr3	36449871	36450250	0.8	0.1	2.2	transcriptic
NM_00800	Fgf2	chr3	37246371	37246621	0.1	0.2	1.5	transcriptic
NM_19865	Gm5148	chr3	37624779	37626218	1.2	0.3	3.7	transcriptic

NM_17785	6030405A1	chr3	54720589	54721018	0.0	0.0	1.4	transcriptic
NA	chr3:12977	chr3	1.3E+08	1.3E+08	2.3	1.8	0.7	CpG Islands
NM_00103	Musk	chr4	58296685	58297424	0.8	0.8	2.4	transcriptic
NM_15339	Ttc39a	chr4	1.09E+08	1.09E+08	2.4	2.2	0.8	transcriptic
NM_15339	Ttc39a	chr4	1.09E+08	1.09E+08	2.9	1.9	0.8	transcriptic
NM_19406	Foxo6	chr4	1.2E+08	1.2E+08	0.3	0.2	1.5	Primary Tra
NA	chr4:12926	chr4	1.29E+08	1.29E+08	0.3	0.8	2.1	CpG Islands
NM_00793	Epha8	chr4	1.37E+08	1.37E+08	0.6	0.5	1.6	transcriptic
NM_00108	Aadacl3	chr4	1.44E+08	1.44E+08	0.2	0.7	2.1	transcriptic
NM_00872	Nppb	chr4	1.47E+08	1.47E+08	0.4	0.6	1.8	transcriptic
NM_02742	2610109H(	chr4	1.48E+08	1.48E+08	0.5	0.2	2.0	transcriptic
NM_17684	Fbxo2	chr4	1.48E+08	1.48E+08	3.7	3.0	0.8	transcriptic
NM_00108	Ptchd2	chr4	1.48E+08	1.48E+08	0.6	0.9	2.0	Primary Tra
NM_02202	Rbp7	chr4	1.49E+08	1.49E+08	3.2	1.8	0.5	transcriptic
NM_15342	Nphp4	chr4	1.52E+08	1.52E+08	0.6	0.5	1.8	transcriptic
NR_02736:	A930003O:	chr5	22252651	22252950	0.6	0.7	1.7	transcriptic
NM_17517	Klhl5	chr5	65522502	65523242	1.0	1.3	2.8	transcriptic
NM_00965	Alb	chr5	90887060	90887393	0.4	0.2	1.6	transcriptic
NM_02369	Crybb1	chr5	1.13E+08	1.13E+08	0.9	0.5	2.0	transcriptic
NM_01878	Tfip11	chr5	1.13E+08	1.13E+08	0.6	0.9	1.9	transcriptic
NM_00108	Oas1b	chr5	1.21E+08	1.21E+08	0.1	0.1	1.2	transcriptic
NM_02140	Srrm3	chr5	1.36E+08	1.36E+08	0.9	0.7	3.1	Primary Tra
NM_02556	Fis1	chr5	1.37E+08	1.37E+08	0.0	0.0	1.1	transcriptic
NM_14556	Agfg2	chr5	1.38E+08	1.38E+08	2.4	1.5	0.5	transcriptic
NM_00102	Pilrb2	chr5	1.38E+08	1.38E+08	0.5	0.3	1.6	transcriptic
NM_03303	Ocm	chr5	1.45E+08	1.45E+08	0.0	0.0	1.7	transcriptic
NM_00101	Wdr91	chr6	34862841	34863825	2.1	1.6	0.4	transcriptic
NM_17342	Zfp775	chr6	48560543	48560787	0.9	0.9	2.1	transcriptic
NM_00108	Ccdc129	chr6	55786592	55787131	0.8	0.9	2.0	transcriptic
NM_00116	Smyd1	chr6	71211535	71211909	2.7	2.4	0.8	transcriptic
NM_14556	Krcc1	chr6	71219681	71220726	0.4	0.4	1.9	transcriptic
NM_00110	2510049J1:	chr6	1.16E+08	1.16E+08	0.7	0.1	2.0	transcriptic
NM_02658	D6Wsu116	chr6	1.16E+08	1.16E+08	1.7	2.1	0.5	transcriptic
NM_02663	Art4	chr6	1.37E+08	1.37E+08	1.2	1.3	2.9	transcriptic
NM_01065	Sspn	chr6	1.46E+08	1.46E+08	2.6	2.0	0.8	transcriptic
NM_00110	Ttyh1	chr7	4070072	4070301	2.1	2.0	0.8	transcriptic
NM_01133	Clcn4-2	chr7	7253199	7253628	3.5	3.3	1.2	transcriptic
NM_00746	Apoc1	chr7	20277618	20277967	1.9	1.9	0.8	transcriptic
NM_15311	Cadm4	chr7	25266457	25266726	1.6	1.5	3.2	transcriptic
NM_01998	Tex101	chr7	25457230	25457684	3.2	2.3	0.9	transcriptic
NM_14618	B3gnt8	chr7	26410201	26411064	3.4	2.4	0.8	transcriptic
NM_03261	Spnb4	chr7	28160186	28160836	0.8	1.2	2.9	Primary Tra
NM_01117	Klk6	chr7	51078563	51079137	1.1	0.8	2.3	transcriptic
NM_00111	Nav2	chr7	56214536	56215185	0.9	1.1	2.5	transcriptic
NA	chr7:74948	chr7	74948300	74948975	1.0	1.0	2.3	CpG Islands
NM_00803	Folr1	chr7	1.09E+08	1.09E+08	0.8	1.0	2.4	transcriptic
NM_13864	Syt17	chr7	1.26E+08	1.26E+08	0.7	0.8	2.0	transcriptic
NM_18328	Tcerg1l	chr7	1.46E+08	1.46E+08	0.0	0.1	1.2	transcriptic
NM_00101	Olfr527	chr7	1.48E+08	1.48E+08	0.5	0.5	1.5	transcriptic
NM_02427	1700094C(	chr8	12573150	12573617	0.9	0.6	1.9	transcriptic

NM_00103	Spag11b	chr8	19139263	19139926	0.2	0.4	1.4	transcriptic
NM_17275	Sorbs2	chr8	46593041	46593310	0.9	0.7	2.1	transcriptic
NM_17790	Hapln4	chr8	72611860	72612504	2.2	2.0	0.6	Primary Tra
NM_00797	F2rl3	chr8	75283119	75283968	0.5	0.9	2.1	transcriptic
NM_17318	Rln3	chr8	86568574	86568908	3.5	3.4	1.6	transcriptic
NM_00103	Ccdc102a	chr8	97436989	97437638	2.5	1.9	0.8	Primary Tra
NM_01888	Gpr56	chr8	97506751	97508365	0.2	0.9	2.2	transcriptic
NM_01157	Cirh1a	chr8	1.09E+08	1.09E+08	0.5	1.0	2.0	transcriptic
NM_00956	Zfpm1	chr8	1.25E+08	1.25E+08	0.6	0.9	1.9	transcriptic
NM_00110	Gm7244	chr9	31079528	31080397	1.2	1.2	2.7	transcriptic
NM_14895	Pknox2	chr9	36957405	36957849	2.0	1.6	0.4	transcriptic
NM_00755	Cxcr5	chr9	44335213	44335660	1.1	0.8	2.3	transcriptic
NA	chr9:88494	chr9	88494209	88494858	0.5	0.0	1.7	CpG Island
NA	chr9:88753	chr9	88753512	88754171	0.2	0.0	1.7	CpG Island
NA	chr9:88961	chr9	88961199	88961948	0.7	0.0	1.8	CpG Island
NA	chr9:96437	chr9	96437157	96437816	0.9	0.8	4.7	CpG Island
NM_17711	Dlec1	chr9	1.19E+08	1.19E+08	2.7	2.1	1.0	transcriptic
NM_14623	Acaa1b	chr9	1.19E+08	1.19E+08	0.4	0.4	1.5	transcriptic
NM_17825	Reps2	chrX	1.59E+08	1.59E+08	2.9	2.9	1.4	transcriptic
NM_00957	Zfy1	chrY	133246	133600	1.8	2.5	0.6	transcriptic

orientatior	descriptior	DISSTRIBU	gene_id
+	cyclic nucle	DISTAL	12790
+	transmemb	DISTAL	56363
+	melanophil	PROXIMAL	171531
+	prolactin re	PROXIMAL	623503
+	D-2-hydrox	PROXIMAL	98314
+	serine (or c	PROXIMAL	20725
-	ATPase, Ca	DISTAL	381290
-	RIKEN cDN	PROXIMAL	71001
+	protein tyr	DISTAL	320139
+	ladinin	DISTAL	16763
-	regulator o	DISTAL	19736
+	SH2 domai	PROXIMAL	26904
-	Fc receptor	PROXIMAL	435653
+	olfactory re	INTRAGENI	258645
+	zinc finger	INTRAGENI	237256
+	RIKEN cDN	DISTAL	76573
-	predicted g	PROXIMAL	215472
-	GLI pathog	DISTAL	73690
-	cleavage ar	PROXIMAL	432508
-	DNA segme	PROXIMAL	52666
+	ankyrin rep	DISTAL	76389
+	insulin-like	INTRAGENI	16006
+	slit homolo	DISTAL	20564
+	olfactory re	INTRAGENI	258493
+	olfactory re	INTRAGENI	258529
-	COP9 (cons	DISTAL	26572
-	olfactory re	DISTAL	258408
-	predicted g	DISTAL	217122
+	protein pho	INTRAGENI	217124
+	distal-less h	INTRAGENI	13393
+	thyroid hor	DISTAL	21833
+	cDNA sequ	PROXIMAL	193217
-	mesogenin	DISTAL	56184
+	acireductor	DISTAL	104923
+	PRP39 pre-	PROXIMAL	328110
+	UDP-N-ace	DISTAL	108760
-	solute carri	PROXIMAL	20493
+	kinesin ligh	DISTAL	16593
+	tudor dom	PROXIMAL	74691
+	asparagina	PROXIMAL	104816
+	phospholip	DISTAL	104759
+	testis expre	DISTAL	75671
+	metastasis	PROXIMAL	116870
+	cysteine-ric	DISTAL	12925
-	aldo-keto r	PROXIMAL	56043
-	TRAF-inter	DISTAL	212937
+	NK2 transc	PROXIMAL	18092
+	zinc finger	DISTAL	52521

+	K+ voltage-	DISTAL	16539
-	sterile alph	PROXIMAL	320679
+	hematopoi	DISTAL	15202
-	leucine ric	INTRAGENI	378937
-	transducer	DISTAL	57259
-	ceramide k	PROXIMAL	223753
+	keratin 86	INTRAGENI	16679
-	NmrA-like	PROXIMAL	67824
+	myosin, lig	PROXIMAL	107589
+	resistin like	PROXIMAL	57263
-	centrosom	DISTAL	74201
+	SUMO1/se	DISTAL	66315
.	0	INTERGENI	0
+	demilune c	DISTAL	13184
+	demilune c	DISTAL	630537
+	demilune c	DISTAL	620253
+	unkempt-li	PROXIMAL	74154
.	0	INTERGENI	0
+	Notch gen	PROXIMAL	18132
+	histocomp	DISTAL	15006
-	mohawk h	INTRAGENI	210719
-	glycophori	DISTAL	71683
-	toll-like rec	PROXIMAL	225471
+	spectrin be	PROXIMAL	20743
-	RIKEN cDN	DISTAL	67752
-	glucosamin	PROXIMAL	14537
+	RIKEN cDN	DISTAL	225995
+	transient r	DISTAL	226025
-	slit homolo	DISTAL	20562
+	golgi autoa	PROXIMAL	71146
-	calcium ch	DISTAL	12298
-	reticulon 4	DISTAL	269295
+	myosin bin	DISTAL	17868
-	1-aminocy	DISTAL	329470
+	solute carri	DISTAL	20511
+	coiled-coil	INTRAGENI	211936
+	apoptosis,	DISTAL	74268
-	secretogra	PROXIMAL	20394
+	Ras and Ra	PROXIMAL	74030
+	RIKEN cDN	PROXIMAL	78609
+	antimicrob	DISTAL	378700
+	parotid sec	DISTAL	19194
-	RIKEN cDN	DISTAL	629499
+	mannosida	DISTAL	69161
+	seminal ve	DISTAL	20944
-	CCCTC-bin	DISTAL	664799
+	spermatog	DISTAL	70862
+	exosome c	DISTAL	50911
+	fibroblast	DISTAL	14173
-	predicted	DISTAL	381438

-	RIKEN cDN	DISTAL	329641
.	0	INTERGENI	0
+	muscle, ske	DISTAL	18198
+	tetratricop	DISTAL	230603
+	tetratricop	DISTAL	230603
-	forkhead b	INTRAGENI	329934
.	0	INTERGENI	0
-	Eph recept	PROXIMAL	13842
-	arylacetam	PROXIMAL	230883
+	natriuretic	DISTAL	18158
-	RIKEN cDN	DISTAL	70433
+	F-box prote	DISTAL	230904
-	patched d	INTRAGENI	242748
-	retinol bin	DISTAL	63954
+	nephronop	INTRAGENI	260305
-	RIKEN cDN	PROXIMAL	330052
+	kelch-like 5	PROXIMAL	71778
+	albumin	DISTAL	11657
+	crystallin,	DISTAL	12960
+	tuftelin int	DISTAL	54723
+	2'-5' oligoa	INTRAGENI	23961
+	serine/argi	INTRAGENI	58212
+	fission 1 (m	PROXIMAL	66437
-	ArfGAP wit	DISTAL	231801
-	paired imm	PROXIMAL	545812
-	oncomodul	INTRAGENI	18261
-	WD repeat	DISTAL	101240
+	zinc finger	DISTAL	243372
+	coiled-coil	PROXIMAL	232016
-	SET and M	INTRAGENI	12180
+	lysine-rich	DISTAL	57896
-	RIKEN cDN	DISTAL	70291
+	DNA segme	DISTAL	28006
-	ADP-ribosy	PROXIMAL	109978
+	sarcospan	DISTAL	16651
+	tweety ho	DISTAL	57776
-	chloride ch	DISTAL	12727
-	apolipopro	PROXIMAL	11812
+	cell adhesi	PROXIMAL	260299
-	testis expre	PROXIMAL	56746
+	UDP-GlcNA	DISTAL	232984
-	spectrin be	INTRAGENI	80297
+	kallikrein re	DISTAL	19144
+	neuron nav	PROXIMAL	78286
.	0	INTERGENI	0
-	folate rece	PROXIMAL	14275
-	synaptotag	PROXIMAL	110058
-	transcripti	INTRAGENI	70571
+	olfactory re	DISTAL	257939
+	RIKEN cDN	INTRAGENI	78634

+	sperm asso	DISTAL	546038
+	sorbin and	PROXIMAL	234214
+	hyaluronar	INTRAGENI	330790
+	coagulatior	DISTAL	14065
-	relaxin 3	PROXIMAL	212108
-	coiled-coil	INTRAGENI	234582
+	G protein-c	PROXIMAL	14766
+	cirrhosis, a	DISTAL	21771
+	zinc finger	DISTAL	22761
+	predicted g	DISTAL	638580
-	Pbx/knotte	DISTAL	208076
-	chemochin	DISTAL	12145
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
+	deleted in l	DISTAL	320256
-	acetyl-Coe	PROXIMAL	235674
-	RALBP1 ass	PROXIMAL	194590
-	zinc finger	INTRAGENI	22767

Differentially methylated regions found in liver connected with 2 fold in gene expression level.

ACC	Name	chr	start	end	BLivS	BcLivS	MLivS	feature DI
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	2.4	transcriptic
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	2.4	transcriptic
NM_00107	Slc1a2	chr2	1.03E+08	1.03E+08	0.6	0.5	1.6	transcriptic
NM_00110	2510049J1	chr6	1.16E+08	1.16E+08	0.7	0.1	2.0	transcriptic
NM_01888	Gpr56	chr8	97506751	97508365	0.2	0.9	2.2	transcriptic
NM_01888	Gpr56	chr8	97506751	97508365	0.2	0.9	2.2	transcriptic
NM_15339	Ttc39a	chr4	1.09E+08	1.09E+08	2.4	2.2	0.8	transcriptic
NM_15339	Ttc39a	chr4	1.09E+08	1.09E+08	2.9	1.9	0.8	transcriptic

orientatior	descriptior	DISSTRIBU	gene_id	transcript_	BLivS	SE_EXPRS	BcLivS	SE_EXPRS
-	aldo-keto r	PROXIMAL	56043	BC012692	4470.037	0.9853	3786.231	0.9846
-	aldo-keto r	PROXIMAL	56043	AK028605	680.8408	0.9533	523.677	0.9524
+	solute carri	DISTAL	20511	AK013557	6573.665	0.9717	4546.488	0.9682
-	RIKEN cDN.	DISTAL	70291	NM_0011(	134.9231	0.8751	171.7679	0.8442
+	G protein-c	PROXIMAL	14766	AF166382	1049.567	0.9717	1028.454	0.9636
+	G protein-c	PROXIMAL	14766	AK087268	421.4766	0.966	420.3359	0.9705
+	tetratricop	DISTAL	230603	AK076641	218.8697	0.9092	334.7512	0.9327
+	tetratricop	DISTAL	230603	AK076641	218.8697	0.9092	334.7512	0.9327

MLivS	SE_EXPRS
672.7672	0.9829
117.1992	0.8512
1437.916	0.9609
40.0965	0.7854
3604.706	0.9886
1618.711	0.9824
3205.484	0.9746
3205.484	0.9746

Gene ontology analysis for liver.

GOTerm	Nr. Genes	Term PVal	Associated	Group Gen	Nr. Genes	-log(P-value)
negative re	3	0.013555	[Draxin, Sli	Draxin|Exo	13	1.867891
acetylgluc	4	0.039911	[4931440L	4931440L1	4	1.398903

Transcription factor identification for liver.

TF	NES	Targets	Motifs
Srf	4.918	50	7
Gata2	4.788	69	7
Tcf7l1	4.512	27	4
Zfp784	4.203	60	3
Ets1	4.122	51	6
Olig1	4.024	58	7
Neurod1	4.014	38	3
Rest	3.947	53	4
Kdm4d	3.629	12	1
Glis2	3.535	36	5
Thra	3.487	38	6
Nf1	3.414	9	1
Mecom	3.388	9	1
Bach1	3.372	11	9
Zbtb49	3.307	18	2
Jazf1	3.144	13	2

Promoter sequence motifs

# Rank	Motif id	AUC	NES	ClusterCod	Transcripti	Target genes
1	taipale-NN	0.053287	4.91805	M1	Srf	Glipr1,Smyd1,Sspn,Mybpc3,Spnb3
2	tfdimers-M	0.05226	4.78842	M2	Gata2,Gata	Cacnb4,Mybpc3,6030405A18Rik,G
3	jaspar-CN0	0.050072	4.51203	M3		Trpm3,Cacnb4,Spag11b,Krt86,Thra
4	yetfasco-1	0.047622	4.20262	M4		Spnb3,Dlx3,Apoc1,Dcpp3,Dcpp1,R
5	tfdimers-M	0.046983	4.1219	M5	Ets1,Sry,Sf	Sspn,Cxcr5,Pilrb2,Msgn1,Zc3h12d,
6	hdpi-OLIG1	0.046208	4.02406	M6	Olig1	Smyd1,Krt86,Alb,Sspn,Musk,Syt17
7	encode-U	0.046131	4.01428	M7		Dcpp3,Dcpp2,Dcpp1,Gpr56,F2rl3,
8	transfac_p	0.045811	3.97392	M8	Rest	Nppb,Krt86,Spnb4,Lrrc24,Nav2,Dc
9	tfdimers-M	0.044601	3.82105	M7	Neurod1,El	F2rl3,4931440L10Rik,Cacnb4,Dcp
10	homer-M0	0.044252	3.77702	M5	Cdx2,Cdx1,	Pknox2,Msgn1,Slc1a2,Gm5148,My
11	yetfasco-1	0.04308	3.62905	M9	Kdm4d,Kdr	Atp2b4,Cacnb4,Lad1,Sh2d1b1,Spn
12	transfac_p	0.043042	3.62415	M1	Srf	Smyd1,Glipr1,Spnb3,Sspn,Gypc,M
13	taipale-RN	0.042935	3.6107	M1	Neurog2,N	Cacnb4,Thra,Alb,Musk,Krt86,Smy
14	elemento-	0.042838	3.59847	M10		Klk6,Reps2,Zc3h12d,Smyd1,A9300
15	flyfactorsu	0.042335	3.53488	M11	Glis2,Glis3,	Ctcfl,Apoc1,Syt17,Sspn,Crybb1,26
16	tfdimers-M	0.042277	3.52754	M5	Jun,Fos,Irf1	Klhl5,Sspn,Cxcr5,Trpm3,Nppb,Cac
17	yetfasco-9	0.04218	3.51531	M5		Sspn,Mkx,Nav2,Rin2,Ppp1r9b,Trp
18	transfac_p	0.042102	3.50553	M1	Srf	Smyd1,Mybpc3,Nppb,Glipr1,Sspn,
19	transfac_p	0.042035	3.49696	M3	Tcf7l1,Tcf7	Msgn1,Gm5148,Klhl5,Krt86,Trpm
20	elemento-	0.041977	3.48963	M12		Trpm3,Retnlb,Mybpc3,Rln3,Cxcr5,
21	yetfasco-1	0.041957	3.48718	M13		Zc3h12d,Trpm3,Cep97,Sspn,Nav2,

22	transfac_p	0.041948	3.48596	M3	Tcf7,Tcf7l1	Msgn1,Gm5148,Krt86,Klhl5,Slc1a2
23	transfac_p	0.041938	3.48474	M2	Pgr,Nr3c1,	Notch4,Trpm3,Ccdc129,Rin2,Msg
24	taipale-GT	0.041725	3.45783	M4	Zfp784	Atp2b4,Spnb3,Slc1a2,Reps2,Syt17,
25	flyfactorsu	0.041589	3.44071	M5		Msgn1,Pknox2,Mylk,Dcpp1,Rin2,R
26	elemento-	0.041376	3.4138	M10		Klk6,Gpr56,Notch4,Ptpn7,Dcpp1,A
27	jaspar-CN0	0.041376	3.4138	M14	Nf1	Msgn1,Mylk,2510049J12Rik,Smyd
28	elemento-T	0.041308	3.40524	M8		Notch4,Slc10a1,Prlh,Atp2b4,Klk6,
29	elemento-	0.041202	3.39179	M8		Smyd1,Prlh,Atp2b4,Slc10a1,Ctcfl,T
30	taipale-GA	0.041192	3.39057	M11	Glis3	Spnb4,Syt17,Sspn,Cep97,Nkx2-6,A
31	transfac_p	0.041173	3.38812	M15	Mecom	Msgn1,4930579J09Rik,Reps2,Olfr
32	elemento-T	0.041047	3.37222	M16	Bach1,Batf	Gpr56,Klc1,Galntl1,Sh2d1b1,Krt86
33	elemento-T	0.041047	3.37222	M17		Zc3h12d,Syt17,Samd12,Trpm3,Slc
34	homer-M0	0.040902	3.35388	M3	Tcf3,Tcf7l1	Msgn1,Nav2,Slc1a2,Agfg2,Gm514
35	transfac_p	0.040718	3.33064	M6	Tal1,Tcf4,T	Cacnb4,4931440L10Rik,Krt86,Alb,
36	homer-M0	0.04066	3.3233	M5		Pknox2,Msgn1,Gm5148,Krt86,Eph
37	flyfactorsu	0.04064	3.32086	M11	Glis3,Glis1,	Ctcfl,Cxcr5,Apoc1,Msgn1,Klk6,Cng
38	yetfasco-1	0.04064	3.32086	M16	Jdp2,Fosl1,	Gpr56,Galntl1,Sh2d1b1,Krt86,Npp
39	tfdimers-M	0.040611	3.31719	M2	Zbtb14,Yy2	Sorbs2,Zfp775,Alb,Nav2,Syt17,Ccd
40	taipale-TTT	0.040534	3.30741	M18	Zbtb49	Gpr56,Nav2,Lrrc24,Klc1,Dlx3,Tdrd
41	tfdimers-M	0.040466	3.29884	M6	Creb1,Atf2	Cacnb4,Musk,Smyd1,Samd12,Apo
42	flyfactorsu	0.040146	3.25849	M1	Bhlha15,N	Alb,Gpr56,Cacnb4,6030405A18Rik
43	encode-U	0.040001	3.24014	M2		Smyd1,Atp2b4,Reps2,Gpr56,F2rl3,
44	encode-U	0.039817	3.21691	M2		Fcrlb,Crybb1,Art4,Tmeff2,Gm5148
45	yetfasco-2	0.039817	3.21691	M19		Cxcr5,Fgf2,Prpf39,Gypc,Rin2,Alb
46	encode-U	0.039701	3.20223	M2		Klk6,Musk,Prlh,Notch4,Krcc1,6030
47	yetfasco-1	0.039585	3.18755	M20		Msgn1,Klk6,4930579J09Rik,Olfr41
48	iDMMPM	0.039498	3.17655	M20		Notch4,Psp,Rin2,Musk
49	transfac_p	0.039488	3.17533	M16	Jdp2,Bach1	Gpr56,Nppb,Sh2d1b1,Krt86,Zc3h1
50	yetfasco-8	0.039488	3.17533	M16	Jdp2,Bach1	Gpr56,Nppb,Sh2d1b1,Krt86,Zc3h1
51	yetfasco-1	0.03943	3.16799	M8		Galntl1,Ppp1r9b,Mybpc3,Reps2,Ps
52	jaspar-MA	0.039411	3.16554	M16	Jdp2,Bach1	Gpr56,Nppb,Sh2d1b1,Krt86,Zc3h1
53	tfdimers-M	0.039333	3.15576	M13	Jun,Pparg,	Krcc1,Zc3h12d,Fgf2,Gpr56,Spnb4,
54	flyfactorsu	0.039314	3.15331	M21		Spnb4,Samd12,Tob2,Notch4
55	flyfactorsu	0.039246	3.14475	M11	Glis2,Glis3,	Ctcfl,Crybb1,Apoc1,Ppp1r9b,Notc
56	yetfasco-8	0.039236	3.14353	M22	Jazf1,Foxn	Dlx3,Slit1,Galntl1,Cacnb4,Zfp622,
57	yetfasco-2	0.039198	3.13864	M16	Jdp2,Bach2	Gpr56,Nppb,Sh2d1b1,Krt86,Galntl
58	jaspar-MA	0.03911	3.12763	M13	Gata5,Gata	Cxcr5,Msgn1,4931440L10Rik,Pkno
59	homer-M0	0.038975	3.11051	M6	Neurod1,T	Cacnb4,Musk,Sorbs2,4931440L10
60	encode-U	0.038936	3.10562	M18		Slc10a1,Atp2b4,Notch4,Psp,Klk6,
61	homer-M0	0.038907	3.10195	M6	Olig2,Tal1,	Cacnb4,Musk,Alb,Smyd1,Krt86,So
62	transfac_p	0.038839	3.09339	M13	Thrb,Nr2f2	Notch4,Trpm3,4931440L10Rik,Aa
63	yetfasco-2	0.03883	3.09216	M13		Ctcfl,Klk6,Psp,Apoc1,Crip1,Slc10a1
64	swissregul	0.038752	3.08238	M16	Bach2,Bac	Gpr56,Krt86,Nppb,Galntl1,Klc1,Sh
65	swissregul	0.038752	3.08238	M16	Fosl2,Jun,F	Gpr56,Krt86,Klc1,Galntl1,Cacnb4,
66	transfac_p	0.038607	3.06404	M4		D030056L22Rik,Atp2b4,Apoc1,Slc
67	elemento-	0.038558	3.05792	M22	Mef2a,Mef	Spnb3,Slit1,Dlx3,Syt17,Apoc1,Cac
68	tfdimers-M	0.038539	3.05547	M2	Hand2,Ma	Spnb3,Msgn1,Alb,Musk,Smyd1,At

69	homer-M0	0.038491	3.04936	M7	Tal1,Elf1	F2rl3,Cacnb4,4931440L10Rik,Mkx,
70	transfac_p	0.038491	3.04936	M1	Srf	Smyd1,Sspn,Spnb3,Nppb,Kcns2,Gl
71	encode-U	0.038452	3.04447	M11		Syt17,Notch4,Klk6,Trpm3,Ptpn7,Pl
72	transfac_p	0.038258	3.02001	M6		Reps2,Smyd1,Sorbs2,Msgn1,Mkx,
73	taipale-RA	0.038249	3.01879	M1	Neurog2,B	Cacnb4,Thra,Musk,4931440L10Rik
74	tfdimers-M	0.03822	3.01512	M13	Rara,Rarb,	Dcpp1,Dcpp3,Gpr56,Dcpp2,Trpm3
75	hdpi-MYF6	0.038123	3.00289	M6	Myf6	Cacnb4,Cxcr5,Smyd1,Ccdc129,Krt
76	stark-TGA	0.038123	3.00289	M16	Arnt	Gpr56,Klc1,Galntl1,Sh2d1b1,Cacn

,Nppb,Gypc,Psp,Slc1a2,4930579J09Rik,Gm5148,Ttyh1,Slc10a1,Dlx3
ypc,Smyd1,Fcrlb,Msgn1,Atp2b4,Nav2,Kcns2,Rin2
a,Gm5148,Nav2,Msgn1,Sorbs2,Manbal,Dlx3,Olfr319,Dlec1,Cep97,Cnga3,Serpinb8,Golga7b,Fgf2,A93000
tn4rl2,6030405A18Rik,Spag11b,Dcpp2,B3gnt8
Syt17,Nkx2-6,Sorbs2,Zfp775,Slit1,Nav2,Golga7b,Rgs4,Olfr418-ps1,Trpm3,Klhl5,Musk,Mlph,Wdr91,Tica
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pp3,Dcpp2,Dcpp1,Aadacl3,Lad1
2,Dcpp3,Dcpp1,Nphp4,Mkx,Ccdc129
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,Cxcr5,Slc10a1,Cacnb4,4931440L10Rik,Nav2,Zc3h12d,Nkx2-6,Trpm3,Msgn1,Olfr319,Mkx,Rin2,Prlh,Spnb
,Nav2,Rin2,Msgn1

405A18Rik,Slit3,Aadacl3,Krt86,Smyd1,Cacnb4,Gpr56,Fcrlb,Mylk,Trpm3,Rya3,Apoc1
8-ps1,Sspn,Reps2,Mybpc3,Musk,Slc1a2,2610109H07Rik,Notch4,Spag11b,Trpm3,Dcpp1,Nav2

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2d,Klk6,Aadacl3,Cacnb4,Serpinb8
Klk6,Slc10a1

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ya3,Syt17,Prlh
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,Notch4,Tmeff2
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36,Prlh,Alb,Sspn,Musk,Klhl5,Trpm3,Dlx3,Zc3h12d,6030405A18Rik,Atp2b4,Sorbs2,Samd12,Nav2,4922505
4

3O13Rik,Senp7

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39a,Musk,Pknox2,Igfbp1,Rgs4,Cnga3,Cep97,Slc10a1,Apoc1,Gcnt1,Mkx

Rik,Pknox2,Dlx3,B3gnt8,Dcpp3,Cep97,Atp2b4,Tmeff2,Ccdc102a,Slit3,Trpm3,Nkx2-6,Slit1,Gpr56

s2,Apoc1,Klk6,4930579J09Rik,Syt17,4922505G16Rik,Psp,Igfbp1,Msgn1,Prpf39,Ttyh1,Rgs4,4931440L10R

,Zc3h12d,4930579J09Rik,Rya3,8030411F24Rik,Spag11b,2510049J12Rik,Trpm3,Crybb1,Olfr527,Cacnb4,

,Dlx3,Slc1a2,Zfp775,Nppb,Spnb3,Ptchd2,Alb,4931440L10Rik,Crybb1,Epha8,Sh2d1b1,Ccdc129,Syt17,Kcn

ybpc3,Gpr56,Tmeff2,Notch4

,Golga7b

,Sorbs2,Olfr418-ps1,Musk,Golga7b,Gm5148,Olfr463,Krt86,Thra,Lad1,Sspn,Samd12,Pknox2,Ptpn7,Psp,

,Sh2d1b1,Rln3,Atp2b4,Msgn1,Nav2,Trpm3,Lad1,Igfbp1,Sspn,Slit1,Gypc,A930003O13Rik,Olfr418-ps1,Rb

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G16Rik,Notch4,Fbxo2,Fcrlb,Sh2d1b1,4930579J09Rik,Rgs4,Krt86,Olfr418-ps1,Msgn1,Ttyh1,Krcc1,Ccdc102

G16Rik,Aadacl3,Spnb4,Notch4,Syt17,Rin2,Mybpc3 ik,2610109H07Rik,Notch4,Ppp1r9b,Musk,Spag11b

\kx2-6,Prpf39,Cep97,Gpr56,Foxo6,4922505G16Rik,Aven,Krt86,Fcrlb,Tob2,Folr1,Psp,Tex101,Tifab,Dlx3,T

s2,Fis1,Sspn,Gpr56,Prpf39,Manbal,Rin2,8030411F24Rik,Zc3h12d,Krt86

ıven,Spag11b,Slc1a2,Syt17

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8Rik,Igfbp1,Golga7b,4922505G16Rik,Klk6,Prlh,A930003O13Rik,Gypc,Mybpc3,Mkx a,6030405A18Rik,Apoc1,Nav2

tyh1,Golga7b,Pilrb2,Notch4,Ccdc73,Acaa1b,Kcns2,Ccdc129,Zfp622

Samd12,Slc10a1,Reps2,Ccdc129,Spnb4

Differentially methylated regions found in hear.

ACC	Name	chr	start	end	BHtS	BcHtS	MHtS	feature DI
NM_17839	3110035E1	chr1	9590986	9592113	3.2	2.4	0.5	transcriptic
NM_00103	Prex2	chr1	11254246	11254806	2.0	1.8	0.6	transcriptic
NM_17764	1110028C1	chr1	66865360	66865784	0.4	0.5	1.7	transcriptic
NM_17556	Tmem169	chr1	72328106	72328782	0.3	0.4	1.7	transcriptic
NM_05301	Mlph	chr1	92809345	92810869	2.5	2.6	1.2	transcriptic
NM_00110	Prlh	chr1	92848564	92849198	3.4	3.5	1.1	transcriptic
NM_00103	Rbm44	chr1	93041267	93041516	2.4	2.2	4.9	transcriptic
NM_17285	Cntnap5b	chr1	1.02E+08	1.02E+08	1.1	1.2	3.5	transcriptic
NM_17760	AA986860	chr1	1.33E+08	1.33E+08	1.8	1.4	0.3	transcriptic
NM_18271	Nfasc	chr1	1.35E+08	1.35E+08	2.0	2.2	0.2	transcriptic
NM_03119	Ren2	chr1	1.35E+08	1.35E+08	2.9	2.3	0.8	transcriptic
NR_02689(	4931440L1	chr1	1.36E+08	1.36E+08	1.7	1.3	4.0	transcriptic
NM_01375	Phlda3	chr1	1.38E+08	1.38E+08	1.8	1.8	0.7	transcriptic
NA	chr1:13868	chr1	1.39E+08	1.39E+08	3.1	3.1	1.4	CpG Island:
NM_00906	Rgs4	chr1	1.72E+08	1.72E+08	0.1	0.1	2.1	transcriptic
NM_02752	Nos1ap	chr1	1.72E+08	1.72E+08	1.4	1.3	3.0	transcriptic
NM_00107	Fcgr2b	chr1	1.73E+08	1.73E+08	3.3	2.4	0.6	transcriptic
NM_00108	Mosc1	chr1	1.87E+08	1.87E+08	2.9	3.4	1.0	transcriptic
NM_17869	C130074G1	chr1	1.87E+08	1.87E+08	0.5	0.5	1.8	transcriptic
NM_02614	Ppil4	chr10	7509779	7510958	0.2	0.1	2.1	transcriptic
NM_02585	Arl1	chr10	88191503	88192282	0.1	0.0	1.6	transcriptic
NM_00770	Socs2	chr10	94881319	94882076	1.6	1.2	0.1	transcriptic
NM_02657	Yeats4	chr10	1.17E+08	1.17E+08	0.4	0.4	1.7	transcriptic
NM_00101	Cpsf6	chr10	1.17E+08	1.17E+08	0.5	0.2	2.2	transcriptic
NM_00834	Igfbp1	chr11	7095925	7096554	0.9	0.6	2.0	transcriptic
NM_01141	Slit3	chr11	34933219	34933808	0.7	0.3	1.7	transcriptic
NM_17747	Ccdc69	chr11	54893543	54894531	0.3	0.3	1.4	transcriptic
NM_00821	Hand1	chr11	57647574	57647838	1.2	1.1	2.5	transcriptic
NM_01199	Cops3	chr11	59654752	59655702	0.4	0.5	3.0	transcriptic
NM_00881	Pemt	chr11	59849713	59850154	1.4	1.3	2.8	transcriptic
NM_00902	Rai1	chr11	59916430	59916779	2.9	2.5	1.1	transcriptic
NA	chr11:6237	chr11	62374031	62374707	1.0	0.4	2.4	CpG Island:
NM_02621	Fam18b	chr11	62690533	62691505	0.4	0.4	2.3	transcriptic
NM_02744	Rnf167	chr11	70458149	70458403	0.8	0.9	2.0	transcriptic
NM_14543	Nle1	chr11	82723263	82723710	0.5	0.6	1.9	transcriptic
NM_17226	Ppp1r9b	chr11	94850167	94850416	1.9	2.0	0.8	transcriptic
NM_00808	B4galnt2	chr11	95778635	95779069	1.0	1.0	2.2	transcriptic
NM_00108	Osbpl7	chr11	96909374	96910572	2.4	2.2	1.0	transcriptic
NM_00992	Cnp	chr11	1E+08	1E+08	0.8	0.7	1.9	transcriptic
NM_17563	Wnk4	chr11	1.01E+08	1.01E+08	0.9	1.1	2.2	Primary Tra
NM_17280	Sdk2	chr11	1.14E+08	1.14E+08	0.3	0.7	1.9	transcriptic
NM_01954	Msgn1	chr12	11218036	11218673	2.2	2.0	0.8	transcriptic
NM_01049	Id2	chr12	25782627	25782887	0.7	0.7	1.9	transcriptic
NM_01178	Agr2	chr12	36718163	36719728	2.4	1.9	0.8	transcriptic
NM_17780	Prpf39	chr12	66135284	66136843	1.7	1.6	0.4	transcriptic

NM_00109	Trmt61a	chr12	1.13E+08	1.13E+08	0.2	0.3	1.4	transcriptic
NM_02887	Xrcc3	chr12	1.13E+08	1.13E+08	2.9	2.1	0.9	transcriptic
NM_01162	Ppp1r13b	chr12	1.13E+08	1.13E+08	1.3	0.9	2.8	transcriptic
NM_17891	Tmem179	chr12	1.14E+08	1.14E+08	1.2	1.5	3.1	transcriptic
NM_19841	Inf2	chr12	1.14E+08	1.14E+08	2.4	2.0	0.7	transcriptic
NM_17891	Pld4	chr12	1.14E+08	1.14E+08	0.1	0.1	1.3	transcriptic
NM_01992	Gpr132	chr12	1.14E+08	1.14E+08	0.6	0.7	2.2	transcriptic
NM_01058	Jag2	chr12	1.14E+08	1.14E+08	2.8	2.8	1.4	transcriptic
NM_00776	Crip1	chr12	1.14E+08	1.14E+08	0.5	0.6	2.2	transcriptic
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	2.4	transcriptic
NM_02815	1700013B1	chr13	59809897	59810486	0.6	0.6	1.9	transcriptic
NM_00100	Zfp58	chr13	67600723	67600995	0.3	0.1	1.5	transcriptic
NM_14545	Pxk	chr14	8928640	8929546	0.2	0.2	1.2	transcriptic
NM_00836	Il3ra	chr14	15178924	15179295	3.2	4.0	1.3	transcriptic
NM_00103	Defb47	chr14	63616089	63616748	2.4	2.2	1.0	transcriptic
NM_14452	Zfp622	chr15	25911170	25911834	0.0	0.0	1.5	transcriptic
NM_00101	Fam105b	chr15	27560776	27561139	0.3	0.3	1.5	transcriptic
NM_19830	Fam105a	chr15	27595029	27595707	0.8	0.9	2.2	Primary Tra
NM_00763	Cct5	chr15	31532950	31533392	0.4	0.5	1.8	transcriptic
NM_17722	Samd12	chr15	53733253	53734732	0.2	0.4	2.7	transcriptic
NM_02050	Tob2	chr15	81690041	81691672	0.0	0.0	2.0	transcriptic
NM_17826	Cenpm	chr15	82075636	82076139	0.6	0.6	1.7	transcriptic
NM_01676	Mcrs1	chr15	99081644	99081893	1.4	1.4	0.0	transcriptic
NM_17245	Galnt6	chr15	1.01E+08	1.01E+08	0.9	1.0	2.2	transcriptic
NM_01066	Krt86	chr15	1.01E+08	1.01E+08	0.2	0.2	2.0	Primary Tra
NM_00115	Cep97	chr16	55937543	55937892	0.5	0.3	2.0	transcriptic
NA	chr17:1567	chr17	15673304	15673974	0.3	0.1	2.1	CpG Islands
NM_00103	AU023871	chr17	35202992	35203741	2.9	3.3	1.4	transcriptic
NA	chr17:3998	chr17	39985220	39985574	0.6	0.1	1.6	CpG Islands
NM_02912	Atp6v1e2	chr17	87348541	87349395	3.2	2.6	1.2	transcriptic
NM_17262	Ino80c	chr18	24281882	24282837	2.5	2.0	0.6	transcriptic
NM_01381	Galnt1	chr18	24361504	24361738	0.5	0.3	1.6	transcriptic
NM_00746	Apc	chr18	34378573	34379422	2.1	2.2	1.0	transcriptic
NM_02935	Pcdh1	chr18	38369077	38369341	2.3	2.3	0.9	transcriptic
NM_17339	Ticam2	chr18	46733459	46734858	0.7	0.4	4.1	transcriptic
NM_19864	Ablim3	chr18	62071917	62072493	1.5	1.5	0.3	transcriptic
NM_01375	Insl6	chr19	29399892	29400624	2.6	2.1	0.8	transcriptic
NM_14487	Uhrf2	chr19	30102448	30103241	1.6	1.7	0.5	transcriptic
NM_02918	Tmem180	chr19	46430038	46430735	0.6	0.8	1.8	transcriptic
NM_00108	Calhm1	chr19	47220974	47221648	1.2	0.7	3.8	transcriptic
NM_02130	Sec61a2	chr2	5818307	5818549	0.9	1.0	2.1	transcriptic
NM_08055	Psmd5	chr2	34727143	34727614	0.2	0.1	2.1	transcriptic
NM_01071	Lhx2	chr2	38209860	38210590	0.6	0.9	2.9	Primary Tra
NM_01940	Nmi	chr2	51831185	51831734	0.2	0.2	1.6	transcriptic
NM_00111	Mettl8	chr2	70855808	70856104	0.7	0.8	2.0	transcriptic
NM_02563	Metapl1	chr2	71290205	71290560	0.7	0.8	1.9	transcriptic
NM_02567	Mcm8	chr2	1.33E+08	1.33E+08	1.0	0.8	2.2	transcriptic

NM_00103	4922505G1	chr2	1.57E+08	1.57E+08	1.8	1.7	0.3	transcriptio
NM_02696	Manbal	chr2	1.57E+08	1.57E+08	2.2	2.0	0.8	transcriptio
NM_01149	Aurka	chr2	1.72E+08	1.72E+08	1.2	0.9	2.6	transcriptio
NM_02915	Spata16	chr3	26535189	26535925	1.5	1.8	0.3	transcriptio
NM_00982	Ccna2	chr3	36472717	36473089	0.0	0.0	1.5	transcriptio
NM_00103	Ankrd50	chr3	38356348	38356812	2.9	2.4	1.1	transcriptio
NM_00899	Abcd3	chr3	1.21E+08	1.21E+08	2.7	3.1	1.3	Primary Tra
NM_02319	Pla2g12a	chr3	1.3E+08	1.3E+08	2.7	2.5	1.2	transcriptio
NM_00981	Casp6	chr3	1.3E+08	1.3E+08	1.4	1.1	2.9	transcriptio
NA	chr3:12977	chr3	1.3E+08	1.3E+08	2.1	1.8	0.6	CpG Islands
NM_00756	Bmpr1b	chr3	1.42E+08	1.42E+08	4.2	3.9	1.9	transcriptio
NM_02608	1700022I1	chr4	42982913	42983347	2.2	2.3	0.8	transcriptio
NM_00109	Msmp	chr4	43598149	43598523	2.2	2.1	0.7	transcriptio
NM_01999	Alg2	chr4	47488672	47489525	2.3	2.1	0.9	transcriptio
NM_00100	Maneal	chr4	1.25E+08	1.25E+08	1.1	1.4	2.9	transcriptio
NA	chr4:12926	chr4	1.29E+08	1.29E+08	0.2	1.1	2.7	CpG Islands
NM_02366	D4Wsu53e	chr4	1.34E+08	1.34E+08	0.1	0.2	2.2	transcriptio
NM_02798	Mad2l2	chr4	1.48E+08	1.48E+08	0.9	1.0	2.4	transcriptio
NM_02202	Rbp7	chr4	1.49E+08	1.49E+08	2.4	2.0	0.3	transcriptio
NM_00103	Gm833	chr4	1.52E+08	1.52E+08	2.6	2.0	1.0	transcriptio
NM_01138	Ski	chr4	1.55E+08	1.55E+08	1.3	1.1	3.2	transcriptio
NM_00103	Dhrsx	chr4_rando	109368	110464	0.2	0.4	1.7	transcriptio
NM_00115	Lnx1	chr5	75074786	75075145	1.9	1.6	0.5	transcriptio
NM_02140	Srrm3	chr5	1.36E+08	1.36E+08	0.5	0.5	2.1	Primary Tra
NM_01579	Trfr2	chr5	1.38E+08	1.38E+08	1.6	1.6	0.3	transcriptio
NM_00108	Lmtk2	chr5	1.45E+08	1.45E+08	0.8	0.8	1.9	transcriptio
NM_00907	Rpia	chr6	70744414	70745064	2.6	2.5	1.2	transcriptio
NM_15377	Atoh8	chr6	72187182	72187831	2.8	2.4	5.8	transcriptio
NM_00108	Vamp5	chr6	72331874	72332410	1.1	1.3	3.1	transcriptio
NM_00759	Capg	chr6	72494222	72494846	0.7	1.0	2.0	transcriptio
NM_03307	D6Mm5e	chr6	82896481	82896830	3.9	3.4	1.7	transcriptio
NM_00113	Rtkn	chr6	83085941	83086845	2.5	1.4	0.4	transcriptio
NM_00110	2510049J1	chr6	1.16E+08	1.16E+08	0.0	0.0	1.2	transcriptio
NM_00966	Alox5	chr6	1.16E+08	1.16E+08	1.0	1.0	2.3	transcriptio
NM_01012	Emp1	chr6	1.35E+08	1.35E+08	2.3	2.2	1.0	transcriptio
NM_01065	Sspn	chr6	1.46E+08	1.46E+08	1.7	1.3	0.3	transcriptio
NM_17537	Rdh13	chr7	4396574	4397709	2.4	2.2	0.5	transcriptio
NM_01176	Zim1	chr7	6651662	6652106	0.0	0.0	1.1	transcriptio
NM_01133	Clcn4-2	chr7	7253199	7253628	4.0	4.0	1.5	transcriptio
NM_01998	Tex101	chr7	25457230	25457684	2.9	2.7	1.3	transcriptio
NM_19799	2310044H1	chr7	51753120	51753569	0.9	0.6	2.3	transcriptio
NM_02933	1700026D0	chr7	90943020	90943269	2.4	2.0	0.9	transcriptio
NM_02824	Prcp	chr7	1E+08	1E+08	0.9	0.8	2.2	transcriptio
NM_00977	Bub3	chr7	1.39E+08	1.39E+08	1.1	1.2	2.4	transcriptio
NM_00111	Shank2	chr7	1.51E+08	1.51E+08	1.1	1.1	2.3	transcriptio
NM_17724	D030016E1	chr8	48621288	48621749	0.4	0.3	2.1	transcriptio
NM_01988	Uba52	chr8	73034990	73035432	0.2	0.2	1.2	transcriptio

NM_05407	Afg3l1	chr8	1.26E+08	1.26E+08	2.2	1.8	0.3	transcriptic
NM_17568	A230050P2	chr9	20673103	20673362	2.3	2.3	1.0	transcriptic
NM_01687	Eif3g	chr9	20705450	20705821	0.5	0.5	1.7	transcriptic
NM_02202	Nrgn	chr9	37360509	37360947	2.6	2.2	1.1	transcriptic
NM_02528	Tbrg1	chr9	37467057	37467817	0.0	0.6	1.8	transcriptic
NM_14685	Olfr982	chr9	39881443	39882282	1.6	1.5	0.4	transcriptic
NM_17303	Tbcel	chr9	42281560	42282505	0.8	0.7	2.0	transcriptic
NM_14540	Tmprss4	chr9	45013294	45014148	2.1	2.1	0.9	transcriptic
NM_17338	Cilp	chr9	65112120	65112894	2.0	2.0	0.6	transcriptic
NM_01095	Oaz2-ps	chr9	65524516	65525092	3.0	2.8	1.2	transcriptic
NA	chr9:88494	chr9	88494209	88494858	0.4	0.0	1.7	CpG Island
NA	chr9:88753	chr9	88753512	88754171	0.2	0.0	1.9	CpG Island
NA	chr9:88961	chr9	88961199	88961948	0.5	0.0	2.3	CpG Island
NA	chr9:96437	chr9	96437157	96437816	0.7	0.7	4.1	CpG Island
NM_17866	Rbms3	chr9	1.17E+08	1.17E+08	0.3	0.2	1.8	transcriptic
NM_14623	Acaa1b	chr9	1.19E+08	1.19E+08	1.2	1.2	2.5	transcriptic
NM_00913	Scn10a	chr9	1.2E+08	1.2E+08	3.2	1.9	0.9	transcriptic
NM_02623	Wdr48	chr9	1.2E+08	1.2E+08	2.4	2.2	0.9	transcriptic
NA	chrX:11735	chrX	11736083	11736642	1.9	2.4	0.7	CpG Island
NM_01169	Vbp1	chrX	72759694	72760038	0.3	0.3	1.5	transcriptic
NA	chrX:16643	chrX	1.66E+08	1.66E+08	4.2	4.3	1.5	CpG Island

orientatior	descriptior	DISSTRIBU	gene_id
+	RIKEN cDN/	PROXIMAL	76982
+	phosphatid	INTRAGENI	109294
-	RIKEN cDN/	DISTAL	68691
+	transmemb	DISTAL	271711
+	melanophil	DISTAL	171531
+	prolactin re	PROXIMAL	623503
+	RNA bindin	PROXIMAL	329207
+	contactin a	PROXIMAL	241175
+	expressed s	DISTAL	212439
-	neurofascir	DISTAL	269116
+	renin 2 tan	PROXIMAL	19702
-	RIKEN cDN/	PROXIMAL	71001
+	pleckstrin h	DISTAL	27280
.	0	INTERGENI	0
-	regulator o	DISTAL	19736
-	nitric oxide	DISTAL	70729
-	Fc receptor	PROXIMAL	14130
-	MOCO sulp	PROXIMAL	66112
-	RIKEN cDN/	DISTAL	226777
+	peptidylprc	DISTAL	67418
+	ADP-ribosy	DISTAL	104303
-	suppressor	DISTAL	216233
-	YEATS dom	PROXIMAL	64050
-	cleavage ar	PROXIMAL	432508
+	insulin-like	DISTAL	16006
+	slit homolo	DISTAL	20564
-	coiled-coil	DISTAL	52570
-	heart and r	DISTAL	15110
-	COP9 (cons	DISTAL	26572
-	phosphatid	INTRAGENI	18618
+	retinoic aci	DISTAL	19377
.	0	INTERGENI	0
+	family with	DISTAL	67510
+	ring finger	DISTAL	70510
-	notchless h	DISTAL	217011
+	protein pho	DISTAL	217124
-	beta-1,4-N-	DISTAL	14422
+	oxysterol b	DISTAL	71240
+	2',3'-cyclic	DISTAL	12799
+	WNK lysine	INTRAGENI	69847
-	sidekick ho	DISTAL	237979
-	mesogenin	DISTAL	56184
-	inhibitor of	DISTAL	15902
+	anterior gra	PROXIMAL	23795
+	PRP39 pre-	PROXIMAL	328110

+	tRNA meth	DISTAL	328162
-	X-ray repai	INTRAGENI	74335
-	protein ph	DISTAL	21981
-	transmem	PROXIMAL	104885
+	inverted fo	DISTAL	70435
+	phospholip	DISTAL	104759
-	G protein-c	DISTAL	56696
-	jagged 2	DISTAL	16450
+	cysteine-ri	DISTAL	12925
-	aldo-keto r	PROXIMAL	56043
-	RIKEN cDN	DISTAL	72219
-	zinc finger	INTRAGENI	238693
+	PX domain	DISTAL	218699
+	interleukin	PROXIMAL	16188
+	defensin b	PROXIMAL	654465
+	zinc finger	DISTAL	52521
-	family with	PROXIMAL	432940
-	family with	INTRAGENI	223433
-	chaperoni	DISTAL	12465
-	sterile alph	PROXIMAL	320679
-	transducer	DISTAL	57259
-	centromer	PROXIMAL	66570
-	microspher	INTRAGENI	51812
-	UDP-N-ace	DISTAL	207839
+	keratin 86	INTRAGENI	16679
-	centrosom	DISTAL	74201
.	0	INTERGENI	0
-	expressed	PROXIMAL	106722
.	0	INTERGENI	0
-	ATPase, H+	DISTAL	74915
-	INO80 com	DISTAL	225280
+	UDP-N-ace	DISTAL	14423
+	adenomat	DISTAL	11789
-	protocadh	PROXIMAL	75599
-	toll-like rec	PROXIMAL	225471
-	actin bindi	PROXIMAL	319713
-	insulin-like	PROXIMAL	27356
+	ubiquitin-li	DISTAL	109113
+	transmem	DISTAL	75146
-	calcium ho	DISTAL	546729
-	Sec61, alph	DISTAL	57743
-	proteasom	DISTAL	66998
+	LIM home	INTRAGENI	16870
-	N-myc (an	DISTAL	64685
-	methyltran	INTRAGENI	228019
+	methionin	DISTAL	66559
+	minichrom	DISTAL	66634

-	RIKEN cDN	DISTAL	629499
+	mannosida	DISTAL	69161
-	aurora kina	DISTAL	20878
+	spermatog	DISTAL	70862
-	cyclin A2	DISTAL	12428
-	ankyrin rep	DISTAL	99696
-	ATP-bindin	INTRAGENI	19299
+	phospholip	PROXIMAL	66350
+	caspase 6	DISTAL	12368
.	0	INTERGENI	0
-	bone morp	INTRAGENI	12167
+	RIKEN cDN	PROXIMAL	67317
-	microsemir	DISTAL	1E+08
-	asparagine	DISTAL	56737
-	mannosida	DISTAL	215090
.	0	INTERGENI	0
+	DNA segme	DISTAL	27981
+	MAD2 mitc	DISTAL	71890
-	retinol binc	DISTAL	63954
+	predicted g	PROXIMAL	330004
-	ski sarcoma	DISTAL	20481
+	dehydroge	PROXIMAL	236082
-	ligand of nu	DISTAL	16924
+	serine/argi	INTRAGENI	58212
+	transferrin	PROXIMAL	50765
+	lemur tyros	DISTAL	231876
-	ribose 5-ph	DISTAL	19895
-	atonal hom	DISTAL	71093
-	vesicle-ass	DISTAL	53620
+	capping pro	PROXIMAL	12332
+	DNA segme	PROXIMAL	110958
+	rhotekin	INTRAGENI	20166
-	RIKEN cDN	DISTAL	70291
-	arachidona	PROXIMAL	11689
+	epithelial m	DISTAL	13730
+	sarcospan	DISTAL	16651
-	retinol deh	PROXIMAL	108841
-	zinc finger,	DISTAL	22776
-	chloride ch	DISTAL	12727
-	testis expre	PROXIMAL	56746
-	RIKEN cDN	DISTAL	69683
-	RIKEN cDN	PROXIMAL	75556
+	prolylcarbo	DISTAL	72461
+	budding un	DISTAL	12237
+	SH3/ankyri	INTRAGENI	210274
-	RIKEN cDN	DISTAL	320714
-	ubiquitin A	DISTAL	22186

+	AFG3(ATPa	DISTAL	114896
+	RIKEN cDN/	PROXIMAL	319278
-	eukaryotic	DISTAL	53356
-	neurograni	PROXIMAL	64011
-	transformi	DISTAL	21376
+	olfactory re	PROXIMAL	258853
-	tubulin folc	DISTAL	272589
-	transmemk	DISTAL	214523
+	cartilage in	PROXIMAL	214425
+	ornithine d	INTRAGENI	18247
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
.	0	INTERGENI	0
-	RNA bindin	DISTAL	207181
-	acetyl-Coer	PROXIMAL	235674
-	sodium cha	DISTAL	20264
+	WD repeat	DISTAL	67561
.	0	INTERGENI	0
+	von Hippel-	PROXIMAL	22327
.	0	INTERGENI	0

Differentially methylated regions found in heart connected with 2 fold in gene expression level.

ACC	Name	chr	start	end	BHtS	BcHtS	MHtS	feature DI
NM_17839	3110035E1	chr1	9590986	9592113	3.2	2.4	0.5	transcriptic
NM_14623	Acaa1b	chr9	1.19E+08	1.19E+08	1.2	1.2	2.5	transcriptic
NM_01178	Agr2	chr12	36718163	36719728	2.4	1.9	0.8	transcriptic
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	2.4	transcriptic
NM_00966	Alox5	chr6	1.16E+08	1.16E+08	1.0	1.0	2.3	transcriptic
NM_00759	Capg	chr6	72494222	72494846	0.7	1.0	2.0	transcriptic
NM_00834	Igfbp1	chr11	7095925	7096554	0.9	0.6	2.0	transcriptic
NM_00115	Lnx1	chr5	75074786	75075145	1.9	1.6	0.5	transcriptic
NM_02563	Metapl1	chr2	71290205	71290560	0.7	0.8	1.9	transcriptic
NM_02563	Metapl1	chr2	71290205	71290560	0.7	0.8	1.9	transcriptic
NM_02202	Rbp7	chr4	1.49E+08	1.49E+08	2.4	2.0	0.3	transcriptic
NM_03119	Ren2	chr1	1.35E+08	1.35E+08	2.9	2.3	0.8	transcriptic
NM_17891	Tmem179	chr12	1.14E+08	1.14E+08	1.2	1.5	3.1	transcriptic

orientatior	descriptior	DISSTRIBU'	gene_id	BHtS	SE_EXPRS	BcHtS	SE_EXPRS	MHtS
+	RIKEN cDN,	PROXIMAL	76982	21.2637	0.6392	56.5306	0.7584	132.6498
-	acetyl-Coer	PROXIMAL	235674	145.9109	0.9693	241.8808	0.9269	602.4219
+	anterior gr	PROXIMAL	23795	25.6133	0.6756	25.3011	0.7193	67.8274
-	aldo-keto r	PROXIMAL	56043	1951.255	0.9854	1215.558	0.9875	500.5032
-	arachidona	PROXIMAL	11689	2453.25	0.9837	1421.85	0.9862	432.0764
+	capping pr	PROXIMAL	12332	2030.167	0.9748	4190.172	0.9788	535.8003
+	insulin-like	DISTAL	16006	34.2096	0.8141	36.453	0.4364	15.4971
-	ligand of nu	DISTAL	16924	1916.057	0.8479	2026.751	0.8552	876.4042
+	methionine	DISTAL	66559	2527.703	0.9675	2282.671	0.9661	710.4212
+	methionine	DISTAL	66559	21.2985	0.6643	18.0991	0.5638	46.6856
-	retinol binc	DISTAL	63954	2366.59	0.9817	1143.717	0.9725	6062.349
+	renin 2 tan	PROXIMAL	19702	57.1029	0.8608	20.0635	0.7159	6.5649
-	transmemb	PROXIMAL	104885	2034.971	0.9833	1710.814	0.9887	537.5806

SE_EXPRS
0.8865
0.9871
0.8161
0.9897
0.9874
0.9846
0.677
0.8739
0.9157
0.8269
0.9838
0.5476
0.9513

Gene ontology analysis for heart.

GOTerm	Nr. Genes	Term PValu	Associated	Group Gen	Nr. Genes i	-log(P-value)
olfactory b	4	0.010356	[Id2, Lhx2,	Apc|Aurka	15	1.98482
spindle che	4	0.013919	[Apc, Aurk	Apc|Aurka	8	1.85638
negative re	3	0.019331	[Apc, Mad	Fam105b|	4	1.713744
acute infla	5	0.023555	[Alox5, Cas	Apc|Jag2|	3	1.627922
intrinsic ap	3	0.042839	[Phlda3, P	Alox5|Cas	9	1.368157
regulation	4	0.04348	[Apc, Aurk	Ablim3|Ap	44	1.36171
negative re	4	0.043895	[Fam105b,	Igfbp1|Ma	9	1.357585
negative re	5	0.048248	[Ppp1r9b,	Phlda3|Pp	3	1.316524
transferase	6	0.049808	[4931440L	4931440L1	6	1.302697
T cell differ	3	0.049926	[Apc, Jag2,	Apc|Aurka	33	1.301671

Transcription factor identification for heart.

Interval	TF	NES	Targets	Motifs
500bp	3110039M	4.575	36	9
500bp	Twist2	3.937	41	5
500bp	Ebf1	3.758	26	3
500bp	Rest	3.632	16	2
500bp	Hic2	3.314	64	3
500bp	Purg	3.083	43	2

Promoter sequence motifs

# Rank	**Motif id**	**AUC**	**NES**	**ClusterCod**	**Transcripti**	**Target genes**
1	yetfasco-2	0.056698	4.61217	M1		Rbms3,Bub3,Uhrf2,Samd12,Zfp62
2	transfac_p	0.056388	4.57505	M2	Foxo1,Fox	Prex2,Igfbp1,Atoh8,Shank2,Sspn,
3	flyfactorsu	0.051049	3.93655	M3	Twist2,Twi	Nrgn,Defb47,Krt86,Nmi,Atp6v1e2,
4	tfdimers-M	0.049559	3.75837	M4	Ebf1,Stat6,	Socs2,Nos1ap,Bmpr1b,Tmprss4,O
5	encode-U	0.049508	3.75218	M2		Sdk2,Msmp,D4Wsu53e,Phlda3,N
6	encode-U	0.048597	3.64329	M2		3110035E14Rik,Msgn1,Atoh8,Scn1
7	transfac_p	0.048566	3.63958	M2	Foxo3,Fox	Atoh8,Sspn,Nfasc,Prex2,Mosc1,Ha
8	transfac_p	0.048504	3.63216	M5	Rest	Krt86,Tmem179,Nfasc,Cntnap5b,
9	homer-M0	0.047521	3.5146	M3	Neurod1,T	Defb47,Atoh8,Lnx1,Psmd5,49314
10	homer-M0	0.047387	3.49852	M2	Tcf7,Lef1,T	Prex2,1110028C15Rik,Shank2,Ato
11	encode-U	0.046735	3.42056	M2		Mcm8,3110035E14Rik,Rbms3,Ssp
12	hdpi-ZNF2	0.046693	3.41561	M3	Zbtb18	Nrgn,Nmi,Krt86,Atoh8,Cilp,Bmpr1
13	taipale-RT	0.045845	3.31414	M6	Hic2	Agr2,Msmp,Atp6v1e2,Prlh,Tmem1
14	transfac_p	0.045183	3.23495	M3	Tcf3,Myf6,	Ablim3,Atoh8,Lnx1,Nos1ap,Tmprs
15	yetfasco-7	0.044986	3.21144	M6		Nrgn,Atp6v1e2,Socs2,Uhrf2,Fam1
16	taipale-NC	0.044738	3.18174	M6	Ets1,Ets2,E	D030016E14Rik,Bmpr1b,Msmp,R
17	swissregul	0.0442	3.1174	M2	Bptf,Pou5f	Rbms3,Prex2,Nos1ap,Sspn,Shank2
18	transfac_p	0.044148	3.11121	M4	Hsf1,Hsf4,	Cct5,Fcgr2b,Socs2,Hand1,Sdk2,11
19	encode-U	0.044127	3.10874	M5		Cntnap5b,Atoh8,Tbcel,Rbms3,Ms
20	stark-MAT	0.044014	3.09512	M7		Socs2,Defb47,Mettl8,Atoh8,Msm
21	tfdimers-M	0.043962	3.08894	M2	Smad1,Sox	Atoh8,Nfasc,Bmpr1b,Sspn,Rbms3,
22	hdpi-PURG	0.04391	3.08275	M8	Purg	Bmpr1b,Nrgn,Msmp,Sspn,Cilp,Ato
23	hdpi-OLIG1	0.043641	3.05058	M3	Olig1	Defb47,Krt86,Sspn,Nrgn,Psmd5,N

24	transfac_p	0.04361	3.04687	M2	Foxa3,Foxa	Uhrf2,Sspn,Prex2,Atoh8,1110028
25	transfac_p	0.043476	3.03078	M9	E2f1	Rnf167,Mcm8,Bub3,Uhrf2,Socs2,C
26	yetfasco-6	0.043476	3.03078	M4		Atoh8,Emp1,Shank2,Msgn1,Socs2,
27	tfdimers-M	0.043434	3.02583	M8	Myb,Zeb1	Nrgn,Prex2,Cilp,Wnk4,Defb47,Ato

2,Cct5,Ppp1r9b,Socs2,Rpia,Sdk2,Id2,Apc,Vamp5
fasc,Nos1ap,1110028C15Rik,Rbms3,Emp1
Cilp,Msmp,Nfasc
sbpl7,Sdk2,Uhrf2,Mad2l2,4931440L10Rik,Prlh,Prpf39,Lnx1,Atp6v1e2,Msmp,Atoh8
i,Rbms3,Agr2,Gm833
0a,Prcp,Sdk2,Cnp,Nos1ap,Alg2,Rbms3,Uhrf2,Trmt61a
nd1,Nmi,Emp1,Uhrf2,1110028C15Rik,Igfbp1
m833,Calhm1,Tmprss4,Pla2g12a,Nos1ap,Rbms3
0L10Rik,Atp6v1e2,Krt86,Nrgn,Ablim3,Agr2,Nmi,Fcgr2b,Phlda3,Cilp,Calhm1,Emp1,AU023871,Apc,Msgn1
h8,Mcm8,Igfbp1,Sspn,Rbms3,Agr2
,Atoh8,Shank2,Prex2,Cnp
b,Atp6v1e2,Sspn,Fcgr2b,Prlh,Defb47,Mad2l2,Alg2,Lnx1,Msmp
80,Nrgn,Osbpl7,Rai1
s4,Cnp,Nrgn,Tmem180,Nmi,Mad2l2
5a,Rtkn,Trmt61a,Ppp1r9b,Pxk,Cenpm,Abcd3,Ppp1r13b,Gm833,Aurka,Capg,Tmem179,Lnx1,Agr2,Uba52
f167,Fam18b,Mcrs1,Prex2,Acaa1b,Apc,Uhrf2,Ppp1r9b,Socs2,4931440L10Rik,Tmem180,Arl1,Ccdc69,Rb
,Tbcel,1110028C15Rik,Igfbp1,Emp1,Bmpr1b,Nfasc
10028C15Rik
gn1,Msmp,Uhrf2,Bmpr1b
,Lnx1,3110035E14Rik,Rbms3,Bmpr1b,4922505G16Rik,1110028C15Rik,Sspn,Msgn1,Krt86,Prex2,Olfr982,
Prex2,Msgn1,3110035E14Rik,Defb47,Emp1,Aurka,Cnp,Tmprss4,Rtkn,Fcgr2b,Hand1,Prpf39,Igfbp1
h8,Fcgr2b,1110028C15Rik,Krt86
s1ap,Gm833,Fcgr2b

15Rik,Trmt61a,Igfbp1,Emp1
cna2,Msgn1,Aurka,Rbms3
,AA986860,Aurka,Cenpm,Ppp1r9b
h8,AA986860,Emp1,1110028C15Rik,2510049J12Rik,Nos1ap,Prlh,Msgn1,Socs2,Lnx1,Bmpr1b,Trfr2,Ticam

,Mosc1,Osbpl7,Cnp,Ccdc69,Nfasc,Hand1,Bmpr1b,Igfbp1,Shank2,Mad2l2,Sspn,Msmp,Gm833,Rbp7,Olfr9

2,Apc,Tmem180,Fam105b,Krt86,Fam18b,Tob2,Tbcel,Rbms3,Samd12,Inf2,1700026D08Rik,Atoh8,Zfp622,
s3,Atp6v1e2,Mcm8,Nos1ap,Cep97,Tmem179,Cops3,Tob2,Eif3g,Prcp,Cpsf6,Mad2l2,Zim1,Trmt61a,1110

,Aurka,Cep97,1700026D08Rik,Gm833,Atp6v1e2,Uhrf2,Jag2,Emp1,Shank2,Tmem179,Xrcc3,Psmd5,Id2,Ln

2,Tbrg1,Tmprss4,Akr1e1,Hand1,Rbms3,Srrm3,Mlph,Fam105b,Prpf39,Uhrf2,Rai1,Manbal,Jag2,Lmtk2,49

)82,2510049J12Rik,Afg3l1

Nfasc,Cnp,Cops3,Galnt6,Prcp,Ski,Sspn,Rnf167,Msmp,D030016E14Rik,Mlph
)028C15Rik,Galnt1,Tmprss4,Bub3,Cenpm

ntk2,Cct5,Samd12,Cops3,Nfasc,Capg,2510049J12Rik,Ccna2,Nos1ap,Prpf39,Tmprss4,Calhm1,Zfp622,Sdk

31440L10Rik,Rpia,Prcp,Ppil4,1700022I11Rik,Zfp58,D030016E14Rik

2,Ablim3,Tmem180,Alox5

Differentially methylated regions found in spleen.

ACC	Name	chr	start	end	BSplS	BcSplS	MSplS	feature DI
NM_15340	Neurl3	chr1	36332180	36333144	2.0	1.8	0.6	transcriptic
NM_00991	Cnga3	chr1	37273757	37273996	0.7	1.0	2.3	transcriptic
NM_00114	Rfx8	chr1	39777740	39778705	2.5	2.6	0.3	transcriptic
NM_02272	Fzd5	chr1	64782446	64782970	1.6	1.9	0.6	Primary Tra
NM_17764	1110028C1	chr1	66865360	66865784	0.1	0.1	1.3	transcriptic
NM_17498	Gpbar1	chr1	74323533	74323862	2.5	2.2	1.1	transcriptic
NM_00110	Prlh	chr1	92848564	92849198	2.2	3.3	1.0	transcriptic
NM_00115	Rab17	chr1	92864208	92864467	4.6	4.8	1.9	transcriptic
NR_02692	1700020N1	chr1	93301989	93303053	2.6	2.3	0.5	transcriptic
NM_17343	Nav1	chr1	1.37E+08	1.37E+08	2.3	2.6	0.9	transcriptic
NM_17739	Atp6v1g3	chr1	1.4E+08	1.4E+08	0.1	0.1	1.5	transcriptic
NM_00906	Rgs4	chr1	1.72E+08	1.72E+08	0.0	0.0	1.6	transcriptic
NM_00103	1700084C0	chr1	1.72E+08	1.72E+08	2.0	2.1	0.9	transcriptic
NM_02752	Nos1ap	chr1	1.72E+08	1.72E+08	1.0	1.2	3.3	transcriptic
NM_02614	Ppil4	chr10	7509779	7510958	0.2	0.3	1.9	transcriptic
NM_17278	Zc3h12d	chr10	7587001	7587665	3.3	5.0	1.0	Primary Tra
NM_17860	Reep3	chr10	66560967	66561616	2.1	2.6	0.9	transcriptic
NM_17799	C030046I0	chr10	79382162	79382614	2.8	4.1	0.6	transcriptic
NM_02585	Arl1	chr10	88191503	88192282	0.2	0.1	1.8	transcriptic
NM_00101	Cpsf6	chr10	1.17E+08	1.17E+08	0.1	0.2	1.6	transcriptic
NM_00834	Igfbp1	chr11	7095925	7096554	0.1	0.3	1.4	transcriptic
NM_03117	Trim17	chr11	58777609	58778084	3.1	2.5	1.2	transcriptic
NM_00115	Guk1	chr11	59002909	59003853	2.0	1.7	0.7	transcriptic
NM_14582	Nlrp3	chr11	59355460	59356014	2.1	2.5	0.9	transcriptic
NM_01199	Cops3	chr11	59654752	59655702	0.5	0.5	1.9	transcriptic
NM_02621	Fam18b	chr11	62690533	62691505	0.6	1.0	2.1	transcriptic
NM_02960	Abcc3	chr11	94255580	94256234	3.8	2.5	1.2	transcriptic
NM_05316	Mrpl27	chr11	94513270	94514107	1.9	1.3	0.2	transcriptic
NM_00110	Gm11545	chr11	94621760	94622509	1.6	1.6	0.3	transcriptic
NR_00329	D030028A	chr11	96803395	96804329	1.8	1.8	0.6	transcriptic
NM_17256	Rundc1	chr11	1.01E+08	1.01E+08	1.1	1.5	0.0	transcriptic
NM_01035	Grin2c	chr11	1.15E+08	1.15E+08	4.1	4.6	1.3	transcriptic
NM_01738	Sept9	chr11	1.17E+08	1.17E+08	2.2	2.7	1.0	transcriptic
NM_02758	Nt5c1b	chr12	10376841	10377105	0.8	1.0	2.3	transcriptic
NM_01954	Msgn1	chr12	11218036	11218673	1.7	1.5	0.1	transcriptic
NA	chr12:355	chr12	35591672	35592144	2.2	2.4	0.9	CpG Island
NM_01178	Agr2	chr12	36718163	36719728	2.6	2.2	1.1	transcriptic
NM_00925	Serpina3n	chr12	1.06E+08	1.06E+08	0.2	0.2	1.5	transcriptic
NM_01058	Jag2	chr12	1.14E+08	1.14E+08	1.9	3.4	0.8	transcriptic
NM_02539	Nudt14	chr12	1.14E+08	1.14E+08	1.9	3.5	0.7	transcriptic
NM_00114	Btbd6	chr12	1.14E+08	1.14E+08	2.3	3.3	1.0	transcriptic
NM_02422	Crip2	chr12	1.14E+08	1.14E+08	2.4	4.5	1.2	transcriptic
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	2.7	transcriptic
NM_02355	Nol7	chr13	43492724	43493746	1.5	1.5	0.3	transcriptic
NM_02605	Cap2	chr13	46597722	46598271	1.9	2.2	0.8	transcriptic
NM_02770	Zdhhc11	chr13	74098871	74100310	2.5	2.4	0.9	transcriptic
NM_14545	Pxk	chr14	8928640	8929546	0.1	0.1	1.7	transcriptic
NM_00836	Il3ra	chr14	15178924	15179295	2.4	3.8	1.2	transcriptic

NM_01967	Stmn4	chr14	66961053	66961869	3.2	3.6	1.4	transcriptio
NM_14597	Pdlim2	chr14	70576631	70577300	2.5	3.0	1.1	transcriptio
NM_00101	Fam105b	chr15	27562080	27562932	0.7	0.7	1.7	transcriptio
NM_14605	Dap	chr15	31152069	31152423	2.1	2.3	0.9	transcriptio
NM_00763	Cct5	chr15	31532950	31533392	0.6	0.7	2.0	transcriptio
NA	chr15:3706	chr15	37065155	37065724	1.8	2.9	0.5	CpG Islands
NM_02049	Ly6i	chr15	74816146	74816688	0.5	0.5	1.6	transcriptio
NM_00114	BC024139	chr15	75958253	75958802	1.9	2.2	0.9	transcriptio
NM_02050	Tob2	chr15	81690041	81691672	0.0	0.0	1.1	transcriptio
NM_02807	Tnfrsf13c	chr15	82056471	82057120	3.2	4.8	1.6	transcriptio
NM_00111	Tcf20	chr15	82742448	82743905	2.7	2.9	1.0	transcriptio
NM_01345	Acr	chr15	89398905	89399458	1.9	2.2	0.9	transcriptio
NM_01676	Mcrs1	chr15	99081644	99081893	1.3	1.1	0.0	transcriptio
NM_02306	Lima1	chr15	99651840	99653407	1.5	1.5	0.5	transcriptio
NM_01066	Krt86	chr15	1.01E+08	1.01E+08	0.3	0.5	1.7	Primary Tra
NM_02639	Nmral1	chr16	4719145	4719399	0.6	0.0	1.7	transcriptio
NM_17251	Abhd10	chr16	45744899	45745784	0.9	0.5	2.3	transcriptio
NM_05410	2310034C0	chr16	88757863	88758407	0.5	0.4	2.1	transcriptio
NM_01370	Krtap14	chr16	88825671	88826015	1.2	1.6	3.3	transcriptio
NM_02862	Krtap16-7	chr16	89403487	89403731	0.9	0.9	2.2	transcriptio
NA	chr17:1567	chr17	15673304	15673974	0.1	0.1	2.0	CpG Islands
NM_02147	Tulp1	chr17	28501806	28502185	2.8	4.8	1.0	transcriptio
NM_08072	Tmprss3	chr17	31336679	31337333	1.6	2.0	0.5	transcriptio
NM_01358	Psmb9	chr17	34326735	34327079	2.0	1.9	0.9	transcriptio
NM_03074	Btnl6	chr17	34654459	34654708	2.1	1.9	0.7	transcriptio
NM_14548	Prr3	chr17	36117975	36118234	1.9	2.0	0.8	transcriptio
NM_02288	Slc29a1	chr17	45730227	45730851	2.5	3.0	1.2	transcriptio
NM_01172	Xdh	chr17	74299291	74299955	2.7	2.1	0.9	transcriptio
NM_02912	Atp6v1e2	chr17	87348541	87349395	2.6	3.6	1.2	transcriptio
NM_17262	Ino80c	chr18	24281882	24282837	2.8	2.9	1.3	transcriptio
NM_02417	0610009O2	chr18	38407099	38408435	2.4	2.2	0.9	transcriptio
NM_19435	Spire1	chr18	67713103	67714060	1.0	0.5	2.6	transcriptio
NA	chr19:4367	chr19	43675168	43676408	2.7	2.7	1.0	CpG Islands
NA	chr19:4513	chr19	45139820	45140264	1.4	1.8	0.1	CpG Islands
NM_00108	Calhm1	chr19	47220974	47221648	1.5	0.8	3.4	transcriptio
NA	chr19:4722	chr19	47225972	47226621	3.8	3.1	1.6	CpG Islands
NM_02661	Gsto2	chr19	47938883	47939327	1.1	1.1	2.6	transcriptio
NM_02823	Ttc30b	chr2	75775796	75777551	0.5	0.5	1.8	transcriptio
NM_00103	Cstf3	chr2	1.04E+08	1.04E+08	0.9	1.1	2.3	transcriptio
NM_17730	Lrrn4	chr2	1.33E+08	1.33E+08	3.3	4.0	1.3	transcriptio
NM_17765	Cstl1	chr2	1.49E+08	1.49E+08	1.8	1.7	0.7	transcriptio
NM_19435	Rya3	chr2	1.54E+08	1.54E+08	2.4	2.8	1.1	transcriptio
NM_14489	BC018465	chr2	1.54E+08	1.54E+08	1.9	2.7	0.7	transcriptio
NM_00103	4922505G1	chr2	1.57E+08	1.57E+08	1.5	1.6	0.4	transcriptio
NM_02696	Manbal	chr2	1.57E+08	1.57E+08	2.4	2.1	0.9	transcriptio
NM_01149	Aurka	chr2	1.72E+08	1.72E+08	0.8	1.0	2.0	transcriptio
NM_02915	Spata16	chr3	26535189	26535925	1.8	2.1	0.4	transcriptio
NM_00111	Fxr1	chr3	33917468	33917962	0.2	0.3	1.3	transcriptio
NM_00762	Ccna1	chr3	54859447	54859691	0.3	0.6	1.6	transcriptio
NM_02319	Pla2g12a	chr3	1.3E+08	1.3E+08	2.6	3.2	1.1	transcriptio

NM_00947	Uox	chr3	1.46E+08	1.46E+08	2.3	1.9	0.5	transcriptic
NM_01582	Gne	chr4	44097015	44097854	0.5	0.5	1.6	transcriptic
NM_00115	Eps15	chr4	1.09E+08	1.09E+08	0.5	0.2	1.6	transcriptic
NM_00100	Maneal	chr4	1.25E+08	1.25E+08	0.8	0.8	2.6	transcriptic
NA	chr4:13601	chr4	1.36E+08	1.36E+08	2.2	2.0	0.7	CpG Island
NM_00977	C1qb	chr4	1.36E+08	1.36E+08	1.5	1.6	0.5	transcriptic
NM_00783	Ddost	chr4	1.38E+08	1.38E+08	3.2	2.2	1.1	transcriptic
NM_14540	Tmem51	chr4	1.42E+08	1.42E+08	2.2	1.9	0.6	transcriptic
NM_00940	Tnfrsf8	chr4	1.45E+08	1.45E+08	1.5	2.0	0.5	transcriptic
NM_17340	Fbxo44	chr4	1.48E+08	1.48E+08	2.4	2.2	0.8	transcriptic
NM_00927	Srm	chr4	1.48E+08	1.48E+08	1.9	2.0	0.7	transcriptic
NM_02202	Rbp7	chr4	1.49E+08	1.49E+08	2.4	2.5	0.4	transcriptic
NM_15342	Nphp4	chr4	1.52E+08	1.52E+08	0.3	0.8	1.9	transcriptic
NM_01138	Ski	chr4	1.55E+08	1.55E+08	0.2	0.2	1.8	transcriptic
NM_02927	Nop14	chr5	35005467	35005791	1.0	0.8	2.4	transcriptic
NA	chr5:37554	chr5	37554388	37554837	1.7	1.3	0.2	CpG Island
NM_02061	Srd5a3	chr5	76567962	76568202	2.5	3.0	1.2	transcriptic
NM_02626	4930519G	chr5	1.15E+08	1.15E+08	1.2	1.2	2.8	transcriptic
NM_02002	Rfc2	chr5	1.35E+08	1.35E+08	1.0	0.8	2.6	transcriptic
NM_02050	Cldn13	chr5	1.35E+08	1.35E+08	3.2	3.4	1.4	transcriptic
NA	chr5:13637	chr5	1.36E+08	1.36E+08	2.0	3.1	0.3	CpG Island
NA	chr5:14391	chr5	1.44E+08	1.44E+08	0.8	0.9	1.9	CpG Island
NM_03303	Ocm	chr5	1.45E+08	1.45E+08	0.0	0.1	1.1	transcriptic
NM_02686	Rasl11a	chr5	1.48E+08	1.48E+08	1.8	1.9	0.7	transcriptic
NM_00108	B3galtl	chr5	1.5E+08	1.5E+08	1.9	2.3	0.7	transcriptic
NM_02423	Stambp	chr6	83523664	83524823	2.2	2.1	0.7	transcriptic
NM_00103	Cml3	chr6	85715204	85716243	2.0	2.2	1.0	transcriptic
NM_13831	H1foo	chr6	1.16E+08	1.16E+08	2.0	2.2	0.6	transcriptic
NM_00108	Ankrd26	chr6	1.19E+08	1.19E+08	2.3	1.6	0.4	transcriptic
NM_01065	Sspn	chr6	1.46E+08	1.46E+08	2.1	1.8	0.5	transcriptic
NM_17537	Rdh13	chr7	4396574	4397709	1.7	2.7	0.7	transcriptic
NM_02328	Ceacam11	chr7	18557783	18558060	1.0	0.9	2.3	transcriptic
NM_01687	Tomm40	chr7	20302460	20302910	1.8	2.0	0.8	transcriptic
NM_01579	Fbxo17	chr7	29517379	29518030	1.9	1.7	0.5	Primary Tra
NM_00100	Zfp619	chr7	46771038	46771921	1.8	1.5	0.4	transcriptic
NA	chr7:74948	chr7	74948300	74948975	0.1	0.3	1.4	CpG Island
NM_01055	Il16	chr7	90883272	90883721	3.5	3.5	0.9	transcriptic
NM_18185	Trim66	chr7	1.17E+08	1.17E+08	1.5	2.2	0.3	transcriptic
NM_13335	Prss8	chr7	1.35E+08	1.35E+08	2.4	2.5	0.6	transcriptic
NM_01148	Star	chr8	26919076	26919336	2.4	2.3	1.1	transcriptic
NM_17724	D030016E1	chr8	48621288	48621749	0.7	0.3	2.0	transcriptic
NM_01198	Homer3	chr8	72805778	72806020	1.6	1.8	0.5	transcriptic
NM_00100	Crtc1	chr8	72963749	72963983	2.0	2.3	0.8	transcriptic
NM_00818	Gtl3	chr8	97961015	97961430	0.1	0.1	1.2	transcriptic
NM_02944	Cdyl2	chr8	1.19E+08	1.19E+08	2.4	3.9	0.9	transcriptic
NM_02968	Pkd1l2	chr8	1.2E+08	1.2E+08	3.3	2.9	0.5	transcriptic
NM_00100	Pabpn1l	chr8	1.25E+08	1.25E+08	2.7	3.1	1.1	transcriptic
NM_05407	Afg3l1	chr8	1.26E+08	1.26E+08	1.7	2.3	0.1	transcriptic
NM_02370	Capn9	chr8	1.27E+08	1.27E+08	3.6	3.5	1.5	transcriptic
NM_00746	Birc3	chr9	7875534	7875775	0.0	0.0	1.5	transcriptic

NM_00969	Aplp2	chr9	31019661	31020509	2.2	2.8	1.0	transcriptic
NM_02528	Tbrg1	chr9	37467057	37467817	0.2	0.5	2.2	transcriptic
NM_14641	Olfr877	chr9	37661972	37662731	1.6	1.5	0.5	transcriptic
NM_14685	Olfr982	chr9	39881443	39882282	1.9	1.7	0.4	transcriptic
NM_13322	Pdzd3	chr9	44062282	44062506	1.7	2.8	0.6	transcriptic
NM_13895	Ttc36	chr9	44611850	44612094	1.0	0.9	2.3	transcriptic
NM_14540	Tmprss4	chr9	45013294	45014148	1.1	1.4	0.0	transcriptic
NM_17338	Cilp	chr9	65112120	65112894	2.0	2.0	0.7	transcriptic
NA	chr9:88494	chr9	88494209	88494858	0.1	0.0	1.2	CpG Island
NA	chr9:88753	chr9	88753512	88754171	0.1	0.0	1.3	CpG Island
NA	chr9:88961	chr9	88961199	88961948	0.2	0.0	1.9	CpG Island
NM_17790	Slc9a9	chr9	94567367	94567985	1.8	1.8	0.4	transcriptic
NM_01127	Rnf7	chr9	96379973	96381584	3.5	4.1	1.5	transcriptic
NA	chr9:96437	chr9	96437157	96437816	1.0	1.8	4.1	CpG Island
NM_17866	Rbms3	chr9	1.17E+08	1.17E+08	0.0	0.2	1.2	transcriptic
NM_00111	Itga9	chr9	1.19E+08	1.19E+08	4.6	5.3	2.3	transcriptic
NM_17711	Dlec1	chr9	1.19E+08	1.19E+08	2.4	2.2	0.8	transcriptic
NM_00913	Scn10a	chr9	1.2E+08	1.2E+08	2.4	2.5	0.8	transcriptic
NM_02897	Gorasp1	chr9	1.2E+08	1.2E+08	2.7	3.3	1.2	transcriptic
NM_15328	Csrnp1	chr9	1.2E+08	1.2E+08	3.3	3.1	1.5	transcriptic
NA	chr9:12048	chr9	1.2E+08	1.2E+08	0.1	0.0	1.5	CpG Island
NM_02691	Lyzl4	chr9	1.22E+08	1.22E+08	2.0	3.4	0.9	transcriptic
NM_00102	DXBay18	chrX	70362024	70362550	2.3	3.1	1.0	transcriptic

descriptior	DISSTRIBU	gene_id
neuralized	DISTAL	214854
cyclic nucle	DISTAL	12790
regulatory	PROXIMAL	619289
frizzled hor	INTRAGENI	14367
RIKEN cDN	DISTAL	68691
G protein-c	DISTAL	227289
prolactin re	PROXIMAL	623503
RAB17, me	PROXIMAL	19329
RIKEN cDN	PROXIMAL	67086
neuron nav	INTRAGENI	215690
ATPase, H+	DISTAL	338375
regulator o	DISTAL	19736
RIKEN cDN	DISTAL	78465
nitric oxide	DISTAL	70729
peptidylpr	DISTAL	67418
zinc finger	INTRAGENI	237256
receptor ac	DISTAL	28193
RIKEN cDN	DISTAL	109284
ADP-ribosy	DISTAL	104303
cleavage ar	PROXIMAL	432508
insulin-like	DISTAL	16006
tripartite m	INTRAGENI	56631
guanylate	DISTAL	14923
NLR family,	PROXIMAL	216799
COP9 (cons	DISTAL	26572
family with	DISTAL	67510
ATP-bindin	DISTAL	76408
mitochond	DISTAL	94064
predicted g	PROXIMAL	217122
RIKEN cDN	DISTAL	319371
RUN domai	DISTAL	217201
glutamate	DISTAL	14813
septin 9	PROXIMAL	53860
5'-nucleoti	PROXIMAL	70881
mesogenin	DISTAL	56184
0	INTERGENI	0
anterior gr	PROXIMAL	23795
serine (or c	DISTAL	20716
jagged 2	DISTAL	16450
nudix (nucl	DISTAL	66174
BTB (POZ)	DISTAL	399566
cysteine ric	DISTAL	68337
aldo-keto r	PROXIMAL	56043
nucleolar p	PROXIMAL	70078
CAP, adeny	INTRAGENI	67252
zinc finger,	DISTAL	71164
PX domain	DISTAL	218699
interleukin	PROXIMAL	16188

stathmin-li	DISTAL	56471
PDZ and LI	INTRAGENI	213019
family with	DISTAL	432940
death-asso	DISTAL	223453
chaperonin	DISTAL	12465
0	INTERGENI	0
lymphocyt	DISTAL	57248
cDNA sequ	DISTAL	271278
transducer	DISTAL	57259
tumor necr	DISTAL	72049
transcripti	PROXIMAL	21411
acrosin pre	INTRAGENI	11434
microsphe	INTRAGENI	51812
LIM domai	DISTAL	65970
keratin 86	INTRAGENI	16679
NmrA-like	PROXIMAL	67824
abhydrolas	DISTAL	213012
RIKEN cDN	DISTAL	117172
keratin ass	INTRAGENI	23927
keratin ass	INTRAGENI	170656
0	INTERGENI	0
tubby like	PROXIMAL	22157
transmemb	DISTAL	140765
proteasom	DISTAL	16912
butyrophili	PROXIMAL	624681
proline-ric	DISTAL	75210
solute carri	DISTAL	63959
xanthine d	PROXIMAL	22436
ATPase, H+	DISTAL	74915
INO80 com	DISTAL	225280
RIKEN cDN	DISTAL	66839
spire homo	DISTAL	68166
0	INTERGENI	0
0	INTERGENI	0
calcium ho	DISTAL	546729
0	INTERGENI	0
glutathione	DISTAL	68214
tetratricop	PROXIMAL	72421
cleavage st	DISTAL	228410
leucine ric	DISTAL	320974
cystatin-lik	PROXIMAL	228756
antimicrob	DISTAL	378700
cDNA sequ	PROXIMAL	228802
RIKEN cDN	DISTAL	629499
mannosida	DISTAL	69161
aurora kina	DISTAL	20878
spermatog	DISTAL	70862
fragile X m	DISTAL	14359
cyclin A1	PROXIMAL	12427
phospholip	PROXIMAL	66350

urate oxida	DISTAL	22262
glucosamin	PROXIMAL	50798
epidermal g	DISTAL	13858
mannosida	DISTAL	215090
0	INTERGENI	0
complemer	PROXIMAL	12260
dolichyl-di-	DISTAL	13200
transmemb	DISTAL	214359
tumor necr	DISTAL	21941
F-box prote	DISTAL	230903
spermidine	DISTAL	20810
retinol binc	DISTAL	63954
nephronop	INTRAGENI	260305
ski sarcoma	DISTAL	20481
NOP14 nuc	DISTAL	75416
0	INTERGENI	0
steroid 5 al	DISTAL	57357
RIKEN cDN/	DISTAL	67593
replication	DISTAL	19718
claudin 13	PROXIMAL	57255
0	INTERGENI	0
0	INTERGENI	0
oncomodul	INTRAGENI	18261
RAS-like, fa	DISTAL	68895
beta 1,3-ga	INTRAGENI	381694
STAM bind	DISTAL	70527
camello-lik	PROXIMAL	93674
H1 histone	DISTAL	171506
ankyrin rep	DISTAL	232339
sarcospan	DISTAL	16651
retinol deh	PROXIMAL	108841
carcinoemb	INTRAGENI	66996
translocase	DISTAL	53333
F-box prote	INTRAGENI	50760
zinc finger	DISTAL	70227
0	INTERGENI	0
interleukin	INTRAGENI	16170
tripartite m	DISTAL	330627
protease, s	PROXIMAL	76560
steroidoger	PROXIMAL	20845
RIKEN cDN/	DISTAL	320714
homer hom	DISTAL	26558
CREB regul	PROXIMAL	382056
gene trap lo	DISTAL	14894
chromodor	DISTAL	75796
polycystic k	PROXIMAL	76645
poly(A)binc	PROXIMAL	382035
AFG3(ATPa	DISTAL	114896
calpain 9	PROXIMAL	73647
baculoviral	DISTAL	11796

amyloid be	PROXIMAL	11804
transformi	DISTAL	21376
olfactory re	PROXIMAL	258412
olfactory re	PROXIMAL	258853
PDZ domai	DISTAL	170761
tetratricop	DISTAL	192653
transmemb	DISTAL	214523
cartilage in	PROXIMAL	214425
0	INTERGENI	0
0	INTERGENI	0
0	INTERGENI	0
solute carri	DISTAL	331004
ring finger	DISTAL	19823
0	INTERGENI	0
RNA bindin	DISTAL	207181
integrin alp	PROXIMAL	104099
deleted in l	DISTAL	320256
sodium cha	DISTAL	20264
golgi reass	DISTAL	74498
cysteine-se	PROXIMAL	215418
0	INTERGENI	0
lysozyme-li	INTRAGENI	69032
DNA segme	PROXIMAL	574405

Differentially methylated regions found in spleen connected with 2 fold in gene expression level.

ACC	Name	chr	start	end	BSplS	BcSplS	MSplS	feature DI
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	2.7	transcriptio
NM_00759	Capg	chr6	72492485	72493556	2.3	2.6	1.2	transcriptio
NM_02050	Cldn13	chr5	1.35E+08	1.35E+08	3.2	3.4	1.4	transcriptio
NM_00991	Cnga3	chr1	37273757	37273996	0.7	1.0	2.3	transcriptio
NR_00329	D030028A	chr11	96803395	96804329	1.8	1.8	0.6	transcriptio
NR_00329	D030028A	chr11	96803395	96804329	1.8	1.8	0.6	transcriptio
NM_17340	Fbxo44	chr4	1.48E+08	1.48E+08	2.4	2.2	0.8	transcriptio
NM_00100	Maneal	chr4	1.25E+08	1.25E+08	0.8	0.8	2.6	transcriptio
NM_00867	Nbl1	chr4	1.39E+08	1.39E+08	2.6	3.1	1.5	transcriptio
NM_02639	Nmral1	chr16	4719145	4719399	0.6	0.0	1.7	transcriptio
NM_02752	Nos1ap	chr1	1.72E+08	1.72E+08	1.0	1.2	3.3	transcriptio
NM_02752	Nos1ap	chr1	1.72E+08	1.72E+08	1.0	1.2	3.3	transcriptio
NM_00925	Serpina3n	chr12	1.06E+08	1.06E+08	0.2	0.2	1.5	transcriptio

orientatior	descriptior	DISSTRIBU	gene_id	gene_id	transcript_	BSplS	SE_EXPRS	BsSplS
-	aldo-keto r	PROXIMAL	56043	56043	BC012692	538.4099	0.9403	536.3072
+	capping pr	DISTAL	12332	12332	BC003480	12069.52	0.9931	13475.73
-	claudin 13	PROXIMAL	57255	57255	BC115481	4588.142	0.9458	4632.86
+	cyclic nucle	DISTAL	12790	12790	BC035272	41.079	0.8114	45.9222
+	RIKEN cDN	DISTAL	319371	319371	NR_00329	484.5903	0.9286	441.8987
+	RIKEN cDN	DISTAL	319371	319371	AK086164	470.4624	0.9347	549.4412
-	F-box prot	DISTAL	230903	230903	AK170958	159.9348	0.8735	125.6946
-	mannosida	DISTAL	215090	215090	BC065047	69.2616	0.8173	71.7084
-	neuroblast	PROXIMAL	17965	17965	BC099858	386.8472	0.9311	415.1514
-	NmrA-like	PROXIMAL	67824	67824	AK146521	76.0386	0.8411	85.586
-	nitric oxide	DISTAL	70729	70729	AK018149	568.0599	0.9183	525.6917
-	nitric oxide	DISTAL	70729	70729	NM_0011	198.4316	0.8594	170.0955
+	serine (or c	DISTAL	20716	20716	BC013651	3328.975	0.9732	3102.373

SE_EXPRS	MSplS	SE_EXPRS
0.9387	71.7177	0.81
0.996	4014.975	0.9895
0.9648	1125.991	0.954
0.8108	12.5645	0.6437
0.9285	89.9653	0.8401
0.9334	151.3386	0.8765
0.8531	51.2342	0.7404
0.8128	28.0201	0.6812
0.9303	840.3752	0.9652
0.8373	34.1256	0.7402
0.9142	1234.956	0.9458
0.8316	463.9802	0.898
0.9664	6661.088	0.9821

Gene ontology analysis for spleen.

GOTerm	Nr. Genes	Term PVal	Associated	Group Gen	Nr. Genes i	-log(P-value)
photorece	4	0.02976	[Cnga3, Np	[Cnga3, Np	4	1.526373
retina deve	5	0.049365	[Cnga3, Np	[Cnga3, Np	5	1.306584

Transcription factor identification for spleen.

Interval	TF	NES	Targets	Motifs
500bp	Jdp2	4.334	55	8
500bp	Mafa	4.176	69	7
500bp	Rest	3.878	41	2
500bp	Zeb1	3.843	24	4
500bp	Rfx8	3.838	37	13
500bp	Spr	3.833	28	3
500bp	Foxo3	3.777	8	1
500bp	Nifa	3.467	36	5
500bp	Vsx1	3.182	16	3

Promoter sequence motifs

# Rank	Motif id	AUC	NES	ClusterCod	Transcripti	Target genes
1	transfac_pu	0.053127	4.33429	M1		Il16,Xdh,Sept9,Slc9a9,Krt86,Tmprs
2	jaspar-POL	0.051764	4.17574	M2		BC018465,Calhm1,Xdh,Pdlim2,Ne
3	encode-UW	0.050362	4.01259	M2		Atp6v1e2,Trim66,BC018465,Nos1
4	tfdimers-M	0.049948	3.96434	M2	Mafa,Nr3c	Il16,Stmn4,Agr2,Tmprss4,Pdlim2,
5	jaspar-PF0	0.049207	3.87817	M3	Rest	Krt86,Crip2,Rbms3,Pxk,BC018465,
6	transfac_pu	0.048901	3.84255	M4	Zeb1	Trim66,Prr3,Nos1ap,Ttc36,Tmprss
7	jaspar-CN0	0.048862	3.83796	M5	Rfx1,Rfx2,	Cops3,Prr3,Trim66,Rundc1,BC024
8	hdpi-SPR	0.048822	3.83336	M6	Spr,Spr-ps1	Rbms3,Pdzd3,Tcf20,Ttc36,Calhm1,
9	transfac_pr	0.048704	3.81958	M1	Jdp2,Bach1	Pdlim2,Sept9,Krt86,Zc3h12d,Stmn
10	yetfasco-8	0.048704	3.81958	M1	Jdp2,Bach1	Pdlim2,Sept9,Krt86,Zc3h12d,Stmn
11	elemento-	0.048348	3.77821	M4		Trim66,Il16,Nos1ap,Fzd5,Prr3,Tcf2
12	taipale-GT	0.048338	3.77707	M7	Foxo3,Fox	Uox,Fam105b,Slc29a1,Ly6i,Tob2,2
13	jaspar-MA	0.048032	3.74145	M1	Jdp2,Bach1	Pdlim2,Sept9,Krt86,Stmn4,Zc3h12
14	jaspar-CN0	0.047865	3.72192	M5	Rfx1,Rfx5,	Cops3,Prr3,Trim66,Rundc1,Ccna1,
15	taipale-NG	0.047825	3.71732	M5	Rfx5,Rfx1,	Prr3,Rundc1,Trim66,Cops3,Ccna1,
16	yetfasco-1	0.047262	3.65183	M1	Mybl2,My	Stmn4,Aurka,Xdh,Pdlim2,Zc3h12d,
17	taipale-NG	0.046561	3.57026	M5	Rfx3,Rfx1,	Prr3,Rundc1,Trim66,Ccna1,Cops3
18	jaspar-CN0	0.046453	3.55762	M5	Rfx3,Rfx4,	Cops3,Nphp4,Prr3,BC024139,Trim
19	taipale-SG	0.046216	3.53005	M5	Rfx5,Rfx1,	Prr3,Rundc1,Trim66,Cops3,Ccna1,
20	taipale-NA	0.046137	3.52086	M1	Nfe2,Bach1	Pdlim2,Sept9,Zc3h12d,Abcc3,Tnfrs
21	transfac_pu	0.045673	3.46686	M8	Nfic,Nfia,N	BC018465,Agr2,Stmn4,B3galtl,Rbm
22	tfdimers-M	0.045505	3.44733	M8	Pura	Agr2,Acr,Rbms3,Stmn4,Il16,BC018
23	taipale-NG	0.044833	3.3692	M5	Rfx1,Rfx3,	Prr3,Trim66,Rundc1,Cops3,Ccna1,
24	taipale-NG	0.044755	3.36001	M5	Rfx2,Rfx1,	Prr3,Trim66,Rundc1,Cops3,Ccna1,
25	yetfasco-2	0.044261	3.30257	M1	Bach2,Jdp2	Il16,Pdlim2,Tnfrsf8,Krt86,Sept9,St
26	hdpi-C2orf	0.044192	3.29452	M5		Atp6v1e2,Krtap14,Nt5c1b,Rundc1,
27	hdpi-AFF4	0.044142	3.28878	M6	Aff4,Spr,Sp	Rbms3,Tcf20,Pdzd3,Calhm1,Trim6
28	encode-UW	0.044044	3.27729	M2		Msgn1,Pkd1l2,Rundc1,Neurl3,Eps

29	taipale-NN	0.044044	3.27729	M4	Tcf4,Tcf3,L	Trim66,Pdlim2,Prlh,Tmprss4,Zc3h1
30	elemento-	0.043649	3.23133	M6		Gpbar1,Rbms3,Nav1,Cstl1,Star,Tri
31	transfac_p	0.043224	3.18193	M9	Vsx1,Lbx2,	Krtap14,Sspn,Stmn4,Atp6v1e2,Mc
32	yetfasco-4	0.043224	3.18193	M9	Vsx1,Lbx2,	Krtap14,Sspn,Stmn4,Atp6v1e2,Mc
33	jaspar-PF0	0.043086	3.16585	M9	Vsx1,Alx1,	Krtap14,Sspn,Neurl3,Tmprss3,Msg
34	transfac_p	0.042997	3.15551	M2	Neurod1,N	Cilp,Trim66,Zc3h12d,Rundc1,Guk1
35	jaspar-MA	0.042948	3.14976	M8		Rbms3,Pdzd3,Tnfrsf13c,Sept9,Cilp,
36	encode-UW	0.042839	3.13712	M2		Tmprss3,Sspn,Krtap14,Pdzd3,Slc2
37	hdpi-TRIM	0.04276	3.12793	M3	Trim21	Rbms3,Gpbar1,Tnfrsf13c,BC01846
38	homer-M0	0.04276	3.12793	M5	Rfx3,Rfx1,R	Rundc1,Prr3,Ccna1,Cops3,Trim66,
39	encode-UW	0.042711	3.12219	M2		Rbms3,Stmn4,1700084C01Rik,Xdh
40	yetfasco-5	0.042711	3.12219	M8		Rbms3,Pdzd3,Tnfrsf13c,Sept9,Cilp,
41	encode-UW	0.042602	3.10955	M8		Pdzd3,Slc29a1,1700084C01Rik,BC
42	homer-M0	0.042395	3.08542	M5	Rfx1,Rfx2,R	Ccna1,Prr3,Cops3,Rundc1,Trim66,
43	taipale-AT	0.042089	3.04981	M1	Bach1,Jdp2	Pdlim2,Sept9,Krt86,Abcc3,Tnfrsf8,
44	jaspar-CN0	0.04198	3.03717	M10		Cdyl2,Cilp,Slc9a9,Rundc1,Atp6v1e
45	yetfasco-1	0.04196	3.03487	M5	Rfx2,Rfx3,R	Rundc1,Prr3,Cops3,Nphp4,Trim66,
46	elemento-	0.041862	3.02338	M4		Prr3,Trim66,Tcf20,Tmem51,Krt86,
47	taipale-NG	0.041842	3.02108	M5	Rfx4,Rfx1,R	Prr3,Trim66,Rundc1,Cops3,Ccna1,

s4,Pdlim2,Tnfrsf8,Stmn4,Olfr877,Abcc3,Nt5c1b,Star,Agr2
rl3,Trim66,Slc29a1,Il16,Stmn4,Capn9,Prlh,C1qb,Olfr877,Rbms3,Slc9a9,Sspn,Gpbar1,Lrrn4,Tnfrsf13c,Zc3
p,Xdh,1700084C01Rik,Star,Pxk,Pdzd3,Krtap16-7,Slc9a9,Prlh,Neurl3,Stmn4,Slc29a1,Nlrp3,Tmprss4,Sept
ilp,Trim66,Gpbar1,Slc9a9,Ceacam11,Abcc3,Prlh,Olfr982,Xdh,Tcf20,Tmprss3
Prr3,Srd5a3,Nos1ap,Gtl3,Xdh,Fbxo44,Agr2,Tmprss3,Grin2c,Rgs4,Pla2g12a,Reep3,Ceacam11,Eps15,Tmp
4,Il16,Atp6v1g3,Msgn1,Nlrp3,Pdlim2,Tcf20
139,Eps15,Ccna1,Nt5c1b,Nphp4,1700084C01Rik,Crip2
,Tnfrsf13c,BC024139,Trim66,Sept9,Rya3
4,Krtap14,Il16,BC018465,Nos1ap,Xdh,Abcc3,Agr2,Tmprss4,Tnfrsf8
4,Krtap14,Il16,BC018465,Nos1ap,Xdh,Abcc3,Agr2,Tmprss4,Tnfrsf8
0,Tmprss4,Pdlim2,Pkd1l2,Pla2g12a,Psmb9
310034C09Rik,Nol7,Nt5c1b
d,Krtap14,Il16,BC018465,Xdh,Nos1ap,Abcc3,Tnfrsf8,Tmprss4,Agr2
Eps15,Nt5c1b,Nphp4,BC024139,Crip2,Gtl3,1700084C01Rik
Nphp4,Eps15,Crip2,Gtl3,Nt5c1b
,Sept9,Olfr877,Itga9,Lima1,Slc29a1,Slc9a9,Acr

66,Rundc1,Ccna1,Nt5c1b,Eps15,Gtl3,Crip2
Eps15,Nphp4,Crip2,Gtl3,Nt5c1b
f8,Slc9a9,Krt86,Krtap16-7,Ceacam11
ns3,1700084C01Rik,Xdh,Tomm40
465,Cdyl2,Msgn1,Atp6v1e2,Tmprss4,Xdh,Rya3,Capn9,Sept9,Neurl3,Crip2
Nphp4,Eps15,Crip2,Nt5c1b,Gtl3,Mcrs1
Nphp4,Eps15,Crip2,Nt5c1b
mn4,Agr2,Abcc3,Krtap14,Zc3h12d,Krtap16-7,Tmprss4,Xdh,Neurl3,Gsto2,Gm11545,Cilp,BC018465,Slc29
,Mcrs1,BC018465,Rbms3,Gpbar1,Srm,Trim66
6,Ttc36,Sept9,BC024139,Rya3,Tnfrsf13c
15,Fzd5,Sspn,Nos1ap,Slc9a9,Rbms3,Capn9,Ttc36

2d,Il16,Xdh,Slc29a1,Msgn1,Csrnp1,Calhm1,Nos1ap
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rs1,Krt86,Neurl3,Nav1,Eps15,Ttc36,Cstf3,Msgn1,Rundc1,Tmprss3,Aplp2
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,Msgn1,Stmn4,Slc29a1,Krt86,B3galtl,Il16,Igfbp1,Star,Tnfrsf13c,Calhm1,Pdlim2,Olfr982,Gpbar1,Pabpn1l,
,Gpbar1
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5,Calhm1,Neurl3,Prss8,Stmn4,Sept9,Lrrn4
Nphp4,Eps15,Gtl3,BC024139,Crip2,Nt5c1b,1700084C01Rik,Mcrs1
,Scn10a,Slc29a1,Cilp,Nos1ap,BC018465,Il16,Calhm1,Eps15,Atp6v1g3,Pkd1l2,Sspn,D030028A08Rik,Capn
,Gpbar1
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Eps15,BC024139,Gtl3,Crip2,Stmn4,Nphp4
Zc3h12d,Gsto2,Il16,Krtap14,Agr2
2,Igfbp1,Rbms3,Agr2
,Ccna1,Crip2,Mcrs1,Gtl3,Eps15,BC024139,1700084C01Rik,Krt86,Ttc36,Pdzd3,Xdh,Pxk,Tmprss4,Aurka,Tn
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rss4,Lima1,Neurl3,Zfp619,Cstf3,Nop14,Tnfrsf13c,Nol7,Aplp2,Stmn4,Homer3,Pdzd3,Ttc30b,Itga9,Sept9,B

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,Nol7,Csrnp1,Aplp2,Capn9

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9,Slc9a9,Csrnp1,1110028C15Rik,Cml3,Gsto2

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frsf13c,Cml3,Atp6v1g3,BC018465,Uox,Aplp2,Pkd1l2,Slc29a1,Capn9,Abcc3,Pabpn1l dost,Fzd5,Prr3,Gpbar1,Acr,Cilp,Tcf20,Uox

tnl6,Manbal,Tbrg1

,Star,Olfr982,Rgs4,Pkd1l2,Trim66,Pla2g12a,Gne,Nlrp3,Atp6v1g3,Itga9,Srd5a3,Rasl11a,Nt5c1b,Calhm1,A pn,Eps15,Ttc36,BC018465,Rya3,Slc9a9,Ccna1,Cml3,Acr,Rasl11a,Ceacam11,Prr3,Csrnp1 rl1,Cml3,Tmem51,Manbal,Fam18b,Rbp7,Rya3,Cnga3