

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

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2 **normal strains**

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6 **ABSTRACT**7 **Aims**

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

10 **Materials and Methods**

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

13 **Results and conclusion**

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

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

22



23 **INTRODUCTION**

24 The regeneration phenomena such as scarless skin wound healing [1] and perfect heart
25 *repair [2], and spinal cord regeneration [3] have been observed in mammals in embryonic and
26 neonatal periods. Regenerative abilities in mammals are known to decline along with development
27 but the adult mouse of the MRL/MpJ mouse appears to be a remarkable exception to this common
28 rule. The first report on the MRL/MpJ enhanced capacity for regeneration pertained the closure of
29 the punches in the ear pinnae [4], which are used for permanent animal marking, which is to say the
30 holes remain for life in most laboratory murine strains. The discovery was followed by a number of
31 studies showing enhanced regenerative responses in different organs and tissues [5-16]. It is
32 important to notice that the ear hole closure in the MRL/MpJ mouse is not a typical example of
33 cutaneous full-thickness wound healing but it involves the restoration of tissue architecture, which is
34 associated with vascularisation, the regrowth of peripheral nerves and muscles, the emergence of
35 sebaceous glands and hair follicles, as well as cartilage formation [4, 16]. The ability to close punches
36 in the ear pinnae in the MRL/MpJ mouse was connected with several molecular features commonly
37 observed in classical models of regeneration, i.e. in the amphibians. In particular, the regeneration
38 process in the MRL/MpJ mouse is driven by the formation of blastema-like structure [4] and the
39 fibroblast-like cells in the MRL/MpJ mouse show a higher accumulation in the G₂ phase of the cell
40 cycle [17]. Another important feature is that the wound edges are remodelled by an increased
41 activity of matrix metalloproteinases (MMPs) [18]. What is more, the adult MRL/MpJ mouse seems
42 to retain some characteristics of embryonic metabolism with increased aerobic glycolysis and
43 expression of stem cell transcription markers [19, 20].

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

56 profiling show that the nature of DNA methylation-mediated regulation is far more complex, since
57 the majority of tissue specific DNA methylation occurs outside of the promoter regions [22].

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

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

78

79 MATERIALS AND METHODS

80 *Animals, sample collection and processing*

81 The tissue samples, ears, hearts, livers, spleens, bone marrow, were collected from adult, 2-
82 month-old, females of the MRL/MpJ, C67BL/6J and BLAB/c mice, three of each strain. The tissues of
83 MRL/MpJ and C67BL/6J mice were purchased from the Jackson Laboratories (Bar Harbor, USA), while
84 those of BALB/c mice from the Tri-City Academic Laboratory Animal Centre - Research & Services
85 Centre. The tissues were collected in RNALater reagent (Qiagen cat. no. 76104) and transported on
86 dry ice. Tissues were disrupted with mortar and pestle in liquid nitrogen, and divided into two
87 portions, one used for DNA and another for RNA extraction. DNA isolation was performed with
88 DNeasy Blood and Tissues Kit (Qiagen, cat. no. 69504) with RNase A treatment (Qiagen, cat. no.
89 19101). RNA was extracted with RNeasy Mini Kit (Qiagen, cat. no. 74104) with on-column DNA
90 digestion with RNase Free DNase Set Kit (Qiagen, cat. no. 79254).

91 *MeDIP-chip*

92 Methylated DNA immunoprecipitation (MeDIP) was carried out for pooled samples from
93 three mice for each strain and tissue following microarray analysis using Mouse DNA Methylation
94 3x720K CpG Island Plus RefSeq Promoter Arrays (Roche, NimbleGen). The method is described in
95 details in a previous paper [25]. Raw data was quantile normalized with background correction
96 separately for each channel, following computing biweighted log₂ ratios, determining KS Scores (with
97 750 bp sliding window and 500 bp spacing between nearby probes) and mapping DNA probes to
98 genes and CpG islands with NimbleScan v. 2.6 (Roche, NimbleGen). The genomic coordinates of
99 genes and CpG islands were mapped to mm9 genome (NCBI37/mm9 build). The data files have been
100 deposited in Gene Expression Omnibus Database under accession number GSE89518
101 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89518>). Gene expression profiles from
102 the corresponding tissues were downloaded from Gene Expression Omnibus Database (GSE64624) as
103 they were reported in a previous study focused on transcriptomic analysis of the MRL/MpJ mouse
104 [20].

105 *Identification of the differentially methylated regions*

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

111 located within a primary transcript, and *intergenic* located within a CpG island located over 5000 bp
112 upstream and over 500 bp downstream of any of primary transcripts in the analysis.

113 **Bioinformatics tools**

114 Gene ontology analysis was performed on the differentially methylated genes with ClueGO
115 [28] using right-sided hypergeometric test with Benjamini-Hochberg correction. Transcription factors
116 targeting the promoter regions of genes annotated to DMRs were predicted with iRegulon [29] using
117 a 500 bp interval flanking transcription start sites. Principal component analysis (PCA) was carried out
118 in R environment by performing multidimensional scaling with *cmdscale* function on the matrix of
119 distance *dist* calculated for transposed matrix of KS Scores citation.

120 **MDRE-qPCR**

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

129

130 **RESULTS**131 ***Global DNA methylation profiles and differentially methylated regions***

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

142 Further analysis was concentrated on the characterization of the most significant differences
143 in DNA methylation profiles between the MRL/MpJ and the reference strains. A genomic region was
144 considered as differentially methylated (differentially methylated region - DMR) characteristic for the
145 MRL/MpJ mouse, if it was significantly more/less enriched for the MRL/MpJ mouse than for both the
146 reference strains; thereafter referred as hyper- and hypomethylated, respectively (detailed criteria of
147 DMR are given in Materials and Methods). Different numbers of DMRs were found for each of
148 examined tissues (Table 1), with the highest number in bone marrow and the smallest in the ear. The
149 majority of DMRs in all tissues were between 250-750 bp in length and they were located between
150 5000 bp and 500 bp upstream of transcription start sites, that reflected the promoter structure and
151 the microarray design.

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

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

159 ***Gene ontology analysis***

160 The results of ontology analyses for the genes connected with the DMRs found in five tissues
161 under the study are presented in Figure 2. We decided to focus on the results obtained for the ear
162 auricle because the manifestation of increased regeneration capacity in the MRL/MpJ mouse is the

163 most spectacular in this organ and we were able to find potential associations between the genes
164 differentially methylated genes in the ear pinnae and regeneration. In the ear auricle, we identified
165 81 DMRs, out of which 36 were hypomethylated (lower enrichment) and 45 were hypermethylated
166 (higher enrichment) in the MRL/MpJ comparing to the two control strains. These 81 DMRs were
167 associated with 73 genes and 6 intergenic CpG islands.

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

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

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

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

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

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

192 **DMRs and gene expression**

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



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

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

208 ***Genes related to apoptosis***

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

214 We observed a lower DNA methylation level in the promoter region of *Bcl2/11* (Figure 4).
215 *Bcl2/11* (*Bim*) is a member of Bcl2 family of proteins involved in the regulation of apoptosis. The
216 expression of *Bcl2/11* and that of *Bax* and *Bid*, the other members of the Bcl2 family, was reported to
217 fall between the day 5 and 14 post injury in the blastema-like structure of the MRL/MpJ mouse[34].

218 Another gene from this group was *Ghrhr*, which had a lower level of DNA methylation in the
219 promoter region (Figure 4). *Ghrhr* encodes a receptor of growth hormone releasing hormone (Ghrh).
220 Ghrh stimulates the growth hormone synthesis and release in the pituitary gland, but it also plays an
221 important role in peripheral organs[35]. Both mouse embryonic fibroblasts (MEFs) and wound
222 associated fibroblasts express *Ghrhr*. The Ghrh stimulation induces the expression of α -Smooth
223 Muscle Actin (α SMA) in fibroblasts and promotes cell migration. In addition, Ghrh and its agonist JI-
224 38 accelerate dorsal skin wound closure [36].

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

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



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

237 **Genes related to development**

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

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

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

265 **Genes related to inflammation**

266 The third group of genes that were significantly enriched among those located in the vicinity
267 of DMRs was involved in cellular response to molecules of bacterial origin, which may play a role in

268 the regulation of inflammatory response (Table 3). This group included *Fcgr2b*, encoding an
269 immunoglobulin receptor, *Ticam2*, encoding toll/interleukin-1 receptor domain-containing protein,
270 *Ikbkg*, involved in modification of NF- κ B signalling. Their overrepresentation may suggest the
271 epigenetic background of differences observed in the inflammatory phase of wound healing in the
272 MRL/MpJ mouse. *Ticam2* involved in Toll-like receptor signalling displays increased methylation and
273 decreased expression in the MRL/MpJ mouse. Toll-like receptors interact with endogenous ligands
274 released following inflammation, but also tissue injury, to induce expression of various cytokines,
275 thus playing an important role in tissue regeneration[53].

276 **DMRs and master regulators**

277 We found that the genes located close to DMRs show enriched number of sequence motifs
278 recognized by Smad1 transcription factor, a mediator of Tgf β /Bmp signalling. Smad1 may be
279 activated by Tgfb1 and Tgfb3, known as critical regulators of wound healing [54]. Although Smad1
280 overexpression in keratinocytes decreases their proliferation and migration and increases apoptosis,
281 thus resulting in delayed healing of dorsal skin wounds [55], it is worth to examine the role of Tgf β
282 signalling in the MRL/MpJ mouse during ear closure, since its splenocytes express Tgf β 1 at high levels
283 [56].

284 **DMRs located within QTL intervals**

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

294 **DMRs and differential gene expression**

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

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

306 **CONCLUSIONS**

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

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

319

320 **SUMMARY POINTS**

- 321 • Adult mice of the MRL/MpJ strain are known for enhanced regenerative capacity in different
322 tissues
- 323 • Ear-pinnae hole closure is a particular manifestation of the regenerative abilities in the
324 MRL/MpJ mouse
- 325 • The study interrogates the epigenetic basis of the regeneration potential in the MRL/MpJ
326 mouse.
- 327 • Methylome profiling was performed in ear pinnae, bone marrow, spleen, liver and heart of
328 the MRL/MpJ mouse and two reference strains C567BL/6 and BALB/c using MeDIP and
329 microarray analysis
- 330 • A number of DMRs distinguishing the MRL/MpJ mouse from the references were identified
331 in ear pinnae and other examined tissues
- 332 • The genes located in the vicinity of DMRs are related to development, inflammation, and
333 apoptosis.
- 334 • The promoter regions of genes located in the vicinity of DMRs in the ear pinnae are enriched
335 in Smad1 transcription factor binding sites.
- 336 • Many genes located in the vicinity of DMRs in the ear pinnae are located within QTL intervals
337 of ear hole closure loci.
- 338 • The results indicate potential epigenetic determinants of the regenerative phenomenon of
339 the MRL/MpJ mouse.
- 340



341 Competing financial interests

342 The authors declare no conflict of interests.

343 Ethical Statement

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

347 Authors' Contributions

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

352

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535

536 **Table 1** Size and position distributions of DMRs.

		Ear	Bone Marrow	Liver	Heart	Spleen	Common
DNA methylation level	Hypomethylated	36	72	46	75	114	2
	Hypermethylated	45	209	122	116	57	8
Genes	Hypomethylated	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

537

538



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

540 **A. Genomic coordinates and methylation levels in the DMRs**

Gene	Chr	Start	End	Bone marrow			Liver			Ear			Heart			Spleen		
				B6	Bc	M	B6	Bc	M	B6	Bc	M	B6	Bc	M	B6	Bc	M
<i>Rbp7</i>	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(<i>Trim43a</i>)	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(<i>Trim43c</i>)	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(<i>Trim43b</i>)	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</i>)	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
<i>Cpsf6</i>	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
<i>Cops3</i>	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
<i>Msgn1</i>	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
<i>Akr1e1</i>	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(<i>Pdcd2</i>)	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									

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

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

544 **B. Expression and functions of differentially methylated genes**

Gene symbol	Full name	Function	Gene expression fold difference (microarray data)									
			Bone marrow		Liver		Ear		Heart		Spleen	
			M/Bc	M/B6	M/Bc	M/B6	M/Bc	M/B6	M/Bc	M/B6	M/Bc	M/B6
<i>Akr1e1</i>	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
<i>Cops3</i>	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
<i>Cpsf6</i>	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
<i>Msgn1</i>	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
<i>Rbp7</i>	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			

545

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

547

548

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

Functional cluster	-log(BH)	Genes	Hypomethylated	Hypermethylated
positive regulation of neuron apoptotic process	1.92	20	<i>Bcl2l11, Fcgr2b, Gas2l2, Ghrhr, Hsd17b1, Kcnab2, Kifc3, Mid1, Nos1ap, Osbpl7, Tnf</i>	<i>Akr1e1, Ankrd1, Cnga3, Cops3, Cyp2d22, Npc111, Pcsk9, Ticam2, Vapb</i>
microtubule binding	1.91	10	<i>Bcl2l11, Gas2l2, Inf2, Kifc3, Tnf</i>	<i>Ankrd1, Npc111, Pxx, Tnnt2, Vapb</i>
anterior/posterior pattern specification	1.82	8	<i>Bcl2l11, En1, Mcrs1, Msgn1, Ring1</i>	<i>Cnga3, Ski, Yeats4</i>
hexosaminidase activity	1.87	3	<i>Naga</i>	<i>4931440L10Rik, Maneal</i>
leukocyte homeostasis	1.93	3	<i>Bcl2l11, Fcgr2b</i>	<i>Ikbkg</i>
cellular response to molecule of bacterial origin	1.81	8	<i>Fcgr2b, Osbpl7, Tnf</i>	<i>Akr1e1, Ankrd1, Ikbkg, Pcsk9, Ticam2</i>
negative regulation of protein complex disassembly	1.99	6	<i>Gas2l2, Mid1, Osbpl7, Tnf</i>	<i>Akr1e1, Pcsk9</i>
oxidoreductase activity	1.74	3	<i>Hsd17b1, Kcnab2</i>	<i>Akr1e1</i>
regulation of neuron death	1.70	7	<i>Bcl2l11, Kcnab2, Nos1ap, Tnf</i>	<i>Cnga3, Htra4, Pcsk9</i>
response to insulin	1.59	3	<i>Ghrhr, Prlh</i>	<i>Pcsk9</i>

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

553

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

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

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

558

559 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				
<i>Prlh</i>	1	45.81	1.9	2.9	0.6			Sth1	
<i>En1</i>	1	52.74	1.8	2.1	0.7			Sth1	
<i>Ren2</i>	1	57.91	2.1	2.5	0.8			Sth1	
<i>Optc</i>	1	58.02	3.6	3.7	1.6			Sth1	
<i>4931440L10Rik</i>	1	58.24	1.3	1.0	2.6			Sth1	
<i>Tnnt2</i>	1	59.32	1.0	0.9	2.9			Sth1	
<i>Uox</i>	3	72.09	2.0	2.0	0.8			Sth2	
<i>Uox</i>	3	72.09	0.3	0.2	2.0			Sth2	
<i>Pcsk9</i>	4	49.67	0.9	1.1	2.4			Sth4	
<i>Bsnd</i>	4	49.67	2.5	1.9	0.7			Sth4	
<i>Maneal</i>	4	57.92	0.7	0.6	2.6			Sth4	
<i>Gjb4</i>	4	61.51	1.9	1.5	5.1	Heal8		Sth4	
<i>Rbp7</i>	4	79.40	2.5	1.9	0.5	Heal8			Heal8
<i>Kcnab2</i>	4	83.08	2.3	2.4	1.1	Heal8			Heal8
<i>Ski</i>	4	86.17	0.1	0.4	1.6	Heal8			Heal8
<i>Ghrhr</i>	6	27.38	2.0	1.9	0.8			Sth5	
<i>Tmem40</i>	6	53.68	2.5	2.3	1.0			Sth5	
<i>H1foo</i>	6	53.72	1.9	1.9	0.7			Sth5	
<i>Slc28a1</i>	7	45.71	1.5	1.8	0.5			Sth6	Heal6
<i>Lonrf1</i>	8	23.05	0.6	0.7	1.8		Heal1		
<i>D030016E14Rik</i>	8	26.86	0.6	0.0	2.1		Heal1		
<i>Tm6sf2</i>	8	34.15	1.3	1.4	0.2		Heal1		
<i>Kifc3</i>	8	47.12	2.3	2.8	1.1	Heal1	Heal1		
<i>Gm8884</i>	9	26.42	3.5	2.6	1.0			Sth8	
<i>Eif1b</i>	9	71.67	0.7	0.6	2.0	Sth9b			
<i>Gas2l2</i>	11	50.33	2.9	3.2	1.3	Heal10			
<i>Gas2l2</i>	11	50.33	1.9	1.8	0.6	Heal10			
<i>Osbpl7</i>	11	60.75	1.9	2.1	0.7	Heal10			Heal10
<i>Hsd17b1</i>	11	64.17	1.8	1.7	0.6	Heal10			
<i>Inf2</i>	12	61.20	0.7	0.7	1.9		Heal5		Heal5
<i>Btbd6</i>	12	61.50	2.5	2.1	0.9		Heal5		Heal5
<i>Akr1e1</i>	13	2.57	0.0	0.0	3.1		Heal2		
<i>Gm7120</i>	13	67.25	1.7	1.3	3.7		Heal3		
<i>Naga</i>	15	38.56	2.7	2.0	1.0		Heal4		Heal4
<i>Cyp2d22</i>	15	38.57	0.4	0.9	2.3		Heal4		Heal4
<i>Ticam2</i>	18	24.65	0.6	0.4	3.7	Heal9			

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

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

Tissue	Gene	MeDIP			mRNA			DMR localisation
		B6	Bc	M	B6	Bc	M	
Bone marrow	<i>2610109H07Rik</i>	0.9	0.7	2.1	260	854	128	distal
	<i>Akr1e1</i>	0.0	0.0	3.5	533	432	91	proximal
	<i>Cd72</i>	1.0	1.8	3.8	7919	9353	3919	distal
	<i>Fcamr</i>	0.7	1.2	2.4	140	160	20	proximal
	<i>Gm16515</i>	0.6	0.7	2.0	2550	2077	6913	distal
	<i>Gpr132</i>	1.1	1.1	3.2	461	353	119	distal
	<i>H2-Aa</i>	1.7	1.9	0.4	103	98	38	distal
	<i>Nlrp3</i>	2.2	2.0	0.7	1162	1630	569	proximal
	<i>Ntm</i>	0.3	0.9	2.0	95	119	580	proximal
	<i>Phlda3</i>	1.8	1.8	0.4	89	145	341	Distal
	<i>Plscr4</i>	0.5	0.2	2.2	84	102	38	Distal
	<i>Spata16</i>	3.1	3.4	0.3	21	28	74	Distal
	<i>Ticam2</i>	0.6	0.4	2.1	1033	1323	174	Proximal
<i>Tnni1</i>	1.3	1.3	2.7	532	276	1387	Distal	
Liver	<i>2510049I12Rik</i>	0.7	0.1	2.0	135	172	40	Distal
	<i>Akr1e1</i>	0.0	0.0	2.4	4470	3786	673	Proximal
	<i>Gpr56</i>	0.2	0.9	2.2	1050	1028	3605	Proximal
	<i>Slc1a2</i>	0.6	0.5	1.6	6574	4546	1438	Distal
	<i>Ttc39a</i>	2.4	2.2	0.8	219	335	3205	Distal
Ears	<i>Akr1e1</i>	0.0	0.0	3.1	918	691	129	Proximal
	<i>Bpifb5 (bc018465)</i>	2.4	2.5	1.0	27	24	86	Distal
	<i>Fcgr2b</i>	1.7	2.2	0.4	146	99	43	Proximal
	<i>Krtap14</i>	1.2	1.2	3.1	56	6	5171	intragenic
	<i>Optc</i>	3.6	3.7	1.6	161	159	57	intragenic
	<i>Rbp7</i>	2.5	1.9	0.5	166	267	805	distal
	<i>Ticam2</i>	0.6	0.4	3.7	120	136	49	proximal
<i>Zfp428</i>	1.0	0.8	3.1	42	47	95	distal	
Heart	<i>3110035E14Rik</i>	3.2	2.4	0.5	21	57	133	proximal
	<i>Acaa1b</i>	1.2	1.2	2.5	146	242	602	proximal
	<i>Agr2</i>	2.4	1.9	0.8	26	25	68	proximal
	<i>Akr1e1</i>	0.0	0.0	2.4	1951	1216	501	proximal
	<i>Alox5</i>	1.0	1.0	2.3	2453	1422	432	proximal
	<i>Capg</i>	0.7	1.0	2.0	2030	4190	536	proximal
	<i>Fcgr2b</i>	3.3	2.4	0.6	48	115	16	proximal
	<i>Lnx1</i>	1.9	1.6	0.5	1916	2027	876	distal
	<i>Metap11</i>	0.7	0.8	1.9	2528	2283	710	distal
	<i>Rbp7</i>	2.4	2.0	0.3	2367	1144	6062	distal
	<i>Tmem179</i>	1.2	1.5	3.1	2035	1711	538	proximal
Spleen	<i>Akr1e1</i>	0.0	0.0	2.7	538	536	72	proximal
	<i>Capg</i>	2.3	2.6	1.2	12070	13476	4015	distal
	<i>Cldn13</i>	3.2	3.4	1.4	4588	4633	1126	proximal
	<i>Cnga3</i>	0.7	1.0	2.3	41	46	13	distal
	<i>D030028A08Rik</i>	1.8	1.8	0.6	470	549	151	distal
	<i>Maneal</i>	0.8	0.8	2.6	69	72	28	distal
	<i>Nbl1</i>	2.6	3.1	1.5	387	415	840	proximal
	<i>Nmral1</i>	0.6	0.0	1.7	76	86	34	proximal
	<i>Nos1ap</i>	1.0	1.2	3.3	568	526	1235	distal
<i>Serpina3n</i>	0.2	0.2	1.5	3329	3102	6661	distal	

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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.

568 **Figure Legends**569 **Figure 1 Principal Component Analysis of DNA methylation profiles.**570 **Figure 2 Ontology analyses for genes associated with DMRs in the tissues of the MRL/MpJ mouse.**571 The results are presented as $-\log(\text{BH})$; Benjamini-Hochberg corrected p-value. The significance of
572 $p=0.05$ corresponds to $-\log(\text{BH}) = 1.3$.573 **Figure 3 Ontology network for the genes associated with DMRs in the ear pinnae of the MRL/MpJ**
574 **mouse.**575 Ontological terms associated with the genes located close to the DMRs in the ears are presented by
576 nodes. Gene set enrichment was performed with ClueGO.577 **Figure 4 Verification of the DMRs by MDRE-qPCR in the ear pinnae.**578 The methylation level is shown as 1-McrBC/TaqI ratio. The verified genes belong to *anterior/posterior*
579 *pattern formation* (*Ski*, *Bcl2l11*), positive regulation of neuron apoptotic process (*Bcl2l11*, *Cyp2d22*,
580 *Ghrhr*, *Ticam2*), or showed big differences in MeDIP score (*Krtap14*, *Gjb4*, *Gm8884*). Statistical
581 significance was calculated with one-way ANOVA with *post hoc* Tukey's multiple comparison test;
582 *p-value<0.05; **p-value<0.01; ***p-value<0.001.

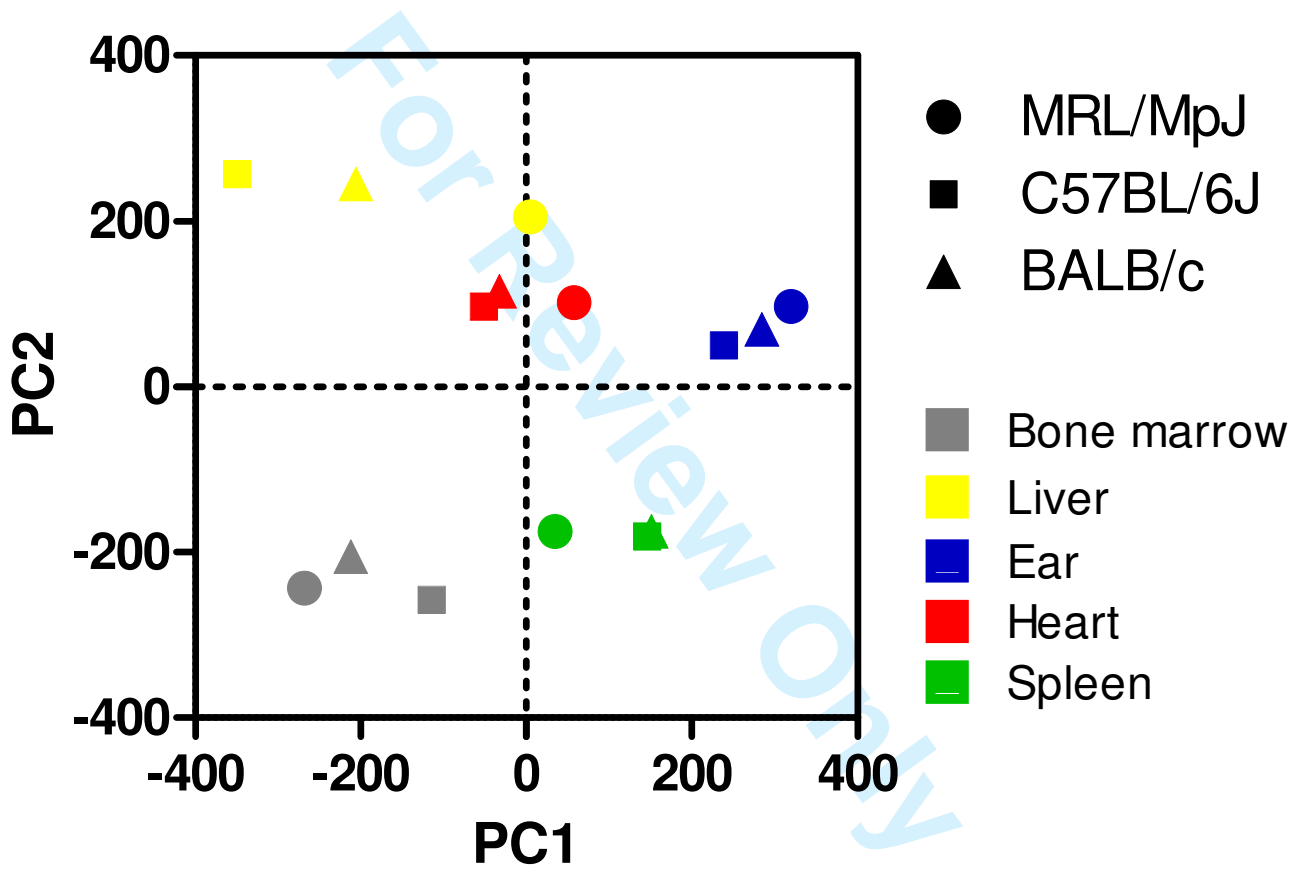


Figure 1

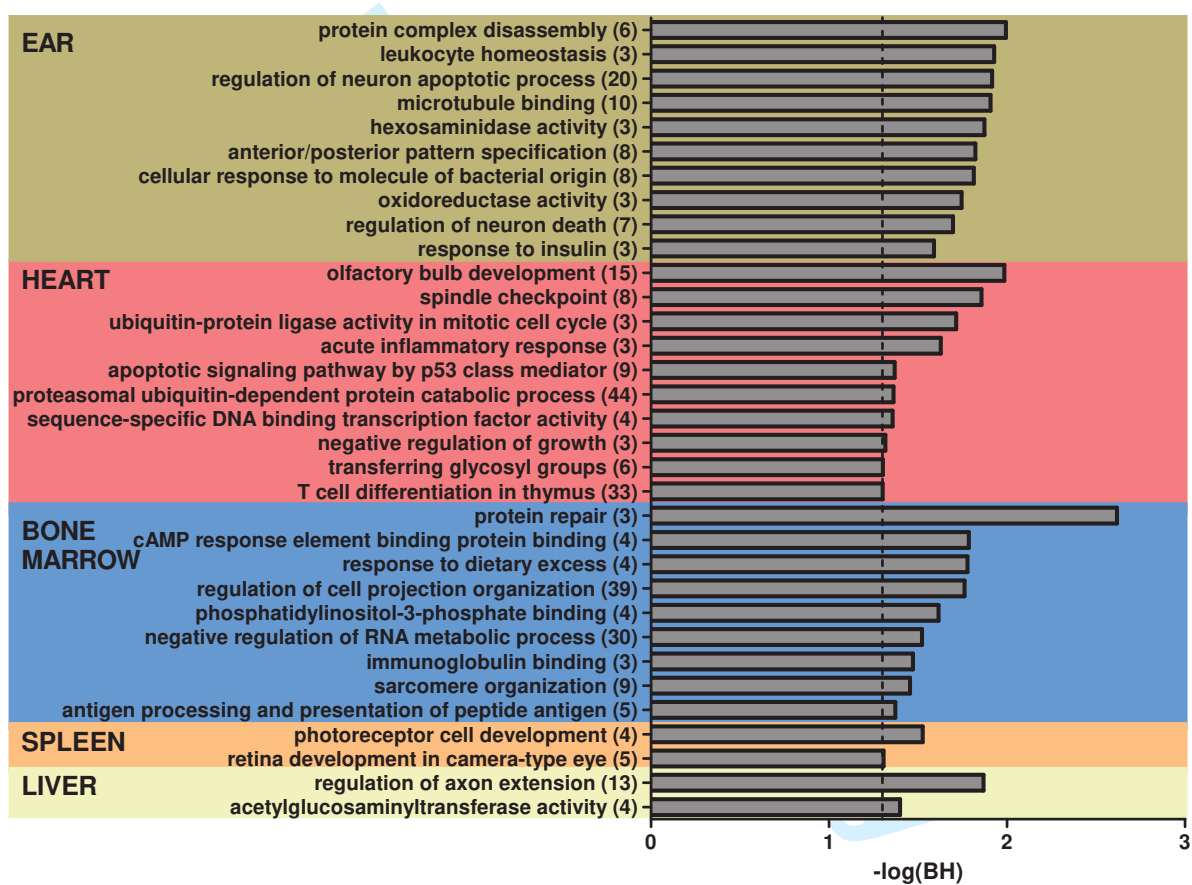


Figure 2



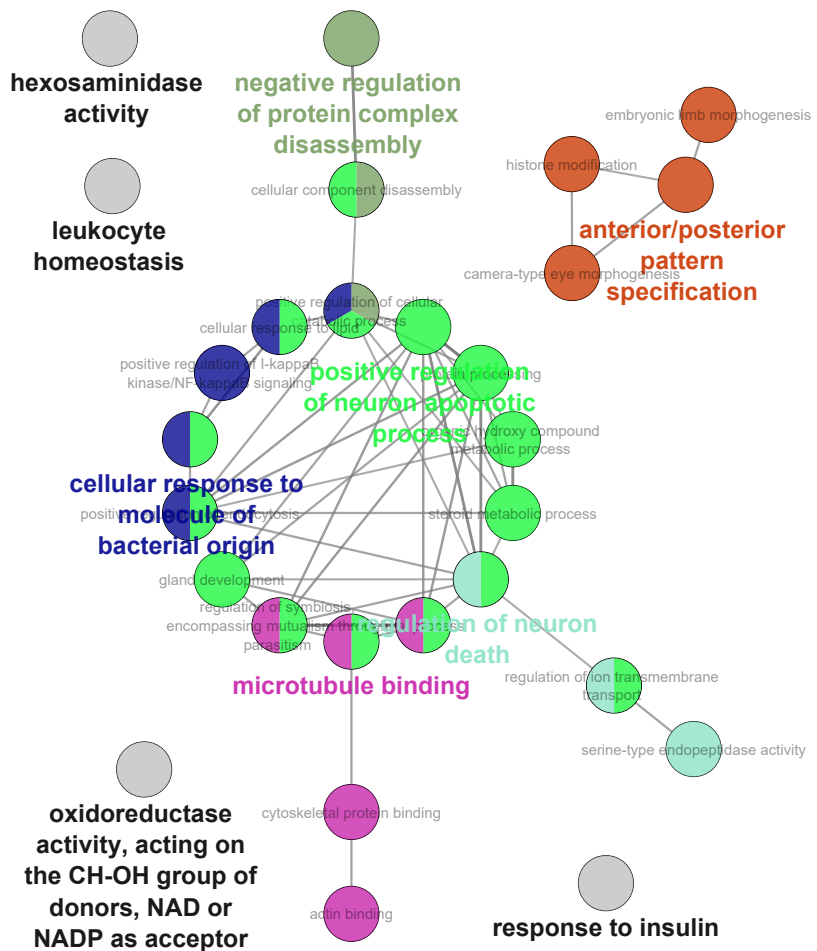


Figure 3

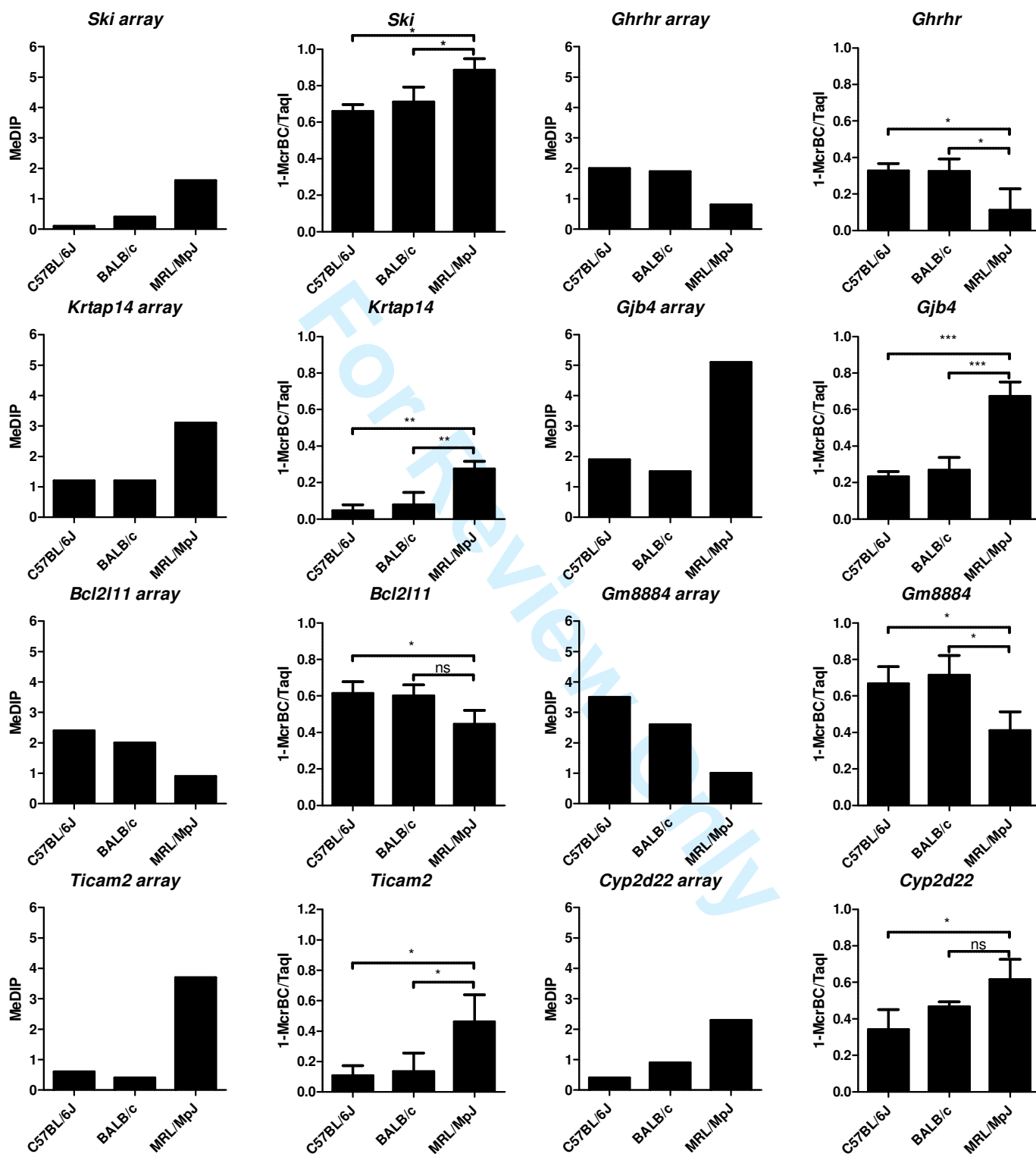


Figure 4

TableS1. Primer sequences used for validation of DMRs.

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

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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 Islands
NA	chr17:1567	chr17	15673304	15673974	0.1	0.2	2.1	CpG Islands
NA	chr9:88494	chr9	88494209	88494858	0.1	0.0	1.4	CpG Islands
NA	chr9:88753	chr9	88753512	88754171	0.1	0.0	1.3	CpG Islands
NA	chr9:88961	chr9	88961199	88961948	0.5	0.0	1.7	CpG Islands
NA	chr9:96437	chr9	96437157	96437816	0.2	0.5	3.9	CpG Islands
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 descriptor DISTRIBU' gene_id

-	RIKEN cDN, PROXIMAL	71001
-	aldo-keto r PROXIMAL	56043
-	ankyrin rep DISTAL	107765
+	ADP-ribose DISTAL	104303
-	arylsulfatas DISTAL	77041
+	cDNA sequ DISTAL	228802
+	BCL2-like 1 DISTAL	12125
-	Bartter syn DISTAL	140475
+	BTB (POZ) c DISTAL	399566
+	cyclic nucle DISTAL	12790
-	COP9 (cons DISTAL	26572
-	cleavage ar PROXIMAL	432508
-	cytochrom DISTAL	56448
-	cytochrom 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 arr PROXIMAL	237891
-	growth arr 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 far DISTAL	16582
-	keratin ass 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

+	progesterone	DISTAL	52023
+	peptidylpro	DISTAL	67418
+	prolactin re	PROXIMAL	623503
+	PX domain	DISTAL	218699
-	retinol bind	DISTAL	63954
+	renin 2 tan	PROXIMAL	19702
-	regulator of	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 sarcoma	DISTAL	20481
+	solute carri	DISTAL	434203
-	transformin	DISTAL	21376
-	toll-like rec	PROXIMAL	225471
+	transmembr	PROXIMAL	107770
-	transmembr	DISTAL	94346
-	tumor necr	PROXIMAL	21926
+	troponin T2	DISTAL	21956
-	tumor prot	DISTAL	21985
+	transferrin	PROXIMAL	50765
+	urate oxida	DISTAL	22262
+	urate oxida	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

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orientation	description	DISTRIBUTION	gene_id	transcript_id	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

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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

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Gene ontology analysis for ear.

GOTerm	Nr. Genes	Term PVal	Associated Genes in cl	Nr. Genes	-log(P-value)
negative re	3	0.010148	[Gas2l2, Mi Akr1e1 Ga	6	1.993614
leukocyte f	3	0.011834	[Bcl2l11, Fc Bcl2l11 Fc	3	1.926853
positive reg	3	0.012147	[Bcl2l11, Pc Akr1e1 An	20	1.915519
microtubul	4	0.012383	[Bcl2l11, G; Ankrd1 Bcl	10	1.90717
hexosamin	3	0.013399	[4931440L: 4931440L1	3	1.872913
anterior/pc	4	0.015072	[En1, Msgn Bcl2l11 Cn	8	1.821818
cellular res	4	0.015362	[Ankrd1, Fc 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 to	3	0.025752	[Ghrhr, Pcs Ghrhr Pcsk	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	Smad2	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_pi	0.090821	4.82278	M1	Smad1	Kifc3,Tpd52,Optc,Tnnt2,Gas2l2,Gjl
2	transfac_pi	0.090365	4.79098	M2	Tal1	Optc,Tnnt2,Mid1,Krtap14,Cyp4f14
3	homer-MO	0.085689	4.46435	M2	Neurod1,T	Optc,Tnnt2,Krtap14,4931440L10Ri
4	homer-MO	0.081923	4.2013	M3	Foxa3,Foxa	Tpd52,Zfp428,Gjb4,Uox,Mid1,Bcl2
5	tfdimers-M	0.081737	4.1883	M2	Meis1,Nr1f	Ankrd1,Cyp4f14,BC018465,Bsnd,4
6	hdpi-SMAP	0.08064	4.1117	M4	Smad2	Cyp4f14,Gas2l2,Gjb4,BC018465,Hs
7	transfac_pi	0.078467	3.95994	M2	Myf6,Tcf3,	Tnnt2,Ankrd1,Optc,Cyp4f14,BC018
8	taipale-AA	0.078095	3.93392	M5	Msc	Tnnt2,Ankrd1,BC018465,Gpr50,Cy
9	homer-MO	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_pi	0.075301	3.73881	M2	Tcf3,Myc,N	Nos1ap,Ankrd1,Hsd17b1,Gjb4,Mic
15	transfac_pi	0.074266	3.66654	M2	Tal1,Tcf4,T	Optc,Krtap14,4931440L10Rik,Tnnt
16	transfac_pi	0.073977	3.64631	M7	Tbx5	Msgn1,Mid1,Gpr50,Cyp4f14,Bsnd,
17	tfdimers-M	0.073749	3.63041	M6	Pou3f2,Pdx	Kifc3,Krtap14,Mid1,Tpd52,En1,Cng
18	jaspar-MAC	0.072921	3.5726	M2	Tcf3,Tal1,T	Optc,Tnnt2,BC018465,Tpd52,Cyp4

19	transfac_pi	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,Tn
21	yetfasco-6f	0.071721	3.48877	M9	Gjb4,Tpd52,BC018465,Cyp4f14,Nc
22	encode-UV	0.071576	3.47866	M1	Optc,Tnnt2,Cops3,Pibf1,Zc3h12d,C
23	tfdimers-M	0.071556	3.47721	M2	Yy1,Tcf3,Zf Krtap14,Tpd52,Cyp4f14,Optc,Gas2
24	transfac_pi	0.071411	3.46709	M3	Pou2f1,Pou Zfp428,Kcnab2,Ankrd1,Optc,Mid1,
25	transfac_pi	0.071245	3.45553	M3	Pou2f1,Pou Zfp428,Msgn1,Kcnab2,Ankrd1,Bsn
26	transfac_pi	0.071204	3.45264	M2	Tcf3,Myf6, Gpr50,Gjb4,Tpd52,BC018465,Cyp4
27	tfdimers-M	0.071183	3.4512	M2	Yy1,Mafa,N Tnnt2,Optc,Krtap14,Gjb4,Cyp4f14,
28	taipale-RTA	0.071121	3.44686	M3	Foxp3,Foxj: Bcl2l11,Gas2l2,En1,Mid1,Uox,VapI
29	yetfasco-1f	0.0711	3.44541	M10	Jazf1,Foxn4 Pibf1,Tnf,En1,Krtap14,Prlh,Fcgr2b,
30	jaspar-MAC	0.071059	3.44252	M3	Foxa2,Foxa Gjb4,Uox,Ankrd1,Mid1,Ghrhr,Tpd5
31	swissregulc	0.071059	3.44252	M3	Foxa2,Foxa Gjb4,Uox,Ankrd1,Mid1,Ghrhr,Tpd5
32	transfac_pi	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_pi	0.070562	3.40784	M11	Tmem40,Kifc3,Gjb4,Krtap14,lkbgk
35	tfdimers-M	0.070397	3.39627	M12	Neurod1,El En1,Mid1,4931440L10Rik,Gjb4,Op
36	transfac_pi	0.070376	3.39483	M1	Osbp17,Ghrhr,Npc1l1,Tpd52,Rgs4,l
37	tfdimers-M	0.069507	3.33413	M2	Nr3c1,Pgr, Tnnt2,Ankrd1,Optc,Tmem40
38	taipale-AAc	0.069362	3.32401	M5	Myf6,Msc Ankrd1,BC018465,Gpr50,Npc1l1,T
39	transfac_pi	0.069073	3.30378	M2	Tcf3,Myod: Tnnt2,Optc,Gjb4,Tpd52,Ankrd1,Cy
40	yetfasco-2l	0.068907	3.29221	M1	Gata2,Gata Cyp4f14,BC018465,Fcgr2b,Gas2l2,
41	homer-MO	0.068866	3.28932	M2	Olig2,Tal1, Optc,Tnnt2,Krtap14,Zc3h12d,Uox,l
42	tfdimers-M	0.068804	3.28499	M6	Yy1,Pax7,V Mid1,Npc1l1,Krtap14,Kifc3,Tpd52,
43	transfac_pi	0.068659	3.27487	M6	Hnf1b,Hmt Mid1,Npc1l1,En1,Gas2l2,Msgn1,Ai
44	encode-UV	0.067976	3.22717	M4	Pibf1,Cyp4f14,Ghrhr,Gm7120,Tme
45	elemento-1	0.067955	3.22573	M13	Pibf1,Slc28a1,Trfr2,H1foo,BC01846
46	transfac_pi	0.067624	3.2026	M14	Nkx2-5 Msgn1,Cops3,Fam18b,BC018465,C
47	transfac_pi	0.067583	3.19971	M2	Tcf3,Tal1,T Optc,Tnnt2,Krtap14,Ankrd1,Tpd52
48	homer-MO	0.067479	3.19249	M15	Six2 Ankrd1,Gjb4,Tpd52,Vapb,Bsnd,Kifc
49	transfac_pi	0.06721	3.1737	M1	Tfcp2,Tfcp2 Gas2l2,Slc28a1,Mid1,BC018465,Cy
50	transfac_pi	0.067107	3.16647	M15	Msgn1,Tpd52,Nos1ap,Mid1,En1,Zf
51	transfac_pi	0.066983	3.1578	M1	Gata5,Gata Gpr50,Bsnd,4931440L10Rik,Gjb4,l
52	yetfasco-8f	0.066983	3.1578	M1	Gata5,Gata Gpr50,Bsnd,4931440L10Rik,Gjb4,l
53	transfac_pi	0.066858	3.14913	M2	Myf6,Tcf3,l Ankrd1,Tnnt2,Gpr50,Gjb4,Npc1l1,l
54	transfac_pi	0.066589	3.13034	M11	Nfia,Nf1,Yy BC018465,Optc,Cyp4f14
55	jaspar-MAC	0.06663	3.11011	M1	Gata5,Gata Gpr50,4931440L10Rik,Bsnd,Gjb4,l
56	taipale-NT/	0.066176	3.10143	M15	Dmbx1,Gsc Tpd52,En1,Zfp428,Cnga3,Ankrd1,k
57	homer-MO	0.066072	3.09421	M10	Jazf1,Foxn4 En1,Htra4,Tnf,Prlh,Optc,BC018465
58	tfdimers-M	0.065865	3.07975	M9	Tfap2a,Nel 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-MO	0.065638	3.06386	M6	Pax4,Shox2 Mcrs1,Npc1l1,Krtap14,Mid1,Msgn
62	swissregulc	0.065534	3.05663	M1	Smad2,Sm: Gas2l2,Bsnd,Pibf1,Prlh,Gjb4,Rya3,
63	transfac_pi	0.065513	3.05518	M6	Lhx5,Alx1, Krtap14,Msgn1,En1,Mid1,Npc1l1,l
64	hdpi-PKNO	0.06541	3.04796	M5	Pknox2 Prlh,Ankrd1,En1,Gpr50,Gas2l2,Slc2
65	transfac_pi	0.065286	3.03929	M2	Myod1,Tcf: Tnnt2,Gjb4,Tpd52,Bsnd,Ankrd1,Cy
66	transfac_pi	0.065265	3.03784	M9	Tnnt2,Gjb4,Bsnd,Optc,Mid1,Cnga3
67	taipale-AG	0.065244	3.0364	M7	Tbx4,Eome Bsnd,Prlh,Nos1ap,Gjb4,Cyp4f14,Tf
68	transfac_pi	0.065244	3.0364	M6	Lhx5,Otp,A Krtap14,Mid1,En1,Npc1l1,Mcrcs1,l

69	jaspar-CNO	0.065141	3.02917	M12		Mid1,4931440L10Rik,Optc,Uox,Tn
70	jaspar-CNO	0.064934	3.01472	M16	Gbx2	Msgn1,Ankrd1,Kifc3,Uox,Slc28a1,F
71	transfac_pr	0.064934	3.01472	M6	Lhx5,Otp,LlEn1,Krtap14,Mid1,Msgn1,Npc111,f	

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34,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,Osbp17,Tnnt2,Optc,Mid1,Tmem40,Kifc3,Cnga3,Krtap14,Ghrhr,Gas2l2,Tbrg1,Tpd52
 ;d17b1,Slc28a1,Tnnt2,Pibf1,Bsnd,Optc,Tmem40,Mid1
 3465,Gpr50,Fcgr2b,Tpd52,Zc3h12d,4931440L10Rik,Bsnd
 p4f14,Gjb4,Tpd52
 14,Tpd52,Zc3h12d,4931440L10Rik,Mid1,BC018465,Msgn1,Gas2l2,Fcgr2b,Zfp428,Tnf,Gjb4,Kifc3
 /apb,Cnga3
 nnt2,Hsd17b1,Tmem40,Optc,Pibf1,Bsnd,Slc28a1,Kifc3,Msgn1,Mid1
 465,Npc1l1
 jb4,Tmem40,Pxk,Tpd52,Hsd17b1,Optc,Mid1,Slc28a1,Kifc3,Msgn1
 l1,Tnnt2,Tpd52
 2,Tpd52,Ankrd1,Zc3h12d,BC018465,Uox,Cyp4f14,Gpr50
 Prlh,Rya3
 za3,Vapb
 f14,Uox,Krtap14,Ankrd1,4931440L10Rik

l11,Ikbkg,En1,Ghrhr
 int2,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
 lf14,Tnnt2
 .Mid1,Gas2l2,Gpr50,Zfp428,Tnf,Tpd52,Nos1ap,BC018465,4931440L10Rik,Kifc3
 o,Ankrd1,Gjb4
 Bcl2l11,Hsd17b1,Cpsf6,BC018465,Cyp4f14,Cnga3,Tnnt2,Tpd52,Gjb4,Htra4,Npc1l1,Optc,Gpr50,Ring1,No
 52,Bcl2l11
 52,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,Osbl7
 :m40,Fcgr2b,Tnf,Npc1l1,En1,Kifc3,Gjb4,Bsnd,Pxk,Tpd52,Nos1ap,Msgn1,Slc28a1,Eif1b,Prlh,Rbp7,Trfr2,BC
 55,Gas2l2,Fcgr2b
 Cpsf6
 ,BC018465,Kifc3,Cyp4f14,Gas2l2,Bsnd,Tnf,Uox,Tmem40
 c3
 p4f14,Hsd17b1
 p428,Hsd17b1
 vmsgn1
 vmsgn1
 Cyp4f14,Bsnd,Tnf,Optc,4931440L10Rik,BC018465,Nos1ap,Tpd52,Kifc3

 vmsgn1
 kifc3,Mid1
 ;
 c,Inf2,Kifc3,Tpd52,Bsnd,Gas2l2
 Rbp7,En1
 rga3
 1,En1
 Tnnt2,BC018465,Kifc3
 vcrs1
 28a1,Tnnt2,Ghrhr,Bsnd,Osbl7,Krtap14,Mid1,Fam18b,Msgn1,Gm5148,Optc,4931440L10Rik,Kifc3,D0300
 p4f14,Gpr50,Optc,BC018465,Bcl2l11
 l,Cyp4f14,Nos1ap,Npc1l1,Prlh,En1,Pxk,BC018465,Hsd17b1,Bcl2l11,Slc28a1,Gas2l2
 d52,Msgn1,Ankrd1,Gpr50,BC018465
 vmsgn1

nt2,Tnf,Rbp7

igs4,Optc

Vlcrs1,Kifc3,Pibf1,Vapb,Uox,Hsd17b1,Tpd52,Osbp17,Zfp428,Cops3,Cnga3

For Review Only

For Review Only

!,Pxx,Arl1,Rya3,Nos1ap,Ikbkg

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

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

am105b,Tnnt2

7,Cpsf6,Pcsk9,Mcrs1
'018465,Gas2l2

l16E14Rik,Inf2,Tmem40,Tpd52,Tnf,Hsd17b1,Zc3h12d,Rya3,Pxk,Uox,BC018465

For Review Only

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	Psm1	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	lpo9	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 Island:
NA	chr1:17218	chr1	1.72E+08	1.72E+08	2.1	2.0	0.3	CpG Island:
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	chr1:17300	chr1	1.73E+08	1.73E+08	0.4	0.7	2.4	CpG Island:
NA	chr1:17300	chr1	1.73E+08	1.73E+08	0.0	0.0	1.2	CpG Island:
NA	chr1:17300	chr1	1.73E+08	1.73E+08	0.3	0.5	2.0	CpG Island:
NA	chr1:17300	chr1	1.73E+08	1.73E+08	0.1	0.3	1.7	CpG Island:
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	Msr3	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 Island:

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 Asp	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	Znr1	chr17	37094580	37094946	0.1	0.4	1.9	transcriptic
NM_14647	Olf90	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 Gylt1b	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 Island:
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 5730508B0	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 2610109HC	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_015348 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 Island:
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 Island:
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_026888	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	Olf877	chr9	37661972	37662731	3.0	1.8	0.2	transcriptic
NM_14685	Olf982	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

orientatiior descriptor DISTRIBU' gene_id

-	minichrom	DISTAL	17215
-	PHD finger	DISTAL	213109
-	regulatory	PROXIMAL	619289
-	amyotroph	PROXIMAL	73463
-	RIKEN cDN,	DISTAL	68691
+	transmemł	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 tyrı	DISTAL	320139
-	importin 9	INTRAGENI	226432
+	pleckstrin ł	DISTAL	27280
+	troponin I,	DISTAL	21952
+	troponin Tı	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 recoł	DISTAL	27058
+	peptidylprc	DISTAL	67418
+	Rho-relateı	DISTAL	69288
+	cDNA sequ	DISTAL	103220
+	ADP-ribosy	DISTAL	104303
+	nuclear rec	DISTAL	22025
-	cleavage ar	PROXIMAL	432508
-	methionineı	DISTAL	320183
-	HORMA do	INTRAGENI	75828
+	insulin-like	DISTAL	16006
+	slit homolo	DISTAL	20564
-	solute carri	INTRAGENI	215332
+	SH3 bindinı	PROXIMAL	79566
+	wingless-ty	PROXIMAL	216795
-	zinc finger	DISTAL	237775
+	NLR family,	PROXIMAL	216799
-	COP9 (cons	DISTAL	26572
+	alkB, alkyla	DISTAL	268420
-	transmemł	DISTAL	216821
-	predicted g	DISTAL	24083
.	0	INTERGENI	0

+	family with	DISTAL	67510
+	kinesin fam	INTRAGENI	16562
+	slingshot h	PROXIMAL	237860
+	transmemt	INTRAGENI	103743
+	collagen, t _γ	INTRAGENI	12842
+	protein phc	DISTAL	217124
-	leucine ric	DISTAL	69297
+	cyclin-depe	DISTAL	69131
-	keratin 19	PROXIMAL	16669
+	tetratricop	DISTAL	74407
-	calcium act	PROXIMAL	76025
+	leucine ric	DISTAL	217366
-	mesogenin	DISTAL	56184
+	family with	PROXIMAL	76820
.	0	INTERGENI	0
+	anterior gr	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 cDN	PROXIMAL	72219
-	zinc finger	INTRAGENI	238693
-	a disintegri	DISTAL	271127
-	leucine ric	PROXIMAL	432779
-	betaine-ho	DISTAL	64918
+	family with	PROXIMAL	320557
+	predicted g	PROXIMAL	633640
+	ribonuclea	PROXIMAL	67053
+	defensin bε	DISTAL	654465
+	retinitis pig	DISTAL	271209
-	methionine	PROXIMAL	110265
-	erythrocytε	PROXIMAL	13829
+	Kruppel-lik	DISTAL	12224
.	0	INTERGENI	0
+	zinc finger	DISTAL	52521
-	family with	PROXIMAL	432940
+	K+ voltage-	DISTAL	16539
+	regulating !	DISTAL	116838
-	sterile alph	PROXIMAL	320679
-	kelch-like 3	PROXIMAL	268807
-	transducer	DISTAL	57259
-	centromerε	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 1 PROXIMAL	67824
-	ATPase typ INTRAGENI	224088
+	karyopheri INTRAGENI	16646
-	abhydrolas DISTAL	213012
+	resistin like PROXIMAL	57263
+	ubiquitin s ζ DISTAL	30940
-	T-cell lymp ρ PROXIMAL	21844
.	0 INTERGENI	0
+	selenoprot. PROXIMAL	27361
.	0 INTERGENI	0
-	FK506 bind PROXIMAL	14229
-	salt induci ρ INTRAGENI	17691
.	0 INTERGENI	0
+	histocomp ρ DISTAL	14999
+	transporte ρ DISTAL	21355
-	histocomp ρ DISTAL	14960
+	neuraminic DISTAL	18010
+	lymphocyte PROXIMAL	114652
+	histocomp ρ DISTAL	15006
+	tripartite r ρ PROXIMAL	224762
-	zinc ribbon INTRAGENI	66136
-	olfactory r ϵ PROXIMAL	258469
.	0 INTERGENI	0
+	G protein-c DISTAL	77596
-	transmem ρ PROXIMAL	381107
-	cytochrom ρ DISTAL	20463
-	3-hydroxya PROXIMAL	107766
-	toll-like rec PROXIMAL	225471
+	phorbol-12 DISTAL	58801
-	melanocori INTRAGENI	17202
+	spectrin be INTRAGENI	20743
-	estrogen r ϵ INTRAGENI	26379
+	ubiquitin-li DISTAL	109113
+	deoxynucle DISTAL	21673
+	deoxynucle PROXIMAL	21673
-	predicted g DISTAL	627939
+	elongation PROXIMAL	12686
-	calcium ho ρ DISTAL	546729
+	phosphotri DISTAL	19212
+	methyltran PROXIMAL	66617
-	N-myc (anc DISTAL	64685
-	activin A re PROXIMAL	269275
+	methionine DISTAL	66559
-	tetratricop ρ PROXIMAL	72421
-	tetratricop ρ PROXIMAL	78802

+	receptor-a5	DISTAL	19400
-	glycosyltra	DISTAL	228366
-	BCL2 modif	DISTAL	171543
+	dispatched	INTRAGENI	214240
+	bromo adjc	PROXIMAL	228536
-	small nucle	PROXIMAL	20638
-	RIKEN cDN,	PROXIMAL	77705
+	RIKEN cDN,	DISTAL	73388
+	cDNA sequ	PROXIMAL	228802
+	discs, large	PROXIMAL	228836
+	myosin, ligl	DISTAL	98932
-	RIKEN cDN,	DISTAL	629499
+	mannosida	DISTAL	69161
+	mannosida	PROXIMAL	69161
-	junctophilii	INTRAGENI	59091
-	solute carri	PROXIMAL	114644
-	glucosamin	DISTAL	654821
+	TH1-like hc	PROXIMAL	57314
+	LSM14 hon	DISTAL	241846
-	glucocortic	INTRAGENI	229004
-	zinc finger	INTRAGENI	170753
+	spermatogi	DISTAL	70862
+	fragile X m	DISTAL	14359
-	cyclin A2	DISTAL	12428
-	predicted g	DISTAL	381438
.	0	INTERGENI	0
+	NMD3 horr	DISTAL	97112
-	relaxin fam	DISTAL	242093
-	homeodor	PROXIMAL	15257
-	Moloney le	PROXIMAL	17454
-	RIKEN cDN,	PROXIMAL	70617
+	H2A histon	INTRAGENI	51788
-	bone morp	INTRAGENI	12167
+	BTB and CN	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
-	arylaceta	PROXIMAL	230883
+	Friend viru	INTRAGENI	14349
-	RIKEN cDN	DISTAL	70433
-	angiopieti	PROXIMAL	654812
-	TAR DNA b	DISTAL	230908
-	retinol binc	DISTAL	63954
+	calsyntenin	INTRAGENI	65945
+	solute carri	DISTAL	56485
-	espin	DISTAL	56226
+	nephronop	INTRAGENI	260305
-	ski sarcoma	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
-	methypho	INTRAGENI	231803
+	transforma	DISTAL	100683
-	replication	INTRAGENI	69263
+	HOXA11 an	DISTAL	15397
-	SET and M	INTRAGENI	12180
-	INO80 com	PROXIMAL	70020
-	forkhead b	DISTAL	108655
-	RIKEN cDN	DISTAL	70291
+	DNA segme	DISTAL	28006
+	chemokine	DISTAL	20315
-	leukocyte r	DISTAL	243813
-	zinc finger,	DISTAL	22776
-	chloride ch	DISTAL	12727
+	creatine kir	DISTAL	12715
-	Ly6/Plaur d	PROXIMAL	232973
.	0	INTERGENI	0
-	FXD doma	DISTAL	18301
-	sodium cha	DISTAL	20266
+	kallikrein r	PROXIMAL	317652
+	izumo sper	DISTAL	73456
.	0	INTERGENI	0
-	interleukin	INTRAGENI	16170
+	prolylcarb	DISTAL	72461
-	tripartite r	DISTAL	330627
-	uromodulir	DISTAL	22242
+	leucine car	DISTAL	30949
-	transcriptic	INTRAGENI	70571
+	syntaxin bii	DISTAL	20911
+	zinc finger,	PROXIMAL	320158
+	coiled-coil	INTRAGENI	212392
-	CREB regul	DISTAL	382056

+	Jun proto-c	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 k	PROXIMAL	76645
-	polycystic k	DISTAL	76645
-	chromatin	DISTAL	234852
+	AFG3(ATPa	DISTAL	114896
-	eukaryotic	DISTAL	53356
-	neurotrimin	PROXIMAL	235106
+	sorting nex	PROXIMAL	102607
-	transformin	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
-	calsyntenin	PROXIMAL	64085
+	poly(rC) bir	PROXIMAL	59092
+	deleted in I	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	2610109HC	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

el.

orientation	descriptor	DISSTRIBU	gene_id	transcript_	BBMrS	SE_EXPRS	BcBBMrS	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_00111	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
-	histocomp	DISTAL	14960	AK170844	102.7279	0.836	98.2533	0.7597
+	NLR family,	PROXIMAL	216799	BC116175	1161.682	0.9414	1629.876	0.9337
-	neurotrimin	PROXIMAL	235106	BC023307	95.2075	0.7797	119.2547	0.8144
+	pleckstrin	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

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Gene ontology analysis for bone marrow.

GO Term	Nr. Genes	Term PVal	Associated Group	Gen Nr.	Genes	-log(P-value)
protein rep	3	0.002417	[Msra, Msr Msra Msrt	3	2.616761	
cAMP resp	3	0.016402	[Creb3, Crt Creb3 Crtc	4	1.785109	
response to	4	0.016682	[Acvr1c, M Acvr1c Mc	4	1.777759	
regulation of	16	0.017355	[Adamts16 Adamts16	39	1.760586	
phosphatid	4	0.02425	[Fam21, Jpl Fam21 Jph	4	1.61528	
negative re	25	0.030079	[Bach2, Bal Bach2 Bah	30	1.521731	
immunogl	3	0.033783	[Fcamr, Fcε Fcamr Fcγ	3	1.471307	
sarcomere	4	0.035096	[Foxp1, Krt Adamts16	9	1.454743	
antigen prc	5	0.042434	[Fcgr3, H2- Fcgr3 H2-A	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_pi	0.045426	4.23369	M1	Srf	Myl9,Jph2,Ckm,Smyd1,Espn,Zmat4
2	tiffin-TIFDM	0.044759	4.13255	M2		Tcf20,Six4,Snx19,Arl1,Hmgb4,Mll3
3	encode-UM	0.044001	4.01762	M3		Bmpr1b,Vgf,Ill16,Tnnt2,Klf5,Krt86,I
4	jaspar-PFO	0.043164	3.89074	M4		BC048943,Tnni1,Jph2,Tnnt2,Trim6
5	transfac_pi	0.042035	3.71972	M1	Srf	Myl9,Msrb3,Krt19,Col1a1,Ckm,Jph
6	hdpi-SSX3	0.041702	3.66915	M5	Ssxa1,Gm2	Ntm,Kcns2,Uhrf2,Six4,Espn,Cops3,
7	elemento-1	0.041046	3.56985	M6		Bahd1,Cdk12,Six4,Trim31,Crtc1,Ar
8	jaspar-MAC	0.040786	3.53032	M1	Srf	Myl9,Tnnt2,Krt19,Msrb3,Ckm,Smy
9	flyfactorsui	0.04044	3.47791	M7	Msx3,Msx2	Krt86,Foxp1,Tcf20,Espn,Msgn1,Brr
10	encode-UM	0.040434	3.47699	M8		BC018465,Scn11a,Klhl38,Zmat4,Kl
11	transfac_pi	0.040422	3.47515	M9	Mterf,Gm9	Tiam1,Foxp1,H2-Aa,Rxfp4,Msrb3,I
12	tiffin-TIFDM	0.040343	3.4632	M8		Cdk12,Trim66,Pcbp4,Ppp1r9b,Jph2
13	hdpi-DAZAI	0.0403	3.45676	M5	Dazap1	Ntm,Kcns2,Six4,Uhrf2,Foxp1,Mcm
14	transfac_pi	0.039936	3.4016	M10	Snai1,Tcf3,	Ssh2,Ill16,Rapsn,Tnnt2,Pcyt1b,Smy
15	yetfasco-1	0.039578	3.34735	M11		Sgip1,Rims2,Lypd4,Bmf,H2afz,Ssh2
16	taipale-TG/	0.039518	3.33816	M10	Meis3,Tgif2	Ill16,Klhl38,Tiam1,Kcns2,Ssh2,Tnnt
17	factorbook	0.039324	3.30873	M1	Srf	Myl9,Jph2,Ckm,Vgf,Smyd1,Tnnt2,Z
18	transfac_pi	0.039287	3.30322	M12	Pdx1	Msgn1,Scn11a,Clstn2,Vgf,Hormad:

19	hdpi-MEIS3	0.03916	3.28391	M13	Meis3	Smyd1,Six4,Tnnt2,Rapsn,I116,Kcns:
20	tfdimers-M	0.039105	3.27563	M3	Yy1,Mycs,C	Tnnt2,I116,Klhl38,Angptl7,Rapsn,A,
21	taipale-TGF	0.038996	3.25908	M10	Gm7148	I116,Kcns2,Ssh2,Tiam1,Klhl38,Trim
22	hdpi-EIF5A	0.038662	3.20852	M2	Eif5a2	Trim66,Klf5,Espn,Tcf20,Krt19,Klhl3
23	tiffin-TIFDM	0.038553	3.19197	M14		Tnnt2,Rp1l1,Phf3,Six4,Spnb3,AA98
24	encode-UM	0.038529	3.18829	M10		1700058C13Rik,Gm5148,Zmat4,Hr
25	transfac_pi	0.038474	3.18001	M1	Srf	Myl9,Smyd1,Ckm,Msrb3,Zmat4,Jp
26	transfac_pi	0.038462	3.17817	M1	Srf	Myl9,Vgf,Ckm,Msrb3,Tnnt2,Zmat4
27	transfac_pi	0.038426	3.17266	M12	Nkx2-5	Foxp1,Msgn1,Alkbh5,Zmat4,Lsm14
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,Trir
31	jaspar-PF0	0.038122	3.12669	M1	Srf	Myl9,Ckm,Msgn1,Zmat4,Tnnt2,Ca
32	encode-UM	0.037837	3.08347	M13		Csrnp1,Bmpr1b,Tepp,Col1a1,Catsp
33	taipale-TTC	0.037764	3.07244	M15	Hsf1,Hsf2,H	1110028C15Rik,Ubqln1,H2afz,BC0
34	homer-MO	0.03757	3.04302	M16	Rela,Rel,Re	Espn,Ntm,Msrb3,Bahd1,Msra,1110
35	hdpi-ZDHH	0.037546	3.03934	M12	Zdhhc15	Tcf20,Lsm14b,Rims2,Smyd1,Ccna2
36	yetfasco-18	0.037443	3.02371	M10	Cnot4	Tcf20,Pter,Gm5148,Nos1ap,Tnnt2,
37	swissregulc	0.037382	3.01451	M4	Mef2d,Mef	Tcf20,BC048943,Hmgb4,Smyd1,Klf
38	homer-MO	0.037352	3.00992	M4	Mef2c,Mef	BC048943,Tcf20,Klhl38,Jph2,Tnni1

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4,Tnnt2,Msrb3,Spnb3,I16,Kcns2,Bmpr1b,Retnlb,Fkbp5,Vgf,Col1a1
 ,Ubqln1,Rfc3,Angptl7,Vgf,Trim66,Ccna2,Cd72,Ntm,Sik1,Kcns2,Csrnp1,Ppp1r9b,Bmf,Tmem232,Tmem11,
 BC048943,Agr2,Tnni1,Col1a1,1700058C13Rik,Stxbp2,I122ra1,BC018465,Msgn1
 i6,Msra,Igfbp1,Lrrc14b,Fam169a,1110028C15Rik,Hmgb4,Klhl38,Ubqln1,Phf3,Agr2
 i2,Spnb3,Gmeb2,Tnnt2,I16,Smyd1,Bmpr1b,Lsm14b,Fkbp5,Mov10
 .Klhl38,Bmpr1b,1110028C15Rik,Mcm3,4930488L21Rik,Ino80b,Foxp1
 l1,Vgf,Mc4r,Nos1ap,Rims2,Sgip1,Ttc30b,Ssh2,Lcmt1
 rd1,Vgf,Jph2,Bmpr1b,Cant1,Wnt9a,Lsm14b,Spnb3,Ly6g5c
 rpr1b,Alkbh5,Zmat4,Elovl3,Rp1l1
 f5,Oasl1,Pcyt1b,Umod,I16,Angptl7,Tnni1,Smyd1,Gyltl1b,Olf90,Nos1ap,Krt19,Jph2,Rhobtb1,H2-Aa,Klk1
 Mov10,Elovl3,Olf90,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,I16
 2,Six4,Rims2,My19,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
 8, 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, Ptg
 h2, Tnnt2, Vgf, Bmpr1b, Kcns2, Col1a1, Cant1, Spnb3, Retnlb, Gm5148, Ubqln1, Tnni1, Krt19, Als2cr11, Fkbp5, BC
 l, Jph2, Fkbp5, Col1a1, Krt19, Gm5148, Als2cr11, Gmeb2, Smyd1, Msgn1, Spnb3, Lsm14b, Bmpr1b, Espn, Il16, Kcr
 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, Gylt1b, Il16, Msgn1, Tiam1, Uhrf2, Calhm1, BC018465, Klhl38, I
 nt1, Gmeb2, Krt19, Jph2, Espn, Il16, Bmpr1b, Msra, Spnb3, Hmgb4, Als2cr11, Eif5, Fkbp5, Kcns2, Acvr1c
 er4, Jph2, Hmgb4, 4930488L21Rik, Olfr90, Gpr110
 18465, Acvr1c, Izumo1, Als2cr11, Sept3, Pcsk9, Plscr4, Ticam2, D4Wsu53e, Aadacl3, Alkbh5, Il22ra1
 0028C15Rik, Zfp704, Fcamr, Six4, Klhl38, Pter, 4930488L21Rik, H2-Aa
 l, 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

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Espn,Fkbp5,Prpf39

5,Bmpr1b,Fxyd5,Ntm,Tiam1,Olfr877,Gpr110,Lypd4,Calhm1,1110028C15Rik,2510049J12Rik,4732456N1C

l,Bach2,Aadacl3,Esrra

mem11,2610109H07Rik,Pcyt1b,Trip11

on7,Il22ra1,Cpsf6,Angptl7,Ssh2,2510049J12Rik,Pkd1l2,St3gal2,Ttc25,Lcmt1,Spnb3
030307,Il16,Espn,Hmgb4,Six4,Tepp,Lsm14b,Hes6,Gmeb2,Ttc25,Lcmt1,Mov10,4922505G16Rik,Igfbp1,Bi
rs2,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

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)Rik,Agr2,AA986860,Fam49a,Tnnt2,Pkd1l2,BC030307,Kcns2,Lsm14b,Rapsn

mf,Msgn1,Msra,Prpf39,Izumo1,Pcyt1b,2610109H07Rik,Mepce,Tmem11,Uhrf2,Ppp1r9b,Dntt,Apool,Kpnz

l4b,Pkd1l2,Fkbp5,Mfap2,Lcmt1,Rhobtb1,Umod,Hes6,Tcf20,Tbrg1,Klf5,Tmem232,Rp111

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α1,Ino80b,Acvr1c,Cox7a2l,Rbp7,Hormad2,Nos1ap,Umod,BC018465,Tcf20,Aadacl3,Usp25,4930488L21Ril

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c,Snrpb,Gm16515,Rims2,Sept3

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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	transcriptic
NM_01979	Tmeff2	chr1	50982423	50983087	0.6	0.5	1.8	transcriptic
NM_05301	Mlph	chr1	92811145	92811789	1.8	1.5	0.5	transcriptic
NM_00110	Prlh	chr1	92848564	92849198	3.8	3.6	1.8	transcriptic
NM_17888	D2hgdh	chr1	95721562	95721811	0.0	0.0	1.0	transcriptic
NM_00115	Serpinb8	chr1	1.09E+08	1.09E+08	0.3	0.3	1.4	transcriptic
NM_21361	Atp2b4	chr1	1.36E+08	1.36E+08	0.7	0.7	1.9	transcriptic
NR_026896	4931440L1	chr1	1.36E+08	1.36E+08	1.7	1.6	3.6	transcriptic
NM_17708	Ptpn7	chr1	1.37E+08	1.37E+08	2.7	3.6	1.1	transcriptic
NM_13366	Lad1	chr1	1.38E+08	1.38E+08	2.3	1.9	0.9	transcriptic
NM_00906	Rgs4	chr1	1.72E+08	1.72E+08	0.0	0.0	1.4	transcriptic
NM_01200	Sh2d1b1	chr1	1.72E+08	1.72E+08	0.7	0.3	1.9	transcriptic
NM_00102	Fcrlb	chr1	1.73E+08	1.73E+08	0.5	1.1	2.2	transcriptic
NM_14665	Olf418-ps	chr1	1.75E+08	1.75E+08	0.6	1.1	2.2	transcriptic
NM_17278	Zc3h12d	chr10	7587001	7587665	4.2	2.3	0.6	Primary Tra
NM_02966	1700027D2	chr10	76023854	76024088	0.7	0.9	1.9	transcriptic
NM_17499	Gm4792	chr10	93761597	93763163	0.9	0.7	2.5	transcriptic
NM_02860	Glipr1	chr10	1.11E+08	1.11E+08	0.9	1.0	2.2	transcriptic
NM_00101	Cpsf6	chr10	1.17E+08	1.17E+08	0.5	0.1	1.6	transcriptic
NM_02802	D10Ert61	chr10	1.27E+08	1.27E+08	1.4	1.5	3.3	transcriptic
NM_02381	Ankrd36	chr11	5467066	5467900	0.6	0.8	2.3	transcriptic
NM_00834	Igfbp1	chr11	7098112	7098566	2.3	2.4	0.7	transcriptic
NM_01141	Slit3	chr11	34933219	34933808	0.4	0.1	2.0	transcriptic
NM_14650	Olf319	chr11	58515470	58515919	0.7	0.9	2.1	transcriptic
NM_14653	Olf313	chr11	58630713	58631267	1.8	1.8	4.5	transcriptic
NM_01199	Cops3	chr11	59654752	59655702	0.9	0.6	2.7	transcriptic
NM_14641	Olf463	chr11	87709058	87709487	1.2	0.8	2.5	transcriptic
NM_00110	Gm11545	chr11	94625051	94625306	0.1	0.1	1.5	transcriptic
NM_17226	Ppp1r9b	chr11	94854043	94854312	0.6	0.6	1.8	Primary Tra
NM_01005	Dlx3	chr11	94982160	94982394	0.8	1.0	2.5	transcriptic
NM_17806	Thra	chr11	98601916	98602155	0.4	0.3	1.6	transcriptic
NR_003364	BC018473	chr11	1.17E+08	1.17E+08	2.4	2.2	1.0	transcriptic
NM_01954	Msgn1	chr12	11218036	11218673	2.0	1.8	0.3	transcriptic
NM_13405	Adi1	chr12	29357759	29358225	1.5	1.6	3.5	transcriptic
NM_17780	Prpf39	chr12	66135284	66136843	2.6	1.5	0.4	transcriptic
NM_00108	Galnt1	chr12	81618420	81618689	1.1	1.2	2.5	transcriptic
NM_01138	Slc10a1	chr12	82068540	82068884	1.9	1.8	0.5	transcriptic
NM_00102	Klc1	chr12	1.13E+08	1.13E+08	0.9	0.4	2.1	transcriptic
NM_02905	Tdrd9	chr12	1.13E+08	1.13E+08	2.9	3.1	1.2	transcriptic
NM_00108	Aspg	chr12	1.13E+08	1.13E+08	0.3	0.1	1.6	transcriptic
NM_17891	Pld4	chr12	1.14E+08	1.14E+08	0.0	0.0	1.2	transcriptic
NM_02938	Tex22	chr12	1.14E+08	1.14E+08	0.1	0.0	1.4	transcriptic
NM_05408	Mta1	chr12	1.14E+08	1.14E+08	3.0	2.8	1.2	transcriptic
NM_00776	Crip1	chr12	1.14E+08	1.14E+08	0.7	0.7	1.8	transcriptic
NM_01885	Akr1e1	chr13	4607703	4608482	0.0	0.0	2.4	transcriptic
NM_14597	Tifab	chr13	56281547	56282296	1.3	0.9	2.9	transcriptic
NM_01092	Nkx2-6	chr14	69789892	69790521	0.8	0.8	2.8	transcriptic
NM_14452	Zfp622	chr15	25911170	25911834	0.1	0.2	1.4	transcriptic

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 Nmr1	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 Mlx	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	transcripti
NA	chr3:12977	chr3	1.3E+08	1.3E+08	2.3	1.8	0.7	CpG Island:
NM_00103	Musk	chr4	58296685	58297424	0.8	0.8	2.4	transcripti
NM_15339	Ttc39a	chr4	1.09E+08	1.09E+08	2.4	2.2	0.8	transcripti
NM_15339	Ttc39a	chr4	1.09E+08	1.09E+08	2.9	1.9	0.8	transcripti
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 Island:
NM_00793	Epha8	chr4	1.37E+08	1.37E+08	0.6	0.5	1.6	transcripti
NM_00108	Aadacl3	chr4	1.44E+08	1.44E+08	0.2	0.7	2.1	transcripti
NM_00872	Nppb	chr4	1.47E+08	1.47E+08	0.4	0.6	1.8	transcripti
NM_02742	2610109HC	chr4	1.48E+08	1.48E+08	0.5	0.2	2.0	transcripti
NM_17684	Fbxo2	chr4	1.48E+08	1.48E+08	3.7	3.0	0.8	transcripti
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	transcripti
NM_15342	Nphp4	chr4	1.52E+08	1.52E+08	0.6	0.5	1.8	transcripti
NR_027362	A930003O	chr5	22252651	22252950	0.6	0.7	1.7	transcripti
NM_17517	Klh15	chr5	65522502	65523242	1.0	1.3	2.8	transcripti
NM_00965	Alb	chr5	90887060	90887393	0.4	0.2	1.6	transcripti
NM_02369	Crybb1	chr5	1.13E+08	1.13E+08	0.9	0.5	2.0	transcripti
NM_01878	Tfip11	chr5	1.13E+08	1.13E+08	0.6	0.9	1.9	transcripti
NM_00108	Oas1b	chr5	1.21E+08	1.21E+08	0.1	0.1	1.2	transcripti
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	transcripti
NM_14556	Agfg2	chr5	1.38E+08	1.38E+08	2.4	1.5	0.5	transcripti
NM_00102	Pilrb2	chr5	1.38E+08	1.38E+08	0.5	0.3	1.6	transcripti
NM_03303	Ocm	chr5	1.45E+08	1.45E+08	0.0	0.0	1.7	transcripti
NM_00101	Wdr91	chr6	34862841	34863825	2.1	1.6	0.4	transcripti
NM_17342	Zfp775	chr6	48560543	48560787	0.9	0.9	2.1	transcripti
NM_00108	Ccdc129	chr6	55786592	55787131	0.8	0.9	2.0	transcripti
NM_00116	Smyd1	chr6	71211535	71211909	2.7	2.4	0.8	transcripti
NM_14556	Krcc1	chr6	71219681	71220726	0.4	0.4	1.9	transcripti
NM_00110	2510049J1	chr6	1.16E+08	1.16E+08	0.7	0.1	2.0	transcripti
NM_02658	D6Wsu116	chr6	1.16E+08	1.16E+08	1.7	2.1	0.5	transcripti
NM_02663	Art4	chr6	1.37E+08	1.37E+08	1.2	1.3	2.9	transcripti
NM_01065	Sspn	chr6	1.46E+08	1.46E+08	2.6	2.0	0.8	transcripti
NM_00110	Ttyh1	chr7	4070072	4070301	2.1	2.0	0.8	transcripti
NM_01133	Clcn4-2	chr7	7253199	7253628	3.5	3.3	1.2	transcripti
NM_00746	Apoc1	chr7	20277618	20277967	1.9	1.9	0.8	transcripti
NM_15311	Cadm4	chr7	25266457	25266726	1.6	1.5	3.2	transcripti
NM_01998	Tex101	chr7	25457230	25457684	3.2	2.3	0.9	transcripti
NM_14618	B3gnt8	chr7	26410201	26411064	3.4	2.4	0.8	transcripti
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	transcripti
NM_00111	Nav2	chr7	56214536	56215185	0.9	1.1	2.5	transcripti
NA	chr7:74948	chr7	74948300	74948975	1.0	1.0	2.3	CpG Island:
NM_00803	Folr1	chr7	1.09E+08	1.09E+08	0.8	1.0	2.4	transcripti
NM_13864	Syt17	chr7	1.26E+08	1.26E+08	0.7	0.8	2.0	transcripti
NM_18328	Tcerg1l	chr7	1.46E+08	1.46E+08	0.0	0.1	1.2	transcripti
NM_00101	Olfir527	chr7	1.48E+08	1.48E+08	0.5	0.5	1.5	transcripti
NM_02427	1700094C0	chr8	12573150	12573617	0.9	0.6	1.9	transcripti

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 F2r13	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 Repts2	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	

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orientation descriptor DISSTRIBU' gene_id

+	cyclic nucle	DISTAL	12790
+	transmemt	DISTAL	56363
+	melanophil	PROXIMAL	171531
+	prolactin rε	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 rε	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 rε	INTRAGENI	258493
+	olfactory rε	INTRAGENI	258529
-	COP9 (cons	DISTAL	26572
-	olfactory rε	DISTAL	258408
-	predicted g	DISTAL	217122
+	protein phc	INTRAGENI	217124
+	distal-less	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 ricl	INTRAGENI	378937
-	transducer	DISTAL	57259
-	ceramide k	PROXIMAL	223753
+	keratin 86	INTRAGENI	16679
-	NmrA-like 1	PROXIMAL	67824
+	myosin, ligl	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 gene	PROXIMAL	18132
+	histocomp:	DISTAL	15006
-	mohawk hc	INTRAGENI	210719
-	glycophorir	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-aminocyc	DISTAL	329470
+	solute carri	DISTAL	20511
+	coiled-coil	INTRAGENI	211936
+	apoptosis,	DISTAL	74268
-	secretograi	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-binc	DISTAL	664799
+	spermatogi	DISTAL	70862
+	exosome c:	DISTAL	50911
+	fibroblast g	DISTAL	14173
-	predicted g	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 do INTRAGENI	242748
-	retinol binc DISTAL	63954
+	nephronop INTRAGENI	260305
-	RIKEN cDN, PROXIMAL	330052
+	kelch-like 5 PROXIMAL	71778
+	albumin DISTAL	11657
+	crystallin, t DISTAL	12960
+	tuftelin int DISTAL	54723
+	2'-5' oligoa INTRAGENI	23961
+	serine/argi INTRAGENI	58212
+	fission 1 (r PROXIMAL	66437
-	ArfGAP wit DISTAL	231801
-	paired imr 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 hon DISTAL	57776
-	chloride ch DISTAL	12727
-	apolipopro PROXIMAL	11812
+	cell adhesic PROXIMAL	260299
-	testis expr PROXIMAL	56746
+	UDP-GlcNA DISTAL	232984
-	spectrin be INTRAGENI	80297
+	kallikrein r DISTAL	19144
+	neuron nav PROXIMAL	78286
.	0 INTERGENI	0
-	folate recej PROXIMAL	14275
-	synaptotag PROXIMAL	110058
-	transcriptic INTRAGENI	70571
+	olfactory r DISTAL	257939
+	RIKEN cDN, INTRAGENI	78634



+	sperm asso	DISTAL	546038
+	sorbin and	PROXIMAL	234214
+	hyaluronan	INTRAGENI	330790
+	coagulator	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 I	DISTAL	320256
-	acetyl-Coer	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

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orientation	description	DISTRIBU	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_00110	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

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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

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Gene ontology analysis for liver.

GO Term	Nr. Genes	Term PVal	Associated Group	Gen Nr.	Genes i -log(P-value)
negative re	3	0.013555	[Draxin, Slii Draxin Exo	13	1.867891
acetylglucc	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-CNO	0.050072	4.51203	M3		Trpm3,Cacnb4,Spag11b,Krt86,Thra
4	yetfasco-1C	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-UM	0.046131	4.01428	M7		Dcpp3,Dcpp2,Dcpp1,Gpr56,F2rl3,M
8	transfac_pi	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,Dcpp
10	homer-MO	0.044252	3.77702	M5	Cdx2,Cdx1,	Pknox2,Msgn1,Slc1a2,Gm5148,My
11	yetfasco-1C	0.04308	3.62905	M9	Kdm4d,Kdr	Atp2b4,Cacnb4,Lad1,Sh2d1b1,Spn
12	transfac_pi	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,Smyc
14	elemento-C	0.042838	3.59847	M10		Klk6,Reps2,Zc3h12d,Smyd1,A9300
15	flyfactorsu	0.042335	3.53488	M11	Glis2,Glis3,	Ctcf1,Apoc1,Syt17,Sspn,Crybb1,26
16	tfdimers-M	0.042277	3.52754	M5	Jun,Fos,Irf1	Klh15,Sspn,Cxcr5,Trpm3,Nppb,Cacr
17	yetfasco-9E	0.04218	3.51531	M5		Sspn,Mkx,Nav2,Rin2,Ppp1r9b,Trpr
18	transfac_pi	0.042102	3.50553	M1	Srf	Smyd1,Mybpc3,Nppb,Glipr1,Sspn,
19	transfac_pi	0.042035	3.49696	M3	Tcf7l1,Tcf7	Msgn1,Gm5148,Klh15,Krt86,Trpm3
20	elemento-C	0.041977	3.48963	M12		Trpm3,Retnlb,Mybpc3,Rln3,Cxcr5,
21	yetfasco-1C	0.041957	3.48718	M13		Zc3h12d,Trpm3,Cep97,Sspn,Nav2,

22	transfac_pi	0.041948	3.48596	M3	Tcf7,Tcf7l1	Msgn1,Gm5148,Krt86,Klhl5,Slc1a2
23	transfac_pi	0.041938	3.48474	M2	Pgr,Nr3c1,	Notch4,Trpm3,Ccdc129,Rin2,Msgr
24	taipale-GT	0.041725	3.45783	M4	Zfp784	Atp2b4,Spnb3,Slc1a2,Reps2,Syt17,
25	flyfactorsui	0.041589	3.44071	M5		Msgn1,Pknox2,Mylk,Dcpp1,Rin2,R
26	elemento-C	0.041376	3.4138	M10		Klk6,Gpr56,Notch4,Ptpn7,Dcpp1,A
27	jaspar-CNO	0.041376	3.4138	M14	Nf1	Msgn1,Mylk,2510049J12Rik,Smyd:
28	elemento-1	0.041308	3.40524	M8		Notch4,Slc10a1,Prlh,Atp2b4,Klk6,N
29	elemento-1	0.041202	3.39179	M8		Smyd1,Prlh,Atp2b4,Slc10a1,Ctcf1,T
30	taipale-GA	0.041192	3.39057	M11	Glis3	Spnb4,Syt17,Sspn,Cep97,Nkx2-6,A
31	transfac_pi	0.041173	3.38812	M15	Mecom	Msgn1,4930579J09Rik,Reps2,Olfr4
32	elemento-1	0.041047	3.37222	M16	Bach1,Batf	Gpr56,Klc1,Galntl1,Sh2d1b1,Krt86
33	elemento-1	0.041047	3.37222	M17		Zc3h12d,Syt17,Samd12,Trpm3,Slc:
34	homer-MO	0.040902	3.35388	M3	Tcf3,Tcf7l1	Msgn1,Nav2,Slc1a2,Agfg2,Gm5148
35	transfac_pi	0.040718	3.33064	M6	Tal1,Tcf4,T	Cacnb4,4931440L10Rik,Krt86,Alb,S
36	homer-MO	0.04066	3.3233	M5		Pknox2,Msgn1,Gm5148,Krt86,Eph
37	flyfactorsui	0.04064	3.32086	M11	Glis3,Glis1,	Ctcf1,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	flyfactorsui	0.040146	3.25849	M1	Bhlha15,Nr	Alb,Gpr56,Cacnb4,6030405A18Rik
43	encode-UM	0.040001	3.24014	M2		Smyd1,Atp2b4,Reps2,Gpr56,F2rl3,
44	encode-UM	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-UM	0.039701	3.20223	M2		Klk6,Musk,Prlh,Notch4,Krcc1,6030
47	yetfasco-1	0.039585	3.18755	M20		Msgn1,Klk6,4930579J09Rik,Olfr41.
48	iDMMPMM	0.039498	3.17655	M20		Notch4,Psp,Rin2,Musk
49	transfac_pi	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-MAC	0.039411	3.16554	M16	Jdp2,Bach1	Gpr56,Nppb,Sh2d1b1,Krt86,Zc3h1
53	tfdimers-M	0.039333	3.15576	M13	Jun,Pparg,F	Krcc1,Zc3h12d,Fgf2,Gpr56,Spnb4,I
54	flyfactorsui	0.039314	3.15331	M21		Spnb4,Samd12,Tob2,Notch4
55	flyfactorsui	0.039246	3.14475	M11	Glis2,Glis3,	Ctcf1,Crybb1,Apoc1,Ppp1r9b,Notch
56	yetfasco-8	0.039236	3.14353	M22	Jazf1,Foxn4	Dlx3,Slit1,Galntl1,Cacnb4,Zfp622,R
57	yetfasco-2	0.039198	3.13864	M16	Jdp2,Bach2	Gpr56,Nppb,Sh2d1b1,Krt86,Galntl
58	jaspar-MAC	0.03911	3.12763	M13	Gata5,Gata	Cxcr5,Msgn1,4931440L10Rik,Pkno
59	homer-MO	0.038975	3.11051	M6	Neurod1,Ti	Cacnb4,Musk,Sorbs2,4931440L10f
60	encode-UM	0.038936	3.10562	M18		Slc10a1,Atp2b4,Notch4,Psp,Klk6,G
61	homer-MO	0.038907	3.10195	M6	Olig2,Tal1,	Cacnb4,Musk,Alb,Smyd1,Krt86,Sor
62	transfac_pi	0.038839	3.09339	M13	Thrb,Nr2f2	Notch4,Trpm3,4931440L10Rik,Aac
63	yetfasco-2	0.03883	3.09216	M13		Ctcf1,Klk6,Psp,Apoc1,Crip1,Slc10a1
64	swissregulc	0.038752	3.08238	M16	Bach2,Bach	Gpr56,Krt86,Nppb,Galntl1,Klc1,Sh:
65	swissregulc	0.038752	3.08238	M16	Fosl2,Jun,F	Gpr56,Krt86,Klc1,Galntl1,Cacnb4,S
66	transfac_pi	0.038607	3.06404	M4		D030056L22Rik,Atp2b4,Apoc1,Slc:
67	elemento-C	0.038558	3.05792	M22	Mef2a,Mef	Spnb3,Slit1,Dlx3,Syt17,Apoc1,Cacr
68	tfdimers-M	0.038539	3.05547	M2	Hand2,Max	Spnb3,Msgn1,Alb,Musk,Smyd1,At

69	homer-MO	0.038491	3.04936	M7	Tal1,Elf1	F2rl3,Cacnb4,4931440L10Rik,Mkx,
70	transfac_pi	0.038491	3.04936	M1	Srf	Smyd1,Sspn,Spnb3,Nppb,Kcns2,Gl
71	encode-UM	0.038452	3.04447	M11		Syt17,Notch4,Klk6,Trpm3,Ptpn7,Pl
72	transfac_pi	0.038258	3.02001	M6		Reps2,Smyd1,Sorbs2,Msgn1,Mkx,l
73	taipale-RA	0.038249	3.01879	M1	Neurog2,Bl	Cacnb4,Thra,Musk,4931440L10Rik
74	tfdimers-M	0.03822	3.01512	M13	Rara,Rarb,1	Dcpp1,Dcpp3,Gpr56,Dcpp2,Trpm3
75	hdpi-MYF6	0.038123	3.00289	M6	Myf6	Cacnb4,Cxcr5,Smyd1,Ccdc129,Krt8
76	stark-TGAN	0.038123	3.00289	M16	Arnt	Gpr56,Klc1,Galnt1,Sh2d1b1,Cacnt

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, Nppb, Gypc, Psp, Slc1a2, 4930579J09Rik, Gm5148, Ttyh1, Slc10a1, Dlx3
 iypc, 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, Ticar
 , Cacnb4, Slc1a2, 6030405A18Rik, Trpm3, Spnb4
 vmsgn1, Cacnb4, Nav2, Ccdc129, Sspn, Klk6, Samd12, Trpm3, Fcrlb, 8030411F24Rik, Retnlb, Spnb3, Golga7b, Ttc3
 pp3, Dcpp2, Dcpp1, Aadacl3, Lad1
)2, Dcpp3, Dcpp1, Nphp4, Mxk, Ccdc129
 /lk, Gpr56, Aven, Trpm3, Crybb1, Klhl5, Rgs4
 b3, Cxcr5, Krt86, Prlh, Sspn, Slc1a2, Rin2, 6030405A18Rik
 ybpc3, Nppb, Syt17, Psp, Crybb1, Gm5148, Slc10a1
 l1, 4931440L10Rik, Gpr56, Sorbs2
 l03O13Rik, Sorbs2, Ccdc129, Msgn1, Zfp775, Spag11b, Gpr56
 l0109H07Rik, Tob2, Ptchd2, Notch4, Fbxo2, Spnb4, Cxcr5, Mybpc3, Ppp1r9b, Klk6, Cnga3, Zfp775, 6030405A18
 rb4, Krt86, 4930579J09Rik
 n3, 4922505G16Rik
 Slc1a2, Kcns2, Olfr418-ps1, Spnb3, Retnlb, Gm5148, Gypc, Cxcr5, Trpm3, Slc10a1, Crybb1, 8030411F24Rik, Rep
 }, Sspn, Slc1a2, Nav2, Cxcr5, 6030405A18Rik
 Fgf2, Slc10a1, Atp2b4, Cnga3, Notch4
 Cxcr5, Nppb, Msgn1, Syt17, Slc1a2, Cops3

,Cxcr5,Trpm3,Sspn,6030405A18Rik,Nav2
 1,Spag11b,Slc10a1,Reps2
 ,Art4,Apoc1,Sorbs2,Samd12,Cops3,Krcc1,Slit1,Prlh,Dlec1,Olfr463,Nav2,4931440L10Rik,Mybpc3,Sh2d1b1
 eps2,Mkx,Spag11b,Alb,Olfr418-ps1,Zc3h12d,Dcpp2,Dcpp3
 t2b4,Dcpp3,Zc3h12d,Trpm3,Slc10a1,Mybpc3,Prlh,Dcpp2,Retnlb,Samd12,Apoc1,Smyd1
 1,Serpinb8,Agfg2,Olfr418-ps1,Dlx3,Cacnb4
 Nav2,Ptchd2
 Trpm3,Mybpc3,Reps2,Musk,Slit3,Cops3,Ttyh1,Notch4,Spag11b,Fcrlb,Nav2,Olfr463,Aadacl3,Gm5148,Klk6
 t2b4,Dlx3,Crybb1,Foxo6
 18-ps1,Trpm3,Spag11b,B3gnt8,Sh2d1b1,Mkx
 ,Nppb,Aadacl3,Cacnb4
 1a2,Mkx,Nppb,Cacnb4,Klhl5,Pknox2,Krt86,Spag11b,Olfr418-ps1,Tmeff2,4922505G16Rik,Gpr56,Spnb4
 3,Slit1,Krt86,Klhl5
 Sorbs2,Kcns2,Musk,Smyd1,Zc3h12d
 a8,6030405A18Rik,Prpf39,Trpm3,4930579J09Rik
 a3,Syt17,Crybb1,2610109H07Rik,Fbxo2,Ppp1r9b,Slit1,A930003O13Rik,Zfp775,Cep97,6030405A18Rik,M
 b,Klc1
 lc129,Rya3,Epha8,Gm5148,Trpm3,4931440L10Rik,Musk,At2b4,Cacnb4,Zc3h12d,Igfbp1,Rgs4,Krt86,Rln3
 9,Mlph,Adi1,4922505G16Rik,Rgs4,Gm4792,Cops3,Folr1
 c1,Igfbp1,8030411F24Rik,Gpr56,4931440L10Rik,Krt86,Pilrb2
 ;,Trpm3,Olfr463,Nav2,Sspn,Reps2,Thra,Slc1a2,Sorbs2,Krt86,Glipr1,Syt17
 .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

 2d,Klk6,Cacnb4,Aadacl3,Serpinb8
 2d,Klk6,Cacnb4,Aadacl3,Serpinb8
 ;p,Cacnb4,Ttyh1,Spnb4,Smyd1
 2d,Klk6,Aadacl3,Cacnb4,Serpinb8
 Klk6,Slc10a1

 14,Ptchd2,Sspn,Spnb4,Cxcr5,2610109H07Rik
 Rya3,Syt17,Prlh
 1
 x2,6030405A18Rik,Prlh,Samd12,Ccdc102a,Krt86
 Rik,Alb,Krt86,Zc3h12d,Kcns2,Smyd1,Gpr56,Mybpc3,8030411F24Rik,6030405A18Rik,Scg5,Tmeff2,Notch4
 ipr56
 rbs2,Thra,Zc3h12d,4931440L10Rik,Trpm3,Prlh,Gpr56,Notch4,Kcns2,8030411F24Rik
 dacl3,Mybpc3,Fcrlb,Smyd1,Rin2,Slc10a1
 .,Notch4,Tmeff2
 2d1b1,Klk6,Cacnb4,Zc3h12d
 h2d1b1,Zc3h12d,Nppb,Aadacl3,Klk6
 1a2,Samd12,Sorbs2
 1b4,Trpm3,4930579J09Rik,Ptpn7
 p2b4,Sh2d1b1,Notch4,Kcns2,Slc10a1,Art4,Aadacl3,Cep97,Sorbs2,Crybb1,Cnga3,Zc3h12d,4931440L10Rik

.Tmeff2,Ccdc129,Smyd1,Dcpp2,Dcpp3,Dcpp1,Trpm3,Reps2,Ptpn7,Lad1,Cnga3,Rgs4,Pld4,Prpf39,Gpr56
ipr1,Mybpc3,Retnlb,Slc10a1,Trpm3,Gypc,Syt17,Musk,Slc1a2,8030411F24Rik,Klk6,Cxcr5,Reps2,4922505C
knox2,Nppb

Vybpc3,Cxcr5,Ccdc129,Atp2b4,Zfp775,Alb

;Krt86,Smyd1,Sorbs2,Alb,Gpr56

36,Prlh,Alb,Sspn,Musk,Klhl5,Trpm3,Dlx3,Zc3h12d,6030405A18Rik,Atp2b4,Sorbs2,Samd12,Nav2,4922505
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3O13Rik,Senp7

12,Slc1a2,Spnb3,Krt86,Kcns2,Senp7,Fgf2,Atp2b4,Spag11b,Manbal,2610109H07Rik

9a,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

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

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

ybpc3,Gpr56,Tmeff2,Notch4

l,Golga7b

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

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

l,Fcrlb,Slc1a2,Tifab,Olfr418-ps1,8030411F24Rik,Krt86,Gpr56,Trpm3,Rin2,Nav2,Manbal,Rya3,6030405A1:

316Rik,Notch4,Fbxo2,Fcrlb,Sh2d1b1,4930579J09Rik,Rgs4,Krt86,Olf418-ps1,Msgn1,Ttyh1,Krcc1,Ccdc102

G16Rik,Aadacl3,Spnb4,Notch4,Syt17,Rin2,Mybpc3

For Review Only

For Review Only

ik,2610109H07Rik,Notch4,Ppp1r9b,Musk,Spag11b

Nkx2-6,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

ven,Spag11b,Slc1a2,Syt17

For Review Only

p7,2510049J12Rik,Slc1a2,Fcrlb,Ttc39a,Ttyh1,Crybb1,Klk6,Aadacl3,Cep97,Gm5148,4922505G16Rik,Rya3,

8Rik,Igfbp1,Golga7b,4922505G16Rik,Klk6,Prlh,A930003O13Rik,Gypc,Mybpc3,Mkx

!a,6030405A18Rik,Apoc1,Nav2

For Review Only

For Review Only

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

For Review Only

.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	t4931440L1	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 Islands
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 Islands
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 Pvk	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 Psmc5	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	transcriptic
NM_02696 Manbal	chr2	1.57E+08	1.57E+08	2.2	2.0	0.8	transcriptic
NM_01149 Aurka	chr2	1.72E+08	1.72E+08	1.2	0.9	2.6	transcriptic
NM_02915 Spata16	chr3	26535189	26535925	1.5	1.8	0.3	transcriptic
NM_00982 Ccna2	chr3	36472717	36473089	0.0	0.0	1.5	transcriptic
NM_00103 Ankrd50	chr3	38356348	38356812	2.9	2.4	1.1	transcriptic
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	transcriptic
NM_00981 Casp6	chr3	1.3E+08	1.3E+08	1.4	1.1	2.9	transcriptic
NA chr3:12977	chr3	1.3E+08	1.3E+08	2.1	1.8	0.6	CpG Island:
NM_00756 Bmpr1b	chr3	1.42E+08	1.42E+08	4.2	3.9	1.9	transcriptic
NM_02608 170002211:	chr4	42982913	42983347	2.2	2.3	0.8	transcriptic
NM_00109 Msmg	chr4	43598149	43598523	2.2	2.1	0.7	transcriptic
NM_01999 Alg2	chr4	47488672	47489525	2.3	2.1	0.9	transcriptic
NM_00100 Maneal	chr4	1.25E+08	1.25E+08	1.1	1.4	2.9	transcriptic
NA chr4:12926	chr4	1.29E+08	1.29E+08	0.2	1.1	2.7	CpG Island:
NM_02366 D4Wsu53e	chr4	1.34E+08	1.34E+08	0.1	0.2	2.2	transcriptic
NM_02798 Mad2l2	chr4	1.48E+08	1.48E+08	0.9	1.0	2.4	transcriptic
NM_02202 Rbp7	chr4	1.49E+08	1.49E+08	2.4	2.0	0.3	transcriptic
NM_00103 Gm833	chr4	1.52E+08	1.52E+08	2.6	2.0	1.0	transcriptic
NM_01138 Ski	chr4	1.55E+08	1.55E+08	1.3	1.1	3.2	transcriptic
NM_00103 Dhrrsx	chr4_randc	109368	110464	0.2	0.4	1.7	transcriptic
NM_00115 Lnx1	chr5	75074786	75075145	1.9	1.6	0.5	transcriptic
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	transcriptic
NM_00108 Lmtk2	chr5	1.45E+08	1.45E+08	0.8	0.8	1.9	transcriptic
NM_00907 Rpia	chr6	70744414	70745064	2.6	2.5	1.2	transcriptic
NM_15377 Atoh8	chr6	72187182	72187831	2.8	2.4	5.8	transcriptic
NM_00108 Vamp5	chr6	72331874	72332410	1.1	1.3	3.1	transcriptic
NM_00759 Capg	chr6	72494222	72494846	0.7	1.0	2.0	transcriptic
NM_03307 D6Mm5e	chr6	82896481	82896830	3.9	3.4	1.7	transcriptic
NM_00113 Rtkn	chr6	83085941	83086845	2.5	1.4	0.4	transcriptic
NM_00110 2510049J1:	chr6	1.16E+08	1.16E+08	0.0	0.0	1.2	transcriptic
NM_00966 Alox5	chr6	1.16E+08	1.16E+08	1.0	1.0	2.3	transcriptic
NM_01012 Emp1	chr6	1.35E+08	1.35E+08	2.3	2.2	1.0	transcriptic
NM_01065 Sspn	chr6	1.46E+08	1.46E+08	1.7	1.3	0.3	transcriptic
NM_17537 Rdh13	chr7	4396574	4397709	2.4	2.2	0.5	transcriptic
NM_01176 Zim1	chr7	6651662	6652106	0.0	0.0	1.1	transcriptic
NM_01133 Clcn4-2	chr7	7253199	7253628	4.0	4.0	1.5	transcriptic
NM_01998 Tex101	chr7	25457230	25457684	2.9	2.7	1.3	transcriptic
NM_19799 2310044H1	chr7	51753120	51753569	0.9	0.6	2.3	transcriptic
NM_02933 1700026DC	chr7	90943020	90943269	2.4	2.0	0.9	transcriptic
NM_02824 Prcp	chr7	1E+08	1E+08	0.9	0.8	2.2	transcriptic
NM_00977 Bub3	chr7	1.39E+08	1.39E+08	1.1	1.2	2.4	transcriptic
NM_00111 Shank2	chr7	1.51E+08	1.51E+08	1.1	1.1	2.3	transcriptic
NM_17724 D030016E1	chr8	48621288	48621749	0.4	0.3	2.1	transcriptic
NM_01988 Uba52	chr8	73034990	73035432	0.2	0.2	1.2	transcriptic

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 Tbc1	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 Islands:
NA	chr9:88753 chr9	88753512	88754171	0.2	0.0	1.9	CpG Islands:
NA	chr9:88961 chr9	88961199	88961948	0.5	0.0	2.3	CpG Islands:
NA	chr9:96437 chr9	96437157	96437816	0.7	0.7	4.1	CpG Islands:
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 Islands:
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 Islands:

orientation	descriptor	DISSTRIBU	gene_id
+	RIKEN cDN	PROXIMAL	76982
+	phosphatid	INTRAGENI	109294
-	RIKEN cDN	DISTAL	68691
+	transmembr	DISTAL	271711
+	melanophil	DISTAL	171531
+	prolactin r	PROXIMAL	623503
+	RNA bindin	PROXIMAL	329207
+	contactin a	PROXIMAL	241175
+	expressed	DISTAL	212439
-	neurofascin	DISTAL	269116
+	renin 2 tan	PROXIMAL	19702
-	RIKEN cDN	PROXIMAL	71001
+	pleckstrin f	DISTAL	27280
.	0	INTERGENI	0
-	regulator o	DISTAL	19736
-	nitric oxide	DISTAL	70729
-	Fc receptor	PROXIMAL	14130
-	MOCO sulph	PROXIMAL	66112
-	RIKEN cDN	DISTAL	226777
+	peptidylpro	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 gr	PROXIMAL	23795
+	PRP39 pre-	PROXIMAL	328110

+	tRNA meth	DISTAL	328162
-	X-ray repai	INTRAGENI	74335
-	protein pho	DISTAL	21981
-	transmemk	PROXIMAL	104885
+	inverted fo	DISTAL	70435
+	phospholip	DISTAL	104759
-	G protein-c	DISTAL	56696
-	jagged 2	DISTAL	16450
+	cysteine-ric	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
-	chaperonin	DISTAL	12465
-	sterile alph	PROXIMAL	320679
-	transducer	DISTAL	57259
-	centromere	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
+	adenomatc	DISTAL	11789
-	protocadhe	PROXIMAL	75599
-	toll-like rec	PROXIMAL	225471
-	actin bindir	PROXIMAL	319713
-	insulin-like	PROXIMAL	27356
+	ubiquitin-li	DISTAL	109113
+	transmemk	DISTAL	75146
-	calcium ho	DISTAL	546729
-	Sec61, alph	DISTAL	57743
-	proteasom	DISTAL	66998
+	LIM homec	INTRAGENI	16870
-	N-myc (anc	DISTAL	64685
-	methyltran	INTRAGENI	228019
+	methionine	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 segmε DISTAL	27981
+	MAD2 mitc DISTAL	71890
-	retinol binc DISTAL	63954
+	predicted g PROXIMAL	330004
-	ski sarcomε DISTAL	20481
+	dehydrogei PROXIMAL	236082
-	ligand of n DISTAL	16924
+	serine/argi INTRAGENI	58212
+	transferrin PROXIMAL	50765
+	lemur tyroε DISTAL	231876
-	ribose 5-ph DISTAL	19895
-	atonal horr DISTAL	71093
-	vesicle-ass DISTAL	53620
+	capping pro PROXIMAL	12332
+	DNA segmε PROXIMAL	110958
+	rhotekin INTRAGENI	20166
-	RIKEN cDN, DISTAL	70291
-	arachidona PROXIMAL	11689
+	epithelial n DISTAL	13730
+	sarcospan DISTAL	16651
-	retinol deh PROXIMAL	108841
-	zinc finger, DISTAL	22776
-	chloride ch DISTAL	12727
-	testis exprε PROXIMAL	56746
-	RIKEN cDN, DISTAL	69683
-	RIKEN cDN, PROXIMAL	75556
+	prolylcarb 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
-	transformin DISTAL	21376
+	olfactory rε 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 chε 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	Metap1	chr2	71290205	71290560	0.7	0.8	1.9	transcriptic
NM_02563	Metap1	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

orientation	descriptor	DISTRIBU	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 n	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
-	transmemt	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

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Gene ontology analysis for heart.

GO Term	Nr. Genes	Term PVal	Associated Group	Gen	Nr. Genes	-log(P-value)
olfactory b	4	0.010356	[Id2, Lhx2, Apc Aurka		15	1.98482
spindle che	4	0.013919	[Apc, Aurka Aurka		8	1.85638
negative re	3	0.019331	[Apc, Mad2 Fam105b F		4	1.713744
acute inflar	5	0.023555	[Alox5, Cas Apc Jag2 F		3	1.627922
intrinsic ap	3	0.042839	[Phlda3, Pp Alox5 Cas		9	1.368157
regulation	4	0.04348	[Apc, Aurka Ablim3 Ap		44	1.36171
negative re	4	0.043895	[Fam105b, Igfbp1 Ma		9	1.357585
negative re	5	0.048248	[Ppp1r9b, F 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-2C	0.056698	4.61217	M1		Rbms3,Bub3,Uhrf2,Samd12,Zfp62:	
2	transfac_pi	0.056388	4.57505	M2	Foxo1,Foxg	Prex2,Igfbp1,Atoh8,Shank2,Sspn,N	
3	flyfactorsui	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-UM	0.049508	3.75218	M2	Sdk2,Msm	p,D4Wsu53e,Phlda3,Nnr	
6	encode-UM	0.048597	3.64329	M2		3110035E14Rik,Msgn1,Atoh8,Scn1	
7	transfac_pi	0.048566	3.63958	M2	Foxo3,Foxl:	Atoh8,Sspn,Nfasc,Prex2,Mosc1,Ha	
8	transfac_pi	0.048504	3.63216	M5	Rest	Krt86,Tmem179,Nfasc,Cntnap5b,C	
9	homer-MO	0.047521	3.5146	M3	Neurod1,Ti	Defb47,Atoh8,Lnx1,Psmd5,493144	
10	homer-MO	0.047387	3.49852	M2	Tcf7,Lef1,T	Prex2,1110028C15Rik,Shank2,Atol	
11	encode-UM	0.046735	3.42056	M2		Mcm8,3110035E14Rik,Rbms3,Sspr	
12	hdpi-ZNF23	0.046693	3.41561	M3	Zbtb18	Nrgn,Nmi,Krt86,Atoh8,Cilp,Bmpr1	
13	taipale-RTC	0.045845	3.31414	M6	Hic2	Agr2,Msm	p,Atp6v1e2,Prlh,Tmem1
14	transfac_pi	0.045183	3.23495	M3	Tcf3,Myf6,	Ablim3,Atoh8,Lnx1,Nos1ap,Tmprs:	
15	yetfasco-7C	0.044986	3.21144	M6		Nrgn,Atp6v1e2,Socs2,Uhrf2,Fam1(
16	taipale-NC	0.044738	3.18174	M6	Ets1,Ets2,E	D030016E14Rik,Bmpr1b,Msm	
17	swissregulc	0.0442	3.1174	M2	Bptf,Pou5f:	Rbms3,Prex2,Nos1ap,Sspn,Shank2	
18	transfac_pi	0.044148	3.11121	M4	Hsf1,Hsf4,	F Cct5,Fcgr2b,Socs2,Hand1,Sdk2,11:	
19	encode-UM	0.044127	3.10874	M5		Cntnap5b,Atoh8,Tbcel,Rbms3,Msg	
20	stark-MAT1	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,Msm	
23	hdpi-OLIG1	0.043641	3.05058	M3	Olig1	Defb47,Krt86,Sspn,Nrgn,Psmd5,Nc	

24	transfac_pi	0.04361	3.04687	M2	Foxa3,Foxa	Uhrf2,Sspn,Prex2,Atoh8,1110028C
25	transfac_pi	0.043476	3.03078	M9	E2f1	Rnf167,Mcm8,Bub3,Uhrf2,Socs2,C
26	yetfasco-62	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,Atol

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2,Cct5,Ppp1r9b,Socs2,Rpia,Sdk2,Id2,Apc,Vamp5
 Ifasc,Nos1ap,1110028C15Rik,Rbms3,Emp1
 .Cilp,Msmg,Nfasc
 sbpl7,Sdk2,Uhrf2,Mad2l2,4931440L10Rik,Prlh,Prpf39,Lnx1,Atp6v1e2,Msmg,Atoh8
 ri,Rbms3,Agr2,Gm833
 LOa,Prpc,Sdk2,Cnp,Nos1ap,Alg2,Rbms3,Uhrf2,Trmt61a
 nd1,Nmi,Emp1,Uhrf2,1110028C15Rik,Igfbp1
 im833,Calhm1,Tmprss4,Pla2g12a,Nos1ap,Rbms3
 l0L10Rik,Atp6v1e2,Krt86,Nrgn,Ablim3,Agr2,Nmi,Fcgr2b,Phlda3,Cilp,Calhm1,Emp1,AU023871,Apc,Msgn1
 h8,Mcm8,Igfbp1,Sspn,Rbms3,Agr2
 n,Atoh8,Shank2,Prex2,Cnp
 b,Atp6v1e2,Sspn,Fcgr2b,Prlh,Defb47,Mad2l2,Alg2,Lnx1,Msmg
 l80,Nrgn,Osopl7,Rai1
 s4,Cnp,Nrgn,Tmem180,Nmi,Mad2l2
 05a,Rtkn,Trmt61a,Ppp1r9b,Pxk,Cenpm,Abcd3,Ppp1r13b,Gm833,Aurka,Capg,Tmem179,Lnx1,Agr2,Uba52
 rf167,Fam18b,Mcrs1,Prex2,Acaa1b,Apc,Uhrf2,Ppp1r9b,Socs2,4931440L10Rik,Tmem180,Arl1,Ccdc69,Rbr
 ;,Tbcel,1110028C15Rik,Igfbp1,Emp1,Bmpr1b,Nfasc
 10028C15Rik
 gn1,Msmg,Uhrf2,Bmpr1b
),Lnx1,3110035E14Rik,Rbms3,Bmpr1b,4922505G16Rik,1110028C15Rik,Sspn,Msgn1,Krt86,Prex2,Olf982,
 Prex2,Msgn1,3110035E14Rik,Defb47,Emp1,Aurka,Cnp,Tmprss4,Rtkn,Fcgr2b,Hand1,Prpf39,Igfbp1
 h8,Fcgr2b,1110028C15Rik,Krt86
 os1ap,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

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L,Mosc1,Osbp17,Cnp,Ccdc69,Nfasc,Hand1,Bmpr1b,Igfbp1,Shank2,Mad2l2,Sspn,Msmg, Gm833,Rbp7,Olfml5

l,Apc,Tmem180,Fam105b,Krt86,Fam18b,Tob2,Tbcel,Rbms3, Samd12,Inf2,1700026D08Rik,Atoh8,Zfp622, Ns3,Atp6v1e2,Mcm8,Nos1ap,Cep97,Tmem179,Cops3,Tob2,Eif3g,Prpc,Cpsf6,Mad2l2,Zim1,Trmt61a,111C

,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:

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82,2510049J12Rik,Afg3l1

Nfasc,Cnp,Cops3,Galnt6,Prpc,Ski,Sspn,Rnf167,Msmg,D030016E14Rik,Mlph
D028C15Rik,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

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2,Ablim3,Tmem180,Alox5

Differentially methylated regions found in spleen.

ACC	Name	chr	start	end	BSpIS	BcSpIS	MSpIS	feature DI
NM_15340	Neur13	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_026924	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	C03004610	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_003293	D030028A0	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	chr12:3559	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	transcripti	
NM_14597 Pdlim2	chr14	70576631	70577300	2.5	3.0	1.1	transcripti	
NM_00101 Fam105b	chr15	27562080	27562932	0.7	0.7	1.7	transcripti	
NM_14605 Dap	chr15	31152069	31152423	2.1	2.3	0.9	transcripti	
NM_00763 Cct5	chr15	31532950	31533392	0.6	0.7	2.0	transcripti	
NA	chr15:3706	chr15	37065155	37065724	1.8	2.9	0.5	CpG Island:
NM_02049 Ly6i	chr15	74816146	74816688	0.5	0.5	1.6	transcripti	
NM_00114 BC024139	chr15	75958253	75958802	1.9	2.2	0.9	transcripti	
NM_02050 Tob2	chr15	81690041	81691672	0.0	0.0	1.1	transcripti	
NM_02807 Tnfrsf13c	chr15	82056471	82057120	3.2	4.8	1.6	transcripti	
NM_00111 Tcf20	chr15	82742448	82743905	2.7	2.9	1.0	transcripti	
NM_01345 Acr	chr15	89398905	89399458	1.9	2.2	0.9	transcripti	
NM_01676 Mcrs1	chr15	99081644	99081893	1.3	1.1	0.0	transcripti	
NM_02306 Lima1	chr15	99651840	99653407	1.5	1.5	0.5	transcripti	
NM_01066 Krt86	chr15	1.01E+08	1.01E+08	0.3	0.5	1.7	Primary Tra	
NM_02639 Nmr1	chr16	4719145	4719399	0.6	0.0	1.7	transcripti	
NM_17251 Abhd10	chr16	45744899	45745784	0.9	0.5	2.3	transcripti	
NM_05410 2310034C0	chr16	88757863	88758407	0.5	0.4	2.1	transcripti	
NM_01370 Krtap14	chr16	88825671	88826015	1.2	1.6	3.3	transcripti	
NM_02862 Krtap16-7	chr16	89403487	89403731	0.9	0.9	2.2	transcripti	
NA	chr17:1567	chr17	15673304	15673974	0.1	0.1	2.0	CpG Island:
NM_02147 Tulp1	chr17	28501806	28502185	2.8	4.8	1.0	transcripti	
NM_08072 Tmprss3	chr17	31336679	31337333	1.6	2.0	0.5	transcripti	
NM_01358 Psmb9	chr17	34326735	34327079	2.0	1.9	0.9	transcripti	
NM_03074 Btnl6	chr17	34654459	34654708	2.1	1.9	0.7	transcripti	
NM_14548 Prr3	chr17	36117975	36118234	1.9	2.0	0.8	transcripti	
NM_02288 Slc29a1	chr17	45730227	45730851	2.5	3.0	1.2	transcripti	
NM_01172 Xdh	chr17	74299291	74299955	2.7	2.1	0.9	transcripti	
NM_02912 Atp6v1e2	chr17	87348541	87349395	2.6	3.6	1.2	transcripti	
NM_17262 Ino80c	chr18	24281882	24282837	2.8	2.9	1.3	transcripti	
NM_02417 06100090z	chr18	38407099	38408435	2.4	2.2	0.9	transcripti	
NM_19435 Spire1	chr18	67713103	67714060	1.0	0.5	2.6	transcripti	
NA	chr19:4367	chr19	43675168	43676408	2.7	2.7	1.0	CpG Island:
NA	chr19:4513	chr19	45139820	45140264	1.4	1.8	0.1	CpG Island:
NM_00108 Calhm1	chr19	47220974	47221648	1.5	0.8	3.4	transcripti	
NA	chr19:4722	chr19	47225972	47226621	3.8	3.1	1.6	CpG Island:
NM_02661 Gsto2	chr19	47938883	47939327	1.1	1.1	2.6	transcripti	
NM_02823 Ttc30b	chr2	75775796	75777551	0.5	0.5	1.8	transcripti	
NM_00103 Cstf3	chr2	1.04E+08	1.04E+08	0.9	1.1	2.3	transcripti	
NM_17730 Lrrn4	chr2	1.33E+08	1.33E+08	3.3	4.0	1.3	transcripti	
NM_17765 Cstl1	chr2	1.49E+08	1.49E+08	1.8	1.7	0.7	transcripti	
NM_19435 Rya3	chr2	1.54E+08	1.54E+08	2.4	2.8	1.1	transcripti	
NM_14489 BC018465	chr2	1.54E+08	1.54E+08	1.9	2.7	0.7	transcripti	
NM_00103 4922505G1	chr2	1.57E+08	1.57E+08	1.5	1.6	0.4	transcripti	
NM_02696 Manbal	chr2	1.57E+08	1.57E+08	2.4	2.1	0.9	transcripti	
NM_01149 Aurka	chr2	1.72E+08	1.72E+08	0.8	1.0	2.0	transcripti	
NM_02915 Spata16	chr3	26535189	26535925	1.8	2.1	0.4	transcripti	
NM_00111 Fxr1	chr3	33917468	33917962	0.2	0.3	1.3	transcripti	
NM_00762 Ccna1	chr3	54859447	54859691	0.3	0.6	1.6	transcripti	
NM_02319 Pla2g12a	chr3	1.3E+08	1.3E+08	2.6	3.2	1.1	transcripti	

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 B3galt1	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 Cdy12	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	Olf877	chr9	37661972	37662731	1.6	1.5	0.5	transcriptic
NM_14685	Olf982	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

descriptor DISTRIBU' 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 rε	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
peptidylprc	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 r	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-lil DISTAL	56471
PDZ and LIF INTRAGENI	213019
family with DISTAL	432940
death-asso DISTAL	223453
chaperonin DISTAL	12465
0 INTERGENI	0
lymphocyte DISTAL	57248
cDNA sequ DISTAL	271278
transducer DISTAL	57259
tumor necr DISTAL	72049
transcriptic PROXIMAL	21411
acrosin pre INTRAGENI	11434
microspher INTRAGENI	51812
LIM domaii DISTAL	65970
keratin 86 INTRAGENI	16679
NmrA-like 1 PROXIMAL	67824
abhydrolas DISTAL	213012
RIKEN cDN. DISTAL	117172
keratin assi INTRAGENI	23927
keratin assi INTRAGENI	170656
0 INTERGENI	0
tubby like ζ PROXIMAL	22157
transmemk DISTAL	140765
proteasom DISTAL	16912
butyrophili PROXIMAL	624681
proline-rich DISTAL	75210
solute carri DISTAL	63959
xanthine dε PROXIMAL	22436
ATPase, H+ DISTAL	74915
INO80 com DISTAL	225280
RIKEN cDN. DISTAL	66839
spire homc 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 rich DISTAL	320974
cystatin-lik PROXIMAL	228756
antimicrob DISTAL	378700
cDNA sequ PROXIMAL	228802
RIKEN cDN. DISTAL	629499
mannosida DISTAL	69161
aurora kinε DISTAL	20878
spermatog DISTAL	70862
fragile X mε DISTAL	14359
cyclin A1 PROXIMAL	12427
phospholip PROXIMAL	66350



urate oxida	DISTAL	22262
glucosamin	PROXIMAL	50798
epidermal	┘DISTAL	13858
mannosida	DISTAL	215090
0	INTERGENI	0
compleme	PROXIMAL	12260
dolichyl-di-	DISTAL	13200
transmemt	DISTAL	214359
tumor necr	DISTAL	21941
F-box prote	DISTAL	230903
spermidine	DISTAL	20810
retinol binc	DISTAL	63954
nephronop	INTRAGENI	260305
ski sarcom	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
carcinoem	INTRAGENI	66996
translocase	DISTAL	53333
F-box prote	INTRAGENI	50760
zinc finger	┘DISTAL	70227
0	INTERGENI	0
interleukin	INTRAGENI	16170
tripartite r	DISTAL	330627
protease, s	PROXIMAL	76560
steroidoge	PROXIMAL	20845
RIKEN cDN.	DISTAL	320714
homer hon	DISTAL	26558
CREB regul.	PROXIMAL	382056
gene trap l	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
transformir DISTAL	21376
olfactory rε PROXIMAL	258412
olfactory rε PROXIMAL	258853
PDZ domaii DISTAL	170761
tetratricop DISTAL	192653
transmemk 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 alç PROXIMAL	104099
deleted in I DISTAL	320256
sodium chε DISTAL	20264
golgi reassε DISTAL	74498
cysteine-se PROXIMAL	215418
0 INTERGENI	0
lysozyme-li INTRAGENI	69032
DNA segmε PROXIMAL	574405



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

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

orientation	descriptor	DISTRIBU	gene_id	gene_id	transcript_	BSpIS	SE_EXPRS	BsSpIS
-	aldo-keto r	PROXIMAL	56043	56043	BC012692	538.4099	0.9403	536.3072
+	capping pro	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 prote	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 1	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_00110	198.4316	0.8594	170.0955
+	serine (or c	DISTAL	20716	20716	BC013651	3328.975	0.9732	3102.373

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SE_EXPRS	MSPIS	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.

GO Term Nr. Genes Term PVal Associated Group Gen Nr. Genes i -log(P-value)

photorecept	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_pi	0.053127	4.33429	M1		Il16,Xdh,Sept9,Slc9a9,Krt86,Tmprs
2	jaspar-POLI	0.051764	4.17574	M2		BC018465,Calhm1,Xdh,Pdlim2,Neu
3	encode-UM	0.050362	4.01259	M2		Atp6v1e2,Trim66,BC018465,Nos1:
4	tfdimers-M	0.049948	3.96434	M2	Mafa,Nr3c:	Il16,Stmn4,Agr2,Tmprss4,Pdlim2,C
5	jaspar-PF01	0.049207	3.87817	M3	Rest	Krt86,Crip2,Rbms3,Pxk,BC018465,
6	transfac_pi	0.048901	3.84255	M4	Zeb1	Trim66,Prr3,Nos1ap,Ttc36,Tmprss
7	jaspar-CNO	0.048862	3.83796	M5	Rfx1,Rfx2,R	Cops3,Prr3,Trim66,Rundc1,BC024:
8	hdpi-SPR	0.048822	3.83336	M6	Spr,Spr-ps1	Rbms3,Pdzd3,Tcf20,Ttc36,Calhm1,
9	transfac_pi	0.048704	3.81958	M1	Jdp2,Bach1	Pdlim2,Sept9,Krt86,Zc3h12d,Stmn
10	yetfasco-84	0.048704	3.81958	M1	Jdp2,Bach1	Pdlim2,Sept9,Krt86,Zc3h12d,Stmn
11	elemento-C	0.048348	3.77821	M4		Trim66,Il16,Nos1ap,Fzd5,Prr3,Tcf2
12	taipale-GTA	0.048338	3.77707	M7	Foxo3,Foxc	Uox,Fam105b,Slc29a1,Ly6i,Tob2,2
13	jaspar-MAC	0.048032	3.74145	M1	Jdp2,Bach1	Pdlim2,Sept9,Krt86,Stmn4,Zc3h12
14	jaspar-CNO	0.047865	3.72192	M5	Rfx1,Rfx5,R	Cops3,Prr3,Trim66,Rundc1,Ccna1,l
15	taipale-NG	0.047825	3.71732	M5	Rfx5,Rfx1,R	Prr3,Rundc1,Trim66,Cops3,Ccna1,l
16	yetfasco-17	0.047262	3.65183	M1	Mybl2,Myk	Stmn4,Aurka,Xdh,Pdlim2,Zc3h12d,
17	taipale-NG	0.046561	3.57026	M5	Rfx3,Rfx1,R	Prr3,Rundc1,Trim66,Ccna1,Cops3
18	jaspar-CNO	0.046453	3.55762	M5	Rfx3,Rfx4,R	Cops3,Nphp4,Prr3,BC024139,Trim
19	taipale-SGT	0.046216	3.53005	M5	Rfx5,Rfx1,R	Prr3,Rundc1,Trim66,Cops3,Ccna1,l
20	taipale-NA	0.046137	3.52086	M1	Nfe2,Bach1	Pdlim2,Sept9,Zc3h12d,Abcc3,Tnfrs
21	transfac_pi	0.045673	3.46686	M8	Nfic,Nfia,N	BC018465,Agr2,Stmn4,B3galtl,Rbn
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,R	Prr3,Trim66,Rundc1,Cops3,Ccna1,l
24	taipale-NG	0.044755	3.36001	M5	Rfx2,Rfx1,R	Prr3,Trim66,Rundc1,Cops3,Ccna1,l
25	yetfasco-20	0.044261	3.30257	M1	Bach2,Jdp2	Il16,Pdlim2,Tnfrsf8,Krt86,Sept9,Str
26	hdpi-C2orf1	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-UM	0.044044	3.27729	M2		Msgn1,Pkd1l2,Rundc1,Neurl3,Eps1



29	taipale-NN	0.044044	3.27729	M4	Tcf4,Tcf3,Li
30	elemento-C	0.043649	3.23133	M6	Trim66,Pdlim2,Prlh,Tmprss4,Zc3h1
31	transfac_pi	0.043224	3.18193	M9	Gpbar1,Rbms3,Nav1,Cstl1,Star,Trin
32	yetfasco-4	0.043224	3.18193	M9	Vsx1,Lbx2,Krtap14,Sspn,Stmn4,Atp6v1e2,Mc
33	jaspar-PFO	0.043086	3.16585	M9	Vsx1,Lbx2,Krtap14,Sspn,Stmn4,Atp6v1e2,Mc
34	transfac_pi	0.042997	3.15551	M2	Vsx1,Alx1,Krtap14,Sspn,Neur13,Tmprss3,Msg
35	jaspar-MAC	0.042948	3.14976	M8	Neurod1,N Cilp,Trim66,Zc3h12d,Rundc1,Guk1
36	encode-UM	0.042839	3.13712	M2	Rbms3,Pdzd3,Tnfrsf13c,Sept9,Cilp,
37	hdpi-TRIM	0.04276	3.12793	M3	Tmprss3,Sspn,Krtap14,Pdzd3,Slc2
38	homer-MO	0.04276	3.12793	M5	Trim21 Rbms3,Gpbar1,Tnfrsf13c,BC01846
39	encode-UM	0.042711	3.12219	M2	Rfx3,Rfx1,Rundc1,Prr3,Ccna1,Cops3,Trim66,
40	yetfasco-5	0.042711	3.12219	M8	Rbms3,Stmn4,1700084C01Rik,Xdh
41	encode-UM	0.042602	3.10955	M8	Rbms3,Pdzd3,Tnfrsf13c,Sept9,Cilp,
42	homer-MO	0.042395	3.08542	M5	Pdzd3,Slc29a1,1700084C01Rik,BC
43	taipale-ATC	0.042089	3.04981	M1	Rfx1,Rfx2,R Ccna1,Prr3,Cops3,Rundc1,Trim66,
44	jaspar-CNO	0.04198	3.03717	M10	Bach1,Jdp2 Pdlim2,Sept9,Krt86,Abcc3,Tnfrsf8,
45	yetfasco-1	0.04196	3.03487	M5	Cdyl2,Cilp,Slc9a9,Rundc1,Atp6v1e
46	elemento-	0.041862	3.02338	M4	Rfx2,Rfx3,Rundc1,Prr3,Cops3,Nphp4,Trim66,
47	taipale-NG	0.041842	3.02108	M5	Prr3,Trim66,Tcf20,Tmem51,Krt86,
					Rfx4,Rfx1,Prr3,Trim66,Rundc1,Cops3,Ccna1,

is4,Pdlim2,Tnfrsf8,Stmn4,Olf877,Abcc3,Nt5c1b,Star,Agr2
 Nr1h3,Trim66,Slc29a1,Ill16,Stmn4,Capn9,Prlh,C1qb,Olf877,Rbms3,Slc9a9,Sspn,Gpbar1,Lrrn4,Tnfrsf13c,Zc3
 hap,Xdh,1700084C01Rik,Star,Pxk,Pdzd3,Krtap16-7,Slc9a9,Prlh,Neurl3,Stmn4,Slc29a1,Nlrp3,Tmprss4,Sept9,
 Cilp,Trim66,Gpbar1,Slc9a9,Ceacam11,Abcc3,Prlh,Olf982,Xdh,Tcf20,Tmprss3
 Prr3,Srd5a3,Nos1ap,Gtl3,Xdh,Fbxo44,Agr2,Tmprss3,Grin2c,Rgs4,Pla2g12a,Reep3,Ceacam11,Eps15,Tmpr
 4,Ill16,Atp6v1g3,Msgn1,Nlrp3,Pdlim2,Tcf20
 139,Eps15,Ccna1,Nt5c1b,Nphp4,1700084C01Rik,Crip2
 ,Tnfrsf13c,BC024139,Trim66,Sept9,Rya3
 4,Krtap14,Ill16,BC018465,Nos1ap,Xdh,Abcc3,Agr2,Tmprss4,Tnfrsf8
 4,Krtap14,Ill16,BC018465,Nos1ap,Xdh,Abcc3,Agr2,Tmprss4,Tnfrsf8
 10,Tmprss4,Pdlim2,Pkd1l2,Pla2g12a,Psm9
 310034C09Rik,Nol7,Nt5c1b
 d,Krtap14,Ill16,BC018465,Xdh,Nos1ap,Abcc3,Tnfrsf8,Tmprss4,Agr2
 Eps15,Nt5c1b,Nphp4,BC024139,Crip2,Gtl3,1700084C01Rik
 Nphp4,Eps15,Crip2,Gtl3,Nt5c1b
 ,Sept9,Olf877,Itga9,Lima1,Slc29a1,Slc9a9,Acr

66,Rundc1,Ccna1,Nt5c1b,Eps15,Gtl3,Crip2
 Eps15,Nphp4,Crip2,Gtl3,Nt5c1b
 sf8,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,Slc29a
 ,Mcrs1,BC018465,Rbms3,Gpbar1,Srm,Trim66
 6,Ttc36,Sept9,BC024139,Rya3,Tnfrsf13c
 15,Fzd5,Sspn,Nos1ap,Slc9a9,Rbms3,Capn9,Ttc36

l2d,Il16,Xdh,Slc29a1,Msgn1,Csrnp1,Calhm1,Nos1ap
m66,Tmprss3,Calhm1,Tcf20,Sept9,Slc29a1,Lyzl4,1110028C15Rik,Prss8,Prr3,Lima1,Igfbp1,Atp6v1g3,Tob2
rs1,Krt86,Neurl3,Nav1,Eps15,Ttc36,Cstf3,Msgn1,Rundc1,Tmprss3,Aplp2
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;n1,Stmn4,Aplp2,Ttc36,Rundc1,Manbal,Nav1,Mcrs1
,Msgn1,Stmn4,Slc29a1,Krt86,B3galtl,Il16,Igfbp1,Star,Tnfrsf13c,Calhm1,Pdlim2,Olf982,Gpbar1,Pabpn1l,
,Gpbar1
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5,Calhm1,Neurl3,Prss8,Stmn4,Sept9,Lrrn4
Nphp4,Eps15,Gtl3,BC024139,Crip2,Nt5c1b,1700084C01Rik,Mcrs1
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,Gpbar1
018465,Rbms3,B3galtl,Gsto2,Rya3,Calhm1,Msgn1,Neurl3,Xdh,Sept9,Nop14,Stmn4,Capn9,Prr3,Sspn,Serf
Eps15,BC024139,Gtl3,Crip2,Stmn4,Nphp4
Zc3h12d,Gsto2,Il16,Krtap14,Agr2
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,Ccna1,Crip2,Mcrs1,Gtl3,Eps15,BC024139,1700084C01Rik,Krt86,Ttc36,Pdzd3,Xdh,Pxk,Tmprss4,Aurka,Tn
Pla2g12a,Pdlim2,Nos1ap,Rbms3
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9,Capn9,Ttc36,Ttc30b,Rbms3,Zc3h12d,Nt5c1b,Sspn,Olf877,4922505G16Rik,Calhm1,Lrrn4,Csrnp1,I16,D
rss4,Lima1,Neurl3,Zfp619,Cstf3,Nop14,Tnfrsf13c,Nol7,Aplp2,Stmn4,Homer3,Pdzd3,Ttc30b,Itga9,Sept9,B

1,Atp6v1e2,Slc9a9,Pdzd3,Tob2,Prr3,Tomm40,Csrnp1,4922505G16Rik,Ceacam11,Lima1,Nos1ap,Olf877

!,Nol7,Csrnp1,Aplp2,Capn9

Rbms3,Prlh,Pdzd3,Nos1ap,Tmprss3,Pkd1l2,Sept9,Lrrn4,Neurl3,Tcf20,Capn9,Rgs4,C1qb,Nlrp3,Manbal,Ssi

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

ina3n,H1foo,Aplp2,Ttc36,Srm,Rgs4,Lima1

frsf13c,Cml3,Atp6v1g3,BC018465,Uox,Aplp2,Pkd1l2,Slc29a1,Capn9,Abcc3,Pabpn1l

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dost,Fzd5,Prr3,Gpbar1,Acr,Cilp,Tcf20,Uox

tnl6,Manbal,Tbrg1

,Star,Olf982,Rgs4,Pkd1l2,Trim66,Pla2g12a,Gne,Nlrp3,Atp6v1g3,Itga9,Srd5a3,Rasl11a,Nt5c1b,Calhm1,Ai

pn,Eps15,Ttc36,BC018465,Rya3,Slc9a9,Ccna1,Cml3,Acr,Rasl11a,Ceacam11,Prr3,Csrnp1

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rl1,Cml3,Tmem51,Manbal,Fam18b,Rbp7,Rya3,Cnga3