Gene Expression Profiling Analysis Reveals Fur Development in Rex Rabbits (*Oryctolagus cuniculus*)

Journal:	<i>Genome</i>
Manuscript ID	gen-2017-0003.R2
Manuscript Type:	Article
Date Submitted by the Author:	31-Jul-2017
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Is the invited manuscript for consideration in a Special Issue? :	This submission is not invited
Keyword:	Chinchilla rex rabbit, fur development, key gene, transcriptome

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Manuscripts

1 **Gene Expression Profiling Analysis Reveals Fur Development in Rex**

2 **Rabbits (*Oryctolagus cuniculus*)**

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10

Draft

11 Abstract

12 Fur is an important economic trait in rabbits. The identification of genes that
13 influence fur development and knowledge regarding the actions of these genes
14 provides useful tools for improving fur quality. However, the mechanism of fur
15 development is unclear. To obtain candidate genes related to fur development, the
16 transcriptomes of tissues from backs and bellies of Chinchilla rex rabbits were
17 compared. Of the genes analyzed, 336 showed altered expression in the two groups
18 (285 upregulated and 51 downregulated), $P \leq 0.05$, fold-change ≥ 2 or ≤ 0.5). Using GO
19 and KEGG to obtain gene classes that were differentially enriched, we found several
20 genes to be involved in many important biological processes. In addition, we
21 identified several signaling pathways involved in fur development, including the Wnt
22 and MAPK signaling pathways, revealing mechanisms of skin and hair follicle
23 development, and epidermal cell and keratinocytes differentiation. The obtained rabbit
24 transcriptome and differentially expressed gene profiling data provided
25 comprehensive gene expression information for SFRP2, FRZB, CACNG1, SLC25A4
26 and SLC16A3. To validate the RNA-seq data, the expression levels of eight
27 differentially expressed genes involved in fur development were confirmed by
28 qRT-PCR. The results of rabbit transcriptomic profiling provide a basis for
29 understanding the molecular mechanisms of fur development.

30 Keywords

31 Chinchilla rex rabbit, fur development, key gene, transcriptome

32

33 **Introduction**

34 The Chinchilla rex rabbit is an important rabbit breed with varied natural coat
35 colors; consumers highly appreciate the properties of rex furs, such as beauty, softness,
36 color, lightness, and warmth retention (Pan et al. 2015). The characteristics of
37 Chinchilla rex rabbit fur differs between the back and belly, especially the length and
38 diameter of the wools (Tao 2010).

39 In recent years, many studies have revealed the mechanisms of skin and fur
40 development. RNA-seq was used to explore the mechanisms of keratinocyte
41 development in mouse skin, and transcription factor (TF) p63 was found to be highly
42 expressed in stratified epithelia, which affected the epidermal phenotype (Rizzo et al.
43 2014). Many genes involved in skin development, including those for transcription
44 factors and growth factors, have been identified in rex rabbits with the plaice
45 phenotype (Pan et al. 2015). In cashmere goats, genes related to hair follicle
46 development and cycling were identified in anagen, catagen and telogen stages by
47 transcriptomic investigation of fur development (Geng et al. 2013). It is generally
48 known that fur development is influenced by many factors, including the proliferation
49 of keratinocytes, development of the epidermis and hair follicle (HF) morphogenesis
50 (Danilenko et al. 1995). Multiple genes involved in HF morphogenesis, regulation of
51 proliferation, differentiation and migration of skin are controlled by members of the
52 Wnt signaling pathway, such as the frizzled and secreted frizzled-related protein
53 (SFRP) families (Ehrlund et al. 2013; Kim and Yoon 2014). Epidermal growth factor
54 is regulated by the MAPK/ERK pathway and plays a vital role in the animal skin

development, enhancing epidermal growth and keratinization, directly stimulating the proliferation of epidermal cells and promoting keratinocyte proliferation and migration. However, fur characteristics are different at different parts of an animal, and the mechanism of fur development regulation is still unclear in rabbits.

Rabbit genome sequencing has been used to study the polygene-related phenotypic changes during rabbit domestication (Carneiro et al. 2014) and differential gene expression in animal skin between anagen and telogen was shown by transcriptome sequencing (Xu et al. 2013). In this study, the skin from the backs and bellies of Chinchilla rex rabbits was collected, and gene expression profiling was used to obtain the differentially expressed genes related to the fur development. After functional annotation, enrichment analysis and assessment of biological functions, candidate genes were identified. These key genes were verified by quantitative real-time PCR. The results obtained serve to improve our understanding of fur development and the differential expression profiles of the candidate genes enable us to clarify the mechanisms of fur development, providing a valuable theoretical basis for further research on the hair and fur of animals.

Materials and methods

Ethics statement

All animal experiments were reviewed and approved by the Institutional Animal Care and Use Committee of the School of Animal Science and Technology, Yangzhou University, and performed in accordance with the Regulations for the Administration

of Affairs Concerning Experimental Animals (China, 1988) and the Standards for the administration of experimental practices (Jiangsu, China, 2008). All surgery was performed according to recommendations proposed by the European Commission (1997), and all efforts were made to minimize suffering of the animals.

Tissue collection

The Chinchilla rex rabbits used in the experiments were obtained from Zhejiang Yuyao Xinnong Rabbit Co., Ltd. During our experiments, rabbits were raised in a controlled environment and had free access to water and food. All rabbits were housed in a suitable, clean and disease free environment, and a secure cage. The health of the rabbits were monitored twice a day (7 am and 6 pm) and recorded. Three healthy, 20-day-old rabbits with the same fur traits were evaluated. Fur on the back (B group) and belly (F group) were different. Three biological samples were taken for each of the two groups (one sample of back and belly fur from each rabbit) to ensure the same genetic background and fur phenotype in each group. After transfer to the laboratory, skin tissue samples (1.5 cm²) were collected from the back and belly of each rabbit. Animals were anesthetized with by injection with 0.7% sodium pentobarbital solution into the ear vein of the rabbits; in order to prevent bacterial infection iodine solution was smeared on the resultant lesion. Fur was removed from the surface, and then the skin was cut into pieces. The pieces were placed in tubes containing RNase, immediately preserved in liquid nitrogen and stored at -70°C until use in subsequent experiments.

RNA extraction, cDNA library construction, and Illumina sequencing

99 Total RNA was extracted following the manufacturer's instructions using the
100 mirVana™ miRNA isolation kit (Ambion); the integrity of the RNA was determined
101 with an Agilent Bioanalyzer 2100 (Agilent technologies, Santa Clara, CA, US) to
102 obtain a RNA Integrity Number (RIN). An RNeasy micro kit (Cat#74004, QIAGEN,
103 GmbH, Germany) was used to further purify the qualified total RNA, and DNA was
104 removed with the RNase-Free DNase set (QIAGEN, GmbH, Germany). RNA quality
105 was monitored using NanoDrop ND-1000 and Agilent Bioanalyzer 2100. After RNA
106 extraction and purification, 3 µg RNA was used for construction of the back and belly
107 cDNA libraries. Ribosomal RNA (rRNA) was depleted from the total RNA and the
108 remaining RNA was subsequently fragmented. These steps were followed by first and
109 second cDNA strand synthesis, end repair, 3'-end adenylation, adapter ligation, and
110 enrichment of the cDNA templates. Finally, the library concentration was determined
111 using a Qubit® 2.0 fluorometer and a Qubit™ dsDNA HS kit (Invitrogen). Cluster
112 generation was completed the sample library, and the first primers hybridized to cBot
113 matched the Illumina HiSeq 2500 platform. After cluster generation, the sequencing
114 reagent was prepared according to the HiSeq 2500 user guide using paired-end
115 technology. Sequencing was controlled by data collection software (Illumina, San
116 Francisco, USA) and the data were analyzed in real time.

117 **Transcriptome mapping and analysis of differentially expressed genes**

118 The cDNA library was sequenced using an Illumina HiSeq 2500 sequencing
119 platform. Original image files were obtained, and bases were called and filtered, after
120 which the results were stored in fastq format. The original sequencing reads were used

121 for transcriptome sequencing analysis. As the raw reads contained sequences of low
122 quality, clean reads were obtained using fastx (version: 0.0.13), which included the
123 removal of low-quality sequence fragments, 3' end bases that were 10 below the
124 quality score of Q=10 ($Q = -10\log^{\text{error_ratio}}$), adapter sequences, reads containing runs of
125 N's blurs, and any sequences shorter than 20 nucleotides with low overall quality. We
126 then used the TopHat algorithm (version:2.0.9) (Trapnell et al. 2009) to map the clean
127 reads to the *Oryctolagus cuniculus* genome by spliced mapping, allowing two bases
128 of mispairing and multiple hits less than or equal to two, according to Ensembl
129 OryCun2.0. Gene expression was quantified using Cufflinks (version:2.1.1) (Trapnell
130 et al. 2010). Additionally, the fragments per kilobase of exon model per million
131 mapped reads (FPKM) were defined as follows:

$$\text{FPKM} = \frac{\text{transcript reads}}{\text{transcript length} \times \text{total mapped reads in run}} \times 10^9$$

132 The fold-change and Fisher-test were used to analyze the differentially expressed
133 genes that were selected with a false discovery rate (FDR) of less than 0.05 and a
134 fold-change greater than or equal to 2 or less than or equal to 0.5.

135 **Gene annotation and network analysis**

136 The differentially expressed genes obtained from the two skin types were used for
137 functional annotation and mapped to Gene Ontology (GO; www.geneontology.org/)
138 terms and Kyoto Encyclopedia of Genes and Genomes (KEGG;
139 www.genome.jp/kegg/) pathways to identify pathways potentially associated with
140 skin development. P values less than or equal to 0.05 and FDR less than or equal to
141 0.05 were considered statistically significant. After comparing the hypergeometrics

142 with the background of the genome, we screened the GO terms looking for significant
143 enrichment of the differentially expressed genes. P values correspond to differential
144 gene expression after Bonferroni correction, and corrected P values less than or equal
145 to 0.05 were the threshold for significance of differences in gene expression. The
146 STRING database was used to perform network analysis and the union of all
147 differentially expressed genes between the B and F groups was used to build the
148 network.

149 **Quantitative real-time PCR confirmation of differentially expressed genes**

150 To validate the sequencing data, eight known differentially expressed candidate
151 genes were selected for validation by qRT-PCR, which was performed on a 7500
152 real-time PCR system (Applied Biosystems) using the AceQ qPCR SYBR® Green
153 Master Mix (Vazyme) according to the manufacturer's instructions. The primer
154 sequences are listed in Table 1. We chose the rabbit glyceraldehyde-3-phosphate
155 dehydrogenase (GAPDH) gene as an internal control. The results of the experiments
156 were normalized to the expression of the constitutive GAPDH gene. Quantitative
157 variation and relative fold-change were calculated based on the $2^{-\Delta\Delta Ct}$ method
158 (Schmittgen and Livak 2008). Error bars represent the mean $\pm$ S.D. as determined
159 using GraphPad Prism 5, and a paired t-test was performed to test significant
160 differences between the two groups using SPSS 21.0.

161 **Western blotting**

162 Protein lysates from six skin samples were obtained using RIPA Lysis Buffer
163 (PPLYGEN). Protein concentrations were determined with the Enhanced BCA Protein

164 Kit (Beyotime). The protein lysates were diluted to 0.5µg/µL, and 2.5µg protein was
165 detected and analyzed with the Wes automated Western blotting system (Protein
166 Simple) (Harris 2015). The following antibodies were used: 1:100 Anti-GAPDH
167 mouse monoclonal antibody (Abcam), 1:50 Anti-SFRP2 monoclonal antibody
168 (Sangon Biotech).

169 **Results**

170 **Results of transcriptome sequencing**

171 To evaluate whether the RNA-seq data were sufficient for further analysis, their
172 global quality was firstly assessed. After trimming clean reads were generated with a
173 ratio of greater than 85% for each sample (Table 2); and the total clean reads that
174 mapped to the rabbit genome had mapping ratios greater than 80% (Table 3). All
175 reads were deposited in the Short Read Archive (SRA) of the National Center for
176 Biotechnology Information (NCBI) under the accession number SRR3528284. We
177 then obtained the mapped read distribution, which showed whether the reads mapped
178 to genes, coding regions, splice sequences, intron sequences, intergenic regions, or
179 non-coding regions (5'UTR and 3'UTR, non-coding RNA regions) (Figure 1). Our
180 results showed that we were able to detect 17,327 expressed genes, including 8445
181 upregulated genes and 8882 downregulated genes (Table S1).

182 To identify the key differentially expressed genes, the parameters of a fold-change
183 greater than or equal to 2 or less than or equal to 0.5 and FDR less than or equal to
184 0.05 were used to further select the significantly differentially expressed genes. These

185 cut-offs identified 285 upregulated genes and 51 downregulated genes (Table S2).
186 Volcano plots of differentially expressed genes were constructed to explore the
187 relationship between fold-change and significance as shown in Figure 2. This analysis
188 identified 336 genes that were significantly differentially expressed between the back
189 and belly regions of the rex rabbits.

190 **Functional annotation of differentially expressed genes**

191 GO functional enrichment and KEGG pathway analyses were performed to
192 determine the functions of the differentially expressed genes. According to the GO
193 analysis, categories of biological process (n=563), molecular function (n=204), and
194 cellular component (n=132) contained 214 differentially expressed genes (Table S3),
195 which were all considered statistically significant (Figure S1). In the biological
196 process category, most GO terms focused on ion activity, development,
197 morphogenesis, cellular processes, biological regulation, and metabolic processes. In
198 the molecular function category, a high proportion of the GO terms were related to
199 binding, activity regulation, enzymatic activity, and ionic equilibrium. In the cellular
200 component category, we found the terms Z disc, I band, muscle contraction, myofibril,
201 titin binding, and M band sarcoplasmic reticulum showed the greatest enrichment of
202 differentially expressed genes. These GO terms revealed the biological functions of
203 the genes. According to the GO analysis, many GO terms were related to the functions
204 of skin and epithelial cells, such as epithelial cell proliferation, regulation of cell
205 proliferation, skin development and regulation of cell development. This suggests that

the genes in these GO categories may play roles in fur development. We then identified the fur development related genes from the GO terms and their distribution in the molecular function categories (Figure 3).

Meanwhile, KEGG pathway analysis identified 66 differentially expressed genes (Table S4), and results of the KEGG enrichment are shown in Figure S2. Analysis of all the KEGG signaling pathways showed a definite relationship between several pathways, such as the Wnt and MAPK signaling pathways. We identified the SFRP2 and FRZB genes from the Wnt signaling pathway (Figure S3) and calcium channel, voltage-dependent, beta 1 subunit (CACNB1), voltage-dependent calcium channel gamma-1 subunit (CACNG1), and calcium channel, voltage-dependent, L type, alpha 1S subunit (CACNA1S) from the MAPK signaling pathway. These genes were found to influence HF and skin development related signaling pathways, suggesting that these genes may play a role in fur development (Chu et al. 2014; Fuchs and Raghavan 2002; Kim and Yoon 2014).

Network analysis of differentially expressed gene interactions

To explore interactions of the differentially expressed genes, RNA-seq data was used to construct a differentially expressed gene interaction network. We identified interacting partners of the differentially expressed genes using the STRING database, which predicts functional associations between proteins (Figure 4).

Validation of differentially expressed genes

To confirm our RNA-seq results, qRT-PCR was performed on samples from the

227 backs and bellies of the rabbits. Eight target genes were selected and specific primers
228 were designed for validation. As shown in Figure 5A, we found that FRZB, SFRP2,
229 DUSP26, PTP4A3, EN1, and CACNA1S were upregulated, and HBB1 and MRPL36
230 were downregulated by qRT-PCR. The protein levels of SFRP2 among the six
231 samples were further assessed by Western blotting, and we found the highest
232 expression of the SFRP2 protein in the back group (Figure 5B). These data indicate
233 that the results from the transcriptome study are consistent with the overall changes in
234 expression of the differentially expressed genes.

235

236 Discussion

237 The characteristics of fur are different on different body parts of Chinchilla rex
238 rabbits, especially the back and belly (Tao 2010). Fur development is regulated by
239 many factors, such as rearing conditions, nutrition, environment, and gene regulation
240 (Harkness et al. 2013; McNitt et al. 2013). Our study revealed several fur
241 development related genes by transcriptomics, and the functional enrichment and
242 pathway analysis of these genes will contribute to our understanding of the
243 mechanisms of fur development.

244 The Wnt signaling pathway plays an indispensable role at various stages during
245 tissue regeneration and skin development (Stoick-Cooper et al. 2007). In this pathway,
246 Wnt proteins are important in conveying inductive signals between the mesenchyme
247 of follicles and the follicular epithelium. As a family of secreted glycoproteins, Wnts

also play roles in embryonic development and maintenance of homeostasis by regulating migration, differentiation, proliferation and apoptosis of cells in mature tissues (Fujimaki et al. 2015; Millar 2002). Several transcription factors have been identified that regulate the differentiation of keratinocytes via the MAPK signaling pathway (Eckert and Welter 1996), which governs many cellular processes, including cell fate, proliferation, differentiation, homeostasis, and survival in all eukaryotes (Whelan et al. 2012). For example, activator protein I is a keratinocyte transcription factor that plays a crucial role in the regulation of epidermal differentiation and the expression of genes in the MAPK pathway (Briata et al. 1993; Eckert and Welter 1996; Smeyne et al. 1992).

Many genes that are related to fur development such as Secreted frizzled-related protein 2 (SFRP2) and Frizzled-related protein (FRZB) are glycoproteins that are involved in the processes of development and disease in diverse cells and tissues (Ezan et al. 2004; Hoang et al. 1996; Kim and Yoon 2014). SFRP2 inhibited mouse keratinocyte proliferation in the catagen phase and was regarded as a Wnt inhibitor in HFs. In the back skin of mice, the Wnt target genes *Ccnd1* and *C-myc*, were shown to have an inverse relationship between the two genes and SFRP2 throughout the HF cycle, while SFRP2 may inhibit the proliferation of keratinocytes in the catagen phase (Kim and Yoon 2014). Moreover, SFRP2 can control cell apoptosis and fate, and mediate regulation of the Wnt pathway that has effects on intestinal epithelial cells (Skah et al. 2015). However, the SFRP2 protein was highly expressed in the back group in our study; suggesting that the protein product of SFRP2 acted as an activator

270 in skin development. This means that SFRP2 could play a positive role in controlling
271 epidermal cell and keratinocyte differentiation.

272 FRZB (also called SFRP-3 or Fritz) is a member of secreted frizzled-related protein
273 family, which includes secreted proteins (SFRP1-5) that bind and inhibit Wnts
274 (Ehrlund et al. 2013; Ladher et al. 2000). As an antagonist of Wnt proteins in chick
275 development, FRZB inhibited the activity of Xwnt-8 during the gastrula stages
276 (Ladher et al. 2000). With the activation of downstream targets of the pathway, a
277 knockdown of FRZB upregulated the Wnt/ β -catenin pathway (Qin et al. 2014). In this
278 study, FRZB was up-regulated in the back group, suggesting that FRZB may promote
279 the growth of HFs and skin development. However many previous studies have
280 regarded FRZB as an inhibitor, although it is probably an activator that influences the
281 target genes in the Wnt pathway.

282 In our study, the fur phenotypes, such as the length and diameter of the wool, were
283 different between the back and belly skin of rex rabbits. These differences may be
284 influenced by the structure of HF and skin, especially the development of epidermal
285 cells and keratinocytes. Bioinformatic analysis revealed that genes in the Wnt
286 signaling pathway may have effects on the development of HF and skin. We also
287 found that SFRP2 mRNA and protein were highly expressed in the back group,
288 leading to the longer, thicker and greater density than belly group.

289 The regulation of fur development related genes involves the differential expression
290 of genes associated with many biological signaling pathways. The mechanism of HF
291 and skin development will be clarified by functional studies of the candidate genes.

292 Therefore, with RNA sequencing and function analysis, the functions of these key
293 genes, such as SFRP2 and FRZB, should be verified by further study including their
294 function in hair cycle regulation, differentiation of keratinocytes and their role in the
295 Wnt pathway.

296

297 **Conclusion**

298 Gene expression profiling analysis was used to assess fur development in Chinchilla
299 rex rabbits. This study found several genes associated with HF and skin development,
300 including SFRP2, FRZB, CACNG1, CACNB1, CACNA1S, PTPLA, PTP4A3, TTN,
301 DUSP26, EN1, MT3, SLC25A4 and SLC16A3. The mechanisms regulating fur
302 development are complex, and fur development related genes should be studied
303 further.

304

305 **Acknowledgments**

306 This work was supported by the Modern Agricultural Industrial System Special
307 Funding (CARS-44-1) and the Priority Academic Program Development of Jiangsu
308 Higher Education Institutions (2011-137).

309

310 **References**

311 Briata, P., D'Anna, F., Franzi, A.T., and Gherzi, R. 1993. AP-1 activity during normal
312 human keratinocyte differentiation: evidence for a cytosolic modulator of AP-1/DNA
313 binding. Experimental cell research 204(1): 136-146.
314 Carneiro, M., Rubin, C.-J., Di Palma, F., Albert, F.W., Alföldi, J., Barrio, A.M.,

- 315 Pielberg, G., Rafati, N., Sayyab, S., and Turner-Maier, J. 2014. Rabbit genome
316 analysis reveals a polygenic basis for phenotypic change during domestication.
317 Science 345(6200): 1074-1079.
- 318 Chu, Q., Cai, L., Fu, Y., Chen, X., Yan, Z., Lin, X., Zhou, G., Han, H., Widelitz, R.B.,
319 and Chuong, C.-m. 2014. Dkk2/Frzb in the dermal papillae regulates feather
320 regeneration. Dev Biol 387(2): 167-178.
- 321 Danilenko, D.M., Ring, B.D., Yanagihara, D., Benson, W., Wiemann, B., Starnes,
322 C.O., and Pierce, G.F. 1995. Keratinocyte growth factor is an important endogenous
323 mediator of hair follicle growth, development, and differentiation. Normalization of
324 the nu/nu follicular differentiation defect and amelioration of chemotherapy-induced
325 alopecia. The American journal of pathology 147(1): 145.
- 326 Eckert, R.L., and Welter, J.F. 1996. Transcription factor regulation of epidermal
327 keratinocyte gene expression. Mol Biol Rep 23(1): 59-70.
- 328 Ehrlund, A., Mejhert, N., Lorente-Cebrián, S., Åström, G., Dahlman, I.,
329 Laurencikiene, J., and Rydén, M. 2013. Characterization of the Wnt inhibitors
330 secreted frizzled-related proteins (SFRPs) in human adipose tissue. The Journal of
331 Clinical Endocrinology & Metabolism 98(3): E503-E508.
- 332 Ezan, J., Leroux, L., Barandon, L., Dufourcq, P., Jaspard, B., Moreau, C., Allières, C.,
333 Daret, D., Couffignal, T., and Duplâa, C. 2004. FrzA/sFRP-1, a secreted antagonist of
334 the Wnt-Frizzled pathway, controls vascular cell proliferation in vitro and in vivo.
335 Cardiovasc Res 63(4): 731-738.
- 336 Fuchs, E., and Raghavan, S. 2002. Getting under the skin of epidermal morphogenesis.
337 Nature Reviews Genetics 3(3): 199-209.
- 338 Fujimaki, S., Wakabayashi, T., Takemasa, T., Asashima, M., and Kuwabara, T. 2015.
339 The regulation of stem cell aging by Wnt signaling. Histology and histopathology
340 30(12): 1411-1430.
- 341 Geng, R., Yuan, C., and Chen, Y. 2013. Exploring differentially expressed genes by
342 RNA-Seq in cashmere goat (*Capra hircus*) skin during hair follicle development and
343 cycling. Plos One 8(4): e62704.
- 344 Harkness, J.E., Turner, P.V., VandeWoude, S., and Wheler, C.L. 2013. Harkness and

- 345 Wagner's biology and medicine of rabbits and rodents. John Wiley & Sons.
- 346 Harris, V.M. 2015. Protein detection by Simple Western™ analysis. Western Blotting:
347 Methods and Protocols: 465-468.
- 348 Hoang, B., Moos, M., Vukicevic, S., and Luyten, F.P. 1996. Primary structure and
349 tissue distribution of FRZB, a novel protein related to *Drosophila* frizzled, suggest a
350 role in skeletal morphogenesis. *J Biol Chem* 271(42): 26131-26137.
- 351 Kim, B.-K., and Yoon, S.K. 2014. Expression of sfrp2 is increased in catagen of hair
352 follicles and inhibits keratinocyte proliferation. *Annals of dermatology* 26(1): 79-87.
- 353 Ladher, R., Church, V., Allen, S., Robson, L., Abdelfattah, A., Brown, N., Hattersley,
354 G., Rosen, V., Luyten, F., and Dale, L. 2000. Cloning and expression of the Wnt
355 antagonists Sfrp-2 and Frzb during chick development. *Dev Biol* 218(2): 183-198.
- 356 McNitt, J.I., Lukefahr, S.D., Cheeke, P.R., and Patton, N.M. 2013. Rabbit production.
357 CABI.
- 358 Millar, S.E. 2002. Molecular mechanisms regulating hair follicle development.
359 *Journal of Investigative Dermatology* 118(2): 216-225.
- 360 Pan, L., Liu, Y., Wei, Q., Xiao, C., Ji, Q., Bao, G., and Wu, X. 2015.
361 Solexa-Sequencing Based Transcriptome Study of Plaice Skin Phenotype in Rex
362 Rabbits (*Oryctolagus cuniculus*). *Plos One* 10.
- 363 Qin, S., Zhang, Z., Li, J., and Zang, L. 2014. FRZB knockdown upregulates β -catenin
364 activity and enhances cell aggressiveness in gastric cancer. *Oncology reports* 31(5):
365 2351-2357.
- 366 Rizzo, J.M., Romano, R.A., Bard, J., and Sinha, S. 2014. RNA-seq Studies Reveal
367 New Insights into p63 and the Transcriptomic Landscape of the Mouse Skin. *Journal*
368 *of Investigative Dermatology* 135(2): 629-632.
- 369 Schmittgen, T.D., and Livak, K.J. 2008. Analyzing real-time PCR data by the
370 comparative CT method. *Nature protocols* 3(6): 1101-1108.
- 371 Skah, S., Nadjar, J., Sirakov, M., and Plateroti, M. 2015. The secreted
372 Frizzled-Related Protein 2 modulates cell fate and the Wnt pathway in the murine
373 intestinal epithelium. *Experimental cell research* 330(1): 56-65.
- 374 Smeyne, R.J., Schilling, K., Robertson, L., Luk, D., Oberdick, J., Curran, T., and

- 375 Morgan, J.I. 1992. Fos-IacZ transgenic mice: Mapping sites of gene induction in the
376 central nervous system. *Neuron* 8(1): 13-23.
- 377 Stoick-Cooper, C.L., Moon, R.T., and Weidinger, G. 2007. Advances in signaling in
378 vertebrate regeneration as a prelude to regenerative medicine. *Genes & development*
379 21(11): 1292-1315.
- 380 Tao, Y. 2010. Studies on the quality of rex rabbit fur. *World Rabbit Sci* 2(1): 21-24.
- 381 Trapnell, C., Pachter, L., and Salzberg, S.L. 2009. TopHat: discovering splice
382 junctions with RNA-Seq. *Bioinformatics* 25(9): 1105-1111.
- 383 Trapnell, C., Williams, B.A., Pertea, G., Mortazavi, A., Kwan, G., van Baren, M.J.,
384 Salzberg, S.L., Wold, B.J., and Pachter, L. 2010. Transcript assembly and
385 quantification by RNA-Seq reveals unannotated transcripts and isoform switching
386 during cell differentiation. *Nature Biotechnology* 28(5): 511-515.
- 387 Whelan, J.T., Hollis, S.E., Cha, D.S., Asch, A.S., and Lee, M.H. 2012. Post -
388 transcriptional regulation of the Ras - ERK/MAPK signaling pathway. *Journal of*
389 *cellular physiology* 227(3): 1235-1241.
- 390 Xu, T., Guo, X., Wang, H., Hao, F., Du, X., Gao, X., and Liu, D. 2013. Differential
391 gene expression analysis between anagen and telogen of *Capra hircus* skin based on
392 the de novo assembled transcriptome sequence. *Gene* 520(1): 30-38.

393

394

395 **Figure Legends**

396 **Figure 1. Mapped region distribution of each sample.** Mapped read distribution for
397 each sample, showing the percentage of reads that mapped to each type of genomic
398 region (genes, coding regions, splice sequences, intron sequences, intergenic regions,
399 and non-coding regions (5'UTR and 3'UTR)) in the Ensembl OryCun2.0 database.

400 **Figure 2. Volcano plot of differentially expressed genes.** Red dots show
401 upregulated genes, green dots show downregulated genes, and two blue lines show a
402 2-fold change in expression ($P=0.05$).

403 **Figure 3. GO enrichment of genes related to fur development.** Within the
404 molecular function category, we identified genes induced by fur development in rex
405 rabbits. GO categories included biological processes, cellular component, and
406 molecular function.

407 **Figure 4. Diagram of the interaction network.** Thicker lines show stronger
408 interactions of differentially expressed genes and their partner genes.

409 **Figure 5. Analysis of differentially expressed genes involved in the regulation of**
410 **fur development in rabbits.** (A) The mRNA levels of FRZB, SFRP2, DUSP26,
411 PTP4A3, EN1, CACNA1S, HBB1 and MRPL36 between back and belly groups. The
412 expression level of genes in the back group was normalized to the belly group. (B)
413 The protein levels of SFRP2 between the back and belly group. Each group had three
414 biological replicates. Error bars represent the mean $\pm$ S.D. of triplicate experiments. *,
415 $P<0.05$; **, $P<0.01$.

416

417 **Table 1. Primer sequences used in qRT-PCR for validation of differentially**
 418 **expressed genes.**

Gene	Primers
GAPDH	Forward primer: 5'-TCACCATCTTCCAGGAGCGA-3' Reverse primer: 5'- CACAATGCCGAAGTGGTCGT-3'
FRZB	Forward primer: 5'-CATCAAGTACCGCCACTCGT-3' Reverse primer: 5'-GCCCCTCTACAGTTTCCATTGCT-3'
SFRP2	Forward primer: 5'-CCAGCCCGACTTCTCCTACAAGC-3' Reverse primer: 5'-TCCAGCACCTCTTTCATGGTCT-3'
EN1	Forward primer: 5'-CTCCTGGGGCTTATCCGTCC-3' Reverse primer: 5'-CTCCCAGTTCCAGCCAAGGTC-3'
CACNA1S	Forward primer: 5'-TCATCCTCAGCGAGATCGACAC-3' Reverse primer: 5'-GATCAGCCTCATGACCCGGAAC-3'
DUSP26	Forward primer: 5'-TAACTGGCTCTGGGCATCCAT-3' Reverse primer: 5'-CCGCTCCAGCTCGAAGACGTT-3'
PTP4A3	Forward primer: 5'- AGAACATGCGCTTCCTCATCACC-3'

	Reverse primer: 5'-TGTCGTAGGTCACTTCGCACAC-3'
HBB1	Forward primer: 5'-GCTGCTGGTTGTCTACCCAT-3'
	Reverse primer: 5'-AGCCAGCACCTTCTTGCCAT-3'
MRPL36	Forward primer: 5'-CCCGCGCTGGGCTTCAAGAC-3'
	Reverse primer: 5'-
	GGGTTGCTCTCGCAGTACACGAAC-3'

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421 **Table 2. Summary of RNA-seq data for each sample.**

Sample ID	Raw reads	Quality trimmed	Adaptor trimmed	Clean reads	Clean ratio	rRNA ratio
B1	62,459,166	59,686,034	58,308,948	54,544,462	87.30%	0.30% ⁴²³
B2	42,040,878	41,785,111	41,048,067	40,089,926	95.40%	0.70% ⁴²⁴
B3	57,515,444	56,961,934	56,014,421	54,639,520	95.00%	0.20% ⁴²⁵
F1	45,589,348	45,273,339	44,450,260	43,352,936	95.10%	2.60% ⁴²⁶
F2	56,952,408	56,446,129	55,441,949	53,996,816	94.80%	0.90% ⁴²⁷
F3	49,299,600	48,995,596	48,156,222	47,052,794	95.40%	0.10%

428 Clean ratio= (Clean reads/Raw reads)×%

429

430 **Table 3. Mapping statistics for each sample.**

Sample	All reads	Mapped	Mapped	Mapped broken	Mapped unique	Mapped multiple	Mapping ratio
ID		reads	paired	paired reads	reads	reads	
			reads				
B1	54,391,204	44,245,125	42,943,776	1,301,349	39,786,635	4,458,490	81.30%
B2	39,826,940	33,675,819	32,120,474	1,555,345	30,460,340	3,215,479	84.60%
B3	54,509,484	45,897,437	44,222,232	1,675,205	41,895,083	4,002,354	84.20%
F1	42,242,866	35,960,580	34,407,676	1,552,904	32,706,780	3,253,800	85.10%
F2	53,524,836	45,300,446	43,337,930	1,962,516	40,933,492	4,366,954	84.60%
F3	47,012,530	39,549,833	37,741,242	1,808,591	35,663,951	3,885,882	84.10%

431 Mapping ratio=Mapped reads/All read

432 **Supporting Information**

433 **Figure S1. Bar plot of GO enrichment results.** GO functional enrichment analysis
434 of the differentially expressed genes, which were all considered statistically
435 significant.

436 **Figure S2. Bar plot of KEGG enrichment results.** KEGG pathway analysis of the
437 differentially expressed genes, which were all considered statistically significant.

438 **Figure S3. Expressed genes annotated in the Wnt signaling pathway.** The
439 expressed genes are in the red box.

440 **Table S1. Gene expression in the two groups.**

441 **Table S2. Differentially expressed genes in the two groups.**

442 **Table S3. Significant GO terms of the differentially expressed genes.**

443 **Table S4. Significant KEGG pathways of the differentially expressed genes.**

Figure 1. Mapped region distribution of each sample. Mapped read distribution for each sample, showing the percentage of reads that mapped to each type of genomic region (genes, coding regions, splice sequences, intron sequences, intergenic regions, and non-coding regions (5'UTR and 3'UTR)) in the Ensembl OryCun2.0 database.

78x53mm (300 x 300 DPI)

Figure 2. Volcano plot of differentially expressed genes. Red dots show upregulated genes, green dots show downregulated genes, and two blue lines show a 2-fold change in expression ($P=0.05$).

190x189mm (300 x 300 DPI)

Figure 3. GO enrichment of genes related to fur development. Within the molecular function category, we identified genes induced by fur development in rex rabbits. GO categories included biological processes, cellular component, and molecular function.

219x112mm (300 x 300 DPI)

Figure 5. Analysis of differentially expressed genes involved in the regulation of fur development in rabbits. (A) The mRNA levels of FRZB, SFRP2, DUSP26, PTP4A3, EN1, CACNA1S, HBB1 and MRPL36 between back and belly groups. The expression level of genes in the back group was normalized to the belly group. (B) The protein levels of SFRP2 between the back and belly group. Each group had three biological replicates. Error bars represent the mean $\pm$ S.D. of triplicate experiments. *, $P<0.05$; **, $P<0.01$.

64x59mm (300 x 300 DPI)

169x127mm (300 x 300 DPI)

169x127mm (300 x 300 DPI)

93x66mm (300 x 300 DPI)

Supplemental Table S1. Gene expression in the two groups

Gene_id	gene_name	Description/locus	Group B_FPKM	Group F_FPKM
ENSOCUG000000022631	ZNF536	zinc finger GL018722:	0.996739667	1.023735333
ENSOCUG000000016727	NELL2	NEL-like 2 8:1590416-	0.990464667	1.031116333
ENSOCUG000000027292	IQCF1	IQ motif co 9:1906113	0.997219	1.048545
ENSOCUG000000024960	-	Uncharacte X:7874588	0.957098333	1.013687
ENSOCUG000000011337	AURKC	aurora kina GL018763:	0.997992	1.061457667
ENSOCUG000000026745	-	Uncharacte 4:8993441-	0.947800667	1.010491
ENSOCUG000000026058	FTCD	formimidoy 14:163823	0.983903333	1.053086
ENSOCUG000000009801	CHIC1	cysteine-ric X:5216642	0.928247	1.000059333
ENSOCUG000000029407	HMG A2	high mobili 4:44715270	0.930181	1.020447667
ENSOCUG000000004393	SYT15	Uncharacte 18:8796448	0.958430333	1.052739333
ENSOCUG000000013116	CDH24	cadherin 24 17:4327209	0.924978667	1.023153333
ENSOCUG000000025458	SMARCC1	GL018812:	0.957120667	1.064048667
ENSOCUG000000014204	FUT4	fucosyltran: 1:1223209	0.990621333	1.12166
ENSOCUG000000004266	FAM222A	family with GL019210:	0.968984333	1.103016667
ENSOCUG000000009414	C17orf64	chromosom 19:267550:	0.875599333	1.001547
ENSOCUG000000026685	-	Uncharacte 17:4054230	0.967109	1.106463
ENSOCUG000000017614	-	Uncharacte AAGW020	0.886652667	1.022333667
ENSOCUG000000008688	WDR96	cilia and fla 18:5206084	0.896277333	1.033549667
ENSOCUG000000026933	NPTXR	neuronal pe 4:84388278	0.960864	1.114302333
ENSOCUG000000009852	RSPH4A	radial spok 12:1055359	0.96107	1.122411333
ENSOCUG000000000714	RARB	retinoic aci 14:1167619	0.903852333	1.062696333
ENSOCUG000000024411	C7orf61	chromosom 6:2732760:	0.969506667	1.142842333
ENSOCUG000000027729	NAT8L	N-acetyltra GL018796:	0.951567	1.131805
ENSOCUG000000010719	WDR76	Oryctolagu 17:2839849	0.849363667	1.012293333
ENSOCUG000000020972	CYP2C14	cytochrome 18:4238150	0.944429	1.12879
ENSOCUG000000021395	EFR3B	EFR3 hom 2:17403029	0.897589667	1.073314
ENSOCUG000000004927	BCAS1	breast carci GL018712:	0.932518667	1.117866
ENSOCUG000000011843	HSD11B2	Oryctolagu 5:23014000	0.867844	1.043334
ENSOCUG000000014290	DUOXA2	dual oxidas 17:2737440	0.890958	1.072581667
ENSOCUG000000022517	-	Uncharacte GL019254:	0.869515	1.065269333
ENSOCUG000000023847	CEP57L1	centrosoma 12:970500:	0.994793667	1.223215
ENSOCUG000000021957	GPR141	G protein-c 10:211207:	0.968751667	1.199024667
ENSOCUG000000011835	IL8	Oryctolagu 15:763689	0.906659667	1.142488
ENSOCUG000000007260	-	Uncharacte 12:308509	0.819123667	1.032323
ENSOCUG000000029474	-	Uncharacte GL018733:	0.996402	1.256937
ENSOCUG000000024036	COL6A5	collagen, ty 14:963914-	0.844292333	1.071333333
ENSOCUG000000024132	-	Uncharacte 12:141424:	0.824246667	1.046397
ENSOCUG000000000184	NCKAP5	NCK-assoc 7:69801660	0.943987333	1.203175
ENSOCUG000000010247	ATP6V0D2	ATPase, H- 3:1015814:	0.873308	1.113754333
ENSOCUG000000016641	GPR97	G protein-c 5:13738039	0.938584667	1.204249333
ENSOCUG000000001103	CASP1	caspase 1, ε 1:1115730:	0.915474333	1.177220333
ENSOCUG000000009903	TSPYL5	TSPY-like 3:11315250	0.932270333	1.203201333
ENSOCUG000000017597	GRM2	glutamate r 9:18908130	0.945418333	1.221070667
ENSOCUG000000006811	NLGN3	neuroligin 1 X:4961553	0.814141	1.057413333
ENSOCUG000000022089	-	14:108525	0.997062	1.295206667
ENSOCUG000000005126	RHOH	ras homolo 2:29498138	0.972153667	1.270073667
ENSOCUG000000012342	CDC25A	cell divisio 9:1598326:	0.775478	1.019443667
ENSOCUG000000005537	RSPH9	radial spok 12:330792:	0.827265333	1.093829333

ENSOCUG00000029142	-	Uncharacte	GL019297:	0.788135333	1.056076333
ENSOCUG00000003039	TTPA	tocopherol	3:78846210	0.751806667	1.016696
ENSOCUG00000010823	PFAS	phosphorib	19:1099682	0.875111	1.191824
ENSOCUG00000012589	SMPDL3B	sphingomy	13:137537	0.846829333	1.154351333
ENSOCUG00000016476	IL18R1	Oryctolagu	2:90028850	0.918324667	1.25298
ENSOCUG00000004096	-	Uncharacte	GL018981:	0.961117667	1.325837
ENSOCUG00000016904	PLXNC1	plexin C1	[4:7348792	0.796695667	1.101224
ENSOCUG00000016711	KIAA1958	KIAA1958	1:673403-7	0.732293667	1.021946
ENSOCUG00000005141	CHST11	carbohydr	4:8355175	0.790493	1.105705333
ENSOCUG00000007927	SKA1	spindle and	9:91095294	0.821681	1.155120667
ENSOCUG00000001278	INTU	inturned pl	15:103461	0.890661667	1.26131
ENSOCUG00000011911	SLC47A2	solute carri	GL018817:	0.983549	1.395183333
ENSOCUG00000021441	NKG7	natural kill	GL019218:	0.949191933	1.351603333
ENSOCUG00000003060	GCH1	GTP cyclot	17:7354730	0.942627667	1.363585
ENSOCUG00000012911	CD4	Oryctolagu	8:32816210	0.821646167	1.188965
ENSOCUG00000017568	P2RY6	pyrimidine	1:14318678	0.896901333	1.303623333
ENSOCUG00000005480	TAF4B	TAF4b RN	9:6746283	0.817886667	1.190033333
ENSOCUG00000010671	SH2D2A	SH2 domai	13:361453	0.913819333	1.331801267
ENSOCUG00000012227	CD226	CD226 mol	9:1100004	0.946290667	1.379721
ENSOCUG00000006864	-	Uncharacte	GL018823:	0.89239	1.308917667
ENSOCUG00000027632	-	Uncharacte	X:1093751	0.781524667	1.152628667
ENSOCUG000000021757	SNX22	sorting nex	17:809002	0.795779333	1.181112333
ENSOCUG00000029436	-	Uncharacte	2:98623374	0.809129333	1.202876667
ENSOCUG00000021915	PLD6	phospholip	GL018920:	0.88066	1.311156667
ENSOCUG00000017387	CLSPN	claspin	[So GL018704:	0.790943333	1.184944
ENSOCUG00000005666	DHRS9	dehydroger	7:1088269	0.933061333	1.403514667
ENSOCUG00000017194	-	Uncharacte	18:697364	0.735858333	1.111137333
ENSOCUG00000016478	RAD54B	RAD54 hor	3:1100058	0.861068667	1.302413333
ENSOCUG00000025918	HIST2H2AA	histone clus	13:4215888	1.995073333	3.021513333
ENSOCUG00000001150	GIMAP8	GTPase, Im	GL018806:	0.85779	1.304510333
ENSOCUG00000011798	KL	klotho	[Sou GL018702:	0.734362	1.122955667
ENSOCUG00000026204	TIFAB	TRAF-inter	3:1807562	0.723977	1.11653
ENSOCUG00000025147	-	Uncharacte	5:22550888	0.800703333	1.239217
ENSOCUG00000015121	-		7:16235652	0.955665333	1.47956
ENSOCUG00000000814	-		11:1817224	0.876733667	1.357444667
ENSOCUG00000002818	FAM64A	family with	19:1366587	0.925319667	1.449379
ENSOCUG00000003854	TPMT	Oryctolagu	GL018711:	0.940892	1.490363333
ENSOCUG00000027017	PARVG	parvin, gar	GL019802:	0.845958333	1.344465333
ENSOCUG00000010254	-	Uncharacte	9:50740448	0.889781333	1.41457
ENSOCUG00000023856	-	Uncharacte	GL018806:	1.998684667	3.19599
ENSOCUG00000001961	RAD51AP1	RAD51 ass	8:30635518	0.946447667	1.514251667
ENSOCUG00000014423	IKZF1	IKAROS f&	GL018745:	0.937168667	1.502113667
ENSOCUG00000002703	FOXO1	forkhead bc	8:29085630	1.88338	3.02239
ENSOCUG00000018028	7SK	7SK RNA	[3:14741397	0.797222333	1.282107
ENSOCUG00000010608	TFF1	trefoil fact	AAGW020	0.974026667	1.57875
ENSOCUG00000017214	RIC3	RIC3 acety	1:14988172	0.782333667	1.270771333
ENSOCUG00000015423	ZDHHC23	zinc finger,	14:1052645	0.818654333	1.343337
ENSOCUG00000014702	ECE2	endothelin	14:8137692	0.767028333	1.259272
ENSOCUG00000002953	CIDEB	cell death-i	17:4434920	1.910874333	3.153893333
ENSOCUG00000026073	FANCA	Fanconi an	GL018965:	0.819283667	1.360099333

ENSOCUG00000024620	-	Uncharacte	GL018888:	0.946872333	1.57626
ENSOCUG00000022346	CD5	Oryctolagu	GL018717:	0.751347667	1.256100333
ENSOCUG00000026826	CLDN19	claudin 19	13:123991:	0.795301	1.331820333
ENSOCUG00000004047	SKA3	spindle and 8:	4346250:	0.842874333	1.415257667
ENSOCUG00000001241	MFSD4	major facili	16:665632:	0.910825667	1.536063333
ENSOCUG00000007701	KANK4	KN motif a	13:104258:	0.978564	1.655673333
ENSOCUG00000005587	PPP1R14D	protein pho	17:312396:	0.676969333	1.14546
ENSOCUG00000004490	GUCY1A2	guanylate c	1:1096041:	0.957888	1.621616667
ENSOCUG00000029646	-	Uncharacte	15:504735:	1.888431667	3.197566667
ENSOCUG00000027626	CD247	Oryctolagu	13:254577:	0.765721333	1.302995667
ENSOCUG00000010249	UBE2T	ubiquitin-c	16:693396:	1.91891	3.278626667
ENSOCUG00000007559	TRPV5	Oryctolagu	7:9203870-	0.663733667	1.136422333
ENSOCUG00000003707	DLX1	distal-less	17:1118183:	0.723108	1.246341
ENSOCUG00000001826	-	Uncharacte	X:7824048	1.914093333	3.301093333
ENSOCUG00000013586	STIL	SCL/TAL1	13:119314:	0.65507	1.134847667
ENSOCUG00000009512	PLA1A	phospholip:	14:991413:	0.925354667	1.60829
ENSOCUG00000027340	DTX1	deltex 1,	E3:21:879170:	0.695185667	1.212846667
ENSOCUG00000027908	SKIDA1	SKI/DACH	16:396965:	0.717188333	1.252806333
ENSOCUG00000010701	HEMGN	hemogen	[5:1:151274:	0.625745667	1.098020667
ENSOCUG00000027725	-	GL018986:		0.659656333	1.179256
ENSOCUG00000027803	SH3GL3	SH3-domai	GL018737:	0.761494667	1.364984333
ENSOCUG00000008068	BCHE	butyrylchol	14:604055:	0.825007667	1.49073
ENSOCUG00000028021	PRIMA1	proline rich	20:124479:	0.963417667	1.741577333
ENSOCUG00000025201	-	Uncharacte	GL018781:	0.623264667	1.128159333
ENSOCUG00000000360	CDH6	cadherin 6,	11:530841:	1.929906667	3.508823333
ENSOCUG00000012683	ADAM33	ADAM me	4:1055040:	1.80474	3.28882
ENSOCUG00000013264	-	Uncharacte	1:5001214:	0.616182333	1.123139667
ENSOCUG00000012907	TBX21	T-box 21	[5:19:395596:	0.870307	1.589593
ENSOCUG00000025273	-	Uncharacte	5:2245672:	0.681738	1.245309667
ENSOCUG00000006283	HAVCR2	hepatitis A	3:3856575:	0.724179	1.324900333
ENSOCUG00000015626	NGEF	neuronal gu	GL018736:	1.683613333	3.084123333
ENSOCUG00000004499	SLC4A1	solute carri	19:445586:	0.631047667	1.157443333
ENSOCUG00000025914	-	Uncharacte	GL018758:	0.603481	1.108976333
ENSOCUG00000024419	-	Uncharacte	GL018760:	1.989326667	3.656466667
ENSOCUG00000022161	SARDH	sarcosine d	GL019710:	0.734066667	1.349451667
ENSOCUG00000006970	SLC44A4	solute carri	12:207138:	0.683752	1.262846333
ENSOCUG00000018769	U3	Small nucle	19:293237:	0.705956667	1.318503333
ENSOCUG00000001813	ARG1	Arginase-1	12:121799:	0.777843333	1.458750333
ENSOCUG00000014135	SUCNR1	succinate re	14:459955:	0.838891	1.579467
ENSOCUG00000012133	-	Uncharacte	AAGW020	0.641683	1.221364
ENSOCUG00000011604	ESM1	endothelial	11:709571:	0.563956	1.076042667
ENSOCUG00000017822	SSC5D	GL019887:		1.553153333	3.009753333
ENSOCUG00000007493	-	Uncharacte	GL018707:	0.518416333	1.006032
ENSOCUG00000015578	-	X:5007808		0.603243333	1.170802333
ENSOCUG00000009734	ALX3	ALX home	13:540961:	0.950042	1.855696667
ENSOCUG00000008274	PROX1	prospero hc	16:591733:	1.678253333	3.290476667
ENSOCUG00000011371	GPR17	G protein-c	7:5937485:	0.721820667	1.421425
ENSOCUG00000006154	GIN54	GIN5 comp	GL018706:	0.702296667	1.388320667
ENSOCUG00000029219	DHH	desert hedg	4:3338811:	0.637350333	1.266614333
ENSOCUG00000024629	RASAL3	RAS protei	GL018829:	0.841543667	1.678566667

ENSOCUG00000002433	FBXO41	F-box prote 2:11313759	0.925904667	1.849834
ENSOCUG000000029274	KLRD1	killer cell k 8:28570335	0.535946333	1.076417667
ENSOCUG000000023873	NT5M	5',3'-nucleo GL018920:	0.921070333	1.856960667
ENSOCUG000000019713	7SK	7SK RNA 15:6871639	0.538436667	1.085546667
ENSOCUG000000014085	CREG2	cellular rep 2:91012342	0.804755	1.622756667
ENSOCUG000000026452	-	GL018747:	0.8363	1.68666
ENSOCUG00000002587	TSHZ2	teashirt zin GL018712:	1.67897	3.42523
ENSOCUG000000010181	ARHGEF39	Rho guanin 1:18263740	0.724022333	1.493150667
ENSOCUG000000024754	GNAT3	guanine nu 7:35479467	0.966445667	2.007965667
ENSOCUG000000016067	-	protein dist AAGW020	0.597756667	1.242733333
ENSOCUG000000023339	SMCO3	single-pass 8:24791874	0.604865667	1.261352
ENSOCUG00000001856	CTSE	Oryctolagu 16:6624345	1.823376667	3.810233333
ENSOCUG000000024499	-	Uncharacte 5:22371610	0.926768333	1.937256667
ENSOCUG000000021283	TCFL5	transcriptio GL019426:	1.440208667	3.013743333
ENSOCUG000000023068	-	Uncharacte 13:3877050	1.572746667	3.308873333
ENSOCUG000000015887	WSCD2	WSC doma GL018777:	1.735885333	3.65613
ENSOCUG000000024631	-	Uncharacte GL019405:	0.626704	1.322647
ENSOCUG000000027828	SNORA23	Small nucle 1:15122497	3.8138	8.055876667
ENSOCUG000000026226	-	Histone H2 12:1083870	1.59725	3.3821
ENSOCUG000000025025	AADACL3	arylacetami GL018739:	0.746197	1.588669667
ENSOCUG000000029126	-	Uncharacte 17:4457802	1.44101	3.068400667
ENSOCUG000000005408	-	Uncharacte GL018792:	0.968348	2.064088
ENSOCUG000000028219	FASLG	Fas ligand (13:272822-	0.478263333	1.032536
ENSOCUG000000006050	SGOL1	shugoshin-l 14:6259397	0.939288667	2.039056667
ENSOCUG000000007602	HS3ST1	heparan sul 2:1876129-	4.980853333	10.81929333
ENSOCUG000000028438	7SK	7SK RNA GL019070:	0.85164	1.85487
ENSOCUG000000005178	-	Uncharacte 14:1601015	3.685403333	8.053566667
ENSOCUG000000026584	-	GL018886:	0.888253667	1.961163333
ENSOCUG000000003735	HCAR1	hydroxycar GL018824:	0.614571333	1.372053
ENSOCUG000000004080	RASL10B	RAS-like, f 19:2479334	0.746795	1.713354333
ENSOCUG000000023446	BIK	BCL2-inter GL019017:	1.320933333	3.040476667
ENSOCUG000000009271	HTR1B	Oryctolagu 12:6427794	0.510793	1.176407333
ENSOCUG000000027635	GCG	Glucagon 7:10127707	0.922597333	2.12677
ENSOCUG000000005876	ZNF775	zinc finger GL018806:	0.510061	1.181373333
ENSOCUG000000013536	NTRK3	neurotrophi GL018934:	0.647137667	1.506474
ENSOCUG000000021112	RAB39A	RAB39A, r 1:10862397	0.689555333	1.612065
ENSOCUG000000009384	CD8B	CD8b mole 2:99543307	0.865408333	2.03609
ENSOCUG000000010651	TEX101	testis expre GL019267:	0.501935667	1.184960333
ENSOCUG000000000476	FGF2	fibroblast g 15:9865440	1.335057667	3.177233333
ENSOCUG000000005012	SH2D1A	SH2 domai X:9883210	0.684652667	1.630928667
ENSOCUG000000017860	GOLGA7B	golgin A7 f 18:4600130	12.5513	30.0356
ENSOCUG000000014458	-	Histone H2 12:1086684	1.75342	4.23365
ENSOCUG000000007576	FGF16	fibroblast g X:6931797	0.545968	1.322293333
ENSOCUG000000021032	-	T cell rece GL018758:	0.508373	1.233231
ENSOCUG000000005039	CA1	carbonic an 3:10097797	1.669944667	4.052078667
ENSOCUG000000022954	NFE2	nuclear fact 4:38046520	1.65162	4.026096667
ENSOCUG000000029339	AWAT2	acyl-CoA v X:4859201	0.483232667	1.181483333
ENSOCUG000000014146	-	Uncharacte GL019021:	4.65289	11.41576667
ENSOCUG000000012279	C14orf37	chromosom 17:7646078	0.701853333	1.728567333
ENSOCUG000000026750	RPL35A	Uncharacte 3:13105920	0.506037333	1.249713333

ENSOCUG000000025343 -	Uncharacte 7:4049935-	26.6003	65.79433333
ENSOCUG000000006500 SLC4A4	Oryctolagu: 15:784907:	1.593633333	3.95266
ENSOCUG000000026714 CD5L	CD5 molec 13:3540739	10.11470333	25.11476667
ENSOCUG000000003837 -	Uncharacte 2:98664529	0.448673333	1.11452
ENSOCUG000000004369 C5orf46	chromosom 3:29847859	4.0662	10.15034667
ENSOCUG000000023770 ABHD15	abhydrolas 19:186302:	0.68016	1.702713333
ENSOCUG000000005930 ZFPM2	zinc finger 3:12068089	0.595073333	1.494253
ENSOCUG000000000017 LIPE	lipase, horn GL018789:	3.935206667	9.926643333
ENSOCUG000000027079 ASF1B	anti-silenci GL019579:	0.957143333	2.424546667
ENSOCUG000000027509 CX3CR1	Oryctolagu: 9:4397515-	0.579353333	1.471875333
ENSOCUG000000029078 -	Uncharacte 13:3959764	0.87646	2.237426667
ENSOCUG000000028103 -	Uncharacte X:7296176	0.662356667	1.7167
ENSOCUG000000029439 HOXA10	homeobox . 10:1189029	1.580596	4.102266667
ENSOCUG000000026199 KLRK1	Uncharacte 8:28488357	0.642763333	1.677726667
ENSOCUG000000029129 GPR37L1	G protein-c 16:6952789	1.332886667	3.50723
ENSOCUG000000026247 -	Uncharacte 3:74042336	0.462810333	1.229020333
ENSOCUG000000005775 MYBL2	v-myb avia GL018718:	0.477168667	1.268985667
ENSOCUG000000023030 RPL32	Uncharacte 6:10158286	3.55528	9.456573333
ENSOCUG000000014031 TGM6	transglutam 4:9531654-	2.804306667	7.488303333
ENSOCUG000000004932 E2F7	E2F transcr 4:5615777:	0.686045333	1.832025
ENSOCUG000000015801 ATP13A4	ATPase typ 14:8927968	0.568859	1.519556667
ENSOCUG000000029697 -	Uncharacte 17:4460020	0.627984	1.685164
ENSOCUG000000011077 ITI-HC3	Oryctolagu: 9:19828564	0.474549333	1.277461667
ENSOCUG000000024403 -	Uncharacte GL019650:	0.611833333	1.65806
ENSOCUG000000002916 TRAT1	T cell recep 14:110666:	0.578092333	1.585127
ENSOCUG000000028085 -	Uncharacte 13:710921:	0.428263333	1.183283667
ENSOCUG000000014900 C4orf36	chromosom 15:666291:	1.975624	5.48325
ENSOCUG000000017622 NOVA1	neuro-onco 17:4651504	4.444203333	12.3745
ENSOCUG000000004914 RAB36	RAB36, mc GL018810:	0.691740667	1.935276667
ENSOCUG000000022000 -	Uncharacte GL019052:	0.72358	2.062052
ENSOCUG000000025019 -	Uncharacte 2:98664529	0.353196667	1.0152
ENSOCUG000000009838 FIGN	fidgetin [Sc 7:10288297	1.149461	3.315996667
ENSOCUG000000000575 HAVCR1	hepatitis A 3:38519798	2.384353333	6.937033333
ENSOCUG000000027526 -	Uncharacte 4:2624044:	3.33951	9.81301
ENSOCUG000000028229 -	GL019052:	4.677856667	13.8054
ENSOCUG000000026231 -	Uncharacte GL019270:	0.45155	1.333685333
ENSOCUG000000012145 -	Uncharacte 13:1241706	0.754003333	2.233416
ENSOCUG000000004068 CHST8	carbohydra AAGW020	0.502624333	1.493162333
ENSOCUG000000006287 -	13:305147:	0.828858667	2.474433333
ENSOCUG000000006830 -	Uncharacte 14:642835:	0.724922667	2.169238333
ENSOCUG000000025868 GABRD	gamma-am AAGW020	1.122538	3.360183333
ENSOCUG000000008464 PRKG2	protein kin 15:690772:	0.956610333	2.864416667
ENSOCUG000000028050 -	Uncharacte 2:9814389:	0.976547333	2.924776667
ENSOCUG000000010340 ALOX15B	arachidonat 19:111578:	0.593774333	1.783221333
ENSOCUG000000009088 STEAP1	Oryctolagu: 10:3845097	1.429391	4.371483333
ENSOCUG000000016886 -	Oryctolagu: GL018717:	0.769586667	2.389336667
ENSOCUG000000011055 NHE-3	Oryctolagu: GL018897:	0.454786667	1.419509333
ENSOCUG000000024191 -	21:462819:	1.853773333	5.857189
ENSOCUG000000022366 snoU85	Small nucle 8:32552666	0.369756667	1.170993333
ENSOCUG000000000252 DIRAS2	DIRAS fam 1:7746367:	0.814241667	2.599636667

ENSOCUG00000021122 -	Uncharacte 2:9846132:	1.409720667	4.565916667
ENSOCUG00000025765 -	Uncharacte AAGW020	0.446159	1.470185333
ENSOCUG00000017459 EPB42	erythrocyte 17:2906080	0.658069333	2.179034667
ENSOCUG00000025226 BMP5	bone morph 12:4567158	0.413147333	1.368103333
ENSOCUG00000007445 PMP2	Oryctolagu: 3:97128687	1.662827333	5.540076667
ENSOCUG00000027505 SIT1	signaling th 1:1827454:	0.466230333	1.566207667
ENSOCUG00000003184 -	10:230645:	0.365420667	1.252748
ENSOCUG00000011557 -	Uncharacte 5:3553529:	0.316093667	1.088242333
ENSOCUG00000029280 ITLN2	intelectin 2 13:321962:	1.72329	5.959335333
ENSOCUG00000023583 NUPR1L	nuclear pro GL018788:	0.327069333	1.133056667
ENSOCUG00000029664 -	Uncharacte GL019400:	0.501011967	1.748186267
ENSOCUG00000009954 CHST4	carbohydra 5:2801379:	0.372398	1.29986
ENSOCUG00000003128 C10orf128	chromosom GL019147:	0.777290667	2.72834
ENSOCUG00000001157 HOXC12	homeobox 4:37739048	0.50463	1.784233333
ENSOCUG00000001864 AQP8	aquaporin 8:1570766:	1.197601	4.240723333
ENSOCUG00000001662 SLC7A11	solute carri 15:263817:	0.838137333	2.970946667
ENSOCUG00000003931 GJA3	gap junction 8:4448978:	0.737026	2.615041333
ENSOCUG00000025452 -	Uncharacte 16:8026230	0.544123333	1.962246667
ENSOCUG00000010243 -	Uncharacte 11:6414858	0.614643667	2.241785
ENSOCUG00000002208 -	Uncharacte 19:172148:	0.359243333	1.313743333
ENSOCUG00000015146 -	Uncharacte GL018764:	1.38211	5.09245
ENSOCUG00000024602 -	7:14697179	0.401887333	1.509735
ENSOCUG00000001208 RXFP1	relaxin/insu GL018701:	0.604177333	2.269936667
ENSOCUG00000013533 IGHM	immunoglo GL019133:	1.057376	3.972820333
ENSOCUG00000026223 -	Uncharacte 21:7796448	0.303056333	1.142250333
ENSOCUG00000003339 C11orf71	chromosom 1:10199580	0.525226333	2.051922333
ENSOCUG00000029191 -	Uncharacte 21:458640:	0.696014667	2.731580667
ENSOCUG00000027644 TSPO2	translocato 12:3079039	0.438137667	1.762885667
ENSOCUG00000010287 SAPCD2	suppressor GL018999:	0.303073	1.220324333
ENSOCUG00000002609 NRGN	1:92485617	0.632243333	2.597566667
ENSOCUG00000009208 ACVR1C	activin A re 7:9633717:	1.046276333	4.36883
ENSOCUG00000023724 -	Uncharacte 2:9862790:	0.269577667	1.136604333
ENSOCUG00000006893 MARCO	macrophag 7:63885199	0.823379333	3.502337333
ENSOCUG00000027233 -	Uncharacte 19:1293124	1.189971667	5.08188
ENSOCUG00000022958 -	Uncharacte GL018758:	0.617884	2.647823333
ENSOCUG00000022477 ALOX12	arachidonat 19:121730:	0.761354	3.900773667
ENSOCUG00000014832 STEAP2	Oryctolagu: 10:3839080	0.390523333	2.01984
ENSOCUG00000026955 -	GL018747:	0.234284	1.215015
ENSOCUG00000009086 KLB	klotho beta 2:28738439	1.298456667	6.877696667
ENSOCUG00000024749 -	Uncharacte AAGW020	0.220450333	1.197746667
ENSOCUG00000010761 NPY	Oryctolagu: 10:9173130	0.231228667	1.274295
ENSOCUG00000019570 7SK	7SK RNA 7:12854278	0.245793	1.37086
ENSOCUG00000024878 HIST1H2AC	histone clus 12:109439:	0.59779	3.467386667
ENSOCUG00000004420 -	Uncharacte GL018810:	0.229043333	1.330296667
ENSOCUG00000011138 ASIP	Oryctolagu: 4:5435026-	0.441273333	2.618416667
ENSOCUG00000027760 -	Uncharacte AAGW020	0.206191333	1.256665667
ENSOCUG00000000407 DCT	dopachrom 8:9636606:	0.609787667	3.825333333
ENSOCUG00000025501 -	Uncharacte GL019618:	0.201555	1.320265333
ENSOCUG00000026224 HAMP	hepcidin an GL018786:	0.241785333	1.636441333
ENSOCUG00000029041 MMP23B	matrix met: GL018828:	0.155864333	1.089520333

ENSOCUG00000017845	MAB21L1	mab-21-like GL018702:	0.379245	2.79361
ENSOCUG00000024556	-	Uncharacterized AAGW020	0.187713	1.422983333
ENSOCUG00000018579	7SK	7SK RNA [6:1277457:	0.219948667	1.677423333
ENSOCUG00000025369	CLDN17	claudin 17 [14:1596980	0.223600333	1.723762333
ENSOCUG00000025011	snoU89	Small nucleolar RNA 8:3296863:	0.421433333	3.268873333
ENSOCUG00000015546	SLC24A4	solute carrier 20:1349799:	0.131180933	1.022830667
ENSOCUG00000027375	-	Uncharacterized 12:1116000	0.179472333	1.434786667
ENSOCUG00000009965	TYR	Oryctolagus 1:12756260	0.194426933	1.770066
ENSOCUG00000023644	7SK	7SK RNA [12:1225429:	0.164045333	1.49551
ENSOCUG00000016646	C10orf67	chromosome 10:18724:	0.125553667	1.200549667
ENSOCUG00000010189	OB	Oryctolagus 7:16060258	0.297447667	3.438422667
ENSOCUG00000026355	GSC	Oryctolagus GL018909:	0.233999	3.052023333
ENSOCUG00000029335	-	Uncharacterized 21:458883:	0.078496167	1.055434367
ENSOCUG00000011093	TRAV19	T cell receptor 17:423085:	0.062193	1.940761667
ENSOCUG00000021336	TRAV5	T cell receptor 17:421011:	1.00E-05	1.125755333
ENSOCUG00000022215	-	Uncharacterized GL019864:	1.00E-05	1.128003333
ENSOCUG00000028265	SCARNA13	Small Cajal 17:687724:	1.00E-05	1.141256667
ENSOCUG00000028173	-	Uncharacterized 2:9858581:	1.00E-05	1.162463333
ENSOCUG00000013324	HCRT	hypocretin 19:430028:	1.00E-05	1.173685333
ENSOCUG00000026861	-	Uncharacterized GL019260:	1.00E-05	1.210323333
ENSOCUG00000028651	7SK	7SK RNA [X:3766904	1.00E-05	1.324093333
ENSOCUG00000028534	SCARNA13	Small Cajal GL019009:	1.00E-05	1.456773333
ENSOCUG00000022649	APLN	Uncharacterized X:1040738	1.00E-05	1.49757
ENSOCUG00000025864	-	Uncharacterized GL019480:	1.00E-05	1.69256
ENSOCUG00000018249	SNORA73	Small nucleolar RNA 13:137020:	1.00E-05	1.791583333
ENSOCUG00000009468	GNG3	guanine nucleotide-binding protein 17:	1.00E-05	1.886516667
ENSOCUG00000019656	SNORA74	Small nucleolar RNA 18:5991800	1.00E-05	2.376926667
ENSOCUG0000002853	VGF	VGF nerve GL018831:	1.00E-05	2.400596
ENSOCUG00000023180	-	Uncharacterized 2:98664529	1.00E-05	2.559893333
ENSOCUG00000022854	-	Uncharacterized GL019739:	1.00E-05	2.563186667
ENSOCUG00000028699	U2	U2 spliceosomal RNA 12:1272810	1.00E-05	3.103563333
ENSOCUG00000012715	TBX5	T-box 5 [Sc 21:9757700	1.00E-05	3.583366667
ENSOCUG00000014604	TMPRSS11	transmembrane protein 15:813701:	16.6667	38.63506667
ENSOCUG00000022767	-	Uncharacterized 7:4123778-	15.3201	35.015
ENSOCUG00000000501	KRT82	keratin 82 [4:3645714:	13.9974	36.68553333
ENSOCUG00000024778	-	Uncharacterized 19:4205504	51.31616667	128.7837333
ENSOCUG00000007342	DSG4	desmoglein 9:72638264	13.80638667	30.1153
ENSOCUG00000017905	PCK1	phosphoenolpyruvate carboxykinase GL019719:	9.04342	26.71173333
ENSOCUG00000013802	ALDOC	aldolase C, 19:1958020	10.33132333	24.06363333
ENSOCUG00000021675	-	Uncharacterized 19:421059:	41.174	104.9704
ENSOCUG00000027394	-	Uncharacterized 2:9814389:	7.71983	22.62971333
ENSOCUG00000000725	MC5R	melanocortin receptor 9:4833691:	5.318493333	16.72933
ENSOCUG00000016071	ELOVL3	ELOVL fat 18:5022204	6.72973	13.36550667
ENSOCUG00000026053	MYCN	v-myc avian 2:1649054:	6.262503333	13.14029333
ENSOCUG00000017782	ACE2	angiotensin-converting enzyme 2:1396877	6.198853333	13.41788333
ENSOCUG00000023092	-	Uncharacterized 4:36335214	4.504123333	14.75333667
ENSOCUG00000029278	KRT78	keratin 78 [4:36772250	5.319533333	12.35142667
ENSOCUG00000015615	KRTAP3-1	keratin associated protein 19:4206690	674.4783333	1591.683667
ENSOCUG00000023053	-	Uncharacterized 19:4231530	46.20983333	118.8643333
ENSOCUG00000007460	SOD3	Oryctolagus 2:1539109:	19.27243333	51.47133333

ENSOCUG00000003849	C6orf226	chromosom 12:324190	5.965666667	11.36153333
ENSOCUG00000001230	XDH	xanthine de 2:1547262	5.949923333	11.83316
ENSOCUG000000021249	-	Uncharacte 13:389941	5.299616667	11.55007667
ENSOCUG000000026651	-	Uncharacte GL019133	3.743377667	12.03156633
ENSOCUG00000009045	ASS1	argininosuc GL019049	3.38385	12.18141333
ENSOCUG00000005302	CIDEC	cell death-i GL018802	3.978993333	11.00131333
ENSOCUG000000024526	-	Uncharacte 2:98664529	3.817931333	11.76538667
ENSOCUG000000022099	-	Uncharacte GL019218	20.88821	45.4856
ENSOCUG000000029454	AADACL2	arylacetami 14:457542	4.310533333	9.35858
ENSOCUG00000005355	-	19:421516	4.16098	9.574283333
ENSOCUG000000025985	-	Uncharacte 4:3640743	14.61788667	39.19756667
ENSOCUG000000017620	-	Oryctolagu GL018733	2.960006667	9.916707
ENSOCUG00000003668	LCK	LCK proto- GL018704	3.976513333	7.05741
ENSOCUG000000013829	KCTD4	potassium c 8:4984311	3.71446	7.920183333
ENSOCUG00000005636	-	Uncharacte GL018810	3.351413333	7.2229
ENSOCUG000000014207	ELF5	E74-like fa 1:1737640	3.023756667	7.96725
ENSOCUG000000010762	CHAC1	ChaC, catic 17:311281	14.28763333	32.21733333
ENSOCUG000000009827	TUBB2A	tubulin, bet GL018715	13.57597	29.95286667
ENSOCUG000000023380	CYP3A6	Oryctolagu GL018760	3.934346667	6.013876667
ENSOCUG000000010465	EPHA3	EPH recept 14:1274670	3.823623333	6.00033
ENSOCUG000000003157	DCBLD1	discoidin, C 12:106423	3.946113333	6.215593333
ENSOCUG000000028069	-	Uncharacte 2:9890482	3.98422	6.336808333
ENSOCUG000000017475	ZBTB37	zinc finger 13:121272	3.852053333	6.127976667
ENSOCUG000000016706	KIF11	kinesin fam 18:404007	3.906093333	6.21591
ENSOCUG000000013023	GK	Uncharacte X:1674232	3.805396667	6.1646
ENSOCUG000000006361	FAM180B	family with 1:1869059	3.791463333	6.157566667
ENSOCUG000000008600	FPR	Oryctolagu GL018792	3.70059	6.020786667
ENSOCUG000000023825	SNCA	synuclein, ε 15:601627	3.72031	6.147736667
ENSOCUG000000008504	CD300LG	CD300 mol 19:4426338	3.988673333	6.61095
ENSOCUG000000003970	TAGLN3	transgelin 3 14:107184	3.614453333	6.00644
ENSOCUG000000011972	EBF2	early B-cell 2:4363903	3.881473333	6.594096667
ENSOCUG000000004719	TNFAIP8L2	Oryctolagu 13:410402	3.921163333	6.7017
ENSOCUG000000003142	AR	Androgen r X:4628842	3.78285	6.60129
ENSOCUG000000006003	ERP27	endoplasmic 8:24645920	3.567175	6.747026667
ENSOCUG000000021520	RASD2	RASD fam: GL019302	3.501166667	6.7593
ENSOCUG000000015927	CITED4	Cbp/p300-i 13:1257160	3.503213333	6.932386667
ENSOCUG000000021409	-	Uncharacte 20:143358	3.198942333	6.605353333
ENSOCUG000000015593	KRT39	keratin 39 [19:420056	29.30243333	65.12703333
ENSOCUG000000023482	SP6	Sp6 transcr 19:3948978	12.03303	27.86526667
ENSOCUG000000023989	-	Uncharacte 2:98469700	1.049253333	7.050029667
ENSOCUG000000012398	SLC30A1	solute carri 16:6135224	27.5823	61.2351
ENSOCUG000000010870	CLMN	calmin (cal) GL018909	2.966573333	5.073766667
ENSOCUG000000027615	-	Uncharacte GL018806	2.746173667	5.003370333
ENSOCUG000000006381	LY86	lymphocyte 12:362030	2.80954	5.189996667
ENSOCUG000000027805	PLCXD2	phosphatidy 14:107473	2.979693333	5.83939
ENSOCUG000000008329	ADAMTS15	ADAM me 3:1299392	2.412195333	5.070086667
ENSOCUG000000001968	COL9A3	collagen, ty GL019426	2.619656667	5.898216667
ENSOCUG000000007677	-	Uncharacte 13:126722	2.36484	5.386623333
ENSOCUG000000022798	-	chromosom 2:9304629	2.141992333	5.129496667
ENSOCUG000000014595	TBX3	T-box 3 [Sc 21:998180	2.360853333	5.97282

ENSOCUG00000002875	STOX1	storkhead b 18:1785750	2.212096667	5.61857
ENSOCUG000000029489	-	Uncharacte AAGW020	26.17462333	59.03168667
ENSOCUG000000014497	EFHD1	EF-hand dc GL018736:	11.13194667	24.28383333
ENSOCUG000000009880	DUSP14	dual specifi 19:2544040	24.92663333	53.56686667
ENSOCUG000000011173	-	Uncharacte 19:4241752	20.35146	56.95026667
ENSOCUG000000022878	C1orf53	chromosom 16:7330124	20.01014	56.4038
ENSOCUG000000015331	GPRC5D	G protein-c 8:26808777	58.02383333	149.4059333
ENSOCUG000000006802	LCORL	ligand depe 2:8406292-	2.954113333	4.178353333
ENSOCUG000000010209	CLDN15	claudin 15 GL018831:	2.95895	4.2383
ENSOCUG000000001171	NUF2	NUF2, ND 13:2960330	2.768123333	4.01928
ENSOCUG000000015108	-	7:15953924	2.997216667	4.361306667
ENSOCUG000000026716	MBLAC2	metallo-bet 11:1021999	2.7893	4.134826667
ENSOCUG000000025990	PRSS27	protease, se GL018828:	2.773933333	4.149983333
ENSOCUG000000003535	CP	ceruloplasn 14:4292839	2.85923	4.279366667
ENSOCUG000000027782	MSMP	microsemir 1:18090637	2.710991	4.08488
ENSOCUG000000001437	-	GL018914:	2.610386667	4.007493333
ENSOCUG000000003204	MAP3K9	mitogen-ac GL018749:	2.807212	4.34948
ENSOCUG000000025420	EID2B	EP300 inter 5:462544-4	2.807646667	4.410546667
ENSOCUG000000025618	PRR7	proline rich 3:57965128	2.769646667	4.384843333
ENSOCUG000000009840	SLC46A2	solute carri 1:456316-4	2.880703333	4.570346667
ENSOCUG000000008207	CAPN8	calpain 8 [S 16:4956260	2.543743333	4.051963333
ENSOCUG000000013808	GPR68	G protein-c 20:1448820	2.769563333	4.477196667
ENSOCUG000000007896	MILR1	mast cell in 19:4929750	2.508773333	4.181866667
ENSOCUG000000022891	NOVA2	neuro-onco GL019168:	2.809806667	4.74119
ENSOCUG000000011780	CYFIP2	cytoplasmic 3:38752688	2.351143333	4.03425
ENSOCUG000000027617	-	GL019085:	2.790073333	4.82811
ENSOCUG000000002901	-	Uncharacte GL018806:	2.373363	4.109770667
ENSOCUG000000010624	POLR3G	polymerase 11:1024740	2.813543333	4.92549
ENSOCUG000000007182	GAS2L3	growth arre 4:79820997	2.289923333	4.022866667
ENSOCUG000000009277	RND2	Rho family 19:4369841	2.549446667	4.612143333
ENSOCUG000000023337	HOXB3	homeobox 19:3849778	2.404633333	4.404326667
ENSOCUG000000014362	ITGAL	integrin, al GL018752:	2.294422333	4.247367333
ENSOCUG000000007526	CTH	cystathionin 13:9562249	2.341996667	4.500646667
ENSOCUG000000004261	SLC35G1	solute carri 18:4158568	2.449236667	4.86335
ENSOCUG000000011441	-	solute carri 8:5864933-	2.381616667	4.791443333
ENSOCUG000000011230	MMP16	matrix met 3:10346475	2.064953333	4.17235
ENSOCUG000000026950	-	Uncharacte GL019171:	2.027043333	4.341756667
ENSOCUG000000018292	7SK	7SK RNA [11:1166590	2.240676667	4.86655
ENSOCUG000000014767	PAG1	phosphoprc 3:9665550	2.07418	4.5711
ENSOCUG000000017793	CD38	Oryctolagu 2:6298523-	2.234327667	4.997563333
ENSOCUG000000016256	HAND2	heart and n 2:51438992	0.046627667	5.0414
ENSOCUG000000029124	-	Uncharacte 2:9848156:	1.00E-05	5.101146667
ENSOCUG000000021624	GNPTG	N-acetylglu AAGW020	1.00E-05	5.3016
ENSOCUG000000003454	PRDM6	PR domain 3:7295523-	0.772645333	4.304963333
ENSOCUG000000017941	-	Oryctolagu 15:762810:	0.544083	4.044773333
ENSOCUG000000004318	PRM3	protamine 6:4835743-	1.00E-05	4.150166667
ENSOCUG000000028998	-	Uncharacte 13:3924779	1.00E-05	4.1879
ENSOCUG000000025346	-	Uncharacte GL018714:	1.00E-05	4.227533333
ENSOCUG000000015682	-	Oryctolagu GL018717:	1.00E-05	4.244593333
ENSOCUG000000020067	SNORA81	Small nucle 14:7883899	1.00E-05	4.493966667

ENSOCUG00000018026	U3	Small nucle	19:293237	1.00E-05	4.718743333
ENSOCUG00000001156	HOXC13	homeobox	4:37314596	19.42003333	41.6063
ENSOCUG00000006938	CSDC2	cold shock	GL018734	7.760876667	15.13086
ENSOCUG00000015168	PLB1	Oryctolagu	2:15745924	7.710403333	15.49623333
ENSOCUG00000027219	IGJ	immunoglo	15:7930209	7.293583333	15.01868
ENSOCUG00000009450	ARHGAP18	Rho GTPas	12:119574	7.959926667	14.1733
ENSOCUG00000003423	SDR9C7	short chain	GL018714	7.79285	14.10433333
ENSOCUG00000009993	DACT2	dishevelled	GL018930	7.467833333	14.2987
ENSOCUG00000002140	DACH1	dachshund	8:7279297	7.10093	14.14693333
ENSOCUG00000027057	-	Uncharacte	14:4582474	7.002896667	14.03551667
ENSOCUG00000008934	IL12RB2	interleukin	13:9885716	1.98756	2.029033333
ENSOCUG00000000875	FAM124A	family with	GL018705	1.94971	2.0432
ENSOCUG00000011321	-	Uncharacte	15:4389999	1.866493333	2.006633333
ENSOCUG00000009941	KIAA0226L	KIAA0226	8:48785358	1.90937	2.058543333
ENSOCUG00000007339	PLCB1	phospholip	4:27356194	1.95906	2.12927
ENSOCUG00000001178	FAM78B	family with	13:2673158	1.98062	2.15293
ENSOCUG00000014388	ZCWPW1	zinc finger,	6:2737170	1.980933333	2.154246667
ENSOCUG000000023919	-	Uncharacte	15:461978	1.88962	2.066459667
ENSOCUG00000023661	-	Uncharacte	2:5457724	1.875723333	2.056833333
ENSOCUG00000001393	SYP	synaptophy	X:3376844	1.86881	2.059758
ENSOCUG00000011254	BEND3	BEN doma	12:9516544	1.965173333	2.18946
ENSOCUG00000005788	SLC22A7	Oryctolagu	12:3274719	1.880373333	2.10763
ENSOCUG00000017084	HCN1	Oryctolagu	11:6583062	1.876666667	2.129656667
ENSOCUG00000011827	RASSF6	Ras associa	15:764728	1.869993333	2.12242
ENSOCUG00000010513	CEP55	centrosoma	18:412071	1.76409	2.017865333
ENSOCUG00000003504	-	Uncharacte	19:2456692	1.94815	2.243566667
ENSOCUG00000012434	CCDC18	coiled-coil	13:712442	1.813753333	2.09355
ENSOCUG00000012546	ZNF462	zinc finger	1:6112090	1.951086667	2.259953333
ENSOCUG00000023139	-	Uncharacte	GL018700	1.790230333	2.080729
ENSOCUG00000029676	ZNF214	zinc finger	1:1484943	1.876593333	2.18309
ENSOCUG00000003812	EPHB1	EPH recept	14:2867450	1.858753333	2.171283333
ENSOCUG00000010319	TBC1D30	TBC1 dom	4:43570212	1.971956667	2.311986667
ENSOCUG00000029468	ZNF83	zinc finger	GL018792	1.72752	2.040195667
ENSOCUG00000003824	-	Uncharacte	3:13618039	1.83478	2.17161
ENSOCUG00000011244	ESPL1	extra spindl	4:3710105	1.948596667	2.308923333
ENSOCUG00000015480	POLE2	polymerase	17:687962	1.69789	2.029416667
ENSOCUG00000002595	ANKRD33B	ankyrin rep	11:3550666	1.704654667	2.039986667
ENSOCUG00000002369	ITK	IL2-inducit	3:38647944	1.960436667	2.354496667
ENSOCUG00000005253	GNAL	guanine nu	9:5002141	1.789106667	2.15826
ENSOCUG00000008092	ACOT11	acyl-CoA tl	13:112262	1.958193333	2.36651
ENSOCUG00000001041	MELK	maternal en	1:1735659	1.84243	2.232573333
ENSOCUG00000005948	DMXL2	Dmx-like 2	17:2090750	1.826606667	2.214373333
ENSOCUG00000023894	-	Uncharacte	17:151881	1.881518	2.28827
ENSOCUG00000003319	HLA-DPA1	major histo	12:2351939	1.760171333	2.156396667
ENSOCUG00000015252	BBS12	Bardet-Bie	15:9858039	1.984253333	2.46147
ENSOCUG00000011383	C4orf32	chromosom	15:3725190	1.95721	2.42925
ENSOCUG00000009148	SERPINB8P	Oryctolagu	9:10393990	1.88528	2.34808
ENSOCUG00000004027	TRAF3IP3	TRAF3 int	16:628908	1.623813333	2.022646
ENSOCUG00000021174	-	Uncharacte	GL018989	1.716123333	2.137965333
ENSOCUG00000004941	ZNF852	zinc finger	9:8249967	1.604713333	2.012943333

ENSOCUG00000017539	SYK	spleen tyros 1:77228940	1.843566667	2.31382
ENSOCUG00000006258	WDR72	WD repeat 17:1883550	1.98726	2.514353333
ENSOCUG00000010775	CDKL5	cyclin-depe X:4345275	1.973393333	2.50031
ENSOCUG00000024968	-	40S ribosor GL018790:	1.631046667	2.072296667
ENSOCUG00000008075	ATP8B4	ATPase, ck 17:223394	1.659643	2.148496667
ENSOCUG00000006682	-	GL018789:	1.572912667	2.046076667
ENSOCUG00000014516	CCDC68	coiled-coil 9:9547820:	1.994516667	2.595246667
ENSOCUG00000022964	-	2:5487763:	1.962935	2.555643333
ENSOCUG00000008522	LHX6	LIM homec GL018699:	1.761214667	2.297426667
ENSOCUG00000006720	FGD2	FYVE, Rho 12:268806:	1.964300333	2.568653333
ENSOCUG00000010148	-	Uncharacte GL018902:	1.724713333	2.25894
ENSOCUG00000012783	DAGLA	diacylglyce GL018717:	1.713603333	2.252546667
ENSOCUG00000013105	PLCG2	phospholip: 5:3609502:	1.964836667	2.58285
ENSOCUG00000014109	CDCA2	cell divisio 2:4415205:	1.570723333	2.074523333
ENSOCUG00000025892	-	Uncharacte GL018806:	1.777481667	2.365329667
ENSOCUG00000000547	SGOL2	shugoshin-17:1411678:	1.671336667	2.229046667
ENSOCUG00000027535	PEG10	paternally e 10:342773:	1.93218	2.588683333
ENSOCUG00000014255	DUOX2	dual oxidas 17:2737440	1.725205333	2.314516667
ENSOCUG00000014936	-	14:306052:	1.75659	2.365573333
ENSOCUG00000003656	CDH2	Uncharacte 9:69300650	1.683873333	2.271343333
ENSOCUG00000025069	-	Histone H2 12:110204:	1.903891667	2.578356667
ENSOCUG00000024656	NCX1	Uncharacte 2:1460470:	1.96932	2.66815
ENSOCUG00000012699	FYB	FYN bindir 11:601480:	1.791023667	2.4325
ENSOCUG00000016491	KIF14	kinesin fam 16:707593:	1.95574	2.658486667
ENSOCUG00000017719	NEK5	NIMA-rela GL018705:	1.87061	2.55597
ENSOCUG00000029283	ZNF484	Uncharacte 1:7002926:	1.964193333	2.685123333
ENSOCUG00000000436	-	Uncharacte GL018782:	1.623165333	2.229139
ENSOCUG00000026148	KBTBD8	kelch repea 9:3421771:	1.697836667	2.344276667
ENSOCUG00000008174	STAMBPL1	STAM binc 18:367968:	1.99713	2.772866667
ENSOCUG00000027052	-	Uncharacte GL018752:	1.735913333	2.416443333
ENSOCUG00000009580	WNT10B	wingless-ty 4:33265510	1.698615333	2.36553
ENSOCUG00000000121	LRR1	leucine rich 17:687569:	1.94109	2.71305
ENSOCUG00000011054	PIK3CD	phosphatid 13:140429:	1.740573333	2.434047667
ENSOCUG00000016477	SELP	selectin P (13:217256:	1.697575333	2.37622
ENSOCUG00000026180	XKR8	XK, Kell bl 13:137530:	1.52324	2.134616667
ENSOCUG00000001906	HRH1	histamine r 9:1252342:	1.83964	2.581376667
ENSOCUG00000001304	AGAP2	ArfGAP wi GL018714:	1.86485	2.648243333
ENSOCUG00000004485	E2F8	E2F transcr 1:1581551:	1.925683333	2.742383333
ENSOCUG00000004162	PRRT3	proline-rich GL018802:	1.573516667	2.2414
ENSOCUG00000012557	SOX6	SRY (sex d GL018733:	1.483994333	2.114926667
ENSOCUG00000022315	KIAA1199	cell migrati GL018737:	1.812793333	2.588753333
ENSOCUG00000010078	GPB1	G protein-c GL019453:	1.694896667	2.42075
ENSOCUG00000000528	TCF15	transcriptio 4:8193969-	1.75927	2.515316667
ENSOCUG00000029622	-	Uncharacte 13:3571400	1.848846667	2.646743333
ENSOCUG00000026015	-	Uncharacte 5:22586300	1.914563333	2.744716667
ENSOCUG00000012739	PIK3CG	phosphatid 7:4334946:	1.758716667	2.533983333
ENSOCUG00000024118	CDT1	chromatin I GL019360:	1.61473	2.3374
ENSOCUG00000025837	NFAM1	NFAT activ GL018734:	1.686166667	2.441779667
ENSOCUG00000001366	-	Uncharacte 7:10862160	1.456276	2.110396667
ENSOCUG00000005507	GNA14	guanine nu 1:63848019	1.41317	2.052763333

ENSOCUG00000021352	-	Uncharacte	GL018724:	1.580506667	2.29982
ENSOCUG00000015410	NDC80	NDC80 kin	9:59439910	1.424253333	2.075876667
ENSOCUG00000003325	SOWAHC	sonondowal	2:83058560	1.64339	2.398246667
ENSOCUG00000026297	NXPH2	neurexophi	7:76530820	1.734313333	2.532136667
ENSOCUG00000001933	PTPRJ	protein tyrc	1:18729054	1.425153333	2.085213333
ENSOCUG00000010020	DNAJC6	DnaJ (Hsp4	13:1009634	1.964823333	2.877396667
ENSOCUG00000009729	RNF43	ring finger	19:2985014	1.903423333	2.795926667
ENSOCUG00000010144	TTC22	tetratricope	13:1121268	1.666573333	2.470151
ENSOCUG00000022067	DLX4	distal-less	19:3767024	1.767885667	2.649450667
ENSOCUG00000004077	SLC4A11	solute carri	4:10162600	1.97041	2.959176667
ENSOCUG00000000699	CENPE	centromere	15:4642357	1.402413333	2.11086
ENSOCUG00000021348	ZNF771	zinc finger	GL018763:	1.534803333	2.312306667
ENSOCUG00000006792	NCAPG	non-SMC c	2:8357628-	1.89015	2.855356667
ENSOCUG00000004450	CCNF	cyclin F [S	GL018968:	1.36318	2.063706667
ENSOCUG00000029391	ZNF668		GL018752:	1.93849	2.93985
ENSOCUG00000011299	CHEK2	checkpoint	GL018723:	1.368686667	2.079073333
ENSOCUG00000009143	CCNE1	cyclin E1 [	GL018722:	1.628930667	2.47792
ENSOCUG00000006806	ZWINT	ZW10 inter	18:2971834	1.37674	2.098016667
ENSOCUG00000006954	PRF1	perforin 1	(18:1642992	1.392940333	2.1247638
ENSOCUG00000011694	HECW2	HECT, C2	7:13662787	1.853886667	2.829153333
ENSOCUG00000022021	IL22RA2	interleukin	12:1275648	1.433616667	2.191200333
ENSOCUG00000027916	FZD5	frizzled cla	7:14864675	1.868406667	2.86084
ENSOCUG00000015382	MAB21L3	mab-21-lik	13:4814520	1.823203333	2.794033333
ENSOCUG00000013471	LIPG	lipase, endc	9:90453684	1.595716667	2.449046667
ENSOCUG00000006436	-	Uncharacte	7:7973608-	1.580766333	2.430946667
ENSOCUG00000021020	KDM8	lysine (K)-	s 6:17405711	1.809826667	2.789063333
ENSOCUG00000011957	AURKB	aurora kina	19:1105280	1.884393333	2.936153333
ENSOCUG00000017771	BMX	BMX non-i	X:1339703	1.520502667	2.37085
ENSOCUG00000002510	SNCB	synuclein,	13:5709923	1.898353333	2.964493333
ENSOCUG00000008255	CENPM	centromere	GL018734:	1.420224333	2.221293333
ENSOCUG00000027480	-	Uncharacte	AAGW020	1.69222	2.674317333
ENSOCUG00000015756	CASC5	cancer susc	17:3137580	1.344683	2.159333333
ENSOCUG00000014008	CHAF1B	chromatin ε	GL018727:	1.660576667	2.683563333
ENSOCUG00000021564	-	Uncharacte	GL018704:	1.315353333	2.131116667
ENSOCUG00000003606	KIF21B	kinesin fam	16:7039684	1.534061	2.489773333
ENSOCUG00000023797	-	Uncharacte	13:1269757	1.5455	2.517083333
ENSOCUG00000010075	TRABD2A	TraB doma	2:10131211	1.302249667	2.132636667
ENSOCUG00000024415	-	60S ribosor	3:81763132	1.640428	2.728886667
ENSOCUG00000014866	HEPH	hephaestin	X:4473128	1.461666667	2.47022
ENSOCUG00000022391	-	Uncharacte	10:2147387	1.36099	2.323061
ENSOCUG00000023219	ASPG	asparaginas	GL018751:	1.376586667	2.352026
ENSOCUG00000006383	GHRL	ghrelin/obe	GL018802:	1.530533333	2.630573333
ENSOCUG00000023214	P2RY11	purinergic	1 GL018833:	1.592063333	2.747746667
ENSOCUG00000000574	PLEKHH1	pleckstrin	h 20:4656675	1.184193333	2.06347
ENSOCUG00000010412	-		7:16271330	1.374603333	2.419471
ENSOCUG00000009079	MATN4	matrilin 4	[GL018725:	1.160174333	2.047083333
ENSOCUG00000024221	INMT	indolethyla	10:1506360	1.492246667	2.678473333
ENSOCUG00000028503	SCARNA6	Small Cajal	GL018736:	1.242883333	2.26955
ENSOCUG00000020988	ANGPTL6	angiopoieti	GL018833:	1.167913333	2.14669
ENSOCUG00000027953	-	Histone H2	12:1080440	1.188574667	2.199893333

ENSOCUG00000009751	HCK	HCK proto:4:7202138-	1.505083	2.819153
ENSOCUG00000005976	-	Uncharacte GL018806:	1.177090667	2.208276
ENSOCUG000000011446	LHFPL5	lipoma HM12:2583260	1.241106333	2.32966
ENSOCUG000000002020	LGI3	leucine-rich GL018798:	1.286196667	2.41606
ENSOCUG000000023227	-	Uncharacte 15:2432499	1.150374667	2.162853333
ENSOCUG000000010754	NIPA1	non imprint 17:775946:	1.237428667	2.3435
ENSOCUG000000021982	-	Uncharacte 13:722319:	1.104136	2.094323333
ENSOCUG000000009872	TMEM178A	transmembr 2:14656978	1.105146	2.106333333
ENSOCUG000000015935	TCF7	transcriptio 3:1694602:	1.180053333	2.252643667
ENSOCUG000000022454	FOXE1	forkhead bc 1:15222380	1.245960667	2.39084
ENSOCUG000000001351	CD96	CD96 mole 14:107561:	1.2781401	2.472095333
ENSOCUG000000002794	ZNF618	zinc finger GL018699:	1.286974	2.49089
ENSOCUG000000015037	UGT8	UDP glyco: 15:347808:	1.312493	2.552846667
ENSOCUG000000017070	P2RY4	pyrimidinei X:4881466	1.096158	2.149730667
ENSOCUG000000002661	-	Uncharacte 12:104750:	1.505538433	2.961990333
ENSOCUG000000007928	APOM	apolipoprot 12:2046768	1.043916	2.07522
ENSOCUG000000016173	WNT2	Oryctolagu: 7:27896340	1.145591	2.456020667
ENSOCUG000000015611	SCUBE3	signal pepti 12:253228:	1.124546333	2.449663333
ENSOCUG000000011287	-	Uncharacte 4:7271374:	1.267438	2.80013
ENSOCUG000000017125	GPR19	G protein-c 8:2707312:	1.270506667	2.819016667
ENSOCUG000000016862	SHH	sonic hedge 13:1151960	1.069206667	2.61601
ENSOCUG000000006095	GLB1L2	galactosida GL018742:	1.000369	2.463367667
ENSOCUG000000021306	HIST1H2AE	12:1101238	1.07994	2.726696667
ENSOCUG000000010806	AP1S3	adaptor-rel: 7:1652652:	1.001401667	2.94855
ENSOCUG000000018093	U5	U5 spliceos GL018739:	94.259	240.57
ENSOCUG000000002612	KRT84	keratin 84 [4:3644335:	14.36623333	30.1767
ENSOCUG000000013134	ST8SIA1	ST8 alpha-18:17831289	6.973943333	12.61317333
ENSOCUG000000027708	U1	U1 spliceos 17:5435280	6.006766667	12.0019
ENSOCUG000000006831	GNG4	guanine nu: 16:326429:	3.995823333	14.35868667
ENSOCUG000000016227	SVEP1	sushi, von 11:2642081-	12.93697	25.08766667
ENSOCUG000000008528	-	Uncharacte 19:4208964	12.44433333	25.8798
ENSOCUG000000022283	DCUN1D3	DCN1, def: 6:1174094:	5.867193333	10.16083333
ENSOCUG000000021137	SFRP5	secreted fri: 18:459213:	5.932106667	10.63611667
ENSOCUG000000008647	S100A3	S100 calciu 13:389083:	86.49603333	192.172
ENSOCUG000000029367	C1QA	complemen 13:1304898	12.78452667	24.19966667
ENSOCUG000000002203	PTN	pleiotrophin 7:1421173-	12.79536	24.4085
ENSOCUG000000026465	BTNL9	butyrophilin 11:3168549	12.84696667	24.91473333
ENSOCUG000000007366	ENDOU	endonuclea 8:42324-50	12.24523333	24.39976667
ENSOCUG000000011380	CIDEA	cell death-i 9:4984499:	12.16893333	24.81196667
ENSOCUG000000015143	-	13:130475:	11.85092333	23.26806667
ENSOCUG000000011686	-	solute carri 9:17681390	11.05005333	23.53626667
ENSOCUG000000012871	CDNF	cerebral do: 16:4634350	1.875466667	1.039599333
ENSOCUG000000022728	-	Uncharacte GL018709:	1.755956667	1.004676333
ENSOCUG000000015966	-	GL018710:	1.896828667	1.108823667
ENSOCUG000000027809	-	Uncharacte 13:605583:	1.840848667	1.093688333
ENSOCUG000000013668	-	Uncharacte 1:11742784	1.68368	1.028569333
ENSOCUG000000017762	-	7:15858630	1.597009333	1.020511333
ENSOCUG000000022800	C5orf52	chromosom 21:3222510	1.90118	1.218157667
ENSOCUG000000003033	GDNF	glial cell de 11:5882268	1.562350667	1.006111
ENSOCUG000000003724	MEGF10	multiple EC3:11015809	1.891346667	1.224504667

ENSOCUG00000015838	COL9A2	collagen, ty 13:126185	1.642273333	1.063896667
ENSOCUG00000013331	-	Glutathione X:6195658	1.94693	1.266960667
ENSOCUG00000015454	AGBL1	ATP/GTP t GL018797	1.567169667	1.039077667
ENSOCUG00000002903	ST8SIA2	ST8 alpha-l GL018759	1.98966	1.348098333
ENSOCUG00000022375	CRYGS	Oryctolagu 14:790446	1.86267	1.272636667
ENSOCUG00000008298	FAXC	failed axon 12:869151	1.554619667	1.068041667
ENSOCUG00000024121	CABYR	calcium bin 9:6530087	1.5498	1.068086667
ENSOCUG00000012952	-	Uncharacte 13:244525	1.517684667	1.051259
ENSOCUG00000027366	WAC	Uncharacte GL018707	1.502686667	1.051390333
ENSOCUG00000016341	RAB37	RAB37, mc GL018989	1.50327	1.066223333
ENSOCUG00000024604	-	Uncharacte 4:5348996	1.816143767	1.290131
ENSOCUG00000027207	FANCE	Fanconi an 12:255231	1.987136667	1.411923333
ENSOCUG00000027691	-	Uncharacte 4:3685107	1.475090667	1.053766
ENSOCUG00000014768	NRCAM	neuronal ce 7:4471602	1.534273333	1.100664667
ENSOCUG00000016324	CIT	citron rho-i 21:126851	1.919873333	1.377306667
ENSOCUG00000006107	GRAMD2	GRAM dor 17:340305	1.396295333	1.001789667
ENSOCUG00000016450	NTF3	neurotroph 8:3152859	1.88259	1.351855333
ENSOCUG00000011599	CACNA1C	calcium cha 8:3501363	1.75896	1.263952667
ENSOCUG00000025713	ASGR1	asialoglyco 19:119517	1.893463333	1.364566667
ENSOCUG00000007204	SLC39A5	solute carri 4:3979373	1.91009	1.377426667
ENSOCUG00000014561	CDH20	cadherin 20:1017803	1.939686667	1.402016667
ENSOCUG00000023917	EBF4	early B-cell 4:9574724	1.979113333	1.45335
ENSOCUG00000022301	SLC37A1	solute carri GL019109	1.763036667	1.295517667
ENSOCUG00000023860	ADRA2B	adrenocept 2:9517815	1.914973333	1.412356333
ENSOCUG00000010801	PPEF1	protein pho X:4536499	1.891703333	1.40221
ENSOCUG00000005785	BAI2	brain-speci GL018704	1.777016667	1.317364667
ENSOCUG00000005993	-	Uncharacte GL018831	1.599891667	1.190124333
ENSOCUG00000003044	SPA17	Oryctolagu 1:9255234	1.66152	1.245673
ENSOCUG00000024851	DOC2B	double C2- 19:167961	1.379916667	1.040501
ENSOCUG00000009667	GABRE	gamma-am GL018731	1.642746667	1.240084333
ENSOCUG00000016937	PDZD3	PDZ domai GL018823	1.505362667	1.136387333
ENSOCUG00000029194	KRT3	Keratin, ty 4:3673370	1.628387	1.230174
ENSOCUG00000029334	-	Uncharacte GL018731	1.485906667	1.123929333
ENSOCUG00000003273	GPIIB	Oryctolagu 19:446483	1.884293333	1.43532
ENSOCUG00000021330	-	chromosom GL018717	1.792933333	1.368993667
ENSOCUG00000017803	-	Uncharacte GL018999	1.51071	1.157155667
ENSOCUG00000004997	MST1	macrophag 9:1719170	1.68629	1.292186667
ENSOCUG00000004155	ACOX2	Oryctolagu 9:2526640	1.447036667	1.109627667
ENSOCUG00000029704	-	Uncharacte 9:3603739	1.65746	1.272715
ENSOCUG00000004594	MND1	meiotic nuc 15:954567	1.804341	1.38907
ENSOCUG00000025849	TEX29	testis expre GL019372	1.679752	1.294285667
ENSOCUG00000004441	PBLD	phenazine t 18:183300	1.837673333	1.41802
ENSOCUG00000028095	-	Uncharacte 12:594498	1.593034667	1.230398
ENSOCUG00000023544	-	Uncharacte GL018991	1.394068667	1.076866667
ENSOCUG00000024498	-	Uncharacte 13:524887	1.327180333	1.028714
ENSOCUG00000007717	IL2RB	interleukin GL018973	1.749690333	1.356434667
ENSOCUG00000002982	MYRFL	myelin reg 4:4890654	1.744876667	1.355623333
ENSOCUG00000029750	-	Uncharacte GL019624	1.561436667	1.217280667
ENSOCUG00000021776	POU2F2	POU class : GL018789	1.579729667	1.231807333
ENSOCUG00000025997	HAUS8	HAUS augi GL018776	1.51404	1.182116667

ENSOCUG00000014235	GALNT9	polypeptide GL018821:	1.30083	1.018289667
ENSOCUG00000013397	RPL23A	Uncharacte GL018706:	1.451859333	1.137510333
ENSOCUG00000003665	CCR5	Oryctolagu 9:1456070:	1.397687333	1.095179333
ENSOCUG00000022648	-	Uncharacte 9:4340243:	1.39908	1.096987333
ENSOCUG00000027361	-	Uncharacte 18:5214918:	1.751054667	1.37495
ENSOCUG00000007165	ISLR2	immunoglo GL019108:	1.635706667	1.287178333
ENSOCUG00000025408	-	Uncharacte AAGW020:	1.568634667	1.237609
ENSOCUG00000007425	CADPS2	Ca++-depe 7:21978279:	1.533596667	1.210673333
ENSOCUG00000023484	HHIPL1	HHIP-like GL018761:	1.39895	1.106772333
ENSOCUG00000025569	CCR7	chemokine 19:416754:	1.774905	1.404659
ENSOCUG00000007453	SMAD9	SMAD fam GL018702:	1.299726667	1.033378
ENSOCUG00000006702	GPR37	G protein-c 7:1979460:	1.297145333	1.03746
ENSOCUG00000022131	-	GL018765:	1.51129	1.215440667
ENSOCUG00000017394	SCNN1G	sodium cha 6:1400826:	1.84429	1.488233333
ENSOCUG00000016911	TDRD12	tudor doma 5:2736728:	1.549726667	1.250633333
ENSOCUG00000021238	-	Uncharacte GL018980:	1.479643333	1.19479
ENSOCUG00000017128	NMU	Neuromedi 15:932005:	1.766536667	1.429456667
ENSOCUG00000002909	GRB14	growth fact 7:1038596:	1.926763333	1.566033333
ENSOCUG00000000945	SRSF12	serine/argir 12:759577:	1.679433333	1.36564
ENSOCUG00000015552	PLXNA4	plexin A4 [7:1062232:	1.82562	1.488053333
ENSOCUG00000025473	MMP17	matrix met: GL019345:	1.546096667	1.2687
ENSOCUG00000012312	CLEC4D	C-type lecti 8:3350003:	1.57747	1.294929
ENSOCUG00000017835	DNMT3B	DNA (cyto: 4:6631097-	1.644773333	1.350323333
ENSOCUG00000004484	GLRB	glycine rec: 15:678724:	1.805873667	1.484493333
ENSOCUG00000026986	-	Uncharacte 2:9917989:	1.318225	1.084754333
ENSOCUG00000006139	SEMA5B	sema doma 14:9615328:	1.86989	1.543071667
ENSOCUG00000014251	WDR31	WD repeat 1:11368-33	1.501403333	1.239486667
ENSOCUG00000006100	-	Uncharacte 2:11795919:	1.753626667	1.449523
ENSOCUG00000017727	-	Uncharacte GL018705:	1.686663333	1.405536667
ENSOCUG00000003302	MAP6	microtubul 1:1410938:	1.996316667	1.66467
ENSOCUG00000013508	IL17RB	interleukin 9:2081058:	1.380478333	1.154452333
ENSOCUG00000022568	-	Uncharacte 4:3731459:	1.60144	1.340149333
ENSOCUG00000027783	-	Uncharacte GL019061:	1.464323333	1.226852667
ENSOCUG00000007931	-	GL018806:	1.97903	1.660356667
ENSOCUG00000000134	NTNG2	netrin G2 [GL018764:	1.679126667	1.409230667
ENSOCUG00000017325	KCNAB3	potassium v 19:111578:	1.221798333	1.028991
ENSOCUG00000007487	SLCO1C1	Uncharacte 8:18919288:	1.499976667	1.264222
ENSOCUG00000025132	RPL23A	Uncharacte 9:5169835:	1.235870667	1.047354333
ENSOCUG00000012275	TEX9	testis expre 17:1609448:	1.732163333	1.469910667
ENSOCUG00000014006	-	Uncharacte X:9773696:	1.195793333	1.016046
ENSOCUG00000000868	CCL20	chemokine 7:16968670:	1.435256667	1.221311
ENSOCUG00000007439	NUDT15	nudix (nucl GL018705:	1.625606667	1.383326667
ENSOCUG00000011291	-	20:211124:	1.456186667	1.23948
ENSOCUG00000025910	-	6:1925980:	1.794286667	1.53164
ENSOCUG00000005262	ZMYND10	zinc finger, 9:1780746:	1.751165	1.494863333
ENSOCUG00000004707	OLFM2	olfactomed GL018833:	1.234873667	1.057153333
ENSOCUG00000009890	DPY19L2	dpy-19-like 10:188267:	1.927466667	1.65107
ENSOCUG00000015026	KIAA1614	KIAA1614 GL019023:	1.521773333	1.307423333
ENSOCUG00000017829	-	Uncharacte GL018828:	1.373729667	1.180857333
ENSOCUG00000022745	-	Uncharacte GL018752:	1.983858667	1.706443333

ENSOCUG00000004230	SLC9A7	solute carrier X:3172607	1.99612	1.717903333
ENSOCUG00000002281	CYP2U1	cytochrome 15:415845	1.854056667	1.603186667
ENSOCUG000000013016	MAPK4	mitogen-activated protein kinase 9:9121887	1.308778333	1.132165667
ENSOCUG000000023520	FLRT1	fibronectin type III domain containing 1:19379	1.35175	1.170663333
ENSOCUG000000017756	C3orf33	chromosome 14:500297	1.433056667	1.242256667
ENSOCUG000000023184	TAS1R1	taste receptor 13:143078	1.3029	1.131121333
ENSOCUG000000011936	FHIT	fragile histidine triad 9:2653089	1.150207333	1.002367333
ENSOCUG00000000809	CDCA5	cell division cycle associated 1:18942	1.504005667	1.311732
ENSOCUG000000027244	-	Uncharacterized protein GL019453	1.911203333	1.668396667
ENSOCUG000000029183	UBAP1L	ubiquitin associated 17:719946	1.628716667	1.424226
ENSOCUG000000017930	SPIN4	spindlin family 4:4163981	1.55883	1.3677
ENSOCUG000000005611	ZNF691	zinc finger protein 13:1238940	1.999816667	1.755826667
ENSOCUG000000029515	-	Uncharacterized protein 4:2006760	1.662343333	1.463217
ENSOCUG000000025363	-	Uncharacterized protein 18:4025889	1.69325	1.494593333
ENSOCUG000000006484	KIF27	kinesin family 18:18728	1.188729333	1.050405333
ENSOCUG000000001836	LPHN1	latrophilin 1:19579	1.794343333	1.58619
ENSOCUG000000007068	CNBD2	cyclic nucleotide binding domain 2:3867130	1.465923333	1.297916667
ENSOCUG000000000877	C19orf59	mast cell-expressed protein 1:18767	1.667343667	1.47878
ENSOCUG000000002733	CACNA1G	calcium channel 19:371125	1.803726667	1.602421333
ENSOCUG000000000960	SDK2	sidekick cell 19:568693	1.881143333	1.67468
ENSOCUG000000001727	SLC19A1	solute carrier GL019369	1.961293333	1.748496667
ENSOCUG000000012102	-	8:1009342	1.591133333	1.420928667
ENSOCUG000000010629	-	Uncharacterized protein X:8796820	1.698616667	1.526072667
ENSOCUG000000023729	S100Z	S100 calcium binding protein 1:18855	1.904956667	1.714157
ENSOCUG000000027203	AZGP1	alpha-2-glycosylated protein 1:18760	1.39052	1.25373
ENSOCUG000000029203	ZFP37	ZFP37 zinc finger 1:341707-3	1.78479	1.610693333
ENSOCUG000000003061	SV2B	synaptic vesicle protein 1:18759	1.236621667	1.117786667
ENSOCUG000000006731	BDNF	brain-derived neurotrophic factor 1:1666519	1.80234	1.63072
ENSOCUG000000000777	-	Uncharacterized protein AAGW020	1.777123333	1.611552
ENSOCUG000000015415	TDRP	testis development protein 1:18917	1.539813333	1.396498
ENSOCUG000000026037	GNB1L	guanine nucleotide binding protein 1:18826	1.47546	1.339703333
ENSOCUG000000015778	SLC25A47	solute carrier GL018904	1.88136	1.709276667
ENSOCUG000000027589	U3	Small nuclear RNA 19:293237	1.43042	1.299626667
ENSOCUG000000027186	STYXL1	serine/threonine kinase 6:2686367	1.88462	1.714984333
ENSOCUG000000029022	ZNF713	zinc finger protein GL018788	1.707846667	1.556
ENSOCUG000000015001	CYB5R2	cytochrome b5 reductase 1:1492138	1.415656667	1.290476667
ENSOCUG000000004365	-	Uncharacterized protein GL019105	1.236762667	1.128261667
ENSOCUG000000029301	ZSCAN23	zinc finger protein 12:105022	1.137278	1.037674667
ENSOCUG000000013621	GDF9	Oryzotolagus 3:1588159	1.68613	1.539673333
ENSOCUG000000021310	-	GL018717	1.164693	1.064857333
ENSOCUG000000021262	USP35	ubiquitin specific protease 1:1385278	1.359813333	1.24489
ENSOCUG000000008401	SCNN1B	amiloride-sensitive sodium channel 6:1410757	1.522211667	1.393873667
ENSOCUG000000017764	FIGF	c-fos inducible protein X:1211430	1.893863333	1.736473333
ENSOCUG000000016105	COLQ	collagen-like protein 14:153242	1.337779667	1.226673333
ENSOCUG000000002189	KCNIP4	Kv channel 2:11313618	1.19756	1.099689333
ENSOCUG000000010871	DNALI1	dynein, axonemal 1:18704	1.417895667	1.302408333
ENSOCUG000000017400	POP1	processing protein 3:1139000	1.29799	1.192417
ENSOCUG000000017204	DAB1	Dab, reelin 13:109553	1.578136667	1.459276667
ENSOCUG000000005892	ARHGAP33	Rho GTPase GL018786	1.161136667	1.076672667
ENSOCUG000000024545	PASK	PAS domain GL018993	1.92608	1.786593333

ENSOCUG00000000066	USP27X	ubiquitin sꝑ X:3409874	1.909876667	1.77364
ENSOCUG00000012794	SFR1	SWI5-depe 18:520499	1.94476	1.806816667
ENSOCUG00000010352	-	16:674607	1.524442667	1.424082667
ENSOCUG00000023744	CDKL1	cyclin-depe 17:693924	1.639046667	1.532432667
ENSOCUG00000012203	SGSM1	small G prc GL018766	1.32139	1.23569
ENSOCUG00000011606	SLC35E4	solute carri 21:319380	1.827293333	1.709506667
ENSOCUG00000015833	SAMSN1	SAM doma 14:142370	1.186953333	1.112869
ENSOCUG00000006044	PPIL6	peptidylpro 12:973537	1.35354	1.269669667
ENSOCUG00000007434	PGLYRP1	peptidoglyc AAGW020	1.829993333	1.718673333
ENSOCUG00000027001	SAC3D1	SAC3 dom: GL018942	1.079033333	1.013996667
ENSOCUG00000005671	-	solute carri 15:466324	1.177475	1.107479333
ENSOCUG00000002706	MYCBPAP	MYCBP as 19:371970	1.841813333	1.734996667
ENSOCUG00000006012	-	Uncharacte 20:314217	1.754306667	1.652633333
ENSOCUG00000025440	-	Uncharacte GL018752	1.885076667	1.776366667
ENSOCUG00000016140	TBXAS1	thromboxa GL018774	1.213963667	1.145967667
ENSOCUG00000027804	SOBP	sine oculis 12:955794	1.134944667	1.072644333
ENSOCUG00000004897	FLT3	fms-related GL018735	1.911733333	1.80688
ENSOCUG00000005972	HESX1	HESX hom 9:2407351	1.458578	1.37974
ENSOCUG00000002264	SAC	adenylate c 13:250928	1.450513	1.372502667
ENSOCUG00000013076	APOBR	apolipoprot 6:1860189	1.221762	1.158266333
ENSOCUG00000028039	CHGB	chromograi 4:12352370	1.724583333	1.635163333
ENSOCUG00000006769	BTNL2	butyrophili 12:2301970	1.88719	1.789401333
ENSOCUG00000012065	PTPRR	protein tyrc 4:4965248	1.12297	1.065053333
ENSOCUG00000003737	ACRBP	acrosin bin 8:3267374	1.208349	1.14621
ENSOCUG00000026633	ZNF597	zinc finger GL018828	1.101384	1.045708667
ENSOCUG00000025890	-	Uncharacte GL019309	1.724933333	1.645088667
ENSOCUG00000012282	MNS1	meiosis-spe 17:160944	1.291255	1.23451
ENSOCUG00000011100	RANBP17	RAN bindin 3:5218605	1.086969	1.040466333
ENSOCUG00000001898	GLP1R	glucagon-li 12:288808	1.054539	1.011141
ENSOCUG00000027991	SAPCD1	suppressor 12:205808	1.975903667	1.89674
ENSOCUG00000010889	RFESD	Rieske (Fe- 11:153056	1.3237	1.271944333
ENSOCUG00000003485	C11orf80	chromosom 1:1944005	1.122772333	1.080827
ENSOCUG00000010080	LRRC36	leucine rich 5:2292042	1.242686667	1.196430667
ENSOCUG00000008358	CABP1	calcium bin 21:119321	1.410323333	1.359102333
ENSOCUG00000005493	DFNB59	deafness, at 7:1181097	1.449143333	1.398960667
ENSOCUG00000002551	CNTLN	centlein, ce 1:3653944	1.465276667	1.415784
ENSOCUG00000013559	SLAMF7	SLAM fam 13:323198	1.196838	1.156757
ENSOCUG00000002655	HEPACAM	hepatic and 1:9232174	1.42166	1.37428
ENSOCUG00000017191	ART4	Uncharacte 8:2475007	1.317910667	1.274003667
ENSOCUG00000006973	EMR2	egf-like mo GL018901	1.210092667	1.170738667
ENSOCUG00000005398	CCNE2	Uncharacte 3:11048650	1.97825	1.914523333
ENSOCUG00000026315	-	Uncharacte GL018829	1.556800667	1.509476667
ENSOCUG00000022810	USP51	ubiquitin sꝑ X:3676960	1.151671	1.116908333
ENSOCUG00000016517	EEFSEC	eukaryotic 9:7127235	1.985196667	1.925896667
ENSOCUG00000004892	RNF2	ring finger GL018801	1.531377	1.488913333
ENSOCUG00000027319	DNAH10	dynein, axo GL019178	1.060366	1.031793333
ENSOCUG00000006248	-	Uncharacte GL018910	1.707079333	1.661428667
ENSOCUG00000022122	ZNF467	zinc finger GL018806	1.630996667	1.590001
ENSOCUG00000016195	MTBP	MDM2 bin 3:1362738	1.192419	1.162776
ENSOCUG00000024024	-	Uncharacte GL018776	1.515963333	1.479948667

ENSOCUG00000022761	IL3RA	interleukin 2:3431058	1.883086667	1.843276667
ENSOCUG00000002630	HAPLN1	hyaluronan 11:387796	1.403066667	1.374030333
ENSOCUG000000027187	PRG4	proteoglyca 16:8407160	1.68551	1.651061667
ENSOCUG000000025281	-	GL018702	1.503227667	1.472776667
ENSOCUG00000003303	CD83	CD83 mole 12:7795779	1.435837	1.408394
ENSOCUG000000015372	DQX1	DEAQ box 2:11201574	1.813553333	1.780356667
ENSOCUG000000004447	ALPL	alkaline ph 13:1316919	1.118957	1.098953
ENSOCUG000000025911	PTGES3	Uncharacte 16:2623669	1.667746667	1.639324
ENSOCUG000000011985	CACNA1A	calcium cha GL018984	1.466119667	1.443306667
ENSOCUG000000025760	MEIS3	Meis home GL018835	1.58126	1.557396
ENSOCUG000000025279	C9orf152	chromosom 1:2982146	1.638293333	1.614986667
ENSOCUG000000017402	ARSG	arylsulfatas 19:5225050	1.805766667	1.78282
ENSOCUG000000010206	DEFB125	defensin, b 4:7866260	1.55775	1.538913333
ENSOCUG000000023151	SLAMF1	signaling ly 13:324334	1.358307333	1.345446333
ENSOCUG000000010048	AFMID	arylformam GL019309	1.37231	1.361414333
ENSOCUG000000003943	CLCF1	cardiotroph 1:1948117	1.303280333	1.294182667
ENSOCUG000000025677	CCR3	chemokine 9:1449051	1.754981333	1.74283
ENSOCUG000000002466	STAT4	signal trans 7:13146689	1.992986667	1.97946
ENSOCUG000000025236	-	Oryctolagu 9:15250350	1.655698	1.64483
ENSOCUG000000024068	OR52W1	olfactory re 1:14720889	1.021841333	1.016842333
ENSOCUG000000011488	FANCI	Fanconi an GL018738	1.718433333	1.712313333
ENSOCUG000000005995	DNM3	dynamini 3 13:2036128	1.194913333	1.190725667
ENSOCUG000000025176	-	15:1471228	1.19739	1.193714667
ENSOCUG000000022096	-	Uncharacte 16:339821	1.246953333	1.243408
ENSOCUG000000011789	ARMC2	armadillo r 12:9680122	1.103583333	1.102126667
ENSOCUG000000013288	MTTP	microsomal 15:5020938	1.337237333	1.335557333
ENSOCUG000000006031	TLR6	toll-like rec 2:2824601	1.360363333	1.35931
ENSOCUG000000014019	SPIRE2	spire-type a GL018965	1.771213333	1.772346667
ENSOCUG000000010372	-	Uncharacte 16:346383	1.73125	1.735526667
ENSOCUG000000009066	SAMD12	sterile alph 3:1340476	1.849783333	1.854546667
ENSOCUG000000017825	METTL25	methyltrans 4:6162939	1.9287	1.93664
ENSOCUG000000017565	-	kielin/chor 7:1567438	1.118078333	1.122972333
ENSOCUG000000025186	-	Uncharacte 4:83004479	1.40187	1.40951
ENSOCUG000000013310	AMT	aminometh 9:1689237	1.30985	1.317058667
ENSOCUG000000023803	CENPL	centromere 13:1158969	1.304656667	1.314386
ENSOCUG000000023096	HPX	Oryctolagu 1:1474461	1.87397	1.888736667
ENSOCUG000000017309	HTR4	5-hydroxyt 3:3042602	1.78884	1.804326667
ENSOCUG000000029071	ZNF81	zinc finger X:3295454	1.400920667	1.413683333
ENSOCUG000000026770	-	1:1749342	1.237611333	1.251580333
ENSOCUG000000015932	-	synapsin II 9:11735390	1.499856667	1.51696
ENSOCUG000000009356	PKDREJ	Uncharacte GL018928	1.903486667	1.927713333
ENSOCUG000000012469	TCTEX1D4	Tctex1 don 13:121822	1.469928333	1.489259
ENSOCUG000000008845	ZNF583	zinc finger GL018811	1.66146	1.68587
ENSOCUG000000008581	CDYL2	chromodon 5:35045034	1.226148	1.244669
ENSOCUG000000004525	NDUFAF2	NADH deh 11:769984	1.636916667	1.662063667
ENSOCUG000000016881	RHEBL1	Ras homolc 4:33360199	1.83851	1.867196667
ENSOCUG000000000515	LGALS4	lectin, gala 5:949252-9	1.171245	1.193450333
ENSOCUG000000028133	SHROOM1	shroom fan 3:1585449	1.458600667	1.490503333
ENSOCUG000000004332	MYRIP	myosin VII 9:3603739	1.483453333	1.516401
ENSOCUG000000021288	-	Uncharacte 5:1262241	1.423013333	1.454956667

ENSOCUG00000009582	CLEC5A	C-type lecti	GL018758:	1.164077333	1.190662667
ENSOCUG00000014250	TRDC	T cell rece	17:4273249	1.244684	1.274379
ENSOCUG00000012987	-	Uncharacte	17:2064290	1.117648	1.146482
ENSOCUG00000026025	CCDC65	coiled-coil	4:33208160	1.073935	1.101930333
ENSOCUG00000026462	LUZP2	leucine zip	1:16368197	1.796973333	1.845726667
ENSOCUG00000003491	CCDC85A	coiled-coil	2:12965643	1.709203333	1.756916667
ENSOCUG00000002418	SAAL1	serum amyl	GL018733:	1.923153333	1.978033333
ENSOCUG00000008721	HLA-DPB1	major histo	12:2355400	1.73073	1.780152333
ENSOCUG00000001918	MORN3	MORN rep	21:5990745	1.189362	1.223383333
ENSOCUG00000002656	TRAPPC3L	trafficking	12:1047507	1.278759667	1.316126
ENSOCUG00000000554	NME6	NME/NM29	1:16038670	1.658806667	1.708173333
ENSOCUG000000027980	RPL23A	Uncharacte	4:53194045	1.084247	1.116549
ENSOCUG00000003040	ADAMTS3	ADAM me	15:7751805	1.835273333	1.89305
ENSOCUG000000023195	-	Uncharacte	GL019183:	1.533921	1.583506667
ENSOCUG00000009115	-	Uncharacte	21:6474248	1.301520333	1.343858333
ENSOCUG00000014499	CLSTN3	calsyntenin	8:33100542	1.179313333	1.21786
ENSOCUG00000009489	-	Rho GTPas	17:3776008	1.500013333	1.552606667
ENSOCUG00000009809	SP110	SP110 nucl	7:17209307	1.290371	1.335873333
ENSOCUG00000011158	FAM131B	family with	7:8747339-	1.401142333	1.451116667
ENSOCUG00000006292	TFEC	transcriptio	7:29221335	1.380121	1.429424333
ENSOCUG000000022962	-		GL018805:	1.408136667	1.45877
ENSOCUG000000026975	TSSK6	testis-speci	GL019137:	1.329777333	1.379497
ENSOCUG000000029728	-		16:6701155	1.727876667	1.79688
ENSOCUG00000012201	PPAT	phosphorib	15:9244227	1.879476667	1.956286667
ENSOCUG000000027280	-	Uncharacte	AAGW020	1.34147	1.396446667
ENSOCUG00000012963	SCAI	suppressor	GL018699:	1.869085	1.947263333
ENSOCUG00000011952	-	Glutathione	12:4245289	1.011156667	1.054546667
ENSOCUG00000015149	TSPEAR	thrombospc	GL019021:	1.105144	1.154271667
ENSOCUG00000001255	REM2	RAS (RAD	17:4311545	1.445953333	1.511237
ENSOCUG00000008307	-	Uncharacte	13:3498068	1.236194667	1.293715
ENSOCUG000000022748	STX11	syntaxin 11	12:1349062	1.167753	1.222766667
ENSOCUG000000028144	PIH1D2	PIH1 doma	1:10430832	1.20492	1.262073333
ENSOCUG00000013017	ELOVL2	ELOVL fat	12:4729514	1.025432333	1.074369
ENSOCUG00000000674	KCNA5	Oryctolagu	8:31128085	1.509963333	1.582531667
ENSOCUG000000021600	-	PDZ domai	1:13472788	1.125984	1.180531667
ENSOCUG00000015702	EPOR	erythropoie	GL019404:	1.22221	1.283056667
ENSOCUG00000008587	TNFSF4	Tumor necr	13:699462-	1.53803	1.615026667
ENSOCUG00000002952	-	Uncharacte	8:28312995	1.145066667	1.203105667
ENSOCUG000000023590	SOWAHB	sonondowal	15:7352019	1.822706667	1.915111667
ENSOCUG000000022539	-	Uncharacte	GL018910:	1.009602667	1.061352
ENSOCUG00000005035	MAP3K13	mitogen-ac	14:8010120	1.771436667	1.862556667
ENSOCUG00000010678	-		19:3141525	1.011299333	1.063881667
ENSOCUG00000011399	TTLL5	tubulin tyrc	20:2918385	1.723756667	1.814326667
ENSOCUG00000009012	FCRL5	Fc receptor	13:3561749	1.050573	1.105783333
ENSOCUG00000013648	SLC16A9	solute carri	18:2644592	1.113186667	1.171856667
ENSOCUG000000021351	GAPT	GRB2-bind	11:7442525	1.225408667	1.291443333
ENSOCUG000000029691	-	Uncharacte	GL018889:	1.292450667	1.363285
ENSOCUG00000011196	LAG3	lymphocyte	8:32792469	1.82373	1.927394667
ENSOCUG00000001548	RASEF	RAS and E	1:69537918	1.232279	1.30314
ENSOCUG00000005239	SNX20	sorting nex	GL018732:	1.49352	1.579475667

ENSOCUG00000002376	HAUS7	HAUS augi	GL018816:	1.65215	1.747303333
ENSOCUG000000021929	CCRL2	chemokine 9:	14578329:	1.180958667	1.24955
ENSOCUG000000028058	CHAC2	ChaC, catic 2:	13246087:	1.37701	1.457126667
ENSOCUG000000013170	1-Mar	mitochondr	16:5227570:	1.708246667	1.810126667
ENSOCUG00000002945	MEOX1	mesenchyrr	19:4410222:	1.65088	1.751733333
ENSOCUG00000003533	RASGRF2	Ras protein 11:	1452934:	1.069708	1.135145
ENSOCUG000000011402	IL7R	interleukin 11:	5714897:	1.519966667	1.616303333
ENSOCUG00000004575	SLA2	Src-like-ad:	4:3370121-	1.163584	1.239255
ENSOCUG00000004026	CEP128	centrosoma 20:	2436490:	1.182054667	1.25918
ENSOCUG00000001536	ST1A8	Oryctolagu:	6:18528008:	1.871541	1.994348
ENSOCUG000000024161	KCNJ15	potassium i	GL018727:	1.169504333	1.248829667
ENSOCUG000000021369	SWSAP1	SWIM-type	GL019404:	1.849803333	1.97689
ENSOCUG000000029709	-	Uncharacte	13:1336022:	1.56074	1.668853333
ENSOCUG000000007702	TBC1D10C	TBC1 dom:	1:19483940:	1.509773333	1.620896667
ENSOCUG00000003274	OIP5	Opa interac	17:3073764:	1.022859667	1.0986
ENSOCUG000000021002	LCN2	lipocalin 2	GL018847:	1.63993	1.761589667
ENSOCUG000000013003	SCN3A	sodium cha	7:10449248:	1.135991333	1.221758333
ENSOCUG00000003095	KIAA1524	KIAA1524 14:	1108138:	1.465416667	1.576193333
ENSOCUG000000009071	KIF24	kinesin fam	1:19527230:	1.070306	1.152717667
ENSOCUG000000025002	-	40S ribosor	13:5019492:	1.432357333	1.546974
ENSOCUG000000022672	AMIGO3	adhesion m	9:17207706:	1.701306667	1.84094
ENSOCUG000000029125	-	Uncharacte	11:2377777:	1.568456667	1.69765
ENSOCUG000000010196	REEP1	receptor ac:	2:10002031:	1.691830333	1.83199
ENSOCUG000000022112	-	Uncharacte	16:6889794:	1.126904	1.221377667
ENSOCUG000000024529	-	Uncharacte	3:10073124:	1.185739667	1.287926667
ENSOCUG000000029050	-	zinc finger	5:1376768-	1.125923333	1.223213333
ENSOCUG000000006897	TTC16	tetratricope	GL018699:	1.783836667	1.94034
ENSOCUG000000029457	-	Uncharacte	GL019214:	1.744396667	1.897503333
ENSOCUG000000016180	F2	coagulation	1:18608468:	1.454746667	1.585413333
ENSOCUG000000015475	USP43	ubiquitin s	19:9724792:	1.801453333	1.963876667
ENSOCUG000000022079	-	Uncharacte	11:7205758:	1.35876	1.48306
ENSOCUG000000017170	-	SLIT-ROB	GL018802:	1.414084333	1.544796667
ENSOCUG000000006103	-	Uncharacte	12:3873792:	1.154670333	1.26271
ENSOCUG000000022143	-	Uncharacte	3:33240087:	1.576203333	1.72415
ENSOCUG000000016496	MLPH	Uncharacte	GL018840:	1.018769	1.114777333
ENSOCUG000000006288	NINL	ninein-like	GL018741:	1.069699333	1.172298
ENSOCUG000000024922	-	Uncharacte	9:13471120:	1.67106	1.831803333
ENSOCUG000000005877	GPR171	G protein-c	14:4499987:	1.521439333	1.668537
ENSOCUG000000008159	CD27	CD27 mole	8:32506939:	1.044983333	1.147123333
ENSOCUG000000026872	-	Uncharacte	4:34945138:	1.179304667	1.295443333
ENSOCUG000000006673	A4GALT	alpha 1,4-g	GL018734:	1.22804	1.351226667
ENSOCUG000000000107	MPPE1	metallopho:	9:50021415:	1.276583333	1.40466
ENSOCUG000000016447	KCNE3	potassium v	1:14214910:	1.789483333	1.972577333
ENSOCUG000000015307	SLC35F1	solute carri	12:1071370:	1.726243	1.904588333
ENSOCUG000000027125	-	Uncharacte	6:12357072:	1.497763333	1.652686667
ENSOCUG000000002364	TNFRSF9	tumor necr	13:1419110:	1.772371333	1.956912
ENSOCUG000000023913	APOBEC3H		4:8431620:	1.506840333	1.667708333
ENSOCUG000000025805	SPATA9	spermatoge	11:1530562:	1.269733333	1.40593
ENSOCUG000000008746	TRAIP	TRAF inter	9:17356580:	1.49766	1.664115
ENSOCUG000000014409	CCDC15	coiled-coil	1:92223898:	1.501346667	1.66853

ENSOCUG00000006424	CEP152	centrosoma 17:2360508	1.223000667	1.36013
ENSOCUG00000015922	RNASEL	ribonucleas GL019670:	1.057307	1.176456333
ENSOCUG00000010832	ASXL3	additional s 9:7497630:	1.030386	1.146569
ENSOCUG00000006934	SLC23A1	solute carri 3:2162233:	1.580533333	1.761186667
ENSOCUG00000015805	NOX5	NADPH ox GL018793:	1.126387333	1.255428333
ENSOCUG00000009422	C22orf23	chromosom GL018972:	1.501451667	1.678393333
ENSOCUG00000005329	APOB	Apolipopro 2:17008170	1.384161667	1.550476667
ENSOCUG00000012388	EMILIN3	elastin micr GL018718:	1.000231	1.120431
ENSOCUG00000003108	TMEM44	transmemb 14:904284:	1.285903	1.44132
ENSOCUG00000001384	RTTN	rotatin [Sou 9:1101369:	1.782336667	1.999046667
ENSOCUG00000006243	WDFY4	WDFY fam GL018819:	1.553605333	1.74383
ENSOCUG00000010516	HIC2	hypermethy 21:5391890	1.744113333	1.95923
ENSOCUG00000011794	NUP210L	nucleoporin 13:3839584	1.55046	1.746293333
ENSOCUG00000023239	ADORA3	Oryctolagu 13:5264598	1.058358333	1.19215
ENSOCUG00000005852	CHM-I	Oryctolagu 8:5411190:	1.102039333	1.241370667
ENSOCUG00000002066	C11orf49	chromosom 1:18629158	1.710403333	1.92904
ENSOCUG00000029316	-	Uncharacte 18:5311070	1.76516	1.992266667
ENSOCUG00000027937	-	Uncharacte AAGW020	1.521840667	1.71792
ENSOCUG00000013168	TSPAN33	tetraspanin 7:1541646:	1.178551333	1.331676667
ENSOCUG00000004912	GNAZ	guanine nu GL018810:	1.425866667	1.611443333
ENSOCUG00000016650	DEPDC1B	DEP domai 11:7663510	1.202167	1.358824333
ENSOCUG00000006156	WDPCP	WD repeat 2:1229337:	1.335006667	1.511763333
ENSOCUG00000004008	CNDP1	carnosine d 9:11468159	1.601923333	1.815703333
ENSOCUG00000021584	DOK3	docking prc 3:5800813:	1.286393333	1.46188
ENSOCUG00000029059	AQP10	aquaporin 113:382554:	1.087187667	1.235546667
ENSOCUG00000010502	SCN3B	sodium cha 1:9445608:	1.349173333	1.539816667
ENSOCUG00000017841	OSBP2	oxysterol b 21:3240594	1.52387	1.742736667
ENSOCUG00000015289	-	10:3218440	1.073659	1.228033333
ENSOCUG00000008800	ZWILCH	zwilch kine 17:585789:	1.53491	1.758996667
ENSOCUG00000029485	-	Uncharacte 2:9541446:	1.523393333	1.755943333
ENSOCUG00000012895	-	Glutathione 12:4223240	1.33346	1.537376667
ENSOCUG00000013958	MMAB	methyalmal GL018892:	1.64089	1.897016667
ENSOCUG00000004709	C1orf56	chromosom 13:4112559	1.635113333	1.89146
ENSOCUG00000002800	KIF12	kinesin fam GL018699:	1.542354333	1.787346667
ENSOCUG00000004650	C9orf91	chromosom GL018699:	1.59399	1.852166667
ENSOCUG00000017794	TULP2	tubby like j GL019028:	1.44155	1.675513333
ENSOCUG00000022139	PGER8	Uncharacte GL018750:	1.473792	1.717298667
ENSOCUG00000015222	SLC9C2	solute carri 13:905003-	1.274817	1.485727667
ENSOCUG00000002773	C3orf67	chromosom 9:2549159:	1.545733333	1.80529
ENSOCUG00000020999	-	X:2677029	1.518713333	1.77417
ENSOCUG00000009004	-	15:2687590	1.198602667	1.400719
ENSOCUG00000009504	CD80	Oryctolagu 14:992159:	1.316676667	1.54023
ENSOCUG00000028997	ZNF793	zinc finger 5:1281977-	1.136632667	1.330551
ENSOCUG00000017473	FAM216B	family with 8:5226856:	1.113050667	1.303163333
ENSOCUG00000007550	MIS18BP1	MIS18 binc 17:645052:	1.407553333	1.648983333
ENSOCUG00000029631	-	Uncharacte 1:18229448	1.046662667	1.226878
ENSOCUG00000017867	FRAS1	Fraser extra 15:718474:	1.33846	1.56947
ENSOCUG00000011550	CD86	Oryctolagu 14:969289:	1.61045	1.893673333
ENSOCUG00000027402	-	Uncharacte 16:6852320	1.413826667	1.664436667
ENSOCUG00000011222	KIAA1257	KIAA1257 9:8036613-	1.131511333	1.333956333

ENSOCUG00000023896	E2F2	E2F transcr 13:129694	1.119333	1.322905
ENSOCUG00000008990	RLTPR	RGD motif 5:23207880	1.278285333	1.517623333
ENSOCUG00000015956	LRMP	lymphoid-r 8:14979232	1.292884	1.538148667
ENSOCUG00000026154	-	Uncharacte GL019404	1.422733	1.696416667
ENSOCUG00000008012	STMN1	Stathmin [3:69407538	1.152303333	1.377083333
ENSOCUG00000001497	FABP7	fatty acid b 12:111910	1.084885667	1.297827667
ENSOCUG00000005237	PCDH17	protocadhei 8:58807440	1.005320667	1.203901
ENSOCUG00000001186	SRPX2	sushi-repea X:8864399	1.41449	1.694673333
ENSOCUG00000005836	NRG1	neuregulin 2:74984999	1.637891	1.962863333
ENSOCUG00000009195	CLEC4E	C-type lecti 8:3349079	1.077794667	1.291786667
ENSOCUG00000006448	ABCB9	ATP-bindir GL019055	1.161013667	1.391693333
ENSOCUG000000025119	RELT	RELT tumc 1:1430955	1.064371333	1.277127667
ENSOCUG00000000962	ORC1	origin reco 13:1143340	1.057558	1.270413333
ENSOCUG00000024410	-	Uncharacte 9:59598268	1.057873333	1.270854333
ENSOCUG00000003187	REM1	RAS (RAD4:7698033-	1.47972	1.779926667
ENSOCUG00000001296	HES2	hes family 113:143198	1.637657667	1.97018
ENSOCUG00000003660	-	Uncharacte 9:14545404	1.318549333	1.592103333
ENSOCUG00000002498	-	Uncharacte 3:10086648	1.57497	1.906936667
ENSOCUG00000023002	-	Uncharacte GL018825	1.463029333	1.777183333
ENSOCUG00000021631	SNORA53	Small nucle 4:77885029	1.177456667	1.431936667
ENSOCUG00000016005	EXO5	exonucleas 13:126036	1.609893333	1.958686667
ENSOCUG00000003763	PTPN22	protein tyrc 13:5033859	1.151777667	1.404081667
ENSOCUG00000007289	PNMA1	paraneoplas 20:3129954	1.189724333	1.4517
ENSOCUG00000022039	AKAP17A	A kinase (P X:6797672	1.337935667	1.635383333
ENSOCUG00000000979	MAP4K1	mitogen-ac 5:2565159-	1.378455333	1.68624
ENSOCUG00000022191	-	4:74386162	1.157262333	1.42247
ENSOCUG00000003084	CPB1	carboxypep 14:426182	1.341457333	1.657464333
ENSOCUG00000003511	GPR85	G protein-c 7:3236368	1.508550667	1.865723333
ENSOCUG00000016081	-	Uncharacte GL018831	1.582193333	1.958123333
ENSOCUG00000022986	CCDC163P	13:1211428	1.242323333	1.537636667
ENSOCUG00000007995	-	17:2894278	1.611811	1.995383333
ENSOCUG00000001107	ARHGAP4	Rho GTPas GL018816	1.536403333	1.90582
ENSOCUG00000015540	ADAT1	adenosine c 5:3023758	1.533526667	1.903053333
ENSOCUG00000005151	KIAA0895	KIAA0895 10:198325	1.012174	1.258093333
ENSOCUG00000000723	TMEM55A	transmemb 3:1065960	1.240775	1.542344
ENSOCUG00000011397	TREM1	triggering r 12:309916	1.474564667	1.84872
ENSOCUG00000012109	-	Uncharacte 4:84078830	1.41939	1.78387
ENSOCUG00000022434	CDCA3	cell divisio 8:32864290	1.177577333	1.49314
ENSOCUG00000017181	PKMYT1	protein kin GL018828	1.547913333	1.96551
ENSOCUG00000000953	RMI2	RecQ medi 6:4885172-	1.406293333	1.792265333
ENSOCUG00000010195	ZC2HC1C	zinc finger, 20:3004818	1.162159667	1.481306667
ENSOCUG00000003116	-	Uncharacte GL018758	1.267328667	1.619039333
ENSOCUG00000001719	DIAPH3	diaphanous 8:6110605	1.176409	1.504616667
ENSOCUG00000014665	REPS2	RALBP1 a: X:2830155	1.104039333	1.413648
ENSOCUG00000013772	TUBD1	tubulin, del 19:284352	1.398165333	1.792123333
ENSOCUG00000011170	HJURP	Holliday ju GL018736	1.47631	1.899116667
ENSOCUG00000010001	HSF4	heat shock 5:22779280	1.373886667	1.772753333
ENSOCUG00000009913	-	Uncharacte 6:1174094	1.086172667	1.40233
ENSOCUG00000008742	-	Uncharacte GL019398	1.44797	1.872521333
ENSOCUG00000024128	-	Uncharacte 5:22494668	1.173539667	1.520716667

ENSOCUG00000006860	GLDN	gliomedin [17:211223:	1.359439333	1.76535
ENSOCUG00000013497	ULK4	unc-51 like 9:2186331-	1.204866667	1.56592
ENSOCUG00000024762	CKS2	CDC28 pro X:7142075	1.061476667	1.380976667
ENSOCUG00000011279	1-Mar	membrane- GL018701:	1.145148	1.499183333
ENSOCUG00000023082	ABHD16B	abhydrolase GL019070:	1.489624333	1.964726667
ENSOCUG00000029609	-	chromosom 12:122170:	1.03397	1.365213333
ENSOCUG00000013801	SHCBP1	SHC SH2- α GL018743:	1.249870333	1.65527
ENSOCUG00000008964	HOXD10	homeobox 7:1156766:	1.154009333	1.536043333
ENSOCUG00000001921	KIAA0825	KIAA0825 11:138520:	1.32547	1.770696667
ENSOCUG00000009932	ESCO2	establishme 2:4184972:	1.20658	1.612066667
ENSOCUG00000017310	SLC6A2	solute carri 5:1187371:	1.140333	1.530143
ENSOCUG00000009777	GAREML	GRB2 asso 2:15971590	1.178185333	1.585603333
ENSOCUG00000012527	SLC26A7	solute carri 3:1068744:	1.227177667	1.654993333
ENSOCUG00000009337	-	GL018710:	1.268084667	1.712876667
ENSOCUG00000025123	GCNT4	glucosamin GL018859:	1.021546667	1.38874
ENSOCUG00000013312	KCNH4	potassium v 19:429850:	1.330729	1.820417
ENSOCUG00000023559	-	septin 1 [Sc GL018752:	1.129202	1.545721667
ENSOCUG00000004688	PKHD1L1	polycystic 13:12488800	1.326523333	1.83736
ENSOCUG00000017111	-	Uncharacte X:4885099	1.368293667	1.896906667
ENSOCUG00000012007	PRR5L	proline rich 1:17568070	1.40859	1.962656667
ENSOCUG00000025809	RTN4RL2	reticulon 4 1:1905472:	1.416883333	1.975623333
ENSOCUG00000005974	LINGO1	leucine rich GL018768:	1.127515333	1.572551333
ENSOCUG00000016509	-	complemen 16:7428779	1.398379333	1.954642667
ENSOCUG00000007327	CNTNAP1	contactin as 19:434108:	1.010277667	1.413116667
ENSOCUG00000027921	-	X:6108226	1.136238333	1.591596667
ENSOCUG00000008771	IL1A	Oryctolagu 2:9755930:	1.192904667	1.671163333
ENSOCUG00000024009	-	Uncharacte GL018719:	1.018469667	1.429852333
ENSOCUG00000001717	SKAP1	src kinase a 19:389171:	1.191262	1.678249333
ENSOCUG00000025070	CCDC114	coiled-coil GL019039:	1.314703667	1.852398333
ENSOCUG00000005819	ZAP70	zeta-chain (2:9440989:	1.058933	1.494141
ENSOCUG00000013763	DLGAP1	discs, large 9:5802671:	1.405106667	1.98446
ENSOCUG00000023708	-	Uncharacte 5:22397050	1.313515667	1.871943333
ENSOCUG00000005122	TMEM125	transmemb 13:1233899	1.372473333	1.956903333
ENSOCUG00000001561	TNFRSF17	tumor necr 6:5381482-	1.395893333	1.993968667
ENSOCUG00000005503	SPDL1	spindle app 3:5101221:	1.3128	1.88209
ENSOCUG00000014013	CSPG5	chondroitin 9:15492258	1.293433333	1.85446
ENSOCUG00000010292	EFHC2	EF-hand dc X:2959414	1.353686667	1.944073333
ENSOCUG00000029428	GIMAP2	GTPase, IV GL018806:	1.081693	1.553729667
ENSOCUG00000011218	-	Uncharacte 9:8011531-	1.384044667	1.990406333
ENSOCUG00000005865	SCUBE1	signal pepti GL018988:	1.008741667	1.452043333
ENSOCUG00000021638	AHRR	aryl-hydroc GL018897:	1.247943333	1.800404
ENSOCUG00000005728	GPRIN2	G protein r 18:882576:	1.175014333	1.727546667
ENSOCUG00000029731	-	Uncharacte 12:231451:	1.264089	1.86183
ENSOCUG00000021541	SHMT1	Serine hydr GL018817:	1.146305667	1.688793333
ENSOCUG00000025874	-	Uncharacte AAGW020	1.015716667	1.52473
ENSOCUG00000005217	TSPAN1	tetraspanin 13:120338:	1.005655	1.512343
ENSOCUG00000012464	CD6	CD6 molec 1:1935933:	1.046814	1.583948
ENSOCUG00000026358	STRA6	stimulated l GL019108:	1.193865	1.811353333
ENSOCUG00000001823	-	Uncharacte 13:1282610	1.148467	1.7685
ENSOCUG00000010409	RBM11	RNA bindii 14:142004:	1.140026667	1.76192

ENSOCUG00000028059	NLRC3	NLR family GL018828:	1.271398333	1.987536667
ENSOCUG00000009374	IRF4	interferon r GL018747:	1.216388667	1.910226667
ENSOCUG00000015747	GINS1	GINS comp GL018741:	1.233986667	1.93932
ENSOCUG00000011838	-	Alveolar m 15:762963:	1.199156667	1.885876667
ENSOCUG00000016029	IQCD	IQ motif co 21:888206:	1.252833333	1.982513333
ENSOCUG00000022194	-	Uncharacte 16:661295:	1.161373	1.854923333
ENSOCUG00000013787	OGDHL	oxoglutarat 18:5815210	1.044362667	1.675459
ENSOCUG00000011143	FOSL1	FOS-like ar 1:1936974:	1.079160333	1.733734333
ENSOCUG00000008474	CD2	CD2 molec 13:475518:	1.123117333	1.809496667
ENSOCUG00000026993	-	Uncharacte GL018806:	1.127106333	1.816736667
ENSOCUG00000001627	SLC6A11	solute carri 9:12745130	1.035366333	1.684471333
ENSOCUG00000025701	CRHR1	Oryctolagu 19:461872:	1.050968333	1.710851333
ENSOCUG00000014120	-	Uncharacte 20:3038458	1.055867333	1.72545
ENSOCUG00000011479	SOX5	SRY (sex d 8:1618984:	1.033016667	1.718873333
ENSOCUG00000029266	-	Uncharacte 12:1046459	1.006967967	1.686644333
ENSOCUG00000002337	PRR11	proline rich 19:2911909	1.018207667	1.707209667
ENSOCUG00000006899	KIF18B	kinesin fam 19:4538154	1.115417667	1.963969667
ENSOCUG00000009679	THEM5	thioesterase 13:4034254	1.02877	1.845956667
ENSOCUG00000022805	-	Uncharacte 13:4180504	5.95437	9.006656667
ENSOCUG00000012215	TRPV3	transient re 19:1487908	5.985993333	9.458423333
ENSOCUG00000003246	SULF1	sulfatase 1 3:8553288:	5.651036667	9.067006667
ENSOCUG00000002848	CCL5	chemokine 19:249224:	5.793343	9.340006667
ENSOCUG00000003500	FAM84B	family with 3:1422784:	5.610746667	9.333996667
ENSOCUG00000002601	OTUB2	OTU deubi GL018883:	5.714233333	9.557743333
ENSOCUG00000008791	SNAPC5	small nucle 17:590221:	5.354796667	9.269536667
ENSOCUG00000005133	MKI67	marker of p GL018726:	5.186306667	9.9445
ENSOCUG00000025315	FAM26D	family with 12:104750:	15.7287	45.7133
ENSOCUG00000015603	KRT40	keratin 40 [19:420272:	11.44153333	22.71786667
ENSOCUG00000027223	-	Uncharacte 2:9814389:	2.05678	11.26439333
ENSOCUG00000004116	LYG2	lysozyme C 2:9299020:	7.713843333	25.49601
ENSOCUG00000017110	KRTAP27-1	keratin assc 14:1599368	7.411	25.72763333
ENSOCUG00000029401	-	Uncharacte X:4184105	4.804163333	8.2285
ENSOCUG00000006225	PROSER2	proline and 16:1646584	4.910903333	8.772136667
ENSOCUG00000029190	PLAC8	placenta-sp 15:6723544	4.854729333	8.691393
ENSOCUG00000003263	SLCO5A1	solute carri 3:8562768:	4.324526667	8.752366667
ENSOCUG00000025113	MYCL	v-myc avia 13:126607:	4.24159	8.749516667
ENSOCUG00000011992	-	Uncharacte 19:421516:	4.151636667	8.669606667
ENSOCUG00000023492	-	Uncharacte 19:4228458	63.5601	166.5076
ENSOCUG00000013493	SLC7A1	solute carri GL018735:	4.99782	7.101203333
ENSOCUG00000024278	-	Uncharacte GL018806:	4.789573333	7.285116667
ENSOCUG00000012503	METTL21B	methyltrans GL018714:	4.845316667	7.644526667
ENSOCUG00000005252	NCMAP	noncompac 13:128851:	4.513253333	7.597543333
ENSOCUG00000029712	-	Uncharacte 11:8030330	4.349636667	7.549756667
ENSOCUG00000023107	-	Uncharacte 14:71120-7	4.540556667	7.910716667
ENSOCUG00000001515	CCL19	chemokine 1:1913243:	4.020616667	7.806293333
ENSOCUG00000007886	FAM49A	family with 2:16549449	9.38582	17.37606667
ENSOCUG00000013779	FOXN1	forkhead bc 19:196121:	15.82536667	31.14026667
ENSOCUG00000011944	ENPP6	ectonucleot 2:6141455:	1.64716	9.255593333
ENSOCUG00000000663	ACTBL2	actin, beta-l 11:733828:	5.587856667	20.85736
ENSOCUG00000007938	ALDH1A3	aldehyde de GL019481:	8.146093333	16.06287667

ENSOCUG00000014720	LYG1	lysozyme C2:9293841	1.68771	8.731236667
ENSOCUG00000019393	SNORA74	Small nucle3:2154319	32.88742333	67.20363333
ENSOCUG00000000560	HEYL	hes-related 13:126885	8.5672	15.9607
ENSOCUG00000023667	-	Uncharacte 8:3781332	0.944613333	1.00E-05
ENSOCUG00000022130	-	GL018833	0.89434	1.00E-05
ENSOCUG00000023186	-	7:1567822	0.87308	1.00E-05
ENSOCUG00000021709	-	bolA family GL018775	0.763176667	1.00E-05
ENSOCUG00000029558	-	Uncharacte 12:1550880	0.684567667	1.00E-05
ENSOCUG00000025328	UBA52	1:3716535	0.643123333	1.00E-05
ENSOCUG00000026970	-	Uncharacte 8:3437539	0.623779	1.00E-05
ENSOCUG00000026579	-	Uncharacte AAGW020	0.606823667	1.00E-05
ENSOCUG00000028681	7SK	7SK RNA X:7093496	0.578166667	1.00E-05
ENSOCUG00000022523	-	Uncharacte AAGW020	0.571673333	1.00E-05
ENSOCUG00000020815	7SK	7SK RNA 9:4943854	0.533766667	1.00E-05
ENSOCUG00000001512	FAM159B	family with 11:808980	0.533035667	1.00E-05
ENSOCUG00000021322	-	13:336546	0.523463333	1.00E-05
ENSOCUG00000020668	7SK	7SK RNA 15:1652420	0.511986667	1.00E-05
ENSOCUG00000022847	-	14:1331710	0.507146667	1.00E-05
ENSOCUG00000026536	-	Uncharacte 2:9848156	0.49603	1.00E-05
ENSOCUG00000023760	-	GL018718	0.49232	1.00E-05
ENSOCUG00000027512	-	Uncharacte 10:214738	0.484130667	1.00E-05
ENSOCUG00000005978	-	18:183879	0.483986667	1.00E-05
ENSOCUG00000013247	-	14:870236	0.473526667	1.00E-05
ENSOCUG00000021652	PIRT	phosphoino 19:8765260	0.448626667	1.00E-05
ENSOCUG00000011028	IL25	interleukin 17:435691	0.432347333	1.00E-05
ENSOCUG00000028653	SCARNA6	Small Cajal GL018736	0.42964	1.00E-05
ENSOCUG00000002404	-	3:14795220	0.42898	1.00E-05
ENSOCUG00000000243	INS	Oryctolagu AAGW020	0.427803333	1.00E-05
ENSOCUG00000027830	-	15:615663	0.415193333	1.00E-05
ENSOCUG00000025571	-	Uncharacte GL018852	0.404940333	1.00E-05
ENSOCUG00000010595	-	Uncharacte 2:1233651	0.40432	1.00E-05
ENSOCUG00000024674	-	Uncharacte 12:858380	0.40309	1.00E-05
ENSOCUG00000023984	-	GL018907	0.394426667	1.00E-05
ENSOCUG00000008927	-	13:9897240	0.394153333	1.00E-05
ENSOCUG00000028083	PPY	Pancreatic 119:443278	0.390671667	1.00E-05
ENSOCUG00000025754	7SK	7SK RNA 17:552139	0.388753333	1.00E-05
ENSOCUG00000026642	TRBV3-1	T cell recep GL018758	0.38512	1.00E-05
ENSOCUG00000011105	-	Uncharacte 14:119161	0.380123333	1.00E-05
ENSOCUG00000023249	7SK	7SK RNA 6:2432068	0.375046667	1.00E-05
ENSOCUG00000023199	-	GL018703	0.357308667	1.00E-05
ENSOCUG00000023111	-	Uncharacte X:1224000	0.353974667	1.00E-05
ENSOCUG00000014272	IL19	interleukin 16:655198	0.35326	1.00E-05
ENSOCUG00000019862	7SK	7SK RNA 12:262847	0.352036667	1.00E-05
ENSOCUG00000027421	-	Uncharacte 1:71421040	0.34825	1.00E-05
ENSOCUG00000024235	-	17:643218	0.347770667	1.00E-05
ENSOCUG00000019601	RNase_MR	RNase MR 1:1826986	0.34542	1.00E-05
ENSOCUG00000007390	LINC00935	Uncharacte 4:3308579	0.343366667	1.00E-05
ENSOCUG00000023206	-	Uncharacte 18:451402	0.339033333	1.00E-05
ENSOCUG00000016466	ACBD7	acyl-CoA b 16:465758	0.334786333	1.00E-05
ENSOCUG00000007694	CNIH3	cornichon f 16:486260	0.334508667	1.00E-05

ENSOCUG00000023445 -	Uncharacte 14:1576710	0.334210333	1.00E-05
ENSOCUG00000000445 BEX4	brain expre X:8681741	0.326905667	1.00E-05
ENSOCUG000000026771 -	GL018747:	0.324968333	1.00E-05
ENSOCUG00000018217 7SK	7SK RNA 12:7082929	0.313538	1.00E-05
ENSOCUG00000022088 -	12:4402022	0.308245	1.00E-05
ENSOCUG000000025093 FAM57B	family with 6:18419510	0.303574	1.00E-05
ENSOCUG000000023287 -	GL018965:	0.301507333	1.00E-05
ENSOCUG00000013068 PYY	Peptide YY 19:4433714	0.301044333	1.00E-05
ENSOCUG00000003616 CD70	CD70 mole GL019202:	0.29089	1.00E-05
ENSOCUG000000028197 -	9:10580458	0.279619333	1.00E-05
ENSOCUG000000026359 GP9	glycoprotei 9:7908173-	0.276541667	1.00E-05
ENSOCUG00000018302 7SK	7SK RNA 2:7430256:	0.273679333	1.00E-05
ENSOCUG000000009617 -	Uncharacte X:8819477	0.271046333	1.00E-05
ENSOCUG000000023927 SPRN	Uncharacte 18:6966008	0.259701667	1.00E-05
ENSOCUG000000029230 -	Uncharacte 1:19271379	0.25835	1.00E-05
ENSOCUG00000018760 7SK	7SK RNA 16:497703:	0.253963667	1.00E-05
ENSOCUG000000007035 OSTN	osteocrin [5 14:869421:	0.253333	1.00E-05
ENSOCUG000000006459 -	3:76011332	0.252271333	1.00E-05
ENSOCUG000000021207 -	7:74355211	0.251125	1.00E-05
ENSOCUG00000019412 7SK	7SK RNA 12:128188:	0.248906667	1.00E-05
ENSOCUG000000021188 -	9:624813-6	0.247715333	1.00E-05
ENSOCUG000000020981 -	Uncharacte AAGW020	0.240628	1.00E-05
ENSOCUG000000025987 BOD1	Uncharacte 8:5393812:	0.240196667	1.00E-05
ENSOCUG000000026648 -	GL018740:	0.239396	1.00E-05
ENSOCUG000000021429 7SK	7SK RNA 18:1996734	0.238654667	1.00E-05
ENSOCUG00000001424 OTOR	otoraplin [54:19403200	0.238068667	1.00E-05
ENSOCUG000000003864 -	GL018820:	0.233770333	1.00E-05
ENSOCUG000000005554 -	Uncharacte GL019089:	0.232532667	1.00E-05
ENSOCUG000000025854 -	Uncharacte 2:11511208	0.232216667	1.00E-05
ENSOCUG000000021787 -	Uncharacte AAGW020	0.231455	1.00E-05
ENSOCUG000000025893 -	Uncharacte 16:2272950	0.227709333	1.00E-05
ENSOCUG000000021033 CST9	4:13387518	0.225797	1.00E-05
ENSOCUG000000024687 -	8:6190361:	0.224829333	1.00E-05
ENSOCUG000000027525 -	GL018700:	0.223203667	1.00E-05
ENSOCUG000000023794 -	7:9014588-	0.223119	1.00E-05
ENSOCUG000000021688 -	Uncharacte GL018701:	0.215167	1.00E-05
ENSOCUG000000027665 -	Olfactory r GL018699:	0.211631	1.00E-05
ENSOCUG000000023572 -	6:3987906-	0.211544333	1.00E-05
ENSOCUG000000024198 -	Uncharacte GL018820:	0.205819	1.00E-05
ENSOCUG00000014341 -	X:1043257	0.205744	1.00E-05
ENSOCUG000000027030 -	X:6011857	0.201784333	1.00E-05
ENSOCUG000000009984 DEFB124	defensin, b4:7711274-	0.198846	1.00E-05
ENSOCUG000000020916 -	18:216963:	0.196783333	1.00E-05
ENSOCUG00000018884 7SK	7SK RNA 11:6049628	0.195930667	1.00E-05
ENSOCUG000000025917 -	Uncharacte 17:421492:	0.194317333	1.00E-05
ENSOCUG00000011637 GUCA2B	guanylate c 13:1245268	0.186854333	1.00E-05
ENSOCUG00000013045 UBE2E2	ubiquitin-c12:734801:	0.185575	1.00E-05
ENSOCUG00000001516 -	15:443450:	0.183133667	1.00E-05
ENSOCUG000000022269 CRYBB1	crystallin, t GL018723:	0.181181667	1.00E-05
ENSOCUG000000020396 7SK	7SK RNA GL018719:	0.180869	1.00E-05

ENSOCUG00000003834 -	Uncharacte 2:98664529	0.180483667	1.00E-05
ENSOCUG000000021237 -	Uncharacte GL018699:	0.176967	1.00E-05
ENSOCUG000000021407 -	Uncharacte 5:27698040	0.176947	1.00E-05
ENSOCUG000000024651 -	7:14205094	0.173806667	1.00E-05
ENSOCUG000000021548 -	Uncharacte 15:7506554	0.171412	1.00E-05
ENSOCUG000000027110 PPP4R1L	15:2406374	0.167887333	1.00E-05
ENSOCUG000000025495 -	Uncharacte 8:28427700	0.166364	1.00E-05
ENSOCUG000000000522 -	Uncharacte 6:7695322-	0.166103	1.00E-05
ENSOCUG000000027272 GPR3	G protein-c 13:1380464	0.165367333	1.00E-05
ENSOCUG000000015761 ANKRD33	ankyrin rep 4:36060310	0.163336667	1.00E-05
ENSOCUG000000022425 POU4F3	POU class 3:28339562	0.154787667	1.00E-05
ENSOCUG000000023416 -	14:7380169	0.152563	1.00E-05
ENSOCUG000000026722 -	13:1284262	0.150995667	1.00E-05
ENSOCUG000000029689 -	Uncharacte GL019186:	0.150940333	1.00E-05
ENSOCUG000000026587 -	Uncharacte GL019438:	0.150013333	1.00E-05
ENSOCUG000000027428 -	Uncharacte 1:70723062	0.14521	1.00E-05
ENSOCUG000000024291 PWP2	Uncharacte 4:12787657	0.144022333	1.00E-05
ENSOCUG000000025240 -	Uncharacte 4:48453272	0.143796	1.00E-05
ENSOCUG000000028138 -	Uncharacte 6:18207334	0.142845333	1.00E-05
ENSOCUG000000003433 GMCSF	Oryctolagu 3:15143062	0.142529333	1.00E-05
ENSOCUG000000006744 CES5A	carboxylest 5:12161088	0.141122667	1.00E-05
ENSOCUG000000022645 HPCAL4	hippocalcin 13:1268260	0.140776333	1.00E-05
ENSOCUG000000001614 -	Uncharacte 13:3426429	0.140509333	1.00E-05
ENSOCUG000000026641 -	GL018760:	0.139880667	1.00E-05
ENSOCUG000000015677 PLAC8L1	PLAC8-like 3:28041489	0.139536	1.00E-05
ENSOCUG000000022739 -	X:9670319	0.139495333	1.00E-05
ENSOCUG000000004512 -	GL019369:	0.139080333	1.00E-05
ENSOCUG000000026808 -	GL018795:	0.137973	1.00E-05
ENSOCUG000000024891 KBTBD11	kelch repea GL018865:	0.137892333	1.00E-05
ENSOCUG000000023135 -	Uncharacte X:7583396	0.135572	1.00E-05
ENSOCUG000000024445 -	Uncharacte 9:90025789	0.134421	1.00E-05
ENSOCUG000000026814 -	Uncharacte 3:66798494	0.133977333	1.00E-05
ENSOCUG000000023936 -	X:7864683	0.132966	1.00E-05
ENSOCUG000000026819 RXFP4	relaxin/insu 13:3690190	0.132775	1.00E-05
ENSOCUG000000026302 -	GL018749:	0.128273333	1.00E-05
ENSOCUG000000007106 -	Ribonuclea 17:4136877	0.128180333	1.00E-05
ENSOCUG000000025812 -	Uncharacte 7:98073558	0.127575333	1.00E-05
ENSOCUG000000001019 DMRTA2	DMRT-like 13:1162510	0.1273699	1.00E-05
ENSOCUG000000024306 -	Uncharacte 5:29085409	0.125679	1.00E-05
ENSOCUG000000020945 -	Uncharacte 4:63510919	0.125464667	1.00E-05
ENSOCUG000000002237 -	Uncharacte GL018827:	0.124793333	1.00E-05
ENSOCUG000000023080 -	Olfactory r 17:3978502	0.122935667	1.00E-05
ENSOCUG000000015954 -	8:69358558	0.122413333	1.00E-05
ENSOCUG000000021138 -	2:99592778	0.121513333	1.00E-05
ENSOCUG000000001411 GALR3	galanin rec 1:GL018972:	0.121116	1.00E-05
ENSOCUG000000008168 -	Uncharacte 18:6406822	0.121059333	1.00E-05
ENSOCUG000000023296 -	Uncharacte GL018738:	0.120296567	1.00E-05
ENSOCUG000000015565 KCNJ5	potassium i 1:87949182	0.1199365	1.00E-05
ENSOCUG000000016681 -	Olfactory r 1:19122097	0.119526667	1.00E-05
ENSOCUG000000005612 -	12:1392492	0.119131667	1.00E-05

ENSOCUG00000016749 -	Uncharacte 15:599170	0.118961667	1.00E-05
ENSOCUG00000027629 -	Uncharacte GL019806	0.118822667	1.00E-05
ENSOCUG00000028220 MIOX	myo-inosit GL019140	0.118270667	1.00E-05
ENSOCUG00000007942 LY6G5C	lymphocyte 12:204887	0.117877333	1.00E-05
ENSOCUG00000027248 PCP2	Purkinje ce GL018767	0.11698	1.00E-05
ENSOCUG00000002990 -	Uncharacte X:3305657	0.116579767	1.00E-05
ENSOCUG00000008028 NAP1L5	nucleosome 15:613465	0.11351	1.00E-05
ENSOCUG00000027298 -	Uncharacte 17:421492	0.111679333	1.00E-05
ENSOCUG00000023690 -	Uncharacte X:3145774	0.111637333	1.00E-05
ENSOCUG00000009701 CSF3	colony stim 19:412287	0.110520333	1.00E-05
ENSOCUG00000002718 -	Uncharacte GL018705	0.109981	1.00E-05
ENSOCUG00000022127 KBTBD13	kelch repea 17:722157	0.108658	1.00E-05
ENSOCUG00000027821 -	GL018777	0.108581667	1.00E-05
ENSOCUG00000027221 -	7:2197827	0.107503333	1.00E-05
ENSOCUG00000010970 -	7:1032023	0.106957667	1.00E-05
ENSOCUG00000013269 -	5:1977753	0.106774667	1.00E-05
ENSOCUG00000023292 -	U1 small m 2:1638280	0.106180667	1.00E-05
ENSOCUG00000013027 -	Olfactory r GL018747	0.106005	1.00E-05
ENSOCUG00000021583 -	Uncharacte 13:124348	0.103748	1.00E-05
ENSOCUG00000020929 -	GL019079	0.103568	1.00E-05
ENSOCUG00000013186 TNFRSF13C	tumor necr GL018734	0.102137333	1.00E-05
ENSOCUG00000023967 -	Uncharacte AAGW020	0.101307333	1.00E-05
ENSOCUG00000024276 -	X:5228961	0.101098333	1.00E-05
ENSOCUG00000008477 -	Uncharacte GL019577	0.099908333	1.00E-05
ENSOCUG00000024246 -	17:4865314	0.099538	1.00E-05
ENSOCUG00000011472 FOXJ1	forkhead bc GL018843	0.0993415	1.00E-05
ENSOCUG00000022551 ARTN	artemin [Sc 13:122752	0.099268333	1.00E-05
ENSOCUG00000027104 TAS2R41	taste recept 7:8624967	0.098643	1.00E-05
ENSOCUG00000023668 -	Oryctolagu GL018713	0.098099333	1.00E-05
ENSOCUG00000025899 -	17:1239448	0.096530333	1.00E-05
ENSOCUG00000015251 -	19:433248	0.096003333	1.00E-05
ENSOCUG00000000602 -	AAGW020	0.095660667	1.00E-05
ENSOCUG00000023240 -	Uncharacte 7:1418556	0.095647	1.00E-05
ENSOCUG00000016070 -	Uncharacte 1:1251492	0.095362333	1.00E-05
ENSOCUG00000013112 PSMB11	proteasome 17:432671	0.093568333	1.00E-05
ENSOCUG00000022591 SSB	Single-strai X:9866000	0.092624	1.00E-05
ENSOCUG00000025488 -	Oryctolagu GL018713	0.092408667	1.00E-05
ENSOCUG00000001600 -	Uncharacte 14:811874	0.092333333	1.00E-05
ENSOCUG00000024592 -	Uncharacte 17:439971	0.092235667	1.00E-05
ENSOCUG00000016484 AIFM3	apoptosis-i 21:492392	0.092064267	1.00E-05
ENSOCUG00000026171 TMEM253	transmemb 17:4141134	0.09182	1.00E-05
ENSOCUG00000024837 -	12:336522	0.091509	1.00E-05
ENSOCUG00000016030 HMGB3	high mobili 1:1632479	0.091479	1.00E-05
ENSOCUG00000026947 -	Uncharacte GL018717	0.0913553	1.00E-05
ENSOCUG00000016064 C17orf105	chromosom 19:4421288	0.090445667	1.00E-05
ENSOCUG00000025270 -	Uncharacte 2:5600126	0.090425	1.00E-05
ENSOCUG00000014523 SPATA17	spermatoge 16:553165	0.089939967	1.00E-05
ENSOCUG00000015568 C8orf74	chromosom 2:3930120	0.089709	1.00E-05
ENSOCUG00000014410 -	Uncharacte GL018705	0.089506	1.00E-05
ENSOCUG00000007213 HMGB4	high mobili GL018704	0.089044667	1.00E-05

ENSOCUG00000016373 -	Uncharacte	12:1267524	0.088244667	1.00E-05
ENSOCUG00000006726 -	Uncharacte	AAGW020	0.086255667	1.00E-05
ENSOCUG00000015175 RESP18	regulated e	7:16055388	0.085560667	1.00E-05
ENSOCUG00000003909 GLIPR1L1	GLI pathog	4:5415269	0.085548	1.00E-05
ENSOCUG00000022173 -	Uncharacte	GL019699	0.085195	1.00E-05
ENSOCUG00000023154 -	Uncharacte	X:4868046	0.083640667	1.00E-05
ENSOCUG00000017530 SLC10A5	solute carri	3:9733681	0.083272667	1.00E-05
ENSOCUG00000000239 ATP6V1G3	ATPase, H-	16:7267708	0.081506667	1.00E-05
ENSOCUG00000011640 -	Uncharacte	14:307493	0.081419	1.00E-05
ENSOCUG00000026071 PIP5KL1	phosphatid	GL018847	0.081087	1.00E-05
ENSOCUG00000007301 -	Uncharacte	GL018781	0.081061333	1.00E-05
ENSOCUG00000026837 CACNG2	calcium ch	4:85248430	0.080213667	1.00E-05
ENSOCUG00000000506 -	Uncharacte	3:1439140	0.079377333	1.00E-05
ENSOCUG00000010645 -	40S ribos	13:2026739	0.078774667	1.00E-05
ENSOCUG00000026905 -		13:9531519	0.078353	1.00E-05
ENSOCUG00000010266 MYO3B	Uncharacte	7:11007230	0.0778732	1.00E-05
ENSOCUG00000012140 -	Uncharacte	GL018700	0.077371333	1.00E-05
ENSOCUG00000027590 -		1:5075996	0.076540667	1.00E-05
ENSOCUG00000024857 -		GL018724	0.076399	1.00E-05
ENSOCUG00000025182 -	Olfactory r	1:19255410	0.075961333	1.00E-05
ENSOCUG00000015848 -	Uncharacte	X:2304500	0.075726667	1.00E-05
ENSOCUG00000015346 -		13:1259808	0.075511333	1.00E-05
ENSOCUG00000005183 CLPSL1	colipase-lik	12:258128	0.075027333	1.00E-05
ENSOCUG00000024591 -		15:4129208	0.074805667	1.00E-05
ENSOCUG00000000869 -	Uncharacte	AAGW020	0.074565667	1.00E-05
ENSOCUG00000023868 -		12:9777200	0.073892667	1.00E-05
ENSOCUG00000000178 CYP26A1	cytochrome	18:408383	0.073497333	1.00E-05
ENSOCUG00000024030 -		GL018817	0.072602	1.00E-05
ENSOCUG00000015369 TLX2	T-cell leuk	2:11202568	0.0725	1.00E-05
ENSOCUG00000023676 -	Uncharacte	AAGW020	0.072074	1.00E-05
ENSOCUG00000013907 FAM83E	family with	GL019039	0.072058633	1.00E-05
ENSOCUG00000011071 -	Uncharacte	8:2907921	0.071862733	1.00E-05
ENSOCUG00000027097 -	Uncharacte	8:16787929	0.071743933	1.00E-05
ENSOCUG00000027926 OR2V1	olfactory re	11:3185969	0.071026667	1.00E-05
ENSOCUG00000026544 LCN9	Uncharacte	1:367323-3	0.0710138	1.00E-05
ENSOCUG00000012984 -		AAGW020	0.070849333	1.00E-05
ENSOCUG00000021193 OR52B2	olfactory re	1:1471746	0.070789	1.00E-05
ENSOCUG00000016008 FANCD2OS	FANCD2 o	GL018802	0.070225333	1.00E-05
ENSOCUG00000005850 GABRR3	gamma-am	14:1225328	0.069952667	1.00E-05
ENSOCUG00000017811 -	Uncharacte	1:1053255	0.069374667	1.00E-05
ENSOCUG00000006178 OR56A3	olfactory re	1:1469812	0.069171	1.00E-05
ENSOCUG00000014968 DDC	dopa decar	GL018745	0.069046	1.00E-05
ENSOCUG00000026282 -	Uncharacte	1:19216329	0.069024667	1.00E-05
ENSOCUG00000021294 TMEM95	transmemb	19:117975	0.068847333	1.00E-05
ENSOCUG00000026520 C5orf49	chromosom	GL018756	0.068805	1.00E-05
ENSOCUG00000007698 C1orf111	chromosom	13:306313	0.068784667	1.00E-05
ENSOCUG00000024095 -		9:15750688	0.068531333	1.00E-05
ENSOCUG00000007395 -	Olfactory r	GL019045	0.067653	1.00E-05
ENSOCUG00000027144 -	Olfactory r	1:1911169	0.067587667	1.00E-05
ENSOCUG00000022893 KLF14	Kruppel-lik	7:9249868	0.067183	1.00E-05

ENSOCUG00000027287 -	Uncharacte	11:256177	0.066855667	1.00E-05	
ENSOCUG00000027826 -	Olfactory r	AAGW020	0.066653	1.00E-05	
ENSOCUG00000016947	CCDC153	coiled-coil	GL018823	0.066394667	1.00E-05
ENSOCUG00000001597	ADAMDEC	ADAM-like	2:4533438	0.066166533	1.00E-05
ENSOCUG00000028222 -	Olfactory r	1:9270939	0.066059333	1.00E-05	
ENSOCUG00000025360 -		1:1515679	0.064984667	1.00E-05	
ENSOCUG00000026374 -	Uncharacte	GL018981	0.06479	1.00E-05	
ENSOCUG00000016383 -		1:8374787	0.064683667	1.00E-05	
ENSOCUG00000016150 -		X:6881685	0.064598	1.00E-05	
ENSOCUG00000025144 -	Olfactory r	1:1481890	0.063858667	1.00E-05	
ENSOCUG00000029162 -	Uncharacte	17:612704	0.063382667	1.00E-05	
ENSOCUG00000026446 -	Uncharacte	2:9866452	0.063311333	1.00E-05	
ENSOCUG00000026780 -	Olfactory r	17:429580	0.061427667	1.00E-05	
ENSOCUG00000025891	SF3A2	splicing fac	1:4708015	0.061314867	1.00E-05
ENSOCUG00000028016 -	Uncharacte	7:3570700	0.061298667	1.00E-05	
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ENSOCUG00000024831 -		4:5810627	0.060468333	1.00E-05	
ENSOCUG00000009516	CHRNA6	cholinergic	GL018706	0.059754867	1.00E-05
ENSOCUG00000021047 -		GL018702	0.058430333	1.00E-05	
ENSOCUG00000026738 -	Olfactory r	13:343381	0.057363333	1.00E-05	
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ENSOCUG00000021906 -	slowmo	hoi	12:435974	0.056444667	1.00E-05
ENSOCUG00000026637 -		18:431258	0.056047333	1.00E-05	
ENSOCUG00000023930	LYZL6	lysozyme-li	19:456721	0.055796333	1.00E-05
ENSOCUG00000022204 -	Uncharacte	GL019073	0.055531	1.00E-05	
ENSOCUG00000005906 -		15:219462	0.055300667	1.00E-05	
ENSOCUG00000021771	LCTL	lactase-like	17:584048	0.055273867	1.00E-05
ENSOCUG00000022822	GBX1	gastrulation	13:125612	0.0550904	1.00E-05
ENSOCUG00000008058 -		14:923226	0.054127667	1.00E-05	
ENSOCUG00000023656 -		7:6393611	0.053828333	1.00E-05	
ENSOCUG00000002529	GRXCR1	glutaredoxi	2:3198462	0.053126667	1.00E-05
ENSOCUG00000005891	ELAVL2	ELAV like	1:2987421	0.053082833	1.00E-05
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ENSOCUG00000006233 -		3:1679605	0.050934333	1.00E-05	
ENSOCUG00000021790 -	Uncharacte	10:817494	0.050870333	1.00E-05	
ENSOCUG00000002123	GRM8	glutamate r	7:1707043	0.050724667	1.00E-05
ENSOCUG00000021622 -	Uncharacte	GL018890	0.050251333	1.00E-05	
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ENSOCUG00000007072 -	Olfactory r	GL018890	0.050191333	1.00E-05	
ENSOCUG00000021113	FTH1	Ferritin [S	13:118381	0.049962333	1.00E-05
ENSOCUG00000014961 -	Uncharacte	14:951214	0.0499251	1.00E-05	

ENSOCUG00000024594	-	Uncharacte	1:92994068	0.049271567	1.00E-05
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ENSOCUG00000027920	CA7	carbonic an	5:22255029	0.047767967	1.00E-05
ENSOCUG00000028168	-		12:7385920	0.047706	1.00E-05
ENSOCUG00000028017	-		18:3914695	0.047642667	1.00E-05
ENSOCUG00000006064	-	Uncharacte	14:7168259	0.047555333	1.00E-05
ENSOCUG00000013365	-	Uncharacte	1:93416755	0.047356333	1.00E-05
ENSOCUG00000021460	-	Uncharacte	GL0188415	0.046142333	1.00E-05
ENSOCUG00000025120	SLC18A3	solute carri	18:5728754	0.046003333	1.00E-05
ENSOCUG00000007630	CACNG7	Oryctolagu	GL0189245	0.045603	1.00E-05
ENSOCUG00000014732	RIMKLA	ribosomal r	13:1242610	0.045518333	1.00E-05
ENSOCUG00000022903	-	Olfactory r	17:3996684	0.044913333	1.00E-05
ENSOCUG00000003708	C4orf22	chromosom	15:6930482	0.044872667	1.00E-05
ENSOCUG00000017073	ARR3	arrestin 3,	r X:4882955	0.044799533	1.00E-05
ENSOCUG00000008039	-	Olfactory r	13:3427572	0.044544667	1.00E-05
ENSOCUG00000024721	-	Uncharacte	15:9865440	0.044473333	1.00E-05
ENSOCUG00000021232	NTSR2	neurotensin	2:16050544	0.044256333	1.00E-05
ENSOCUG00000021560	RPS4X	Uncharacte	1:10602035	0.044105	1.00E-05
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ENSOCUG00000017404	-	Uncharacte	1:10184000	0.044050667	1.00E-05
ENSOCUG00000009530	NPVF	neuropeptic	10:1007258	0.043921333	1.00E-05
ENSOCUG00000021373	-	Olfactory r	12:2189885	0.043652	1.00E-05
ENSOCUG00000010210	CXorf22	chromosom	X:2213090	0.04364769	1.00E-05
ENSOCUG00000006710	NTSR1	neurotensin	GL0197905	0.043629	1.00E-05
ENSOCUG00000015617	SLC25A31	solute carri	15:1035600	0.043317067	1.00E-05
ENSOCUG00000025716	-	Uncharacte	12:3093715	0.042717	1.00E-05
ENSOCUG00000011949	-	Glutathione	12:4257000	0.042677333	1.00E-05
ENSOCUG00000014487	ODF3	outer dense	GL0193555	0.042602667	1.00E-05
ENSOCUG00000003800	TAS2R3	taste recept	GL0187585	0.042549667	1.00E-05
ENSOCUG00000029228	LRRC19	leucine rich	1:26481675	0.042456	1.00E-05
ENSOCUG00000011580	SPATA32	spermatoge	19:4511899	0.041954	1.00E-05
ENSOCUG00000024058	-	Transporter	AAGW020	0.041609667	1.00E-05
ENSOCUG00000017844	-	Uncharacte	GL0198925	0.041585333	1.00E-05
ENSOCUG00000027698	-	Uncharacte	GL0187115	0.041533667	1.00E-05
ENSOCUG00000025908	-	Uncharacte	1:15695234	0.0411413	1.00E-05
ENSOCUG00000028181	ORYCUNV	Uncharacte	GL0187475	0.040966667	1.00E-05
ENSOCUG00000027720	-		GL0187375	0.040956667	1.00E-05
ENSOCUG00000025601	RGS11	regulator of	GL0193195	0.04063	1.00E-05
ENSOCUG00000023563	-		2:22803295	0.040567333	1.00E-05
ENSOCUG00000025389	-		3:47619344	0.040508	1.00E-05
ENSOCUG00000007843	-	paraneoplas	GL0192845	0.040460667	1.00E-05
ENSOCUG00000009770	CCDC83	coiled-coil	1:13081299	0.040352667	1.00E-05
ENSOCUG00000024155	ORYCUNV	Uncharacte	GL0187475	0.039564333	1.00E-05
ENSOCUG00000010100	IL2	Oryctolagu	15:9831245	0.039459667	1.00E-05
ENSOCUG00000008297	-	proteoglyca	1:19047525	0.039198	1.00E-05
ENSOCUG00000003089	PRG3	proteoglyca	1:19046644	0.039082667	1.00E-05
ENSOCUG00000029681	NRXN3	neurexin 3	20:2639210	0.038894667	1.00E-05

ENSOCUG00000024199	ORYCUNV	Uncharacte	GL018763:	0.038146	1.00E-05
ENSOCUG00000014664	PLCZ1	phospholip	8:21164500	0.0378526	1.00E-05
ENSOCUG00000006218	-		GL018700:	0.037706333	1.00E-05
ENSOCUG00000006115	LRIT1	leucine-rich	GL018716:	0.037518767	1.00E-05
ENSOCUG00000015660	TRIM31	tripartite m	12:221003:	0.0375	1.00E-05
ENSOCUG00000024257	ORYCUNV	Uncharacte	GL018752:	0.037433333	1.00E-05
ENSOCUG00000021544	-	Olfactory r	17:429371:	0.037337667	1.00E-05
ENSOCUG00000022038	-	Uncharacte	GL019776:	0.037117667	1.00E-05
ENSOCUG00000003870	FGF19	fibroblast g	AAGW020	0.036845	1.00E-05
ENSOCUG00000004746	SPATA16	spermatoge	14:678991:	0.036621767	1.00E-05
ENSOCUG00000003497	SHCBP1L	SHC SH2-c	GL019071:	0.0363748	1.00E-05
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ENSOCUG00000014297	APOF	apolipoprot	4:39937979	0.035934333	1.00E-05
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ENSOCUG00000016758	-	Uncharacte	2:1553250:	0.035272667	1.00E-05
ENSOCUG00000024564	-	Uncharacte	GL018856:	0.035267	1.00E-05
ENSOCUG00000029464	-	Uncharacte	GL018772:	0.034986	1.00E-05
ENSOCUG00000028137	IHH	indian hedg	7:1602890:	0.034766967	1.00E-05
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Draft

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Draft

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0.458450909	0.870312	0.887418
0.33855609	0.857774	0.874685
0.429333475	0.856831	0.873775
0.392243909	0.85673	0.873724
0.341136889	0.844064	0.860857
0.317914306	0.822428	0.838839
0.503514769	0.81114	0.827472
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Draft

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0.463998302	0.757224	0.773427
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0.603343443	0.741603	0.75841
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Draft

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1.89E-06	0.681754	0.699518
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2.41E-06	0.677407	0.695387
2.39E-06	0.677407	0.695387
2.37E-06	0.677407	0.695387
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2.23E-06	0.677407	0.695387

Draft

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Draft

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Draft

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Draft

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0.406098129	0.635908	0.659546
0.396061657	0.635908	0.659546
0.339625127	0.635908	0.659546
0.391815272	0.63289	0.656456
0.47607039	0.630554	0.654071
0.552909498	0.625855	0.649275
0.500484646	0.625855	0.649275
0.278286129	0.615365	0.638431
0.515670515	0.60088	0.623477
0.480851217	0.60088	0.623477
0.577432297	0.60034	0.622992
0.55773238	0.60034	0.622992
0.450096962	0.600255	0.622941
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0.524217383	0.59372	0.616344
0.515637334	0.59372	0.616344
0.501858624	0.59372	0.616344
0.490446142	0.59372	0.616344
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0.813558341	0.586647	0.628934
0.809343107	0.586647	0.628934
0.808560755	0.586647	0.628934
0.808015157	0.586647	0.628934
0.807943359	0.586647	0.628934
0.807770103	0.586647	0.628934
0.806163926	0.586647	0.628934
0.805824325	0.586647	0.628934
0.804530136	0.586647	0.628934
0.80447358	0.586647	0.628934
0.797613845	0.586647	0.628934
0.795680178	0.586647	0.628934
0.788658353	0.586647	0.628934
0.787537755	0.586647	0.628934
0.784645726	0.586647	0.628934
0.784550352	0.586647	0.628934
0.78276583	0.586647	0.628934
0.781866256	0.586647	0.628934
0.780986026	0.586647	0.628934
0.780172496	0.586647	0.628934
0.77736667	0.586647	0.628934
0.775001599	0.586647	0.628934
0.774548549	0.586647	0.628934
0.773272899	0.586647	0.628934
0.77170172	0.586647	0.628934

Draft

0.770067881	0.586647	0.628934
0.769430537	0.586647	0.628934
0.768642	0.586647	0.628934
0.763847873	0.586647	0.628934
0.758184005	0.586647	0.628934
0.757368812	0.586647	0.628934
0.755085474	0.586647	0.628934
0.751286965	0.586647	0.628934
0.748558477	0.586647	0.628934
0.748467805	0.586647	0.628934
0.745246033	0.586647	0.628934
0.743051751	0.586647	0.628934
0.741500067	0.586647	0.628934
0.740324561	0.586647	0.628934
0.735592456	0.586647	0.628934
0.731002292	0.586647	0.628934
0.73053385	0.586647	0.628934
0.721972468	0.586647	0.628934
0.721328936	0.586647	0.628934
0.717695572	0.586647	0.628934
0.717182931	0.586647	0.628934
0.716997474	0.586647	0.628934
0.715414309	0.586647	0.628934
0.714928704	0.586647	0.628934
0.713898412	0.586647	0.628934
0.713816922	0.586647	0.628934
0.712290104	0.586647	0.628934
0.709824206	0.586647	0.628934
0.709730539	0.586647	0.628934
0.708723608	0.586647	0.628934
0.70805492	0.586647	0.628934
0.701685593	0.586647	0.628934
0.701349581	0.586647	0.628934
0.700057807	0.586647	0.628934
0.697522435	0.586647	0.628934
0.697471681	0.586647	0.628934
0.696314611	0.586647	0.628934
0.696191251	0.586647	0.628934
0.695357849	0.586647	0.628934
0.694704933	0.586647	0.628934
0.693146279	0.586647	0.628934
0.680163584	0.586647	0.628934
0.678949743	0.586647	0.628934
0.678772023	0.586647	0.628934
0.666161659	0.586647	0.628934
0.664964892	0.586647	0.628934
0.66088912	0.586647	0.628934
0.659101114	0.586647	0.628934
0.649401753	0.586647	0.628934
0.647036566	0.586647	0.628934

Draft

0.639685473	0.586647	0.628934
0.636777136	0.586647	0.628934
0.636298634	0.586647	0.628934
0.635861659	0.586647	0.628934
0.631941946	0.586647	0.628934
0.626102966	0.586647	0.628934
0.623329289	0.586647	0.628934
0.622448499	0.586647	0.628934
0.620679415	0.586647	0.628934
0.620401599	0.586647	0.628934
0.614653579	0.586647	0.628934
0.614295534	0.586647	0.628934
0.611937369	0.586647	0.628934
0.600984754	0.586647	0.628934
0.597024487	0.586647	0.628934
0.596416297	0.586647	0.628934
0.567940374	0.586647	0.628934
0.55730994	0.586647	0.628934
0.661107692	0.583682	0.626065
0.63287433	0.583682	0.626065
0.623252731	0.583682	0.626065
0.620271827	0.583682	0.626065
0.601108707	0.583682	0.626065
0.59786428	0.583682	0.626065
0.577676842	0.583682	0.626065
0.521525131	0.583682	0.626065
0.344072732	0.57966	0.621789
0.503635905	0.578834	0.620942
0.18259128	0.575412	0.617309
0.302551	0.573288	0.615107
0.288056033	0.573288	0.615107
0.583844362	0.570655	0.61251
0.559829779	0.570655	0.61251
0.558567462	0.570655	0.61251
0.494097977	0.570655	0.61251
0.484779921	0.570655	0.61251
0.478872552	0.570655	0.61251
0.381724918	0.564821	0.606285
0.703799028	0.544572	0.584804
0.657446346	0.544572	0.584804
0.633828212	0.544572	0.584804
0.594041144	0.544572	0.584804
0.576129385	0.544572	0.584804
0.573975388	0.544572	0.584804
0.515048115	0.544572	0.584804
0.540157918	0.534378	0.573892
0.508196248	0.531752	0.571107
0.177963739	0.528278	0.567411
0.267908147	0.528204	0.567367
0.507137887	0.528126	0.567318

Draft

0.193295642	0.525001	0.563996
0.489369722	0.513018	0.551157
0.536768437	0.512101	0.550206
94461.3333	0.503454	0.7295
89434	0.503454	0.7295
87308	0.503454	0.7295
76317.6667	0.503454	0.7295
68456.7667	0.503454	0.7295
64312.3333	0.503454	0.7295
62377.9	0.503454	0.7295
60682.3667	0.503454	0.7295
57816.6667	0.503454	0.7295
57167.3333	0.503454	0.7295
53376.6667	0.503454	0.7295
53303.5667	0.503454	0.7295
52346.3333	0.503454	0.7295
51198.6667	0.503454	0.7295
50714.6667	0.503454	0.7295
49603	0.503454	0.7295
49232	0.503454	0.7295
48413.0667	0.503454	0.7295
48398.6667	0.503454	0.7295
47352.6667	0.503454	0.7295
44862.6667	0.503454	0.7295
43234.7333	0.503454	0.7295
42964	0.503454	0.7295
42898	0.503454	0.7295
42780.3333	0.503454	0.7295
41519.3333	0.503454	0.7295
40494.0333	0.503454	0.7295
40432	0.503454	0.7295
40309	0.503454	0.7295
39442.6667	0.503454	0.7295
39415.3333	0.503454	0.7295
39067.1667	0.503454	0.7295
38875.3333	0.503454	0.7295
38512	0.503454	0.7295
38012.3333	0.503454	0.7295
37504.6667	0.503454	0.7295
35730.8667	0.503454	0.7295
35397.4667	0.503454	0.7295
35326	0.503454	0.7295
35203.6667	0.503454	0.7295
34825	0.503454	0.7295
34777.0667	0.503454	0.7295
34542	0.503454	0.7295
34336.6667	0.503454	0.7295
33903.3333	0.503454	0.7295
33478.6333	0.503454	0.7295
33450.8667	0.503454	0.7295

Draft

33421.0333	0.503454	0.7295
32690.5667	0.503454	0.7295
32496.8333	0.503454	0.7295
31353.8	0.503454	0.7295
30824.5	0.503454	0.7295
30357.4	0.503454	0.7295
30150.7333	0.503454	0.7295
30104.4333	0.503454	0.7295
29089	0.503454	0.7295
27961.9333	0.503454	0.7295
27654.1667	0.503454	0.7295
27367.9333	0.503454	0.7295
27104.6333	0.503454	0.7295
25970.1667	0.503454	0.7295
25835	0.503454	0.7295
25396.3667	0.503454	0.7295
25333.3	0.503454	0.7295
25227.1333	0.503454	0.7295
25112.5	0.503454	0.7295
24890.6667	0.503454	0.7295
24771.5333	0.503454	0.7295
24062.8	0.503454	0.7295
24019.6667	0.503454	0.7295
23939.6	0.503454	0.7295
23865.4667	0.503454	0.7295
23806.8667	0.503454	0.7295
23377.0333	0.503454	0.7295
23253.2667	0.503454	0.7295
23221.6667	0.503454	0.7295
23145.5	0.503454	0.7295
22770.9333	0.503454	0.7295
22579.7	0.503454	0.7295
22482.9333	0.503454	0.7295
22320.3667	0.503454	0.7295
22311.9	0.503454	0.7295
21516.7	0.503454	0.7295
21163.1	0.503454	0.7295
21154.4333	0.503454	0.7295
20581.9	0.503454	0.7295
20574.4	0.503454	0.7295
20178.4333	0.503454	0.7295
19884.6	0.503454	0.7295
19678.3333	0.503454	0.7295
19593.0667	0.503454	0.7295
19431.7333	0.503454	0.7295
18685.4333	0.503454	0.7295
18557.5	0.503454	0.7295
18313.3667	0.503454	0.7295
18118.1667	0.503454	0.7295
18086.9	0.503454	0.7295

Draft

18048.3667	0.503454	0.7295
17696.7	0.503454	0.7295
17694.7	0.503454	0.7295
17380.6667	0.503454	0.7295
17141.2	0.503454	0.7295
16788.7333	0.503454	0.7295
16636.4	0.503454	0.7295
16610.3	0.503454	0.7295
16536.7333	0.503454	0.7295
16333.6667	0.503454	0.7295
15478.7667	0.503454	0.7295
15256.3	0.503454	0.7295
15099.5667	0.503454	0.7295
15094.0333	0.503454	0.7295
15001.3333	0.503454	0.7295
14521	0.503454	0.7295
14402.2333	0.503454	0.7295
14379.6	0.503454	0.7295
14284.5333	0.503454	0.7295
14252.9333	0.503454	0.7295
14112.2667	0.503454	0.7295
14077.6333	0.503454	0.7295
14050.9333	0.503454	0.7295
13988.0667	0.503454	0.7295
13953.6	0.503454	0.7295
13949.5333	0.503454	0.7295
13908.0333	0.503454	0.7295
13797.3	0.503454	0.7295
13789.2333	0.503454	0.7295
13557.2	0.503454	0.7295
13442.1	0.503454	0.7295
13397.7333	0.503454	0.7295
13296.6	0.503454	0.7295
13277.5	0.503454	0.7295
12827.3333	0.503454	0.7295
12818.0333	0.503454	0.7295
12757.5333	0.503454	0.7295
12736.99	0.503454	0.7295
12567.9	0.503454	0.7295
12546.4667	0.503454	0.7295
12479.3333	0.503454	0.7295
12293.5667	0.503454	0.7295
12241.3333	0.503454	0.7295
12151.3333	0.503454	0.7295
12111.6	0.503454	0.7295
12105.9333	0.503454	0.7295
12029.6567	0.503454	0.7295
11993.65	0.503454	0.7295
11952.6667	0.503454	0.7295
11913.1667	0.503454	0.7295

Draft

11896.1667	0.503454	0.7295
11882.2667	0.503454	0.7295
11827.0667	0.503454	0.7295
11787.7333	0.503454	0.7295
11698	0.503454	0.7295
11657.9767	0.503454	0.7295
11351	0.503454	0.7295
11167.9333	0.503454	0.7295
11163.7333	0.503454	0.7295
11052.0333	0.503454	0.7295
10998.1	0.503454	0.7295
10865.8	0.503454	0.7295
10858.1667	0.503454	0.7295
10750.3333	0.503454	0.7295
10695.7667	0.503454	0.7295
10677.4667	0.503454	0.7295
10618.0667	0.503454	0.7295
10600.5	0.503454	0.7295
10374.8	0.503454	0.7295
10356.8	0.503454	0.7295
10213.7333	0.503454	0.7295
10130.7333	0.503454	0.7295
10109.8333	0.503454	0.7295
9990.8333	0.503454	0.7295
9953.8	0.503454	0.7295
9934.15	0.503454	0.7295
9926.8333	0.503454	0.7295
9864.3	0.503454	0.7295
9809.9333	0.503454	0.7295
9653.0333	0.503454	0.7295
9600.3333	0.503454	0.7295
9566.0667	0.503454	0.7295
9564.7	0.503454	0.7295
9536.2333	0.503454	0.7295
9356.8333	0.503454	0.7295
9262.4	0.503454	0.7295
9240.8667	0.503454	0.7295
9233.3333	0.503454	0.7295
9223.5667	0.503454	0.7295
9206.4267	0.503454	0.7295
9182	0.503454	0.7295
9150.9	0.503454	0.7295
9147.9	0.503454	0.7295
9135.53	0.503454	0.7295
9044.5667	0.503454	0.7295
9042.5	0.503454	0.7295
8993.9967	0.503454	0.7295
8970.9	0.503454	0.7295
8950.6	0.503454	0.7295
8904.4667	0.503454	0.7295

Draft

8824.4667	0.503454	0.7295
8625.5667	0.503454	0.7295
8556.0667	0.503454	0.7295
8554.8	0.503454	0.7295
8519.5	0.503454	0.7295
8364.0667	0.503454	0.7295
8327.2667	0.503454	0.7295
8150.6667	0.503454	0.7295
8141.9	0.503454	0.7295
8108.7	0.503454	0.7295
8106.1333	0.503454	0.7295
8021.3667	0.503454	0.7295
7937.7333	0.503454	0.7295
7877.4667	0.503454	0.7295
7835.3	0.503454	0.7295
7787.32	0.503454	0.7295
7737.1333	0.503454	0.7295
7654.0667	0.503454	0.7295
7639.9	0.503454	0.7295
7596.1333	0.503454	0.7295
7572.6667	0.503454	0.7295
7551.1333	0.503454	0.7295
7502.7333	0.503454	0.7295
7480.5667	0.503454	0.7295
7456.5667	0.503454	0.7295
7389.2667	0.503454	0.7295
7349.7333	0.503454	0.7295
7260.2	0.503454	0.7295
7250	0.503454	0.7295
7207.4	0.503454	0.7295
7205.8633	0.503454	0.7295
7186.2733	0.503454	0.7295
7174.3933	0.503454	0.7295
7102.6667	0.503454	0.7295
7101.38	0.503454	0.7295
7084.9333	0.503454	0.7295
7078.9	0.503454	0.7295
7022.5333	0.503454	0.7295
6995.2667	0.503454	0.7295
6937.4667	0.503454	0.7295
6917.1	0.503454	0.7295
6904.6	0.503454	0.7295
6902.4667	0.503454	0.7295
6884.7333	0.503454	0.7295
6880.5	0.503454	0.7295
6878.4667	0.503454	0.7295
6853.1333	0.503454	0.7295
6765.3	0.503454	0.7295
6758.7667	0.503454	0.7295
6718.3	0.503454	0.7295

Draft

6685.5667	0.503454	0.7295
6665.3	0.503454	0.7295
6639.4667	0.503454	0.7295
6616.6533	0.503454	0.7295
6605.9333	0.503454	0.7295
6498.4667	0.503454	0.7295
6479	0.503454	0.7295
6468.3667	0.503454	0.7295
6459.8	0.503454	0.7295
6385.8667	0.503454	0.7295
6338.2667	0.503454	0.7295
6331.1333	0.503454	0.7295
6142.7667	0.503454	0.7295
6131.4867	0.503454	0.7295
6129.8667	0.503454	0.7295
6112.6667	0.503454	0.7295
6063.87	0.503454	0.7295
6052.7667	0.503454	0.7295
6046.8333	0.503454	0.7295
5975.4867	0.503454	0.7295
5843.0333	0.503454	0.7295
5736.3333	0.503454	0.7295
5716.7667	0.503454	0.7295
5644.4667	0.503454	0.7295
5604.7333	0.503454	0.7295
5579.6333	0.503454	0.7295
5553.1	0.503454	0.7295
5530.0667	0.503454	0.7295
5527.3867	0.503454	0.7295
5509.04	0.503454	0.7295
5412.7667	0.503454	0.7295
5382.8333	0.503454	0.7295
5312.6667	0.503454	0.7295
5308.2833	0.503454	0.7295
5303.9333	0.503454	0.7295
5269.5	0.503454	0.7295
5231.5333	0.503454	0.7295
5212.98184	0.503454	0.7295
5158.9	0.503454	0.7295
5149.6667	0.503454	0.7295
5134.5667	0.503454	0.7295
5130.1	0.503454	0.7295
5093.4333	0.503454	0.7295
5087.0333	0.503454	0.7295
5072.4667	0.503454	0.7295
5025.1333	0.503454	0.7295
5023.2733	0.503454	0.7295
5019.1333	0.503454	0.7295
4996.2333	0.503454	0.7295
4992.51	0.503454	0.7295

Draft

4927.1567	0.503454	0.7295
4900.2333	0.503454	0.7295
4869.2333	0.503454	0.7295
4781.0667	0.503454	0.7295
4780.2533	0.503454	0.7295
4776.7967	0.503454	0.7295
4770.6	0.503454	0.7295
4764.2667	0.503454	0.7295
4755.5333	0.503454	0.7295
4735.6333	0.503454	0.7295
4614.2333	0.503454	0.7295
4600.3333	0.503454	0.7295
4560.3	0.503454	0.7295
4551.8333	0.503454	0.7295
4491.3333	0.503454	0.7295
4487.2667	0.503454	0.7295
4479.9533	0.503454	0.7295
4454.4667	0.503454	0.7295
4447.3333	0.503454	0.7295
4425.6333	0.503454	0.7295
4410.5	0.503454	0.7295
4406.7733	0.503454	0.7295
4405.0667	0.503454	0.7295
4392.1333	0.503454	0.7295
4365.2	0.503454	0.7295
4364.769	0.503454	0.7295
4362.9	0.503454	0.7295
4331.7067	0.503454	0.7295
4271.7	0.503454	0.7295
4267.7333	0.503454	0.7295
4260.2667	0.503454	0.7295
4254.9667	0.503454	0.7295
4245.6	0.503454	0.7295
4195.4	0.503454	0.7295
4160.9667	0.503454	0.7295
4158.5333	0.503454	0.7295
4153.3667	0.503454	0.7295
4114.13	0.503454	0.7295
4096.6667	0.503454	0.7295
4095.6667	0.503454	0.7295
4063	0.503454	0.7295
4056.7333	0.503454	0.7295
4050.8	0.503454	0.7295
4046.0667	0.503454	0.7295
4035.2667	0.503454	0.7295
3956.4333	0.503454	0.7295
3945.9667	0.503454	0.7295
3919.8	0.503454	0.7295
3908.2667	0.503454	0.7295
3889.4667	0.503454	0.7295

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3814.6	0.503454	0.7295
3785.26	0.503454	0.7295
3770.6333	0.503454	0.7295
3751.8767	0.503454	0.7295
3750	0.503454	0.7295
3743.3333	0.503454	0.7295
3733.7667	0.503454	0.7295
3711.7667	0.503454	0.7295
3684.5	0.503454	0.7295
3662.1767	0.503454	0.7295
3637.48	0.503454	0.7295
3630.8333	0.503454	0.7295
3627.6	0.503454	0.7295
3621.1	0.503454	0.7295
3593.4333	0.503454	0.7295
3585.7	0.503454	0.7295
3561.8667	0.503454	0.7295
3561.1	0.503454	0.7295
3531.5	0.503454	0.7295
3527.2667	0.503454	0.7295
3526.7	0.503454	0.7295
3498.6	0.503454	0.7295
3476.6967	0.503454	0.7295
3464.3667	0.503454	0.7295

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Supplemental Table S2. The differentially expressed gene

Gene_id	Gene_name	Description	locus	Group B_FPKM	Group F_FPKM
ENSOCUG000000021179-			GL019111:	19868.53333	1.00E-05
ENSOCUG000000026797-			AAGW020	7202.266667	1.00E-05
ENSOCUG000000023307	5S_rRNA	5S ribosom	11:8384034	2910.753333	1.00E-05
ENSOCUG000000025865-			AAGW020	1800.563333	1.00E-05
ENSOCUG000000018677-			13:309807:	1310.606667	1.00E-05
ENSOCUG000000028924	U6	U6 spliceos	1:2514450	932.4266667	1.00E-05
ENSOCUG000000018974	Y_RNA	Y RNA [Sc	7:3031346-	821.8	1.00E-05
ENSOCUG000000025175	U6	U6 spliceos	1:1906998:	465.9133333	1.00E-05
ENSOCUG000000025525	5S_rRNA	5S ribosom	9:4342323	383.9833333	1.00E-05
ENSOCUG000000020172-			GL018965:	290.7456667	1.00E-05
ENSOCUG000000020605	5S_rRNA	5S ribosom	1:9198902	284.9963333	1.00E-05
ENSOCUG000000028838	SNORA40	Small nucle	4:4834227	236.927	1.00E-05
ENSOCUG000000020814	5S_rRNA	5S ribosom	12:147082:	220.8463333	1.00E-05
ENSOCUG000000019387	5S_rRNA	5S ribosom	X:1026209	197.4093333	1.00E-05
ENSOCUG000000025322	5S_rRNA	5S ribosom	1:1745621	188.5663333	1.00E-05
ENSOCUG000000019535	snoU6-53	Small nucle	17:416629	156.383	1.00E-05
ENSOCUG000000018766	SNORA66	Small nucle	13:717060:	141.8548333	1.00E-05
ENSOCUG000000026436-			7:6204293:	130.35	1.00E-05
ENSOCUG000000024376	5S_rRNA	5S ribosom	9:4341173	127.9943333	1.00E-05
ENSOCUG000000024416	5S_rRNA	5S ribosom	9:4341888	127.9943333	1.00E-05
ENSOCUG000000026611	5S_rRNA	5S ribosom	9:4342082	127.9943333	1.00E-05
ENSOCUG000000018670	SNORA65	Small nucle	GL018699:	97.40366667	1.00E-05
ENSOCUG000000025836-		Uncharacter	GL018720:	90.872	1.00E-05
ENSOCUG000000019359	SNORA61	Small nucle	13:136971:	89.42126667	1.00E-05
ENSOCUG000000028757	SNORA21	Small nucle	19:403005:	86.63733333	1.00E-05
ENSOCUG000000027907	SNORA71	Small nucle	4:1946654-	79.263	1.00E-05
ENSOCUG000000020979	SNORA31	Small nucle	3:1405490:	76.19633333	1.00E-05
ENSOCUG000000019923	SNORA68	Small nucle	13:118502:	75.71133333	1.00E-05
ENSOCUG000000029045-		Uncharacter	4:7839108-	34.023	1.00E-05
ENSOCUG000000019492	SNORA48	Small nucle	19:116015:	33.0339	1.00E-05
ENSOCUG000000029018-		Uncharacter	7:1268515:	32.45896667	1.00E-05
ENSOCUG000000019650	SNORA42	Small nucle	13:369203:	31.46656667	1.00E-05
ENSOCUG000000018902	SNORA57	Small nucle	GL018717:	26.7226	1.00E-05
ENSOCUG000000027978	SNORD15	Small nucle	1:1413079	23.2878	1.00E-05
ENSOCUG000000018472	U4	U4 spliceos	GL018715:	18.26726667	1.00E-05
ENSOCUG000000028449	SNORA18	Small nucle	5:2350666:	12.68623333	1.00E-05
ENSOCUG000000027788	U2	U2 spliceos	19:439006:	11.6302	1.00E-05
ENSOCUG000000019885	SNORA25	Small nucle	1:1231903:	11.3631	1.00E-05
ENSOCUG000000023289-		Uncharacter	AAGW020	10.74416667	1.00E-05
ENSOCUG000000022460	snoU109	Small nucle	16:777644:	9.1159	1.00E-05
ENSOCUG000000022414	U2	U2 spliceos	19:438939:	8.722633333	1.00E-05
ENSOCUG000000025425	U3	Small nucle	15:192642:	6.590666667	1.00E-05
ENSOCUG000000027893	SNORA2	Small nucle	4:3298890:	6.342533333	1.00E-05
ENSOCUG000000026960	U2	U2 spliceos	19:438493:	4.54	1.00E-05
ENSOCUG000000020237	U2	U2 spliceos	3:2174888:	4.0715	1.00E-05

ENSOCUG00000010964-	14:410650	8.707646667	0.671497333
ENSOCUG00000025833-	14:286335	8.83117	0.96739
ENSOCUG00000010829 MYL4	myosin, lig 19:466604	9.982684867	1.478484333
ENSOCUG00000027420-	14:117265	145.3351517	22.02369667
ENSOCUG00000017655-	Uncharacte 14:118855	5.00421	0.764393333
ENSOCUG00000006901 ANKRD1	Oryctolagu 18:389079	5.282653733	0.817438
ENSOCUG00000013346 MYOZ3	myozenin 3:323612	15.44709667	2.404926667
ENSOCUG00000001849 SMPX	small musc X:748949	161.2807033	25.22266667
ENSOCUG00000022110 TCEAL7	transcriptio X:867411	23.21665667	4.121073333
ENSOCUG00000015238-	Uncharacte 12:151335	390.928	76.18466667
ENSOCUG00000011736 CA3	carbonic ar 3:1010757	247.744492	52.50103333
ENSOCUG00000018543 SNORA73	Small nucle 13:137019	28.32506667	6.018966667
ENSOCUG00000025586 MYL2	myosin, lig 21:709262	113.8373713	24.94596667
ENSOCUG00000012392 MYL3	myosin, lig 9:1487404	472.3030067	105.6394333
ENSOCUG00000016660 SFRP2	secreted fri 15:100071	27.07488333	6.087516667
ENSOCUG00000018609 SNORA21	Small nucle 19:403005	161.2493333	36.91033333
ENSOCUG00000015658-	long interg 2:9566380	75.92373333	17.3856
ENSOCUG00000005860 MSS51	MSS51 mit 18:140151	9.628735667	2.210953333
ENSOCUG00000017368 MYL6B	myosin, lig 4:3972165	385.2902733	89.13616667
ENSOCUG00000017913 YIPF7	Yip1 doma 2:3339515	7.380269667	1.709933333
ENSOCUG00000011454 HRASLS	HRAS-like 14:891130	5.096299333	1.20116
ENSOCUG00000022189-	12:123469	7.413541	1.759053333
ENSOCUG00000017131 LMOD2	leiomodini 7:2091136	57.57983	13.83980333
ENSOCUG00000010113-	12:836655	8.796195667	2.15023
ENSOCUG00000007983 TNNC1	Troponin C 9:1952363	1134.514743	278.16
ENSOCUG00000006310 PPM1J	protein pho 13:514437	6.870769	1.720686667
ENSOCUG00000006570 ABRA	actin-bindin 3:1220781	16.476574	4.29863
ENSOCUG00000012444 FBXO40	F-box prote 14:973648	6.006916667	1.567966667
ENSOCUG00000006986 SCIN	scinderin [10:264805	19.3975	5.063686667
ENSOCUG00000025599-	GL019111	6076.733333	1590.31
ENSOCUG00000003951 ATP1B4	ATPase, Na X:9480283	6.7004863	1.75546
ENSOCUG00000008959 MYOZ2	myozenin 2 15:944651	67.28834367	17.9381
ENSOCUG00000024073 DUSP26	dual specif 2:7420892	34.95524	9.320313333
ENSOCUG00000023632 SNORD97	Small nucle 1:1525866	102.2928667	27.31073333
ENSOCUG00000014521 C10orf71	chromosom 18:553539	8.236597133	2.1998
ENSOCUG00000009959 CASQ1	Oryctolagu 13:328899	290.723379	78.09223333
ENSOCUG00000008850 CACNG1	Oryctolagu 19:504213	37.43841267	10.07795
ENSOCUG00000000788 GADL1	glutamate c 14:177993	5.457648667	1.478429
ENSOCUG00000012592 ASB5	Oryctolagu 2:5370162	21.45505133	5.833863333
ENSOCUG00000011211 RSMTCK	creatine kir 11:165195	10.59811633	2.88749
ENSOCUG00000010424 TNNT1	troponin I t 16:701017	269.5459833	75.80913333
ENSOCUG00000023019 FOSB	FBJ murine GL019006	118.3252667	33.51292333
ENSOCUG00000025317 PTP4A3	protein tyr GL019882	79.93277333	22.80596667
ENSOCUG00000007471-	Cytochrom GL018752	541.8979767	155.809
ENSOCUG00000026126 MB	Myoglobin 4:8592447	722.8693433	207.9653333
ENSOCUG00000001522 SH3BGR	SH3 domai GL018907	81.57835633	23.50546667
ENSOCUG00000024729 HSPB3	Uncharacte 11:704716	9.230223333	2.686916667

ENSOCUG00000025023 -	Oryctolagu 9:10337708	129.5630733	38.06893333
ENSOCUG00000017871 ACTN2	actinin, alp 16:2641435	349.8069467	103.1885
ENSOCUG00000023172 SOCS3	GL019170:	63.70896667	18.82820667
ENSOCUG00000011023 NRAP	nebulin-rel: 18:6115875	66.20849267	19.83893333
ENSOCUG00000021287 HSPB6	heat shock GL018786:	166.8031333	50.32816667
ENSOCUG00000023462 MYLPF	myosin ligl GL018752:	882.6428067	266.764
ENSOCUG00000008066 DHRS7C	dehydroger 19:9698225	43.4202	13.16046667
ENSOCUG00000012560 MYOZ1	myozenin 118:1378375	608.1104533	184.6756667
ENSOCUG00000016643 ITGB1BP2	integrin bet X:4975947	13.78375167	4.189813333
ENSOCUG00000017035 TRIM54	tripartite m 2:15877788	19.53343333	5.94522
ENSOCUG00000013131 MYOM2	myomesin : GL018865:	97.42797467	30.12246667
ENSOCUG00000014182 MYL1	myosin, lig 7:15116255	2490.106663	774.4553333
ENSOCUG00000010594 CASQ2	Oryctolagu 13:4846359	33.72092	10.49121333
ENSOCUG00000024802 -	Uncharacte AAGW020	10.44519667	3.252936667
ENSOCUG00000003384 PRKAG3	protein kin: 7:16009255	7.750675	2.414053333
ENSOCUG00000021185 FNDC5	fibronectin GL018704:	13.4252	4.194873333
ENSOCUG00000009100 ANKRD23	ankyrin rep 2:94641859	117.0913633	37.1957
ENSOCUG00000016283 RPL3L	ribosomal l GL019283:	48.516351	15.43159667
ENSOCUG00000017551 XIRP2	xin actin-bi 7:10675605	52.36394767	16.6633
ENSOCUG00000016424 AMPD1	AMP deam 13:4949635	54.89815533	17.51773333
ENSOCUG00000011821 TPM3	tropomyosi 13:3836888	156.70029	50.0294
ENSOCUG00000000968 DES	desmin [Sc 7:16062156	347.7070333	111.3746
ENSOCUG00000010198 TPM2	Tropomyos 1:18090635	2453.236733	786.836
ENSOCUG00000015051 PPP1R3C	protein pho 18:3959399	22.45380133	7.201983333
ENSOCUG00000025140 SRL	Oryctolagu GL018787:	37.88071533	12.16381667
ENSOCUG00000014268 SIX1	20:8229769	12.37461333	3.977326667
ENSOCUG00000013564 TRIM63	tripartite m 13:1392230	42.3056	13.6724
ENSOCUG00000007450 -	Cytochrom GL018752:	25.42336667	8.237803333
ENSOCUG00000011505 -	Uncharacte GL019066:	23.91191767	7.78895
ENSOCUG00000025160 TCAP	titin-cap [S 19:4089279	438.9892	143.8236667
ENSOCUG00000027310 SLC16A3	solute carri GL019266:	14.86857333	4.886446667
ENSOCUG00000014414 MYOT	myotilin [S 3:20207681	101.2987763	33.35463333
ENSOCUG00000026908 -	Uncharacte GL019355:	218.263	71.8963
ENSOCUG00000027228 SMTNL1	smoothelin 1:19062686	28.70399833	9.634346667
ENSOCUG00000012459 FHL3	four and a l GL018704:	132.1617033	44.37636667
ENSOCUG00000021380 SMCO1	single-pass 14:9225735	5.050987733	1.700833333
ENSOCUG00000005950 CAV3	caveolin 3 GL018703:	18.50879833	6.25213
ENSOCUG00000022163 -	Uncharacte 18:1232798	7.071343333	2.401323333
ENSOCUG00000010229 MYH8	myosin, he: 19:9145212	126.5555113	43.06603333
ENSOCUG00000029574 CYP2F1	cytochromε GL018789:	284.807	97.4666
ENSOCUG00000007837 LRRC39	leucine rich 13:6397495	22.90906933	7.859933333
ENSOCUG00000009828 ARPP21	cAMP-regt 14:2256992	5.7872511	1.98956
ENSOCUG00000008064 TRDN	triadin [So 12:1123859	43.2182435	14.8979
ENSOCUG00000013155 HHATL	hedgehog a 9:1440802-	11.38994933	3.93124
ENSOCUG00000027853 PGAM2	phosphogly 10:4463981	542.7079167	187.3336667
ENSOCUG00000001526 SYPL2	Oryctolagu 13:5472114	57.67747167	19.91823333
ENSOCUG00000006734 MYO18B	myosin XV GL018766:	12.30282047	4.260086667

ENSOCUG00000022984-	Uncharacte GL018883:	15.8602	5.49439
ENSOCUG00000008601 ASB16	ankyrin rep 19:444919:	9.213305667	3.207606667
ENSOCUG00000002173 PYGM	Oryctolagu GL019294:	530.706	186.0513333
ENSOCUG00000014862 BIN1	bridging in 7:5859356:	28.75333333	10.08661333
ENSOCUG00000010649 MKX	mohawk hc 16:680173:	5.42281	1.907096667
ENSOCUG00000007793 ANKRD2	ankyrin rep 18:457547:	21.81358	7.689566667
ENSOCUG00000008571 MYOM1	myomesin 9:5883363:	75.98302667	26.96463333
ENSOCUG00000023698 ASB12	ankyrin rep X:4288185:	16.39346667	5.822266667
ENSOCUG00000009244 THBS4	thrombospo 11:747006:	37.10992	13.19623333
ENSOCUG00000002108-	Uncharacte 19:124704:	929.4095067	330.816
ENSOCUG00000023774 FITM1	fat storage- 17:441795:	44.532086	15.91446667
ENSOCUG00000010852 HSPB7	heat shock GL018791:	52.30673667	18.79246667
ENSOCUG00000015301 SCN1B	Oryctolagu GL018786:	54.51526333	19.60946667
ENSOCUG00000001457 MYF6	myogenic f4:5997836:	15.01316667	5.404183333
ENSOCUG00000016259 DDIT4L	DNA-damε 15:496440:	57.75949667	20.79876667
ENSOCUG00000016462 IL1RL1	interleukin 2:9007806:	7.72277	2.782473333
ENSOCUG00000028008 APOBEC2	apolipoprot 12:308025:	165.8807733	59.78406667
ENSOCUG00000004480 CSRP3	cysteine an 1:1581129:	92.46186667	33.4775
ENSOCUG00000011901 EN1	engrailed h 7:6400934:	7.304793333	2.647146667
ENSOCUG00000004509 MYH3	myosin, he: 19:892681:	96.976193	35.21193333
ENSOCUG00000008892 RAPSNI	receptor-as 1:1867483:	5.024189	1.828803333
ENSOCUG00000001757 TNNT3	troponin T AAGW020	597.7033333	217.904
ENSOCUG00000021115 PKIA	cAMP-dep 3:9436287:	29.71504333	10.84700333
ENSOCUG00000017445 PFKM	phosphofru GL018949:	188.4263667	69.0504
ENSOCUG00000022132 KCNA7	potassium v GL019028:	8.081243667	2.966013333
ENSOCUG00000012980 KLHL41	kelch-like f7:1092272:	90.76475333	33.50716667
ENSOCUG00000021153 MAP3K7C	MAP3K7 C 14:158427:	14.54108667	5.374206667
ENSOCUG00000012976 HSPB2-C1	Uncharacte 1:1044606:	9.561723333	3.534753333
ENSOCUG00000021070 ACA64	Small nucle GL018779:	172.5043333	63.77166667
ENSOCUG00000022885-	Uncharacte GL018757:	95.3722	35.34893333
ENSOCUG00000026736 SGCA	sarcoglycan 19:374748:	20.9226	7.755636667
ENSOCUG00000023342 RTN2	reticulon 2 GL019006:	29.27852333	10.85697
ENSOCUG00000013394 KERA	keratocan [4:7026081:	16.01538333	5.94413
ENSOCUG00000005171 AK1	adenylate k GL018847:	178.7841	66.37896667
ENSOCUG00000006329 ALDOA	Oryctolagu 6:1844374:	3549.770667	1321.590333
ENSOCUG00000028843 SNORA48	Small nucle 19:116015:	106.6229	39.74506667
ENSOCUG00000027154 CKM	creatine kir GL019006:	1146.6364	429.3466667
ENSOCUG00000025341 ADSSL1	adenylosuc AAGW020	65.327204	24.53756667
ENSOCUG00000025110-	20:1157620	8.317223333	3.124563333
ENSOCUG00000017722 GMPR	guanosine r GL018711:	17.74819	6.71151
ENSOCUG00000013760 NEURL	neuralized 18:514202:	19.90326933	7.535283333
ENSOCUG00000013251 STAC3	SH3 and cy GL018714:	45.82181267	17.35881667
ENSOCUG00000022445 MYH2	myosin, he: 19:902757:	381.391699	145.0050333
ENSOCUG00000005808 PDLIM3	PDZ and L 2:6293828:	73.09453667	27.83003333
ENSOCUG00000026890-	Uncharacte GL019066:	22.93158333	8.78758
ENSOCUG00000019382 7SK	7SK RNA 12:270034:	5.102123333	1.958256667
ENSOCUG00000009072 DUSP13	dual specif 18:123279:	13.24886667	5.103263333

ENSOCUG00000016537SRPK3	SRSF prote GL018816:	9.81983	3.81888
ENSOCUG00000012693LDB3	LIM domai 18:8393772	54.465601	21.1908
ENSOCUG00000002752S100A1	S100 calcit 13:3883129	18.32079433	7.16315
ENSOCUG000000021799-	13:1079970	71.88773333	28.21923333
ENSOCUG00000017004TMEM182	transmemb 2:89613620	10.357889	4.069976667
ENSOCUG00000009276MYBPC1	myosin bin 4:80935715	292.1764367	114.8120333
ENSOCUG00000001264CMYA5	cardiomyo 11:509806-	22.84334077	8.979716667
ENSOCUG000000027792TMEM52	transmemb AAGW020	30.56981333	12.02886667
ENSOCUG00000007566ACTA1	actin, alpha GL018838:	3758.033867	1490.837
ENSOCUG00000015430TRIM72	tripartite m GL018752:	10.12949133	4.023046667
ENSOCUG000000022842-	13:3051477	5476.833333	2176.9
ENSOCUG000000025973POPDC3	popeye dor 12:9322845	9.182574333	3.65423
ENSOCUG000000024481CAPN3	calpain 3, (17:2978168	40.15153533	15.99893333
ENSOCUG00000016243MT3	Oryctolagu 5:12893441	65.00805	25.91333333
ENSOCUG00000012404MG33A	Oryctolagu GL018776:	119.2813567	47.5556
ENSOCUG00000004821MLLT11	AF1q; Unc 13:4111091	10.28124333	4.102956667
ENSOCUG00000001205RBFOX1	RNA bindi 6:1578018-	11.25862667	4.542426667
ENSOCUG00000013367COL11A1	collagen, ty 13:6105345	14.52371667	5.871773333
ENSOCUG00000008188LMOD3	leiomodini 9:36532519	33.1275461	13.46701333
ENSOCUG00000011037MYH7	myosin, he 17:4360597	126.0784917	51.35136667
ENSOCUG000000020919TMOD4	Oryctolagu 13:4101888	39.23698033	16.00943333
ENSOCUG000000025995ASB2	ankyrin rep 20:1232813	17.63076	7.22492
ENSOCUG000000023317-	actinin, alp 1:19416791	157.2613407	64.70706667
ENSOCUG00000017433-	hemicentin GL019049:	7.854743333	3.240853333
ENSOCUG00000005702PTPLA	protein tyr 16:4370602	15.53638	6.411506667
ENSOCUG00000014122-	tropomyosi 17:9208775	480.0403333	198.6743333
ENSOCUG000000026636MHC	Oryctolagu 19:9056196	368.27513	152.5336667
ENSOCUG00000017458NEB	nebulin [Sc 7:90491559	70.52658067	29.45853333
ENSOCUG00000017328MYLK2	myosin lig 4:7410542-	16.3351523	6.824063333
ENSOCUG00000013103COX7A1	cytochrome GL018786:	307.77753	129.5753333
ENSOCUG00000006209HFE2	hemochron 13:4270358	17.5475	7.391783333
ENSOCUG000000024308MMP11	matrix met: GL019236:	261.5936667	110.6312
ENSOCUG00000011182-	Uncharacte GL018951:	8.40492	3.55593
ENSOCUG00000009223DOK5	docking pr GL018712:	6.31928	2.677046667
ENSOCUG000000022868-	Uncharacte 13:6044938	69.00503333	29.31376667
ENSOCUG00000006084CMBL	carboxyme 11:3526880	47.49233667	20.18073333
ENSOCUG00000018756SNORA4	Small nucle 14:7883899	151.7151333	64.7683
ENSOCUG000000021402-	Uncharacte GL018699:	30.94377667	13.22816667
ENSOCUG00000011179TNMD	tenomoduli X:8877767	8.644693333	3.708096667
ENSOCUG000000027082-	Uncharacte 17:3600791	36.45373333	15.64243333
ENSOCUG000000024272NEXN	nexilin (F a 13:8752898	46.00752333	19.8325
ENSOCUG00000005991ALPK3	alpha-kinas GL018738:	26.08434	11.32364
ENSOCUG00000008657CGREF1	cell growth 2:15885479	27.01596667	11.77962
ENSOCUG00000009681-	Uncharacte 13:5446427	15.02588767	6.577043333
ENSOCUG000000026398-	Uncharacte 13:6047311	21.77343333	9.543836667
ENSOCUG00000013151KLHL40	kelch-like 19:1440802-	13.07617633	5.746143333
ENSOCUG00000013865PLN	Oryctolagu 12:1074437	66.50786667	29.34573333

ENSOCUG00000010371FRZB	frizzled-rel 7:1229236	20.03972667	8.850653333
ENSOCUG00000004685ENY2	enhancer of 11:7483491	153.5949333	68.15573333
ENSOCUG00000002688ATP2A1	ATPase, C ₆ :18725418	566.39853	252.074
ENSOCUG00000003619CACNA1S	voltage-dep 16:7032466	25.48051497	11.36246
ENSOCUG00000013549MLF1	myeloid leu 14:5299762	85.26407	38.0387
ENSOCUG00000016777TTN	titin [Sourc 7:11822549	39.83853967	17.82053333
ENSOCUG00000019855SNORA40	Small nucle 1:12318609	114.7503333	51.33966667
ENSOCUG00000021107VAMP1	vesicle-ass 8:32523676	10.60414333	4.747433333
ENSOCUG00000027846DNAJB5	DnaJ (Hsp α 1:18869864	10.19262667	4.581296667
ENSOCUG00000023161RYR1	ryanodine r 5:2456216-	45.50247733	20.52133333
ENSOCUG00000002594SLC25A4	Oryctolagu 2:62603666	11.72456667	5.289
ENSOCUG00000022657GAPDH	Glyceralde 1:67461814	2381.022	1075.959333
ENSOCUG00000004422BTG2	BTG famil: 16:6847108	89.52196667	40.4901
ENSOCUG00000004988LOXL4	lysyl oxida 18:4635010	10.92119	4.942613333
ENSOCUG00000009858KLHL30	kelch-like 1 GL018969:	14.82710833	6.73078
ENSOCUG00000024395-	Uncharacte X:7070897	7.04227	3.200146667
ENSOCUG00000003372ART3	ADP-ribos: 15:7427884	54.64816667	24.93093333
ENSOCUG00000012081CACNB1	calcium ch: 19:4050257	29.92180333	13.68057
ENSOCUG00000009266CAND2	cullin-asso 9:11163772	8.492666667	3.88333
ENSOCUG00000009702FMOD	Fibromodu 16:6844037	34.73266667	16.04226667
ENSOCUG00000000303PPP1R3A	Oryctolagu 7:31525844	11.94047327	5.541333333
ENSOCUG00000001833CAP2	CAP, aden: GL018711:	20.12941	9.349483333
ENSOCUG00000026762-	AAGW020	5581.883333	2613.038333
ENSOCUG00000025533CHCHD10	coiled-coil- GL019236:	29.84431	13.99956667
ENSOCUG00000005294RRAGD	Ras-related 12:7619698	26.94454	12.67566667
ENSOCUG00000022352-	12:1017196	111.6327	52.5875
ENSOCUG00000000286PGM1	phosphoglu 13:1028192	75.71373333	35.92543333
ENSOCUG00000024465COL8A1	Oryctolagu 14:1209125	34.847	16.6083
ENSOCUG00000028162UBE2QL1	ubiquitin-c: GL018756:	20.711131333	9.923723333
ENSOCUG00000003928	6-Sep septin 6 [Sc X:6833851	9.352086667	4.484603333
ENSOCUG00000024335TMEM238	transmemb 6:11629592	10.48943333	5.0305
ENSOCUG00000022294MURC	muscle-rel 1:12553800	18.32934667	8.79238
ENSOCUG00000026468BDKRB1	Oryctolagu GL018779:	8.793416667	4.22182
ENSOCUG00000021265-	4:35443191	7.823883333	3.757103333
ENSOCUG00000016799CYB5R1	cytochrome 16:6881226	57.35706667	27.59983333
ENSOCUG00000006135-	Uncharacte 2:10451069	21.70842333	10.50664667
ENSOCUG00000016222TXLNB	taxilin beta 12:1296812	12.600005	6.098473333
ENSOCUG00000011876SLN	Oryctolagu 1:10882034	511.03784	248.171
ENSOCUG00000012700CORO6	coronin 6 [19:1857875	23.56486333	11.44444333
ENSOCUG00000014350ADAMTS1	ADAM me 5:31919262	11.84485667	5.77528
ENSOCUG00000016975CRYM	crystallin, r 6:12137414	33.9774	16.56660333
ENSOCUG00000003641LHX8	LIM homeo 13:9049907	8.910123333	4.35161
ENSOCUG00000026022DERL3	derlin 3 [Sc GL019236:	10.60679	5.188546667
ENSOCUG00000009444ALDH1A1	retinal dehy 1:59416688	101.3726	49.732
ENSOCUG00000002473OLFML2A	olfactomed GL018699:	44.46506667	21.81606667
ENSOCUG00000003788SGCG	Oryctolagu 8:41421536	15.62589333	7.672526667
ENSOCUG00000029113MT-ND6	NADH-ubi MT:11771-	1548.816333	765.0503333

ENSOCUG00000006728 MYOM3	myomesin 13:129235	17.14396367	8.479133333
ENSOCUG000000023599 APOD	apolipoprotein 14:912261	362.1856667	179.1716667
ENSOCUG000000024524 -	12:4644570	31.62469667	15.68258
ENSOCUG000000024316 -	AAGW020	9.97123	4.952223333
ENSOCUG000000021586 -	Oryctolagus GL018725	3012.174413	1499.522
ENSOCUG000000019019 -	12:9693270	1333.416667	2845.356667
ENSOCUG0000000281475_8S_rRNA	5.8S ribosome GL019111	2631.370333	6923.65
ENSOCUG00000000568 HBB1	Oryctolagus 1:14623649	989.0313333	2837.970667
ENSOCUG000000012040 KRTAP11	-keratin associated 14:160985	462.043	1333.298
ENSOCUG000000014311 -	Uncharacterized 4:36357980	64.30313333	218.6652333
ENSOCUG000000005594 -	Uncharacterized 14:1600431	310.514	1154.621667
ENSOCUG000000017116 -	Uncharacterized 14:1599724	171.5336667	645.004
ENSOCUG000000023455 -	GL018835	29.2465	121.755
ENSOCUG000000016589 KRTAP15	-keratin associated 14:160047	75.49793333	341.6386667
ENSOCUG000000005599 -	Uncharacterized 14:159993	70.15253333	351.2556667
ENSOCUG000000006582 PLA2G2A	phospholipase 13:132962	16.03706667	85.78023
ENSOCUG000000027358 -	GL019111	118756.1	646888.1
ENSOCUG000000027336 -	CEBPZ opj 2:14910318	135.991	754.4556667
ENSOCUG000000027177 -	GL019111	42856.13333	301560.6667
ENSOCUG000000010359 -	Uncharacterized 1:9867122	7.212	52.0896
ENSOCUG000000019413 SNORD22	Small nuclear RNA GL018717	60.762	461.4916667
ENSOCUG000000027160 -	GL019111	102394.8667	793224.6667
ENSOCUG000000026447 SNORA71	Small nuclear RNA 4:1945782	9.620366667	258.5243333
ENSOCUG000000020113 -	1:17139534	841.3	48723.8
ENSOCUG000000019830 SNORA12	Small nuclear RNA 18:4818140	1.00E-05	18.94603333
ENSOCUG000000014954 MRPL36	mitochondrial GL019196	1.00E-05	19.49926667
ENSOCUG000000019530 SNORA5	Small nuclear RNA 10:453025	1.00E-05	25.07086667
ENSOCUG000000019496 SNORA29	Small nuclear RNA 12:1496289	1.00E-05	29.07386667
ENSOCUG000000019045 SNORA33	Small nuclear RNA 12:1230749	1.00E-05	37.85066667
ENSOCUG000000018667 U8	U8 small nuclear RNA 19:110781	1.00E-05	38.106
ENSOCUG000000024092 SNORA16	Small nuclear RNA 13:136970	1.00E-05	41.99
ENSOCUG000000021204 SNORA71	Small nuclear RNA 4:1948855	1.00E-05	44.927
ENSOCUG000000019843 SNORA5	Small nuclear RNA 10:453025	1.00E-05	48.72933333
ENSOCUG000000019868 SNORA72	Small nuclear RNA 3:1138454	1.00E-05	51.62033333
ENSOCUG000000023699 SNORA28	Small nuclear RNA GL018751	1.00E-05	51.952
ENSOCUG000000028597 SNORA9	Small nuclear RNA 11:152336	1.00E-05	57.20033333
ENSOCUG000000018058 SNORA44	Small nuclear RNA 13:1369710	1.00E-05	57.22533333
ENSOCUG000000028334 SCARNA1	Small Cajal body RNA 13:3692038	1.00E-05	59.11133333
ENSOCUG000000025177 SNORA11	Small nuclear RNA 1:10427620	1.00E-05	71.539
ENSOCUG000000023202 SNORA51	Small nuclear RNA 15:1300489	1.00E-05	71.67233333
ENSOCUG000000019857 SNORA30	Small nuclear RNA 1:15122491	1.00E-05	74.05433333
ENSOCUG000000018158 SNORA9	Small nuclear RNA 10:451860	1.00E-05	86.67033333
ENSOCUG000000023501 U5	U5 spliceosomal RNA GL018739	1.00E-05	120.285
ENSOCUG000000020613 5S_rRNA	5S ribosomal RNA GL018802	1.00E-05	186.7333333
ENSOCUG000000028172 -	9:49804488	1.00E-05	213.9613333
ENSOCUG000000028922 5S_rRNA	5S ribosomal RNA GL018717	1.00E-05	251.4166667
ENSOCUG000000020092 -	12:2274802	1.00E-05	417.1233333

ENSOCUG00000020132 -	GL018715:	1.00E-05	422.56
ENSOCUG00000019006 U6	U6 spliceos X:1066721	1.00E-05	582.57
ENSOCUG00000021914 U6	U6 spliceos GL019106:	1.00E-05	582.57
ENSOCUG00000024616 -	3:21027824	1.00E-05	11959.73333
ENSOCUG00000024819 -	GL019301:	1.00E-05	19622.66667
ENSOCUG00000019646 SNORD30 Small nucleol	GL018717:	1.00E-05	31299.36667
ENSOCUG00000019971 -	15:1045711	1.00E-05	35535.33333
ENSOCUG00000029114 -	MT:14103-	1.00E-05	35831.33333
ENSOCUG00000026701 -	GL019111:	1.00E-05	37244.33333

Draft

s in the two groups

Fold_change-G	P-value	FDR	Expression patterns
1986853333		0	0 UP
720226666.7		0	0 UP
291075333.3		0	0 UP
180056333.3		0	0 UP
131060666.7		0	0 UP
93242666.67		0	0 UP
82180000		0	0 UP
46591333.33	4.58E-245	1.37E-242	UP
38398333.33	1.05E-201	2.55E-199	UP
29074566.67	1.47E-152	2.93E-150	UP
28499633.33	2.17E-149	4.18E-147	UP
23692700	4.84E-124	7.48E-122	UP
22084633.33	1.35E-115	1.93E-113	UP
19740933.33	1.85E-103	2.43E-101	UP
18856633.33	1.03E-98	1.29E-96	UP
15638300	7.68E-82	8.02E-80	UP
14185483.33	6.14E-74	5.94E-72	UP
13035000	3.80E-68	3.43E-66	UP
12799433.33	1.44E-66	1.26E-64	UP
12799433.33	1.44E-66	1.26E-64	UP
12799433.33	1.44E-66	1.26E-64	UP
9740366.667	8.63E-51	6.18E-49	UP
9087200	4.09E-47	2.81E-45	UP
8942126.667	1.37E-46	9.28E-45	UP
8663733.333	5.15E-45	3.39E-43	UP
7926300	2.42E-41	1.46E-39	UP
7619633.333	9.05E-40	5.35E-38	UP
7571133.333	3.02E-39	1.76E-37	UP
3402300	7.42E-18	2.17E-16	UP
3303390	2.44E-17	6.94E-16	UP
3245896.667	8.04E-17	2.22E-15	UP
3146656.667	2.64E-16	7.12E-15	UP
2672260	1.00E-13	2.26E-12	UP
2328780	3.47E-12	6.74E-11	UP
1826726.667	1.24E-09	1.84E-08	UP
1268623.333	1.32E-06	1.27E-05	UP
1163020	4.16E-06	3.64E-05	UP
1136310	4.16E-06	3.64E-05	UP
1074416.667	1.30E-05	0.0001025	UP
911590	4.06E-05	0.00028351	UP
872263.3333	0.000125517	0.00077951	UP
659066.6667	0.001162783	0.00529919	UP
634253.3333	0.001162783	0.00529919	UP
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407150	0.010164013	0.03134778	UP

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9.128862196	0.000125517	0.00077951 UP
6.751972033	0.000178519	0.0010539 UP
6.599035297	2.22E-53	1.64E-51 UP
6.546642656	0.003469471	0.01322092 UP
6.462451872	0.003469471	0.01322092 UP
6.423105071	1.22E-06	1.19E-05 UP
6.394276442	1.00E-58	7.91E-57 UP
5.633643178	4.36E-09	6.02E-08 UP
5.131321263	6.05E-130	1.01E-127 UP
4.718849826	1.72E-80	1.78E-78 UP
4.705968356	3.47E-10	5.57E-09 UP
4.563357789	1.75E-37	9.78E-36 UP
4.470896823	5.00E-149	9.52E-147 UP
4.447607261	9.50E-10	1.43E-08 UP
4.368677244	9.45E-52	6.85E-50 UP
4.367047058	1.02E-24	3.91E-23 UP
4.355015334	0.000567186	0.00287273 UP
4.322490945	6.27E-120	9.36E-118 UP
4.316115444	0.001418955	0.00624968 UP
4.242814723	0.010389537	0.03202624 UP
4.214506099	0.001418955	0.00624968 UP
4.160451462	4.68E-19	1.43E-17 UP
4.090816176	0.001494521	0.00654755 UP
4.078640865	0	0 UP
3.993039019	0.003887805	0.01443102 UP
3.832982601	5.10E-06	4.39E-05 UP
3.831023193	0.003887805	0.01443102 UP
3.830707008	8.13E-07	8.18E-06 UP
3.821099869	0	0 UP
3.81694046	0.003887805	0.01443102 UP
3.751141072	3.01E-21	1.01E-19 UP
3.750436144	3.15E-11	5.59E-10 UP
3.745518858	4.85E-31	2.29E-29 UP
3.744248174	0.001494521	0.00654755 UP
3.722820652	8.53E-85	9.18E-83 UP
3.714883748	5.23E-12	1.00E-10 UP
3.691518948	0.010389537	0.03202624 UP
3.677674657	1.15E-07	1.32E-06 UP
3.670356029	0.000211144	0.00121222 UP
3.555587189	2.02E-77	2.06E-75 UP
3.530735458	8.69E-35	4.65E-33 UP
3.504906172	8.16E-24	3.02E-22 UP
3.477963254	6.94E-152	1.37E-149 UP
3.475912701	5.04E-202	1.25E-199 UP
3.47061207	3.65E-24	1.37E-22 UP
3.43524734	0.000567186	0.00287273 UP

3.403380709	6.01E-37	3.31E-35 UP
3.389979956	4.03E-97	4.88E-95 UP
3.383698075	4.74E-19	1.44E-17 UP
3.337301032	8.00E-20	2.54E-18 UP
3.314309746	1.43E-46	9.63E-45 UP
3.308702849	5.95E-240	1.75E-237 UP
3.299290298	4.28E-13	9.17E-12 UP
3.292856412	1.12E-165	2.49E-163 UP
3.289824767	8.97E-05	0.00057335 UP
3.285569471	8.13E-07	8.18E-06 UP
3.234395634	1.76E-27	7.45E-26 UP
3.215300555	0	0 UP
3.214205921	2.43E-10	3.96E-09 UP
3.211005236	0.000579179	0.00292834 UP
3.210647791	0.003849448	0.0143009 UP
3.20038269	8.97E-05	0.00057335 UP
3.147981173	1.85E-32	9.16E-31 UP
3.143961836	3.07E-14	7.22E-13 UP
3.142471639	1.99E-15	5.12E-14 UP
3.133861801	8.58E-16	2.25E-14 UP
3.132164088	1.86E-42	1.17E-40 UP
3.121959884	1.66E-92	1.91E-90 UP
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3.117724701	3.65E-07	3.89E-06 UP
3.114212945	4.34E-11	7.58E-10 UP
3.111289156	8.63E-05	0.00055427 UP
3.094233639	1.10E-12	2.28E-11 UP
3.086182765	5.93E-08	7.11E-07 UP
3.069979608	1.43E-07	1.62E-06 UP
3.052273733	5.60E-115	7.95E-113 UP
3.042819116	3.50E-05	0.00024865 UP
3.037022632	9.50E-28	4.06E-26 UP
3.035802955	3.59E-58	2.81E-56 UP
2.979340408	9.69E-09	1.29E-07 UP
2.978200182	2.09E-35	1.13E-33 UP
2.969713513	0.010389537	0.03202624 UP
2.960398829	5.71E-06	4.84E-05 UP
2.944769343	0.003849448	0.0143009 UP
2.938638679	1.99E-33	1.03E-31 UP
2.922098442	2.93E-73	2.82E-71 UP
2.914664585	3.65E-07	3.89E-06 UP
2.908809536	0.010389537	0.03202624 UP
2.900962115	1.20E-12	2.47E-11 UP
2.897291778	0.000225533	0.00128589 UP
2.897012194	2.29E-137	4.09E-135 UP
2.895712221	3.99E-16	1.07E-14 UP
2.887927273	0.000226111	0.00128876 UP

2.886617077	3.57E-05	0.00025256 UP
2.872330252	0.00145729	0.006412 UP
2.852470824	5.31E-133	9.10E-131 UP
2.850642965	2.52E-08	3.19E-07 UP
2.843489842	0.010389537	0.03202624 UP
2.836776238	9.22E-07	9.16E-06 UP
2.817877245	2.46E-20	8.03E-19 UP
2.815650263	1.41E-05	0.00011054 UP
2.812160036	1.15E-10	1.93E-09 UP
2.809445452	5.35E-230	1.52E-227 UP
2.798214161	1.28E-12	2.62E-11 UP
2.783388556	1.51E-14	3.62E-13 UP
2.780048241	6.33E-15	1.57E-13 UP
2.778063908	3.57E-05	0.00025256 UP
2.777063544	1.07E-15	2.78E-14 UP
2.775505486	0.003849448	0.0143009 UP
2.774665267	3.98E-42	2.45E-40 UP
2.761910736	3.86E-24	1.44E-22 UP
2.759497018	0.003849448	0.0143009 UP
2.754071811	6.89E-25	2.67E-23 UP
2.747254945	0.010389537	0.03202624 UP
2.742966321	2.18E-146	4.11E-144 UP
2.739470287	1.01E-08	1.34E-07 UP
2.728823681	5.03E-47	3.44E-45 UP
2.724614747	0.001494521	0.00654755 UP
2.708816124	2.38E-23	8.62E-22 UP
2.705717806	8.88E-05	0.00057023 UP
2.705060985	0.00145729	0.006412 UP
2.705030969	3.23E-43	2.07E-41 UP
2.698022006	1.71E-24	6.50E-23 UP
2.697728233	2.31E-06	2.11E-05 UP
2.696749031	1.01E-08	1.34E-07 UP
2.694319157	1.41E-05	0.00011054 UP
2.693384802	2.46E-44	1.59E-42 UP
2.685984135	0	0 UP
2.68267005	3.57E-27	1.50E-25 UP
2.670654017	4.68E-274	1.45E-271 UP
2.662334244	3.30E-17	9.31E-16 UP
2.661883421	0.003581026	0.01360115 UP
2.64444067	1.43E-05	0.00011124 UP
2.641343192	5.70E-06	4.83E-05 UP
2.63968527	3.39E-12	6.58E-11 UP
2.630196279	2.12E-91	2.42E-89 UP
2.626462419	3.97E-19	1.22E-17 UP
2.609544759	9.32E-07	9.25E-06 UP
2.605441574	0.010389537	0.03202624 UP
2.596155794	0.000217275	0.00124495 UP

2.571390041	0.00145729	0.006412 UP
2.570247513	4.05E-14	9.42E-13 UP
2.557644937	1.39E-05	0.00010876 UP
2.547472941	5.93E-18	1.74E-16 UP
2.544950462	0.001357199	0.00602207 UP
2.544824164	2.58E-69	2.36E-67 UP
2.543882131	9.32E-07	9.25E-06 UP
2.541371034	2.50E-08	3.17E-07 UP
2.520754359	0	0 UP
2.517865729	0.001357199	0.00602207 UP
2.515886505	0	0 UP
2.512861624	0.00145729	0.006412 UP
2.509638268	4.87E-11	8.43E-10 UP
2.508671855	8.28E-17	2.28E-15 UP
2.508250484	5.04E-29	2.25E-27 UP
2.505813286	0.001357199	0.00602207 UP
2.478548911	0.000559758	0.00283926 UP
2.473480471	8.88E-05	0.00057023 UP
2.459902971	4.21E-09	5.83E-08 UP
2.455212001	3.69E-30	1.72E-28 UP
2.450866281	2.85E-10	4.63E-09 UP
2.440270619	3.35E-05	0.00023884 UP
2.430358055	5.27E-37	2.92E-35 UP
2.423665167	0.008559301	0.02748972 UP
2.423202658	8.50E-05	0.00054656 UP
2.41621716	1.21E-108	1.67E-106 UP
2.414385873	1.20E-83	1.28E-81 UP
2.39409681	3.43E-17	9.68E-16 UP
2.393757429	3.51E-05	0.00024917 UP
2.375278706	2.97E-69	2.70E-67 UP
2.37391969	3.35E-05	0.00023884 UP
2.364555991	5.07E-59	4.03E-57 UP
2.36363483	0.003581026	0.01360115 UP
2.360541592	0.009648455	0.03055726 UP
2.354014553	8.19E-17	2.26E-15 UP
2.353350391	7.92E-12	1.49E-10 UP
2.342428832	9.86E-35	5.24E-33 UP
2.339233958	5.75E-08	6.92E-07 UP
2.331302042	0.003581026	0.01360115 UP
2.330438785	1.67E-09	2.45E-08 UP
2.319804529	8.12E-12	1.52E-10 UP
2.303529607	3.55E-07	3.80E-06 UP
2.293449761	1.49E-07	1.68E-06 UP
2.284596119	8.50E-05	0.00054656 UP
2.28141303	5.26E-06	4.49E-05 UP
2.275643953	0.000217275	0.00124495 UP
2.266355586	1.09E-15	2.83E-14 UP

2.264208744	5.54E-06	4.70E-05 UP
2.253587861	6.29E-34	3.28E-32 UP
2.246953395	6.53E-121	9.84E-119 UP
2.242517463	8.39E-07	8.43E-06 UP
2.241508516	2.54E-19	7.89E-18 UP
2.23554138	6.55E-10	1.00E-08 UP
2.235120342	1.60E-25	6.32E-24 UP
2.233658187	0.001357199	0.00602207 UP
2.224834454	0.001357199	0.00602207 UP
2.21732558	4.40E-11	7.67E-10 UP
2.216783261	0.001227051	0.00553819 UP
2.212929362	0	0 UP
2.210959387	3.83E-20	1.24E-18 UP
2.209598296	0.001357199	0.00602207 UP
2.202881142	0.000202634	0.00117465 UP
2.200608514	0.008559301	0.02748972 UP
2.191982384	5.20E-13	1.11E-11 UP
2.187175193	1.35E-07	1.54E-06 UP
2.186954667	0.003581026	0.01360115 UP
2.165072267	3.29E-08	4.11E-07 UP
2.154801481	0.001227051	0.00553819 UP
2.152997046	1.24E-05	9.80E-05 UP
2.136165881	0	0 UP
2.131802412	1.35E-07	1.54E-06 UP
2.125690167	7.84E-07	7.90E-06 UP
2.122799144	3.40E-24	1.27E-22 UP
2.107524567	7.46E-17	2.07E-15 UP
2.098167784	3.29E-08	4.11E-07 UP
2.08705066	1.24E-05	9.80E-05 UP
2.085376559	0.003213511	0.01244257 UP
2.085167146	0.002819175	0.0110266 UP
2.084685451	3.12E-05	0.00022432 UP
2.082849735	0.007403752	0.02447249 UP
2.082424315	0.008559301	0.02748972 UP
2.078167139	5.27E-13	1.12E-11 UP
2.066160975	1.14E-05	9.12E-05 UP
2.066091678	0.001087138	0.00497934 UP
2.059216589	4.16E-102	5.41E-100 UP
2.059065928	7.89E-06	6.53E-05 UP
2.050957992	0.001227051	0.00553819 UP
2.050957539	6.47E-08	7.72E-07 UP
2.047546387	0.007403752	0.02447249 UP
2.044269943	0.002819175	0.0110266 UP
2.038377704	1.83E-21	6.17E-20 UP
2.038179812	2.88E-10	4.67E-09 UP
2.036603326	0.000184884	0.00108629 UP
2.024463314	3.84E-301	1.21E-298 UP

2.02190047	7.26E-05	0.00047533 UP
2.021444983	6.68E-72	6.32E-70 UP
2.016549361	1.67E-07	1.88E-06 UP
2.013485525	0.003213511	0.01244257 UP
2.008756399	0	0 UP
0.468629006	0.000831341	0.0039454 DOWN
0.380055366	1.80E-05	0.00013694 DOWN
0.348499491	4.76E-07	4.94E-06 DOWN
0.346541433	0.000432797	0.00226012 DOWN
0.294071135	0.013403258	0.03892696 DOWN
0.268931381	6.92E-13	1.45E-11 DOWN
0.26594202	4.74E-08	5.78E-07 DOWN
0.240207794	0.007488757	0.02471575 DOWN
0.220987671	1.26E-07	1.44E-06 DOWN
0.199719293	1.80E-09	2.61E-08 DOWN
0.186955277	0.003319497	0.01283573 DOWN
0.183580591	0	0 DOWN
0.180250485	3.85E-23	1.38E-21 DOWN
0.142114467	0	0 DOWN
0.138453741	0.004505496	0.01637305 DOWN
0.131664349	2.81E-22	9.77E-21 DOWN
0.129086841	0	0 DOWN
0.037212616	2.05E-27	8.63E-26 DOWN
0.017266716	0	0 DOWN
5.28E-07	0.013008502	0.03836567 DOWN
5.13E-07	0.013921514	0.04035772 DOWN
3.99E-07	0.001292689	0.00574466 DOWN
3.44E-07	0.000512035	0.00261789 DOWN
2.64E-07	2.87E-05	0.00020795 DOWN
2.62E-07	3.05E-05	0.00022019 DOWN
2.38E-07	1.19E-05	9.50E-05 DOWN
2.23E-07	2.66E-06	2.40E-05 DOWN
2.05E-07	1.03E-06	1.01E-05 DOWN
1.94E-07	3.97E-07	4.19E-06 DOWN
1.92E-07	3.97E-07	4.19E-06 DOWN
1.75E-07	5.95E-08	7.13E-07 DOWN
1.75E-07	5.95E-08	7.13E-07 DOWN
1.69E-07	2.06E-08	2.63E-07 DOWN
1.40E-07	4.27E-10	6.75E-09 DOWN
1.40E-07	4.27E-10	6.75E-09 DOWN
1.35E-07	1.63E-10	2.70E-09 DOWN
1.15E-07	2.00E-12	4.03E-11 DOWN
8.31E-08	2.45E-17	6.96E-16 DOWN
5.36E-08	3.35E-27	1.41E-25 DOWN
4.67E-08	2.72E-31	1.30E-29 DOWN
3.98E-08	7.54E-37	4.14E-35 DOWN
2.40E-08	7.18E-62	5.87E-60 DOWN

2.37E-08	8.96E-63	7.43E-61 DOWN
1.72E-08	5.60E-87	6.22E-85 DOWN
1.72E-08	5.60E-87	6.22E-85 DOWN
8.36E-10	0	0 DOWN
5.10E-10	0	0 DOWN
3.19E-10	0	0 DOWN
2.81E-10	0	0 DOWN
2.79E-10	0	0 DOWN
2.68E-10	0	0 DOWN

Draft

Supplementary Table S3. The significant GO terms of differentially expressed genes

GO_term	Type	Number	Diff_gene	cluster	fi	P-value	FDR
The significant GO terms of up-regulated genes							
titin binding	molecular_function	7	3.27%	4.10E-11	6.51E-09		
actin binding	molecular_function	17	7.94%	2.99E-10	3.17E-08		
structural constituent of muscle	molecular_function	7	3.27%	9.40E-10	8.94E-08		
FATZ binding	molecular_function	3	1.40%	1.55E-06	5.29E-05		
tropomyosin binding	molecular_function	4	1.87%	3.08E-06	0.000101		
motor activity	molecular_function	6	2.80%	3.48E-06	0.0001		
cytochrome-c oxidase activity	molecular_function	5	2.34%	4.77E-06	0.00013		
cytoskeletal protein binding	molecular_function	6	2.80%	6.13E-06	0.000162		
titin Z domain binding	molecular_function	2	0.93%	3.65E-05	0.001087		
G-protein coupled receptor activity	molecular_function	2	0.93%	3.68E-05	0.000761		
microfilament motor activity	molecular_function	3	1.40%	4.15E-05	0.000841		
actin filament binding	molecular_function	6	2.80%	5.18E-05	0.001028		
glyceraldehyde-3-phosphate dehydrogenase activity	molecular_function	2	0.93%	7.24E-05	0.001813		
telethonin binding	molecular_function	2	0.93%	7.24E-05	0.001813		
voltage-gated calcium channel activity	molecular_function	4	1.87%	7.32E-05	0.001182		
actin monomer binding	molecular_function	3	1.40%	7.40E-05	0.001174		
muscle alpha-actinin binding	molecular_function	2	0.93%	0.000125	0.002597		
troponin I binding	molecular_function	2	0.93%	0.000125	0.002597		
fructose binding	molecular_function	2	0.93%	0.000125	0.002597		
high voltage-gated calcium channel activity	molecular_function	2	0.93%	0.000296	0.005311		
cation binding	molecular_function	2	0.93%	0.000418	0.007244		
nucleic acid binding	molecular_function	2	0.93%	0.000508	0.00499		
poly(A) RNA binding	molecular_function	1	0.47%	0.000547	0.00531		
oxidoreductase activity	molecular_function	3	1.40%	0.000551	0.009042		
intramolecular transferase activity	molecular_function	2	0.93%	0.00057	0.005321		
creatine kinase activity	molecular_function	1	0.47%	0.0009	0.014048		
phosphofructokinase activity	molecular_function	1	0.47%	0.0009	0.014048		
interleukin-33 receptor activity	molecular_function	1	0.47%	0.0009	0.014048		
nickel cation binding	molecular_function	1	0.47%	0.0009	0.014048		
metalloenzyme activity	molecular_function	1	0.47%	0.0009	0.014048		
ligase regulator activity	molecular_function	1	0.47%	0.0009	0.014048		
cadmium ion binding	molecular_function	1	0.47%	0.0009	0.014048		
voltage-gated sodium channel activity	molecular_function	1	0.47%	0.0009	0.014048		
ATPase inhibitor activity	molecular_function	1	0.47%	0.0009	0.014048		
interleukin-33 binding	molecular_function	1	0.47%	0.0009	0.014048		
troponin T binding	molecular_function	1	0.47%	0.0009	0.014048		
translation factor activity	molecular_function	1	0.47%	0.0009	0.014048		
NADP binding	molecular_function	3	1.40%	0.000971	0.005108		
calcium channel regulator activity	molecular_function	2	0.93%	0.001223	0.017919		
protein tyrosine/serine kinase activity	molecular_function	4	1.87%	0.001385	0.007051		
connexin binding	molecular_function	1	0.47%	0.001786	0.024635		
adenylosuccinate dehydrogenase activity	molecular_function	1	0.47%	0.001786	0.024635		
bradykinin receptor activity	molecular_function	1	0.47%	0.001786	0.024635		
troponin C binding	molecular_function	1	0.47%	0.001786	0.024635		

GMP reductase ac	molecular_function	1	0.47%	0.001786	0.024635
calcium-dependen	molecular_function	1	0.47%	0.001786	0.024635
phosphoserine phc	molecular_function	1	0.47%	0.001786	0.024635
sodium channel re	molecular_function	2	0.93%	0.001848	0.025132
ATPase binding	molecular_function	3	1.40%	0.002419	0.009477
calcium-dependen	molecular_function	3	1.40%	0.002669	0.010331
protein-lysine 6-o	molecular_function	1	0.47%	0.002952	0.035123
glycogen phospho	molecular_function	1	0.47%	0.002952	0.035123
sodium ion bindin	molecular_function	1	0.47%	0.002952	0.035123
actinin binding	molecular_function	1	0.47%	0.002952	0.035123
6-phosphofructoki	molecular_function	1	0.47%	0.002952	0.035123
thyroid hormone r	molecular_function	1	0.47%	0.002952	0.035123
phosphoglycerate	molecular_function	1	0.47%	0.002952	0.035123
AMP deaminase a	molecular_function	1	0.47%	0.002952	0.035123
ryanodine-sensitiv	molecular_function	1	0.47%	0.002952	0.035123
calcium channel a	molecular_function	3	1.40%	0.003528	0.011911
actin-dependent A	molecular_function	1	0.47%	0.004391	0.04918
aldehyde dehydrog	molecular_function	1	0.47%	0.004391	0.04918
endopeptidase acti	molecular_function	1	0.47%	0.004391	0.04918
acetylcholine rece	molecular_function	1	0.47%	0.004391	0.04918
hydrolase activity,	molecular_function	1	0.47%	0.006097	0.063787
chitin binding	molecular_function	1	0.47%	0.006097	0.063787
phosphorylase acti	molecular_function	1	0.47%	0.006097	0.063787
LIM domain bindi	molecular_function	1	0.47%	0.006097	0.063787
fructose-bisphosph	molecular_function	1	0.47%	0.006097	0.063787
filamin binding	molecular_function	1	0.47%	0.006097	0.063787
thyroid hormone b	molecular_function	1	0.47%	0.006097	0.063787
voltage-gated sodi	molecular_function	1	0.47%	0.006097	0.063787
sodium channel in	molecular_function	1	0.47%	0.006097	0.063787
phosphopyruvate l	molecular_function	1	0.47%	0.006097	0.063787
tau protein binding	molecular_function	1	0.47%	0.006097	0.063787
interleukin-1 rece	molecular_function	1	0.47%	0.006097	0.063787
enzyme inhibitor a	molecular_function	2	0.93%	0.006207	0.016322
Wnt-protein bindin	molecular_function	2	0.93%	0.006989	0.018329
protein phosphata	molecular_function	1	0.47%	0.008063	0.081664
receptor agonist ac	molecular_function	1	0.47%	0.008063	0.081664
ion channel bindin	molecular_function	3	1.40%	0.010108	0.0248
cAMP-dependent	molecular_function	1	0.47%	0.010283	0.10092
phosphogluconate	molecular_function	1	0.47%	0.010283	0.10092
peptide binding	molecular_function	1	0.47%	0.010283	0.10092
oxidoreductase act	molecular_function	1	0.47%	0.010283	0.10092
hormone binding	molecular_function	1	0.47%	0.012749	0.029316
coreceptor activity	molecular_function	1	0.47%	0.012749	0.118989
protein kinase B b	molecular_function	1	0.47%	0.012749	0.118989
retinol dehydroger	molecular_function	1	0.47%	0.012749	0.118989
voltage-gated ion c	molecular_function	3	1.40%	0.014488	0.03178
ligand-dependent i	molecular_function	2	0.93%	0.015412	0.03373

RNA polymerase I molecular_function	2	0.93%	0.015412	0.13974
deaminase activity molecular_function	1	0.47%	0.015455	0.138806
adenylate kinase a molecular_function	1	0.47%	0.015455	0.138806
NAD(P)+-protein- molecular_function	1	0.47%	0.015455	0.138806
protein kinase A c molecular_function	1	0.47%	0.015455	0.138806
protein kinase inhi molecular_function	1	0.47%	0.015455	0.138806
enzyme regulator i molecular_function	1	0.47%	0.015455	0.138806
protein tyrosine pt molecular_function	4	1.87%	0.015504	0.031878
TBP-class protein molecular_function	1	0.47%	0.018396	0.03734
vinculin binding molecular_function	1	0.47%	0.018396	0.156363
phospholipase acti molecular_function	1	0.47%	0.018396	0.156363
alpha-actinin bindi molecular_function	1	0.47%	0.018396	0.156363
NAD binding molecular_function	2	0.93%	0.019627	0.165357
S100 protein bindi molecular_function	1	0.47%	0.021564	0.178512
calcium-transporti molecular_function	1	0.47%	0.021564	0.178512
copper ion binding molecular_function	2	0.93%	0.022773	0.042262
carboxy-lyase acti molecular_function	1	0.47%	0.02856	0.226575
carbonate dehydra molecular_function	1	0.47%	0.02856	0.226575
nucleobase-contain molecular_function	1	0.47%	0.02856	0.226575
phosphatidylserine molecular_function	1	0.47%	0.032376	0.252638
structural constitut molecular_function	1	0.47%	0.032376	0.252638
receptor signaling molecular_function	1	0.47%	0.036396	0.279429
phosphatase activi molecular_function	4	1.87%	0.036895	0.061837
p53 binding molecular_function	2	0.93%	0.040355	0.067401
calcium-dependen molecular_function	1	0.47%	0.040615	0.067716
cysteine-type endo molecular_function	1	0.47%	0.040615	0.302077
alpha-tubulin bind molecular_function	1	0.47%	0.040615	0.302077
protein kinase acti molecular_function	1	0.47%	0.040615	0.302077
RNA polymerase I molecular_function	1	0.47%	0.040615	0.302077
voltage-gated sodi molecular_function	1	0.47%	0.040615	0.302077
NADH dehydroge molecular_function	1	0.47%	0.045028	0.332297
cation channel acti molecular_function	1	0.47%	0.045028	0.332297
nucleoside diphosj molecular_function	1	0.47%	0.049628	0.357922
adenyl nucleotide molecular_function	1	0.47%	0.049628	0.357922
electron carrier acti molecular_function	2	0.93%	0.049998	0.078544
extracellular matri molecular_function	1	0.47%	0.054411	0.386558
lyase activity molecular_function	2	0.93%	0.057969	0.089444
R-SMAD binding molecular_function	1	0.47%	0.059371	0.412561
DNA binding molecular_function	7	3.27%	0.062303	0.094748
protein complex sc molecular_function	1	0.47%	0.069803	0.471292
syntaxin binding molecular_function	1	0.47%	0.075265	0.504592
protein kinase C b molecular_function	1	0.47%	0.075265	0.504592
pyridoxal phospho molecular_function	2	0.93%	0.075798	0.111702
protein C-terminu molecular_function	3	1.40%	0.080006	0.117177
glutathione transfe molecular_function	1	0.47%	0.080884	0.118283
cholesterol bindin molecular_function	1	0.47%	0.080884	0.523823
extracellular matri molecular_function	1	0.47%	0.092578	0.57604

insulin receptor bi molecular_function	1	0.47%	0.092578	0.57604
oxidoreductase act molecular_function	1	0.47%	0.092578	0.57604
protein serine/thre molecular_function	1	0.47%	0.098643	0.140161
drug binding molecular_function	1	0.47%	0.098643	0.605856
hydrolase activity, molecular_function	1	0.47%	0.098643	0.605856
protein binding, bi molecular_function	1	0.47%	0.104847	0.635758
RNA polymerase I molecular_function	1	0.47%	0.111186	0.154074
identical protein b molecular_function	8	3.74%	0.111793	0.154019
zinc ion binding molecular_function	18	8.41%	0.114372	0.157344
binding molecular_function	1	0.47%	0.117504	0.161187
protein disulfide o molecular_function	1	0.47%	0.137808	0.77629
protein binding molecular_function	117	54.67%	0.155511	0.204767
catalytic activity molecular_function	12	5.61%	0.166016	0.216503
RNA polymerase I molecular_function	1	0.47%	0.181104	0.232674
cation-transporting molecular_function	1	0.47%	0.181104	0.942138
kinase binding molecular_function	1	0.47%	0.181104	0.942138
chaperone binding molecular_function	1	0.47%	0.204051	0.259008
protein heterodimer molecular_function	1	0.47%	0.207652	0.262182
transcription coref molecular_function	2	0.93%	0.24656	0.304442
sequence-specific molecular_function	5	2.34%	0.261085	0.318249
ubiquitin-protein t molecular_function	4	1.87%	0.26256	0.31923
oxidoreductase act molecular_function	8	3.74%	0.271146	0.326748
kinase activity molecular_function	5	2.34%	0.283683	0.339279
metalloendopeptid molecular_function	2	0.93%	0.356356	0.415749
transporter activity molecular_function	3	1.40%	0.364799	0.423522
transcription coact molecular_function	2	0.93%	0.399707	0.45626
protein tyrosine ki molecular_function	3	1.40%	0.417458	0.472556
Rho guanyl-nucle molecular_function	1	0.47%	0.452963	0.505534
metallopeptidase a molecular_function	2	0.93%	0.463582	0.515572
phosphoprotein ph molecular_function	1	0.47%	0.471094	0.522705
protein complex bi molecular_function	1	0.47%	0.480174	0.530924
ATPase activity molecular_function	2	0.93%	0.489633	0.538257
ATP binding molecular_function	17	7.94%	0.492608	0.540903
protein dimerizatio molecular_function	2	0.93%	0.515907	0.563884
enzyme binding molecular_function	1	0.47%	0.523405	0.569464
protein kinase acti molecular_function	4	1.87%	0.524598	0.570111
lipid binding molecular_function	1	0.47%	0.53477	0.579842
GTPase activity molecular_function	1	0.47%	0.542465	0.586849
magnesium ion bi molecular_function	2	0.93%	0.562295	0.605549
receptor binding molecular_function	1	0.47%	0.587512	0.630566
sequence-specific molecular_function	5	2.34%	0.627571	0.666795
monooxygenase ac molecular_function	1	0.47%	0.634582	0.673492
transferase activity molecular_function	7	3.27%	0.658987	0.697838
cysteine-type pept molecular_function	1	0.47%	0.706196	0.741234
oxidoreductase act molecular_function	1	0.47%	0.723902	0.758981
protein serine/thre molecular_function	3	1.40%	0.754197	0.786413
protein kinase bin molecular_function	2	0.93%	0.757671	0.789171

GTP binding	molecular_function	4	1.87%	0.770198	0.800468
protein domain sp	molecular_function	1	0.47%	0.785106	0.814184
serine-type peptid	molecular_function	1	0.47%	0.894985	0.914191
transferase activity	molecular_function	6	2.80%	0.918583	0.933288
peptidase activity	molecular_function	3	1.40%	0.954944	0.965081
RNA polymerase I	molecular_function	1	0.47%	0.962655	0.970813
hydrolase activity	molecular_function	9	4.21%	0.987836	0.992004
transferase activity	molecular_function	1	0.47%	0.993224	0.995315
nucleotide binding	molecular_function	17	7.94%	0.999516	0.999516
Z disc	cellular_component	18	8.41%	5.77E-19	5.50E-16
I band	cellular_component	10	4.67%	7.41E-15	3.53E-12
myofibril	cellular_component	10	4.67%	2.94E-13	6.99E-11
M band	cellular_component	7	3.27%	4.10E-11	6.51E-09
sarcoplasmic retic	cellular_component	8	3.74%	2.80E-10	3.33E-08
T-tubule	cellular_component	7	3.27%	1.89E-09	1.63E-07
A band	cellular_component	5	2.34%	1.10E-08	8.08E-07
contractile fiber	cellular_component	5	2.34%	4.99E-08	3.39E-06
sarcoplasmic retic	cellular_component	5	2.34%	7.62E-08	3.63E-06
sarcomere	cellular_component	6	2.80%	8.03E-08	3.48E-06
actin cytoskeleton	cellular_component	12	5.61%	1.93E-07	7.98E-06
troponin complex	cellular_component	3	1.40%	3.08E-06	9.77E-05
myosin complex	cellular_component	6	2.80%	3.48E-06	0.000127
cytoskeleton	cellular_component	10	4.67%	5.93E-05	0.001129
striated muscle thi	cellular_component	2	0.93%	7.24E-05	0.001813
sarcoplasmic retic	cellular_component	2	0.93%	7.24E-05	0.001813
sarcolemma	cellular_component	5	2.34%	7.76E-05	0.00121
stress fiber	cellular_component	5	2.34%	8.68E-05	0.001332
dystroglycan com	cellular_component	2	0.93%	0.000199	0.002492
muscle tendon jun	cellular_component	2	0.93%	0.000199	0.003865
filamentous actin	cellular_component	3	1.40%	0.00028	0.003177
mitochondrial res	cellular_component	2	0.93%	0.000296	0.005311
junctional membr	cellular_component	2	0.93%	0.000296	0.005311
sarcoglycan compl	cellular_component	2	0.93%	0.000296	0.005311
voltage-gated calci	cellular_component	3	1.40%	0.000399	0.004088
myosin filament	cellular_component	1	0.47%	0.0009	0.014048
longitudinal sarco	cellular_component	1	0.47%	0.0009	0.014048
H zone	cellular_component	1	0.47%	0.0009	0.014048
lipid tube	cellular_component	1	0.47%	0.0009	0.014048
calcium ion-transp	cellular_component	1	0.47%	0.0009	0.014048
terminal cisterna	cellular_component	1	0.47%	0.0009	0.014048
transcription expo	cellular_component	1	0.47%	0.0009	0.014048
dystrophin-associa	cellular_component	2	0.93%	0.00097	0.014661
fascia adherens	cellular_component	2	0.93%	0.001223	0.0064
synaptic vesicle	cellular_component	4	1.87%	0.0015	0.007598
bleb	cellular_component	1	0.47%	0.001786	0.024635
DUBm complex	cellular_component	1	0.47%	0.001786	0.024635
muscle myosin coi	cellular_component	1	0.47%	0.001786	0.024635

female germ cell n	cellular_component	1	0.47%	0.001786	0.024635
GMP reductase co	cellular_component	1	0.47%	0.001786	0.024635
costamere	cellular_component	2	0.93%	0.001848	0.007392
plasma membrane	cellular_component	12	5.61%	0.001984	0.007839
extracellular matri	cellular_component	8	3.74%	0.002435	0.009502
6-phosphofructoki	cellular_component	1	0.47%	0.002952	0.035123
apical dendrite	cellular_component	1	0.47%	0.004391	0.04918
integral componen	cellular_component	21	9.81%	0.005833	0.017353
outer dense fiber	cellular_component	1	0.47%	0.006097	0.063787
SAGA complex	cellular_component	1	0.47%	0.006097	0.063787
actomyosin contra	cellular_component	1	0.47%	0.006097	0.063787
euchromatin	cellular_component	1	0.47%	0.006097	0.063787
phosphopyruvate l	cellular_component	1	0.47%	0.006097	0.063787
Cul5-RING ubiqui	cellular_component	1	0.47%	0.006097	0.063787
mitochondrial resp	cellular_component	1	0.47%	0.008063	0.081664
smooth endoplasm	cellular_component	1	0.47%	0.010283	0.10092
sodium channel co	cellular_component	1	0.47%	0.010283	0.10092
intercalated disc	cellular_component	2	0.93%	0.010705	0.024978
neuromuscular jun	cellular_component	2	0.93%	0.011786	0.112207
axon terminus	cellular_component	1	0.47%	0.012749	0.118989
sodium:potassium	cellular_component	1	0.47%	0.012749	0.118989
sperm flagellum	cellular_component	1	0.47%	0.015455	0.033669
node of Ranvier	cellular_component	1	0.47%	0.018396	0.156363
nuclear envelope l	cellular_component	1	0.47%	0.018396	0.156363
perikaryon	cellular_component	1	0.47%	0.021564	0.041556
podosome	cellular_component	1	0.47%	0.021564	0.178512
septin complex	cellular_component	1	0.47%	0.021564	0.178512
microtubule associ	cellular_component	1	0.47%	0.024954	0.203044
nuclear inner mem	cellular_component	1	0.47%	0.024954	0.203044
inclusion body	cellular_component	1	0.47%	0.024954	0.203044
endoplasmic retic	cellular_component	5	2.34%	0.027174	0.048627
voltage-gated sodi	cellular_component	1	0.47%	0.032376	0.252638
mitochondrial mer	cellular_component	2	0.93%	0.033865	0.262107
sperm principal pi	cellular_component	1	0.47%	0.040615	0.302077
integral componen	cellular_component	2	0.93%	0.045035	0.072299
collagen trimer	cellular_component	2	0.93%	0.047481	0.345053
cleavage furrow	cellular_component	1	0.47%	0.049628	0.357922
Cul3-RING ubiqui	cellular_component	1	0.47%	0.059371	0.091458
cytoplasmic ribon	cellular_component	1	0.47%	0.059371	0.412561
focal adhesion	cellular_component	7	3.27%	0.061139	0.093127
cytoplasmic vesicl	cellular_component	1	0.47%	0.075265	0.504592
cell cortex	cellular_component	2	0.93%	0.075798	0.504614
cortical cytoskelet	cellular_component	1	0.47%	0.086657	0.549983
respiratory chain	cellular_component	1	0.47%	0.092578	0.132932
mitochondrial inte	cellular_component	1	0.47%	0.092578	0.57604
large ribosomal su	cellular_component	1	0.47%	0.092578	0.57604
basement membra	cellular_component	2	0.93%	0.096087	0.136734

dendritic spine	cellular_component	1	0.47%	0.098643	0.605856
nuclear pore	cellular_component	1	0.47%	0.111186	0.665715
postsynaptic densi	cellular_component	1	0.47%	0.124252	0.708309
growth cone	cellular_component	1	0.47%	0.13097	0.176606
actin filament	cellular_component	1	0.47%	0.137808	0.77629
caveola	cellular_component	1	0.47%	0.151822	0.201582
ruffle membrane	cellular_component	1	0.47%	0.151822	0.845231
centrosome	cellular_component	1	0.47%	0.173832	0.224238
filopodium	cellular_component	1	0.47%	0.188665	0.240763
nucleus	cellular_component	39	18.22%	0.217314	0.273654
voltage-gated pota	cellular_component	1	0.47%	0.219767	0.276377
membrane raft	cellular_component	2	0.93%	0.225266	0.282919
mitochondrial inn	cellular_component	3	1.40%	0.369692	0.428159
integral componen	cellular_component	1	0.47%	0.372888	0.43029
proteinaceous extr	cellular_component	2	0.93%	0.406	0.462889
Golgi apparatus	cellular_component	4	1.87%	0.431652	0.487465
cell surface	cellular_component	2	0.93%	0.435062	0.488996
cell-cell junction	cellular_component	2	0.93%	0.470071	0.52218
nucleolus	cellular_component	4	1.87%	0.476413	0.527378
peroxisome	cellular_component	1	0.47%	0.489263	0.53972
midbody	cellular_component	1	0.47%	0.525665	0.570619
perinuclear region	cellular_component	4	1.87%	0.540566	0.585459
trans-Golgi netwo	cellular_component	1	0.47%	0.571168	0.613715
neuron projection	cellular_component	1	0.47%	0.607467	0.648328
receptor complex	cellular_component	1	0.47%	0.66157	0.699794
protein complex	cellular_component	3	1.40%	0.672684	0.709973
intracellular memt	cellular_component	3	1.40%	0.732158	0.766792
external side of pl	cellular_component	1	0.47%	0.766876	0.797887
nuclear membrane	cellular_component	1	0.47%	0.776441	0.806076
transcription facto	cellular_component	1	0.47%	0.806106	0.834145
nucleoplasm	cellular_component	1	0.47%	0.836483	0.861831
synapse	cellular_component	1	0.47%	0.896216	0.914467
cytosol	cellular_component	7	3.27%	0.897641	0.91494
apical plasma men	cellular_component	1	0.47%	0.911394	0.926974
cytoplasm	cellular_component	39	18.22%	0.929728	0.9426
lysosomal membr	cellular_component	1	0.47%	0.991257	0.994391
muscle contractio	biological_process	11	5.14%	3.34E-14	1.06E-11
cardiac muscle co	biological_process	9	4.21%	4.07E-11	7.76E-09
ventricular cardiac	biological_process	7	3.27%	1.89E-09	1.80E-07
skeletal muscle co	biological_process	5	2.34%	1.10E-08	9.55E-07
striated muscle co	biological_process	5	2.34%	1.91E-08	1.21E-06
signal transductio	biological_process	1	0.47%	3.73E-08	2.22E-06
cardiac muscle tis	biological_process	5	2.34%	4.99E-08	2.79E-06
sarcomere organiz	biological_process	6	2.80%	6.09E-08	3.05E-06
regulation of the f	biological_process	5	2.34%	7.62E-08	4.54E-06
skeletal muscle ce	biological_process	7	3.27%	3.01E-07	1.19E-05
cardiac myofibril	biological_process	4	1.87%	1.03E-06	3.76E-05

regulation of relea biological_process	4	1.87%	1.52E-06	5.38E-05
regulation of striat biological_process	3	1.40%	3.08E-06	0.000117
regulation of ATP biological_process	3	1.40%	3.08E-06	0.000117
G-protein coupled biological_process	2	0.93%	1.10E-05	0.000283
skeletal muscle fib biological_process	4	1.87%	1.24E-05	0.000312
plasma membrane biological_process	3	1.40%	1.41E-05	0.000344
regulation of calci biological_process	2	0.93%	3.65E-05	0.000869
negative regulatio biological_process	2	0.93%	3.65E-05	0.001087
negative regulatio biological_process	2	0.93%	3.65E-05	0.001087
sarcoplasmic retic biological_process	2	0.93%	3.65E-05	0.001087
detection of muscl biological_process	2	0.93%	3.65E-05	0.001087
regulation of myot biological_process	2	0.93%	7.24E-05	0.001351
cellular response t biological_process	2	0.93%	7.24E-05	0.001813
regulation of relax biological_process	2	0.93%	7.24E-05	0.001813
muscle filament sl biological_process	2	0.93%	7.24E-05	0.001813
muscle cell cellula biological_process	3	1.40%	9.58E-05	0.001448
muscle organ deve biological_process	4	1.87%	0.0001	0.001491
adult heart develo biological_process	3	1.40%	0.000122	0.001786
regulation of calci biological_process	3	1.40%	0.000122	0.00258
cardiac muscle fib biological_process	2	0.93%	0.000125	0.001783
skeletal muscle thi biological_process	2	0.93%	0.000125	0.002597
release of sequeste biological_process	2	0.93%	0.000125	0.002597
negative regulatio biological_process	2	0.93%	0.000125	0.002597
hydrogen ion trans biological_process	5	2.34%	0.000133	0.001707
calcium ion transp biological_process	6	2.80%	0.000145	0.001835
negative regulatio biological_process	2	0.93%	0.000199	0.003865
myofibril assembl biological_process	2	0.93%	0.000199	0.003865
response to activit biological_process	2	0.93%	0.000199	0.003865
regulation of cardi biological_process	2	0.93%	0.000199	0.003865
cardiac muscle hy biological_process	2	0.93%	0.000199	0.003865
collagen fibril org biological_process	4	1.87%	0.000229	0.002623
glycolytic process biological_process	4	1.87%	0.000292	0.003266
negative regulatio biological_process	2	0.93%	0.000296	0.003273
regulation of calci biological_process	2	0.93%	0.000296	0.005311
negative regulatio biological_process	2	0.93%	0.000296	0.005311
response to muscl biological_process	2	0.93%	0.000418	0.004238
negative regulatio biological_process	2	0.93%	0.000418	0.007244
glycogen metaboli biological_process	3	1.40%	0.000551	0.005298
regulation of heart biological_process	3	1.40%	0.000551	0.009042
regulation of musc biological_process	2	0.93%	0.000753	0.006895
nucleotide metabo biological_process	2	0.93%	0.000753	0.011951
negative regulatio biological_process	1	0.47%	0.0009	0.008009
positive regulation biological_process	1	0.47%	0.0009	0.014048
muscle tissue deve biological_process	1	0.47%	0.0009	0.014048
heart growth biological_process	1	0.47%	0.0009	0.014048
IMP salvage biological_process	1	0.47%	0.0009	0.014048
muscle structure d biological_process	1	0.47%	0.0009	0.014048

negative regulation of biological_process	1	0.47%	0.0009	0.014048
muscle system process biological_process	1	0.47%	0.0009	0.014048
negative regulation of biological_process	1	0.47%	0.0009	0.014048
autolysis biological_process	1	0.47%	0.0009	0.014048
regulation of the cell cycle biological_process	1	0.47%	0.0009	0.014048
negative regulation of biological_process	1	0.47%	0.0009	0.014048
negative regulation of biological_process	1	0.47%	0.0009	0.014048
positive regulation of biological_process	1	0.47%	0.0009	0.014048
naphthalene metabolism biological_process	1	0.47%	0.0009	0.014048
skeletal muscle fiber development biological_process	1	0.47%	0.0009	0.014048
corticospinal neuron development biological_process	1	0.47%	0.0009	0.014048
positive regulation of biological_process	1	0.47%	0.0009	0.014048
forward locomotion biological_process	1	0.47%	0.0009	0.014048
response to muscle contraction biological_process	1	0.47%	0.0009	0.014048
regulation of tissue morphogenesis biological_process	1	0.47%	0.0009	0.014048
skeletal muscle adaptation biological_process	1	0.47%	0.0009	0.014048
skeletal muscle myogenesis biological_process	1	0.47%	0.0009	0.014048
positive regulation of biological_process	1	0.47%	0.0009	0.014048
sarcomerogenesis biological_process	1	0.47%	0.0009	0.014048
tendon sheath development biological_process	1	0.47%	0.0009	0.014048
regulation of signal transduction biological_process	1	0.47%	0.0009	0.014048
regulation of skeletal muscle development biological_process	1	0.47%	0.0009	0.014048
regulation of protein synthesis biological_process	1	0.47%	0.0009	0.014048
muscle cell fate specification biological_process	1	0.47%	0.0009	0.014048
regulation of nerve conduction biological_process	1	0.47%	0.0009	0.014048
regulation of myofibrillogenesis biological_process	1	0.47%	0.0009	0.014048
negative regulation of biological_process	1	0.47%	0.0009	0.014048
adrenergic receptor activity biological_process	1	0.47%	0.0009	0.014048
positive regulation of biological_process	1	0.47%	0.0009	0.014048
negative regulation of biological_process	1	0.47%	0.0009	0.014048
cadmium ion homeostasis biological_process	1	0.47%	0.0009	0.014048
tendon formation biological_process	1	0.47%	0.0009	0.014048
regulation of muscle contraction biological_process	1	0.47%	0.0009	0.014048
evasion or tolerance of stress biological_process	1	0.47%	0.0009	0.014048
membrane depolarization biological_process	1	0.47%	0.0009	0.014048
positive regulation of biological_process	1	0.47%	0.0009	0.014048
negative regulation of biological_process	1	0.47%	0.0009	0.014048
phosphocreatine binding biological_process	1	0.47%	0.0009	0.014048
negative regulation of biological_process	1	0.47%	0.0009	0.014048
regulation of cell cycle arrest biological_process	1	0.47%	0.0009	0.014048
regulation of muscle contraction biological_process	1	0.47%	0.0009	0.014048
regulation of respiration biological_process	1	0.47%	0.0009	0.014048
positive regulation of biological_process	1	0.47%	0.0009	0.014048
interleukin-33-mediated signaling biological_process	1	0.47%	0.0009	0.014048
regulation of sodium ion transport biological_process	2	0.93%	0.00097	0.005189
muscle cell differentiation biological_process	2	0.93%	0.00097	0.014661
glycogen biosynthesis biological_process	2	0.93%	0.001223	0.017919

negative regulation of biological_process	2	0.93%	0.001223	0.017919
myotube differentiation biological_process	2	0.93%	0.001223	0.017919
regulation of ventricular biological_process	2	0.93%	0.001515	0.007633
regulation of G2/M biological_process	2	0.93%	0.001515	0.021215
myoblast fusion biological_process	2	0.93%	0.001515	0.021215
heart contraction biological_process	2	0.93%	0.001515	0.021215
regulation of calcium biological_process	1	0.47%	0.001786	0.008807
negative regulation of biological_process	1	0.47%	0.001786	0.024635
negative regulation of biological_process	1	0.47%	0.001786	0.024635
regulation of membrane biological_process	1	0.47%	0.001786	0.024635
self proteolysis biological_process	1	0.47%	0.001786	0.024635
regulation of skeletal biological_process	1	0.47%	0.001786	0.024635
negative regulation of biological_process	1	0.47%	0.001786	0.024635
G1 to G0 transition biological_process	1	0.47%	0.001786	0.024635
negative regulation of biological_process	1	0.47%	0.001786	0.024635
relaxation of skeletal biological_process	1	0.47%	0.001786	0.024635
negative regulation of biological_process	1	0.47%	0.001786	0.024635
somatic muscle development biological_process	1	0.47%	0.001786	0.024635
tendon development biological_process	1	0.47%	0.001786	0.024635
zinc ion homeostasis biological_process	1	0.47%	0.001786	0.024635
regulation of skeletal biological_process	1	0.47%	0.001786	0.024635
thyroid hormone transport biological_process	1	0.47%	0.001786	0.024635
maintenance of microtubule biological_process	1	0.47%	0.001786	0.024635
positive regulation of biological_process	1	0.47%	0.001786	0.024635
lipid tube assembly biological_process	1	0.47%	0.001786	0.024635
negative regulation of biological_process	1	0.47%	0.001786	0.024635
negative regulation of biological_process	1	0.47%	0.001786	0.024635
cellular response to biological_process	1	0.47%	0.001786	0.024635
endothelial cell-cell biological_process	1	0.47%	0.001786	0.024635
spongiotrophoblasts biological_process	1	0.47%	0.001786	0.024635
positive regulation of biological_process	1	0.47%	0.001786	0.024635
striated muscle cell biological_process	1	0.47%	0.001786	0.024635
'de novo' AMP biosynthesis biological_process	1	0.47%	0.001786	0.024635
negative regulation of biological_process	1	0.47%	0.001786	0.024635
sequestering of calcium biological_process	1	0.47%	0.001786	0.024635
tendon cell differentiation biological_process	1	0.47%	0.001786	0.024635
regulation of cell cycle biological_process	1	0.47%	0.001786	0.024635
extraocular skeletal muscle biological_process	1	0.47%	0.001786	0.024635
cellular metal ion homeostasis biological_process	1	0.47%	0.001786	0.024635
cellular calcium ion homeostasis biological_process	4	1.87%	0.00189	0.007496
glucose metabolic process biological_process	3	1.40%	0.002186	0.008598
neuromuscular system biological_process	2	0.93%	0.002644	0.010273
positive regulation of biological_process	7	3.27%	0.002843	0.010957
skeletal muscle tissue biological_process	3	1.40%	0.002937	0.011275
skeletal muscle satellite cell biological_process	1	0.47%	0.002952	0.011284
purine nucleotide metabolism biological_process	1	0.47%	0.002952	0.035123
regulation of skeletal muscle biological_process	1	0.47%	0.002952	0.035123

negative regulation of biological process	1	0.47%	0.002952	0.035123
regulation of p38N biological process	1	0.47%	0.002952	0.035123
positive regulation of biological process	1	0.47%	0.002952	0.035123
cellular lipid catabolism biological process	1	0.47%	0.002952	0.035123
development of prebiotic biological process	1	0.47%	0.002952	0.035123
actin-mediated cellular biological process	1	0.47%	0.002952	0.035123
negative regulation of biological process	1	0.47%	0.002952	0.035123
cellular response to biological process	1	0.47%	0.002952	0.035123
sclerotome development biological process	1	0.47%	0.002952	0.035123
negative regulation of biological process	1	0.47%	0.002952	0.035123
intracellular protein biological process	1	0.47%	0.002952	0.035123
cellular response to biological process	1	0.47%	0.002952	0.035123
negative regulation of biological process	1	0.47%	0.002952	0.035123
ether lipid metabolism biological process	1	0.47%	0.002952	0.035123
negative regulation of biological process	1	0.47%	0.002952	0.035123
microspike assembly biological process	1	0.47%	0.002952	0.035123
IMP biosynthetic pathway biological process	1	0.47%	0.002952	0.035123
negative regulation of biological process	1	0.47%	0.002952	0.035123
actin filament severing biological process	1	0.47%	0.002952	0.035123
negative regulation of biological process	2	0.93%	0.003111	0.010539
protein import into biological process	2	0.93%	0.003626	0.012198
chondrocyte development biological process	2	0.93%	0.004192	0.014052
ATP biosynthetic pathway biological process	2	0.93%	0.004192	0.047509
regulation of cytoskeleton biological process	1	0.47%	0.004391	0.014616
regulation of glucose biological process	1	0.47%	0.004391	0.04918
purine ribonucleoside biological process	1	0.47%	0.004391	0.04918
fructose 1,6-bisphosphate biological process	1	0.47%	0.004391	0.04918
histone modification biological process	1	0.47%	0.004391	0.04918
positive regulation of biological process	1	0.47%	0.004391	0.04918
regulation of stem cell biological process	1	0.47%	0.004391	0.04918
leptin-mediated signaling biological process	1	0.47%	0.004391	0.04918
negative regulation of biological process	1	0.47%	0.004391	0.04918
thyroid hormone response biological process	1	0.47%	0.004391	0.04918
fructose 6-phosphate biological process	1	0.47%	0.004391	0.04918
Wnt signaling pathway biological process	1	0.47%	0.004391	0.04918
negative regulation of biological process	1	0.47%	0.004391	0.04918
negative regulation of biological process	1	0.47%	0.004391	0.04918
AMP biosynthetic pathway biological process	1	0.47%	0.004391	0.04918
glycogen catabolic pathway biological process	1	0.47%	0.004391	0.04918
regulation of established biological process	1	0.47%	0.004391	0.04918
caveola assembly biological process	1	0.47%	0.004391	0.04918
nucleus localization biological process	1	0.47%	0.004391	0.04918
convergent extension biological process	1	0.47%	0.004391	0.04918
negative regulation of biological process	1	0.47%	0.004391	0.04918
positive regulation of biological process	1	0.47%	0.004391	0.04918
mRNA modification biological process	1	0.47%	0.004391	0.04918
heart morphogenesis biological process	3	1.40%	0.004561	0.01383

negative regulation of biological_process	3	1.40%	0.004561	0.050494
cardiac muscle tissue biological_process	2	0.93%	0.00481	0.01449
endoplasmic reticulum biological_process	2	0.93%	0.00481	0.052629
somitogenesis biological_process	3	1.40%	0.004948	0.014812
calcium ion transport biological_process	4	1.87%	0.005648	0.016857
muscle tissue morphogenesis biological_process	1	0.47%	0.006097	0.018083
negative regulation of biological_process	1	0.47%	0.006097	0.063787
membrane raft organization biological_process	1	0.47%	0.006097	0.063787
positive regulation of biological_process	1	0.47%	0.006097	0.063787
regulation of ventricular contraction biological_process	1	0.47%	0.006097	0.063787
positive regulation of biological_process	1	0.47%	0.006097	0.063787
negative regulation of biological_process	1	0.47%	0.006097	0.063787
cornea development biological_process	1	0.47%	0.006097	0.063787
positive regulation of biological_process	1	0.47%	0.006097	0.063787
cellular response to biological_process	1	0.47%	0.006097	0.063787
positive regulation of biological_process	1	0.47%	0.006097	0.063787
muscle cell development biological_process	1	0.47%	0.006097	0.063787
myoblast migration biological_process	1	0.47%	0.006097	0.063787
negative regulation of biological_process	1	0.47%	0.006097	0.063787
convergent extension biological_process	1	0.47%	0.006097	0.063787
positive regulation of biological_process	1	0.47%	0.006097	0.063787
membrane depolarization biological_process	1	0.47%	0.006097	0.063787
positive regulation of biological_process	1	0.47%	0.006097	0.063787
positive regulation of biological_process	1	0.47%	0.006097	0.063787
regulation ofryanodine receptor activity biological_process	1	0.47%	0.006097	0.063787
midbrain-hindbrain development biological_process	1	0.47%	0.006097	0.063787
positive regulation of biological_process	1	0.47%	0.006097	0.063787
enucleate erythrocyte biological_process	1	0.47%	0.008063	0.021089
negative regulation of biological_process	1	0.47%	0.008063	0.081664
negative regulation of biological_process	1	0.47%	0.008063	0.081664
proteoglycan metabolism biological_process	1	0.47%	0.008063	0.081664
otic vesicle formation biological_process	1	0.47%	0.008063	0.081664
negative regulation of biological_process	1	0.47%	0.008063	0.081664
ossification involving bone morphogenesis biological_process	1	0.47%	0.008063	0.081664
neural crest cell differentiation biological_process	1	0.47%	0.008063	0.081664
negative regulation of biological_process	1	0.47%	0.008063	0.081664
energy reserve metabolism biological_process	1	0.47%	0.008063	0.081664
basement membrane organization biological_process	1	0.47%	0.008063	0.081664
oxidative phosphorylation biological_process	1	0.47%	0.008063	0.081664
regulation of branching morphogenesis biological_process	1	0.47%	0.008063	0.081664
negative regulation of biological_process	1	0.47%	0.008063	0.081664
fructose metabolic process biological_process	1	0.47%	0.008063	0.081664
cholesterol catabolic process biological_process	1	0.47%	0.008063	0.081664
negative regulation of biological_process	1	0.47%	0.008063	0.081664
forebrain neuron development biological_process	1	0.47%	0.008063	0.081664
synaptic transmission biological_process	1	0.47%	0.008063	0.081664
regulation of cardiac contraction biological_process	1	0.47%	0.008063	0.081664

negative regulation of biological_process	4	1.87%	0.009944	0.024462
regulation of atrial biological_process	1	0.47%	0.010283	0.025165
cellular response to biological_process	1	0.47%	0.010283	0.10092
forebrain neuron development biological_process	1	0.47%	0.010283	0.10092
SNARE complex assembly biological_process	1	0.47%	0.010283	0.10092
locomotion biological_process	1	0.47%	0.010283	0.10092
cardiac conduction biological_process	1	0.47%	0.010283	0.10092
response to unfolded biological_process	1	0.47%	0.010283	0.10092
neuronal action potential biological_process	1	0.47%	0.010283	0.10092
negative regulation of biological_process	1	0.47%	0.010283	0.10092
positive regulation of biological_process	1	0.47%	0.010283	0.10092
negative regulation of biological_process	1	0.47%	0.010283	0.10092
negative regulation of biological_process	1	0.47%	0.010283	0.10092
sperm axoneme assembly biological_process	1	0.47%	0.010283	0.10092
cellular response to biological_process	2	0.93%	0.010705	0.10399
regulation of membrane biological_process	3	1.40%	0.011452	0.026592
endothelial cell differentiation biological_process	2	0.93%	0.011786	0.027301
protein dephosphorylation biological_process	5	2.34%	0.012166	0.028043
removal of superoxide biological_process	1	0.47%	0.012749	0.118989
cardiac muscle cell biological_process	1	0.47%	0.012749	0.118989
negative regulation of biological_process	1	0.47%	0.012749	0.118989
protein targeting to biological_process	1	0.47%	0.012749	0.118989
positive regulation of biological_process	1	0.47%	0.012749	0.118989
regulation of protein biological_process	1	0.47%	0.012749	0.118989
somite development biological_process	1	0.47%	0.012749	0.118989
cardiac muscle cell biological_process	1	0.47%	0.012749	0.118989
cardiac left ventricle biological_process	1	0.47%	0.012749	0.118989
positive regulation of biological_process	1	0.47%	0.012749	0.118989
protein localization biological_process	1	0.47%	0.012749	0.118989
positive regulation of biological_process	1	0.47%	0.012749	0.118989
positive regulation of biological_process	1	0.47%	0.012749	0.118989
peptidyl-tyrosine cleavage biological_process	4	1.87%	0.014252	0.031334
branching involved in biological_process	1	0.47%	0.015455	0.138806
nucleoside triphosphate biological_process	1	0.47%	0.015455	0.138806
positive regulation of biological_process	1	0.47%	0.015455	0.138806
positive regulation of biological_process	1	0.47%	0.015455	0.138806
zinc ion transport biological_process	1	0.47%	0.015455	0.138806
response to reactive biological_process	1	0.47%	0.015455	0.138806
protein N-linked glycosylation biological_process	1	0.47%	0.015455	0.138806
monovalent inorganic biological_process	1	0.47%	0.015455	0.138806
positive regulation of biological_process	1	0.47%	0.015455	0.138806
cellular zinc ion homeostasis biological_process	1	0.47%	0.015455	0.138806
positive regulation of biological_process	1	0.47%	0.015455	0.138806
positive regulation of biological_process	1	0.47%	0.015455	0.138806
positive regulation of biological_process	1	0.47%	0.015455	0.138806
positive regulation of biological_process	1	0.47%	0.015455	0.138806
muscle organ morphogenesis biological_process	1	0.47%	0.015455	0.138806

astrocyte developr biological_process	1	0.47%	0.015455	0.138806
histone deubiquitin biological_process	1	0.47%	0.015455	0.138806
regulation of mem biological_process	1	0.47%	0.015455	0.138806
nucleotide phosph biological_process	1	0.47%	0.015455	0.138806
protein ubiquitinat biological_process	6	2.80%	0.016357	0.03356
cellular response t biological_process	2	0.93%	0.016751	0.034295
regulation of ion t biological_process	3	1.40%	0.018011	0.036795
protein homotetra biological_process	2	0.93%	0.018156	0.037012
protein polymeriz biological_process	2	0.93%	0.018156	0.155715
mRNA transport biological_process	1	0.47%	0.018396	0.156363
dentate gyrus deve biological_process	1	0.47%	0.018396	0.156363
transcription elong biological_process	1	0.47%	0.018396	0.156363
regulation of G1/S biological_process	1	0.47%	0.018396	0.156363
response to mecha biological_process	1	0.47%	0.018396	0.156363
activation of prote biological_process	1	0.47%	0.018396	0.156363
carboxylic acid m biological_process	1	0.47%	0.018396	0.156363
positive regulation biological_process	1	0.47%	0.018396	0.156363
placenta blood ves biological_process	1	0.47%	0.018396	0.156363
epithelial cell prol biological_process	1	0.47%	0.018396	0.156363
cardiac muscle hy biological_process	1	0.47%	0.018396	0.156363
negative regulatio biological_process	1	0.47%	0.018396	0.156363
positive regulation biological_process	1	0.47%	0.018396	0.156363
plasma membrane biological_process	1	0.47%	0.018396	0.156363
positive regulation biological_process	2	0.93%	0.019627	0.038211
response to stress biological_process	2	0.93%	0.019627	0.165357
response to endopl biological_process	2	0.93%	0.019627	0.165357
response to hypox biological_process	3	1.40%	0.02099	0.040533
calcium ion impor biological_process	1	0.47%	0.021564	0.178512
positive regulation biological_process	1	0.47%	0.021564	0.178512
cellular response t biological_process	1	0.47%	0.021564	0.178512
myoblast different biological_process	1	0.47%	0.021564	0.178512
regulation of I-kap biological_process	1	0.47%	0.021564	0.178512
pentose-phosphate biological_process	1	0.47%	0.021564	0.178512
negative regulatio biological_process	1	0.47%	0.021564	0.178512
negative regulatio biological_process	1	0.47%	0.021564	0.178512
negative regulatio biological_process	1	0.47%	0.021564	0.178512
endothelial cell m biological_process	1	0.47%	0.021564	0.178512
DNA demethylatic biological_process	1	0.47%	0.021564	0.178512
lipid particle organ biological_process	1	0.47%	0.021564	0.178512
purine nucleotide biological_process	1	0.47%	0.021564	0.178512
planar cell polarity biological_process	1	0.47%	0.021564	0.178512
hematopoietic ster biological_process	1	0.47%	0.024954	0.046218
JAK-STAT cascac biological_process	1	0.47%	0.024954	0.203044
negative regulatio biological_process	1	0.47%	0.024954	0.203044
negative regulatio biological_process	1	0.47%	0.024954	0.203044
regulation of endo biological_process	1	0.47%	0.024954	0.203044
muscle fiber devel biological_process	1	0.47%	0.024954	0.203044

regulation of neur biological_process	1	0.47%	0.024954	0.203044
ERK1 and ERK2 c biological_process	1	0.47%	0.024954	0.203044
trophoblast giant c biological_process	1	0.47%	0.024954	0.203044
collagen catabolic biological_process	1	0.47%	0.024954	0.203044
membrane depolar biological_process	1	0.47%	0.024954	0.203044
regulation of Wnt biological_process	1	0.47%	0.024954	0.203044
actin filament orga biological_process	2	0.93%	0.026193	0.047137
substantia nigra de biological_process	2	0.93%	0.026193	0.211318
outflow tract morp biological_process	2	0.93%	0.026193	0.211318
intrinsic apoptotic biological_process	1	0.47%	0.02856	0.051011
establishment of p biological_process	1	0.47%	0.02856	0.226575
peroxisome organi biological_process	1	0.47%	0.02856	0.226575
cellular response t biological_process	1	0.47%	0.02856	0.226575
regulation of cardi biological_process	1	0.47%	0.02856	0.226575
positive regulation biological_process	1	0.47%	0.02856	0.226575
regulation of trans biological_process	1	0.47%	0.02856	0.226575
positive regulation biological_process	1	0.47%	0.02856	0.226575
focal adhesion ass biological_process	1	0.47%	0.02856	0.226575
behavioral respons biological_process	1	0.47%	0.02856	0.226575
positive regulation biological_process	1	0.47%	0.02856	0.226575
heart trabecula for biological_process	1	0.47%	0.02856	0.226575
negative regulatio biological_process	2	0.93%	0.031842	0.055317
digestive tract mor biological_process	1	0.47%	0.032376	0.056142
cytoplasmic micro biological_process	1	0.47%	0.032376	0.252638
negative regulatio biological_process	1	0.47%	0.032376	0.252638
central nervous sy biological_process	1	0.47%	0.032376	0.252638
protein monoubiq biological_process	1	0.47%	0.032376	0.252638
negative regulatio biological_process	1	0.47%	0.032376	0.252638
ventricular system biological_process	1	0.47%	0.032376	0.252638
negative regulatio biological_process	2	0.93%	0.033865	0.057673
negative regulatio biological_process	1	0.47%	0.036396	0.061763
detection of mech biological_process	1	0.47%	0.036396	0.279429
positive regulation biological_process	1	0.47%	0.036396	0.279429
positive regulation biological_process	1	0.47%	0.036396	0.279429
female gonad deve biological_process	1	0.47%	0.036396	0.279429
regulation of heart biological_process	1	0.47%	0.036396	0.279429
negative regulatio biological_process	2	0.93%	0.038121	0.063781
hindbrain develop biological_process	1	0.47%	0.040615	0.302077
camera-type eye n biological_process	1	0.47%	0.040615	0.302077
positive regulation biological_process	1	0.47%	0.040615	0.302077
negative regulatio biological_process	1	0.47%	0.040615	0.302077
negative regulatio biological_process	1	0.47%	0.040615	0.302077
ATP metabolic pr biological_process	1	0.47%	0.040615	0.302077
positive regulation biological_process	1	0.47%	0.040615	0.302077
positive regulation biological_process	1	0.47%	0.045028	0.073276
glucose transport biological_process	1	0.47%	0.045028	0.332297
protein localizatio biological_process	1	0.47%	0.045028	0.332297

nucleoside diphosph	biological_process	1	0.47%	0.045028	0.332297
iron ion homeosta	biological_process	1	0.47%	0.045028	0.332297
negative regulatio	biological_process	1	0.47%	0.045028	0.332297
negative regulatio	biological_process	2	0.93%	0.047481	0.076098
ventricular septum	biological_process	1	0.47%	0.049628	0.079271
cell-cell junction c	biological_process	1	0.47%	0.049628	0.357922
positive regulation	biological_process	1	0.47%	0.049628	0.357922
intrinsic apoptotic	biological_process	1	0.47%	0.049628	0.357922
eye development	biological_process	1	0.47%	0.049628	0.357922
post-anal tail morp	biological_process	1	0.47%	0.049628	0.357922
negative regulatio	biological_process	1	0.47%	0.049628	0.357922
protein ADP-ribos	biological_process	1	0.47%	0.054411	0.085336
positive regulation	biological_process	1	0.47%	0.054411	0.386558
negative regulatio	biological_process	1	0.47%	0.054411	0.386558
apoptotic mitochon	biological_process	1	0.47%	0.054411	0.386558
associative learnin	biological_process	1	0.47%	0.054411	0.386558
cartilage condensa	biological_process	1	0.47%	0.054411	0.386558
cell death	biological_process	1	0.47%	0.054411	0.386558
release of sequeste	biological_process	1	0.47%	0.054411	0.386558
cartilage developn	biological_process	2	0.93%	0.055242	0.085374
response to heat	biological_process	1	0.47%	0.059371	0.412561
positive regulation	biological_process	1	0.47%	0.059371	0.412561
regulation of heart	biological_process	1	0.47%	0.059371	0.412561
cochlea morphoge	biological_process	1	0.47%	0.059371	0.412561
learning or memor	biological_process	1	0.47%	0.064503	0.097938
lactation	biological_process	1	0.47%	0.064503	0.43862
regulation of cell c	biological_process	1	0.47%	0.069803	0.105647
triglyceride metab	biological_process	1	0.47%	0.069803	0.471292
bone morphogene	biological_process	1	0.47%	0.069803	0.471292
one-carbon metab	biological_process	1	0.47%	0.069803	0.471292
chromatin modific	biological_process	1	0.47%	0.075265	0.113016
negative regulatio	biological_process	1	0.47%	0.075265	0.504592
cellular response t	biological_process	1	0.47%	0.075265	0.504592
carbohydrate phos	biological_process	1	0.47%	0.075265	0.504592
neuromuscular jun	biological_process	1	0.47%	0.075265	0.504592
endoplasmic retict	biological_process	1	0.47%	0.075265	0.504592
proximal/distal pa	biological_process	1	0.47%	0.075265	0.504592
cellular response t	biological_process	1	0.47%	0.075265	0.504592
carbohydrate meta	biological_process	5	2.34%	0.076764	0.112777
cell cycle arrest	biological_process	2	0.93%	0.079011	0.115899
mRNA export fror	biological_process	1	0.47%	0.080884	0.523823
synaptic transmiss	biological_process	2	0.93%	0.082292	0.119788
sodium ion transp	biological_process	2	0.93%	0.082292	0.529336
heart development	biological_process	4	1.87%	0.085095	0.123491
cellular response t	biological_process	1	0.47%	0.086657	0.125567
social behavior	biological_process	1	0.47%	0.086657	0.549983
positive regulation	biological_process	1	0.47%	0.086657	0.549983

inner ear morphog	biological_process	2	0.93%	0.092538	0.133076
protein kinase B si	biological_process	1	0.47%	0.098643	0.605856
positive regulation	biological_process	1	0.47%	0.098643	0.605856
cellular response t	biological_process	1	0.47%	0.098643	0.605856
response to drug	biological_process	2	0.93%	0.099702	0.140202
brown fat cell diff	biological_process	1	0.47%	0.104847	0.635758
limb development	biological_process	1	0.47%	0.104847	0.635758
apoptotic signalin	biological_process	1	0.47%	0.104847	0.635758
protein methylatio	biological_process	1	0.47%	0.104847	0.635758
peptidyl-threonine	biological_process	1	0.47%	0.104847	0.635758
protein ubiquitinat	biological_process	1	0.47%	0.104847	0.635758
cell cycle	biological_process	2	0.93%	0.110937	0.153953
negative regulatio	biological_process	1	0.47%	0.111186	0.665715
negative regulatio	biological_process	1	0.47%	0.111186	0.665715
Wnt signaling pat	biological_process	2	0.93%	0.11481	0.157719
midbrain develop	biological_process	1	0.47%	0.117655	0.161162
negative regulatio	biological_process	1	0.47%	0.117655	0.682975
negative regulatio	biological_process	1	0.47%	0.117655	0.682975
protein complex a	biological_process	1	0.47%	0.117655	0.682975
dephosphorylation	biological_process	4	1.87%	0.117713	0.160319
patterning of bloo	biological_process	1	0.47%	0.124252	0.168741
positive regulation	biological_process	1	0.47%	0.124252	0.708309
embryonic forelim	biological_process	1	0.47%	0.124252	0.708309
positive regulation	biological_process	1	0.47%	0.124252	0.708309
negative regulatio	biological_process	1	0.47%	0.13097	0.742166
regulation of prote	biological_process	1	0.47%	0.13097	0.742166
protein oligomeriz	biological_process	1	0.47%	0.13097	0.742166
pigmentation	biological_process	1	0.47%	0.13097	0.742166
protein localizatio	biological_process	1	0.47%	0.137808	0.184519
negative regulatio	biological_process	1	0.47%	0.137808	0.77629
positive regulation	biological_process	1	0.47%	0.14476	0.192743
fatty acid metaboli	biological_process	1	0.47%	0.14476	0.810653
positive regulation	biological_process	1	0.47%	0.151822	0.845231
mitochondrion org	biological_process	1	0.47%	0.151822	0.845231
extrinsic apoptotic	biological_process	1	0.47%	0.151822	0.845231
negative regulatio	biological_process	2	0.93%	0.152444	0.201006
neuron developme	biological_process	1	0.47%	0.158991	0.20906
cellular response t	biological_process	1	0.47%	0.158991	0.869884
cellular response t	biological_process	1	0.47%	0.158991	0.869884
response to toxic s	biological_process	1	0.47%	0.158991	0.869884
positive regulation	biological_process	1	0.47%	0.158991	0.869884
negative regulatio	biological_process	5	2.34%	0.163056	0.212935
glucose homeostas	biological_process	2	0.93%	0.166049	0.216249
regulation of RNA	biological_process	1	0.47%	0.166264	0.216234
skeletal system mc	biological_process	1	0.47%	0.166264	0.889232
neural tube develo	biological_process	1	0.47%	0.166264	0.889232
nucleobase-contain	biological_process	1	0.47%	0.173636	0.224594

cellular response to biological_process	1	0.47%	0.173636	0.923472
extracellular matrix biological_process	2	0.93%	0.175397	0.225951
positive regulation of biological_process	1	0.47%	0.181104	0.942138
cellular response to biological_process	1	0.47%	0.181104	0.942138
dorsal/ventral pattern biological_process	1	0.47%	0.188665	0.976136
sperm motility biological_process	1	0.47%	0.188665	0.976136
multicellular organismal biological_process	4	1.87%	0.201339	0.255907
potassium ion transport biological_process	2	0.93%	0.204717	0.258818
transcription, DNA biological_process	1	0.47%	0.21596	0.272309
odontogenesis of crown biological_process	1	0.47%	0.22774	0.2849
cholesterol homeostasis biological_process	1	0.47%	0.235787	0.294193
BMP signaling pathway biological_process	1	0.47%	0.243904	0.303129
regulation of gene expression biological_process	3	1.40%	0.246212	0.304408
anterior/posterior axis biological_process	2	0.93%	0.251994	0.310749
negative regulation of biological_process	1	0.47%	0.252089	0.310464
skin development biological_process	1	0.47%	0.260337	0.318562
intracellular signaling biological_process	5	2.34%	0.261257	0.318052
embryonic digit morphogenesis biological_process	1	0.47%	0.268648	0.325385
embryonic limb morphogenesis biological_process	1	0.47%	0.277016	0.3334
regulation of transcription biological_process	8	3.74%	0.281478	0.33749
sodium ion transport biological_process	1	0.47%	0.285441	0.340954
positive regulation of biological_process	1	0.47%	0.311026	0.369198
positive regulation of biological_process	3	1.40%	0.31248	0.370001
protein localization biological_process	1	0.47%	0.328316	0.387787
positive regulation of biological_process	1	0.47%	0.333106	0.392472
protein transport biological_process	1	0.47%	0.336269	0.395708
transmembrane receptor biological_process	1	0.47%	0.337023	0.396106
peptidyl-serine phosphorylation biological_process	1	0.47%	0.345769	0.405385
protein homooligomerization biological_process	2	0.93%	0.350273	0.409655
cellular response to biological_process	1	0.47%	0.354552	0.414151
negative regulation of biological_process	1	0.47%	0.363369	0.422894
cell redox homeostasis biological_process	1	0.47%	0.372217	0.43056
phosphorylation biological_process	5	2.34%	0.37411	0.431178
MAPK cascade biological_process	1	0.47%	0.381096	0.438698
oxidation-reduction biological_process	10	4.67%	0.386936	0.444883
response to lipopolysaccharide biological_process	1	0.47%	0.390003	0.447868
ATP catabolic process biological_process	4	1.87%	0.392906	0.449575
neuron projection biological_process	1	0.47%	0.398935	0.455926
protein stabilization biological_process	1	0.47%	0.407891	0.464488
proteolysis biological_process	4	1.87%	0.413124	0.468765
positive regulation of biological_process	1	0.47%	0.416869	0.472452
proteasome-mediated biological_process	1	0.47%	0.425867	0.481503
regulation of Rho GTPase biological_process	1	0.47%	0.434883	0.490532
response to oxidative stress biological_process	1	0.47%	0.443916	0.498358
GTP catabolic process biological_process	1	0.47%	0.448685	0.501936
cell adhesion biological_process	1	0.47%	0.452808	0.505954
regulation of cell signaling biological_process	1	0.47%	0.462023	0.515042

positive regulation biological_process	1	0.47%	0.498357	0.545957
nervous system de biological_process	1	0.47%	0.507457	0.555286
post-embryonic de biological_process	1	0.47%	0.51656	0.563305
in utero embryonic biological_process	3	1.40%	0.551765	0.596232
positive regulation biological_process	1	0.47%	0.552976	0.596863
positive regulation biological_process	6	2.80%	0.560843	0.604669
positive regulation biological_process	1	0.47%	0.589335	0.631809
negative regulation biological_process	1	0.47%	0.598406	0.640813
protein phosphory biological_process	5	2.34%	0.601912	0.643843
negative regulation biological_process	5	2.34%	0.610502	0.650838
positive regulation biological_process	1	0.47%	0.625557	0.666141
potassium ion tran biological_process	1	0.47%	0.65259	0.691832
metabolic process biological_process	13	6.07%	0.663166	0.700703
axon guidance biological_process	1	0.47%	0.688404	0.724957
regulation of trans biological_process	1	0.47%	0.698808	0.734288
inflammatory resp biological_process	1	0.47%	0.732721	0.766539
apoptotic process biological_process	1	0.47%	0.741516	0.774038
regulation of cell f biological_process	1	0.47%	0.827996	0.855865
cation transport biological_process	1	0.47%	0.853363	0.877323
protein autophosph biological_process	1	0.47%	0.870112	0.892615
cellular response to biological_process	1	0.47%	0.874802	0.895497
transcription from biological_process	1	0.47%	0.903436	0.919862
negative regulation biological_process	3	1.40%	0.919625	0.933351
lipid metabolic pr biological_process	1	0.47%	0.943784	0.955832
positive regulation biological_process	8	3.74%	0.947416	0.958491
negative regulation biological_process	5	2.34%	0.965616	0.972768
transmembrane tra biological_process	5	2.34%	0.976164	0.981318

The significant GO terms of down-regulated genes

calcium ion bindin molecular_function	1	0.47%	7.27E-07	2.77E-05
oxygen binding molecular_function	1	0.47%	5.60E-05	0.001089
oxygen transporter molecular_function	1	0.47%	0.00057	0.0092
phospholipase A2 molecular_function	1	0.47%	0.075265	0.504592
ion channel activit molecular_function	1	0.47%	0.122531	0.166643
metal ion binding molecular_function	1	0.47%	0.176895	0.227574
heme binding molecular_function	1	0.47%	0.254674	0.312435
phospholipid bindi molecular_function	1	0.47%	0.29392	0.350641
structural molecu molecular_function	1	0.47%	0.602338	0.643575
structural constitut molecular_function	1	0.47%	0.861051	0.884272
membrane cellular_component	1	0.47%	0.000902	0.004852
hemoglobin compl cellular_component	1	0.47%	0.006097	0.063787
extracellular regio cellular_component	1	0.47%	0.091765	0.132164
intermediate filam cellular_component	1	0.47%	0.235823	0.293468
endoplasmic retic cellular_component	1	0.47%	0.263979	0.320545
mitochondrion cellular_component	1	0.47%	0.283654	0.339671
ribonucleoprotein cellular_component	1	0.47%	0.494458	0.542309
extracellular vesic cellular_component	1	0.47%	0.678786	0.715619
extracellular space cellular_component	1	0.47%	0.696067	0.732217

ribosome	cellular_component	1	0.47%	0.843777	0.868406
intracellular	cellular_component	1	0.47%	0.877442	0.897234
oxygen transport	biological_process	1	0.47%	0.000753	0.011951
phosphatidic acid	biological_process	1	0.47%	0.0009	0.014048
phospholipid meta	biological_process	1	0.47%	0.104847	0.147218
lipid catabolic pro	biological_process	1	0.47%	0.166264	0.889232
ion transport	biological_process	1	0.47%	0.258125	0.316261
transport	biological_process	1	0.47%	0.569678	0.612806
ion transmembran	biological_process	1	0.47%	0.955112	0.964228
translation	biological_process	1	0.47%	0.969733	0.975883

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Supplemental Table S4. The significant KEGG ways of differentially ex

Pathway_ID	Pathway_DES	Diff_gene_in_this	P-value
ocu04260	Cardiac muscle contraction - Oryz	15	3.56E-15
ocu05414	Dilated cardiomyopathy - Oryctol	11	2.65E-10
ocu05410	Hypertrophic cardiomyopathy (H	11	2.65E-10
ocu04261	Adrenergic signaling in cardiomy	12	9.80E-09
ocu05412	Arrhythmogenic right ventricular	7	2.05E-06
ocu04530	Tight junction - Oryctolagus cuni	9	4.86E-06
ocu00010	Glycolysis / Gluconeogenesis - O	5	0.000166851
ocu00030	Pentose phosphate pathway - Ory	3	0.000447537
ocu05010	Alzheimer's disease - Oryctolagus	7	0.000987367
ocu01230	Biosynthesis of amino acids - Ory	4	0.001699944
ocu00190	Oxidative phosphorylation - Oryc	6	0.001998665
ocu04932	Non-alcoholic fatty liver disease (	6	0.003248325
ocu05012	Parkinson's disease - Oryctolagus	6	0.003558092
ocu00500	Starch and sucrose metabolism - (	3	0.009055494
ocu00052	Galactose metabolism - Oryctolag	2	0.011199545
ocu00051	Fructose and mannose metabolism	2	0.012414351
ocu04810	Regulation of actin cytoskeleton -	6	0.013128566
ocu01200	Carbon metabolism - Oryctolagus	4	0.014205948
ocu04020	Calcium signaling pathway - Oryc	5	0.014827989
ocu04670	Leukocyte transendothelial migra	4	0.017799147
ocu00230	Purine metabolism - Oryctolagus	5	0.019083082
ocu04973	Carbohydrate digestion and absor	2	0.02131934
ocu04910	Insulin signaling pathway - Oryct	4	0.021970257
ocu00910	Nitrogen metabolism - Oryctolagu	1	0.02727234
ocu00520	Amino sugar and nucleotide sugar	2	0.030940473
ocu05016	Huntington's disease - Oryctolagu	5	0.031910867
ocu04921	Oxytocin signaling pathway - Ory	4	0.032195899
ocu05230	Central carbon metabolism in can	2	0.045206613
ocu04964	Proximal tubule bicarbonate recla	1	0.060614202
ocu04710	Circadian rhythm - Oryctolagus c	1	0.060614202
ocu05143	African trypanosomiasis - Oryctol	1	0.060614202
ocu04911	Insulin secretion - Oryctolagus cu	2	0.065617615
ocu04520	Adherens junction - Oryctolagus c	2	0.068861179
ocu05416	Viral myocarditis - Oryctolagus c	2	0.068861179
ocu00250	Alanine, aspartate and glutamate m	1	0.078044067
ocu04510	Focal adhesion - Oryctolagus cuni	4	0.088474661
ocu00592	alpha-Linolenic acid metabolism -	1	0.090581016
ocu01100	Metabolic pathways - Oryctolagu	19	0.095991746
ocu05030	Cocaine addiction - Oryctolagus c	1	0.117642046
ocu03018	RNA degradation - Oryctolagus c	2	0.122516892
ocu00591	Linoleic acid metabolism - Oryct	1	0.124788535
ocu04130	SNARE interactions in vesicular t	1	0.124788535
ocu04960	Aldosterone-regulated sodium rea	1	0.124788535
ocu05146	Amoebiasis - Oryctolagus cunicul	2	0.131379983
ocu04961	Endocrine and other factor-regula	1	0.132076782

ocu04022	cGMP-PKG signaling pathway - O	3	0.156256042
ocu04978	Mineral absorption - Oryctolagus	1	0.162545891
ocu05144	Malaria - Oryctolagus cuniculus (	1	0.162545891
ocu00565	Ether lipid metabolism - Oryctola	1	0.162545891
ocu04919	Thyroid hormone signaling pathw	2	0.164570882
ocu00260	Glycine, serine and threonine met	1	0.170467826
ocu05031	Amphetamine addiction - Oryctol	1	0.194890728
ocu04270	Vascular smooth muscle contracti	2	0.21735379
ocu00330	Arginine and proline metabolism	1	0.220208034
ocu05200	Pathways in cancer - Oryctolagus	1	0.225936733
ocu04024	cAMP signaling pathway - Orycto	3	0.228819775
ocu00480	Glutathione metabolism - Oryctol	1	0.22882654
ocu04972	Pancreatic secretion - Oryctolagus	2	0.234295503
ocu04150	mTOR signaling pathway - Orycto	1	0.237528154
ocu04152	AMPK signaling pathway - Oryct	2	0.251700543
ocu04918	Thyroid hormone synthesis - Oryc	1	0.264093914
ocu04975	Fat digestion and absorption - Ory	1	0.273090668
ocu04970	Salivary secretion - Oryctolagus c	1	0.282152319
ocu04920	Adipocytokine signaling pathway	1	0.282152319
ocu05203	Viral carcinogenesis - Oryctolagu	3	0.318026547
ocu04610	Complement and coagulation casc	1	0.318981344
ocu04727	GABAergic synapse - Oryctolagu	1	0.328318261
ocu04971	Gastric acid secretion - Oryctolag	1	0.328318261
ocu04666	Fc gamma R-mediated phagocyto	1	0.337700932
ocu04912	GnRH signaling pathway - Orycto	1	0.337700932
ocu05322	Systemic lupus erythematosus - O	2	0.344730197
ocu04976	Bile secretion - Oryctolagus cunic	1	0.347126434
ocu05202	Transcriptional misregulation in c	2	0.364349808
ocu00830	Retinol metabolism - Oryctolagus	1	0.366094586
ocu00982	Drug metabolism - cytochrome P4	1	0.375631739
ocu04010	MAPK signaling pathway - Oryct	3	0.3850554
ocu05100	Bacterial invasion of epithelial ce	1	0.385200727
ocu04723	Retrograde endocannabinoid signi	1	0.423744385
ocu00564	Glycerophospholipid metabolism	1	0.423744385
ocu04725	Cholinergic synapse - Oryctolagu	1	0.45286629
ocu04750	Inflammatory mediator regulation	1	0.462602359
ocu00980	Metabolism of xenobiotics by cyt	1	0.462602359
ocu00590	Arachidonic acid metabolism - Or	1	0.491867507
ocu05034	Alcoholism - Oryctolagus cunicul	2	0.501029077
ocu04726	Serotonergic synapse - Oryctolagi	1	0.501634911
ocu04080	Neuroactive ligand-receptor intera	1	0.503896619
ocu05204	Chemical carcinogenesis - Orycto	1	0.511405311
ocu04066	HIF-1 signaling pathway - Orycto	1	0.521176874
ocu04974	Protein digestion and absorption -	1	0.530947818
ocu04380	Osteoclast differentiation - Orycto	1	0.60889469
ocu04068	FoxO signaling pathway - Orycto	1	0.695451841
ocu04014	Ras signaling pathway - Oryctola	1	0.760984529

ocu04310	Wnt signaling pathway - Oryctola	1	0.761405315
ocu05206	MicroRNAs in cancer - Oryctolag	1	0.789212204
ocu05205	Proteoglycans in cancer - Oryctol:	1	0.823493904
ocu03010	Ribosome - Oryctolagus cuniculu	2	0.874720636
ocu05169	Epstein-Barr virus infection - Ory	1	0.874782983
ocu04141	Protein processing in endoplasmic	1	0.897194096

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expressed genes

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