Dissecting Wnt/β-catenin signaling during gastrulation using RNA interference in mouse embryos

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Summary

Differential gene regulation integrated in time and space drives developmental programs during embryogenesis. To understand how the program of gastrulation is regulated by Wnt/β-catenin signaling, we have used genome-wide expression profiling of conditional β-catenin mutant embryos. Known Wnt/β-catenin target genes, known components of other signaling pathways, as well as a number of uncharacterized genes were downregulated in these mutants. To further narrow down the set of differentially expressed genes, we used whole-mount in situ screening to associate gene expression with putative domains of Wnt activity. Several potential novel target genes were identified by this means and two, *Grsf1* and *Fragilis2*, were functionally analyzed by RNA interference (RNAi) in completely embryonic stem (ES) cell-derived embryos. We show that the gene encoding the RNA-binding factor *Grsf1* is important for axial elongation, mid/hindbrain development and axial mesoderm specification, and that *Fragilis2*, encoding a transmembrane protein, regulates epithelialization of the somites and paraxial mesoderm formation. Intriguingly, the knock-down phenotypes recapitulate several aspects of Wnt pathway mutants, suggesting that these genes are components of the downstream Wnt response. This functional genomic approach allows the rapid identification of functionally important components of embryonic development from large datasets of putative targets.

Key words: Wnt/β-catenin signaling, Gastrulation, RNA interference (RNAi), Target genes, Expression profiling, *Grsf1*, *Fragilis2*, Functional genomics

Introduction

Signaling molecules of the Wnt family regulate many cellular behaviors, including differentiation, proliferation and morphogenesis, and are involved in gastrulation and axial development (reviewed by Sokol, 1999; Yamaguchi, 2001). β-Catenin, besides acting as a central component of the cadherin cell-adhesion complex, plays an essential role in the canonical Wnt/β-catenin signaling pathway (reviewed by Huber et al., 1996). Upon Wnt stimulation, β-catenin enters the nucleus and acts in a complex with members of the Tcf/Lef (T-cell factor/Lymphoid enhancer factor) family of transcription factors to activate target genes (Hecht and Kemler, 2000).

Mutations in a number of Wnt genes and Wnt signaling components highlight the crucial role of the Wnt/β-catenin signaling pathway in the initiation of primitive streak formation, as well as in the patterning and morphogenesis of the gastrulation-stage embryo (Beddington and Robertson, 1999; Lu et al., 2001). Mutant mouse embryos that lack functional Wnt3 or β-catenin fail to establish an anterior-posterior (A-P) axis and do not form a primitive streak, thus they fail to generate endoderm and mesoderm, resulting in an arrest of development before gastrulation (Liu et al., 1999; Haegel et al., 1995; Huelsken et al., 2000). Both *Wnt3a* null mutants and *Lef1;Tcf1* compound homozygous null mutants fail to differentiate paraxial mesoderm, do not form somites caudal to the forelimb buds and exhibit severe posterior truncations (Takada et al., 1994; Galceran et al., 1999). In addition, *Wnt3a* controls directly the expression of *Axin2* and *Dll1* in the paraxial mesoderm, and thereby, links the Notch and Wnt signaling pathways in the processes of somitogenesis (Aulehla et al., 2003; Galceran et al., 2004; Hofmann et al., 2004). By the end of gastrulation and the beginning of neurulation, secreted Fgf8 and Wnt1 molecules from the isthmic organizer play an important role in patterning the mid/hindbrain region along the A-P axis (reviewed by Liu and Joyner, 2001; Wurst and Bally-Cuif, 2001).

Recently, using the Cre/*loxP* system, we have conditionally inactivated β-catenin in the visceral endoderm (VE) and the anterior primitive streak (APS) by using a Cytokeration 19 (*K19*)-driven Cre (Lickert et al., 2002). Similar to in Wnt3 and β-catenin null mutants, A-P axis formation was affected; however, the conditional β-catenin mutants proceeded through gastrulation. This revealed a crucial function for β-catenin during later developmental processes, such as posterior axis elongation and somite formation, processes affected in other Wnt mutants. Additionally, the node, an embryonic structure functionally equivalent to the Spemann/Mangold organizer in frog, failed to form in these mutants. Taken together, these results are consistent with the hypothesis that Wnt/β-catenin signaling is important for the induction of the mouse embryonic organizing centers, the formation of somites, and the proper morphogenesis of the gastrulating embryo.

Here, we have used a functional genomic approach combining Affymetrix GeneChip analysis, whole-mount in situ screening and rapid functional assessment by RNAi in embryonic stem (ES) cell-derived embryos to dissect the Wnt/β-catenin signaling pathway during gastrulation. Intriguingly, the knock-down phenotypes of two potential target genes, *Grsf1* and *Fragilis2* (*Ifitm1* – Mouse Genome Informatics), recapitulate specific but distinct aspects of Wnt pathway mutants, suggesting that these genes are components of the downstream Wnt response. In summary, this approach represents a highly efficient and rapid methodology with which to unravel developmental pathways in the mouse.

Materials and methods

Generation of mutant mice and genotyping

Cytokeratin 19 (*K19*) promoter-driven Cre mice (*K19-Cre*) were previously generated by a knock-in of the Cre recombinase gene into the ATG translation initiation codon of exon1 of *K19* (Harada et al., 1999). The β-catenin floxed (*flox*) allele and the β-catenin floxed deleted (*floxdel*) allele were previously described (Brault et al., 2001). *K19-Cre* mice were mated with β-catenin *floxdel* mice and the offspring, which inherited both alleles, were crossed with homozygous β-catenin *flox* mice; a quarter of the offspring was positive for *K19-Cre*, together with one *flox* and one *floxdel* allele. Littermates, which inherited the *floxed* and *floxdel* β-catenin alleles but did not carry the *K19-Cre* allele served as heterozygous controls. Mutant animals were bred on a mixed 129Sv×C57Bl/6 background. PCR genotyping was performed as described previously (Lickert et al., 2002).

Microarray experiments

Microarray experiments have been submitted to GEO in a MIAME compliant format (Minimum Information About a Microarray Experiment) (Brazma et al., 2001). The accession number is GSE2519.

Sample preparation

Embryos from the above described intercrosses were dissected in PBS and separated into embryonic and extraembryonic portions. The embryonic portions were stored in PBS at –80°C until the PCR genotyping was carried out using the extraembryonic portions. The pooled embryos were homogenized in 250 μl of TRIzol Reagent (Invitrogen), and total RNA was extracted according to the manufacturer's protocol.

Probe preparation and GeneChip hybridization

For each sample, 5 μg total RNA was used for cDNA synthesis according to the Expression Analysis Technical Manual (Affymetrix). The in vitro transcription and labeling of cRNA was carried out using the BioArray High-Yield Transcription Labeling Kit (Enzo). Then 25 μg of labeled cRNA was used to hybridize all three GeneChips from the Affymetrix U74v2 according to the standardized Affymetrix protocol.

Data analysis

MAS 5.0 software was used to generate the expression data set for each GeneChip.dat file and scale normalized to a target value of 150. Comparisons were made to calculate signal log ratios of expression between mut:wt and mut:het using either wild type (wt) or heterozygotes (het) as a baseline, respectively. The resulting table was exported to Microsoft Excel to filter out probe sets with absent calls across all samples (*P*-detection >0.04) and probe sets with no change in expression (0.003 > *P*-signal log ratio <0.997) in both mut:het and mut:wt comparisons. Illogical combinations of absent and present calls with a significant change call were deleted, e.g. an absent call in baseline and present call in mutant with a decrease change. Genes that were consistently up- and downregulated in both comparisons (absolute signal log ratio of ⩾0.5) were hierarchically clustered using Cluster 3.0 software [http://bonsai.ims.u-tokyo.ac.jp/~mdehoon/software/cluster/software.htm, based on the method of Eisen et al. (Eisen et al., 1998)].

Using the Affymetrix Gene Ontology (GO) analysis software (www.affymetrix.com) the numbers of probe sets on U74v2A GeneChip corresponding to the GO terms 'Transcription' (GOID:6350), 'Cell Communication' (GOID:7154), 'Pattern Specification' (GOID:7389) and 'Morphogenesis' (GOID:9653) were calculated as of the November 2003 annotation build. The total numbers of all other probe sets with a GO term were denoted as 'Others'. Additionally, the numbers for the same GO terms were calculated for the 49 downregulated genes from the U74Av2 GeneChip. Percentiles for each GO term category were calculated by dividing the numbers in each category by the total number of probe sets with any GO term.

Whole-mount in situ hybridization, histology and alkaline phosphatase staining

For whole-mount in situ hybridization and histology, embryos were processed as described previously (Lickert et al., 2002). Sense and antisense in situ probes were in vitro transcribed using ESTs available from ATCC (Manassas, VA, USA) with the following I.M.A.G.E. Clone IDs: *Fragilis2*, 657273; *Zic3*, 5120056; *Scap2*, 3599914; *Punc*, 3514346; *EST10*, 3980327; *EST16*, 1328681; *Sox2*, 5707193. Additionally, ESTs from the NIA 15K Mouse cDNA Clone Set with the following H3 clone IDs were used for probe synthesis: *Grsf1*, H3046G05; *EST6*, H3074B02. Additional probes for known genes were as follows: *Axin2* (Aulehla et al., 2003), *Wnt3a* (Gavin et al., 1990), *Wnt8* (Bouillet et al., 1996), *Frzb1* (Hoang et al., 1998), *Notch1* (Conlon et al., 1995), *Dll1* (Hrabe de Angelis et al., 1997), *Gbx2* (Wassarman et al., 1997), *Hoxb1* (Marshall et al., 1992), *T* (Herrmann et al., 1990), *Tbx6* (Chapman et al., 1996), *PAPC* (Rhee et al., 2003), and *Krox20* (Swiatek and Gridley, 1993).

To identify germ cells, embryos were fixed in 4% paraformaldehyde in PBS for 30 minutes and stained for tissue non-specific alkaline phosphatase for 5 minutes [25 mM Tris-maleic acid (pH 9.0), 0.4 mg/ml α-naphthyl phosphate (Sigma), 1 mg/ml Fast Red TR salt (Sigma), 8 mM $MgCl_2$, 0.01% Na-desoxycholate, 0.02% NP-40].

shRNA targeting of ES cells and embryos and northern blot analysis

For construction of the *Grsf1* and *Fragilis2* shRNA transgenes, we have used the pcDNA3.1 *RasGAP* shRNA plasmid described recently (Kunath et al., 2003). *RasGAP* shRNA was released from the plasmid by *Asp*718, *Xba*I digestion, and annealed oligonucleotides corresponding to the target sequence were introduced into the same sites using the following sense- and antisense-strand oligonucleotides (target sequence in bold):

Grsf1 shRNA forward, 5′-GT ACC **AAA GCA CAG GGA AGA AAT TGG TA** C AAG AGA **TA CCA ATT TCT TCC CTG TGC TTT** TTT TTGG AAA T-3′ and *Grsf1* shRNA reverse, 5′-CTA GAT TTC CAA AAA **AAA GCA CAG GGA AGA AAT TGG TA** T CTC TTG **TA CCA ATT TCT TCC CTG TGC TTT** G-3′ (corresponding to bases 982-1004 of the murine *Grsf1* gene, NCBI accession no.: NM_178700); and

Fragilis2 shRNA forward, 5′-GT ACC **GAA CAT CAG CTC CCT GTT CTT CA** C AAG AGA **TG AAG AAC AGG GAG CTG ATG TTC** TTT TTT TGG AAA T-3′ and *Fragilis2* shRNA reverse, 5′-CTA GAT TTC CAA AAA AA **GAA CAT CAG CTC CCT GTT CTT CA** T CTC TTG **TG AAG AAC AGG GAG CTG ATG TTC** G-3′ (corresponding to bases 295-317 of the murine *Fragilis2* gene, NCBI accession no.: BK001123).

The resulting shRNA targeting constructs were confirmed by DNA sequencing. Transgenic ES-cell lines were established as described (Kunath et al., 2003). The mRNA expression level of the individual ES-cell lines for *Grsf1* and *Fragilis2* was determined by northern blotting using the NorthernMax-Gly^{TM} Kit (Ambion), according to the manufacturer's protocol. Pre-selected ES-cell lines were used to generate totally ES cell-derived embryos using the tetraploid aggregation technique as described previously (Nagy et al., 1993; Kunath et al., 2003). Embryos with any contribution of tetraploid EGFP-positive cells were excluded from the analysis. Experimental animals were treated according to guidelines approved by the Canadian Council for Animal Care.

Co-culture of ES cells with Wnt1-expressing fibroblasts

The co-cultivation of ES cells with NIH3T3 fibroblasts was carried out essentially as described previously (Lickert et al., 2000), with the exception that the ES cells were seeded in transwell filters (*Transwell*-COL, collagen-treated, 0.4 μm pore-size; Costar #3491). After 18 hours of co-cultivation, total RNA was isolated from the ES cells using the *RNeasy Mini* Kit (Qiagen). For each sample, 2 μg of RNA was treated with DNaseI and then reverse transcribed using oligo (dT)-primers and SuperSriptII reverse transcriptase (Invitrogen).

Quantitative PCR was performed using the LightCycler Fast Start DNA Master^{Plus} SYBR Green I Kit (Roche) according to the manufacturer's protocol. The following primers were used to amplify mRNAs for *Gapdh*, *Fragilis2* and *Grsf1*: *Gapdh*-fwd, 5′-ACCA-CAGTCCATGCCATCACT-3′; *Gapdh*-rev, 5′-GTCCACCACCCTG-TTGCTGTA-3′; *Fragilis2*-fwd, 5′-GGGCTCCTCG-ACCACACCTCTT-3′; *Fragilis2*-rev, 5′-CCCAGTC-GTATCACCCACCATCT-3′; *Grsf1*-fwd, GATATTCG-GCCTATGACGGCT-3′; *Grsf1*-rev, CAAAATCGA-CAGCCTCTGGAAG.

Results

Expression profiling of gastrulation stage conditional β-catenin mutants

β-Catenin homozygous null mutant embryos arrest before gastrulation (Haegel et al., 1995; Huelsken et al., 2000). To study the effects of disrupting the Wnt/β-catenin signaling pathway during gastrulation, we generated embryos that were compound heterozygous for a *floxed* β-catenin allele and a β-catenin *floxdel* allele (where exon 2-6 were removed by Cre-mediated excision), carrying the *K19-Cre* allele (hereafter termed conditional β-catenin knock out (CKO) (Lickert et al., 2002). We pooled and isolated total RNA from 47 CKO (7.32 μg), 47 heterozygous (6.12 μg), and 41 wild-type (6.44 μg) embryos between late gastrulation and head-fold stage – the time when the first phenotypic alterations can be seen. The high number of embryos collected should normalize any variation in staging. The three individual RNA samples were used for labeled cRNA preparation and GeneChip hybridizations (Affymetrix U74v2 Series containing about 36,000 probe sets). No amplification of the cRNA was used to ensure accurate representation of the individual expression profiles; however, this precludes the use of biological replicates because of limiting amounts of embryonic material. To identify genes directly or indirectly deregulated in the CKO mutant embryos, we compared wild-type (wt) and heterozygous (het) expression profiles against the mutant expression profile. For further study, we focused on the genes with consistent alterations in gene expression, i.e. those differing in both comparisons with an absolute signal log ratio $\geqslant 0.5$. This limited the set of candidates to 262 upregulated and 77 downregulated genes on the three Affymetrix GeneChips (Fig. 1A, and Table S1 in the supplementary material). Here, we concentrated only on the downregulated genes in β-catenin mutants. These genes included the previously described direct target genes *Cdx1*, brachyury (*T*), follistatin, *Axin2,* and *Dll1*, thus validating the expression profiling approach (Table 1). Downregulation of genes such as *Wnt3a*, *Tbx6*, *T*, *Notch1*,

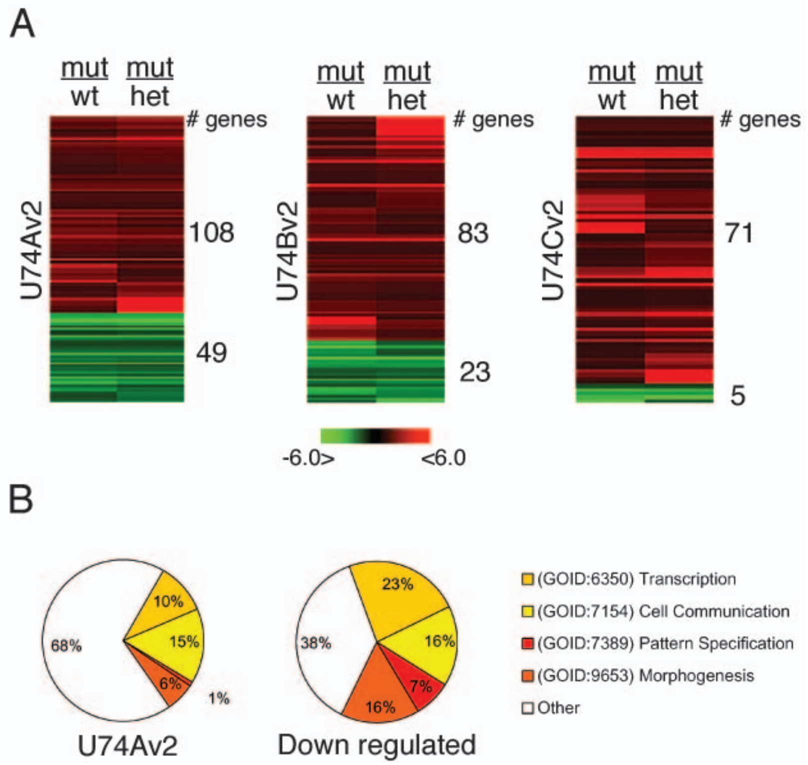

Fig. 1. Gene expression profiling of conditional β-catenin mutant embryos. (A) Hierarchical clustering of differentially regulated genes (see Materials and methods). The number of upregulated (shades of red) and downregulated (shades of green) genes per GeneChip is indicated. Different shades indicate the signal log ratios between the individual comparisons, and a color scale bar represents these values. (B) Enrichment of genes encoding for developmental regulatory factors among the potential β-catenin target genes. Approximately 6000 genes on the U74Av2 GeneChip are annotated and have a gene ontology (GOID) term. The left pie chart represents the percentage of genes with the indicated GO terms among all genes with a GO term. The right pie chart represents the percentage of genes with the indicated GO terms among the 49 downregulated genes of the U74Av2 GeneChip.

Table 1. Selected list of up- and downregulated genes

Gene symbol	Probe set ID	Mutant/wild type	Mutant/ heterozygote	GOID	Functional annotation
Sox2*	100009_r_at	1.3	1.3	(GOID:6350) Transcription	
Pem	101368_at	0.7	0.9	(GOID:6350) Transcription	
Dab2	98045_s_at	0.6	0.7	(GOID:9653) Morphogenesis	
Gbx2*	94200_at	–5.4	–4.4	(GOID:6350) Transcription	Pat
Hoxa1	95297_at	–5.1	–4.5	(GOID:7389) Pattern Specification	Pat
Cdx1	103477_at	–4.2	–4.9	(GOID:6350) Transcription	Pat
Raldh2	101707_at	–3.6	–3.4	(GOID:1523) Retinoid metabolism	Pat
twist	98028_at	–3.2	–3.6	(GOID:6350) Transcription	Pat
Hoxb1*	93888_at	–1.7	–1.8	(GOID:7389) Pattern Specification	Pat
Wnt5a	99390_at	–1.6	–1.8	(GOID:9653) Morphogenesis	Pat
Hoxb2	106927_at	–1.5	–1.4	(GOID:7389) Pattern Specification	Pat
Wnt3a*	102667_at	–2.9	–3.2	(GOID:9653) Morphogenesis	Pat, Mes
Tbx6	93611_at	–1.6	–1.8	(GOID:6350) Transcription	Pat, Mes
T	93941_at	–1.4	–1.4	(GOID:6350) Transcription	Pat, Mes
Meox1	98419_at	–1	–0.7	(GOID:6350) Transcription	Pat, Mes
FGFR1	97509_f_at	–0.6	–0.6	(GOID:7154) Cell Communication	Pat, Mes
Follistatin	98817_at	–0.6	–1	TGF-beta signaling pathway	Pat, Mes
Lef1	103628_at	–0.5	–0.6	(GOID:6350) Transcription	Pat, Mes
Axin2*	163891_at	–0.4	0.1	(GOID:7154) Cell Communication	Pat, Mes
Dll1*	92931_at	–2	–1.5	(GOID:7389) Pattern Specification	Pat, Mes, L-R
Notch1*	97497_at	–1.3	–0.8	(GOID:7389) Pattern Specification	Pat, Mes, L-R
Foxj1	98831_at	–1.2	–1	(GOID:6350) Transcription	L-R
Sox17	92996_at	–0.8	–0.7	(GOID:6350) Transcription	En
EST6†	114959_at	–5	–4.8	RIKEN cDNA C030045D06 gene	
EST16†	138065_at	–4.9	–3.7	None available	
Wnt8*	99361_at	–2.4	–3	(GOID:7154) Cell Communication	
Fragilis2†	160254_at	–1.6	–1.7	Family of IFN-inducible genes	
EST10†	97386_at	–1.5	–1.6	Similar to integrase of retrovirus	
Crabp1	98108_at	–1.5	–1.3	(GOID:5501) Retinoid binding	
Smarcd3	108488_at	–1.4	–1.5	SWI/SNF related regulator of chromatin	
NFkB	98427_s_at	–1.3	–1.1	(GOID:6350) Transcription	
Frzb1*	104672_at	–1.1	–1	(GOID:7275) Development	
Scap2†	102012_at	–1	–0.5	Src associated phosphoprotein 2	
Rbp1	104716_at	–1	–1	(GOID:1523) Retinoid metabolism	
Punc†	94117_f_at	–1	–1	(GOID:7154) Cell Communication	
Irx3	99034_at	–1	–0.9	(GOID:6350) Transcription	
AI447312	106222_at	–0.8	–1	Hypothetical aminotransferases class-II	
Grsf1†	96684_at	–0.8	–0.7	G-rich RNA sequence binding factor 1	
Zic3†	98330_at	–0.8	–0.7	(GOID:6350) Transcription	

Genes were annotated using the Affymetrix Netaffx and NCBI databases.
The Gene symbol, Affymetrix probeset ID, signal $\log_2$ ratio for both comparisons, a GO-term ID (GOID) and a functional annotation are given.
*Genes whose differential expression was confirmed by in situ hybridization.
†Genes for which the expression pattern was tested in wild-type embryos.
Pat, patterning and morphogenesis; Mes, paraxial mesoderm and somites; En, endoderm formation; L-R, left-right axis determination.

Dll1, *Meox1*, *Lef1*, follistatin, *Fgfr1* and *Axin2* is in agreement with defects in paraxial mesoderm specification and somite formation in the mutant embryos. Moreover, components of the retinoic acid signaling cascade, such as *Raldh2*, *Crabp1* and *Rbp1*, as well as components of the FGF signaling cascade, like *Fgfr1*, and components of the Wnt signaling cascade, including *Wnt3a*, *Wnt5a*, *Wnt8* and *Frzb1*, were also downregulated. These results indicate that all the major caudalizing activities were affected, offering a possible explanation for the lack of posterior development in CKO embryos. Additionally, downregulation of the general definitive endoderm marker *Sox17*, is consistent with our previous observation that endoderm formation is affected in CKO mutants. Interestingly, we also found that the downregulation of genes, like *Notch1*, *Dll1* and *Foxj1* (Krebs et al., 2003; Raya et al., 2003; Chen et al., 1998), was implicated in left-right (L-R) asymmetry (Table 1), a process not previously identified as being affected in CKO embryos and which should now be analyzed further (Lickert et al., 2002). Classification of the downregulated genes by Gene Ontology (GO) terms revealed that transcription factors, as well as genes implicated in pattern specification and morphogenesis, were highly enriched among the downregulated genes when compared with all genes on the U74Av2 GeneChip (Fig. 1B). Comparing our data with the reported expression profiles of pre-gastrulation stage β-catenin homozygous null mutants at E6.0 and E6.5 gave almost no overlap in the datasets (Morkel et al., 2003) (see Table S2 in the supplementary material), suggesting that the transcriptional Wnt response changes dynamically over the course of development.

Expression screening establishes new regulatory interactions

To confirm that downregulated genes are differentially expressed in domains of Wnt activity in wild-type and CKO embryos, in situ hybridization was performed at E7.5 (Fig. 2). Wnt ligands, such as *Wnt3a* and *Wnt8*, as well as the secreted

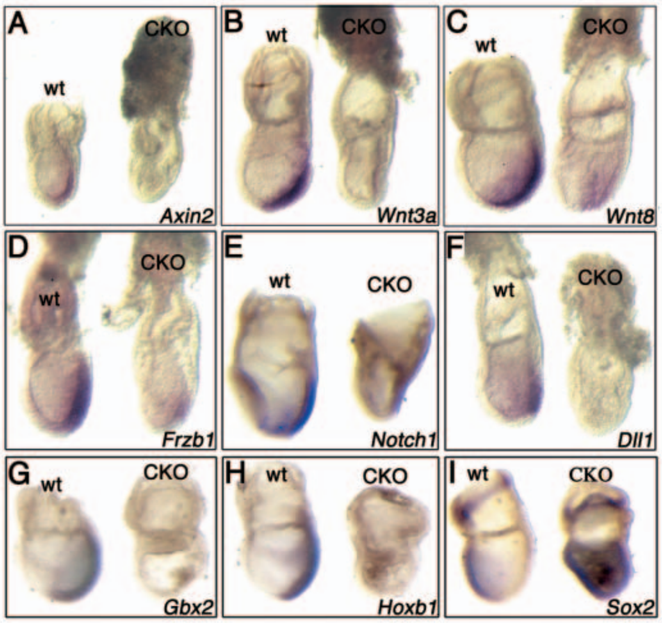

Fig. 2. Confirmation of the GeneChip results by whole-mount in situ hybridization. (A-I) Late-gastrula stage wild-type (wt) and conditional β-catenin mutant (CKO) embryos hybridized with the indicated probes. All embryos are depicted in a lateral view, anterior to the left. (A-H) *Axin2*, *Wnt3a*, *Wnt8*, *Frzb1*, *Notch1*, *Dll1*, *Gbx2* and *Hoxb1* are all expressed in the primitive streak of wild-type embryos, but are downregulated in conditional β-catenin mutants to varying extents. (I) *Sox2* is normally expressed in the extraembryonic chorion and anterior epiblast in wild-type embryos at this stage. The expression in the extraembryonic region is unaffected in mutant embryos, but the whole epiblast expresses *Sox2*.

Wnt inhibitor *Frzb1*, and the negative regulator *Axin2*, showed strong downregulation in the primitive streak (PS) of CKO embryos (Fig. 2A-D). These results suggest both positive- and negative-feedback regulation in the Wnt/β-catenin signaling pathway. We also found that the PS expression of *Notch1* and its ligand *Dll1* was downregulated in β-catenin mutants (Table 1, Fig. 2E,F). In addition, several Hox genes were downregulated in β-catenin mutants (Table 1), and *Hoxb1* was absent in β-catenin mutants (Fig. 2H). Furthermore, *Gbx2*, which is normally expressed in the posterior epiblast at late gastrulation stage (Wassarman et al., 1997), was completely lost in CKO embryos (Fig. 2G). Concordant with the loss of *Gbx2* expression, we found a posterior expansion of the expression of *Sox2*, a marker of the anterior epiblast (Fig. 2I) (Wood and Episkopou, 1999), which was upregulated in the microarray experiments (Table 1).

In summary, all nine genes tested by in situ hybridization accurately reflected the GeneChip results.

Expression screening identifies novel genes regulating embryonic development

To discover new components of Wnt/β-catenin signaling in developing embryos, we investigated further the expression of 16 downregulated genes (EST1-16) for which there was little or no published evidence concerning their developmental roles at the time the screen was conducted. Upon in situ hybridization in wild-type embryos at E7.5 and E8.5, eight of the genes showed expression patterns that strongly overlapped with known regions of high Wnt reporter activity (Fig. 3) (Mohamed et al., 2004). All genes except EST6 showed expression in the PS region at gastrulation stages (Fig. 3). In addition, *Grsf1*, *Punc* and *Zic3* showed expression in the mid/hindbrain region at E8.5, while *Scap2*, *Punc*, *Zic3*, *Fragilis2* and EST16 were expressed in the paraxial mesoderm, somites or neurectoderm of the tailbud region (Fig. 3). Interestingly, EST6 showed strong expression in the extraembryonic ectoderm and in a row of cells anterior to the node, known regions of organizing activity (Fig. 3C). EST10 showed a specific expression pattern in the definitive endoderm around gastrulation by whole-mount in situ hybridization and histological sectioning of stained embryos (Fig. 3F and data not shown).

For further analysis, we used transgenic RNA interference (RNAi) (Kunath et al., 2003) to analyze the function of the newly identified potential Wnt/β-catenin target genes, *Irx3*, *Scap2*, *Smarcd3*, *Fragilis2* and *Grsf1* (Table 1). Because the results for the *Smarcd3* knock-down analysis was recently published (Lickert et al., 2004) and because in a first attempt we were not able to knock down *Scap2* and *Irx3*, we focus here on the analysis of *Grsf1* and *Fragilis2* (Fig. 3A,G).

Knock down of potential Wnt/β-catenin targets, *Grsf1* and *Fragilis2*

Grsf1 codes for the mouse ortholog of the human G-rich sequence specific binding factor1 (GRSF1), which was previously shown to bind to a specific consensus sequence in the 5′-UTR of influenza virus nucleocapsid mRNA and thereby act positively on translation (Park et al., 1999; Kash et al., 2002). *Fragilis2* belongs to a family of interferon-inducible genes with five members (*Fragilis1-5*), clustered on 68 kb of mouse chromosome 7 and associated with germ-cell differentiation (Tanaka and Matsui, 2002; Lange et al., 2003).

Both *Grsf1* and *Fragilis2* contain several putative Wnt-responsive elements in inter- and intragenic regions (see Fig. S1 in supplementary material). To test the hypothesis that *Grsf1* and *Fragilis2* are components of the Wnt-signaling response, we first monitored mRNA expression in ES cells that had been co-cultured in transwell filters on top of Wnt1-expressing 3T3 fibroblasts (Fig. 4A) (Lickert et al., 2000). Quantitative RT-PCR revealed that Wnt1 induced endogenous *Grsf1* mRNA expression in ES cells by twofold, but had no effect on *Fragilis2* expression, which is already highly expressed in ES cells per se (Fig. 4D). We then used in situ hybridization analysis to test the mRNA expression level of both genes in wild-type and CKO embryos at E7.5 (Fig. 4B,C). Consistent with the GeneChip experiments, the expression of both genes is absent in the PS of CKO embryos, but weak *Fragilis2* expression remained at the base of the allantois, where the primordial germ cells (PGCs) are located. Because PGCs and ES cells share many molecular markers and cellular properties, this might suggest that the regulation of *Fragilis2* expression in PGCs and ES cells is independent of Wnt/β-catenin, but is dependent on this signaling system in the paraxial mesoderm emerging from the PS. This idea is further supported by transgenic enhancer studies of a PGC-specific enhancer located in intron1 of *Fragilis2*, which does not depend on two Wnt-responsive elements (data not shown).

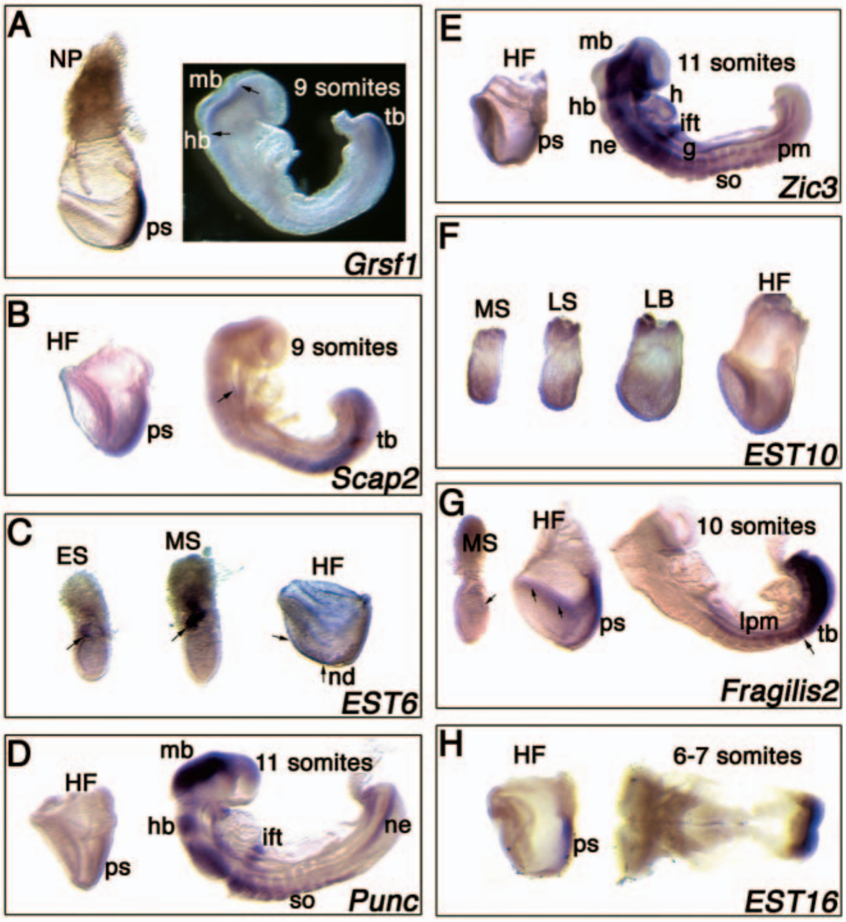

Fig. 3. Whole-mount expression screening to identify potential β-catenin target genes. (A-H) Whole-mount in situ hybridization with the indicated probes on wild-type embryos at different developmental stages. All embryos are depicted in a lateral view, anterior to the left, except for the 6- to 7-somite stage embryo in H, which is depicted in a ventral view. (A) *Grsf1* is strongly expressed in the primitive streak (ps) at neural-plate stage (NP). At 9-somite stage, *Grsf1* is restricted to the posterior neurectoderm in the tailbud (tb), and the midbrain (mb; arrow) and hindbrain region (hb; arrow). (B) *Scap2* is expressed in the primitive streak at head-fold stage. At the 9-somite stage, mRNA expression is detected in the tailbud region and foregut pocket (arrow). (C) *EST6* is expressed (arrows) in the extraembryonic ectoderm at early-streak (ES) and mid-streak (MS) stage. At head-fold stage, *EST6* shows expression in a row of cells anterior to the node (arrows). (D) *Punc* is expressed in the primitive streak at head-fold stage. At the 11-somite stage, expression is seen in the midbrain (mb) and hindbrain (hb), as well as in the somites (so), inflow tract (ift) and posterior neurectoderm. (E) *Zic3* is expressed in the primitive streak at head-fold stage. At 11-somite stage, expression is detected in anterior neurectoderm (ne), heart (h), inflow tract, gut (g), somites, midbrain (mb) and hindbrain (hb), and posterior paraxial mesoderm (pm). (F) *EST10* is strongly expressed throughout the definitive endoderm at mid-streak, late-streak (LS), late-bud (LB) and head-fold stage. (G) *Fragilis2* is first detected in the region where the allantois will form at mid-streak stage (arrow). At head-fold stage, expression is prominent in the primitive streak region and in the lateral-plate mesoderm (arrows). At 10-somite stage, expression is confined to the lateral-plate mesoderm (lpm), paraxial mesoderm and first forming somite (arrow) in the tailbud region. (H) EST16 shows expression in the primitive streak at late head-fold stage. At 6- to 7-somite stage, expression is confined to the posterior neurectoderm.

Taken together with the co-expression of *Grsf1* and *Fragilis2* in the regions of high Wnt activity, these results suggest that both genes represent good candidate Wnt/β-catenin target genes.

To test whether these genes have necessary functions in domains of Wnt activity in embryonic development, we used RNAi in ES cells (Kunath et al., 2003) to knock down *Grsf1* and *Fragilis2*. Stably transfected R1 ES-cell clones were selected and tested for successful silencing at the mRNA level using northern blotting (Fig. 4D). We were able to obtain ES-cell clones for both genes with very low residual levels of specific mRNA expression (Fig. 4D; *Grsf1*, clones 5 and 6; *Fragilis2*, clones 1 and 2), indicating that neither *Grsf1* nor *Fragilis2* function is essential for ES-cell growth or maintenance. To examine the effects of the expected silencing of these genes in embryos, we then used the tetraploid aggregation technique (Nagy et al., 1993) to generate completely ES cell-derived embryos of the efficiently silenced ES-cell lines (*Grsf1*, clones 5 and 6; *Fragilis2*, clones 1 and 2). In situ expression analysis at E7.5 revealed substantial silencing of *Grsf1* and *Fragilis2* mRNA levels, indicating that the silencing effect seen in ES cells is stably maintained in ES cell-derived embryos (Fig. 4E,F).

Grsf1 and *Fragilis2* knock downs recapitulate Wnt signaling phenotypes

Grsf1 shRNA-silenced ES cell-derived embryos did not show any obvious phenotype at E7.5 (clone 5, *n*=7; clone 6, *n*=5). At E9.5 (clone 5, *n*=10; clone 6, *n*=25), we consistently found two phenotypes: (1) truncation of the posterior axis with formation of a large allantois; and (2) abnormal mid/hindbrain development (Fig. 5A). The phenotypes observed were restricted to the expression domains of *Grsf1* in the posterior epiblast and in the mid/hindbrain region, suggesting that the effects seen are specific for *Grsf1* gene knock down (Fig. 3A). Shortening of the tailbud region was clearly seen at E8.5 (clone 5, *n*=6; clone 6, *n*=8), when the mid/hindbrain region still looked morphologically normal (Fig. 5B). The abnormally large allantois is most likely a secondary effect due to the truncation of the posterior axis and failure of chorio-allantoic fusion. A more detailed histological analysis of the mutants at E9.5 revealed an overgrowth of neurepithelium in the mid/hindbrain region of *Grsf1*-silenced embryos (Fig. 5C). Loss of epithelial integrity was seen in the neural tube from the level of the septum transversum in the midtrunk region of *Grsf1*-silenced embryos and extending posteriorly (Fig. 5D), which might be due to secondary effects, because the neural tube rapidly degenerates following a failure of allantoic placental development. To avoid studying a secondary degeneration phenotype at this late stage, we analyzed the expression of marker genes in knock-down embryos prior to the 13-somite stage. At the 7- to 8-somite stage, *Grsf1*-silenced embryos showed slightly reduced levels of *Fgf8* expression in the isthmus region, whereas expression in the tailbud was strongly reduced (Fig. 5E) (Crossley and Martin, 1995). By the 10-somite stage, *Grsf1*-silenced embryos showed barely detectable levels of *Fgf8* in the midline of the mid/hindbrain region and almost no expression in the lateral regions of the neural tube (Fig. 5F). Expression of *Gbx2* in rhombomeres (r) 1 and 2 of knock-down embryos was strongly reduced at the 7- to 8-somite stage (Fig. 5G), whereas the hindbrain marker *Krox20* appeared to be normally expressed in r3 and r5 in these mutants (Fig. 5H). Interestingly, *Gbx2* expression in the tailbud appeared to be normal (Fig. 5G), in contrast to the reduced level of *Fgf8* in this region (Fig. 5E), which indicates that the knock down of *Grsf1* selectively alters the expression of marker genes. Onset of expression of the potential β-catenin target *Gbx2* (Fig. 2G) in the epiblast seemed to be unaffected at head-fold stage (Fig. 5I), indicating that *Grsf1* is important for maintaining *Gbx2* expression at later developmental stages in the mid/hindbrain region.

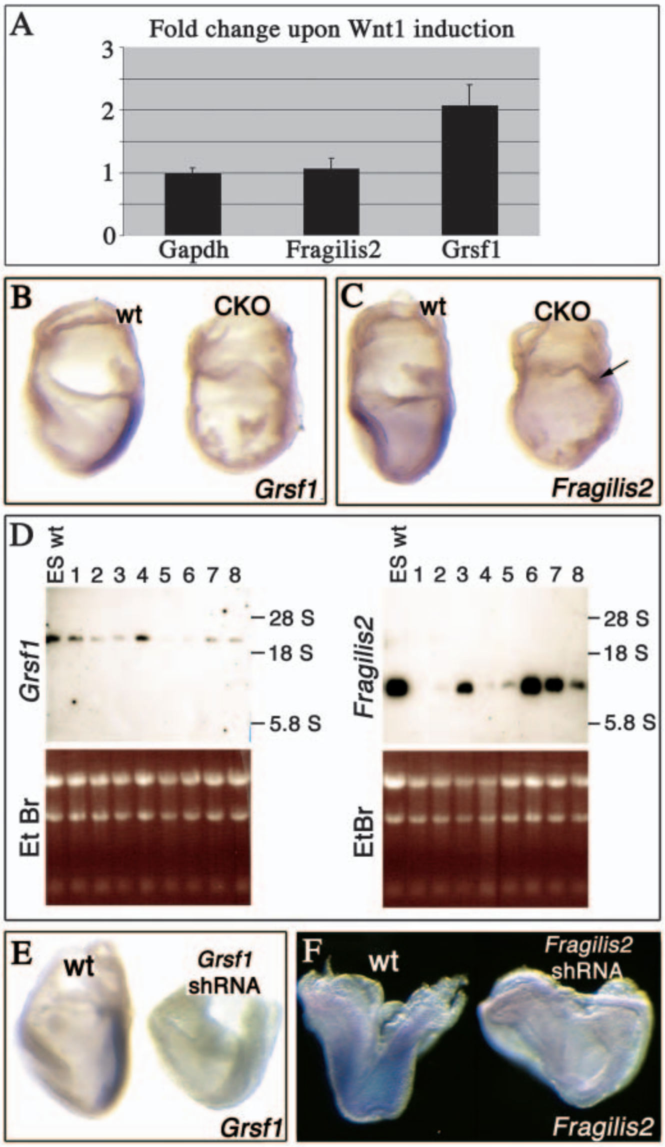

Fig. 4. The response of *Grsf1* and *Fragilis2* to Wnt signaling and shRNA silencing. (A) Co-culture of ES cells on *lacZ* and *Wnt1*-expressing fibroblasts induces *Grsf1* endogenous mRNA expression in Wnt1-treated ES cells, but not *Fragilis2* expression. Gene-specific expression was normalized to Gapdh and the fold change was calculated. Results of three independent co-culture experiments are shown. Whole-mount in situ hybridization of wild-type and β-catenin mutants (B,C), and of wild-type and shRNA-silenced embryos (E,F) with *Grsf1* and *Fragilis2* probes at late-gastrulation stage. All embryos are depicted in a lateral view, anterior to the left. *Grsf1* and *Fragilis2* are strongly downregulated in the primitive streak of β-catenin mutant embryos (B,C) and knock-down embryos (E,F). Arrow in C indicates remaining *Fragilis2* expression at the base of the allantois. (D) Northern blot analysis for *Grsf1* and *Fragilis2* for eight different shRNA ES-cell lines (1-8) and wild-type ES cells. 28S, 18S and 5.8S ribosomal RNAs are indicated as molecular length markers, and the ethidium bromide (EtBr)-stained agarose gels served as loading control.

We next tested the mRNA expression of known Wnt/β-catenin target genes, *Cdx1* and *T*, in *Grsf1* knock-down mutants. At gastrulation stages, *Cdx1* and *T* were normally expressed in the PS of mutant embryos (Fig. 5J-K), whereas the expression domain of *T* in the axial mesoderm did not extend as far anteriorly in the mutants as it did in wild-type embryos (Fig. 5K, arrows). Interestingly, *T* expression in the axial mesoderm of *Grsf1* knock-down embryos was greatly reduced at head-fold stage (Fig. 5L, arrows). Taken together, these results indicate that *Grsf1* function is essential for posterior axis elongation, midbrain development and axial mesoderm specification.

Fragilis2-silenced embryos also did not show any obvious phenotype at E7.5 (clone 1, *n*=6; clone 2, *n*=4). Embryos analyzed between E9.0 and E9.5 (clone 1, *n*=8; clone 2, *n*=13) revealed problems in somite formation and a truncation of the posterior axis (Fig. 6A). Similar to *Grsf1*-silenced embryos, *Fragilis2*-silenced embryos also developed a large allantois, presumably due to the posterior truncation. In *Fragilis2*-silenced embryos at E8.5 (clone 1, *n*=12; clone 2, *n*=8), the somites appeared hollow and were irregular in shape and smaller in size (Fig. 6B, see b′,b″). Additionally, the neural tube appeared kinked, a phenotype frequently seen in mutants affecting somite formation (Conlon et al., 1995). Histological analysis of the *Fragilis2*-silenced embryos at E8.5 revealed abnormalities in epithelialization and/or maintenance of epithelial integrity of the somites (Fig. 6C). As the Fragilis gene family is implicated in PGC development and *Fragilis2* is expressed in this cell population, we stained *Fragilis2*-silenced embryos for tissue non-specific alkaline phosphatase (AP). No difference in the AP staining between wild-type and knock-down embryos was observed, suggesting that the formation of PGCs was normal at head-fold stage (Fig. 6D).

Wnt/β-catenin signaling is implicated in both the formation of paraxial mesoderm (Takada et al., 1994; Galceran et al., 1999) and the subsequent segmentation of presomitic mesoderm into somites (Auhlela et al., 2003; Galceran et al., 2004; Hofmann et al., 2004). To discriminate between possible defects in these two processes in the *Fragilis2* knock-down embryos, we analyzed *T* and *Tbx6*, genes

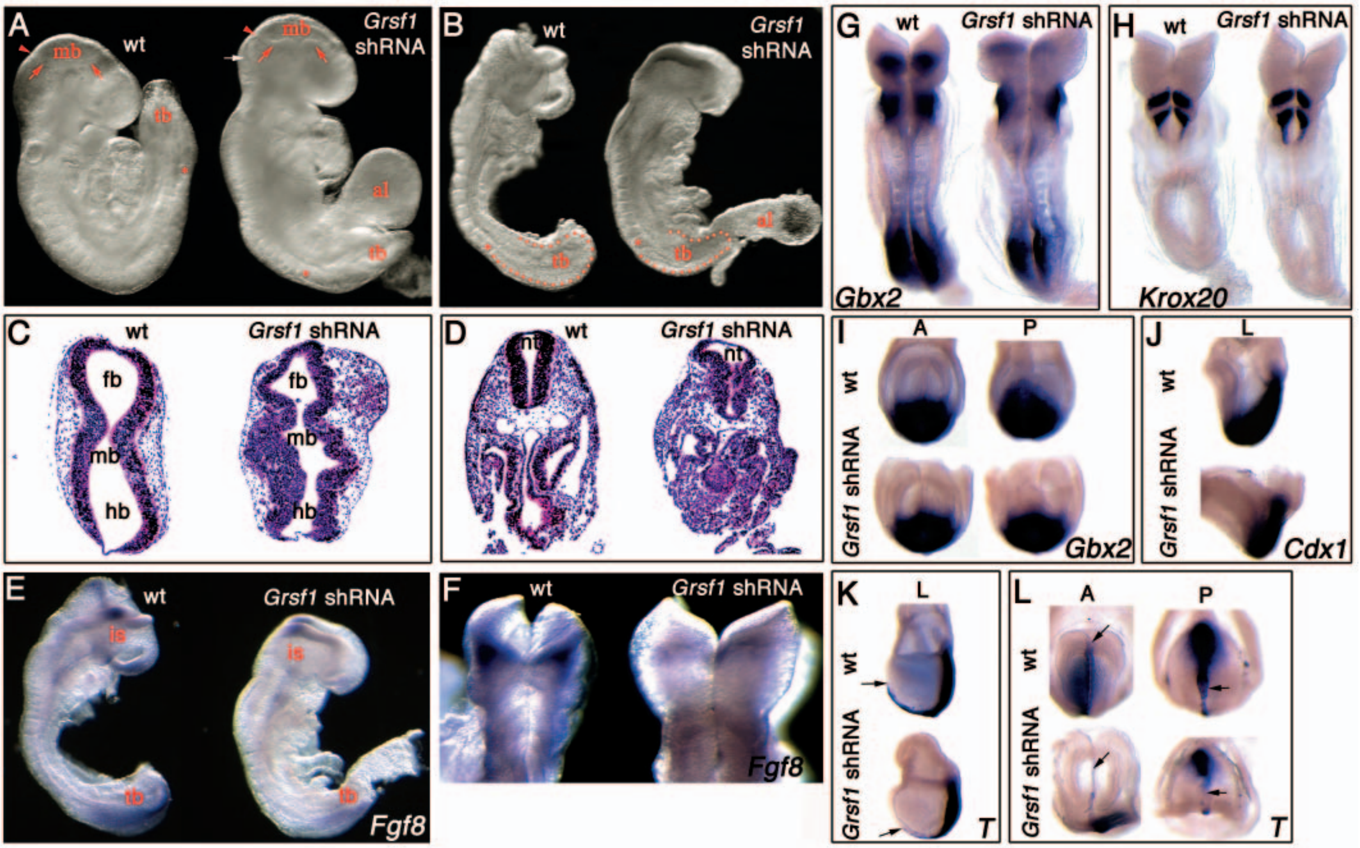

Fig. 5. *Grsf1*-silenced embryos mimic mid/hindbrain and posterior truncation phenotypes of Wnt mutants. (A) Posterior truncations are more pronounced at E9.0 (the first forming somite is indicated by an asterisk in A and B). Additionally, *Grsf1*-silenced embryos show a clear thickening in the midbrain (mb) region (red arrows), a large alantois (al) and abnormal anterior hindbrain development (white arrow; red arrowhead indicates mid/hindbrain boundary). (B) At E8.5, *Grsf1*-silenced embryos show a reduced tailbud (tb) region (indicated by dotted area). (C,D) Comparison of Hematoxylin and Eosin-stained transverse sections of wild-type and *Grsf1*-silenced embryos at E9.0. fb, forebrain; hb, hindbrain; nt, neural tube. (E-K) Whole-mount in situ analysis of wild-type and *Grsf1*-silenced embryos with indicated probes. (E,F) Comparison of *Fgf8* expression in 7-8 somite wild-type and *Grsf1*-silenced embryos. (E) Lateral view, anterior up. (F) Dorsal view on the mid/hindbrain boundary. (G,H) Comparison of hindbrain marker gene expression in wild-type and *Grsf1*-silenced embryos at 7-somite stage; dorsal view, anterior up. (I-L) Expression analysis of potential (*Gbx2*) and known Wnt/β-catenin target genes (*Cdx1* and *T*) in wt and knock-down embryos at gastrulation stage. L, lateral view, anterior to the left; A, anterior view, anterior is up; P, posterior view, posterior is up. (I,J) *Gbx2* and *Cdx1* are normally expressed in *Grsf1*-silenced embryos at head-fold stage. Note, that the posterior axis is slightly shortened in knock-down mutants. (K,L) Comparison of *T* expression in wild-type and *Grsf1*-silenced embryos at E7.5 (K) and head-fold stage (L). Arrow indicates the anterior expression border. A, anterior view; P, posterior view; L, lateral view.

implicated in paraxial mesoderm formation, and *PAPC*, a gene important for epithelialization of the somites (Rhee et al., 2003). Expression of *T* and *Tbx6* was unaffected in mutant embryos at head-fold stage, but decreased in the tailbud region at E8.5 (Fig. 5E). Expression of PAPC in wild-type embryos is restricted to two stripes at the anterior end of the presomitic mesoderm corresponding to the next two presumptive somites (Fig. 5E; somite 0 and –1). Analysis of *Fragilis2* knock-down embryos revealed that PAPC expression is decreased at head-fold stage and was barely detectable in the two presomitic stripes at 10-somite stage (Fig. 5E). Taken together, these results demonstrate that knock down of *Fragilis2* predominantly affects the epithelialization of somites, and to a lesser extent the formation of paraxial mesoderm, suggesting that *Fragilis2* acts downstream of Wnt/β-catenin to regulate these processes.

Discussion

Previous studies have highlighted the important role of Wnt/β-catenin signaling in the control of various developmental processes at the time of gastrulation and axial patterning in the early mouse embryo (Sokol, 1999; Beddington and Robertson, 1999; Yamaguchi, 2001; Lu et al., 2001). To understand mechanistically how the Wnt/β-catenin signaling cascade acts on these developmental processes, it is necessary to identify the target genes of Wnt signaling in different developmental domains. Using GeneChip analysis of conditional β-catenin mutants and wild-type embryos at late-gastrulation stages, we identified many potential Wnt/β-catenin target genes enriched for developmental components involved in pattern specification and morphogenesis, including 26 well-characterized signaling molecules and transcription factors (Table 1 and Fig. 1B). Further clustering of these genes into different functional groups, e.g. genes involved in paraxial

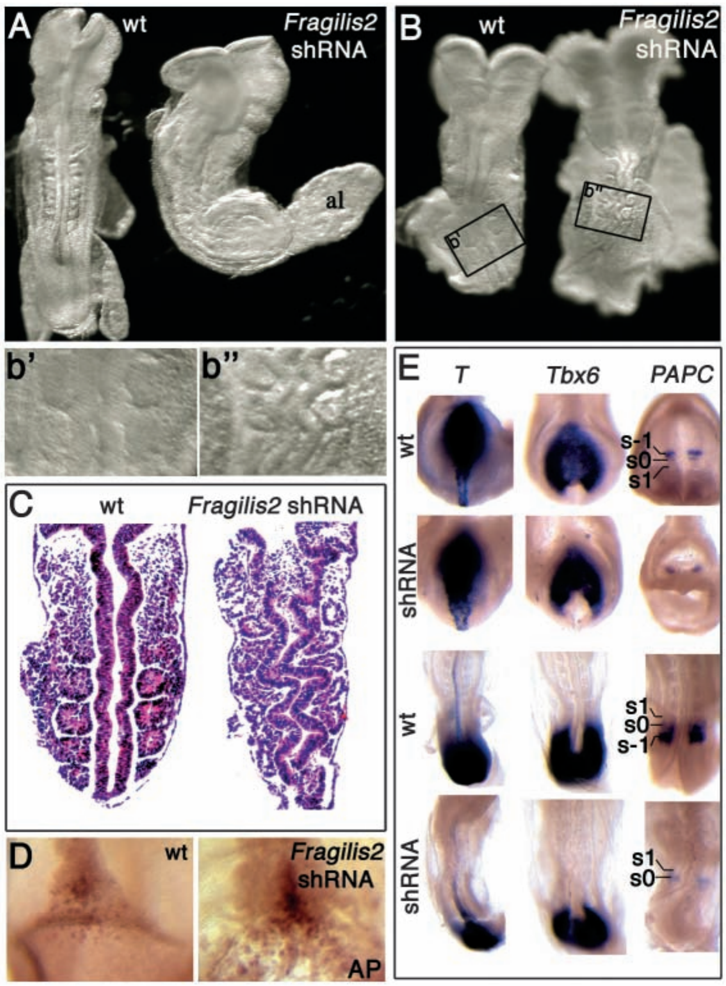

Fig. 6. *Fragilis2*-silenced embryos mimic the somite phenotype of the β-catenin mutants. (A,B,D) Embryos are depicted in a dorsal view; anterior is up. Comparison of wild-type and *Fragilis2*-silenced embryos at E8.75 (A) and E8.5 (B) demonstrates abnormal development in the posterior region, formation of a large allantois (al), a kinked neural tube and abnormal somite formation (magnified in b′ and b″). (C) Comparison of Hematoxylin and Eosin-stained frontal sections of wild-type and *Fragilis2*-silenced embryos at E8.5. (D) Tissue non-specific alkaline phosphatase (AP) staining to detect primordial germ-cell (PGC) formation at head-fold stage. Embryos are depicted in a posterior view, focusing on the embryonic-extraembryonic border. (E) Whole-mount in situ analysis of wild-type and *Fragilis2*-silenced embryos with the indicated probes at the 2- to 3-somite stage (upper panels; posterior view, posterior is up) and the 9- to 10-somite stage (lower panel; dorsal view, posterior is down). *T* and *Tbx6* are normally expressed in *Fragilis2*-silenced embryos at 2-3 somite stage, but expression is slightly reduced at the 9- to 10-somite stage in the tailbud region. In wild-type embryos, *PAPC* is expressed in two presomitic stripes (s0 and s-1). At the 2- to 3-somite stage, only one presomitic stripe is clearly visible in knock-down mutants, and *PAPC* expression further diminishes at the 9- to 10-somite stage.

mesoderm and somite formation, genes important for endoderm formation, factors involved in patterning and morphogenesis, and genes implicated in L-R axis formation (Table 1), reveals the different molecular programs potentially controlled by β-catenin during gastrulation.

As well as identifying sets of genes possibly downregulated by Wnt/β-catenin signaling at gastrulation, we also found a large number of genes that were upregulated in the conditional β-catenin mutants. One possible explanation for this is offered by the morphogenetic defects observed in β-catenin mutant embryos, such as retention of the visceral endoderm (VE) because of a lack of definitive endoderm formation, which normally displaces VE into the extraembryonic region. Consistent with this interpretation, *Dab2* and *Pem*, two marker genes for VE, were upregulated in β-catenin mutants (Table 1). However, we also found genes specifically expressed in the embryo to be upregulated, e.g. *Sox2*, an anterior epiblast marker, which later becomes restricted to the neurectoderm. In situ expression analysis showed that *Sox2* becomes expressed in the posterior region of β-catenin mutants, suggesting that the posterior epiblast has acquired an anterior fate. Further mining of the upregulated set of genes in the conditional β-catenin mutants might reveal novel components of visceral endoderm formation or anterior specification.

The objective of target gene screens is not only to identify characterized and functionally annotated genes, but also to add new players and their respective function to the gene regulatory network. All the genes we tested, whether well characterized or less well annotated, showed the expected expression differences between wild type and β-catenin mutants by in situ hybridization. Thus, we expect that our dataset will provide a rich resource for future data mining to characterize Wnt/β-catenin pathways in gastrulation. Ideally, the relative importance of target genes needs to be tested by assessing their function during development. Using shRNA-mediated gene silencing in ES cells and then in ES-derived embryos (Kunath et al., 2003), we have identified and characterized two novel putative Wnt/β-catenin target genes, *Grsf1* and *Fragilis2*, whose expression is required for normal development. Both genes, when knocked down, recapitulate specific but distinct aspects of the conditional β-catenin mutant phenotype, implicating them as crucial downstream mediators of the Wnt/β-catenin signaling pathway.

The human ortholog GRSF1 is a sequence-specific RNA-binding protein, and has been shown to act positively on translation in vitro and in a cell-culture system (Park et al., 1999; Kash et al., 2002). This raises the interesting possibility that Wnt induction of Grsf1 selectively activates the translation of other mRNA transcripts in the primitive streak and/or the mid/hindbrain region. Using a computational approach for predicting possible target genes of Grsf1, we have screened the genes expressed at late gastrulation stage according to our U74A Affymetrix wild-type data set. From 4694 annotated 5′ UTRs in the ENSEMBL database, we found 386 non-redundant genes with at least one high-affinity Grsf1 consensus binding site (5′-AGGGU-3′; see Table S3 in the supplementary material). Interestingly, among these genes we found developmental regulatory factor genes, such as *T*, *Hoxb1*, *Hoxb8* and *Frzb1,* which are co-expressed with *Grsf1* at gastrulation stage. We also found genes regulating cell proliferation, such as *p53*, cyclin B1, cyclin A2 and *Cdk2*, and genes regulating apoptosis, *Bcl2* and *Bax*, as candidate Grsf1 target genes. In-depth analysis of these potential target genes will be required to dissect the mechanisms by which Grsf1 regulates mid/hindbrain development, posterior elongation and axial mesoderm specification.

Importantly, the observed *Grsf1* knock-down phenotypes remarkably recapitulate distinct aspects of the CKO mutant phenotype and other Wnt pathway mutants (Lickert et al., 2002; McMahon and Bradley, 1990; Thomas and Capecchi, 1990; Brault et al., 2001), suggesting that *Grsf1* is a crucial mediator of the Wnt/β-catenin signaling cascade. Interestingly, the lack of *T* expression in the anterior primitive streak of *Grsf1* knock-down embryos is comparable to lack of *T* expression in Wnt3a mutants (Yamaguchi et al., 1999), offering an explanation for the axis truncation in both mutants. The normal expression of the Wnt/β-catenin target genes, *Cdx1* and *Grsf1*, in *Grsf1* knock-down embryos suggests that Grsf1 acts downstream of the Wnt/β-catenin signaling pathway selectively on target mRNAs and is not involved in signal transduction, e.g. by stabilizing components of the pathway. This might also be the case for mid/hindbrain development, where *Grsf1* is necessary for maintaining *Fgf8* and *Gbx2* expression, two factors important for the establishment of the mid/hindbrain boundary. The comparison of putative mRNA targets of the RNA-binding factor Grsf1 (see Table S3 in the supplementary material) with all the deregulated genes from the β-catenin target gene screen (Table S1 in supplementary material) revealed several potentially co-regulated transcripts (see Table S4 supplementary material), which might explain similarities in the Grsf1 and CKO mutant phenotypes.

Fragilis2 is expressed in the primitive streak, including the base of the allantois, where the PGCs are localized at late gastrulation stage, and in the paraxial and lateral mesoderm, as well as in the first forming somites at E8.5. Studies in the immune system suggest a role for Fragilis2 (human orthologs Leu13/9-27/IFITM1) as part of a transmembrane multiprotein signaling complex implicated in inhibition of cell proliferation and homotypic cell adhesion (Knight et al., 1985; Deblandre et al., 1995; Sato et al., 1997). Histological analysis of Fragilis2-silenced embryos revealed a defect in epithelialization of the somites, consistent with a function in homotypic cell adhesion. Additionally, marker gene analysis revealed that *Fragilis2* knock-down embryos show reduced expression of PAPC, a gene implicated in somite epithelialization, and reduced expression of the paraxial mesoderm markers *T* and *Tbx6* at tailbud stage. These phenotypes are very similar to the paraxial mesoderm and somite segmentation defects seen in several different Wnt mutants (Lickert et al., 2002; Takada et al., 1994; Galceran et al., 1999; Aulehla et al., 2003; Galceran et al., 2004; Hofmann et al., 2004), thus it seems likely that *Fragilis2* is a crucial downstream mediator of the Wnt/β-catenin signaling cascade in these processes, mediating homotypic cell adhesion.

By using RNAi-mediated gene functional studies in ES cell-derived embryos, we have shown that it is possible to rapidly evaluate the relative importance of putative target genes of developmental pathways identified from expression profiling of mutant versus wild-type embryos. The potential for parallel functional analyses of several candidate genes in a relatively high throughput manner is an important component of genome-wide approaches to developmental genomics in the mouse.

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Supplementary material

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/132/11/2599/DC1

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Table S1. Filtered list of 262 upregulated and 77 downregulated genes across all three Affymetrix MGU74v2 GeneChips

AFFYID	NAME	Mut-wt	Mut-het
93133_at	Cluster Incl U70859:Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds /cds=(273,2129) /gb=U70859 /gi=1575775 /ug=Mm.5140 /len=2371	1.6	1.4
161626_f_at	Cluster Incl AV028204:AV028204 Mus musculus cDNA /clone=1300018L03 /clone_end=3 /gb=AV028204 /gi=4807814 /ug=Mm.69193 /len=266 /NOTE=replacement for probe set(s) 96991_f_at on MG-U74A	1.1	1.4
102764_at	Cluster Incl M36387:Tumor rejection antigen P1A /cds=(271,945) /gb=M36387 /gi=202143 /ug=Mm.1297 /len=1174	0.8	1.4
102220_at	Cluster Incl AB017360:Mus musculus UTF1 gene, complete cds /cds=(0,1019) /gb=AB017360 /gi=5672601 /ug=Mm.10205 /len=1020	1.7	1.3
100009_r_at	Cluster Incl X94127:SRY-box containing gene 2 /cds=(0,959) /gb=X94127 /gi=1209429 /ug=Mm.4541 /len=960	1.3	1.3
103776_at	Cluster Incl AA597222:vo28b03.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1051181 /clone_end=5 /gb=AA597222 /gi=2412657 /ug=Mm.24822 /len=277	1	1.3
100078_at	Cluster Incl M64248:Mouse apolipoprotein A-IV (apoa-A) mRNA, complete cds /cds=(92,1267) /gb=M64248 /gi=191884 /ug=Mm.4533 /len=1427	1	1.3
161361_s_at	Cluster Incl AV213431:AV213431 Mus musculus cDNA, 3 end /clone=2410127L14 /clone_end=3 /gb=AV213431 /gi=6154654 /ug=Mm.59362 /len=356 /NOTE=replacement for probe set(s) 94653_at on MG-U74A	0.6	1.3
93573_at	Cluster Incl V00835:Metallothionein 1 /cds=(0,185) /gb=V00835 /gi=53247 /ug=Mm.2041 /len=186	1.1	1.2
95000_g_at	Cluster Incl AJ010338:Mus Musculus mRNA for hypothetical protein /cds=(8,1273) /gb=AJ010338 /gi=3724121 /ug=Mm.2735 /len=1739	0.7	1.2
96047_at	Cluster Incl U63146:Mus musculus retinol binding protein (RBP) mRNA, complete cds /cds=(0,605) /gb=U63146 /gi=1515449 /ug=Mm.2605 /len=606	1	1.1
95518_at	Cluster Incl AW122893:UI-M-BH2.1-apa-d-07-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-apa-d-07-0-UI /clone_end=3 /gb=AW122893 /gi=6098423 /ug=Mm.25311 /len=217	0.8	1.1
92550_at	Cluster Incl M36120:Keratin complex 1, acidic, gene 19 /cds=(0,1211) /gb=M36120 /gi=198583 /ug=Mm.1012 /len=1212	0.8	1.1
161906_f_at	Cluster Incl AV113045:AV113045 Mus musculus cDNA /clone=2610018I11 /clone_end=3 /gb=AV113045 /gi=5267125 /ug=Mm.75972 /len=247 /NOTE=replacement for probe set(s) 98695_f_at on MG-U74A	2	1
93568_i_at	Cluster Incl AI853444:UI-M-BH0-ajy-d-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-ajy-d-09-0-UI /clone_end=3 /gb=AI853444 /gi=5497350 /ug=Mm.204 /len=363	0.9	1
96094_at	Cluster Incl U79573:Mus musculus apolipoprotein A-I gene, complete cds /cds=(0,791) /gb=U79573 /gi=2145136 /ug=Mm.26743 /len=792	0.9	0.9
93840_at	Cluster Incl AA655303:vq85e06.s1 Mus musculus cDNA, 5 end /clone=IMAGE-1109122 /clone_end=5 /gb=AA655303 /gi=2591457 /ug=Mm.2161 /len=292	0.9	0.9
92633_at	Cluster Incl AJ242663:Mus musculus mRNA for cathepsin Z precursor (ctsZ gene) /cds=(104,1024) /gb=AJ242663 /gi=5019547 /ug=Mm.115 /len=1291	0.9	0.9
93626_at	Cluster Incl AF103875:Mus musculus placenta-specific ATP-binding cassette transporter (Abcp) mRNA, partial cds /cds=(0,443) /gb=AF103875 /gi=4185797 /ug=Mm.7458 /len=502	0.7	0.9
93261_at	Cluster Incl AJ000990:Mus musculus mRNA for legumain /cds=(94,1401) /gb=AJ000990 /gi=3676226 /ug=Mm.17185 /len=1889	0.6	0.9
97160_at	Cluster Incl X04017:Mouse mRNA for cysteine-rich glycoprotein SPARC /cds=(89,997) /gb=X04017 /gi=54168 /ug=Mm.35439 /len=2079	0.5	0.9
99475_at	Cluster Incl U88327:Mus musculus suppressor of cytokine signalling-2 (SOCS-2) mRNA, complete cds /cds=(222,818) /gb=U88327 /gi=2245385 /ug=Mm.4132 /len=1121	1.1	0.8
104585_at	Cluster Incl AI316546:uj98c03.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1957924 /clone_end=5 /gb=AI316546 /gi=4031813 /ug=Mm.23982 /len=490	1	0.8
101561_at	Cluster Incl K02236:Metallothionein 2 /cds=(0,185) /gb=K02236 /gi=199131 /ug=Mm.89170 /len=186	1	0.8
96134_at	Cluster Incl AA755260:vp92b12.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1092191 /clone_end=5 /gb=AA755260 /gi=2802458 /ug=Mm.28147 /len=205	1	0.8
98042_at	Cluster Incl AW049787:UI-M-BH1-anm-e-03-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-anm-e-03-0-UI /clone_end=3 /gb=AW049787 /gi=5910316 /ug=Mm.34126 /len=434	0.9	0.8
160249_at	Cluster Incl U44426:Tumor protein D52 /cds=(21,578) /gb=U44426 /gi=1469925 /ug=Mm.2777 /len=2033 /NOTE=replacement for probe set(s) 97225_at on MG-U74A	0.8	0.8
97887_at	Cluster Incl Z22216:Apolipoprotein CII /cds=(0,293) /gb=Z22216 /gi=296375 /ug=Mm.28394 /len=294	0.8	0.8
100479_at	Cluster Incl AA756653:vv58e04.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1226622 /clone_end=5 /gb=AA756653 /gi=2803851 /ug=Mm.5001 /len=393	0.7	0.8
94834_at	Cluster Incl U06119:Cathepsin H /cds=(47,1048) /gb=U06119 /gi=454100 /ug=Mm.2277 /len=1381	0.7	0.8
95465_s_at	Cluster Incl AI849587:UI-M-AH1-agr-e-02-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AH1-agr-e-02-0-UI /clone_end=3 /gb=AI849587 /gi=5493493 /ug=Mm.24750 /len=310	0.7	0.8
102418_at	Cluster Incl AA793009:vp54g03.r1 Mus musculus cDNA, 3 end /clone=IMAGE-1080532 /clone_end=3 /gb=AA793009 /gi=2855964 /ug=Mm.12669 /len=341	1.8	0.7
101368_at	Cluster Incl M32484:Placentae and embryos oncofetal gene /cds=(106,738) /gb=M32484 /gi=200286 /ug=Mm.6923 /len=853	1	0.7
97518_at	Cluster Incl D29016:Mouse mRNA for squalene synthase /cds=(20,1270) /gb=D29016 /gi=468456 /ug=Mm.3204 /len=1634	0.8	0.7
101676_at	Cluster Incl U13705:Glutathione peroxidase 3 /cds=(16,696) /gb=U13705 /gi=536927 /ug=Mm.7156 /len=1415	0.7	0.7
93543_f_at	Cluster Incl J03952:Mouse, glutathione transferase GT8.7 mRNA, complete cds /cds=(12,668) /gb=J03952 /gi=193687 /ug=Mm.2011 /len=1018	0.7	0.7

93569_f_at	Cluster Incl AI853444:UI-M-BH0-ajy-d-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-ajy-d-09-0-UI /clone_end=3 /gb=AI853444 /gi=5497350 /ug=Mm.204 /len=363	0.6	0.7
98045_s_at	Cluster Incl U18869:Mus musculus mitogen-responsive 96 kDa phosphoprotein p96 mRNA, alternatively spliced p67 mRNA, and alternatively spliced p93 mRNA, complete cds /cds=(216,2516) /gb=U18869 /gi=1176369 /ug=Mm.34248 /len=3347	0.6	0.7
94831_at	Cluster Incl M65270:Mouse cathepsin B gene /cds=(25,1044) /gb=M65270 /gi=309151 /ug=Mm.22753 /len=1848	0.6	0.7
99561_f_at	Cluster Incl AF087825:Mus musculus claudin-7 mRNA, complete cds /cds=(0,635) /gb=AF087825 /gi=4191357 /ug=Mm.42189 /len=636	0.6	0.7
160493_at	Cluster Incl D16432:Cd63 antigen /cds=(54,770) /gb=D16432 /gi=484052 /ug=Mm.4426 /len=878 /NOTE=replacement for probe set(s) 100045_at on MG-U74A	0.5	0.7
97444_at	Cluster Incl AI844520:UI-M-AJ1-ahf-a-08-0-UI.s2 Mus musculus cDNA, 3 end /clone=UI-M-AJ1-ahf-a-08-0-UI /clone_end=3 /gb=AI844520 /gi=5488426 /ug=Mm.30241 /len=491	0.9	0.6
99535_at	Cluster Incl AW047630:UI-M-BH1-akm-g-06-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-akm-g-06-0-UI /clone_end=3 /gb=AW047630 /gi=5908159 /ug=Mm.42187 /len=385	0.8	0.6
95350_at	Cluster Incl D00073:Transthyretin /cds=(26,469) /gb=D00073 /gi=220561 /ug=Mm.2108 /len=680	0.8	0.6
103357_at	Cluster Incl X15684:Solute carrier family 2 (facilitated glucose transporter), member 2 /cds=(63,1634) /gb=X15684 /gi=51090 /ug=Mm.18443 /len=2491	0.7	0.6
93785_at	Cluster Incl M64782:Mouse folate-binding protein 1 (FBP1) mRNA, complete cds /cds=(59,826) /gb=M64782 /gi=193227 /ug=Mm.2135 /len=979	0.7	0.6
104717_at	Cluster Incl AI848330:UI-M-AH1-ago-b-10-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AH1-ago-b-10-0-UI /clone_end=3 /gb=AI848330 /gi=5492236 /ug=Mm.24505 /len=456	0.6	0.6
103818_at	Cluster Incl AJ012754:Mus musculus mRNA for glycoprotein-associated amino acid transporter y+LAT1a /cds=(257,1789) /gb=AJ012754 /gi=3970790 /ug=Mm.20906 /len=2158	0.6	0.6
101019_at	Cluster Incl U74683:Cathepsin C /cds=(67,1455) /gb=U74683 /gi=2145015 /ug=Mm.684 /len=1767	0.6	0.6
98627_at	Cluster Incl X81580:Insulin-like growth factor binding protein 2 /cds=(71,988) /gb=X81580 /gi=550378 /ug=Mm.38748 /len=1310	0.6	0.6
97132_at	Cluster Incl AA189890:mu55b11.r1 Mus musculus cDNA, 5 end /clone=IMAGE-643293 /clone_end=5 /gb=AA189890 /gi=1776532 /ug=Mm.34876 /len=344	0.6	0.6
101106_at	Cluster Incl AI853331:UI-M-BH0-air-a-07-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-air-a-07-0-UI /clone_end=3 /gb=AI853331 /gi=5497237 /ug=Mm.7514 /len=347	0.5	0.6
99133_at	Cluster Incl X14309:Antigen identified by monoclonal antibodies 4F2 /cds=(92,1672) /gb=X14309 /gi=49749 /ug=Mm.4114 /len=1828	0.5	0.6
101963_at	Cluster Incl X06086:Cathepsin L /cds=(68,1072) /gb=X06086 /gi=53046 /ug=Mm.930 /len=1374	0.5	0.6
100499_at	Cluster Incl D29797:Mouse mRNA for syntaxin 3A, complete cds /cds=(103,972) /gb=D29797 /gi=924267 /ug=Mm.5122 /len=1073	1.1	0.5
97819_at	Cluster Incl AI843119:UI-M-AK1-aes-f-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AK1-aes-f-05-0-UI /clone_end=3 /gb=AI843119 /gi=5477332 /ug=Mm.282 /len=199	0.9	0.5
104343_f_at	Cluster Incl AI845798:UI-M-AQ1-aeb-h-07-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AQ1-aeb-h-07-0-UI /clone_end=3 /gb=AI845798 /gi=5489704 /ug=Mm.22526 /len=184	0.6	0.5
104554_at	Cluster Incl L25674:Mus musculus ear-2 transcription factor mRNA, complete cds /cds=(113,1282) /gb=L25674 /gi=409757 /ug=Mm.2376 /len=1643	0.6	0.5
101926_at	Cluster Incl L41495:Mus musculus protein-serine/threonine kinase (pim-2) mRNA, complete cds /cds=UNKNOWN /gb=L41495 /gi=765065 /ug=Mm.932 /len=2039	0.6	0.5
161050_at	Cluster Incl AI504506:vo06h07.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1040701 /clone_end=3 /gb=AI504506 /gi=4402357 /ug=Mm.4868 /len=187 /NOTE=replacement for probe set(s) 92928_at on MG-U74A	0.6	0.5
103888_at	Cluster Incl AA636171:vn15d02.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1021251 /clone_end=5 /gb=AA636171 /gi=2559950 /ug=Mm.21285 /len=392	0.5	0.5
101451_at	Cluster Incl AF038939:Mus musculus zinc finger protein (Peg3) mRNA, complete cds /cds=(13,4728) /gb=AF038939 /gi=2791677 /ug=Mm.7952 /len=5560	-0.5	-0.6
98330_at	Cluster Incl D70849:Zinc finger protein of the cerebellum 3 /cds=(538,1938) /gb=D70849 /gi=1345414 /ug=Mm.4265 /len=3509	-0.8	-0.7
96684_at	Cluster Incl AI846123:UI-M-AN1-afj-a-11-0-UI.s2 Mus musculus cDNA, 3 end /clone=UI-M-AN1-afj-a-11-0-UI /clone_end=3 /gb=AI846123 /gi=5490029 /ug=Mm.27453 /len=341	-0.8	-0.7
104548_at	Cluster Incl Y15443:Mus musculus mRNA for 50C15 protein /cds=(20,454) /gb=Y15443 /gi=2624230 /ug=Mm.23697 /len=721	-0.9	-0.8
99034_at	Cluster Incl Y15001:Mus musculus mRNA for iroquois homeobox protein 3 /cds=(0,1523) /gb=Y15001 /gi=2765437 /ug=Mm.39039 /len=1937	-1	-0.9
98817_at	Cluster Incl Z29532:M.musculus mRNA for follistatin /cds=(0,1031) /gb=Z29532 /gi=488368 /ug=Mm.4913 /len=1123	-0.6	-1
104716_at	Cluster Incl X60367:Retinol binding protein 1, cellular /cds=UNKNOWN /gb=X60367 /gi=50547 /ug=Mm.2450 /len=2633	-1	-1
93941_at	Cluster Incl X51683:Brachyury /cds=(108,1418) /gb=X51683 /gi=55053 /ug=Mm.913 /len=2046	-1.4	-1.4
92931_at	Cluster Incl X80903:Delta-like 1 homolog (Drosophila) /cds=(13,2181) /gb=X80903 /gi=806569 /ug=Mm.4875 /len=2857	-2	-1.5
97386_at	Cluster Incl AI853294:UI-M-BH0-ajl-f-03-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-ajl-f-03-0-UI /clone_end=3 /gb=AI853294 /gi=5497200 /ug=Mm.29789 /len=413	-1.5	-1.6
160254_at	Cluster Incl AW123191:UI-M-BH2.1-apg-b-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-apg-b-09-0-UI /clone_end=3 /gb=AW123191 /gi=6098761 /ug=Mm.27846 /len=339 /NOTE=replacement for probe set(s) 97245_at on MG-U74A	-1.6	-1.7

93611_at	Cluster Incl U57331:T-box 6 /cds=(24,1646) /gb=U57331 /gi=1620601 /ug=Mm.727 /len=1712	-1.6	-1.8
93888_at	Cluster Incl X53063:Homeo box B1 /cds=(95,988) /gb=X53063 /gi=51398 /ug=Mm.890 /len=1526	-1.7	-1.8
102667_at	Cluster Incl X56842:Wingless-related MMTV integration site 3A /cds=(128,1186) /gb=X56842 /gi=55433 /ug=Mm.1367 /len=2814	-2.9	-3.2
98028_at	Cluster Incl M63649:Twist gene homolog, (Drosophila) /cds=(166,786) /gb=M63649 /gi=202243 /ug=Mm.3280 /len=1485	-3.2	-3.6
94200_at	Cluster Incl Z48800:Gastrulation brain homeobox 2 /cds=(421,1467) /gb=Z48800 /gi=755766 /ug=Mm.1306 /len=2126	-5.4	-4.4
95297_at	Cluster Incl M22115:Homeo box A1 /cds=(80,1075) /gb=M22115 /gi=193047 /ug=Mm.197 /len=2216	-5.1	-4.5
103477_at	Cluster Incl M80463:Caudal type homeo box 1 /cds=(0,578) /gb=M80463 /gi=402307 /ug=Mm.21968 /len=579	-4.2	-4.9
96038_at	Cluster Incl AI840339:UI-M-AJ0-abd-g-01-0-UI.s2 Mus musculus cDNA, 3 end /clone=UI-M-AJ0-abd-g-01-0-UI /clone_end=3 /gb=AI840339 /gi=5474552 /ug=Mm.2587 /len=497	1	3.2
95954_at	Cluster Incl AA437728:vd19h10.s1 Mus musculus cDNA, 5 end /clone=IMAGE-793027 /clone_end=5 /gb=AA437728 /gi=2142642 /ug=Mm.24927 /len=159	0.9	3.2
160401_r_at	Cluster Incl AI931748:ul65b03.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2135405 /clone_end=3 /gb=AI931748 /gi=5668233 /ug=Mm.30266 /len=519 /NOTE=replacement for probe set(s) 97457_at on MG-U74A	1.9	3
103795_f_at	Cluster Incl AA986114:uc81h03.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1432085 /clone_end=3 /gb=AA986114 /gi=3167989 /ug=Mm.24982 /len=580	1.2	2.9
95511_at	Cluster Incl X69902:Integrin alpha 6 /cds=(181,3402) /gb=X69902 /gi=408127 /ug=Mm.25232 /len=3756	0.9	2.9
104419_at	Cluster Incl AI132380:ue24a03.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1481260 /clone_end=3 /gb=AI132380 /gi=3602396 /ug=Mm.28928 /len=441	0.7	2.9
96868_at	Cluster Incl AI196896:ui55b05.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1886289 /clone_end=5 /gb=AI196896 /gi=3749502 /ug=Mm.30063 /len=1011	0.5	2.7
103806_at	Cluster Incl AF064984:Low density lipoprotein-related protein 5 /cds=(112,4956) /gb=AF064984 /gi=3641528 /ug=Mm.20876 /len=5119	0.5	2.4
102959_at	Cluster Incl U61363:Mus musculus groucho-related gene 4 protein (Grg4) mRNA, partial cds /cds=(0,1733) /gb=U61363 /gi=4028901 /ug=Mm.17915 /len=1930	0.6	2.2
92430_at	Cluster Incl AW045710:UI-M-BH1-akq-e-01-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-akq-e-01-0-UI /clone_end=3 /gb=AW045710 /gi=5906239 /ug=Mm.4152 /len=446	1.1	1.6
102232_at	Cluster Incl AI850740:UI-M-BG1-ail-g-10-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BG1-ail-g-10-0-UI /clone_end=3 /gb=AI850740 /gi=5494646 /ug=Mm.1040 /len=404	0.6	1.3
97317_at	Cluster Incl AW122933:UI-M-BH2.1-apa-h-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-apa-h-09-0-UI /clone_end=3 /gb=AW122933 /gi=6098463 /ug=Mm.28107 /len=399	1.5	1.2
98000_at	Cluster Incl J04634:Lymphocyte antigen 64 /cds=(194,1915) /gb=J04634 /gi=191943 /ug=Mm.3177 /len=2111	1.1	1.1
160369_at	Cluster Incl AI849109:UI-M-AH1-agw-h-03-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AH1-agw-h-03-0-UI /clone_end=3 /gb=AI849109 /gi=5493015 /ug=Mm.29921 /len=374 /NOTE=replacement for probe set(s) 96312_at on MG-U74A	0.7	1.1
99378_f_at	Cluster Incl M18837:Mouse MHC class I Q4 beta-2-microglobulin (Qb-1) gene, complete cds /cds=(0,980) /gb=M18837 /gi=199323 /ug=Mm.56926 /len=981	0.6	1.1
104210_at	Cluster Incl AI839082:UI-M-AK0-adi-f-03-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AK0-adi-f-03-0-UI /clone_end=3 /gb=AI839082 /gi=5473295 /ug=Mm.2775 /len=212	1	1
103868_at	Cluster Incl AA681274:vr76e12.s1 Mus musculus cDNA, 5 end /clone=IMAGE-1134670 /clone_end=5 /gb=AA681274 /gi=2663414 /ug=Mm.21138 /len=412	0.7	0.9
103502_at	Cluster Incl AA866768:ud07g06.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1434490 /clone_end=5 /gb=AA866768 /gi=2962213 /ug=Mm.22367 /len=376	0.6	0.9
99501_at	Cluster Incl AA882416:vx44e09.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1278088 /clone_end=5 /gb=AA882416 /gi=2991527 /ug=Mm.41684 /len=571	0.5	0.9
95661_at	Cluster Incl L08115:CD9 antigen /cds=(54,734) /gb=L08115 /gi=388911 /ug=Mm.2956 /len=1130	0.5	0.9
96771_at	Cluster Incl AI006228:ua88d09.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1364561 /clone_end=5 /gb=AI006228 /gi=3215837 /ug=Mm.29023 /len=382	1	0.8
100095_at	Cluster Incl U37799:Scavenger receptor class B1 /cds=(50,1579) /gb=U37799 /gi=1167551 /ug=Mm.4603 /len=1785	0.9	0.8
95702_at	Cluster Incl AI461803:uc43c04.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1400742 /clone_end=3 /gb=AI461803 /gi=4315833 /ug=Mm.29697 /len=481	1.2	0.7
104714_at	Cluster Incl AW125299:UI-M-BH2.1-apy-c-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-apy-c-05-0-UI /clone_end=3 /gb=AW125299 /gi=6100829 /ug=Mm.24477 /len=374	0.6	0.7
103716_at	Cluster Incl AI851218:UI-M-BH0-ajx-g-06-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-ajx-g-06-0-UI /clone_end=3 /gb=AI851218 /gi=5495124 /ug=Mm.24160 /len=306	0.6	0.7
103377_at	Cluster Incl AW259788:um81b12.y1 Mus musculus cDNA, 5 end /clone=IMAGE-2317727 /clone_end=5 /gb=AW259788 /gi=6632769 /ug=Mm.18600 /len=507	0.5	0.7
162245_f_at	Cluster Incl AV332872:AV332872 Mus musculus cDNA, 3 end /clone=6330539N18 /clone_end=3 /gb=AV332872 /gi=6372924 /ug=Mm.99066 /len=268 /NOTE=replacement for probe set(s) 100253_f_at on MG-U74A	1.2	0.6
92644_s_at	Cluster Incl M12848:Mouse myb proto-oncogene mRNA encoding 71 kd myb protein, complete cds /cds=(161,2071) /gb=M12848 /gi=199934 /ug=Mm.1202 /len=3310	1	0.6
93953_at	Cluster Incl D89871:Mus musculus mRNA for serine protease, complete cds /cds=(244,2529) /gb=D89871 /gi=2696702 /ug=Mm.9431 /len=2614	0.7	0.6
102235_at	Cluster Incl X13945:Lung carcinoma myc related oncogene 1 /cds=(0,1106) /gb=X13945 /gi=53287 /ug=Mm.1055 /len=3076	0.7	0.6

97722_at	Cluster Incl AA879709:vv97e03.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1230364 /clone_end=5 /gb=AA879709 /gi=2988692 /ug=Mm.39052 /len=404	0.5	0.6
94461_at	Cluster Incl AI852144:UI-M-BH0-ajb-e-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-ajb-e-09-0-UI /clone_end=3 /gb=AI852144 /gi=5496055 /ug=Mm.28830 /len=425	0.5	0.6
96491_at	Cluster Incl AI035632:ue19f09.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1480841 /clone_end=3 /gb=AI035632 /gi=3259323 /ug=Mm.25185 /len=768	1.1	0.5
160904_at	Cluster Incl AI841484:UI-M-AH0-acy-c-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AH0-acy-c-05-0-UI /clone_end=3 /gb=AI841484 /gi=5475697 /ug=Mm.5166 /len=412 /NOTE=replacement for probe set(s) 100506_at on MG-U74A	0.9	0.5
92699_at	Cluster Incl AJ249198:Mus musculus mRNA for glycoprotein-associated amino acid transporter b0,+AT1 /cds=(326,1789) /gb=AJ249198 /gi=5824164 /ug=Mm.45874 /len=1930	0.7	0.5
103977_at	Cluster Incl AF087644:Coagulation factor X /cds=(0,1445) /gb=AF087644 /gi=3641315 /ug=Mm.2578 /len=1486	0.7	0.5
96781_at	Cluster Incl AI838293:UI-M-AO0-aby-c-04-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AO0-aby-c-04-0-UI /clone_end=3 /gb=AI838293 /gi=5472506 /ug=Mm.29072 /len=310	0.6	0.5
99591_i_at	Cluster Incl AB030505:Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds /cds=UNKNOWN /gb=AB030505 /gi=5668736 /ug=Mm.42795 /len=4190	0.6	0.5
96269_at	Cluster Incl AA716963:vu69f10.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1196683 /clone_end=5 /gb=AA716963 /gi=2729237 /ug=Mm.29847 /len=273	0.5	0.5
102370_at	Cluster Incl AA822174:vp36a09.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1078744 /clone_end=5 /gb=AA822174 /gi=2892042 /ug=Mm.1187 /len=329	0.5	0.5
103665_at	Cluster Incl AW122523:UI-M-BH2.2-aox-b-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.2-aox-b-05-0-UI /clone_end=3 /gb=AW122523 /gi=6098047 /ug=Mm.20697 /len=423	0.5	0.5
97013_f_at	Cluster Incl AW046124:UI-M-BH1-alf-e-03-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-alf-e-03-0-UI /clone_end=3 /gb=AW046124 /gi=5906653 /ug=Mm.88950 /len=249	0.5	0.5
100600_at	Cluster Incl M58661:CD24a antigen /cds=(72,302) /gb=M58661 /gi=198985 /ug=Mm.6417 /len=1800	-0.5	-0.5
100407_at	Cluster Incl L38580:Galanin /cds=(0,374) /gb=L38580 /gi=927115 /ug=Mm.4655 /len=553	-0.5	-0.5
95016_at	Cluster Incl D50086:Mouse mRNA for neuropilin, complete cds /cds=(347,3118) /gb=D50086 /gi=1783300 /ug=Mm.27448 /len=3652	-0.5	-0.5
101001_at	Cluster Incl AI647612:uk41h01.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1971601 /clone_end=3 /gb=AI647612 /gi=4726290 /ug=Mm.6766 /len=524	-0.7	-0.5
103628_at	Cluster Incl D16503:Lymphoid enhancer binding factor 1 /cds=(1804,2658) /gb=D16503 /gi=391762 /ug=Mm.2029 /len=2740	-0.5	-0.6
94449_at	Cluster Incl AI854522:UI-M-BH0-ajj-d-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-ajj-d-05-0-UI /clone_end=3 /gb=AI854522 /gi=5498428 /ug=Mm.28785 /len=358	-0.5	-0.6
97509_f_at	Cluster Incl U22324:Mus musculus fibroblast growth factor receptor-1 mRNA, long isoform precursor, complete cds /cds=(57,2525) /gb=U22324 /gi=722340 /ug=Mm.3157 /len=2526	-0.6	-0.6
97520_s_at	Cluster Incl X83569:Neuronatin /cds=(66,230) /gb=X83569 /gi=619499 /ug=Mm.3210 /len=1102	-0.7	-0.6
101973_at	Cluster Incl Y15163:Mus musculus mRNA for mrg1 protein /cds=(219,1028) /gb=Y15163 /gi=3059126 /ug=Mm.9524 /len=1943	-0.7	-0.7
100403_at	Cluster Incl AA839903:vw65f04.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1259839 /clone_end=5 /gb=AA839903 /gi=2916497 /ug=Mm.46514 /len=250	-0.8	-0.7
92997_g_at	Cluster Incl D49473:SRY-box containing gene 17 /cds=(642,1517) /gb=D49473 /gi=1487865 /ug=Mm.5080 /len=1984	-0.8	-0.7
98419_at	Cluster Incl Z15103:Mesenchyme homeobox 1 /cds=UNKNOWN /gb=Z15103 /gi=57939 /ug=Mm.3404 /len=2182	-1	-0.7
98852_at	Cluster Incl X97581:M.musculus mRNA for spalt transcription factor /cds=(0,3972) /gb=X97581 /gi=1296844 /ug=Mm.5089 /len=4126	-0.6	-0.8
102833_at	Cluster Incl AW046220:UI-M-BH1-akw-h-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-akw-h-08-0-UI /clone_end=3 /gb=AW046220 /gi=5906749 /ug=Mm.14547 /len=383	-0.7	-0.8
100127_at	Cluster Incl M35523:Cellular retinoic acid binding protein II /cds=(115,531) /gb=M35523 /gi=192705 /ug=Mm.4757 /len=868	-0.8	-0.8
97497_at	Cluster Incl Z11886:Notch gene homolog 1, (Drosophila) /cds=(78,7673) /gb=Z11886 /gi=288502 /ug=Mm.31255 /len=8064	-1.3	-0.8
93724_at	Cluster Incl AI596034:uk22a01.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1969704 /clone_end=3 /gb=AI596034 /gi=4605082 /ug=Mm.86922 /len=516	-0.5	-0.9
94400_at	Cluster Incl AI843094:UI-M-AK1-aes-c-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AK1-aes-c-08-0-UI /clone_end=3 /gb=AI843094 /gi=5477307 /ug=Mm.25783 /len=349	-0.6	-0.9
97977_at	Cluster Incl AA645293:vs81a07.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1152660 /clone_end=5 /gb=AA645293 /gi=2571722 /ug=Mm.3116 /len=276	-0.9	-0.9
99086_g_at	Cluster Incl AI021421:ub12a08.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1366742 /clone_end=5 /gb=AI021421 /gi=3235757 /ug=Mm.38976 /len=470	-1.3	-0.9
94036_at	Cluster Incl AI844806:UI-M-AH1-agx-b-02-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AH1-agx-b-02-0-UI /clone_end=3 /gb=AI844806 /gi=5488712 /ug=Mm.21921 /len=404	-0.6	-1
104672_at	Cluster Incl U68058:Secreted frizzled-related sequence protein 3 /cds=(12,983) /gb=U68058 /gi=1688096 /ug=Mm.3246 /len=2176	-1.1	-1
98831_at	Cluster Incl L13204:HNF-3/forkhead homolog 4 /cds=(153,1418) /gb=L13204 /gi=550487 /ug=Mm.4985 /len=2427	-1.2	-1
98427_s_at	Cluster Incl M57999:Nuclear factor of kappa light chain gene enhancer in B-cells 1, p105 /cds=(291,3206) /gb=M57999 /gi=201931 /ug=Mm.3420 /len=3892	-1.3	-1.1
94117_f_at	Cluster Incl AF026465:Putative neuronal cell adhesion molecule /cds=(226,2607) /gb=AF026465 /gi=3068591 /ug=Mm.10689 /len=3146	-1.2	-1.2

98108_at	Cluster Incl X15789:Murine CRABP mRNA for cellular retinoic acid binding protein /cds=(0,413) /gb=X15789 /gi=49659 /ug=Mm.34797 /len=647	-1.5	-1.3
94813_at	Cluster Incl X65128:Growth arrest specific 1 /cds=(424,1578) /gb=X65128 /gi=51045 /ug=Mm.22701 /len=2961	-1	-1.4
103460_at	Cluster Incl AI849939:UI-M-BG0-ahz-g-03-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BG0-ahz-g-03-0-UI /clone_end=3 /gb=AI849939 /gi=5493845 /ug=Mm.21697 /len=440	-1.9	-1.5
99390_at	Cluster Incl M89798:Wingless-related MMTV integration site 5A /cds=(550,1689) /gb=M89798 /gi=202403 /ug=Mm.56963 /len=1690	-1.6	-1.8
102755_at	Cluster Incl AB016496:Mus musculus mRNA for intelectin, complete cds /cds=(79,1020) /gb=AB016496 /gi=3357908 /ug=Mm.12924 /len=1178	-2.8	-2.8
99361_at	Cluster Incl Z68889:M.musculus mRNA for wnt-8D protein /cds=(56,1120) /gb=Z68889 /gi=1419029 /ug=Mm.558 /len=1747	-2.4	-3
97742_s_at	Cluster Incl D12483:Fibroblast growth factor 8 /cds=(199,1005) /gb=D12483 /gi=220326 /ug=Mm.4012 /len=1178	1.7	4
162276_i_at	Cluster Incl AV367855:AV367855 Mus musculus cDNA, 3 end /clone=8430438I18 /clone_end=3 /gb=AV367855 /gi=6415502 /ug=Mm.99631 /len=198 /NOTE=replacement for probe set(s) 100646_f_at on MG-U74A	1.8	1.5
97413_at	Cluster Incl AI121305:uc30b06.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1399475 /clone_end=5 /gb=AI121305 /gi=3521629 /ug=Mm.29959 /len=358	3	0.7
160702_at	Cluster Incl AA791885:vs54g07.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1150140 /clone_end=5 /gb=AA791885 /gi=2854840 /ug=Mm.23713 /len=390 /NOTE=replacement for probe set(s) 104552_at on MG-U74A	0.5	0.6
96841_at	Cluster Incl AW046627:UI-M-BH1-ald-c-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-ald-c-09-0-UI /clone_end=3 /gb=AW046627 /gi=5907156 /ug=Mm.30018 /len=268	0.5	0.5
129147_r_at	Cluster Incl AI931796:ul66a05.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2135504 /clone_end=3 /gb=AI931796 /gi=5668281 /ug=Mm.19539 /len=263	0.9	0.7
130491_at	Cluster Incl AI853281:UI-M-BH0-ajl-e-01-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-ajl-e-01-0-UI /clone_end=3 /gb=AI853281 /gi=5497187 /ug=Mm.41901 /len=353	0.6	1
130494_f_at	Cluster Incl AI891509:ul59e01.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2123352 /clone_end=3 /gb=AI891509 /gi=5597411 /ug=Mm.41961 /len=504	0.5	0.5
131000_f_at	Cluster Incl AI154242:ud30f03.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1447421 /clone_end=5 /gb=AI154242 /gi=3682711 /ug=Mm.28880 /len=389	0.8	0.8
131216_f_at	Cluster Incl AI463306:vw61a06.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1248274 /clone_end=3 /gb=AI463306 /gi=4317336 /ug=Mm.23689 /len=455	1.2	0.7
138014_at	Cluster Incl AI846692:UI-M-AN1-afi-f-02-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AN1-afi-f-02-0-UI /clone_end=3 /gb=AI846692 /gi=5490598 /ug=Mm.39488 /len=257	1.2	0.9
141090_f_at	Cluster Incl AA725961:vu85f09.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1198217 /clone_end=5 /gb=AA725961 /gi=2743668 /ug=Mm.76286 /len=287	0.6	0.7
165449_f_at	Cluster Incl AI848527:UI-M-AP1-agf-e-12-0-UI.s2 Mus musculus cDNA, 3 end /clone=UI-M-AP1-agf-e-12-0-UI /clone_end=3 /gb=AI848527 /gi=5492433 /ug=Mm.32920 /len=387 /NOTE=replacement for probe set(s) 132394_f_at on MG-U74C	0.5	0.7
165599_at	Cluster Incl AW060997:UI-M-BH1-amn-d-02-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-amn-d-02-0-UI /clone_end=3 /gb=AW060997 /gi=6008748 /ug=Mm.23587 /len=260 /NOTE=replacement for probe set(s) 131211_i_at, 131212_r_at on MG-U74C	0.6	0.5
165601_f_at	Cluster Incl AA021940:mh83d03.r1 Mus musculus cDNA, 5 end /clone=IMAGE-457541 /clone_end=5 /gb=AA021940 /gi=1485705 /ug=Mm.23666 /len=424 /NOTE=replacement for probe set(s) 131215_f_at on MG-U74C	0.9	0.9
165656_i_at	Cluster Incl AI448522:mp66c10.x1 Mus musculus cDNA, 3 end /clone=IMAGE-574194 /clone_end=3 /gb=AI448522 /gi=4283309 /ug=Mm.32022 /len=168 /NOTE=replacement for probe set(s) 130984_r_at on MG-U74C	0.9	0.9
165677_at	Cluster Incl AI876331:uk59h01.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1973329 /clone_end=5 /gb=AI876331 /gi=5550380 /ug=Mm.33150 /len=306 /NOTE=replacement for probe set(s) 130944_at on MG-U74C	0.5	0.5
165695_at	Cluster Incl AI527248:uj50e02.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1923386 /clone_end=3 /gb=AI527248 /gi=4441383 /ug=Mm.33803 /len=540 /NOTE=replacement for probe set(s) 130906_at on MG-U74C	0.7	0.9
165915_i_at	Cluster Incl AV228304:AV228304 Mus musculus cDNA, 3 end /clone=4432415C24 /clone_end=3 /gb=AV228304 /gi=6180823 /ug=Mm.46240 /len=277 /NOTE=replacement for probe set(s) 130223_r_at on MG-U74C	0.7	0.5
166226_f_at	Cluster Incl AV225951:AV225951 Mus musculus cDNA, 3 end /clone=3830432J18 /clone_end=3 /gb=AV225951 /gi=6177266 /ug=Mm.77420 /len=236 /NOTE=replacement for probe set(s) 128528_f_at on MG-U74C	0.5	0.9
166567_f_at	Cluster Incl AV150568:AV150568 Mus musculus cDNA /clone=2900006M09 /clone_end=3 /gb=AV150568 /gi=5355774 /ug=Mm.100399 /len=270 /NOTE=replacement for probe set(s) 128980_f_at on MG-U74C	-0.8	-0.7
167118_f_at	Cluster Incl AV020777:AV020777 Mus musculus cDNA /clone=1190020D07 /clone_end=3 /gb=AV020777 /gi=4797769 /ug=Mm.45800 /len=198 /NOTE=replacement for probe set(s) 140018_s_at on MG-U74C	0.5	0.6
167188_at	Cluster Incl AA673840:vo82f02.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1065627 /clone_end=5 /gb=AA673840 /gi=2647122 /ug=Mm.45996 /len=498 /NOTE=replacement for probe set(s) 140217_at on MG-U74C	0.8	0.8
167192_at	Cluster Incl AW215882:up02f02.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2650875 /clone_end=3 /gb=AW215882 /gi=6526585 /ug=Mm.46043 /len=228 /NOTE=replacement for probe set(s) 140223_at on MG-U74C	0.5	0.6
167479_at	Cluster Incl AW124333:UI-M-BH2.1-apq-f-04-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-apq-f-04-0-UI /clone_end=3 /gb=AW124333 /gi=6099863 /ug=Mm.63694 /len=224 /NOTE=replacement for probe	0.9	1.3

	set(s) 140668_at on MG-U74C		
167965_f_at	Cluster Incl AV370033:AV370033 Mus musculus cDNA, 3 end /clone=9030206H02 /clone_end=3 /gb=AV370033 /gi=6417680 /ug=Mm.85143 /len=247 /NOTE=replacement for probe set(s) 133630_r_at on MG-U74C	0.8	0.6
168454_f_at	Cluster Incl AV164866:AV164866 Mus musculus cDNA /clone=3110030E14 /clone_end=3 /gb=AV164866 /gi=5371303 /ug=Mm.95688 /len=301 /NOTE=replacement for probe set(s) 135506_f_at, 135507_r_at on MG-U74C	0.6	0.6
170064_f_at	Cluster Incl AV305824:AV305824 Mus musculus cDNA, 3 end /clone=5730533E06 /clone_end=3 /gb=AV305824 /gi=6338338 /ug=Mm.74027 /len=320 /NOTE=replacement for probe set(s) 131025_f_at on MG-U74C	0.5	0.6
170808_s_at	Cluster Incl AV333550:AV333550 Mus musculus cDNA, 3 end /clone=6330548H01 /clone_end=3 /gb=AV333550 /gi=6373602 /ug=Mm.97546 /len=325 /NOTE=replacement for probe set(s) 132606_at on MG-U74C	0.6	0.5
129046_f_at	Cluster Incl AA118152:mn11b12.r1 Mus musculus cDNA, 5 end /clone=IMAGE-537599 /clone_end=5 /gb=AA118152 /gi=1673183 /ug=Mm.12130 /len=184	0.5	1.1
129297_at	Cluster Incl AA265229:mu66d04.r1 Mus musculus cDNA, 5 end /clone=IMAGE-644359 /clone_end=5 /gb=AA265229 /gi=1901439 /ug=Mm.24297 /len=415	0.5	1.3
133204_at	Cluster Incl AU044066:AU044066 Mus musculus cDNA, 3 end /clone=J0914D09 /clone_end=3 /gb=AU044066 /gi=3979541 /ug=Mm.17774 /len=419	0.9	2.5
136134_at	Cluster Incl AI836316:UI-M-AQ0-aac-h-07-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AQ0-aac-h-07-0-UI /clone_end=3 /gb=AI836316 /gi=5470524 /ug=Mm.35216 /len=418	0.6	1.2
165792_at	Cluster Incl AI957090:ul75a07.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2136372 /clone_end=3 /gb=AI957090 /gi=5749799 /ug=Mm.42174 /len=479 /NOTE=replacement for probe set(s) 130497_at on MG-U74C	0.9	1.1
128830_r_at	Cluster Incl AA672352:vk91a11.s1 Mus musculus cDNA, 5 end /clone=IMAGE-962012 /clone_end=5 /gb=AA672352 /gi=2644569 /ug=Mm.100122 /len=143	3.1	3.4
129326_at	Cluster Incl AI605536:vo35e07.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1051908 /clone_end=3 /gb=AI605536 /gi=4614703 /ug=Mm.24820 /len=234	2.6	1.3
129347_at	Cluster Incl AI591631:vt35h03.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1165109 /clone_end=3 /gb=AI591631 /gi=4600679 /ug=Mm.25234 /len=239	2.8	2.1
129928_f_at	Cluster Incl AW214436:uo48b10.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2645755 /clone_end=3 /gb=AW214436 /gi=6520959 /ug=Mm.89542 /len=620	1	0.8
130779_f_at	Cluster Incl AI552636:vx31g10.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1276866 /clone_end=3 /gb=AI552636 /gi=4484999 /ug=Mm.34872 /len=365	0.9	1.6
130994_at	Cluster Incl AW124327:UI-M-BH2.1-apq-e-10-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-apq-e-10-0-UI /clone_end=3 /gb=AW124327 /gi=6099857 /ug=Mm.28417 /len=239	3	1.7
132361_at	Cluster Incl AI642127:uc46b09.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1401017 /clone_end=3 /gb=AI642127 /gi=4720602 /ug=Mm.45147 /len=618	0.6	0.9
132794_at	Cluster Incl AI593288:vu15g03.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1180756 /clone_end=3 /gb=AI593288 /gi=4602336 /ug=Mm.80567 /len=461	3.3	0.9
133037_at	Cluster Incl AI196550:ui65c04.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1887270 /clone_end=3 /gb=AI196550 /gi=3749156 /ug=Mm.17489 /len=457	2.8	1.3
133830_at	Cluster Incl AI428510:mo37e12.x1 Mus musculus cDNA, 3 end /clone=IMAGE-555790 /clone_end=3 /gb=AI428510 /gi=4274436 /ug=Mm.27109 /len=467	0.6	1.1
134223_at	Cluster Incl AI647230:vn60a10.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1025562 /clone_end=5 /gb=AI647230 /gi=4725705 /ug=Mm.31085 /len=319	2.5	3.3
134260_at	Cluster Incl AI549876:vw97d02.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1262883 /clone_end=3 /gb=AI549876 /gi=4482239 /ug=Mm.35154 /len=452	2.8	2.7
134932_at	Cluster Incl AI592958:vu88e03.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1209244 /clone_end=3 /gb=AI592958 /gi=4602006 /ug=Mm.87358 /len=449	0.5	0.5
135278_at	Cluster Incl AI852823:UI-M-BH0-ajk-a-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-ajk-a-05-0-UI /clone_end=3 /gb=AI852823 /gi=5496729 /ug=Mm.39241 /len=433	0.8	4
135760_at	Cluster Incl AI852713:UI-M-BH0-aji-f-04-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-aji-f-04-0-UI /clone_end=3 /gb=AI852713 /gi=5496619 /ug=Mm.39664 /len=408	1.2	2.1
136554_r_at	Cluster Incl AI505113:vq69b08.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1107543 /clone_end=3 /gb=AI505113 /gi=4402964 /ug=Mm.35709 /len=165	0.6	1.9
136630_i_at	Cluster Incl AI596386:vj55e07.x1 Mus musculus cDNA, 3 end /clone=IMAGE-932964 /clone_end=3 /gb=AI596386 /gi=4605434 /ug=Mm.36568 /len=226	0.6	1.2
137047_at	Cluster Incl AI607298:uc40a04.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1400430 /clone_end=3 /gb=AI607298 /gi=4616465 /ug=Mm.37249 /len=532	0.9	1.2
138408_at	Cluster Incl AW124077:UI-M-BH2.1-apn-g-07-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-apn-g-07-0-UI /clone_end=3 /gb=AW124077 /gi=6099607 /ug=Mm.65393 /len=433	1.6	3.1
139602_at	Cluster Incl AI649058:uk34f12.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1970927 /clone_end=3 /gb=AI649058 /gi=4729892 /ug=Mm.49585 /len=563	0.7	1.9
140759_at	Cluster Incl AI646554:vv55e10.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1226346 /clone_end=3 /gb=AI646554 /gi=4725029 /ug=Mm.66314 /len=180	0.7	1.4
141010_at	Cluster Incl AI643790:vi45f06.x1 Mus musculus cDNA, 3 end /clone=IMAGE-906755 /clone_end=3 /gb=AI643790 /gi=4722265 /ug=Mm.74094 /len=156	-2.1	-2
165460_at	Cluster Incl AI853126:UI-M-BH0-ajf-e-12-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-ajf-e-12-0-UI /clone_end=3 /gb=AI853126 /gi=5497032 /ug=Mm.39303 /len=293 /NOTE=replacement for probe set(s) 132371_at on MG-U74C	1.9	3.6
165637_i_at	Cluster Incl AI591601:vt45d09.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1166033 /clone_end=3 /gb=AI591601 /gi=4600649 /ug=Mm.28769 /len=559 /NOTE=replacement for probe set(s) 130996_at on MG-	4.6	4.4

	U74C		
165641_at	Cluster Incl AW122960:UI-M-BH2.1-aoz-g-01-0-UI.s2 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-aoz-g-01-0-UI /clone_end=3 /gb=AW122960 /gi=6098490 /ug=Mm.30820 /len=633 /NOTE=replacement for probe set(s) 131009_at on MG-U74C	1.5	1.3
165935_at	Cluster Incl AV062770:AV062770 Mus musculus cDNA /clone=2010004G12 /clone_end=3 /gb=AV062770 /gi=5182598 /ug=Mm.46323 /len=272 /NOTE=replacement for probe set(s) 130201_at on MG-U74C	2.4	1.1
165956_f_at	Cluster Incl AV076385:AV076385 Mus musculus cDNA /clone=2210017P08 /clone_end=3 /gb=AV076385 /gi=5196213 /ug=Mm.46390 /len=339 /NOTE=replacement for probe set(s) 130056_f_at on MG-U74C	4.4	0.8
166030_i_at	Cluster Incl AV269998:AV269998 Mus musculus cDNA, 3 end /clone=4930546J23 /clone_end=3 /gb=AV269998 /gi=6258035 /ug=Mm.50649 /len=231 /NOTE=replacement for probe set(s) 129811_f_at on MG-U74C	2	5.3
166437_f_at	Cluster Incl AV318471:AV318471 Mus musculus cDNA, 3 end /clone=5932402C16 /clone_end=3 /gb=AV318471 /gi=6283888 /ug=Mm.94758 /len=302 /NOTE=replacement for probe set(s) 128806_at on MG-U74C	3.4	3.3
166740_at	Cluster Incl AA624602:vn82g09.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1038496 /clone_end=5 /gb=AA624602 /gi=2528478 /ug=Mm.34419 /len=334 /NOTE=replacement for probe set(s) 135689_at on MG-U74C	0.5	3
167004_r_at	Cluster Incl AI558098:vw66d04.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1259911 /clone_end=3 /gb=AI558098 /gi=4508336 /ug=Mm.45448 /len=395 /NOTE=replacement for probe set(s) 139756_f_at, 139757_r_at on MG-U74C	3.5	4
167216_f_at	Cluster Incl AV023830:AV023830 Mus musculus cDNA /clone=1190033O23 /clone_end=3 /gb=AV023830 /gi=4800822 /ug=Mm.46211 /len=273 /NOTE=replacement for probe set(s) 140252_f_at on MG-U74C	1.1	0.7
167237_f_at	Cluster Incl AV066368:AV066368 Mus musculus cDNA /clone=2010109A18 /clone_end=3 /gb=AV066368 /gi=5186196 /ug=Mm.46351 /len=291 /NOTE=replacement for probe set(s) 140274_f_at on MG-U74C	0.6	0.9
167608_f_at	Cluster Incl AV235587:AV235587 Mus musculus cDNA, 3 end /clone=4732405J01 /clone_end=3 /gb=AV235587 /gi=6188100 /ug=Mm.71217 /len=266 /NOTE=replacement for probe set(s) 140910_f_at on MG-U74C	1.1	1.4
167758_at	Cluster Incl AI644260:vv85d02.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1229187 /clone_end=3 /gb=AI644260 /gi=4722735 /ug=Mm.77756 /len=289 /NOTE=replacement for probe set(s) 141178_at on MG-U74C	0.5	0.7
167843_f_at	Cluster Incl AV321065:AV321065 Mus musculus cDNA, 3 end /clone=6030430K23 /clone_end=3 /gb=AV321065 /gi=6290898 /ug=Mm.80771 /len=244 /NOTE=replacement for probe set(s) 133069_f_at on MG-U74C	0.5	0.6
167853_f_at	Cluster Incl AV062553:AV062553 Mus musculus cDNA /clone=2010003L07 /clone_end=3 /gb=AV062553 /gi=5182381 /ug=Mm.81318 /len=271 /NOTE=replacement for probe set(s) 133083_f_at on MG-U74C	0.6	0.8
168371_f_at	Cluster Incl AV254276:AV254276 Mus musculus cDNA, 3 end /clone=4921508O09 /clone_end=3 /gb=AV254276 /gi=6241735 /ug=Mm.89140 /len=212 /NOTE=replacement for probe set(s) 135345_f_at on MG-U74C	0.6	0.8
168398_f_at	Cluster Incl AV266989:AV266989 Mus musculus cDNA, 3 end /clone=4930522F01 /clone_end=3 /gb=AV266989 /gi=6255026 /ug=Mm.91434 /len=204 /NOTE=replacement for probe set(s) 135420_f_at on MG-U74C	1.2	1
168426_f_at	Cluster Incl AV376588:AV376588 Mus musculus cDNA, 3 end /clone=9130211I04 /clone_end=3 /gb=AV376588 /gi=6424235 /ug=Mm.94255 /len=243 /NOTE=replacement for probe set(s) 135466_f_at on MG-U74C	2.7	3.6
168503_at	Cluster Incl AV379925:AV379925 Mus musculus cDNA, 3 end /clone=9230016F10 /clone_end=3 /gb=AV379925 /gi=6428934 /ug=Mm.98504 /len=234 /NOTE=replacement for probe set(s) 135821_at on MG-U74C	4.6	2.7
168542_f_at	Cluster Incl AV357712:AV357712 Mus musculus cDNA, 3 end /clone=7420408E21 /clone_end=3 /gb=AV357712 /gi=6404714 /ug=Mm.99369 /len=246 /NOTE=replacement for probe set(s) 135880_f_at on MG-U74C	2	2.8
170625_i_at	Cluster Incl AV309412:AV309412 Mus musculus cDNA, 3 end /clone=5730581I16 /clone_end=3 /gb=AV309412 /gi=6362447 /ug=Mm.95740 /len=342 /NOTE=replacement for probe set(s) 132247_at on MG-U74C	4.7	0.5
171194_at	Cluster Incl AV122288:AV122288 Mus musculus cDNA /clone=2610524A15 /clone_end=3 /gb=AV122288 /gi=5308015 /ug=Mm.48061 /len=295 /NOTE=replacement for probe set(s) 139066_at on MG-U74C	1.4	3.5
130826_at	Cluster Incl AU019726:AU019726 Mus musculus cDNA, 3 end /clone=J0521F07 /clone_end=3 /gb=AU019726 /gi=3375310 /ug=Mm.26180 /len=586	-3	-4.1
131812_at	Cluster Incl AW060633:UI-M-BH1-anq-h-06-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-anq-h-06-0-UI /clone_end=3 /gb=AW060633 /gi=6008384 /ug=Mm.76676 /len=431	-3.4	-2.9
135746_at	Cluster Incl AI850592:UI-M-BG1-aij-h-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BG1-aij-h-08-0-UI /clone_end=3 /gb=AI850592 /gi=5494498 /ug=Mm.39635 /len=385	-3.8	-0.9
104990_at	Cluster Incl AA681392:vr41c07.s1 Mus musculus cDNA, 5 end /clone=IMAGE-1123212 /clone_end=5 /gb=AA681392 /gi=2663532 /ug=Mm.34340 /len=440	1.1	0.7
105008_at	Cluster Incl AI563638:vx97c09.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1293904 /clone_end=3 /gb=AI563638 /gi=4522095 /ug=Mm.34550 /len=181	1.3	3.2
105198_at	Cluster Incl AA839576:vw97a03.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1262860 /clone_end=5 /gb=AA839576 /gi=2915671 /ug=Mm.35591 /len=330	1.6	1.5
105273_at	Cluster Incl AI854883:UI-M-BH0-akb-f-10-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-akb-f-10-0-UI /clone_end=3 /gb=AI854883 /gi=5498789 /ug=Mm.36537 /len=461	0.7	3.3
106064_at	Cluster Incl AA920012:vz25b08.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1327479 /clone_end=5 /gb=AA920012 /gi=3066791 /ug=Mm.22538 /len=387	0.5	0.5
106196_at	Cluster Incl AW060432:UI-M-BH1-anj-d-10-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-anj-d-10-0-UI /clone_end=3 /gb=AW060432 /gi=6008183 /ug=Mm.22817 /len=423	0.5	1

106204_at	Cluster Incl AI957179:ul76e06.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2136514 /clone_end=3 /gb=AI957179 /gi=5749888 /ug=Mm.22983 /len=536	0.5	0.5
106292_at	Cluster Incl AW123279:UI-M-BH2.1-apg-f-11-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-apg-f-11-0-UI /clone_end=3 /gb=AW123279 /gi=6098809 /ug=Mm.24020 /len=495	0.6	1.4
106294_at	Cluster Incl AI834916:UI-M-AN1-afe-f-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AN1-afe-f-08-0-UI /clone_end=3 /gb=AI834916 /gi=5469129 /ug=Mm.24036 /len=326	0.5	0.6
106475_at	Cluster Incl AI852981:UI-M-BH0-aiz-h-11-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-aiz-h-11-0-UI /clone_end=3 /gb=AI852981 /gi=5496887 /ug=Mm.41855 /len=385	0.6	0.7
106577_at	Cluster Incl AI849498:UI-M-AH1-agt-d-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AH1-agt-d-08-0-UI /clone_end=3 /gb=AI849498 /gi=5493404 /ug=Mm.24329 /len=379	1.7	0.9
106615_at	Cluster Incl AW208385:uo59g03.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2646868 /clone_end=3 /gb=AW208385 /gi=6514379 /ug=Mm.24624 /len=587	0.6	0.5
107154_f_at	Cluster Incl AW215571:up06a03.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2651212 /clone_end=3 /gb=AW215571 /gi=6526247 /ug=Mm.89024 /len=333	0.5	2.5
107491_at	Cluster Incl AW048191:UI-M-BH1-amc-e-02-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-amc-e-02-0-UI /clone_end=3 /gb=AW048191 /gi=5908720 /ug=Mm.45111 /len=455	0.7	0.5
107498_at	Cluster Incl AW047594:UI-M-BH1-akm-c-03-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-akm-c-03-0-UI /clone_end=3 /gb=AW047594 /gi=5908123 /ug=Mm.45131 /len=439	1	0.8
107621_at	Cluster Incl AA815487:vp20b09.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1069145 /clone_end=5 /gb=AA815487 /gi=2885083 /ug=Mm.27611 /len=389	3.8	0.5
108022_at	Cluster Incl AI845954:UI-M-AK1-aex-h-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AK1-aex-h-05-0-UI /clone_end=3 /gb=AI845954 /gi=5489860 /ug=Mm.27820 /len=317	0.5	0.5
108076_at	Cluster Incl AI836801:UI-M-AJ0-abc-h-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AJ0-abc-h-05-0-UI /clone_end=3 /gb=AI836801 /gi=5471014 /ug=Mm.28162 /len=292	0.7	0.6
108516_at	Cluster Incl AI851393:UI-M-BH0-akh-h-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-akh-h-08-0-UI /clone_end=3 /gb=AI851393 /gi=5495299 /ug=Mm.28435 /len=333	2.8	1
108780_at	Cluster Incl AI845395:UI-M-AO1-aej-a-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AO1-aej-a-05-0-UI /clone_end=3 /gb=AI845395 /gi=5489301 /ug=Mm.23265 /len=495	1	1.3
108784_at	Cluster Incl AI427138:mn38e12.x1 Mus musculus cDNA, 3 end /clone=IMAGE-540238 /clone_end=3 /gb=AI427138 /gi=4273064 /ug=Mm.23282 /len=397	0.9	0.6
108848_g_at	Cluster Incl AW261779:um92d07.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2332237 /clone_end=3 /gb=AW261779 /gi=6638592 /ug=Mm.65980 /len=494	0.5	0.6
109069_at	Cluster Incl AI255982:ui76b01.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1888297 /clone_end=3 /gb=AI255982 /gi=3863507 /ug=Mm.28756 /len=484	0.8	0.8
109133_at	Cluster Incl AW049475:UI-M-BH1-ams-f-06-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-ams-f-06-0-UI /clone_end=3 /gb=AW049475 /gi=5910004 /ug=Mm.28993 /len=222	0.7	0.6
109167_at	Cluster Incl AI466033:vw35b01.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1245769 /clone_end=5 /gb=AI466033 /gi=4320063 /ug=Mm.29148 /len=292	0.8	0.5
109332_at	Cluster Incl AW046226:UI-M-BH1-ala-a-07-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-ala-a-07-0-UI /clone_end=3 /gb=AW046226 /gi=5906755 /ug=Mm.23805 /len=430	0.5	0.8
109622_at	Cluster Incl AI594717:vv12g06.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1211482 /clone_end=3 /gb=AI594717 /gi=4603765 /ug=Mm.62046 /len=446	0.5	0.7
110008_at	Cluster Incl AW124842:UI-M-BH2.1-apk-f-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-apk-f-09-0-UI /clone_end=3 /gb=AW124842 /gi=6100372 /ug=Mm.25025 /len=506	0.5	0.6
110309_at	Cluster Incl AW121524:UI-M-BH2.2-aop-c-10-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.2-aop-c-10-0-UI /clone_end=3 /gb=AW121524 /gi=6096857 /ug=Mm.30208 /len=546	1.1	1.1
110446_at	Cluster Incl AA684172:vm68b07.s1 Mus musculus cDNA, 5 end /clone=IMAGE-1003381 /clone_end=5 /gb=AA684172 /gi=2670758 /ug=Mm.25725 /len=290	0.5	3.6
110467_at	Cluster Incl AI120654:ub71b06.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1383155 /clone_end=5 /gb=AI120654 /gi=3520978 /ug=Mm.25851 /len=487	0.8	0.5
110503_at	Cluster Incl AI481152:vg87a11.x1 Mus musculus cDNA, 3 end /clone=IMAGE-872924 /clone_end=3 /gb=AI481152 /gi=4374378 /ug=Mm.26159 /len=401	0.5	0.9
111347_at	Cluster Incl AI842321:UI-M-AM1-afz-b-04-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AM1-afz-b-04-0-UI /clone_end=3 /gb=AI842321 /gi=5476499 /ug=Mm.34081 /len=361	1.7	0.9
111359_at	Cluster Incl AW108291:um20f02.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2192859 /clone_end=3 /gb=AW108291 /gi=6079091 /ug=Mm.34119 /len=534	2.3	2.3
111494_at	Cluster Incl AI553403:vw52e01.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1247448 /clone_end=3 /gb=AI553403 /gi=4485766 /ug=Mm.27419 /len=416	0.6	0.6
111529_at	Cluster Incl AW048558:UI-M-BH1-alx-e-01-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-alx-e-01-0-UI /clone_end=3 /gb=AW048558 /gi=5909087 /ug=Mm.27612 /len=396	1.1	0.7
112209_at	Cluster Incl AW122818:UI-M-BH2.1-aoz-b-10-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-aoz-b-10-0-UI /clone_end=3 /gb=AW122818 /gi=6098348 /ug=Mm.87253 /len=318	2.2	2.9
112373_at	Cluster Incl AI840826:UI-M-AH0-adb-d-06-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AH0-adb-d-06-0-UI /clone_end=3 /gb=AI840826 /gi=5475039 /ug=Mm.38488 /len=363	0.6	0.7
112392_at	Cluster Incl AI834768:UI-M-AM0-ads-b-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AM0-ads-b-05-0-UI /clone_end=3 /gb=AI834768 /gi=5469001 /ug=Mm.38806 /len=320	0.7	3.7
112400_at	Cluster Incl AW060912:UI-M-BH1-anv-c-03-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-anv-c-03-0-UI /clone_end=3 /gb=AW060912 /gi=6008663 /ug=Mm.28607 /len=477	0.7	0.6
112405_at	Cluster Incl AI557974:vw69e08.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1260230 /clone_end=3 /gb=AI557974 /gi=4508212 /ug=Mm.28632 /len=284	0.7	0.5
112445_at	Cluster Incl AI156718:ue53g05.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1494872 /clone_end=5 /gb=AI156718 /gi=3685187 /ug=Mm.28937 /len=316	1.2	0.8

112828_at	Cluster Incl AW121214:UI-M-BH2.3-aok-d-07-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.3-aok-d-07-0-UI /clone_end=3 /gb=AW121214 /gi=6096547 /ug=Mm.41032 /len=478	0.6	0.6
112922_i_at	Cluster Incl AI173274:ue90g08.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1498430 /clone_end=3 /gb=AI173274 /gi=3720854 /ug=Mm.29644 /len=509	0.8	1.4
112955_at	Cluster Incl AW122703:UI-M-BH2.2-aot-c-01-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.2-aot-c-01-0-UI /clone_end=3 /gb=AW122703 /gi=6098233 /ug=Mm.29888 /len=466	0.9	0.7
113036_at	Cluster Incl AW120709:UI-M-BH2.3-anz-e-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.3-anz-e-08-0-UI /clone_end=3 /gb=AW120709 /gi=6096007 /ug=Mm.9868 /len=432	0.9	0.7
113265_at	Cluster Incl AA840143:ud01f02.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1433883 /clone_end=5 /gb=AA840143 /gi=2915852 /ug=Mm.30607 /len=394	0.5	3.8
113314_at	Cluster Incl AI840767:UI-M-AM0-adn-f-04-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AM0-adn-f-04-0-UI /clone_end=3 /gb=AI840767 /gi=5474980 /ug=Mm.30794 /len=399	1	4.3
113431_at	Cluster Incl AI121269:ue90f05.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1498401 /clone_end=5 /gb=AI121269 /gi=3521593 /ug=Mm.11226 /len=550	3	3.7
114032_f_at	Cluster Incl AI843759:UI-M-AN1-afc-b-03-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AN1-afc-b-03-0-UI /clone_end=3 /gb=AI843759 /gi=5477972 /ug=Mm.31827 /len=453	0.7	3.6
114629_at	Cluster Incl AW124408:UI-M-BH2.1-ape-d-11-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-ape-d-11-0-UI /clone_end=3 /gb=AW124408 /gi=6099938 /ug=Mm.85814 /len=212	0.5	0.6
114749_at	Cluster Incl AW107659:um22d07.x1 Mus musculus cDNA, 3 end /clone=IMAGE-2225293 /clone_end=3 /gb=AW107659 /gi=6078459 /ug=Mm.33503 /len=593	0.5	0.8
114845_s_at	Cluster Incl AI449745:mr67e01.x1 Mus musculus cDNA, 3 end /clone=IMAGE-602520 /clone_end=3 /gb=AI449745 /gi=4292152 /ug=Mm.34037 /len=482	1.1	1
115010_at	Cluster Incl AI848157:UI-M-AH1-agq-b-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AH1-agq-b-08-0-UI /clone_end=3 /gb=AI848157 /gi=5492063 /ug=Mm.11186 /len=446	0.9	1.1
115062_at	Cluster Incl AW122118:UI-M-BH2.2-aor-b-06-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.2-aor-b-06-0-UI /clone_end=3 /gb=AW122118 /gi=6097537 /ug=Mm.12730 /len=391	0.5	1.2
115066_at	Cluster Incl AI550177:mn21c02.y1 Mus musculus cDNA, 5 end /clone=IMAGE-538562 /clone_end=5 /gb=AI550177 /gi=4482540 /ug=Mm.12902 /len=588	1.1	0.6
115112_at	Cluster Incl AW050362:UI-M-BH1-ang-e-10-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-ang-e-10-0-UI /clone_end=3 /gb=AW050362 /gi=5910891 /ug=Mm.34129 /len=515	1.3	3.3
115347_at	Cluster Incl AI639571:vv48b08.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1225623 /clone_end=3 /gb=AI639571 /gi=4702680 /ug=Mm.17643 /len=360	0.7	0.5
115752_at	Cluster Incl AI837128:UI-M-AK0-adc-f-10-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AK0-adc-f-10-0-UI /clone_end=3 /gb=AI837128 /gi=5471341 /ug=Mm.20703 /len=332	0.6	0.5
115792_at	Cluster Incl AI510157:vy01c05.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1294184 /clone_end=5 /gb=AI510157 /gi=4409062 /ug=Mm.21630 /len=271	0.6	0.8
115820_at	Cluster Incl AI852255:UI-M-BH0-aje-a-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-aje-a-09-0-UI /clone_end=3 /gb=AI852255 /gi=5496161 /ug=Mm.34977 /len=365	0.8	0.6
116003_at	Cluster Incl AI594591:vo08f12.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1040879 /clone_end=5 /gb=AI594591 /gi=4603639 /ug=Mm.31072 /len=409	0.5	0.9
116312_at	Cluster Incl AW214291:uo45h06.x2 Mus musculus cDNA, 3 end /clone=IMAGE-2645531 /clone_end=3 /gb=AW214291 /gi=6520777 /ug=Mm.22496 /len=297	0.6	0.5
116418_at	Cluster Incl AA839780:vw51e12.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1247374 /clone_end=5 /gb=AA839780 /gi=2916374 /ug=Mm.37829 /len=439	0.5	0.5
116635_at	Cluster Incl AW061144:UI-M-BH1-anc-a-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-anc-a-09-0-UI /clone_end=3 /gb=AW061144 /gi=6008895 /ug=Mm.38313 /len=459	0.8	0.8
116837_at	Cluster Incl AI839054:UI-M-AK0-adi-b-04-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AK0-adi-b-04-0-UI /clone_end=3 /gb=AI839054 /gi=5473262 /ug=Mm.38847 /len=413	0.5	1.2
162562_at	Cluster Incl AI840292:UI-M-AH0-act-h-04-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AH0-act-h-04-0-UI /clone_end=3 /gb=AI840292 /gi=5474505 /ug=Mm.18818 /len=359 /NOTE=replacement for probe set(s) 106038_at on MG-U74B	0.5	0.8
162607_i_at	Cluster Incl AA655098:vq83g07.s1 Mus musculus cDNA, 5 end /clone=IMAGE-1108956 /clone_end=5 /gb=AA655098 /gi=2591252 /ug=Mm.24146 /len=344 /NOTE=replacement for probe set(s) 106307_r_at on MG-U74B	1.1	0.6
162690_at	Cluster Incl AW045453:UI-M-BH1-akr-h-02-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-akr-h-02-0-UI /clone_end=3 /gb=AW045453 /gi=5906022 /ug=Mm.27628 /len=326 /NOTE=replacement for probe set(s) 107625_at on MG-U74B	0.9	0.7
162704_i_at	Cluster Incl AW121177:UI-M-BH2.3-aok-a-04-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.3-aok-a-04-0-UI /clone_end=3 /gb=AW121177 /gi=6096510 /ug=Mm.28122 /len=448 /NOTE=replacement for probe set(s) 108063_at on MG-U74B	0.6	0.9
162728_at	Cluster Incl AI854587:UI-M-BH0-ake-b-01-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-ake-b-01-0-UI /clone_end=3 /gb=AI854587 /gi=5498493 /ug=Mm.28456 /len=464 /NOTE=replacement for probe set(s) 108522_at on MG-U74B	1.7	1.3
162843_at	Cluster Incl AW124799:UI-M-BH2.1-apk-a-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-apk-a-09-0-UI /clone_end=3 /gb=AW124799 /gi=6100329 /ug=Mm.34012 /len=438 /NOTE=replacement for probe set(s) 111330_at on MG-U74B	0.5	0.5
162869_at	Cluster Incl AI849131:UI-M-AJ1-agy-b-03-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AJ1-agy-b-03-0-UI /clone_end=3 /gb=AI849131 /gi=5493037 /ug=Mm.34614 /len=393 /NOTE=replacement for probe set(s) 111803_at on MG-U74B	3	1
162929_at	Cluster Incl AI843261:UI-M-AO1-aei-b-11-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AO1-aei-b-11-0-UI /clone_end=3 /gb=AI843261 /gi=5477474 /ug=Mm.39487 /len=331 /NOTE=replacement for probe set(s) 112789_at on MG-U74B	1.2	0.6
163015_at	Cluster Incl AA929443:vt30f05.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1164609 /clone_end=5 /gb AA929443 /gi 3078752 / g Mm 45844 /len 342 /NOTE replacement for probe set(s) 113929 at on MG	0.8	0.8

	/gb=AA929443 /gi=3078752 /ug=Mm.45844 /len=342 /NOTE=replacement for probe set(s) 113929_at on MG-U74B		
163262_at	Cluster Incl AI316329:uj99c11.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1958036 /clone_end=5 /gb=AI316329 /gi=4031596 /ug=Mm.26162 /len=469 /NOTE=replacement for probe set(s) 110959_at on MG-U74B	0.5	0.5
163489_at	Cluster Incl AI536506:vp05h01.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1067761 /clone_end=5 /gb=AI536506 /gi=4450641 /ug=Mm.35290 /len=457 /NOTE=replacement for probe set(s) 115868_at on MG-U74B	1	0.7
163626_at	Cluster Incl AI845529:UI-M-AO1-aek-e-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AO1-aek-e-08-0-UI /clone_end=3 /gb=AI845529 /gi=5489435 /ug=Mm.41519 /len=292 /NOTE=replacement for probe set(s) 117268_at on MG-U74B	0.5	1.1
164028_at	Cluster Incl AI550146:mn15e06.y1 Mus musculus cDNA, 5 end /clone=IMAGE-538018 /clone_end=5 /gb=AI550146 /gi=4482509 /ug=Mm.89772 /len=435 /NOTE=replacement for probe set(s) 112717_at on MG-U74B	0.7	0.6
164330_f_at	Cluster Incl AV246750:AV246750 Mus musculus cDNA, 3 end /clone=4832417M20 /clone_end=3 /gb=AV246750 /gi=6234209 /ug=Mm.55261 /len=255 /NOTE=replacement for probe set(s) 112527_f_at on MG-U74B	0.5	0.6
164467_f_at	Cluster Incl AV214487:AV214487 Mus musculus cDNA, 3 end /clone=2410136N07 /clone_end=3 /gb=AV214487 /gi=6155333 /ug=Mm.59365 /len=212 /NOTE=replacement for probe set(s) 113390_f_at on MG-U74B	1.8	0.8
164545_f_at	Cluster Incl AV296659:AV296659 Mus musculus cDNA, 3 end /clone=5730442M11 /clone_end=3 /gb=AV296659 /gi=6328678 /ug=Mm.62763 /len=283 /NOTE=replacement for probe set(s) 106367_f_at on MG-U74B	1	0.9
165359_f_at	Cluster Incl AV028174:AV028174 Mus musculus cDNA /clone=1300018H13 /clone_end=3 /gb=AV028174 /gi=4807784 /ug=Mm.52431 /len=261 /NOTE=replacement for probe set(s) 110910_f_at on MG-U74B	1	1
106125_at	Cluster Incl AI847472:UI-M-AI1-afs-e-09-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AI1-afs-e-09-0-UI /clone_end=3 /gb=AI847472 /gi=5491378 /ug=Mm.41027 /len=481	-2.1	-0.7
106222_at	Cluster Incl AW050335:UI-M-BH1-ang-c-02-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH1-ang-c-02-0-UI /clone_end=3 /gb=AW050335 /gi=5910864 /ug=Mm.23314 /len=501	-0.8	-1
106927_at	Cluster Incl AI882582:ub98b11.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1396509 /clone_end=5 /gb=AI882582 /gi=5567671 /ug=Mm.41857 /len=414	-1.5	-1.4
108488_at	Cluster Incl AI838112:UI-M-AL0-abw-a-05-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AL0-abw-a-05-0-UI /clone_end=3 /gb=AI838112 /gi=5472325 /ug=Mm.28315 /len=491	-1.4	-1.5
108614_f_at	Cluster Incl AI845104:UI-M-BG0-ahs-a-02-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BG0-ahs-a-02-0-UI /clone_end=3 /gb=AI845104 /gi=5489010 /ug=Mm.95694 /len=152	-1.1	-1
109689_at	Cluster Incl AI115717:uc34e06.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1399906 /clone_end=5 /gb=AI115717 /gi=3516041 /ug=Mm.29368 /len=366	-0.6	-0.7
109748_at	Cluster Incl AI852387:UI-M-BH0-aip-b-07-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-aip-b-07-0-UI /clone_end=3 /gb=AI852387 /gi=5496333 /ug=Mm.29635 /len=378	-3.7	-1.8
110311_at	Cluster Incl AW121466:UI-M-BH2.2-aon-f-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.2-aon-f-08-0-UI /clone_end=3 /gb=AW121466 /gi=6096799 /ug=Mm.30219 /len=224	-2	-1.3
110859_at	Cluster Incl AI851594:UI-M-BH0-aki-h-07-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-aki-h-07-0-UI /clone_end=3 /gb=AI851594 /gi=5495500 /ug=Mm.33881 /len=531	-1.5	-0.7
113567_at	Cluster Incl AI848066:UI-M-AP1-agk-a-08-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AP1-agk-a-08-0-UI /clone_end=3 /gb=AI848066 /gi=5491972 /ug=Mm.41925 /len=320	-0.6	-1.2
114959_at	Cluster Incl AI316880:ui35d02.y1 Mus musculus cDNA, 5 end /clone=IMAGE-1853283 /clone_end=5 /gb=AI316880 /gi=4032147 /ug=Mm.26923 /len=559	-5	-4.8
116273_at	Cluster Incl AW123862:UI-M-BH2.1-app-c-06-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH2.1-app-c-06-0-UI /clone_end=3 /gb=AW123862 /gi=6099392 /ug=Mm.31953 /len=451	-2.1	-1.7
116917_at	Cluster Incl AI843367:UI-M-AQ1-adz-e-01-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AQ1-adz-e-01-0-UI /clone_end=3 /gb=AI843367 /gi=5477580 /ug=Mm.39738 /len=320	-1.4	-0.7
162552_at	Cluster Incl AI838713:UI-M-AO0-acf-a-07-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-AO0-acf-a-07-0-UI /clone_end=3 /gb=AI838713 /gi=5472926 /ug=Mm.12715 /len=251 /NOTE=replacement for probe set(s) 106021_at on MG-U74B	-0.5	-0.6
163495_at	Cluster Incl AA867621:vx12b01.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1264201 /clone_end=5 /gb=AA867621 /gi=2963066 /ug=Mm.35584 /len=381 /NOTE=replacement for probe set(s) 115905_at on MG-U74B	-2.7	-3.3
163539_at	Cluster Incl AA790688:vw18d01.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1244161 /clone_end=5 /gb=AA790688 /gi=2850808 /ug=Mm.38269 /len=145 /NOTE=replacement for probe set(s) 116622_at on MG-U74B	-1	-1.3
163658_at	Cluster Incl AI851180:UI-M-BH0-akg-g-11-0-UI.s1 Mus musculus cDNA, 3 end /clone=UI-M-BH0-akg-g-11-0-UI /clone_end=3 /gb=AI851180 /gi=5495051 /ug=Mm.44182 /len=483 /NOTE=replacement for probe set(s) 106994_at on MG-U74B	-1.4	-0.6
163796_at	Cluster Incl AI115603:uh87f01.r1 Mus musculus cDNA, 5 end /clone=IMAGE-1764697 /clone_end=5 /gb=AI115603 /gi=3515927 /ug=Mm.46662 /len=368 /NOTE=replacement for probe set(s) 108978_at on MG-U74B	-0.6	-0.8
163901_at	Cluster Incl AV229258:AV229258 Mus musculus cDNA, 3 end /clone=4631405N17 /clone_end=3 /gb=AV229258 /gi=6181774 /ug=Mm.73467 /len=245 /NOTE=replacement for probe set(s) 110244_at on MG-U74B	-1.6	-1.5
163902_at	Cluster Incl W84234:mf36f06.r1 Mus musculus cDNA, 5 end /clone=IMAGE-407171 /clone_end=5 /gb=W84234 /gi=1541218 /ug=Mm.73487 /len=486 /NOTE=replacement for probe set(s) 110245_at on MG-U74B	-0.7	-0.7
164204_at	Cluster Incl AI645728:vr78e08.x1 Mus musculus cDNA, 3 end /clone=IMAGE-1134854 /clone_end=3 /gb=AI645728 /gi=4724203 /ug=Mm.64913 /len=406 /NOTE=replacement for probe set(s) 108343_at on MG-	-1.7	-1.2

	U74B		
164692_i_at	Cluster Incl AV343909:AV343909 Mus musculus cDNA, 3 end /clone=6430540I04 /clone_end=3 /gb=AV343909 /gi=6384968 /ug=Mm.68548 /len=235 /NOTE=replacement for probe set(s) 106774_r_at on MG-U74B	-0.7	-2.6
165336_f_at	Cluster Incl AV324794:AV324794 Mus musculus cDNA, 3 end /clone=6230427O21 /clone_end=3 /gb=AV324794 /gi=6294711 /ug=Mm.51343 /len=226 /NOTE=replacement for probe set(s) 110886_at on MG-U74B	-1.6	-2.6

Shown are the probe identification, sequence description and signal $\log_2$ ratio for both comparisons.

Table S2. Comparison of expression profiles for homozygous null and conditional β-catenin mutants

AffymetrixID	Symbol	β-cat 6.0	β-cat 6.5	CKO-wt	CKO-het
94200_at	Gbx2	1	0	–5.4	–4.4
94200_at	Gbx2	–1.6	–2	–5.4	–4.4
95297_at	Hoxa1	–1.2	1.3	–5.1	–4.5
114959_at	C030045D06Rik			–5	–4.8
103477_at	Cdx1	1.3	–1	–4.2	–4.9
103477_at	Cdx1	1.2	1	–4.2	–4.9
135746_at	---			–3.8	–0.9
109748_at	5430401D19Rik			–3.7	–1.8
131812_at	Atp8a2			–3.4	–2.9
98028_at	Twist1	–1.2	1.8	–3.2	–3.6
130826_at	---			–3	–4.1
102667_at	Wnt3a	1.1	–1.2	–2.9	–3.2
102755_at	Itln			–2.8	–2.8
163495_at	Skp2			–2.7	–3.3
99361_at	Wnt8a	1	–1	–2.4	–3
116273_at	---			–2.1	–1.7
106125_at	2610024A01Rik			–2.1	–0.7
141010_at	Nkx1–2			–2.1	–2
92931_at	Dll1	1.4	–3	–2	–1.5
110311_at	Nkd1			–2	–1.3
103460_at	5830413E08Rik	–1.1	1.1	–1.9	–1.5
164204_at	AI427833			–1.7	–1.2
93888_at	Hoxb1	2.1	1.2	–1.7	–1.8
93888_at	Hoxb1	2.3	–1.8	–1.7	–1.8
165336_f_at	---			–1.6	–2.6
163901_at	6030401B09Rik			–1.6	–1.5
160254_at	Mil2-pending			–1.6	–1.7
93611_at	Tbx6	1.2	1.1	–1.6	–1.8
99390_at	Wnt5a	1	–1.2	–1.6	–1.8
97386_at	1110032O19Rik	–1.4	–1.6	–1.5	–1.6
110859_at	1300010M03Rik			–1.5	–0.7
98108_at	Crabp1	–1.5	–2.6	–1.5	–1.3
98108_at	Crabp1	1.6	1	–1.5	–1.3
98108_at	Crabp1	1.2	1.8	–1.5	–1.3
106927_at	Hoxb2			–1.5	–1.4
163658_at	6430704M03Rik			–1.4	–0.6
116917_at	LOC279653			–1.4	–0.7
108488_at	Smarcd3			–1.4	–1.5
93941_at	T	–2.5	–4.6	–1.4	–1.4
98427_s_at	Nfkb1	1.1	0	–1.3	–1.1
97497_at	Notch1	–1.9	1.4	–1.3	–0.8
97497_at	Notch1	1	–1.1	–1.3	–0.8
97497_at	Notch1	1.4	–1.4	–1.3	–0.8
97497_at	Notch1	–1.1	1.3	–1.3	–0.8
97497_at	Notch1	–1.5	1.1	–1.3	–0.8
99086_g_at	Usp3			–1.3	–0.9
98831_at	Foxj1	1.2	–1.2	–1.2	–1
94117_f_at	Punc			–1.2	–1.2
108614_f_at	1110012O05Rik			–1.1	–1

104672_at	Frzb	1.7	–4.3	–1.1	–1
163539_at	---			–1	–1.3
94813_at	Gas1	1.3	–1.2	–1	–1.4
99034_at	Irx3			–1	–0.9
98419_at	Meox1	1.1	1.3	–1	–0.7
104716_at	Rbp1	1.3	1.2	–1	–1
97977_at	BC019633	–1.1	–1.9	–0.9	–0.9
104548_at	Phlda2	–2.1	–1.4	–0.9	–0.8
166567_f_at	2900027G03Rik			–0.8	–0.7
106222_at	AI447312			–0.8	–1
100127_at	Crabp2	1.5	2.8	–0.8	–0.8
96684_at	Grsf1	1.1	–1.2	–0.8	–0.7
100403_at	Myl7	3.2	1.3	–0.8	–0.7
100403_at	Myl7	1.5	–1.1	–0.8	–0.7
92997_g_at	Sox17	–1	–2.2	–0.8	–0.7
98330_at	Zic3	–1	–1.2	–0.8	–0.7
98330_at	Zic3	–1.2	–1.2	–0.8	–0.7
98330_at	Zic3	–1.1	–1.3	–0.8	–0.7
101001_at	5031439A09Rik	1.8	–2.1	–0.7	–0.5
101001_at	5031439A09Rik	–1.2	–1.2	–0.7	–0.5
163902_at	Apln			–0.7	–0.7
102833_at	Cbx2	0	1.3	–0.7	–0.8
101973_at	Cited2			–0.7	–0.7
164692_i_at	Gabarapl1			–0.7	–2.6
97520_s_at	Nnat	1.3	1.1	–0.7	–0.6
94400_at	1110051M20Rik	1.1	–1.1	–0.6	–0.9
113567_at	1810034B16Rik			–0.6	–1.2
109689_at	Agtrl1			–0.6	–0.7
94036_at	Cdc42ep4			–0.6	–1
163796_at	Dact1			–0.6	–0.8
97509_f_at	Fgfr1	1.1	1.2	–0.6	–0.6
97509_f_at	Fgfr1	–1.1	1.5	–0.6	–0.6
98817_at	Fst	1.2	–1.6	–0.6	–1
98852_at	Sall3	1.5	–1.6	–0.6	–0.8
162552_at	2310016C16Rik			–0.5	–0.6
100600_at	Cd24a	1.3	–1.5	–0.5	–0.5
100600_at	Cd24a	2.4	1.3	–0.5	–0.5
100407_at	Gal	1.2	–1.2	–0.5	–0.5
100407_at	Gal	1	–1.1	–0.5	–0.5
103628_at	Lef1	1.2	–1	–0.5	–0.6
103628_at	Lef1	1.1	–1.2	–0.5	–0.6
95016_at	Nrp	–1.5	1.4	–0.5	–0.5
94449_at	Pcdhga12	1.1	1.1	–0.5	–0.6
94449_at	Pcdhga12	–1.8	2	–0.5	–0.6
101451_at	Peg3	1.5	1.1	–0.5	–0.6
93724_at	Ror2			–0.5	–0.9
107154_f_at	---			0.5	2.5
108848_g_at	---			0.5	0.6
116418_at	---			0.5	0.5
129297_at	---			0.5	1.3
130494_f_at	---			0.5	0.5
134932_at	---			0.5	0.5

167758_at	---			0.5	0.7
167843_f_at	1110051B16Rik			0.5	0.6
108022_at	1200002M06Rik			0.5	0.5
110503_at	1500009K05Rik			0.5	0.9
165677_at	1700011I11Rik			0.5	0.5
106204_at	1810013D05Rik			0.5	0.5
167192_at	2700083E18Rik			0.5	0.6
99501_at	3100002M17Rik	–1	–1.2	0.5	0.9
99501_at	3100002M17Rik	1.1	–1.2	0.5	0.9
113265_at	5730455O13Rik			0.5	3.8
162843_at	5730469D23Rik			0.5	0.5
129046_f_at	A330103N21Rik			0.5	1.1
106294_at	AI642036			0.5	0.6
160702_at	BC031468			0.5	0.6
164330_f_at	Bcar1			0.5	0.6
110446_at	C130034K06			0.5	3.6
160493_at	Cd63			0.5	0.7
95661_at	Cd9	1.2	1	0.5	0.9
163262_at	Cldn6			0.5	0.5
101963_at	Ctsl	–2.2	–1.2	0.5	0.6
101963_at	Ctsl	1.4	–1	0.5	0.6
101963_at	Ctsl	1.1	1	0.5	0.6
101963_at	Ctsl	1.2	–1	0.5	0.6
97013_f_at	Cyba			0.5	0.5
166740_at	D16Ium22e			0.5	3
103665_at	Elovl6	–1.2	1.1	0.5	0.5
96868_at	Fgb			0.5	2.7
101106_at	G3bp2-pending	1.2	–1.3	0.5	0.6
114749_at	Gpr23			0.5	0.8
106196_at	Htf9c			0.5	1
96269_at	Idi1	–1.1	1	0.5	0.5
166226_f_at	Itm1			0.5	0.9
167118_f_at	Jmj			0.5	0.6
114629_at	Lbcl1			0.5	0.6
103377_at	Lrp2			0.5	0.7
103806_at	Lrp5			0.5	2.4
110008_at	Mint-pending			0.5	0.6
116837_at	Myo6			0.5	1.2
94461_at	Pbef-pending	–1.2	–1.2	0.5	0.6
94461_at	Pbef-pending	0	–1.5	0.5	0.6
94461_at	Pbef-pending	–1.1	–1.1	0.5	0.6
96841_at	Pim3	–1	1.2	0.5	0.5
96841_at	Pim3	1.2	–1	0.5	0.5
96841_at	Pim3	1.2	–1.1	0.5	0.5
96841_at	Pim3	–1.3	–1.1	0.5	0.5
103888_at	Rbpms			0.5	0.5
109332_at	Rent1			0.5	0.8
102370_at	Retsdr2-pending	–1.1	–1.1	0.5	0.5
115062_at	Rev1l			0.5	1.2
163626_at	Rnasep1			0.5	1.1
162562_at	Rnf128			0.5	0.8
109622_at	Sh3bp4			0.5	0.7

170064_f_at	Slc2a3			0.5	0.6
116003_at	Slc35e3			0.5	0.9
99133_at	Slc3a2	–1.3	1.1	0.5	0.6
99133_at	Slc3a2	1.1	1	0.5	0.6
99133_at	Slc3a2	–1.3	1	0.5	0.6
99133_at	Slc3a2	2.3	–1	0.5	0.6
99133_at	Slc3a2	1.5	1.3	0.5	0.6
99133_at	Slc3a2	–1.3	–1	0.5	0.6
97160_at	Sparc	1.1	1.5	0.5	0.9
97160_at	Sparc	1	1.4	0.5	0.9
97722_at	Ssr1	1.5	–1.2	0.5	0.6
165449_f_at	Ube2j1			0.5	0.7
106064_at	Zdhhc12			0.5	0.5
136554_r_at	---			0.6	1.9
141090_f_at	---			0.6	0.7
161050_at	---			0.6	0.5
168454_f_at	---			0.6	0.6
162704_i_at	0610030G03Rik			0.6	0.9
167853_f_at	1110023P21Rik			0.6	0.8
106475_at	1810060K07Rik			0.6	0.7
132361_at	2210411K11Rik			0.6	0.9
111494_at	2310020P08Rik			0.6	0.6
167237_f_at	2510027N19Rik			0.6	0.9
93569_f_at	2610042L04Rik	2.8	1.2	0.6	0.7
133830_at	2810004A10Rik			0.6	1.1
136134_at	2810403A07Rik			0.6	1.2
102232_at	4833420E20Rik	1	–1.1	0.6	1.3
115752_at	6030443O07Rik			0.6	0.5
103716_at	6430546F08Rik	–1.2	–1.5	0.6	0.7
115792_at	9830148O20Rik			0.6	0.8
106615_at	AA407558			0.6	0.5
104714_at	AA959601	–1	–1.4	0.6	0.7
96781_at	AL023001	1.2	–1.1	0.6	0.5
130491_at	Amn			0.6	1
106292_at	Bcl11a			0.6	1.4
99561_f_at	Cldn7			0.6	0.7
94831_at	Ctsb	–1.6	–1.2	0.6	0.7
94831_at	Ctsb	–1.4	–1.5	0.6	0.7
94831_at	Ctsb	1	–1.4	0.6	0.7
94831_at	Ctsb	–1.1	1.9	0.6	0.7
94831_at	Ctsb	–1.7	1.3	0.6	0.7
101019_at	Ctsc	1.1	–1.1	0.6	0.6
101019_at	Ctsc	1.3	–1	0.6	0.6
104717_at	D5Ertd689e	1.5	–1.8	0.6	0.6
170808_s_at	D6Wsu176e			0.6	0.5
98045_s_at	Dab2	–1.2	–1	0.6	0.7
136630_i_at	F11r			0.6	1.2
99378_f_at	H2-Q1	–1.1	1.1	0.6	1.1
99378_f_at	H2-Q1	–1.1	–1.3	0.6	1.1
98627_at	Igfbp2	1.1	–1.8	0.6	0.6
98627_at	Igfbp2	1.1	–1.3	0.6	0.6
93261_at	Lgmn	–1.5	–1.1	0.6	0.9

116312_at	LOC234344			0.6	0.5
168371_f_at	Lrrc5			0.6	0.8
104554_at	Nr2f6	1.2	1.1	0.6	0.5
103502_at	Nrk	1.7	2.8	0.6	0.9
103502_at	Nrk	1.2	1.8	0.6	0.9
101926_at	Pim2	1.5	1.1	0.6	0.5
101926_at	Pim2	1.1	1.2	0.6	0.5
104343_f_at	Pla2g12	1.2	–1.1	0.6	0.5
112828_at	Podxl			0.6	0.6
165599_at	Ranbp2			0.6	0.5
99591_i_at	Rdh11			0.6	0.5
103818_at	Slc7a7	–1.3	1.5	0.6	0.6
97132_at	Soat2	–1	1.1	0.6	0.6
102959_at	Tle4	1.2	1.2	0.6	2.2
161361_s_at	Tnnt1			0.6	1.3
112373_at	Ube2v1			0.6	0.7
95000_g_at	---	–1.1	–1.1	0.7	1.2
165695_at	1810011O16Rik			0.7	0.9
112392_at	1810027I20Rik			0.7	3.7
107491_at	2010204K13Rik			0.7	0.5
115347_at	2700078E11Rik			0.7	0.5
140759_at	4831403C07Rik			0.7	1.4
105273_at	6030405M08Rik			0.7	3.3
93626_at	Abcg2	–1.1	–1.2	0.7	0.9
109133_at	Als2			0.7	0.6
94834_at	Ctsh	–1.3	–1.2	0.7	0.8
160369_at	Dhcr24			0.7	1.1
100479_at	Dnmt3a	1.5	1.2	0.7	0.8
164028_at	Dnmt3b			0.7	0.6
103977_at	F10	1.4	–1.1	0.7	0.5
104419_at	F730017H24Rik	2	–1	0.7	2.9
93785_at	Folr1	–1.3	–1.1	0.7	0.6
93785_at	Folr1	0	1.1	0.7	0.6
165915_i_at	Foxp1			0.7	0.5
114032_f_at	Glcci1			0.7	3.6
101676_at	Gpx3	1	–1.1	0.7	0.7
101676_at	Gpx3	–1.1	–1.1	0.7	0.7
93543_f_at	Gstm1	–1.3	1.1	0.7	0.7
102235_at	Lmyc1	–1.6	–1.2	0.7	0.6
112400_at	mKIAA0182			0.7	0.6
103868_at	Nufip1	1	–1.1	0.7	0.9
108076_at	Nup210			0.7	0.6
95465_s_at	Pr1			0.7	0.8
93953_at	Prss12	2.6	–1.3	0.7	0.6
93953_at	Prss12	1.5	–1.3	0.7	0.6
112405_at	Slc16a3			0.7	0.5
103357_at	Slc2a2	0	–2.1	0.7	0.6
103357_at	Slc2a2	–1.2	–2.3	0.7	0.6
92699_at	Slc7a9			0.7	0.5
139602_at	Tk1			0.7	1.9
167188_at	---			0.8	0.8
167965_f_at	---			0.8	0.6

95518_at	1810015C04Rik			0.8	1.1
109167_at	2400008B06Rik			0.8	0.5
110467_at	2610042L04Rik			0.8	0.5
116635_at	Abca3			0.8	0.8
163015_at	Amn			0.8	0.8
97887_at	Apoc2	–2	0	0.8	0.8
97887_at	Apoc2	1	–1.8	0.8	0.8
97887_at	Apoc2	1	–1.3	0.8	0.8
97887_at	Apoc2	–1.5	–1.1	0.8	0.8
135278_at	Atrx			0.8	4
131000_f_at	BB114266			0.8	0.8
99535_at	Ccrn4l	1.2	–1.1	0.8	0.6
99535_at	Ccrn4l	1	–1.1	0.8	0.6
99535_at	Ccrn4l	1.2	1.1	0.8	0.6
97518_at	Fdft1	–1.1	1.2	0.8	0.7
112922_i_at	Kdelr3			0.8	1.4
92550_at	Krt1–19	1.2	1.2	0.8	1.1
115820_at	Nav1			0.8	0.6
109069_at	Slc40a1			0.8	0.8
160249_at	Tpd52			0.8	0.8
102764_at	Trap1a	1.2	1.2	0.8	1.4
102764_at	Trap1a	3.5	1.2	0.8	1.4
95350_at	Ttr	1.2	1.3	0.8	0.6
108784_at	---			0.9	0.6
133204_at	---			0.9	2.5
137047_at	---			0.9	1.2
165656_i_at	---			0.9	0.9
95954_at	---	–1.1	1	0.9	3.2
130779_f_at	1200003C15Rik			0.9	1.6
113036_at	2310015I10Rik			0.9	0.7
93568_i_at	2610042L04Rik	2.8	1.2	0.9	1
98042_at	4833411K15Rik			0.9	0.8
165601_f_at	9630060C05Rik			0.9	0.9
96094_at	Apoa1	–1	1.4	0.9	0.9
96094_at	Apoa1	–1.2	–1.2	0.9	0.9
96094_at	Apoa1	–1.3	–1.8	0.9	0.9
93840_at	Apom	–1.2	–1.2	0.9	0.9
162690_at	B130036O03			0.9	0.7
160904_at	B230317C12Rik			0.9	0.5
115010_at	BC042513			0.9	1.1
167479_at	Car7			0.9	1.3
92633_at	Ctsz	–2.7	–1.2	0.9	0.9
112955_at	D10Bwg0792e			0.9	0.7
165792_at	Dab2			0.9	1.1
97819_at	Gsto1	–1.2	1.4	0.9	0.5
97444_at	Ifi30	–1.3	1.1	0.9	0.6
97444_at	Ifi30	–1.1	1.1	0.9	0.6
97444_at	Ifi30	–1.4	1.2	0.9	0.6
129147_r_at	Igsf9			0.9	0.7
95511_at	Itga6	–1.1	–2.1	0.9	2.9
100095_at	Scarb1	1.2	1.4	0.9	0.8
103776_at	---	1.1	1.2	1	1.3

129928_f_at	---			1	0.8
113314_at	4833415N24Rik			1	4.3
163489_at	Ankrd3			1	0.7
165359_f_at	Apoa1			1	1
100078_at	Apoa4	–1.1	1.4	1	1.3
100078_at	Apoa4	–1.5	1.2	1	1.3
107498_at	BC019216			1	0.8
104585_at	Crb3	–1.1	1.1	1	0.8
96134_at	Dp1l1	–3.5	2.4	1	0.8
96771_at	Erbb3	1	1.2	1	0.8
104210_at	Itga3	1.1	1.2	1	1
101561_at	Mt2	–1.1	–1.4	1	0.8
101561_at	Mt2	1.4	1.5	1	0.8
92644_s_at	Myb	1.1	–1.1	1	0.6
92644_s_at	Myb	–1.3	1	1	0.6
101368_at	Pem	–1.1	–1.1	1	0.7
164545_f_at	Pgk1			1	0.9
96047_at	Rbp4	1.4	–1.1	1	1.1
96047_at	Rbp4	2.3	1.7	1	1.1
96047_at	Rbp4	1.8	1.6	1	1.1
96047_at	Rbp4	1.5	1.5	1	1.1
96047_at	Rbp4	2.1	1.2	1	1.1
96047_at	Rbp4	2.4	1.5	1	1.1
96038_at	Rnase4	–1.1	–1.1	1	3.2
108780_at	Tmem2			1	1.3
104990_at	---			1.1	0.7
161626_f_at	---			1.1	1.4
92430_at	1110027L01Rik	1.1	–1.1	1.1	1.6
110309_at	2610028H14Rik			1.1	1.1
96491_at	B130024H06Rik	1.7	–1.8	1.1	0.5
162607_i_at	BC026370			1.1	0.6
167608_f_at	D030016E14Rik			1.1	1.4
115066_at	Dnmt3b			1.1	0.6
111529_at	Gats			1.1	0.7
98000_at	Ly64	1.4	1.2	1.1	1.1
98000_at	Ly64	–2.1	–1.1	1.1	1.1
98000_at	Ly64	1.3	1.3	1.1	1.1
93573_at	Mt1	–1.6	–1	1.1	1.2
93573_at	Mt1	–1.1	–1.3	1.1	1.2
114845_s_at	Pepf-pending			1.1	1
167216_f_at	Prkaca			1.1	0.7
99475_at	Socs2	–1.5	–1.3	1.1	0.8
100499_at	Stx3	–1.2	–1.2	1.1	0.5
100499_at	Stx3	1.4	1.5	1.1	0.5
100499_at	Stx3	–1.1	–1.2	1.1	0.5
135760_at	---			1.2	2.1
168398_f_at	---			1.2	1
95702_at	1300006C19Rik			1.2	0.7
131216_f_at	AI466840			1.2	0.7
112445_at	LOC213048			1.2	0.8
162245_f_at	Myo6			1.2	0.6
138014_at	Nup153			1.2	0.9

162929_at	Sall2			1.2	0.6
103795_f_at	Timd2	–1.7	–1.4	1.2	2.9
115112_at	2510015N06Rik			1.3	3.3
105008_at	2610034N15Rik			1.3	3.2
100009_r_at	Sox2	1.4	1.2	1.3	1.3
171194_at	---			1.4	3.5
97317_at	Enpp2	–1	–1.4	1.5	1.2
97317_at	Enpp2	1.2	–1.5	1.5	1.2
165641_at	Nudt6			1.5	1.3
138408_at	---			1.6	3.1
105198_at	4631416I11Rik			1.6	1.5
93133_at	Slc7a3	1.3	–1.1	1.6	1.4
106577_at	Csna			1.7	0.9
97742_s_at	Fgf8	1.6	–3	1.7	4
111347_at	Gmfb			1.7	0.9
162728_at	Prodh			1.7	1.3
102220_at	Utf1			1.7	1.3
162276_i_at	C1qb			1.8	1.5
164467_f_at	Gjb3			1.8	0.8
102418_at	Tex19			1.8	0.7
160401_r_at	Cnot7			1.9	3
165460_at	Ppap2c			1.9	3.6
168542_f_at	---			2	2.8
161906_f_at	2410022L05Rik			2	1
166030_i_at	4921525L17Rik			2	5.3
112209_at	2410003B16Rik			2.2	2.9
111359_at	6330407P03Rik			2.3	2.3
165935_at	2010003K15Rik			2.4	1.1
134223_at	---			2.5	3.3
129326_at	---			2.6	1.3
168426_f_at	Crb3			2.7	3.6
134260_at	---			2.8	2.7
108516_at	0610011L13Rik			2.8	1
129347_at	2900024N03Rik			2.8	2.1
133037_at	Pex7			2.8	1.3
97413_at	1600029D21Rik	–1.1	–1.5	3	0.7
162869_at	Enc1			3	1
130994_at	Nkd2			3	1.7
113431_at	Rnf14			3	3.7
128830_r_at	6330403E24Rik			3.1	3.4
132794_at	---			3.3	0.9
166437_f_at	Fzd8			3.4	3.3
167004_r_at	D830007F02Rik			3.5	4
107621_at	D7Ertd458e			3.8	0.5
165956_f_at	2310002A05Rik			4.4	0.8
168503_at	---			4.6	2.7
165637_i_at	2610034E18Rik			4.6	4.4
170625_i_at	5730536A07Rik			4.7	0.5

The Affymetrix ID (MGU74v2 probe set ID), Gene symbol, signal $\log_2$ ratios for E6.0 and E6.5 β-catenin homozygous null mutants and signal $\log_2$ ratios for both conditional β-catenin mutant (CKO) comparisons. Note that redundant probe set IDs appear because the β-catenin homozygous null mutants data was collected with the Mu11k platform that contains multiple probe sets that map to only one probe set on the MGU74v2 arrays.

Table S3. Genes with Grsf1 high-affinity consensus-binding sites

Transcript ID	Total matches	Locations	Gene ID	Sequence
ENSMUST00000000028.1	1	73	ENSMUSG00000000028.1	TGGAAACACATTCAAATAATGTGTGACTGAATTTACTTTATGTCTAAGAGTATATTGTTTTCTAAGTATGCC**AGGGT**CAGATAATAGACCTTCCTTCCCGAAGTAAAGATGTCTGCCAAACATAGGTGGTTTTGGGTGACTGGACGTTAGCGTCAACACCGGCAACAAGGAACCAATCAGAAAGGAGGAAAGGCTAAGAATTATTGGCTGCTGGCGTGGACCAATCAGAAGAGCTGTGATTTGGCGGGAGTCTTGACGACCTCCGGGGCTGTCCGTGTCTCAGCGCCAGTTCTAGGTATCCGCCGCTGTGGCT
ENSMUST00000000033.1	2	87,502	ENSMUSG00000000033.1	AGCATTTCCTCATTCTCTAGAGGACTTCTCTGAAGCCACAGAAATTAGAGGTGATTTTTCCCGGGTGTTGTAGGGCCCACTGGCTTC**AGGGT**GAACCCTAGTCTCCACTCCCACCCCTCAAAAGAACTGACCTGAATTCCCTAAAATCCATCTGTTGTTTTTCATCTCCCATTTTTAAGCAATTAAAATTAAGCTCCCCTAAATTTCATGTTGGGAATTTTCTTAAACCCAACAGCAACAACAAACCACCTAACTTCTACAAATTAGTCTAGGATTTTGTGGGTTCCCCAAGCTTTCTAACCAAGATATTGGGTTCCCCTCGTTAGGCCTGGATCAAGATGCCCCCCATTTTTGCATAGAATAATTTTCCTCATTCCCCAACTTGGATTCTAATTTTTCTGGAATCTCAAATTTAGTCATTCGCCACAGTTTTCCCATTTATGGAGTCGCCTTCGAGTCCCCCTACTTTGGGCCGCTCATTCCCAGGACCGCAAATCAGACA**AGGGT**CTGACTTGGGATCCCCGAAATTTGATCATTGTTTCCGCTGGCCACTTTCGGCAGCTTCCCGTCCTGCGCATAACAGTGGTATCGGCCTCGTCACTTCTCCTACGGTGTCCCAGCGGCAGCACAGATTTTGGAAAAGTGTGTGTGCCCCAAACACGCACTGGACACTGCGCGGCGGCCAGGACGTGGGCAGTGTTGCTCCCGTGTCCAGGAAAACGACTGGGCATTGCCCCCAGTTTCCCCCAAATTTGGGCATTGTCCCCGGGTCTTCCAACGGACTGGGCGTTGCCCCGGTTCACTGGGGACTGCCCTTGGGGTCTCGCTCACCTTCAGCAGCGTCCACTTCAGCAGCTCCCACTTCATCCGCTCTCCCGCCCTTCTCCTCCGATCCTCCTGCGCCAGCGGACCCGACCTTCGGCCTTGTGGTACCA
ENSMUST00000060749.1	1	73	ENSMUSG00000000122.1	GGTCCCGGATGTTGCGGGCAGTATGAGGCGAGCGCAGGGGGACAGGGACCAGCAGCTGTCGCCGCCGTTCTC**AGGGT**GAAGAAAAACCAGAAACCTTTGCCCCCTGACTTTGGAGACTCAGTTTAACCTTCAAACTGGCG
ENSMUST00000000284.1	1	6	ENSMUSG00000000275.1	GCGGT**AGGGT**GCGCAGCTGTCCCTGCGCGTCACGTCGGGTGAGCCCACGAGCGCG
ENSMUST00000000394.1	1	23	ENSMUSG00000000384.1	CGTAGGCTGATGGAGGTCAGTG**AGGGT**GATCGCCGCCGCAGTCTGGCGTCCTGGAGAGACCGGGTTTCTGAACGGAACAAGACTGGCAGACTTGCCGAAAGAAACGTCATGTGGTTATGTAGCGTGTTCTCGAAAAAGGACTTCGGAGTCACCTACTAGGAGTCTTCCCTCCCTCCCTCCCTCTTCCCTGCGCCCAGCATC
ENSMUST00000000642.1	1	234	ENSMUSG00000000628.1	GCCACATTGTTGCACCAACTCCAGTGCTGGAGTCTCAGGACACCACAGGCTACCCGGAGTTGTTCTGCTTTGGAGATCCGAGGGCAGGAGCATCACGCCAGTGACTCTGATAGGTGCGATCGCCGGATTGGAACAGAACTGTCATTTTTTTCCGAAGTTGAGCCTTAGTGACCCAGTGAGTGAAGTTAGCGACGGGACGCTAAGCAGCTAGACCGGTCGGCAGGAGTGAGACTT**AGGGT**ACCTTCTAGTAGTTGTGATTAAAAAAATTGAAAAAAAGAAAAAAAAAAACCCTGTTTCTGGAAACTTGAGGCCCTCAGCTGGTGAGCCATCGTGGTTAAGCTTCTTTGTGTGGCTCCTGGAGTCTTCGATCCCAGCCGGACACCCGGGCCTGGTTTCAAAGCGGTCGGACAGCGCTGCCTGCTCCATCGGTAGCGCTCGAGCCTCGGTTTCTCTATTTGGCCCCGACTCGCCGCAACAAG
ENSMUST00000062678.1	1	26	ENSMUSG00000000951.1	GCGGAAGCGTCGAGTGCGTGGTCTC**AGGGT**TCTCCTCACCATGGTTCCCGGAGTGCCGCTCCCGCCGGAGATCCAGCTGGCGCAGCGCCTGGCGGGCAATGAACAGGTGA
ENSMUST00000041898.1	1	29	ENSMUSG00000000951.1	CCAGCGGAAGCGTCGAGTGCGTGGTCTC**AGGGT**TCTCCTCACC
ENSMUST00000000977.1	1	29	ENSMUSG00000000951.1	CCAGCGGAAGCGTCGAGTGCGTGGTCTC**AGGGT**TCTCCTCACC
ENSMUST00000000984.1	2	43,187	ENSMUSG00000000958.1	AGCAAATCAGCAAAAAGAGGATCTAGCGAATCAGTTGGTTTC**AGGGT**TGGTTCCTCATACAGGCATCTCAGCGCAGGGACATTTGAAACTGAAATCAGAGGGGAGAGACTTTGGGGGTCAGGGGGAGGCAGAAAAAAGTTTTACCAAACTGCCTCATTCATGCCTGTCCTGTGTCATAACAGGTTG**AGGGT**TCAGCTGTCTGATAAATAAGAGGGCAATGCGAGCAAGCTGGTGAAGGTCTTCCTTCTCTTCGCC
ENSMUST00000052870.1	1	352	ENSMUSG00000001034.1	GAGCGAGCCCGGGGGAACACTCATCACTGGGTTGGCAAGACTCAGGAATCCCAAATTCCCGAGGAGGCGTGGCGGCGGGGTGCCGGCCGGTCGGTGAGTGCGATCCCGGGAGTCCCAGCGCCCCGCCCCTCCCTTTCTTCCGGGGCCGCGCCGCGCCCCCCTGGATCCTGGGCCGTGGGGTTCT

				CTGTGCCAGCGGTCCCCTCTCGCCTGCTGCACAGGTCCTGCCTCCAAACCCACAGAGGCGGAACTGAGAGGCCCTCAGGACGATCTTCTCATCAGCGCTTCGTACAGACCATGGCCGAACCGCTGAAGGAGGAGGACGGCGAAGATGGCTCTGGGGAGCCCCCTGGG**AGGGT**GAAGGCAGAACCCGTTCACACCGCTGCCTCTGTGGTGGCCAAGAACCTGGCCCTGCTCAAAGCCCGCTCCTTCGACGTGACCTTTGACGTGGGGGACGAGTACGAGATCATCGAGACCATAGGCAATGGGGCCTACGGGGTGGTGTCTTCGGCGCGCCGCCGCCTCACGGGTGAGCTGGCTTCCTGA
ENSMUST00000001063.1	1	184	ENSMUSG00000001036.1	AAACGCTGCACAGGCTCGGGTCGCTCCCGCTTCTCCCGCGTCGCCGGCGGCTGCAGCCTTGCACTCGCGCTGGCCAGGAACGGAGGGCATGGCTGCCAGCTTCTGGGACCTGAGGCTTTGGAGGAGGAAATGACTGTGGAGGGCCATTTTGTTCCATCTGCATTTCTGACACGGAAACTTCCT**AGGGT**GCAGGCTTAGGGGACAGGAAAGTTTCTCTTGAAGGGCTTCACATTTGTAACAAAGAAGATAAAAATGACAACTTCATCTATCAGACGGCAGATGAAAAACATTGTGAACAATTACTCAGAGGCTGAAATCAAAGTCCGGGAGGCCACCTCCAATGACCCGTGGGGCCCATCCAGCTCTCTGATGACTGAGATTGCTGACCTGACCTACAATGTGGTAGCGTTCTCGGAGATCATGAGCATGGTTTGGAAGCGACTTAATGACCATGGCAAGAACTGGCGGCATGTATAC
ENSMUST00000001155.1	4	61,782,811,1206	ENSMUSG00000001127.1	ACAAGCCCAAGATGGAGGCGGTGGTGGTGGTAGCGGTGTGACAGGTGAGGGCAGGCCCGGT**AGGGT**TCGGGTTTTGGAGCGGCTGCGGGACCCGGGTATGAAGTCCAGACCGAAAGCTCAGCTCCAAGATGCTTCCGTCTGAATCTCAGCGTTCTCCCGCCCGGAACCAAAGGAGTGGTTTGACCAGGGCGAGACCGTCGTCATCGACCGTGGGAGTGGATGGAGGAGTCGGCCTGCAGGCTGCAGTGGTGGTTTCGCTTGCTGCGCGTGGCAGTGCACCTGCACAGAGCTTGAAGCCCTTGGGGAGGGCGGGACGGAGCCAAATTGGGTCTGGGGTCTGGGGCTTGGGTGCGAAATTCCAAGGTGAATTCTTAAACCCCTTAAAATGTCTAATGACGTTTCCTCACGACGTCCAGGAGATGCAGCTCTCTCCCATGGTTCCTTATTGCCCTTCATATTCTACGCCACCTAGGAAGATGTCTGACGATTACCTCATTATCCCTAGTTCACCCTAATCCCTTTCCATGATTTCACAGTGCGTTTACACCAGTAATCTGTTTGTGACCCCCAGTAGTTATCAGGTACAGTTTTTGGAAACCCTTCCCCCAACCTCACCTCCATCTTCTTCATCTGGATACCATTGTCTTCCTTTGCCTTTCCTCTTGATAGTGTTTTCTGATGAGCCATCATTGCCACTGCATTTGATTTAGTGTGTAATGTGGTCTGTTATCCAGCTGTTTTTCACAGTCTGTAGTGACTCTTATTACATCTCTCTTTAGTCT**AGGGT**ATGGCGAACCTCTGTGGACTCTAG**AGGGT**CTGGTGACCTCTATTAGCTACCTGACAGTACCTTTGATTCTACCATTAGCCTTATAGCTTATGCTCTGGAATACCCACAGTGCCTTTTAAGGTCATTGGTACTGTCTTCATTTCCTTCAATCTAAAAACAAGGTCTGATGATCCTCCATTTTCCTGTCCCCTGTCTGTGTCTGATTACCCATTCTCTGAAGCTAAG
ENSMUST00000001319.1	1	19	ENSMUSG00000001300.1	CGCGCGCTGAGGGACGCGC**AGGGT**GAGCGCACCTGGCCTCGGCGACCGCGGGAGCGGCGCGGCGTGTCCGCCCCGGAGGATTGGGGGTCGCTGCCCGCGGCCGGTCCCAACGCGTCCCGGAGTGCGCAGAACTGGGAGCGGCTTGGGC
ENSMUST00000001522.1	1	98	ENSMUSG00000001482.1	GAACTACAGTGTAGCCAGCCGGTCCGGTACAATGTAGCGGCAGCCAGGTGCAGGGCAGTCTGGGAAGTCACGTGACAAGAGTGATGCCCTCCTCATGC**AGGGT**GAAAGGGGAACATCTCAAGTAAGGGGACAGGAAGGAAGATCCAGTTCCAAGAGGTGGGATGCT
ENSMUST00000057054.1	1	14	ENSMUSG00000001493.1	CACTCATTCACTC**AGGGT**CCCCGGGAAGGGCTTGTCAGTATGGGTGGGTCCAAGGTAGGACAGTCAAAATGTTCAGCATGGTAGGAAACAACTCCGTGCCCGATAGTCAGCGTGTGTCGGGGGCAGGAAGGCAGACGTGAAGCCTAGACAGGTGTGGACACGCACATGTGTGTTCCTGGCCACGTGTTTGTGGAATTTGAGGCAAAATTTTTGTTTTGGTTCCTGGGGTAAAGTTTCCATTCAACATTTTCCTCTACTGTTTAATTTTTTTTTTAATTTTAAATTACAAAACTCTGACTAGAAAAAGCGCAATACCTTTGAAAGGACTGGGGCAGGCAGTGGACAGCAG
ENSMUST00000001533.1	1	14	ENSMUSG00000001493.1	CACTCATTCACTC**AGGGT**CCCCGGGAAGGGCTTGTCAGTATGGGTGGGTCCAAGGTAGGACAGTCAAAATGTTCAGCATGGTAGGAAACAACTCCGTGCCCGATAGTCAGCGTGTGTCGGGGGCAGGAAGGCAGACGTGAAGCCTAGACAGGTGTGGACACGCACATGTGTGTTCCTGGCCACGTGTTTGTGGAATTTGAGGCAAAATTTTTGTTTTGGTTCCTGGGGTAAAGTTTCCATTCAACATTTTCCTCTACTGTTTAATTTTTTTTTTAATTTTAAATTACAAAACTCTGACTAGAAAAAGCGCAATACCTTTGAAAGGACTGGGGCAGGCAGTGGACAGCAG
ENSMUST00000001558.1	1	0	ENSMUSG00000001517.1	**AGGGT**CAAAGCTTGCGATTCTCGATGGAGAGCGAAAGCACAGCCTCACG
ENSMUST00000002070.1	1	24	ENSMUSG00000002017.1	TCCGGGGAAGGAGCGCATGCGCT**AGGGT**ACGCGTTGCCGGCGAGAGGGCAGCCTGACGACTCGGAAATTTGAATACCACAGTAGCATGGAGTGTGACCTC

ENSMUST00000056241.1	1	39	ENSMUSG00000002059.1	CGCTCGCAGAGTGGGACGGCGGGCCTCGCTGCGCGTCT**AGGGT**TGTCGCCCCCTCCTCTCACCGGTCGAGGGCGTCGGCAGTTGCTGCCCCTGCGCAAAGTGACCCCGTGTGGCGGGGCGGCCCCGAGCCCCCCCAGGCCTCTCTGTTATGGTAGGGCCATCCCAGCCCCGAGTTGTCGTCGGGTCTCCGCGGCCCCGGGTTATCGTAGGGGCTATCCGACCCCGTGTCATTGTAGGATCCGCGCGGGCCCGGGCTCCCCGGGACGCGACTCCCCGCCCACAACTAGCGGCCGGGGGATCTCCCCGCCCCCGAGTGGTCTTCGGGACGCCCCGGGCTCGGGTGATTGTGGGCTCTCCCAGACCCGGGGTGATTGTCTCGTCCCCTTGGCCCGCGGTGGTCGTAGCGTCTCCAAGGCCGAGGGCTCCCACAGGCTCTCCGTGGCCCCGGGTGATTGTCGGTACCCCGCGGCCGCGGATAATCGTCGGGTCTCCACGGGTCCCGGCCGCCGGGGCGGATCAGGCCTCTGCGCCTTCCCGGGGAGCCCCGCAAGGCCGCAGACAAG
ENSMUST00000002198.1	1	1180	ENSMUSG00000002129.1	CTCTGGGTCGCCGCCATCTTGTCATTGAGTTGGATACTTCGTGTGGTGATCTTTAATCTTGTCGTCGCACCGGTTGTCGCCACCGAGGTGGACTGGCAGCCCTGAGCGTCGCAGTCATGCAGGCCGGACCCGTGCAGGCGGTACCCCCGCCGCCGCCAGTAGCCACTGAGTCCAAACAGCCAATTGAAGAAGAAGCATCGTCAAAGGAGGATCCCACCCCTTCCAAGCCAGTGGTCGGCATTATTTACCCTCCCCCGGAGGTCAGGAACATCGTCGACAAGACTGCCAGTTTTGTGGCCAGAAATGGGCCTGAATTTGAAGCTAGGATTCGACAGAATGAGATCAACAACCCCAAGTTCAATTTCTTAAATCCCAATGACCCTTACCATGCCTACTACCGCCACAAGGTCAGCGAGTTCAAGGAGGGGAAGGCTCAGGAGCCCTCAGCTGCCATCCCCAAGGTTATGCAGCAGCAGCAGCAAGCTACGCAACAGCAGCTGCCCCAGAAGGTCCAAGCCCAGGTGATCCAAGAGACCATAGTACCGAAGGAGCCCCCTCCTGAGTTTGAGTTCATCGCTGATCCCCCCTCCATCTCAGCCTTCGACCTGGATGTAGTGAAGCTGACAGCTCAGTTTGTGGCCAGGAATGGGCGTCAGTTTCTGACCCAGCTGATGCAGAAAGAGCAGCGCAACTACCAGTTTGACTTTCTCCGACCCCAGCACAGCCTCTTCAACTACTTCACAAAGCTGGTGGAGCAGTATACCAAGATCTTGATTCCACCCAAAGGCTTATTTTCAAAGCTCAAGAAAGAGGCTGAAAATCCTCGAGAAGTTTTGGACCAGGTTTGTTACCGAGTAGAATGGGCCAAATTTCAGGAACGTGAGAGGAAGAAGGAAGAAGAGGAGAAAGAGAAGGAGCGAGTAGCTTATGCTCAGATTGACTGGCATGATTTTGTGGTGGTGGAGACAGTGGATTTTCAACCCAATGAGCAAGGAAACTTTCCACCCCCAAC
ENSMUST00000002378.1	1	367	ENSMUSG00000002307.1	AGGGGAATTTGAACCCCCATGGCCACCGATGACAGCATCATTGTACTTGATGATGACGATGAAGATGAAGCTGCTGCTCAACCAGGGCCCTCCAACCTACCCCCCAATCCTGCCTCAACAGGACCTGGTCCTGGCCTGTCTCAACAGGCCACTGGTCTCTCCGAGCCCCGTGTGGATGGAGGGAGCAGTAACTCCGGTAGTAGGAAGTGCTACAAGTTGGATAATGAGAAGCTCTTTGAAGAGTTCCTTGAACTGTGTAAGACGGAGACATCAGACCACCCTGAGGTGGTTCCGTTCCTCCACAAACTGCAGCAGCGTGCCCAGTCTGTGTTTCTGGCCTCTGCAGAGTTCTGCAACATCCTCTCC**AGGGT**TCTGGCTCGGTCTCGGAAGCGGCCCGCTAAGATCTATGTGTACATTAACGAGCTCTGCACTGTTCTTAAAGCTCACTCCATCAAGAAGAAGTTGAACTTAGCTCCTGCAGCCTCAACGACCAGTGAGGCGTCGGGCCCTAACCCTCCCACAGAGCCCCCCTCTGACCTTACAAACACTGAAAACACTGCCTCTGAGGCCTCAAGGACTCGCGGTTCCCGGAGGCAGATCCAGCGCCTGGAGCAGCTGCTGGCACTGTACGTAGCCGAGATTCGG
ENSMUST00000002452.1	1	46	ENSMUSG00000002379.1	GAGAGTTGACCTAGCCGGCTACCCTTGAGTTCGCCCAGACGCTTT**AGGGT**CGGCCGAGCAAGCCCAGCTAGGT
ENSMUST00000002532.1	1	101	ENSMUSG00000002458.1	CTGCGCACTGCGCCCCCTCCCCGGCGACCAGCAGGACTTCGGAGCGCGCGGGCGGCGTGACTCGGGGACGCGGCGATCTGCCAGGATCCTATGCTGCAGTG**AGGGT**CCAGAGCTGGCACCACAGAATCTGGGCAACCCCCTCCACTCACCC
ENSMUST00000002599.1	1	91	ENSMUSG00000002524.1	GCGACGGCGACTATAGCTCTCGTAAGTGAGTCCCTCGCGGCCAGGGGGCGGCCCTCAGCTCGGAGGACAGGTCAATGGCCAACAAGGAGG**AGGGT**CGGAGCCAGCAGCAGCGGCTGCAGCGGCGGCGGCGGCAGTGGTGGCAGCAGGAGACAAATGGAAACCTCCACAGGGCACAGAATCCATCAAG
ENSMUST00000003183.1	1	54	ENSMUSG00000003099.1	TCACTCGGCACTCCTTCGCGACGGTTCGGCCTGGTGCCGCGAGCGGCCGTTGCC**AGGGT**GGGGGTCGCTTTGCGGC
ENSMUST00000003356.1	1	53	ENSMUSG00000003269.1	TGGCTTTCTTCCTGCGGACCTAGGCTTAACGCCGTCCTTTCCGACCCTGACCC**AGGGT**CCTGCTGCCGTAGCTTGTTTCTACTGTGTACCCCAGATCCAGGCCACGTTGTCCGCTATGGCGGAACCAGAACCTCGTTTCTTTTCCAAGAAATGCACCCAAGATTCAGGACCCCCAACTTTCCCATCATGATGGAGCCAGAATCTGGCCCCCTTACGAGAAATGCACCCCAGGTTCATGCTAGGATCCCTACAGTGGTGGATCCAGAAGCCAGAGTCCTGGTGTCTTTCCAAGATTTGCATCCGAGATCTAGGACCCCAAAGC

				CCTTTTGATGATGAAGCCATGAGTCCAAGGCCCTGTGTCCTTCCAAGTAATGTTTCCAATATCCAAGCATCCTGTTCTACTGTGTTGGGACCAAGGAGCCAGGGCTTCCAAATAAAGCATCTAAAATTCAGACTCAGGAGTTTCTAATTGTGGTGATGGGTCCAGAATCCCAGGGACTGGTTGCCTTTCAAGTAATTGGCCCAGAAATTCATCCTCAGACCTATGAGCTGGGATTCCTAGGCACTTCTGACACAAACTCAGGACTCAGTTTTACTCCCTCTCCTCAGACTTCTGGTACCCATTCCTCTTCTGGACAGGAATCCAGGCCCCCAGCCCAAATCCTTTCTCAGGATGCAGGAGTCCTGACCCCCAGAACTAATTTCTTGACCCTGGTCCCCA
ENSMUST00000003435.1	1	229	ENSMUSG00000003345.1	CAGCTGGGCACCACAAGATTTAAGGCAGTGGGACCTGTTGGCAGAATGTCTTCTCTCTCTGCAAGCAACCCTGAAGCCACCAAGATGAGCACCCCAGTCCGGCCTGTGAGCGTACCCGGGTGTCAATAGCCGGGAGCCGAGGGGCCACCGGGAGCAATGGTGTACTAGGCCGGGCGCGAGCTCAGGTTTCGCACTCGGATCTCACGGCAGAGTCACCGTGGAGAGGCC**AGGGT**ACCACAAACTT
ENSMUST00000019676.1	1	5	ENSMUSG00000003345.1	GGCC**AGGGT**ACCACAAACTT
ENSMUST00000003777.1	1	93	ENSMUSG00000003680.1	GAGAGGGAATTACCGTGAGCCGGTGAGTGGAAGCAGCCGTCCCTCCCCAGCAGGCGCCCTCCCAACCCCGGAGTCTGCAGCAAGTGTTAATG**AGGGT**ATAGTATGTGCTGACCCTGCTGGAGGCCTGGGATGCAAAGTTCCACCGGGGCC
ENSMUST00000003858.1	1	259	ENSMUSG00000003760.1	TCGCGGGCGGTGGGGGGCGGGGTATGGCGCGCTGCGAAGCGCAGGGCGGCTGGCACAAACGGCGGCGCCGAGGCCGGAGGAAAAAGCTCGCCACCCCCATCAGTCCCTTCTCAAGCTCCTAGAGACAACTGTGGACTTGGGGACCAGCGAGCACCCCCAGAGCACTAGAGGAGCCCCTGCTGCCTGCCCTGCCTCACCCTGCCCCACACGAGGCCCAGCGGCCCCGGGCTGCATCAAGTGGAGGAGGAGGAGGCGGAGG**AGGGT**GGCACCATGGGCCCGGGCCGTGCCCTCCATGCCCGGGGGATGAAGACACTGCTGCC
ENSMUST00000061869.1	2	395,420	ENSMUSG00000003873.1	ATGGACGGGTCCGGGGAGCAGCTTGGGAGCGGCGGTGAGGCGGGAGGCGGAGGACTAGGCCCGGTCCAAGAACCCTAGGACCCCTCCGGCTTTGGGCTCGGGCGGGAGCAGGCTGGGGCGCGCGGATCCATTCCCACCGGCTCATCCGCACCCCGAGAGCGGACATCCGCGTGCGCGCCCCCGGGCAGGCCCGGGCTTGTCGCTGGCGCCACTTCCTGCTGGTGGCCTGGGATGGGACAGAAGGCCAGCGCCACCTCCTCCCACCCCCAGCTGGGGGTCTGTTTGCTTTTGGCATTCTGCTCTCTGGGTTTGCTGTGGAGCTGGGATGCAGGCCGGGTCCCGCCCCCTGTCCATCAGAAGCAGTAGCCAGGCCTTCCATGCTACTTGTCACTACT**AGGGT**CCCCAGCTCTGTCTCCCCTC**AGGGT**TATGAGCCTACCTATCCATCCCCCTGA
ENSMUST00000004140.1	2	14,72	ENSMUSG00000004038.1	CTGCCTTCCGCTTT**AGGGT**CTGCTGCTCTGGTTACAGACCTAGGAAGGGGAGTGCCTAATTGGGATTGGTGC**AGGGT**TGGGAGGGACCCGCTGTTTTGTCCTGCCCACGTTTCTCTAGTAGTCTGTATAAAGTCACAACTCCAAACACACAGGTCAGTCCTGCTGAAGCCAGTTTGAGAAGACCACAGCACCAGCACC
ENSMUST00000004200.1	1	41	ENSMUSG00000004096.1	CTTGGGCCTGGCGCCCCCGGCGCCGAGATTTCTGGGAGCTA**AGGGT**CGCATTGGTTCATGAGTGAGTTTCGGAAGGTGCTGCGTAGGACCCCCGCCAGAACTAAAAG
ENSMUST00000061351.1	1	303	ENSMUSG00000004099.1	ATGCGCGGGGCAGCGTTTGGCGCGGGCTGTGCTTCCTGTCGCGCGTGCCCTTAGCTGTTGGCGCCAAAATGGGTGGGGGCCGGGGTGCTGGCAAGCCCATTGACTGGGAGCTTGAGGGAGCAAGGGGATCAGCCCTCTGAAATAGAACAAGCTTGGGGACACCCTCAGGGGTTCCCCTCTTTGGTCAGCCAGGCTCCTGGGTGTGCAGGAAGTGCCCCTCTCCCGGCCTGTGGACACCCTGAAGCCCCCACTCCGCTCCAGCCTCCACTTCCGGTGCCCTGCAGATCCCGCCGCGCCCACCCG**AGGGT**CCCTCCGCCGGTTCCCCTGGCCCTGGTTCAGAAGGGCCCTCCTTCCCAGCCCCGCTGTCAAGTCCTAGGACCTTTTCTCTCTCATCCTGCCGGGCCGGGCCTGGGCAGCTTGAAGCCCTCGTGGGATTTTGTTTTGTTTTCATCCTAACGTAAAGGAGCTCCTGCGATCCTGGAGCTATCAAAGAGACTCTGCCTGGAAAGAGCTGGTGCTGCAGAATGGGCCCTCCACTTTGGCAGTGACATAACTCTGTCCCGAGATCCCAGAGCAATCGAGGAAACCTTTAACTCCATTCAAAGTGTTTATCAGGGGGAAGGAAAGATGAATGGTAGTGAGATGTCTCGGCCCCCGCCCTATTATTTTAGCCCCTGTAA
ENSMUST00000004389.1	1	57	ENSMUSG00000004278.1	GTCCCGCTTCCTTTCTGCCTCCTCTGGCCTGCATCCGTGGGGGAGGTGGCTGGCTGC**AGGGT**TCTCCGGATCTCTTCTGTGTTCCCACTACTCAAGCACCGAGTGGCGTTCT
ENSMUST00000004569.1	1	251	ENSMUSG00000004455.1	ATCCGTGCGCCGCCCGAGGCTGGCCTGAGGAGTCGGCGGCCATCTTGTTCTTCTCGTGGTTCCCAGTGGCGAGAGGAGGAGGAAGCCCGGAGCGGAGCGGGGCGGCTGGGGGGGGTGGACCCGCCGCGGCTGCTGCTGCCACCGCCGCCGCCGCCACCACCGCTCGTGGGGCTCGTGGCGTGAGGAAGGAGGACGAGTGAGACCCCGGGGCGAGCGGGCGGCGGCGCCGCTGCTGCTGCTGCTGCTGCGGG**AGGGT**CGGCGGCGGGACGGCG

ENSMUST00000004574.1	1	113	ENSMUSG00000004460.1	GAAGGGGCGCGCTACCTGTCTCCGCGGCCGGGCAAGAGAGAGACCCCGGCGTGAGGCGGCCTCCCTGGGCCGGAAGGGCTGGTCAGCCGACGCAGCGGCACCGGAGGCTGAG**AGGGT**AGGACCAGGGGACGCC
ENSMUST00000004750.1	1	64	ENSMUSG00000004631.1	GGCAGGCCAAGAATGCTATTATTCTGGTGGTGGGAGCTGGGAGACCCTTGTGCTTGGACGGGAA**AGGGT**CGGGGGACACTCAAGATGAGCCCCGCGACCACTGGCACATTCTTACTGACAGG
ENSMUST00000059625.1	1	7	ENSMUSG00000004947.1	ATACTCG**AGGGT**TCTTCCCAGGCCGAGCCGGAGCTGAGCCCGGAGGTCGGCGGTCCTCTCAACCTGTTCCTTCTGCTTCCCTCAGACTCGGTACCTCGGAATCGGTGTGGCTGAGTCAGCAAGGCCTCAGATTTGCCGGGTTCTTGTTTGCTGTTCCTATCAAGATGGGAGCTCAGACAAGTTATTGCTTCTGAGGATCTGGTGCTTTCATCAAGAAGGGACAGTTTGGTGCCAGCTCTTCAGTGAAGAGGAGGTCCCCCAGAGGTGCTGGGCAATGAACCTGAACCTGCAACCCAGCGTGGTGTGAAGTCTTCAGAGAAAGCAGAAG
ENSMUST00000005072.1	1	79	ENSMUSG00000004947.1	ATGCGCAGCGCGGTGCTTGGAGGCTGCGACGCCGAGTTTCACTCCGGCTGCCTCCGGCTCGGAGTCGGAGACATACTCG**AGGGT**TCTTCCCAGGCCGAGCCGGAGCTGAGCCCGGAGGTCGGCGGTCCTCTCAACCTGTTCCTTCTGCTTCCCTCAGACTCGGTACCTCGGAATCGGTGTGGCTGAGTCAGCAAGGCCTCAGATTTGCCGGGTTCTTGTTTGCTGTTCCTATCAAGATGGGAGCTCAGACAAGTTATTGCTTCTGAGGATCTGGTGCTTTCATCAAGAAGGGACAGTTTGGTGCCAGCTCTTCAGTGAAGAGGAGGTCCCCCAGAGGTGCTGGGCAATGAACCTGAACCTGCAACCCAGCGTGGTGTGAAGTCTTCAGAGAAAGCAGAAG
ENSMUST00000019213.1	1	7	ENSMUSG00000004947.1	ATACTCG**AGGGT**TCTTCCCAGGCCGAGCCGGAGCTGAGCCCGGAGGTCGGCGGTCCTCTCAACCTGTTCCTTCTGCTTCCCTCAGACTCGGTACCTCGGAATCGGTGTGGCTGAGTCAGCAAGGCCTCAGATTTGCCGGGTTCTTGTTTGCTGTTCCTATCAAGATGGGAGCTCAGACAAGTTATTGCTTCTGAGGATCTGGTGCTTTCATCAAGAAGGGACAGTTTGGTGCCAGCTCTTCAGTGAAGAGGAGGTCCCCCAGAGGTGCTGGGCAATGAACCTGAACCTGCAACCCAGCGTGGTGTGAAGTCTTCAGAGAAAGCAGAAG
ENSMUST00000005185.1	1	17	ENSMUSG00000005054.1	CAAGCCAGGTTTTTCT**AGGGT**CCAGGCACCCAGGTCTCCTAGTTGGATCTGTCTTCAGCTTCTCCGTGCTACCCCGACTACTGCTGCCAAG
ENSMUST00000005371.1	1	102	ENSMUSG00000005239.1	AAGTTCTGTAGCTTCAGTTCATTGGGACCATCCTGGCTGTAGGTAGCGACTACAGTTAGGGGGCACCTAGCATTCAGGCCCTCATCCTCCTCCTTCCCAGC**AGGGT**GTCACGCTTCTCCGAAGACTGG
ENSMUST00000006025.1	1	583	ENSMUSG00000005871.1	AGGATGGGCTGCCTACCCCATCAGGATTTTATGTTTTCCTTTGTGCTGACTTTGTGAATGGCTGCACTTCTGTGGCATCGTAAATCTTCAGAACTACTTTGCCATAGATTAAATTAAATGAATGTGGTAGGGATGAACTCTGGTCTCATTCATGTATTCTACTTCCGAAGGCCTATAGGCCATGTCCAAATCAGAAGCTAAAGTGCAGCATTACTCACACAAATTCTTTATCAGTGGTTGTATTCTGTAAGTTTGACATACAGGAGGAGTTAGGTCATCTTTAACCTTGAAACAGTCTCACCAGATAGAGAGCTTACCTGTAGCACTGCAGATCTCTTCCGATGGGACTGAGGCTCTGCCTTTTGCTTGAACCCTGTTTCTCTTCAGCTCAGACCCCATGTTCCATCCTCTTAGGAACTGTTGCTGCTGGGACCATGGCGTTTGGAGCCCAAGCCTGCGAATAAGCACCACTCCTCCTGTCTGGAGAGCTTTGCTGCCTTTGTCTCTTTCTTCAAAACAAAACAAGCAGCTACTCCATTCTTAGTGGTGAATTTCAAAATCCTTTTTAACCTTATAGGTCCA**AGGGT**AGCCAAGG
ENSMUST00000055687.1	1	29	ENSMUSG00000006519.1	AGAGTTGGACCGGGCTGCTGCGTGTGCGC**AGGGT**CCTCGTC
ENSMUST00000017604.1	1	48	ENSMUSG00000006519.1	GACTTGCGAAGTGGGCTGCAGAGTTGGACCGGGCTGCTGCGTGTGCGC**AGGGT**CCTCGTC
ENSMUST00000027415.1	1	126	ENSMUSG00000006576.1	TGCGTGGGGCGCCTGGAGAGGGGTCTTGCGGGCAGGTGGGATCCTGCGGGGACCCGAGCGCGGGGCCCACGCTGGCCTGGTCGGGGCTCCCCAAGAGGTCTCTGCAGCGCCCCCTTCTTCTCACCC**AGGGT**TTGGGTCCCATAGTGATTGAGAGACTCCTAAGTCTTCAGTCTTCAGCCCTGCC
ENSMUST00000007257.1	1	63	ENSMUSG00000007041.1	GGTGGAGCAGCTGGGTGTGGGGTGCACTGGGCCTGTGGGGAAGCCGTGTTGGAGCGAACTAA**AGGGT**CTGATCGGACTTGGGTTGCGCCGAAGGGACAGCCCTGAGTCTGGAGGAGAGAATCCCGGACCGTGAGACCCGCCTTCCCTTGCCCCGGCCCCTCCCAGTTCCCCCAGCGACGGCTGCTTCCTGGTCCCCGACGCAACC
ENSMUST00000007266.1	1	40	ENSMUSG00000007050.1	GGCACTCGTGTCGGTCGCTTGGGGCGGCAGCCAGGCCCC**AGGGT**TTTCCGTACAGCCTTACTGCCCACACCCCAGTGTGAGGAGGCTGCTCGGAGCCG
ENSMUST00000009003.1	1	29	ENSMUSG00000008859.1	CGGCGGCTGCTGCAGAGCGGCCGGGAGG**AGGGT**GGGTCTCCCTAGAGCGGAGCGCCGGAGTCCTCCTCCTCCCGCCGCCGCCCAGGCCGCCGCCGCTGCCGCCGCGCCTCCGGACTCCTCTTGCCGCGCCCCGCGCGGAACTCCGAGCGCGGTCCGATCGGCGCAGCCGAGGCCCAAGAGCCCGCGGGTCGAGCGGCTCGCGGTGCAGATTTTTCTTAATCCTCTGAGGA

				CTCTGGAAAACAGG
ENSMUST00000010051.1	1	55	ENSMUSG00000009907.1	GCCAGAGGCGGGACCAGAGCCCTAAGGGGCTCGAAATTACGGAAGTTTTGTGCGG**AGGGT**CGGGTGGCTGCTGGAGTTCCTGCTGGATTTACGGCTCCGGAGCTGGGGCTGCCGCTGGGGGGTCTCAGAGCCGCCAGCCTCCGCACGGTTTGCGGTGGTGACCCGGGCGCGACTCGACGGCGCTGCTGCGGGCCTTGTCTGTAGTAGGGGACCCCTCGGATCTCCACC
ENSMUST00000061164.1	3	11,300,494	ENSMUSG00000010110.1	CACTTTTAAG**AGGGT**TTTTTCGCCTCCCCCTCCGCCCTCCGAAGTGTGTCCACCTCTGGAGATCGGTTGCTGTTTTCTGTGAGAGGGGGAAGGAAATCACGTATACCAAAGGCAGGATTGAGACCTGGGCTAACTGCAAAGGTCTGCCTGGAAGTTCAGGGCCGCAGGACCAGGCTGTGGCTGTTTTCTCGACTTTAGGGGCCCCGGCCGGAGCTCTGGCAGTCAGAGCCAAGTCGGAAGGAGACTCTGAGGAGGCTTCGCCTTGGGCCTGGAGGAAGCTGACCGTTCTCGCCGTGTCC**AGGGT**GCAGGATCTGCGGGTGGCCGTGGGCTCCAAAGTCTGTCAAATACGGGAAAGGGCCTGGGGATTTGCTAGTTGAGGGGAGCGTTTGGGGAAAGAGGCTGTCTGGAGAATGACATTCTCCTCTCCACAACAGTCTGAGGTTATGCGACTCGATGATCCCGCGGAAACGCTACGGATCTAAGAACACGGATC**AGGGT**GTCTACCTGGGTCTCTCAAAGACACAGGTTCTGTCCCCTGCAACTGCTATCAGTAGCAGCAGTGACAGCACTCCTTTGCCCACTCCGGTGGCCCTGGTCCCCTCCCCTCCCGACACC
ENSMUST00000010254.1	1	193	ENSMUSG00000010110.1	GAGTTAGGAGTACGTCTAGGTGACGTGGCGGCTCCTGTTCTTTGGTCCGGCTTCCACTGCTTACAAGTCCTTCGAGGAGGCGGCAACGATCTGGGAAGAGTGGCGGTGGTGGTGGCGGTAGGAAACAGAAGAGTCTGAGGTTATGCGACTCGATGATCCCGCGGAAACGCTACGGATCTAAGAACACGGATC**AGGGT**GTCTACCTGGGTCTCTCAAAGACACAGGTTCTGTCCCCTGCAACTGCTATCAGTAGCAGCAGTGACAGCACTCCTTTGCCCACTCCGGTGGCCCTGGTCCCCTCCCCTCCCGACACC
ENSMUST00000010278.1	1	28	ENSMUSG00000010134.1	ACGTGTGCGGTCCCTCCGGCGCCGAGTC**AGGGT**CTCTCGTCGAGTCTGGGTCTAGGTTAGATTTGGAATCGTGGAG
ENSMUST00000011240.1	2	27,81	ENSMUSG00000011096.1	GGCGGCGTTGTGAGCTGGGGTTTGGGG**AGGGT**CTGGCCTTCCTGAGGTTGAGGGGCAGTGGGAGGGCGAGCCCCCGTGGGA**AGGGT**ATGGACTGCATAGGTCAGGGGGGCAGTGATCGTCCTGCGACTCCTGGCCGACTGCTGAAAGAGCTCACGCTCAACCCCATGTGTCTGA
ENSMUST00000012566.1	1	12	ENSMUSG00000012422.1	CCCGGCCCGGA**AGGGT**GATGTGGCTGGACCAGCACCGGCCTCACTATG
ENSMUST00000015712.1	1	108	ENSMUSG00000015568.1	AAAGGTTGACTTGCCCTACGGCGCTCCACCGCGCTCCAGTCCTCTTGCGCCTCCTGCTCAACCCGCTCCTGACTGCCCCACGCCGCGTAGTTCCAGCAGCAAAGCAGA**AGGGT**GCACCGGGAG
ENSMUST00000061747.1	1	180	ENSMUSG00000015568.1	AGACTCTCGATTTCTCCTCCTACTCCTCCTCCGAGGAATTCTGCCCCTTGTAACTGTTCTGCCCTCCCCTTTAAAGGTTGACTTGCCCTACGGCGCTCCACCGCGCTCCAGTCCTCTTGCGCCTCCTGCTCAACCCGCTCCTGACTGCCCCACGCCGCGTAGTTCCAGCAGCAAAGCAGA**AGGGT**GCACCGGGAG
ENSMUST00000056450.1	2	371,788	ENSMUSG00000015697.1	CGAACAGTATCGGGGCAAGAACCCTCTATTAGTTCCACTTCTGTATGACTTCCGGAGGATGACAGCACGGCGCAGAGTTAACCGCAAAATGGGCTTTCATGTAATCTATAAGACACCCTGTGGTCTCTGCCTTCGGACGATGCAGGAGATAGAGCGCTACCTTTTTGAGACTGGCTGTGACTTTCTGTTCCTGGAGATGTTCTGTTTGGATCCATATGTTCTTGTTGACAGAAAGTTTCAACCCTTTAAGCCTTTTTACTATATTTTGGACATCACCTATGGCAAGGAAGATGTTCCCCTGTCCTGTGTTAATGAGATTGACACAACTCCCCCACCCCAGGTGGCCTACAGCAAGGAACGCATTCCTGGCA**AGGGT**GTTTTCATTAACACAGGCCCTGAATTTCTGGTTGGCTGTGACTGCAAGGATGGGTGTCGGGATAAGTGAGTTGGTGGGGTGTACAGGCATTGCTGTCTCTGCCTTCAGGTTTATTACAGTTGCTTTTCTTTTCTTTTTTATTTGTATTGCTTTCCCTGTTTTCCTTTACCTCCTCTTTCAGCTAGAGTTCTGCTAAGGTCATTATGAAATACAGATACAGAAACTGGGTACAGTGGCACATACCTGTAACTTCAGAATTTGAAATTCAGCATTGTGGCAGTTTCATCTTGAGTTCTGGGCCAGCCTAGGCTTCATAATAACTTTGAAGCTAGGCTGAGCTAGCTACGCAGTGAGATCTTATTGAAAGAGAGAGAGAGAGAGAGGGAGAATGAATGAACATGAGATAGGGAGACC**AGGGT**CTGATCGTCTTAAATGTCCCCAGGAGTAACCCTGGAAATGTAGGGGTTATGTTCTGTTCCTGTCTCCTCTTGCTGTTTCTGTCTCCCCTTAACCTTTCATCCTTGTGTTCACCATTTAGATTCTACTTTATTCTCACTGTATCTTACTCATGCTTTTTCTCACTACCTTTACCTTATCCCCATCCTCTGTTATTGGTTGATTTTTGCCCTAAGGTAAGG
ENSMUST00000015893.1	1	259	ENSMUSG00000015749.1	AGTCTCGCAGCAGCCATTGAAGGGGAAGGAACTGCGGGCGCGCGCGTGTCTCTCTCCCTCACTCTCTCTGTGTGAAAGTGTGTGCGTGCCCGAGTGTGCGCGCGCGGGTGTGTGGACTCGGAGGTGGGGGCAGCCGAGTTAGTCCCAAGTCGTCGGACTCCATTTGCTATTCTTTTCTTTCTCT

				CCCACACCCGTGTGGTAGTGGGCGTTCGTCTTTGCGTCTCTTTTCATTCATCTCCAGACCTTTAGAGGTTTTTTT**AGGGT**TGGGGATAGTGGGGAGGGCAGGCGAGGGGAAAGGAGGAGGAC
ENSMUST00000015934.1	1	95	ENSMUSG00000015790.1	GCCCTACTCTTCCGGTCACGGTTCTCTTCCGACCTTGCGGGTGTTGGGCAGTAGTCTCAAGCTGGGGTGCTGGCGCAAGAATGCAAGCACATCAG**AGGGT**GGTTCGTCCATGATCGGAGATGCCCATCTGACGCCGCAGCCACCACGTGAGACAGAGCGCCGTCCCGGAAGGAAGCAGATTTCTCGGTCCCGGAAGTGCTCAAAG
ENSMUST00000016639.1	1	203	ENSMUSG00000016495.1	GCTCTGCCGAAGCAAGGTACTGTCCCTGCGCTGATCGCTCTGGAGCTCTGGCTAGAGGCCTCTGCTGCGGTCACCGTCCCCGCACCGTGTCGCGTGAGATCTCCAGAGGGACACTCCTGTTTGCCTTCTATATTTAACCGTGTACCTGAGATTTCCCCCGACACATCCAAAGTCCAAGTCCAAGAGAGCAAGGCCCAGAAGG**AGGGT**CAAG
ENSMUST00000016763.1	2	239,630	ENSMUSG00000016619.1	GCTTTCCAAAGATGAAACAAGGGGTGTGCATTTCAGAACAGTACTGTGTAGCCACGTGCCTGTGGGGCTGACACGTGTCAAACTCACAGGCACTTTCAGGAACTTGTCTCTTCATGGTGGCAGTGCTCTGTGAGCATCTGCCCATGCCTTGAATATTTACCAAAAGAATAAAAGCAAAAAAGATCATGACTGGACTGCCTTCTAGAGCTCCCCGGCCAATTTCAGTTGTAAATTAGTG**AGGGT**GGCTTGCTTTTTTTTCTAACATTCCAGCAATTTGCTGCTAAAGACTATCACTTTTGGAAACAAGAATTACAGGGGAGATGTGTGGGGTGTGACTGTAACTCGGTGTCTTGTCTTTATGCTTTAGGAGCTAGCTCATTGCATCTGACCTGAGTATGGGAATCACTATGAAGTCTGAGTGTCACAGGGAGGCCCCCGGAGGGCACTCTGTTCTTCTTCCACTGTGTGTGTAGCTGGTTCCAACCCATGGCTTAAACTTCATTTATGGTTTAACGTGTTAGAAACTTGCATCTTGTCTGTTTAATGTGAACTGAGGTGTGTATCTCCAGTTTGAAAATCTCACGTTGTGTCTTACATTTGCCTGAAGGAAGTGTGTGTTCTCTGTGGTC**AGGGT**GCATCTGGCAGATGCTAAGCCTGGGCCTTCCCACACTATAGCTCACACTATGACACATTCCCAGCCCTGCC
ENSMUST00000039852.1	2	16,877	ENSMUSG00000017119.1	AGTAGTTCTGTACAA**AGGGT**GGGAATCGCTCCCTGAGGCCGGAATATGAGCGCAAGGTAGTGCCCAAAGCAGTTGCAAAACGAGGTCTCATCCCTCCCTCAGCCTTCCTGCCATGGAAGTCTCCAGTTTCGGTAAATAAGAGACTTGTGTAAGAAGAACTACCAATTCCAGCATGCATTGCGGAACGAAAGGCCTTCTCCACAGCATCTCTTGGAAAGTGTAGTCTTACGGGAAAAGAGCTTCTCACACCGGAAGCAGGCACGAGTACCACAGGAACCCAGTCGGTACAGCGGAGACCTCCTCGCAGTTATGCGTCTTAGCTGCTATGAATCGCAGCGTTCTGTGTTCGTGTTTTGTGCACAGAAAATAGACTAAAAGGAGCTGTGGGTTCCAGGAAGACTACAATTCCCGTCCAGCCCCGCGATTCTCGGAAAAAACAAACAAACCAACCAACTTGAACGTGCTGGGGAGTTGCTGGGGAGTTGATGAGCCAGCGTCTGCCTAAATTTTACAGCTCCTAAGAAGGAAGAATTGCATTTCAGGCTGACCTAGAACTCTTGGACTTCCATTACCATCCTGCATCAACTTCTGAGTAACTGGGACTACAGCTCCAGCCAGACAGCATGGAACCACAGGTTACTCTAAATGTGACTTTTAAAAATGAAACTCAAAGCTTTCTGGTTTCGGATCCAGAAAATACAACCTGGGCTGATGTTGAAGCTATGGTAAAAGTTTCATTTGATCTGAATACTATCCAGATAAAATACCTGGATGAGGAGAACGAGGAGATATCCATCAATAGTCAAGGTGAATATGAAGAAGCACTTAGATGGCTAACATTAAGCAAGGAAATCAGCTACAGATGCAAGTCCACGA**AGGGT**ACCATGTTGTAGATGAAGCACTCCCCAAAAATGTGGTAGAAAACCAAGCGGCTGCCAGGACAGGGAAGAAGCCACTTGCACATTATTCTTCACTGGTGAGAGTCTTGGGATCAGACATGAAGACCACAGAG
ENSMUST00000017365.1	1	120	ENSMUSG00000017221.1	CTGGCATTTCCCAGAAGCCCCAGCGCCGGGAAGGAGTTTGCAGCTGCTCGGTCATCGTGCGGCCCGACGCGAGCCCGCGCTGGTGTGCAGGCCCGGCTCTGTGCCTGGTCTCTGGTGTG**AGGGT**TTACGCGAGGCCCCTGCTTCGGTCCCCGGACTAGGCCTCGACCCCGGGCGCC
ENSMUST00000017384.1	1	126	ENSMUSG00000017240.1	AAAATTAGCTCCACAGTAAGTAAAATAGATTGTTCCTCTCTTTTCAGGTAGTTTGTACCTCCTTTTCAGGCTCCATGGAAGCCATCACCGACAGACGTCATCTCGCTCTCCAGAAAACGTGCCGC**AGGGT**GCAGGCCCCGCCCCGCGGAAAGAAGGGCGGCCCTCCCTGGACGTGAAGCACGCTGGGACTCCGGAGTCTCGAGCTTCCCGGCAGCCTCCGCGGCGGGCGTGGTGCGTAAGGAGCTGACCAGCGGTGGCCGTTCTCCGTAAG
ENSMUST00000017904.1	1	90	ENSMUSG00000017760.1	AGAGCTGATCTAAGAGGTGGCTATAAAGCCCTGGCCGGCTGCGGCCCACCAGACGGTCCCGGGGAATTCGGAACTGCTCGATGCGCAGAT**AGGGT**TCAACCAGTAGGGCTTGGGGACCACTGGGGACCGCTGCCTCCGCTTCTGGTTGACCTTCCCGGGGCACACGGTTGTGGTGGCGTGTGATAGCGAAGACCCAACTGTGGCCAAGGCTGACCAAGTCAGGCAGTGAAAACTCGGGTACAGCGGCCAGACTGGCGGGATCCAGAGCGGTCAGGCCAAGAC
ENSMUST00000017975.1	2	126,235	ENSMUSG00000017831.1	GTCCTCGGAACTCGAGCGCGGCGACTCTGGAGGAGGAGGAGAAAGGAAGGCGGAACGGAGAGGCGGAGACGCAGCCCGGCAGGGGCGGCGGC

				ACGGCGGGCGGCGCTCATAGTCCCGCGCCGGCC**AGGGT**GAGAAGAAGGAGCGAGCAGGCGACGCCGCCGCTGCAGCCGCGGCGCATCCGATCTCCGGGCCGGGCCGGGCCGTGCGTGGCCTCGCTGCCGGGAGACGCGGCCC**AGGGT**AATTTCTCCAGAAAGAAAACAAAATTAATGCCTTGCATCCTGGAAGTTCATTTAGGAATCTGAAATTAGGGACTTCTTTAAAATTTGGAC
ENSMUST00000018005.1	1	114	ENSMUSG00000017861.1	CAGACCTGCAGACACGCTGACGCCTGAGAGCACCGCCTGGGGCCCGGAGCGGCTCGAGCAGCCTGAGTCCTGACCCCGGCCCGGCTCCCGCTCCGGGCTCGGCCGGCGGGCGTA**AGGGT**GCGGCGGGGTCCGGGCCGGGGGGATGTCTCGGCGGACGCGCTGC
ENSMUST00000018050.1	1	530	ENSMUSG00000017906.1	CAAGCGGCAGATTCGAAGCCGGTTCCAGCTCAACCTGGACAAGACCATAGAGAGTTGCAAAGCACAGCTAGGCATAAATGAGATCTCAGAGGATGTTTATACAGCCGTGGAGCACAGCGATTCCGAGGACTCCGAAAAGTCGGAGAGCAGCGACAGCGAGTACGTCAGCGATGAGGAACAGAAGCCCAAGAATGAGCCCGAGGACCCCGAGGACAAAGAGGGGAGTCGGGTGGACAAAGAGGCCCCTGCCATCAAAAGGAAGCCCAAACCCACAAACCAGGTAGAGGTCAAAGAGGAAGCGAAGAGCAACTCTCCTGTCAGCGAGAAGCCGGACCCCACACCCGCCAAGGACAAGGCCAGCCCAGAGCCTGAGAAGGACTTTGTAGAGAAAGCAAAGCCATCACCTCATCCCACAAAGGACAAACTGAAAGGAAAGGATGAAACGGATTCTCCCACAGTGCACTTGGGCTTGGATTCGGACTCGGAGAGCGAACTTGTCATAGACTTAGGAGAGGATCCTTCTGGGAGGG**AGGGT**CGAAAAAACAAGAAAGATCCCAAGGTGCCGTCGCCTAAGCAAGACGCTATAGGTAAACCGCCACCGTCGTCCACTTCGGCGGGCAACCAGTCTCCCCCAGAGACACCGGTACTCACCCGCTCAGCCACCCAAGCACCCGCGGCTGGGGTCACCGTGGCCGCCGCCACCACCAGCACGATGTCTACCGTCACAGTCACGGCACCGGCCACCGCCGTCACGGGAAGCCCGGTGAAGAAGCAGAGGCCGCTCTTACCGAAGGAGACTGTCCCAGCTGTGCAGCGGGTCGTGTGGAACGCATCAAGTAAGTTTCAAACGTCCTCCCAAAAGTGGCACATGCAGAAGATACAGCGCCAGCAGCAGCAGCAGCAACAACAACAGCAGAGCCAACAGCAGAGCCAGCAGCAGCAGCCTCAGTCTTCCCAGGGGACGAGATATCAGACCAGACAGGCTGTGAAAGCTGTCCAGCAGAAGGAGGTC
ENSMUST00000040191.1	1	57	ENSMUSG00000018166.1	GCACCGTGAGACACTGGGACCACAGCTGCTGCTCAACTGGGGAGTACAAATTGCCA**AGGGT**ATGTATTACCTCGAGGAACACAGCATGGTG
ENSMUST00000018441.1	1	16	ENSMUSG00000018297.1	AGTGCTGCTCCGGTAC**AGGGT**CGCGCTCGCGTCTGTCCTTAAGGCTCTCCTCGGTGTCCACGGCACCCTCTTTCCTTGCTTTGCAGCGATCCTACTGCCAGAAATTCGCC
ENSMUST00000018506.1	1	8	ENSMUSG00000018362.1	GGGCTGA**AGGGT**AGCAGACGTTTCCACAGCCGCCGACCCGCAGCTTGAGTGTCCTGCACCACCTTTCGTGGAAATCTGAGCCGGCTGTACAGCTTTCCTCCTTGTTCCTGCAGCC
ENSMUST00000018711.1	1	18	ENSMUSG00000018567.1	ACTTTGTACTGTGGGAA**AGGGT**TTTTCAGTTCACTCGAAACAACAGCAACCTTATCTGCGATGTCATATGTGTAACCCACAAGTTGATTCCAAAGCAGTTACGCTGAAGGCGTAAGAGGACCAGGCTACGGGTTGCGCTAGCAAGCTGAGCTAGTGGCGTATGTTAGCAGGCGGGGCCGGTCCGATGGTCGGGGGCGGGGTTGATGAATAGGGAAGTGGCGCAAATTCGTGGATCGCTCCGCCAAGTCTGTTCGTCGAAGCCGCCTCCGCCGCCGCCCCCTGTCCCGGCCCCCCCCCTGGGTTCCCTCAGCCCAGCTCGGTCCAGCCCGGTTCTCGGGAGA
ENSMUST00000018713.1	1	383	ENSMUSG00000018569.1	GCCCGCACCTGCCGCCGCACCGCCAGCTCCCTGTGCCGCGCACCGCAGCCTGGGGCCCAAGGGCCCGCATACTTTCTGGGGGCCACGCCCTAACGGCCCCTCCACTTCTTTGGGTAGTCTCGGAGCACGCCGGTAGGAACCGCCCGGCCTTCGGGGACCGCTTTTGTCTGGAACCAGTCCTTCGGGCGAAGCCGGTTCCCTCTGCTGTGAGAGTGTCGCTTCACCGGAGGGGACGATTTGTGTTTACCTCGGTTAACAAGATTTGTAGTTACCCGGTCCAAAAAAAAATCTTTTTCTCCTTTGGGTGACTTAAATCTCTATCCAAATTTTCTTGTGTTGCTGCTCCCCGGATTTTTGTTTTTTTGTTTTTTTGCTTTACTGT**AGGGT**CGCCCTCCCGGCGCGTCCCGTCTTTTCTGAGACAAGGAA
ENSMUST00000019117.1	1	31	ENSMUSG00000018973.1	TGACATACTGCCGAAAGGTTGTAGGGCAAG**AGGGT**GTCTCCCCCAAACGGCCCGACCCTCCTTCGGCCTCTAC
ENSMUST00000019183.1	1	220	ENSMUSG00000019039.1	TTTAGTCTTCCGGTCGCCATGGCGACCGGGCGCCTTGGGGTTGGCGAGACGCTGGAGGCCCTTAATGCAGCTGTAGGGCCTGGTAGCCCAGTGTGGTTTAAGGAAACCCATGCCCGGCACCTTCGTGTTCGAGACTTCTTGGCACCGCGAAGCGCGCTACAGGCGCGCTTCAGGGACGGCCAGGTGCCAGAGTGCGTGTTCCGTGCGGTCTCCTGCCTGC**AGGGT**CCCGGAGTGGCCCCTGTACTGCGCTGCGCGCCGACACCCGCGGGTTTATCGCTCCAACTACAGCGGCCCGCTGTCTTCGAACATGTACTCGGTGCCCTGGCCTCCTATGCTACTCCCGCCAAACCTGCCTCACCAGGCCCGCGAGTTGTCCTACACTGCCCAGCACTGCGCTGTAATTCGGGGACGCTCCGATTGAGCCAGCTGCGTGCCGTGCTCGTAGCCGATCATCTAGTAC

				GGGTACTGCGTGCTCATGGGGTACGTGTGTGCTCAGTGCCCCCGGTGCGGGACCCTCACATGTCAACTTTCCTCCAGAAACTTCGGGTGGAATGGCCCACTGCCTCGAAGAGCACCTCGACCGAAACACTGAGAACCTGTGTTCTTGCAAACCTTAATGGTTCTAAGGAAGCGACGCTGCCCCCTGGCGTCCTAGGCCGACTGTGTCTGAAGGAACTGGTAGAACAGAGAGGCACTGCTGGCTATGACCCCAGCATAGACCACTGTTTGGTGACTGAAGATGTGCTCTCTGTGCTCTCGGAGCTGCAGGAGGCTGTGCGCCACTGGCCAGAGGGCGGCCACCCAGGCCGGCGTCCAGATGCTGGTGTAGATGACTGCGTGGTTATACACGTGGTTAGCTGTGAAGAGGCATTCCAGCAACAAAAGCTGGATTTGCTCTGGCAGAAATTGGATGACCGGGCTCCTCACAAGCAGAAACACCTGGTGTGTGGTCCCGTGAAAATGGCTGGTGTACCCGGCACCCAGCTGACTGCCCCTCAGTACTACAGGCTCA
ENSMUST00000019354.1	1	4	ENSMUSG00000019210.1	TCCC**AGGGT**TTTCGTCTCAGGTTTGCTCCGCCGCCACTTTGAACCCAGATTCGAAGCTGTCCCCTGGCCGGACTTTGCCTTCGCC
ENSMUST00000019470.1	1	92	ENSMUSG00000019326.1	GCGAGCGAGAGAGCAAGCAGCCAGCAGGCGGGCGGGCGGGTGGCCGGCCGGCACGGAGGGAGGGGACGAGCAAGCGGTGAGCAAGCCAGCG**AGGGT**GCCCGGGTCCCGAGGGCAACGGAGATTCCTCAGGCCCCTCCGGTGCCCTCCCCGGAGCCCAGAGCACCTCCGGCACCCAGCGGAGCGGACACGGCCCGGCCTGGCC
ENSMUST00000019611.1	1	39	ENSMUSG00000019467.1	CCCAGCTTCCGTGGCCCCTCGGCCCTGAAACTTGAAGC**AGGGT**AGGGGTCCAGC
ENSMUST00000055515.1	1	41	ENSMUSG00000019505.1	AGTGACGAGAGGCTTTGTCCGGTTCGGCGGTCTTTCTGTG**AGGGT**GTTTCGACGCGCTGGGCGGTTTGTGCTTTCATCACATTTGTTAACAGGTCAAAATGCAGATCTTCGTGAAGACCCTGACCGGCAAGACCATCACCCTGGAGGTGGAGCCCAGTGACACCATCGAGAACGTGAAGGCCAAGATCCAGGATAAAGAGGGCATCCCCCCTGACCAGCAGAGGCTGATCTTTGCCGGCAAGCAGCTGGAAGATGGCCGCACCCTCTCTGATTACAACATCCAGAAAGAGTCAACCCTGCACCTGGTCCTCCGTCTGAGGGGTGGCATGCAGATCTTCGTGAAGACCCTGACTGGCAAGACCATCACCCTGGAGGTGGAGCCCAGTGACACCATCGAGAACGTGAAGGCCAAGATCCAGGATAAAGAGGGCATCCCCCCTGACCAGCAGAGGCTGATCTTTGCCGGCAAGCAGCTGGAAGATGGCCGCACCCTCTCTGATTACAACATCCAGAAGGAGTCAACCCTGCACCTGGTCCTTCGCCTGAGAGGTGGC
ENSMUST00000019649.1	1	72	ENSMUSG00000019505.1	ATAAATAGCGGCTCGCGCGGCCACTGAGCTCAGTGACGAGAGGCTTTGTCCGGTTCGGCGGTCTTTCTGTG**AGGGT**GTTTCGACGCGCTGGGCGGTTTGTGCTTTCATCACATTTGTTAACAGGTCAAA
ENSMUST00000019859.1	1	36	ENSMUSG00000019715.1	GAAGCGGAAGGCGGCGCCACCTCGGCGGCGGATTCG**AGGGT**TTGTTGTCAGTCGTGTCAGCTGGTGACATGCC
ENSMUST00000019950.1	1	74	ENSMUSG00000019814.1	AGCCCTGTGGACCCACGTGTGGAGCTGCCGGCAGGTACCGGGGAGCGGCGGTTCGGCTGCCGCGGTTCCGGAG**AGGGT**GTCCCTGCCTCATCATG
ENSMUST00000020099.1	1	80	ENSMUSG00000019942.1	TGGCACTCGGCCTCTAAGCTCCTGGAGTTGCTGCGTCCGCGCAGTCCGGAACTGCGGTGTGGCCCCAGCCGGGACAGAG**AGGGT**CCGTCGTAACCTGTTGAGTAACT
ENSMUST00000020174.1	1	77	ENSMUSG00000019998.1	AGCTGAGACCGGCTGCGCCAGGCAGTGGGCCCCCGGGTGACAGCGGCTGGAGGTGGCCGAGGAAGCCGGCGAGGTC**AGGGT**GACTCCTAGAAATCCACATAGCCTACCTGCATCTGATGAAATCAGCCAGCCAGCCAACCAGCC
ENSMUST00000059116.1	1	14	ENSMUSG00000020088.1	TGTGCTCTGAGGG**AGGGT**CGCGCCGCCAGCCACCGCCGGAGGAGCCCCTCGCGGCGTTGTAAGCATCAATA
ENSMUST00000020285.1	1	48	ENSMUSG00000020088.1	CGCGTAGCTGGCGGACCCGGGGACTGCTGGTCTGTGTGCTCTGAGGG**AGGGT**CGCGCCGCCAGCCACCGCCGGAGGAGCCCCTCGGGCCGTTGTAAGCATCAATA
ENSMUST00000020342.1	1	358	ENSMUSG00000020134.1	CCAGGTTGCTGGCTTCCTTAGTTTCTCGTCTGGCATATATTAGTCAAAGGGAGCACAGAAAATTCAGTCTTCTTGTTCCCTAGATCCCGAAGTCCCTACTGTTCTGCCTCTCTCAGATTTTTATATCTTCTTATATTTTTTTTTCATGTCTATTTATTATGTGCCTACATGTACCATGCTGTGCATGTCGAGGCCAAAGGACAGTTTGCAGCAATTGGTTCTTTCCTTTCACCACGTGAGGTCCCAGATCAAACCTCAGTCAAAGGTAAGCACCTTTACCCACTGAGCCATCCTGCCAGCTCCCTCCCTTCGTATATTTAGAAAAAGCTTTCTATATCTGCTTACATTATTTTATCC**AGGGT**CTTTAATTATACTTTGTAGAAATAATAGGGAAATGGACAACTTTGTTCAGTAAAGTGGCAGACAGACAAATGTACATTTATCTGTTTGTGTCAAATACAGAACCATTGACATGTGTTTCATGTGATTTTCTTGCTGTGTTCATGAAGACTTGGAAAATACTCTATTTAAACTGGAATCATTGTTCATGTTATTAACAAAACCTTTTTCTCTTTAGGAAATAATGCAAAAGGTGTCTCAAGGCTCCTGACCAGTGAACAGAGATTTGAGAAAGACAGCCAAGCTC

ENSMUST00000020358.1	1	39	ENSMUSG00000020149.1	GCGATCACTGAGTGGCGGCGGCTGCTGATTGTGTTCTA**AGGGT**CGGAGTGGGGTCGACGTTTGCTCTACCGGAACAGCTTAGCTCATTCCTCCCTTTCCATTACCTGTGGCGCGGAGAGTTGGGGCGGCGGCTGCGTCAGCAAGGGCGGTGGTGGCGGCGGCGGCGGCGGCAGCTGCAGTGACATGTCCAGCATGAATCCCGAATAT
ENSMUST00000020420.1	1	2	ENSMUSG00000020198.1	A**AGGGT**CTGTGGAAGCTGGGGGGGGCGGGCTTACTGGCTACCCCTTCTCCTCAGACTGCTCTCCGGCTACAGCCGTCGCTCTGGCCTCCACGGCGTCCCCTCCGCGGCGGCCGGAAACACAGCGGGGCGGTTGCCTGAGGTGCGGTCGCCGGGTCCCCGCACCTTCTAGGGCCGCGGCAGCGGCGTTTCCCTCGGAGGCCGCAGCCCACGGGCCGCCGCG
ENSMUST00000020604.1	1	366	ENSMUSG00000020346.1	GGTGGGGCCTGCGGGCGGCAGGGACCTGGCCCCGGCCTGGATCTGGAGCCGGGAGGGCGGAGGCTCCCAGCCCGGACCGATGGGCGGGGCCCAGGTTCCCACAGAGATCAGCCTCCCGGGCCATGTTGGTGTTAAAGCCTGTTTCTTCTCCTGAGCCCCGGCAGAACACAAGTGGACCAGTGGATGACTTCTCTTGTCTGAGCAAGAGATGGCCTAATCCCTGCAATCTCTCTACCACTGGCCTCTGAGCTGTAAAAGCCAGCTGGATGAAGGGATGTAACACGCGCCTGGGAGGGACACTGAAGTCAGGAGTGGGGGGGGAGGGGCCCGGACACACCCCTTCCCCCCCCAGACTCCTCCCCATC**AGGGT**GCACGTGGCCATGGACTTTGGACCTGGATAAGTGGAGAGAAGCTGTACTTTGGGGGATCTGATTCTCAGTTTTGGAAATGAAGTATTAGGTTGGGGGAGGGGGCGGGGTTGATGATCTTCAGGGAAGCGACAGAGAGAAGAAAAGAAAGGTACATGGCTTCTTCCTACTCTCAGCCTAGAAGAATAAACCCTTAGTGTGGGGACCTGAGCCAGGCAAGCCAAAGGCAGCCTTGAGCCCTCCCTCCCCTGCCCTCCCCTGCGGGGGCCAGG
ENSMUST00000020640.1	1	18	ENSMUSG00000020372.1	TCTTTCTTTTTCTCCAC**AGGGT**CGTGGTGGCAGCCGCTGTGGTGCTTGGCTCTCTGAGCTATCCGGTGCCATCCTTGTCGCTGCGGCGACCCTCGCATCAACTGCAGCC
ENSMUST00000020653.1	1	81	ENSMUSG00000020386.1	AGGAGCTGAGAAGAGCTGGGGCCCTGGCAGCCATAGCGCTTTGCACAGCCGGCTTGGAGCGTGTAGGACGGGCACGGAGC**AGGGT**TGCGTTCTCTGAAGTCGCAGACCTGTAAGATCTGGAT
ENSMUST00000003461.1	1	29	ENSMUSG00000020456.1	GGCGCTTGACACCCGGAGCTCGCGGCCG**AGGGT**ACTTGTGGAAGGCTTCAGGACAAA
ENSMUST00000060992.1	1	27	ENSMUSG00000020458.1	ACCCTAGGGCTTTGTCTACGAGTGGC**AGGGT**G
ENSMUST00000018744.1	1	164	ENSMUSG00000020534.1	GCGCTCTCCAGGAATTCGGCGATCCACTTGCCTCTGCCTCCCTAGTGCTGGGATTAAAGGCGTGCGCCACCACAACGCGTTTAGTCCCTTTCATAAAGACCGGAGGAACAGACGTTTACGGCCAGCTCCCGAAACCAAGTGAACTGGAGGCCACCCTGCACCA**AGGGT**TGGAACCTTTTCACAAAATCCACGCTCCTAATACAAGGCAACTCTGAACCAGTGCA
ENSMUST00000051716.1	1	57	ENSMUSG00000020608.1	TTTGGGCGGGTGTGCCCTGCTTGGCGGGCGAGCGGTGGCCGAGGTCCGACGCCCTC**AGGGT**GGCCTTCGTGTCGTGACAGCCGCGGCGTGTAGCTTCCCCGGGGTGACCGCGACTTGTTGGAGATCTG
ENSMUST00000020960.1	1	69	ENSMUSG00000020632.1	TTCTTCCGCCACCCGGATATGAGCCGTTCTCGCGAGAGCCGTCCCTCTTTCTAAGCCGGCGATCCGTC**AGGGT**GAAGCC
ENSMUST00000061672.1	2	62,500	ENSMUSG00000020661.1	CCACAGGCAGAGCCGCCTGAAGCCCAGCGCTGAGGCTGCACTTTTCCGAGGGCTTGACATC**AGGGT**CTATGTTTAAGTCTTAGCTCTTGCTTACAAAGACCACGGCAATTCCTTCTCTGAAGCCCTCGCAGCCCCACAGCGCCCTCGCAGCCCCAGCCTGCCGCCTACTGCCCAGCAATGCCCTCCAGCGGCCCCGGGGACACCAGCAGCTCCTCTCTGGAGCGGGAGGATGATCGAAAGGAAGGAGAGGAACAGGAGGAGAACCGTGGCAAGGAAGAGCGCCAGGAGCCCAGCGCCACGGCCCGGAAGGTGGGGAGGCCTGGCCGGAAGCGCAAGCACCCACCGGTGGAAAGCAGTGACACCCCCAAGGACCCAGCAGTGACCACCAAGTCTCAGCCCATGGCCCAGGACTCTGGCCCCTCAGATCTGCTACCCAATGGAGACTTGGAGAAGCGGAGTGAACCCCAACCTGAGGAGGGGAGCCCAGCTGCAGGGCAGA**AGGGT**GGGGCCCCAGCTGAAGGAGAGGGAACTGAGACCCCACCAGAAGCCTCCAGAGCTGTGGAGAATGGCTGCTGTGTGACCAAGGAAGGCCGTGGAGCCTCTGCAGGAGAGGGCAAAGAACAGAAGCAGACCAACATCGAATCCATGAAAATGGAGGGCTCCCGGGGCCGACTGCGAGGTGGCTTGGGCTGGGAGTCCAGCCTCCGTCAGCGACCCATGCCAAGACTCACCTTCCAGGCAGGGGACCCCTACTACATCAGCAAACGGAAACGGGATGAGTGGCTGGCACGTTGGAAAAGGGAGGCTGAGAAGAAAGCCAAGGTAATTGCAGTA
ENSMUST00000020991.1	1	62	ENSMUSG00000020661.1	CCACAGGCAGAGCCGCCTGAAGCCCAGCGCTGAGGCTGCACTTTTCCGAGGGCTTGACATC**AGGGT**CTATGTTTAAGTCTTAGCTCTTGCTTACAAAGACCACGGCAATTCCTTCTCTGAAGCCCTCGCAGCCCCACAGCGCCCTCGCAGCCCCAGCCTGCCGCCTACTGCCCAGCA
ENSMUST00000002980.1	1	36	ENSMUSG00000020664.1	GCTCCTCGGCGATGACGTATATGTTGCGCAGGCGC**AGGGT**GGGGAGACCTTGGATAAGTCTTACCAGGCGTTCAGCGGAGGTGAAAACCCCTGGTTGGAGGGACGGGACCGAGGGACG

ENSMUST00000015107.1	1	2	ENSMUSG00000020694.1	T**AGGGT**TAGAGAAGACAGTTGGTACAGAAGAAAGGAGACTGAGAAGGACTAGAGAGGAGAAGGCAGTTGGTGAAGAGAATGAACAGTGAAAAGAAAGGCTGGTGAGCCAGGGAAGCTAAGCTGAGCCAGAAAAGATCCTACTGTTAGGAAACAGAGGGAGAATCCATGAAGAACTCACACAAAATAGCAGGAAAAAAAAGACATAAAGCTTCATTTATAGAAAATTAAAATTGCTGGGCAGTGGTGGCATTCGCCTTTAATCCCAGCTCTCGGGAGGCAGAGGCAGGCGGATCTCTATGAGTTTCAGGACAGCCAGGGCTACACAGAGAAACCCTGTCTTGACCCCCCATCTTCCCCCCCAAAAAGGTGAAACTAAAAATTTCATCTGTCTTCAAATGGTTCCTTTAAAACTGCACTCAGGAAACAGGCATCAGGGCATATGCCTATACTGCCAGCTCCTAGGGCCTGGGACAAAAGGACTGAGAATTTAGAACAATCTTGGCTACATAGTGAGACTCTCTGAAAACAGATAAAGTCCTTCAGACACGTTCAGACATCTGGTCAAGGAAGCATCAGAAGAAAACAAAAAGCTGAGTCGTTACTTTGAAGTCCGTGTCTTGGCTCGTGAAACTAGAAATG
ENSMUST00000021052.1	1	34	ENSMUSG00000020710.1	GTCTCCCCATTTGAGAGAGAGAGAGAGAGATGG**AGGGT**ATGGGCTATGGACCTCGGAGGGCTCCGCCACTGACCTGTGTCCCTCCACTGTTCCACTTTCCTCAGCGTCCTGGC
ENSMUST00000021085.1	1	20	ENSMUSG00000020739.1	AGAGAAGCGGCCGCGCGGC**AGGGT**CCCAGCCGCGGGGGGCACGGCGCT
ENSMUST00000021087.1	1	96	ENSMUSG00000020743.1	GTCTGACCTAGTTCACCTGAGCGGGGCAAGGGATATGGTGACCCCGGCGCGGGGTGCGACCTGGCAAGACCAACAACTTCACGCAAAACGCAGGG**AGGGT**CCGGCCCAGCGCTCGGAGGCTTTCGTGGTCAGAAACAAGGCGGAGGTGCTGTCCTTAGTTTCAGGCCAGTGAAAACCTGCCGGGCTTAGACCGTC
ENSMUST00000016008.1	1	115	ENSMUSG00000020802.1	CAGAGTGGCAGTGGCACTGGTCGTAAAAAGAGCATTCCCTTGTCCATCAAAAACTTGAAGCGAAAACACAAGAGGAAGAAGAATAAGGTCACCCGTGACTTCAAGCCTGGAGAC**AGGGT**GGCAGTGGAGGTTGTGACCACG
ENSMUST00000019038.1	1	53	ENSMUSG00000020824.1	AGAAGCAGGCGCCAGAACACAACCGGAGTCCCTGAGGCTCCAGAACAGAGTC**AGGGT**GAGCCAGCCCCAGCCCAGCCCCAGGTTCTGGCTTCCTCTCTTGCTTCTCCCTCCTTTGGTTGCAGCCAGCAGAGCCCACTTAAACTCCGAGGTGACTCCCAGCTGTGTTGGCGAC
ENSMUST00000021197.1	1	13	ENSMUSG00000020840.1	CTTCCGGCGCTT**AGGGT**GCGAGAACCAGGTCCGGCCAGCTAGGCAGCGGACTGTAGTGTAACCCCAGAGCTCACCTGAAAACCCTGAAAACTAACGTTTCCTCCACGAAGCAGTTTGGGCGCC
ENSMUST00000021338.1	1	339	ENSMUSG00000020955.1	GAGCCAGGAGGCAAAGACGCTCATCCCAGGCCCTCTCCGCGTGGCCTCACCCTCAAGGGGACCCACAAGCGCAAACTCAGTGCCTAGCGGGCCCACGCCAGACTCTCGCCCAGAGGCGCTGGGCCCAAACCCCGGAGGCCCAGGAGAGGTGGCTCCGGAGGAGCCCTGCGGACGCCATGCTAAAAGCCAAAATGGCTGCCCCAAGGATGCCCGCAGCGCGCCGCCCGTGAGGAGGGAGCCGGGCGCGCCGTCACCGCTCGCCGGCCGGAGCGGCTCAGGTTCCAGCTACGGTCATCCAGTGCCATAACTTTTAAAGGATATTGCAAAGAAACTGGGAA**AGGGT**GAAAAA
ENSMUST00000047981.1	1	51	ENSMUSG00000021012.1	GCGGCAGCGGCGGCAGCGGCAGCGGCAGCGGCGTAGGGGGCCCAGGCTGC**AGGGT**GGCAGCCCGCGGCGGGCTCCAGGTAACCGAGGCGCCGCGCAGTGCCGAGCCGGCCGCCCGCCGCCGAGCC
ENSMUST00000021564.1	1	149	ENSMUSG00000021136.1	GCCGCGGCCACGCCGAGCGCAGCAGGCGCCACGCGCAGAGCACACGCTCGCACTCCAGCTCCGGGCCTCCGCCGTTCATGACCGTGACCCCGGGCGCAGGCTCCTCCAGCCCCTGCCGCTGGCTCTTCGGCCACTCCCAGCTGCTGCA**AGGGT**CCCCACCTCCCCAAGTGCTTTGAAGCTAGCCTGAGCCCCCCTGCCCGCTGCCCGCTCGTGGCTGCCCGGCTCCGCTGGCACC
ENSMUST00000062658.1	2	1508,1619	ENSMUSG00000021156.1	CTGGGAACTGGCTCCTCACCTCCTGTCTACTGGCTCAGAGTTTGTCAAGCCCTGAGTGTCAGCCGTTGTCATGCTGCTCTTTACAGTAGGCAGAGTCCACACCATGAGCTTAAACCTCCCAGCACCATGGGGTTTCTAACTACACCTCCCAATCCTTCCACAGAGCCTGGATTCCTTCTGAAAACATCCAGGATATCACGGTCAATGTTCACCGACTGCACGTGAAGCGCAGCATGGGCTGGAAGAAGGCCTGTGACGAGCTGGAACTGCATCAGCGCTTCCTCCGTGAAGGAAGGTTCTGGAAGTCTAAGAATGAGGACCGAGGTGAGGAAGAGGCAGAATCCAGTATCTCCTCCACCAGTAACGAGCAGGTGAGTCGCCGGTGTCGGTAAGAAGGCGCTGCTGATTCGGATTCTCCATGTACCCTCCTCACTGTCATAAACAGGTTTTGACATCTTCTTTCCCTTTCCTACAAACATCTGTAAAGTTCTCTGCACAAGTAACCAAACCAGTGCAAAGATGTGAGTGGGTAGAAGCAACCTGGAGCCTGACCCAGCTGGTGGGAGGAGAGTAAGTGCGCCGCTCGGCTCTGCGGGTCCGCTGGCTTTCACCACCAACCCACAGCAATAACGAAGCAAGGGGCTGCTGAGTGGATGGAAGGACTCCCTTCTCTCCTGCGCGTCCACTACAAGTATTTTCAACACAGAGGTATTTCCGTGTGTGCCAAGTAATAAGATATTACTTTTATAATGCCCACAGCTGAAGGTCACTCAAGAGCCAAGAGCAAAGAAAGGACGACGTAATCAGAGTGTGGAGCCCAAAAAGGAA

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ENSMUST00000058861.1	2	70,91	ENSMUSG00000021241.1	CTCCAGGGCCTTGTCCCTAACTGCCGAGGCGGTCAGGGCTGTCATTCCTAGGCGCTCGGGAAGGTATCG**AGGGT**GGAACGTCACTTAGGA**AGGGT**GTTGGGTTCTGCGTCTTCAGGATAGATGGGAGGCTAA
ENSMUST00000021706.1	1	6	ENSMUSG00000021277.1	GGTAC**AGGGT**CCCCATTACTTGAAGGATAAGGCTGGCACGGCTCCGACGTCTGTGTGGAAGCTTCTCCCTCCCTTCTGAGCTTCTCTAGACTCCTTACAGCGCACGGCACAGAATTTCAGTTTCCTAAG
ENSMUST00000060274.1	1	6	ENSMUSG00000021277.1	GGTAC**AGGGT**CCCCATTACTTGAAGGATAAGGCTGGCACGGCTCCGACGTCTGTGTGGAAGCTTCTCCCTCCCTTCTGAGCTTCTCTAGACTCCTTACAGCGCACGGCACAGAATTTCAGTTTCCTAAG
ENSMUST00000001307.1	2	80,303	ENSMUSG00000021282.1	CAACGCTGTCGCTCGGCCGGGGCAACCCATGACTCGCCGGTGGCCTTTGATGTGACAATCTCCCGGCGGCTGAGGGAGC**AGGGT**TTGTGTTCCGTGTTGTCCTCCTCGTTTCGAGCAGTTTCCCTGCCAGTCACAACCCGTGTCAAAATGGTGGCCTCCTGGGTTCCTGGAGTTGTGCTTTGTTACATGGGGATGTCAGCTGTTTTCTCACAAGGACTCGGGCTGTTAGAGCTCGGAGTGTTAGTTGTGTGAGGGACTCGGGGACGGGAAGTTGTCCCGGGGAGGAGTGATGCTAAACCTGT**AGGGT**TGTTGTGTGTTTTCTCCTTTTCTCTTTCAGAGCTGTTGCGCAGCCATTGGTACCTGTATTGGGGAAACATAGCATACAAGCAAGAAGCTTACAGCCTCAGTGGCGAAAATTTTTTCATGTCAGAGACCGAGAACTCTTGCAGTCGTTTATGTCATCCCTTCTTCTCCAGACAGAAGATACCAAAAAGTTGCAATCAAAGATCTCTTCATCTTATTGATAAAGTCACTAATAAGCCAAA
ENSMUST00000050993.1	2	80,303	ENSMUSG00000021282.1	CAACGCTGTCGCTCGGCCGGGGCAACCCATGACTCGCCGGTGGCCTTTGATGTGACAATCTCCCGGCGGCTGAGGGAGC**AGGGT**TTGTGTTCCGTGTTGTCCTCCTCGTTTCGAGCAGTTTCCCTGCCAGTCACAACCCGTGTCAAAATGGTGGCCTCCTGGGTTCCTGGAGTTGTGCTTTGTTACATGGGGATGTCAGCTGTTTTCTCACAAGGACTCGGGCTGTTAGAGCTCGGAGTGTTAGTTGTGTGAGGGACTCGGGGACGGGAAGTTGTCCCGGGGAGGAGTGATGCTAAACCTGT**AGGGT**TGTTGTGTGTTTTCTCCTTTTCTCTTTCAGAGCTGTTGCGCAGCCATTGGTACCTGTATTGGGGAAACATAGCATACAAGCAAGAAGCTTACAGCCTCAGTGGCGAAAATTTTTTCATGTCAGAGACCGAGAACTCTTGCAGTCGTTTATGTCATCCCTTCTTCTCCAGACAGAAGATACCAAAAAGTTGCAATCAAAGATCTCTTCATCTTATTGATAAAGTCACTAATAAGCCAAA
ENSMUST00000021807.1	1	381	ENSMUSG00000021377.1	TTCTGAGGAGCGGGGAGAGAGAGAGCGCGAGAGAGAGCGAGCGCGCGGCGCGAGGACCTCGGCCCCGCGCGACTTCTACACAGCGGCGGCCTTCTCGTGCGCACCCGCGGCCCCCAGCATGTCGGCGGCGGCGGCCCCCGCTGCGGAGGGAGAGGACGCCCCCGTGCCGCCCTCATCCGAGAAGGAACCCGAGATGCCGGGTCCCAGGGAAGAGAGTGAGGAGGAGGAGGAGGATGACGAAGACGATGATGAAGAGGACGAGGAGGAAGAAAAAGAAAAGAGTCTTATCGTGGAAGGCAAGAGAGAGAAGAAGAAAGTAGAGAGACTGACGATGCAAGTGTCTTCCTTACAGAGAGAGCCATTTACAGTGACACAAGGGA**AGGGT**CAGAAACTTTGTGAAATTGAA
ENSMUST00000021921.1	1	66	ENSMUSG00000021466.1	TGGATGTGGGCAGCGGCGGCCGCAAAGACCTCGGGACTCACGCGCAATGTGGCAATGGAAGGCGC**AGGGT**CTGAGTCCCCGGCAGCGGCCACGGCCGCAGCACCCGCAGCGCCCGCCGTGTGAGCGGCAGCAGCGGGTCTGTCACCCGGAGCCGGAGTCCCCGGCGGCCAGCAGCGTCCTCGCGAGCCGAGCGCCCAGGCGCGCCCGGAGCCCGCGGCGGCGGCGGCAAC
ENSMUST00000021990.1	2	64,198	ENSMUSG00000021518.1	GTTTGCAGGCCCTGGAGCTGGTCGCCGCGTTCCCAGGATCAGTCACTCCGCCGTAATGTGGGG**AGGGT**GAGAGCTCTACGATGTCGCCCTACTAGGCTGCTTCTTCAGGCTGCCTTCTCCCCCTGCTCCGGGACGCGGTGGTGGCGCCGCGACCCCGCCCTCGCGCGCGGGTCCTTCCCTGGGCTAGCACCCTTCTC**AGGGT**GCCAGACCCCGCCCCAGCGTCAGGCACCTTCGCTGCTGCGGTCCGTCGCTGCCGGGGTCCCAGCCTTCTAGGGCCGGGGCCTCCGGGGCCGCGGCAGGACGGGGAGAAGAACT
ENSMUST00000022276.1	1	3	ENSMUSG00000021756.1	GG**AGGGT**GGCGTGTGCGGTCGGGAGGCCAGAGCTTCGAGCCATCCGGGCTGCGGCTCCGCTGAGGGACCGGTGGTGTGGGCCGGGATCCGCGGGGCTGAGGGACGCTCAGGAGCGGCGAGGCTCGCGTCCGGAAGGAAGACCCGATAGAAGGAACATGACATCTAGAGGCAGCGAACTTGTTTCCGATTCATGCTTTATCATTTCTTAATTTCGTATGTTGGGAACATCCCTGCAAG
ENSMUST00000022383.1	2	4,17	ENSMUSG00000021835.1	GAG**AGGGT**GGTGCTGG**AGGGT**GGGAAGGCAAGAGCGCGAGGCCTGGCCCGGAAGCTAGGTGAGTTCGGCATCCGAGCTGAGAGACCCCAGCCTAAGACGCCGCTGCGCTGCAACCCAGCCTGAGTATCTGGTCTCCGTCCCTGATGGGATTCTCGTCTAAACCGTCTTGGAGCCTGCAGCGATCCAGTCTCTGGCCCTCGACCAGGTTCATTGCAGCTTTCTAGAGGTCCCCAGAAGCAGCTGCTGGCGAGCCCGCTTCTGCAGGAACCAATGGAG

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ENSMUST00000050772.1	1	257	ENSMUSG00000022199.1	GCAGAGCTGCAGAGCGGGGTCTCCCGGCCCTCTGCGTCCTAGCTCTCCGCACCTAGCCCAGCCAGACAGCAGCTCATTCTCTCGGCGCGGCCCATAGGGCCCCAGCGGTCGGCAAGCTGGCTCCCCGAGTAGCCACCGGGACCCCCGAGCCCAATGGCGGGGGCGGCAACAAAATCGACAGCGCCGTGGAGATCGCCCCCGGCTCCAATGGAGCAGGTCGGGAGCCTCGGAGATGCGGTCCCCCCCGAGCAGCTGC**AGGGT**GAGCGGGAGCGCCGGCGGGAGGGGGAGGGCGACGCGCTGGGCAGCAGCCTGTCGCTGGCCGCGCCCCCGGGACCCCTCAGCTTCGAGGCTCTGCTCGCCCAGGTGGGGGCCCTGGGTGGCGGCCAGCAGCTGCAGCTCGGCCTGTGCTGCCTGCCCGTGCTTTTCGTGGCGCTGGGCATGGCCTCAGACCCCATCTTCACGCTGGCGCCCCCGCTGCACTGCCACTACGGCGCCTTGCCCCCCAACGCTTCGGGCTGGGAGCAGCCCCCCAACTCCAGCGGCGTCAGTGTCGCCGGCGCGGCCCTAGCAGCCAGCGCCGCCAGCGGAGTCGTCACCAGTACGGACCCCTCGTGCAGTGGCTTCGCCCCACCAGACTTCAACCACTGCCTGAAGGACTGGGACTATAACGGACTGCCCGTGCTCACCACCA
ENSMUST00000022815.1	1	60	ENSMUSG00000022204.1	GGAGGTGCTGGAGTCAGACGTGTCAAGTTCGATAACACTTTTGAAAAACCTCCAGGAGC**AGGGT**G
ENSMUST00000022856.1	1	16	ENSMUSG00000022248.1	GCTTTTTGGACGCTC**AGGGT**GTTCTTGGGGCTGGGGTGGCAGGGGCTTTGAGGGGTCGGACGTCACCCACAGCCTGGCGCCAGGGGCTCCCTTAGTGGCCGCTGTGCGGCGAGCGGGCCGAAGTCGCGTTCTCCTGCAAGCCAGGTTTTCACACATCTTCCGGAAGAGGAGCATCCTTCTTCTCGGAGCCGACGGTACCGTGGACCATCC
ENSMUST00000022867.1	2	54,74	ENSMUSG00000022257.1	CCCAGTGTCCCGTCGCAGCGGCCACTCGGAGCTCTCGGTACAGTGCAGAGCCA**AGGGT**CGGGCGAGCGGTCCG**AGGGT**CGGGGCGGCCAAGGAGAGGGGCAGGAGCAGCGGACCCAAGACGAAGCGAGCGACGCTCTCACAAACTTCCACGAGCGCCGGAGCT
ENSMUST00000054014.1	1	360	ENSMUSG00000022430.1	CAAAGCAAAATAGGTGTGTATTTTGGCTTTGGTTTGCTTTTTAAATACAAGAGCAAGACAGAATCTAACTGTTGAGTCTGAGGATGTAGTGAGTAGATGAAGTGCCTTTCCGTGCTGCTCTGTGACTGGTCTGAAGGTAAGTTGGTTGTATTGTTGGTAGACTGTGCCAGGCTTCTCCCAACAGAGTAAAAGTGATTTGGCCCTGCACTTTAATGGTGGTTACTAAGTTCTTCTACATTCTAGCTTCGAAAGGGGGTGGCACTAGATTTTGTCATTCTGAACTCTGGTCTCAGTGTAGCTCCTGTCAGCATATCATTACAGAAGAGGCAGGAGTTTGGGGTATTGGAGGGAGCTCCCAT**AGGGT**AATCACAAACCAAGATGCAGGGCCTGCCTGTGTCCTGAGTGGCACTGATCCTCTTTTACTCTGTTGGGATGAGTCTTTTTTTTTGTACCTACTCAGGGCAGTTACTAACTTCATCTTCTCCCCTCTTGCTGTCATCTGCATTCGTGCTCTCCACCTCTTGGCATGTCTTTACCTTCTCTTTCTCTGCCACATCAACCTACACAATGTCTCCTCATTGACGTGGAAGATGTGGAAGATGTCAAGTTTGTCATCAACTACGATTATCCAAACAGCTCAGAGGATTATGTTCACCGTATTGGCCGAACGGCCCGCAGCACCAACAAGGGCACTGCCTATACTTTCTTTACCCCGGGCAACCTGAAGCAGGCTAGAGAGCTGATCAAAGTATTGGAAGAGGCCAATCAAGCCATCAATCCAAAATTG
ENSMUST00000023108.1	1	55	ENSMUSG00000022471.1	AGTTTAGGGAACAGGGGGTGGAAGCGGGAAATGCGAGTGGGCGTGCCCGCTTGA**AGGGT**CGAAGGGCGTGTTGTGCGTGATGACGCAACGTCGCTGATTGGGCGAGAGACAAGGAGCCCGCGTGGACGTGGTGCCCACCTTCTGCTGTCCCAGTGGCTTGCCCGCCTGCGGTTAAGTGAGCAAACCAAC
ENSMUST00000023292.1	1	138	ENSMUSG00000022620.1	CTGAGATCGACGCTGTCTACCACCAGTTCCTCCTCAATTTCGAACCGCCCTTGTCCCATGGCGCTGGAGCCTCCCGGGTCAATGTGAAGTGACTTCTGCTCCTGATCCCAAGCCTGTGCTGGCACCTCTGGGTGAAC**AGGGT**CAGATCCCCGCTCGTGACGTTAATGAAGCCCTGGTCCTTTAGGGGCTCTGTGGAGTTACACCCCAGGCCACCCCCTTCCGAGTTCTGACAGATTCGCTGGAGCTTCAGAGAGTGGACCTACAGACAGAAGGATTATTTGGGTCTGGCGGCTCAGGGGAGGAGGAGGGCTCGGGACTGGGGCCTCAGGTAGGGGCTGGCCTGGGCGCTCAAGGAACGAGCCTGCTGGAATCGCTCTGCCTTCCCTACCAAGGGACTGAGGACACAGGCCCATCTGTATCTCTGTC
ENSMUST00000023426.1	1	20	ENSMUSG00000022744.1	GAGGAGGCGCGGGGAGAGT**AGGGT**GCTGTGGTCGGAGCTGGAGGGCGAAGCCGGTGGAGTGAGAGGATGGGCGAGCAGTCTGAATGCCAGA
ENSMUST00000023451.1	2	499,669	ENSMUSG00000022767.1	AGCTGCAGAAGGACAACCGAGATGGCCGCCTGCGGAAGCAGGAGCTAGAAGAGCTGGTGCGTGGGCTGGAAGCCGAGAGCGAGAGCCTCACCGGGCGCCTGGAGGAGCTGCGGGAGCGCGAGCGCAGCCTGCAGCGGAGACGAAGTCAAGCATCACGAGCCATTCGAGGCGAGGCATGTGAGGCGGCACGGGAGCGTGCGGAGCGGGCTCGTGGGCTGCTGGAGGCGGCG

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ENSMUST00000023465.1	1	44	ENSMUSG00000022779.1	CCGGAATGGTAGCAGCGCTCCGACCCGGGCGGGGGCGTGGGGG**AGGGT**CCTGCCCTGGCGCGGCTTTTTCGCCATCCAGCCCTCGCCGTGGGGCCTCTGGGCGGCGGTGGAGCCGCGTTTAGTGGGCAGTGGTCGCTTTTCCAACGAGCTCCCCGCGGCCCCGAGGAGTCAGCATTGGCAGTCGTGTTGAGCTACAGAGGAGACATTTCTAAGCTTTTTTATTGCTGCTGTTCTGGGTCTGGGTGCAACGGTCTGTGGGCCCTGACAGCCAGGAGCAAGA
ENSMUST00000023515.1	2	71,107	ENSMUSG00000022817.1	TGGCGGCCCGCAGGAGAGGGGGGAGGAGAAAGCAGAGAAGAGTGGGGGCTGGCGGCCGAGGAAAAAGGGA**AGGGT**CTCCGAGAGTAGACGCGCGGGGGACTCGGCG**AGGGT**GCGTCCGGAGCAGCGACAACTCCGAGCGTCCCAGCGGGCCAGCGAGGAGGATGGTGGCGGCCGGGCGCGGACCAGCCCGGCCGCGGGCGCCGTGAGCCGGAGCGCAGCGCCCGGCATGCGGCTGCGGTCCCCGGCCTCGGCCCCGCTCCGCCCCCGCCGAGCGCCCCAGCCGAGCGGCGCGCATC
ENSMUST00000003321.1	1	26	ENSMUSG00000022822.1	GCCGCTATAAAGGCTTGTTTTGCTC**AGGGT**CCGATGTTCGCGAGCGTGCCCGGGCTGTTTGCTCTCGTGTGGGGAGGCTGGGGTGCAGAATTTCTGAAGTGAAAGGAGGAGTCTGCACCCTGGTCCTCTGTGTGGTGAAG
ENSMUST00000051289.1	1	139	ENSMUSG00000022863.1	CGTTCGCCCTGTCGGCCGCGCGCTCCGCCGCCCGCCAGTCTGGTCGGCGCGCGCTCAGCGGCGGCGGCGGCGGCCCGACGACGCAGCAGCGGCGCTCGCGCTCGGCTCCCCGGCCACGGGACGCGGTCGCACCCGGCG**AGGGT**GCAGCCCCCGGAGCGGCGGCGGCGGCGGGAAAAAA
ENSMUST00000023570.1	1	159	ENSMUSG00000022863.1	CGTGGGCCGCGTCGGGACTGCGTTCGCCCTGTCGGCCGCGCGCTCCGCCGCCCGCCAGTCTGGTCGGCGCGCGCTCAGCGGCGGCGGCGGCGGCCCGACGACGCAGCAGCGGCGCTCGCGCTCGGCTCCCCGGCCACGGGACGCGGTCGCACCCGGCG**AGGGT**GCAGCCCCCGGAGCGGCGGCGGCGGCGGGAAAA
ENSMUST00000057483.1	1	25	ENSMUSG00000022951.1	CGCAGTGAGGGAGGATGCGCAGTG**AGGGT**TCCTTGACCTTTTCTTCTGAGTTCGGCACCCTAAAGAAAACTGTATGTAAACTGCCCGTCGATGCACTCTAGCTACAGTATGGAATGCTGGAGCATCAGAAGCTGTTACGCAGTTTCTTAGGGGAGGAACCGCTGATGGCCACAGCGCCCTGAACACGGCTGA
ENSMUST00000023731.1	1	138	ENSMUSG00000022995.1	GAGCCGGGGAGCGGGCCAGCGGACCATCTTCACCGCGGTCGGGTCGGCTTGCGGAGCGGGAGGCAGCGGCCGGAGAGCCGGGCGGAACCTGCGGGGGCGGAGGCGGCGGTGGCAGCCGCGGCGCAGGGAGCAGGAAC**AGGGT**CAAGTCCTCCATACCAAGGACCAGGCTAAAACCAGATTACACTGCCCCTCCCTGGGCCCTATTGACTTAAAGCAGCCACTGTAATCATG
ENSMUST00000053183.1	1	183	ENSMUSG00000022995.1	GTCGCCGTCGCGGCTTCCGGTGCTAGGTGGAGGGCGGGCAGGAGGGAGCCGGGGAGCGGGCCAGCGGACCATCTTCACCGCGGTCGGGTCGGCTTGCGGAGCGGGAGGCAGCGGCCGGAGAGCCGGGCGGAACCTGCGGGGGCGGAGGCGGCGGTGGCAGCCGCGGCGCAGGGAGCAGGAAC**AGGGT**CAAGTCCTCCATACCAAGGACCAGGCTAAAACCAGATTACACTGCCCCTCCCTGGGCCCTATTGACTTAAAGCAGCCACTGTAATC
ENSMUST00000041991.1	2	325,1323	ENSMUSG00000023008.1	TGCCTCCTGACAAGGCCCGGCTGCTGCGACAGTATGACAACGAGAAGAAGTGGGATCTGATCTGTGACCAGGAAAGATTTCAAGTAAAGAATCCTCCCCACACCTATATCCAGAAACTCCAGAGCTTCTTGGACCCCAATGTAACACGGAAGAAGTTCCGGAGGAGAGTGCAGGAGTCCACTAAAGTCCTACGGGAGCTGGAGATCTCACTTCGCACCAATCACATTGGGTGGGTGAGGGAGTTTCTCAATGATGAGAACAAAGGCCTGGACGTGCTGGTGGATTACCTGTCATTTGCCCAGTGTTCTGTCATGTTTGACTTTG**AGGGT**CTGGAGAGTGGTGATGACGGTGCATTTGACAAGCTCCGGTCCTGGAGCAGGTCAATCGAGGACCTGCAACCGCCCAACGCCCTGTCGGCCCCCTTCACCAACAGCCTCGCTCGCTCTGCGCGTCAGTCCGTGCTCCGGTACAGTACTCTCCCTGGCCGCAGGGCCCTGAAGAACTCCCGCCTGGTGAGCCAGAAGGATGACGTCCATGTCTGCATCCTTTGTC

				TCAGAGCCATCATGAACTATCAGTATGGCTTCAACTTGGTCATGTCCCACCCCCACGCTGTCAATGAGATTGCACTTAGCCTCAACAACAAGAATCCAAGGACCAAAGCCCTGGTCTTGGAGCTGCTGGCAGCTGTGTGTTTGGTGCGGGGAGGTCATGAAATCATCCTGGCTGCCTTTGACAATTTCAAAGAGGTGTGTAAAGAACTGCATCGGTTTGAGAAGCTCATGGAGTATTTCCGAAATGAGGACAGCAACATTGACTTCATGGTGGCCTGCATGCAGTTCATCAACATTGTGGTGCACTCGGTAGAGGACATGAACTTCCGGGTCCACCTGCAATATGAGTTTACCAAGTTGGGGCTGGAGGAATTCCTCCAGAAGTCGAGGCACACGGAGAGCGAGAAGTTGCAGGTGCAGATTCAAGCGTACCTGGACAATGTGTTTGACGTGGGGGGCTT
ENSMUST00000038494.1	1	236	ENSMUSG00000023022.1	TGAACGACGGTGGACCAGGCACAGCTTGGAGTTTTAACTTTCAGTTTACAAAGACGCATGTTTGGCTGTTGCAGCAGGCAAGTTGTAACTGGTACTTACTTCTTGTTCCTCTAGAACCCTGAAAGTCTGCCCCAGCACTTTAGAAGAGGGACCCTGTCTGTGTTAAAGAAGAAGTGGGAGAACCCGGTGGCTGGGGCAGAATTCCACACAGACTCACTGCCAAACAGCAGCAGTG**AGGGT**GGGCACACAGCGGACTACCCTCCTGCTGAAGTGACGGACAAGCCTGCTCCTGGAGTCAGAGCTGACCGGGAAGAGCACACCCAGCCCAAACCTAGATTTGGATCTCGTCCGGAAGCAGTTATCCAGAGCCGGTATCCTCGCTCAGAGAACAGCCACGATTTTAAAGCCCAGGCCACGGAGAGCCAAAAA
ENSMUST00000024619.1	2	335,896	ENSMUSG00000023809.1	AGCCCGCATCCGCGCCGAGGGCCGCCGCGTCGGGCTCCCCGGCGCGCGTGCCCGCCAGCGCGCTGCCTAGCCTGGGATGTGCCGGGGATGCGCGCCCGCCGGCCCTGCGGCTCCTGGCAGCTGGGCGCGGGGCGATGGAGCTGAGCATGAAGAAGTTCACGGTGCGCAGGTTCTTCTCCGTGTACCTGCGCAAGAAGTCGCGCTCCAAGAGCTCCAGTCTGAGTCGCCTCGAGGAAGAAGGCATTGTGAAGGAGATTGACATTAGCAACCATGTGAAGGAAGGCTTTGAGAAGGCAGACCCCTCCCAGTTCGAGCTACTAAAGGTTTTAGGACA**AGGGT**CGTATGGAAAGGTGTTCTTGGTGAGGAAGGTTACAGGATCAGACGCTGGTCAGCTCTACGCCATGAAGGTCCTGAAGAAAGCCACCTTGAAAGTGCGAGACCGGGTCAGATCTAAGATGGAGAGAGACATCCTGGCAGAGGTGAATCACCCTTTCATTGTCAAGCTGCATTATGCCTTTCAGACCGAAGGCAAGCTCTACCTGATCCTGGACTTCCTGCGGGGAGGTGACCTCTTCACCAGGCTTTCCAAAGAGGTGATGTTCACGGAGGAGGATGTCAAGTTCTACCTGGCTGAGCTGGCCTTGGCTCTAGACCACCTCCATGGCCTGGGGATCATCTACAGGGATCTGAAGCCAGAGAATATCCTCCTGGATGAAGAGGGACACATTAAGATCACAGATTTTGGCTTGAGCAAGGAGGCCACCGACCATGACAAGAGAGCCTATTCATTCTGTGGGACTATTGAATACATGGCGCCCGAGGTGGTGAACCGGCGTGGACACACACAGAGTGCCGACTGGTGGTCCTTCGGTGTGCTCATGTTCGAGATGCTCAC**AGGGT**CCCTGCCATTCCAGGGGAAGGACAGGAAGGAAACAATGGCCCTCATCCTCAAAGCCAAGCTGGGTATGCCTCAGTTCCTCAGTGCGGAGGCTCAGAGCCTGCTCAGGGCCCT
ENSMUST00000024642.1	1	95	ENSMUSG00000023865.1	GGCTCCGCAGAGTGACCCTTTTTCTTGGAAAAGCGGTGGCGAGAGAAGTGAAGGTGGCTGTTGGGTAGGGAGTCAAGACTCCTGGAAGGTGGAG**AGGGT**GGCGGGAGG
ENSMUST00000024737.1	1	17	ENSMUSG00000023942.1	CTTATCTCCCAGCTAC**AGGGT**GGCCCTTTATCTCTCCCAGCTTCGCAGGACCCAACCTCCTGCCTGAGCCTGAGCCAGGACCCCTTCCTGGGGAACGCCCAGGTACCTTTGGCTCTCACCGTCCTGCCAACATCGAGTCTATAAATTTGCAAGAGCCAGAGGGAGGGAGCTGCCAGCCAGGCACAGCCGAGAACACTGGAGCC
ENSMUST00000024778.1	1	15	ENSMUSG00000023983.1	AGTCTCTGAGTTCG**AGGGT**TTGGAGGCGCCACCTTTTGATCCTTCGCTATGGGAGTGACGTGT
ENSMUST00000056742.1	1	57	ENSMUSG00000023983.1	GCTTCCTGTGTTTAGGGGGCCGCCGTTCGCGTGAAGGTCTGGAGTCTCTGAGTTCG**AGGGT**TTGGAGGCGCCACCTTTTGATCCTTCGCT
ENSMUST00000024967.1	1	11	ENSMUSG00000024151.1	CGGCCAGCGC**AGGGT**CGCTCTGTGCTCTAGTGGTGTTGGTGTGGAGCGGCTCGGAA
ENSMUST00000063145.1	1	30	ENSMUSG00000024181.1	GAGGCGCGGGCGCGCTCTCCTAGAAGTAG**AGGGT**CGCGCG
ENSMUST00000025014.1	1	30	ENSMUSG00000024181.1	GAGGCGCGGGCGCGCTCTCCTAGAAGTAG**AGGGT**CGCGCG
ENSMUST00000025073.1	1	7	ENSMUSG00000024231.1	GAGCCG**AGGGT**GTGTGTCCCGCAAAGCCCAGAGCTCCGGAGGACGACAGCCTCCCCGAGCCAGCTACCTGCCCGTCCTCCTCCCTTGACCTCCTCGCGCCTGGCCGCAGCGGCATTGTTTTACTAGGCTCCCTCGGGAGCAGGTTTCAACACTAAACTTGCACA
ENSMUST00000025133.1	1	41	ENSMUSG00000024283.1	ACCGCCGGCGCCAGTAACGGGGAGGTGCCGCGAGCCGCCG**AGGGT**GCGCTGAGACCTGGTGCCGGGGCTGCCCGCCGCCCGCCCGCCGCCCGCGCGCCCGCCCGCCTGCCTCGCGGCCGCTCTCCCCCTCCCCGACACACACACACAGCCGGGCATTG
ENSMUST00000025163.1	2	53,165	ENSMUSG00000024309.1	GGGTTTATTGATTACAGCGGGTAGAGCGTGAAGAGGTTAGCGTTTGGCTTGG**AGGGT**TCGGGGATCTCTTCTTTCGCTCTCCTTTGCCTAGGGAGTGGCTATTCTGGACGAAAAGAGGCTGCGGCGCCTCGGAGAGTT

				GCGGGTAGAAAGTGCTGTCCTTCTGC**AGGGT**CAGGGAGGGGGGATTCAGGTGCCTCCCAGAGCTTGAGACCCAGCGACCCCCGCCCAGGAGGCTTTCTCCTTCACC
ENSMUST00000025186.1	1	155	ENSMUSG00000024327.1	TCCCGGAGCCGGTGAGAGGTCCCTGCTGCTCCCTTACGGCGCTTTCCAGGCCTTTACCCCAACCAGTGGGCCATAGAGACGCGGGCCCAGAGAGACCGTAAAGTTGCTGATCAAAGGCTAGAGCGGTGTCGGGGGTGGGGGGCTGCATCCAGGA**AGGGT**GTTGGGGATGAGGTGGACCGGCCTTGGGGACAATGTAAGAGCGGAGCAAGTAGTATAGAGGAAGGGCTTCAAGGGACGCGGATCCCGAATAGGTAGATTGAGAGTCAAGTCGAGTCGTCTCTTGTTCCTCCGGTCAGCGTG
ENSMUST00000056284.1	1	155	ENSMUSG00000024327.1	TCCCGGAGCCGGTGAGAGGTCCCTGCTGCTCCCTTACGGCGCTTTCCAGGCCTTTACCCCAACCAGTGGGCCATAGAGACGCGGGCCCAGAGAGACCGTAAAGTTGCTGATCAAAGGCTAGAGCGGTGTCGGGGGTGGGGGGCTGCATCCAGGA**AGGGT**GTTGGGGATGAGGTGGACCGGCCTTGGGGACAATGTAAGAGCGGAGCAAGTAGTATAGAGGAAGGGCTTCAAGGGACGCGGATCCCGAATAGGTAGATTGAGAGTCAAGTCGAGTCGTCTCTTGTTCCTCCGGTCAGCGTG
ENSMUST00000025295.1	1	63	ENSMUSG00000024427.1	GGCGCGCGTGCGCACTGGAGCTCTCTGCCCTCCCATTCATAAAAAAGCCATTTTCCCAGGCA**AGGGT**TGCAACATCGCCGCTGAGGCAGCGAACAGAGCTGACAGCGCGGAGCTGGCGCTGCAGGGCTCAGGGAGCTTTGCCGGCTCCTCCGACTGACGTCTGCGACTTCAACGGCGACTGACCCACTCGGGTTCGGGGATTTACACAGACGTGGAGCGATGCTTGTGACTCTGCAGCTCCTCAAAGACCCCTAGAAGCCTGTCCCTTGGTGCAGTTCAGGACCTCCAGCCTC
ENSMUST00000007183.1	2	47,62	ENSMUSG00000024463.1	CCTGTCAGATCACCATCCCATATCGTCACGTGCATTCTACTGTCAA**AGGGT**ACAGTGGCTG**AGGGT**CTGTGCCCTGCTCCACGGCAGCCCCCGAATGGTGCCCACCATGGCACCTGATATCTTAGGTTTCTGGGTTCCACCCACAATGCTGTCACTCGTGAACCTCAGTGTGAGTCATTGGCAAGTCCTGGGTCTTCCTTCTCCCCAGAGTAATCACACAGAGCGCTCACACTCTCTCCTCCTGGGAGCCTGTGTGAGAATTAATTACCAGCACATCCCCGAAACTGGTGAAGTCGTGGCTGTAGGAGAATGTGTGGTGGGATACATCTCCTGGAAGGGACCTGCGGAAGTTAGAAATTAAGCGGTGGCTGGCGAGCCCTGCACATTGAGCTGGTTGGGAGAGGGCTACGGATCAGTTGGCTCTGTCTGGAGCCTGTAGAAT
ENSMUST00000025453.1	1	54	ENSMUSG00000024563.1	GGAGGAGCAGCTCGCCAAGCCTGCAGCTCGCGAGCGCCGAGCGAGCCTCCCGG**AGGGT**AGATTTACCGGGCTTTTTCTGAGTGTGGATTGTTACCTTTGGTAAGAAA
ENSMUST00000025477.1	1	71	ENSMUSG00000024584.1	GAGTTCCAGGGCAGCCCTGGCTACATAGAGAGACCCTGTCTCAAAAAGGAGGAGGAAGAGGAAAAAGAGG**AGGGT**TTGATGGAAGCCAGAAATGTTAGAGCATGATAAAGCAGGAATGTTACCAGGTGAAAGCTAGACTGAACTACAGAGATCCCCCATCTCAACATAAAGAAGTGACACACTTCCTCCTACAAGGCCACACCCCCAATCATGCCACTCCTGGGGCCATCTACACTCAGACCGCTCCACTGTGGTAGCTCCTAAGATGTAGCTTCTGCTCTGCACAGCTGACACTGCATTGCCCAAGCTCTTGAAACAATTTGAATTCAGAGGGACAATATGGAAAGATGGATCAAGTCGCAACTAGGAGTTGACAGGTGTCTGGTAACCAGTGCGGCGGTGGAGATGGCAACCTCGCTGGGAACGCGCTGGGGAGCCTGAGCCCGCAGCCGGAGACGCACTGCTCCTTGTGCTCCACCGCCCGCCACGCCGCCGCGCAGACCCTCCATCTTCCATTTCAGCTCCGGGCCAGGCTCGACCCTGCCCCGGGGTGGGGTAGGGAGCGGGCTCCCGCTTCTCTCGGGGCTCCAGGTCGTTCTCCACCCCCGGGCCCTCTGCGACTCAATTGCCTGGGTCCCCCCTCCCCCGCCACACACACTCACACGCGCCCGCGAGCACACACGCACGCACACAACACACTCACACGCCAGCAGGCTGCTGGCCGCTCAATGGACCGATTTCCCCGGTTTCCCTGAACCCAGCCTAGCCCGGG
ENSMUST00000025639.1	1	75	ENSMUSG00000024732.1	TACTGGCCAGAGACAAGAACTCGTAAGAGTAAGGGAGCAGGGCATCAGAGATTTTAAGAAAATGACGTTGAATA**AGGGT**GGACCGTGCGAGGCTCCGTGCAGGCTCTTTACAGAAGTCATTTTGTTATACTCTTAAATCCTAAGCGCAGGGGATAACCCCTCCCGCAAGCACACCCCATTAAACAGAGGAAAGTGAGGCTTAAAGAGAAAGGCACCAAGCGGAGAAACTTTGAAGCTGTTCCTTTTCCCTGTCCGAGCAAACCACAATACAGGCCACTGATGGCCACGGGTGA
ENSMUST00000025711.1	1	58	ENSMUSG00000024797.1	ACCCCTTTGAGTTGAGGTTGGAGCTATGGCGGCTGCGGCAGCTGTGGGGCCTGGCCT**AGGGT**CCGGGCCTGGAGACTCCCCAGAAGGTCCCGAGGCGGACGCTCCGGAGCGTCGGCGGAAGGCTCACGGGATGCTGAAGCTTTACTACGGCCTCTCGGAGGGGGAGGTGGCGGGGCATCCCGCAGGGCCTGACCCTCTGGACCCAACCGATCTCAATGGGGCGCACTTCGACCCGGAAGTTTATCTTGACAAGCTGCGTAGAGAATGTCCTCTGGCCCAGCTGATGGACAGTGAGACGGACATGGTACGGCAGATCCGGGCTCTAGACAGCGACATGCAGACCCTGGTCTATGAGAACTACAACAAGTTCATCTCAGCTACAGACACCATTCGAAAG

ENSMUST00000025749.1	1	53	ENSMUSG00000024830.1	GACGTAGGCACAGCCCGGTGCTGTCAGTCAGAGTTCTGCCTGGTCCGGGCCA**AGGGT**CCCGCGGACCGGCGGGGCC
ENSMUST00000025752.1	1	238	ENSMUSG00000024833.1	TCGCGCAAGCGCGCGCTAGGCAAAGCGTTTGGCGGGTTTTTCCTGATGCTGTGCTCCTCACGGAGAAGCTAAGGTGTAGTCCTCGGAAGCAAGTTTTCTCTCTGGATCGAGACCTCTCGAGGGCTTTTGAAGTATTTCTCTGTGACCTGGTGGCTGGGGTCGTTTGAGGGCTTAGGCCAGGTGGTCTCGTGACACGTCCCTGTCACCTTCCGGTAAAGCGAAAGGATAAGCGTCTGC**AGGGT**AGAGCTGAGGTCGGGGCCCGGCGGCAGGCGCCCGGCCACTCCCGGGTCACC
ENSMUST00000040772.1	1	103	ENSMUSG00000024965.1	CCAGCAACAGCCCGCCCTGGGGAGGGACTAGTACAACTTTCATGATAAGGCCACTACAGGCTGACCTCTGAAGGAAGCAACTGAGCAGGACCAGGCCAGACC**AGGGT**AACAGGTGTCCCACTGCCACCTGCAGCTGCAGCCCGTTGCAGGCTAGCAGAAACAGCCGCAGCC
ENSMUST00000026252.1	1	146	ENSMUSG00000025223.1	CGGGGCTGTGACCCCGCGGGGCGGGCGGAGGCTGTGCATGCGAGTCTTTGTGCGGCCTGCGGAGTGGAGCTCCCAGCCAGACCGGCCTGTCCCACTCGGGACATGAGCTGCTGAAGTTGGCTCCACCTTAGTCCTCACCCTTGCC**AGGGT**CCCTGAGGACTCCCAGGCGCTCCCCGCACCTCCCCTGACCCCCTCAGTTCTCCCAGGTTGTTCCTCAAAGTCATTCAAGCTGTACTCGCCGAAGGAGCCCCCGAACGGCAACGCCTTCCCTCCCTTCCACCCCGGCACC
ENSMUST00000026254.1	1	332	ENSMUSG00000025224.1	CTGGAGGAAGCTGGTGACTCTGGGGCTGACAAAAAGTTCACCAGGAAGCCACCTCGATTTTCCTGTCTTCTGCCAGATCCACGGGAACTAATTGAAATTAAAAACAAAAAAAAGCTGCTGATCACTGGTACAGAGCAGTTCAACCAAAAACCAAAGAAGGGGATCCAATTTCTGCAGGAGAAAGGCCTCCTCACCATCCCAATGGATAACACGGAGGTAGCCCAATGGCTCCGAGAAAACCCTCGGTTAGACAAAAAAATGATTGGAGAGTTTGTGAGTGACCGCAAAAACATGGACCTGTTGGAGAGTTTTGTGAGCACCTTCAGCTTTC**AGGGT**CTGCGGCTTGATGAAGCTCTCCGACTCTACCTGGAAGCCTTCCGTTTGCCTGGGGAAGCACCCGTTATTCACAGGTTGCTGGAGGTATTCACTGAGCACTGGAGGAGTTGTAATGGCTCCCCATTTGCTAATAGTGATGCCTGCTTTGCCCTGGCCTATGCTGTCATCATGCTTAACACTGACCAACATAACCACAATGTTCGAAAGCAGAATGCACCCATGACCCTGGAGGAATTTCGCAAAAACCTAAAAGGTGTGAATGGAGGCAAGGACTTTGAGCAAGACATCCTGGAAGACATGTACCATGCCATCAAGAATGAGGAGATTGTGATGCCTGAGGAGCAGACAGGTCTGGTCCGTGAGAACTATGTGTGGAGCGTGCTGCTTCACCGAGGTGCTAGCCCTGAGGGCGTGTTCCTTCGAGTGCCTCCTGGCAGCTACGATCTTGACCTCTTCACTATGACCTGGGGCCCCACGATCGCTGCTCTCTCTTATGTCTTCGATAAAAGCCTTGAGGAGACCATCATCCAGAAAGCCATCTCAGGCTTCAGGAAGTGTGCCATGATCTCCGCCCACTATGGCCTCAGCGATGTGTTTGACAATCTCATCATCTCTCTGTGCAAATTCACAGCTCTAAGTAGTGAGTCTATTGAGAACCTTCCCAGTGTATTTGGAA
ENSMUST00000026387.1	2	53,69	ENSMUSG00000025337.1	GGTAGCTTCTTCCCTGGTAGGTTCCGGAAGAGCCGCGCACTCCTTGGGCGTTA**AGGGT**TCGCGCGCCGC**AGGGT**CGTTTCAGCCGAGCACTTGGCGTCCCCTCGAGCTCGAGATCTGTGAACAGCCACC
ENSMUST00000026414.1	1	205	ENSMUSG00000025357.1	GTCCCCTCCTGTCCAGCTCGGGCTCCGGCGCCCCTGCTCTGACCGTGCGCTCTCTTGGGTCAAGGTAGAGCCCCCGCGAGCCCCGTGCCACTCGCACACTCTCGCACCCGGCCAAAAGGGCAGCGGAAGGGGCCGCCCCACCGACTGGGTGAGGGCTGCGGCGTCCAGAGAAGGAAGCGTTGACAGCTGGAAGCTGCTGCTGGA**AGGGT**TTGCGCTGGGACTCCGGGACTGCCGTAGCGCTGCGCAAGACGCAAGACCGGGGCTAACCCTCTGAAAAACAAGAAGCTGTACTACCAGGCTGTCTCTGTGATCAACTTCAGGAAGAGAAGAAGG
ENSMUST00000026416.1	1	135	ENSMUSG00000025358.1	GGCGGCAACATTGTTTCAAGTTGGACAAATTGTCAAGGGCTGAGCTCTCCTTGCGTTCCATCCCGAGCTGGGACTGCCGTGCTCACCCGGGGTCCCCCAGGTCCTCCGCTCCGAGTGTCGGGCCCGCTTTCGTC**AGGGT**TCCCGGGCCCCGCTCCCGGGGGCCTGAGCCGCCTCACTAGCGCTCC
ENSMUST00000026446.1	2	70,236	ENSMUSG00000025381.1	GGGGTCCTCGCTGCCTCGGAGGCGCTCCTAAAGCTGCCTGCTCGCGCGAGAGTTTGGAGGGGCGGGCTT**AGGGT**CAGTTTCGGTGGGGGGCTCGCACGGGACCCTCAGATCTCCGCTTAGGTGCCTAGTTAAGTGCGGGAAGCTGGGCCAGGCGGTCACTGGCCACCCTGAACCTGGCGGGAGCCGGAGCGCTCTGGAGAAGCCGGGACAGCCCCGTTTTTCCCAGCCAGCTGCT**AGGGT**TGGGACCCACAGAAAACAAAGTGAGAGTCCGGCTGCTTTCCAGAGCCTGGGCCACGGCGGCGGCCGTGGGAGCAGAGGTGGAGCGACCCTGTTACACTAAAG
ENSMUST00000026584.1	1	100	ENSMUSG00000025510.1	GGCCGAGCGTTCTCTGTACTCCGAGTGATCGCTCCTACCGTGGCTGCCGGGGCTGGTATTTCAAAGCGTGGTTGGTGAGTGCTCCGTGAAGCATAGCCGG**AGGGT**GTGGGGAGCAGTGTCCTGAGTTCCTCGCTCACTGGTGTTCCTAGTCTCCAAGCTGGCCTCAGGGACGCCCAGGAGGCAG

				AGCCTGAGATCTGGTGGCTCTGAGAACCATTTTGACCACTGCTTAAGCTTCTGTAGTTGGAGTGGCAAGATCCCACCTGCTAGGTGAAGGGCAGAGAGTGACTTTTGACCTGTACCTGCTGGTCCTGACTTGAGAGGCCCAGG
ENSMUST00000026666.1	1	52	ENSMUSG00000025579.1	ACAGACCACGTGACCCACGCTGCCCGCTGAGCCTGGGGGTCTTCGGCCTGG**AGGGT**GATTGCGCAGGCCTTCAGAAGTATTCATGCTGCCCCGAACCAACAGGCTTTCACC
ENSMUST00000059097.1	1	24	ENSMUSG00000025647.1	AGATTCGATTTCCTTTTCTTTGAA**AGGGT**AGGAGATTGAAACTGAGTGGCCTCTGATGAAAAGAGGGGAAGTCCTGGGCTGCAGGAGCCCCTTGAGTGAAGGCGGAGGCTAACATGGGG
ENSMUST00000058351.1	1	1365	ENSMUSG00000025791.1	CTGAGCCCTCTGCAGCAGCCAGAGCCGCAGCCACTGTCGCCTCGCAGCCAACCGCCACCATGGTGAAGATCGTGACAGTGAAGACGCAGGCATATCCGGATCAGAAGCCGGGCACCAGCGGATTGCGGAAGCGAGTGAAGGTTTTCCAGAGCAACGCCAACTATGCGGAGAATTTCATCCAGAGCATCGTCTCTACCGTGGAGCCGGCGCTGAGGCAGGAGGCCACGCTGGTTGTGGGCGGGGACGGCCGCTTCTACATGACCGAGGCCATCCAGCTCATCGTACGCATCGCTGCAGCCAACGGGATTGGTCGCCTGGTTATTGGGCAGAATGGAATACTCTCCACCCCTGCCGTATCTTGCATCATCCGAAAAATCAAAGCTATTGGTGGGATCATTCTGACAGCCAGCCATAATCCAGGAGGGCCCAATGGAGATTTTGGAATTAAATTCAATATTTCTAATGGGGGTCCTGCTCCAGAAGCAATCACTGATAAAATTTTCCAAATCAGCAAGACAATCGAAGAATATGCCATTTGCCCTGACTTGAAGGTAGACCTCGGTGTTCTGGGAAAGCAGCAGTTTGACTTGGAAAACAAGTTCAAGCCCTTCACAGTGGAGATTGTGGACTCAGTGGAGGCCTATGCCACAATGCTGAGAAACATCTTCGATTTCAACGCACTGAAGGAGCTACTCTCTGGTCCAAACAGACTGAAGATCCGCATAGACGCCATGCACGGAGTTGTGGGACCGTACGTAAAGAAGATCCTCTGTGAAGAACTTGGTGCCCCTGCAAACTCAGCTGTGAACTGTGTTCCCCTGGAGGATTTTGGAGGCCACCATCCCGACCCCAATCTCACCTATGCTGCTGACCTAGTGGAGACCATGAAGTCAGGAGAGCATGATTTCGGGGCTGCCTTTGATGGTGACGGGGATCGAAACATGATTCTGGGCAAGCACGGGTTCTTTGTGAATCCTTCTGACTCTGTGGCTGTCATCGCTGCCAACATCTT
ENSMUST00000026987.1	1	75	ENSMUSG00000025869.1	GCGCGCACGGGTGGACGGAGACTATTAACACGCGGCTCTGAGAGCGTGGTTCTTGAGTTTGAGCTGCTGTTTCA**AGGGT**TTGAGCTGCTGTTGGGGCAGTTAGCGAG
ENSMUST00000027035.1	2	733,1020	ENSMUSG00000025902.1	CCCATTTAGTGAAGAAACTGAAATATGGCCCACTCACACTGCTGGCGGGTCTGAAGTGCGGTTGGCCCCAACACTCCTCCCAAAGTATCTATCAAGAGAATGGTCAGCAGAAGTTAGATCTAGTTTTTAGAGAAATCAACCAAGACAGGGAAGACAGAGAAAATGCATTCTGGACCCGCTACTGTTTTCAATCGTCATTTCAAACAAAACCCGTAGTTTATTTAAAAAAAAAAAAAACACGGAAAGAGAAAATTAGGCCCTGAGATCTTTGAAAAGATGCCCATTACTAGATACAAAAGAGAAGAGTCACTGTGGAGGTGAGGGACTGCGTCCCTGCTTCTGAGAGGCAGGAGAGCTACATGGGGAGACTGTCTCAAAACTAACAACAGAAGAGATAGAATTTTTTTTTTCTTAAAGAGCACCTGGCTAGAGAATCGATTTGTAAAATTGCTATTTCTACCCTTAGAGTTTCCTTGATTAAACATCTGAAATGCATTTTTTTTTGTTTTACTTTCAAGCTAATGTTTTTCAGAAAAAAATAAAAAGCTTTGAGGAAAAGCACATTATCAGTTAGATTTAAGACCAATTGCTTTTAAATTACCAATTTAAAATATCATTTTTTTTTATTTCTTAAAGCAGATTTAATTTTACCCCCTTTGTATGAATCTTACAGACCTGGAGTTTTAACTACTATCACTGATCTCTACACACAACCTCCAGCTTTAAATGGGAGGG**AGGGT**CACCACTGCTTTATAACATAACAAATTAGAGAAAAGCTGGCTTCTGTATGAGTTCTTTGGAGACAAAGTAGCTCCAGAAACTGCAGACCAGAAGCTATCAAAATCTCTGTGCTTTTTTGGAACCTCCAGTAAGCCAGATTTGGTCTCTGAAATAATACAGGAAAACCTCAGCATGTCACCTCATGGATACAATGAGCAGCACCTCCAGACATCTGAATTTCAGCCTTCCTATTTCCCCAAGAGGTCTTGGCGCCAGCGCCCGGCTCCAGCCAGT
ENSMUST00000055098.1	1	187	ENSMUSG00000025902.1	CTGAAGTGCGGTTGGCCCCAACACTCCTCCCAAAGTATCTATCAAGAGAATGGTCAGCAGAAGTTAGATCTAGTGAGCAGCACCTCCAGACATCTGAATTTCAGCCTTCCTATTTCCCCAAGAGGTCTTGGCGCCAGCGCCCGGCTCCAGCCAGTTTTCCCCAAGGCTAGCTTCCGATCCCTGCCTC**AGGGT**CGGGGGAAGCGGCGTGTCCCGTGGCCATAGCAGAGCTCGGGGTCGGTCTGGAGAGCC
ENSMUST00000027111.1	1	61	ENSMUSG00000025968.1	TTTCCGTCCTCCAGGTCGGGCTGACAGAGGTTGCCGTGGCCGCCATATTGACTTAGCGGCC**AGGGT**TTTGAGGGGTCAGGGAGACCCGGACAGGTCCGCGGAACTACTCGGTGGGCTCCGGAGGAAAGCCATC
ENSMUST00000027195.1	1	73	ENSMUSG00000026034.1	ATCGTCGTAATCGTTTGCAGACTTCTCGCCGTCGCCTTGTAAGCTTTGTCTTCGCCTTGCAAGCTTTGTCTTC**AGGGT**TGGAAAG
ENSMUST00000027298.1	2	11,191	ENSMUSG00000026124.1	CAGGACTGTAT**AGGGT**CAGCACTTCCAGCCTGGTGGTTCAGAGCTCCTGACCTGAGAGGGCTTCAACACCTGGACTCCAGGATCTTCCTTTA

				ACCCTGCTGTCTCTGGTCCAGGCAGAGGGCAGAGACATCTTCATCTTGCAAGACTGTGCATCCTGTAACCTGCTATAGTGATTCCAAGACCTGGAGTAA**AGGGT**GCCTCCGGGGCTAGGATATTTGAGTTTCAACTTCTGTGGTCATCGATCCCCAAGCACAG
ENSMUST00000027344.1	3	387,406,648	ENSMUSG00000026159.1	GGCGGTTGTCCCGCCCGGCCGGTTGGTGTGACCGGTCGGCGCGTGCTGCGCAGCTTCCTCGCCTTGTCCTGCCCGGCGGAGCCGAGCGGAGGCCGAGACCGGAGTCCGCGAGGGCGGAGGCGGCGGCGGCCAGGGCGGCCCGTGGGAAGGGAGCGCGGGGCCCCGGCAGCGCCGCCGGCTCCCGGCCCTGCCGGCCTCCTCGGTCGGAGCCGCGGCCATGGCGGCCAGCGCGAAGCGGAAGCAGGAGGAGAAGCACCTGAAGATGCTGCGGGACATGACGGGGCTGCCGCACAACCGCAAGTGTTTCGACTGCGACCAGCGCGGCCCCACCTACGTGAACATGACGGTCGGCTCGTTCGTGTGCACCTCCTGCTCCGGCAGCCTGAG**AGGGT**TAAATCCACCTCAC**AGGGT**GAAATCTATCTCCATGACAACATTTACACAACAGGAAATTGAATTCCTACAAAAACATGGAAATGAAGTCTGCAAACAGATATGGCTAGGATTATTTGATGACAGATCTTCAGCAATTCCAGACTTCAGGGATCCACAAAAAGTGAAAGAGTTTCTACAAGAGAAATATGAAAAGAAAAGATGGTATGTTCCGCCAGAGCAAGCCAAAGTGGTGGCCTCGGTTCATGCGTCTATTTC**AGGGT**CTTCTGCCAGCAGCACAAGCAGCACCCCGGAGGTCAAGCCCCTGAAATCCCTGTTGGGAGAGTCTGCACCCGCACTGCACCTAAATAAGGGCACACCTAGTCAGTCCCCAGTTGTAGGTCGCTCTCAAGGGCAGCAGCAGGAGAAGAAGCAGTTTGACCTTTTGAGTGATCTTGGCTCAGACATCTTTGCTGCTCCAGCTCCTCAGTCAACAGCTACAGCCAATTTTGCTAACTTTGCACACTTTAACAGTCATGCAGCTCAGAAT
ENSMUST00000027397.1	1	77	ENSMUSG00000026199.1	TGTTGCAGAAATCCAGTTTTCGAACGTGGTCTTGCGTGTGGCTCGGCTCTCGGGACATTAGGGGAGGCTTCTGAGGG**AGGGT**CGAGTGACGAGGCTTGGTGTCGGTGCTAGTAGTTCCGTTGGGTAGACTCTGACTGGTAACTCCTGGACTCGAATTGGGTCTTGGTGCTCTCCATTTCACTCCTGAAGATCCTCACGTATTTACCGCAGAACTGATTTGTGGGAGCGGGTAAAGGCTGAAGGGCATTTCTGCGTGGGGATGGCCAAACCGGCTGGCGATGCGGCAGTAGGATCTCGTTCTGGAGAGTTGTTTCTGCCCTCCGTTTCTTCTTCAGCCACGTCGCCAGCTCCAAGTGCAGCCTCAGCCCCTGCCTCCGTTTCCCTGTTGTCCCTCAACGGGGAAGCTCCACTCATTCGGGGCCTGAGCCTGGTGAGCCAAGCTCCTGGGGAGGCTCTGGCCTGGGCGCCGCGTACTTCCTGTCCAGGAGAGAACACAAGCTCGGGGGGAAAAGTATCTCCATATTCTCTGGAAATTTCAGAGAAATTATTTTGTTCAGCCTGTGACCAGATCTTCCAGAACCACCAGGAACAGAGAGAACATTATAAGCTTGATTGGCATCGCTTTAACTTAAAACAACGTCTCAAGAACAAGCCTCTCCTGTCTGCTTCAGACTTTGAACAGCAAAGCTCCACAGGTGATGCTTGTTACCGGGAAGCCTGCCTGGGAGCAGGGCGGGCTGGGGAGGACCCTGTGGGGCTTGAGGAAAGGTCACAGGTGGAGTACCAAACTTGCAGGGCCCATATTTGTCTTCAGGGGATCTTTCCAGCATCTCAGGATCAGATGACACAGACTCCAGCAGTGAAGAGGACTTGCTGCCACTGGATGAGGGGAGGGCTGAATCCGAGAAACCTAACCGGCCCCCCGGATTCTACCCACATCGGGTCCTTTTCAAAAACGCCCAGGGCCAGTTTCTTTATGCCTATCGTTGTGTCCTAGGCCCTCACCAGGCAA
ENSMUST00000058770.1	1	50	ENSMUSG00000026199.1	GGTCTTGCGTGTGGCTCGGCTCTCGGGACATTAGGGGAGGCTTCTGAGGG**AGGGT**CGAGTGACGAGGCTTGGTGTCGGTGCTAGTAGTTCCGTTGGGTAGACTCTGACTGGTAACTCCTGGACTCGAATTGGGTCTTGGTGCTCTCCATTTCACTCCTGAAGATCCTCACGTATTTACCGCAGAACTGATTTGTGGGAGCGGGTAAAGGCTGAAGGGCATTTCTGCGTGGGGATGGCCAAACCGGCTGGCGATGCGGCAGTAGGATCTCGTTCTGGAGAGTTGTTTCTGCCCTCCGTTTCTTCTTCAGCCACGTCGCCAGCTCCAAGTGCAGCCTCAGCCCCTGCCTCCGTTTCCCTGTTGTCCCTCAACGGGGAAGCTCCACTCATTCGGGGCCTGAGCCTGGTGAGCCAAGCTCCTGGGGAGGCTCTGGCCTGGGCGCCGCGTACTTCCTGTCCAGGAGAGAACACAAGCTCGGGGGGAAAAGTATCTCCATATTCTCTGGAAATTTCAGAGAAATTATTTTGTTCAGCCTGTGACCAGATCTTCCAGAACCACCAGGAACAGAGAGAACATTATAAGCTTGATTGGCATCGCTTTAACTTAAAACAACGTCTCAAGAACAAGCCTCTCCTGTCTGCTTCAGACTTTGAACAGCAAAGCTCCACAGGGGATCTTTCCAGCATCTCAGGATCAGATGACACAGACTCCAGCAGTGAAGAGGACTTGCTGCCACTGGATGAGGGGAGGGCTGAATCCGAGAAACCTAACCGGCCCCCCGGATTCTACCCACATCGGGTCCTTTTCAAAAACGCCCAGGGCCAGTTTCTTTATGCCTATCGTTGTGTCCTAGGCCCTCACCAGGCAAGTAACAGTCCAGATTGTGTGCTCACTCCCAACTTTTGTATACTAGGTTTTCCTCAGCCAATGTATGTCTTATTTTCTTCCTTTTGAGTAAGGCTATATCATACCTGACAGCATAATCTTGAACTGGCCAGAATCTTGAATGGGTCA
ENSMUST00000027401.1	1	72	ENSMUSG00000026201.1	CTTCGCACAGGCCGGAGACCGGTCGGTGTGGAGTTTGTAGTGGCAGACCCTGTGCTCGTTCCCGAGCGACGG**AGGGT**GGACTCGGCCAGAGGTGGGCTCGAGCCCCGCACCTCCTGCGCCGCCACCCCATGCCTGACG

				GGTGCGAGAGCTGGACCTGGCCGAAGGTGGGCCGGGGTTGAAAGAAGCGGCCTGCATGACCCGCCGGGACCCCACCGCATCGCCTGGAAGAGCCCACTCTCCCTGGAAGGAAGACCATCCCTGAAGAGGATGACTGAGACGTT
ENSMUST00000027499.1	1	77	ENSMUSG00000026278.1	GGCGGAGCCTGTGCTTCAGCTCGGGTGTGGACGGGGCGGGCGCTGGGGCGGGGCGCGCGCTCGCGGGTTTGAATGGA**AGGGT**CTAGACCGCCGGAGACGGCAGCGAGCGGGTCCTGAAACCAGAACTCCACCGCCGCCCCGCGCGCCATGAGGCGGGAGAGGTGTGGCGCCTCTCGCCCGCGCTTCGGCC
ENSMUST00000027534.1	2	44,425	ENSMUSG00000026309.1	GTCTCCCGCGGTGAGTGACGGCGCCGCCGCCGCCGCCGCCGCCC**AGGGT**AGCGCGGAGCCTCCGCTCCACTGCACCGCCGCCATGGACGTCTTCGGGGACCTGCCGGAGCCCGAGCGCGCGCCGCGGCCATCTGCCGGGAAGGAAGCACAGGGACGACCCGTGCTCTTTGAGGACCTGCCCCCGGCCAGCAGTACTGACTCAGGCTCTGGGGGACCTTTACTCTTTGATGATCTTCCGCCTGCTGCCAGTGGCAATTCAGGTTCTCTTGCCACATCAGGTTCCCAGGTGGTGAAGACTGAAGGGAAAGGAGCAAAGAGGAAAGCCCCTGAGGAGGAGAAGAATGGCGGTGAAGAGCTTGTGGAAAAGAAAGTTTGTAAAGCCTCTTCGGTGATCTTTGGTCTGAAAGGCTATGTGGCAGAGCGGA**AGGGT**GAGAGGGAGGAGATGCAGGATGCCCATGTCATCCTGAACGATATCACTCAGGAGTGTAATCCTCCATCATCTCTCATTACTCGGGTTTCATACTTTGCTGTGTTTGATGGACATGGAGGAATACGAGCCTCGAAATTTGCTGCACAGAATTTGCACCAGAACTTAATCAGGAAATTTCCTAAAGGAGATATA
ENSMUST00000027629.1	1	29	ENSMUSG00000026380.1	TGGGTGCTGCTTAAAGGTGGACGGCGGCC**AGGGT**TGCCGCGTCCAGCTCGGTGCCACGCCCCGGCCGGTGCTGCGGAAGCCTCAGCC
ENSMUST00000027686.1	2	25,32	ENSMUSG00000026427.1	GCCGAGTCTCAGCATGGCTGCCTCC**AGGGT**TG**AGGGT**CCGGGAGCCGCCACTCCTTCGTTTTGTTGACCGCCCCTGGCGTCTGTGCTCTTCTTGTCTTTCCTGAGCTACTCCAGCAGAC
ENSMUST00000027697.1	1	121	ENSMUSG00000026437.1	TTTTGCCTTCCTCCTCCTCTTACCCACCTTCCTGCACCCCTCCCTTCTCCCTTCTCCCGCAGCTCAGGTTACAGCTTCTTTGGGGGGAAAACCGCTCACCTTTCCAGGGCCAGGAAGAGCC**AGGGT**CCCGAGTAGGGACCCCGGCGGGGCGCGGGGCAGGGCACCTAAGCCTGGCAGCGCGGCCGCGGAGGGCGGGAGCCGGCTCGCCACGACCGGGACACGCGCAGAGTCCGCCGCGGCGGCCAGAGAGGGGCACCGCGCCGGGCAAGCTGAGCAAAGGACCCATCTTGGACCCCTGCTGATC
ENSMUST00000027877.1	1	198	ENSMUSG00000026585.1	GTGAGCGCATGCGCCTTGCGGAGAGTTCGGCCCTGACGGCTCTGGGCGGGTCTGGGCTGCTCCAGTGTTTTGGGGCCCAGGAGCAGTGGGAGGAGCCGGCGGGTTCACCGTGGTAACCGCTGCGCCGCCGCCGCCGCCACCGCCACCGCCACCGCCGCCCCGCCTTGCAGGCCTTGGGACTGTCACCGCTCTGCTTTG**AGGGT**ACTTTGGCCGGGTCTCCGGAAGTAGCCCTCCCAGATTCTCAGACACTCCCATTCTCCCCACGCCGCTGCCGCCGCCGCCGCCGCC
ENSMUST00000056368.1	1	102	ENSMUSG00000026585.1	CGGCGGGTTCACCGTGGTAACCGCTGCGCCGCCGCCGCCGCCACCGCCACCGCCACCGCCGCCCCGCCTTGCAGGCCTTGGGACTGTCACCGCTCTGCTTTG**AGGGT**ACTTTGGCCGGGTCTCCGGAAGTAGCCCTCCCAGATTCTCAGACACTCCCATTCTCCCCACGCCGCTGCCGCCGCCGCCGCCGCC
ENSMUST00000052228.1	1	102	ENSMUSG00000026585.1	CGGCGGGTTCACCGTGGTAACCGCTGCGCCGCCGCCGCCGCCACCGCCACCGCCACCGCCGCCCCGCCTTGCAGGCCTTGGGACTGTCACCGCTCTGCTTTG**AGGGT**ACTTTGGCCGGGTCTCCGGAAGTAGCCCTCCCAGATTCTCAGACACTCCCATTCTCCCCACGCCGCTGCCGCCGCCGCCGCCGCCATGCAAGGCGAGGACGCCAGATACCTCAAAAGGAAAGTTAAAGGGGGG
ENSMUST00000027927.1	1	330	ENSMUSG00000026618.1	TCCTCCGAAGTTGGAGTCTCTTACAGATGCCTCATCCCCTGTTAGCGTTTTAGTTTGGACCACCCAGCCTTGGACAATTCCCGCCAACCAGGCAATTTGCTATATGCCAGAGGCAAAGTATGCTGTGGTGAAATGTTCTGCCTCTGGGCACCTCTACATCCTGGCTGAAGATAAAATAGCACCTGTCGCTTCTGCCTTGGAAACAACATTTGATGTTGTTGCAGCATTTTCAGGTGTGGATCTGGAAGGTGGCACTTGTAGTCACCCTTTAACTCCCGATAAAGTGTCTCCTCTTTTACCTGCTACCCACGTGACTATGGCCAAAGGAAC**AGGGT**TGGTTCACACAGCCCCAGCTCACGGTATGGAAGATTACAGCGTAGCATCTCAGCACAGCCTCCCTATGGACTGTTTAGTGGATGAAGGCGGAATGTTCACCGATGCCGCAGGCCCTGAACTTCAGAACAAGGCTGTACTTAAAGAAGGAACAGATGTGGTTATAAAGATGCTTCAAGCTACCAAGAATGTGTTGAAAGAAGAGAACATTGTGCACAGCTATCCCTGTGACTGGAGAACTAAGACACCCGTGCTGATTCGA
ENSMUST00000062189.1	1	25	ENSMUSG00000026618.1	CAGTTCCTCGCCGCCGAGCTCTTCA**AGGGT**CTCTACCTTTAGGTACCGGGCGGCTGCCGTGGGCCGTGTGCGGAGGGCTCCGCCCGGCTCGTCCACCATGCACTGGGGGCTGTGCCCTCGCGGGCCCGGGGCGGCGGC

				GGTCGCCGCGGCT
ENSMUST00000027931.1	1	81	ENSMUSG00000026622.1	CAGACGAGGGGCTCGGGTTTCGGCGCGGTTGGCCTGCAGCGGGCGAGCCTGGGCTCCGAGCGGCGCGGTGGTGTGGTTGCC**AGGGT**GGCCGCTCGCC
ENSMUST00000060745.1	1	10	ENSMUSG00000026634.1	GCGGAGGAAG**AGGGT**CCGCGGCGGGGACGCGCCAGGCGGCGCCCGGGGAGAGGTAA
ENSMUST00000027961.1	1	18	ENSMUSG00000026651.1	GCTAGCTGAAGCTGCTGA**AGGGT**CCTTCGTTGAGCTGCCGTGGTCTCCGCCGCCTT
ENSMUST00000027980.1	1	16	ENSMUSG00000026669.1	CAGCTAAGAGGAAGGA**AGGGT**TGGTTACAGGAAAGGGAGTCGGATTGAGTCTTCAGCACTGCCTAGTGTACAGCTGCTTAGAGCACTGGCTTCACGTGCCTTCCAAAACCAGCTCAGACTGACCTTCGCCCATTCGTAGGATAAAAACCGTAGCACTTACATAAGCTTTCTCTTACAGGTGTGCTTATCTATTGATCATCCTCAAAAAGTCTTAATTATGGGAGAAGCTATGGACCTGGGAGCCTGTAAAGCCAAGAAGAAGAATGGAGAGCCATGTACACAGACAGTTAACTTGCATGACTGTGAATACTGCCAGTATCACATCCAGGCCCAGTACAAGAAGCTCAGCGCAAAGAGGACTGATCTGCAGTCCACTTTCTCTGGGGGACGGATTCCGAAGAAGTTCCGCAAAGGCACCAGCCTGAAGGAGCGGCTGTGCCAAGATGGTTTCTACTATGGTGGTGTTTCTTCCGAATCCTTCGCAGCGTCCAGGGCGGCGGCCATTGCTCCTAAGAAGAAGGTTCAAACCACGCTGACCAATCTGGTTGTCCGGGGCACAAACTCGATCATCCAGGAAACAAAACAAAAGCTTGGTATTCCCCAGAAGAGCTTGTCCTGCTCTGAGGAGTTCAGGGAATTG
ENSMUST00000028059.1	1	4	ENSMUSG00000026727.1	GGAC**AGGGT**GTGTTCCTGCTGCGGGATCCTGTTTTCGGCTGATCCAGTTCATCGCTCTCCACCCGAGTTTCCCTTGCAGGTCCCTAATCACACCCACCAGGTGTTGCTCGCTGCGAAC
ENSMUST00000028139.1	1	113	ENSMUSG00000026799.1	GGAAAGCCGGCTGTGACAGCTGCAACATGGCGGACGTGCTGAGCGTTGGTGTGAACCTGGAGGCCTTTTCGCAGGCTATTAGCGCCATCCAGGCGCTACGCTCTAGCGTGAGT**AGGGT**CTTCGACTGCCTTAAGGATGGC
ENSMUST00000052987.1	1	494	ENSMUSG00000026814.1	AGGAAGTCTACAAGACAGTCTCCATGCGCCTGAACATCGTCAGCCCTGACCTGTCTGGTAAAGGCCTTGTCCTGCCCTCTGTACTGGGTATCACCTTTGGTGCCTTCCTGATTGGGGCCCTGCTCACAGCTGCACTCTGGTACATCTATTCTCACACACGTGGCCCCAGCAGCATGGCGTAGTGCCCAGCCTGGAGCCTCGGGGAGCCCCCCAGCCAGCCCTTGCCCTGCAGGAGAGACCGAGCAGCCACAAGCTGGAAACCACCGGCCATGAACTTGTCCCAGGAACCAAACACCTCCCCTGCACCTGTTCATTCCTCCCAGTGGAGACTTCAGATTGGAATACCTTGGGATCTCCTCACCCCACTTTACAGAACTGCCCAATCCAGGGGCTCTGGGATATGGCTGCCCGGGATTACAGAAAGACACGGCACTGCCGTGCACACCCATGCTGCTTAGAAGCCTAAGCCTCTGCCTTCAAGCTGGATCCTGTGC**AGGGT**GGGCAGGCAAGAACTCAGACATGCCCAGCCTAGCCCAGGGCGGCCTGCATCTGGCCCCAGAAGCCTCCTCACCTGGACTGGCACAACTTCGGTTGGGGAAACAGAAGCTGAGGGAGCTTAGATGGGGTGGGGGATCCAAGCCCCTCCCAGCCCACCCATTGGCCAGGCAGCAGGGGGGAGTGGCCAGGCGGCTGGTTGTGGGCCAAGTCCTGCATATTCACTAATAAATCAGACATGAAACCAGTGCCCCTCTGGGTTGTATGGGAGAAGAGGAAGATGGGCAATT
ENSMUST00000054313.1	1	791	ENSMUSG00000026842.1	GCCAGCTCTGCCTCGGAAACGCACCAGTGAGAGCAGGTCTGAGCAGGTGGCCAAAAGCACGGCGATGCCCCCTCCCCGGCTGGTGAAGAAGAACGAGGAGGCTGCTGAAGAAGGCTTCAAAGACACAGAATCCAGCCCTGGCTCCAGCCCTCCCAGCTTGACTCCCAAACTCCTCCGCAGGCAGGTCACTGCCTCTCCTTCCTCTGGCCTCTCTCACAAGGAAGAGGCCACCAAGGGCAGTGCCTCAGGCATGGGGACTCCGGCCACTGCAGAGCCAGCACCCCCCAGCAACAAAGTGGGCCTCAGCAAGGCCTCCTCTGAGGAGATGCGCGTAAGGAGGCACAAGCACAGCTCGGAGTCCCCAGGGAGAGACAAGGGGCGACTGGCTAAGCTCAAGCCTGCCCCGCCGCCTCCTCCTGCCTGCACAGGAAAAGCAGGCAAGCCCGCACAGAGCCCCAGCCAAGAGGCCGGGGAGGCAGGGGGGCCCACAAAGACAAAATGCACGAGTCTGGCTATGGATGCTGTGAACACTGACCCCACCAAGGCCGGCCCACCTGGAGAAGGACTGAGAAAGCCTGTGCCCCCATCTGTGCCAAAGCCCCAGTCGACGGCTAAGCCTCCAGGGACTCCCACCAGCCCGGTCTCCACCCCCTCCACAGCACCAGCTCCTTCACCCCTGGCTGGGGACCAGCAGCCATCTTCTGCCGCCTTCATCCCCCTCATATCAACCCGTGTGTCTCTTAGGAAGACCCGCCAGCCGCCAGAGCGCATTGCCAGTGGCACCATCACCA**AGGGT**GTGGTTCTGGACAGTACTGAGGCCCTGTGCCTTGCCATCTCCCGGAACTCAGAGCAGATGGCCAGCCACAGTGCTGTACTGGAGGCTGGCAAGAACCTGTACACTTTCTGTGTGAGCTATGTGGACTCTATCCAGCAGATGAGGAACAAGTTTGCCTTCCGTGAGGCTATCAACAAGCTGGAGAGCAACCTCCGAGAGCTGCAGATCTGCCCTGCC

ENSMUST00000028205.1	1	10	ENSMUSG00000026851.1	CGCAGCGCCA**AGGGT**CTGGTTCCGCT
ENSMUST00000028258.1	1	29	ENSMUSG00000026895.1	ACGGGCGACACGGCCGAGGGCACCTGGTC**AGGGT**CGCGGCTACCGCCGTC
ENSMUST00000028389.1	2	10,105	ENSMUSG00000027004.1	GTGGGGACCA**AGGGT**TCGTCTATGGATCCAGAGCCGGGGGTGGAGTGGGGAAAGGTGTGCGGCTCCTGTCGGGAGCTGCCTGGGGCTACAGCATCACAGATAGAC**AGGGT**CTCACACTCCAGTCCCCTGAAAACTCAAAGCCTTCTCGGAAGGAGGAGCCGGAGGGCAGGGGACCGCGGGGCGGAGCTCTTGTCGGCCGAGGTGGGAAGGCGCAGCTGCGAGCCAAGGCGCTGACCTCCTCTGAGCTCCTCTGGCCGCTCGCAGGATCTTCCCGACCCTGCAGGACTTGGCAAACTCCCACCTCCGCTCCCATTAGTCCTCCCACCCCCACCAAATCTCCTCCCTCGGAGGTCCCCTATCCATCTCACTTTGCAGAATTTATCGCTTCTTCCAACACCTTTTTGCAACACCCCAGAACTCCGAGTCCCTTAACTGAATTTGACTTTTGTTTTTATTTCTCTCTGGCTTCCTCTTCTGCCCCCTCATCTGATTGATGTGCTAAGGCTGATGTCTCTGCCAGAGCGAGAGGAATAAATAGATGCTGCCTCGCCTAGAGGCTTAGACGCTTGGGAAGAGCAGCCGGCGCAGCGAGGCACCGGGCTCCGCCAAGCTAGTGGACCGGACCTGGGAGCACTTGGATCCAAGAGAACTGTGATTGTCCCAGGGGTGGGGGCAGCTCCCCAGGTCGTTGGGATCACCCCTCGGAACCGCAGGGGGAGACTTCGGAACGAAAGTGTCTCCCGCGTCCGTCGCTCGGCTGCGCCCTGCCCCATCCTGCTGGGACC
ENSMUST00000028463.1	1	136	ENSMUSG00000027067.1	GAAACGTAGATTCACGCGGGGCCCCGGGGTGGTGGGGTCTCTGCGATCAGGACACTACCCTCTGAGCGGAGTTGAGATTCCCACCCTGCTGGACATCTACACAACTAACCAGGAATTGGGGCACAGCATCCAGAGA**AGGGT**TCGTTTTCTCTGGTGCAGCCTAGGGCTGTGTGCTCAGGCCACCACGGGCAGGTGAAC
ENSMUST00000028800.1	1	66	ENSMUSG00000027327.1	GTTCTGCTGCTGCTACCGCCGCCTCCGCGGTCGTTTCTGACCGCCTGGCCGCGGGGCTCGCCTGCA**AGGGT**TCCTGCTGCTGTCTCTGGAGCATGGCAGGCTGCTGAGGTTGAGTGGCAGTGTCAAGTAGGAGCTGCGTGTCTTGCCCAGTGGCAGGGAGCGTGTCC
ENSMUST00000028817.1	1	21	ENSMUSG00000027342.1	ATTAGACGGTTGCGGGCGCAG**AGGGT**TGGTAGTTGTCGCTGTAGGCCTTCGCTGCCGCTTCTGCATCGTGAATCGGGGGACCTTGGCAGCCAGACCTCGTTCCTCTTAGAGTAGCTCTCATCTAGTCGCCACAACTCCGCCACC
ENSMUST00000037875.1	1	113	ENSMUSG00000027422.1	TCCCGGCGGAGGGGGCCGTTCGCCAGCTCCGAGGCAGAAAGTGCCACGACTCCACACACGCGCACGCAGCCAGCGAGCGGCCGGAGCGGACGGCGGACGGGGCGGACGGCGCC**AGGGT**CGCAGTGTGTGCAGCTGCTCAGGGGCGGCTTCTCGGTGGAGGCTCGGCCGGCTCCCCTCTTGCGGTTCCGCGGCGGCGGCGGCGGCTGCTCTTGCCCTCTCGCTCTCCCTCTCGCGTCTCCCGCTGCAGGTGGAAAGCAAGCCAGCCAAG
ENSMUST00000029005.1	1	4	ENSMUSG00000027502.1	AGGT**AGGGT**TTCGCCAGAGACCCCGGAAGCGACGGCTTCTCGTCTTTGCTAAGGCTTCTGGTTTTTGCTACGGTTTCTGATTTCGGCTTTGGG
ENSMUST00000029028.1	1	191	ENSMUSG00000027523.1	AGTGGAGGCACCTCTCGGAGTCTTAGACTTCAGAGTCTGAGACTTAGCGAGAGGAGCCTCGAGGAGACTCCTTCTCTCTTCTTTACCCATCCCTTTCTTTTACTTACAGCCACAAGCTGAGGCGCGGAGCTTTAGAAAGTTCGCAGTGGTTTGAAGTCCTTGCGCAGTGGGGCCACTCTCTGCAGAGCCAG**AGGGT**GAGTCGGCTTCTCGGTGAGCACCTAAGAGA
ENSMUST00000029270.1	1	42	ENSMUSG00000027715.1	CGCTCCTCCCGCCTGCAGCCTCTGCTCCGCGGGTCGGCCGCC**AGGGT**CCCGCGCTGCTCCGGAGCGGCGGGCGCTGTGCACGCTCTGCCGCCGACAGAACCGGACCGGAGCCGCG
ENSMUST00000029431.1	1	109	ENSMUSG00000027842.1	CCCCAAAGGAGACAAGGACATGAAGTAAACACCACGCTAAATGCTACAGACCCGCACAGGAACCTCTGGAACATCGGGACCAGCCTCCCGGGGACCGACGGGTACTGGG**AGGGT**CGTTTCTGAGTGAGATCCCATTTCTCTGGCTGGAGACACAGATGGCCTCAAATGAGAGAGATGCTATATCATGGTATCAGAAGAAGATTGGAGCATATGATCAGCAGATATGGGAAAAGTCAATCGAACAGACTCAGATTAAG
ENSMUST00000037340.1	1	450	ENSMUSG00000027942.1	CATCCACCATGTTTTCTGACGGACTCTAGCCTGGTTTTTTTTTTTTTTTTTTTTTTTAATCGAAAACCATATGGAAATGTTCGGAGAGCTCCAGGGAACCTAGGTTCCCTGGCTTCGGCAGAGCCTGGGCTAACGCGCGAGCGCGGCGGGACTGTCCTAGCAGGTGTTCCCGGAGAGAGAGGCGATGGCGTCTAGTAGTAACTGGCTTTCTGGAGTGAATGTCGTGCTGGTGATGGCGTACGGGAGCCTGGTATTCGTACTGCTGTTTATTTTTGTGAAGAGACAAATCATGCGCTTTGCAATGAAATCTAGAAGGGGACCTCATGTTCCTGTAGGACACAATGCCCCCAAGAGATCCCGTTTCATGCTGAAGGCCGGCACCCCTGTTCTTTAATGGGTAAGAATTTCCGCTCCTACTTGCTAGATCTGCGAAATACTAGCACTCCTTTCA**AGGGT**GTTGGCAAGGCCCTCATTGATACTCTCCTGGATGGATATGAGACAGCCCGCTATGGGACAGGGGTCTTTGGCCAGAGTGAGTACTTACGATATCAAG

				AGGCCTTGAGTGAGCTGGCCACTGTGGTCAAA
ENSMUST00000029554.1	1	44	ENSMUSG00000027944.1	GGTTGCTTTCCGGCAGCGAACGCTGAGCCCTGGCTATATCCGAC**AGGGT**AGCGTAAGCTGGTCGTGGTCTCGTGTTGCCCATGGGCTGCAGAGCTTCAAAGTTTCTAGTGCCCCTACTGGA
ENSMUST00000029603.1	1	2	ENSMUSG00000027978.1	CG**AGGGT**GGGGTGGAGGTCGGACTCCGGGCTACAGAGCTCCTGGCGCTCATCGCCTCTGGCGCTCCAGCCTTTGCTTCGCGGGGCTGACCCTTTGGGTCCCGGTGTGA
ENSMUST00000029679.1	1	2	ENSMUSG00000028044.1	AG**AGGGT**GGGAGCGCGTGCTGCTGGGAGTTGTCTGGAGGCCTGCGGCGCGGGGCTGAGCGCCCTCGGACAGAGCAATC
ENSMUST00000029683.1	1	282	ENSMUSG00000028048.1	ACTTGCTGTGCTAGTCGGTTCCAAGAGCTATGATATCTGTCTGTGTTTTATTTGGTAGGTCTTCTATCCCTCCAAGGCACAGAAACTTCCACAGTCTTCTCATTCGCTGGTCCTGAGTAGCTCCAGTTTCCAAGATCTTCTGGAGAGGGCATCATGGCTCTTTGAGGGCACAGATGGAGGGAGGGCTGAAGGTTGAAATCGATGGGGGAAAAGAGTGAAGAGAGTCTTCTTTGGAGTGGGCAGCAAACTCCCTAGCAGAGTGAATGAATGCAGGACGCCTCC**AGGGT**CTACGGGCACTGTCTAATCACTAATAAAGAAGTGTGCTGGTGTC
ENSMUST00000029698.1	1	66	ENSMUSG00000028062.1	TGGGCCACCGGAAGCGACTGAGGGAGAGCAAGAGGCTGCGACTGTAGGGGTGTGTTGGTGCAGGTC**AGGGT**TAAGAGACGCAGGC
ENSMUST00000029700.1	1	91	ENSMUSG00000028064.1	GTGCCTGGAGGGCCGCGCGCCCGTTCCAGCCAGGCTGAGCCTGCTTGCCTTGCCTGGACCCCCTTCTTTGCCTCGGATGGCACCCTGATTC**AGGGT**TTGAACACAGGACTTCTCAGTGTGGCTGGCTCAAGGAACCATCTGGTGACCATCTCAGGCTGACC
ENSMUST00000029723.1	1	739	ENSMUSG00000028082.1	AGCCAAGGACCCCTGTCATCCATTAGAGCGGTAATCAAGAGATCTTCTCGGACCTGTATTCAGAGTGAACTTCATCGGGACAGGAGGCGTCCAGAGATCACCATCGTGGCAGCAGAGCCACTGAGGCCGGCCTCGTGGTTTCCAGGAGCTCCACCTCCAGGACTGGGATTTCCCTCCACGCCTGGAGCAGGCCCTTGGAGACCCAATGACTTGGTTCCCGCTGAGCTCCCGCCATCCTATGAACAAGTGATAAAAGAAATCAACCAAGTCCAGGTCAATGCCACAAATAACAATAACGCTGCTGCCACTCCAAGGAGCACTATCACCTCTGCGACGCAGACGGACTTTCCGGAGGACATAGACAGCGATCCTCCCCCAACACTACAGGCGCCTCTCAAGCCTCTCCAGCCGTCACCCGCAGCCTCAGCTGGTAACCTCCCCCCAGGTGTGGCACCTTTAATCGTCTTCGATATCTGTGAAGAGCAAACTTGTCCTGAAAACCCCAGTGCTACAAGATGTCCAGTGCCAAGGCCAAGATCAAAAAGCAACCTCAGACCAGTAGCTAGGGATGCTAACAGTAAAGAGAAAAACAGCCAGAAAAGCCCAGTGACCCCCAGAGAAGACTGGCCACCCCACTGTCTACTGGACAGCACCTGCAATTTAGATAGCCAGGCAATGATGAACATTATGAACACAGAACAAAGCCAAAATACTATTGTTTCCAGGATCAAAGCATTTG**AGGGT**CAGACGAACACAGAAATCCCAGGACTGCCCAAGAAACCCGAGATTATTCCCCGCACGATTCCCCCGAAGCCTGCTGTTTCCTCAGGGAAACCCTTAGTGGCACCCAAGCCAGCTGCTAACAGAGCTTCTGGGGAATGGGACACATGGGCCGAAAACAGGCTCAAGGTGACTTCCAGAGAAGGGCTCACGCCATACTCATCGCCACAAGAAGCCGGAATCACCCCAGTAACCAAACCTGAATTGCCAAAGAAACCAACTCCTGGCCTTA
ENSMUST00000029773.1	1	188	ENSMUSG00000028129.1	GGGCAGCGAGCAGGGCAGCCGGTCCCAGTCCAGAGCGACCCGGAGCCTCCGCGGGACTCGAGTCCTAGCGAACCTCGAAGCATCATCCGCGTCCGTCTGCGGCGTTCGGGCTTCTCCGGCGCCGCGCAGGGGAGCGAGCTCGTGCATCACCCGCGCGGCCGCCGCTGGGGCTAAGAGCAGGGACACCG**AGGGT**GACTGACCGCTAGAACTCTTCCAGTCGTCCAAACAGCCATGACCCACTTCAACAAGGGCCCTTCCTACGGGCTCTCCGCCGAAGTTAAGAACAAG
ENSMUST00000029812.1	2	206,229	ENSMUSG00000028163.1	CGCGGGCCGGTTCTAGCAGCGCAGGCCGGAGCTCAGGGCCCCGCCGCGCCCGGCCCGCCCCGCGCTTCTCCGCCCGCGCCGCAGCCATGGCGCGCCGCTGAGCCGCCCGCCCGCCCGCCCGCGCCCCGACCCGGCTCGGGCTCCCGCCGGTCCGCGCCGCTCCGCAGCGGGAGCCCGCAGGCGAGGAGAGGCCGCGCCGCATCTCC**AGGGT**ACCCTCAGAGGCCAGAAG**AGGGT**GTCAGAGCCCTTGTAACTGGAGTTTGACGGTCGTGAGCTGCGCATCTTCACC
ENSMUST00000029950.1	1	60	ENSMUSG00000028282.1	CGCGGGGCTGCTGGGGAGAGGCAGCGGGGTGCCGCCTGGGATGGCTTACGCTCTGGGCGA**AGGGT**TGTGCCTGGCTGGGCCTCGAGGAGCCAGCTGCCGTCCTCGGGGAGCGCCCCTCGGAGCGTCTCGGGGGGCGCTGGGGCGAGCACCCGGAACATCGCCGGGTCTACAGCGCGCCCCTCCCCTCCCCCACCCGTGTCTCCCAAGTCCCTACTGCCGAGCTCTCGATGGCACCTATGAGAAGGATATAGGACC
ENSMUST00000030069.1	1	418	ENSMUSG00000028378.1	AAGTCCTGGGCGCTTTGCGAAGCATTCAGAGCGGTCTCCCGGGAAGGAGTTTCTGTGAGCTTGTGGTATACCAGGATGGTGCAGGCCAAGAGCTGGACCCTGAAGAAGCACTTCGAAGGCTTCCCTACGGACGGTAACTTCGAGTTGAAGACGACTGAGCTCCCACCCTTAAATAATGGAGGAG

				GTCCTGCTGGAAGCCCTGTTCCTCTCTGTGGATCCTTACATGAGGAGTTGCAGCCAAAAAACTGAAGGAGGGCGACAGGATGATGGGCGAGCAAGTGGCCAGGAGTCGTGGAAAGTAAAAACTCAGCTTTCCCAAAAGGAACGATTGTAGCGGCTTTATTAGGCAGGACATCACATTCCATTTCTGATGGGAGCCTCACTGCCTACTTTGGCCTGCTTGACATCTGTGGCGTGA**AGGGT**GGAGAAACCGTG
ENSMUST00000030091.1	1	49	ENSMUSG00000028394.1	AGCGACGCGGGAAGTCCAGACACCAGAACTGTCTGGAGACCTGAGCAGG**AGGGT**CGGGCCCCAGCGGAGGCA
ENSMUST00000030121.1	2	123,1092	ENSMUSG00000028413.1	GGATCCACAAAGTTTTGTGTTATCAGCTTATAGATAATAGAACCACACCTAAGGAACATAGACATAAAAGAGCCGCAGGGACCACAGCCTCAGGACCTCACCAAGGGAGGCGAGGGGCCAGAG**AGGGT**CGGTCAGGAAGTCACCTGATGAGCAGTATACTTTCTTTTCTTTCTTTCTTTTTTTTTTTTTTTTTTTGGTTTGTTTTTGCTTTTGTTTTTCGAGACAGGTTTTTTTTCTGTGTAGCCCTGGCTGTCCTGGAACTCACTCTGTAGAACAGGCTGGCCTCGAACTCAGAAATGCACCTGCCTCCCAAGTGGTTTTTTTTTTTTTAAATACTTTCTATGATTGCAACCAAATGTCACTCAGCCTGCTTTCTCATCGATGAATCGGAGACAGTTAACAACCCCTATTACATGGCATATATTGGTTAACAACAAACTCTCCAAACATAGGAGTAGCTAGAATTAGCATTCCCCATCTTAAGGTTCTCATCACATTCAAGGATAAATGGGTCTGAGGCCTCGGGGTCAAGACTTCAAGTGCTTAAATCTTCCAGCTTCCACTTTCAGATCAACAAGGTTAGGTAAAGGAACGCGCAGTGACAAAGTTTTTAGGAGCCCTGAGTTCCACAGCTTATCAGCTGTGAGATTTTACAGGCCATTCATTCTTATTCACTCCAAGGCACTGAAATCTTTGTTTACTACATAGTCTGGGCTGGCTCCAAACTCTGGCTCTTCCTGTCTCCGCAACCAGAGTCTGGGATTACAGGTGTTCACGACCGCGCCTAGATTCCAGTATTCTGTTAAATGGGGACTGTGTTCCAGCGCTGTGTACAACGGGCTGTTCTGTACGCAGGCTTAGGAATTAATGCAGTTTTCTGCCAGTCTCATCCCAACAAGCATGTGTCATCTCCATGTGGCATGCACTAGAGGCCATGTTGCACCTAGAACCAAGTTGGGCAGGTTCCTGAGGTTTCCCAATCCTGCAAACACTTATGTGGGAGTAAGAGTAG
ENSMUST00000030164.1	1	13	ENSMUSG00000028452.1	GGGAGGCTGCCAG**AGGGT**TTGTCACTGCTGTTGCTCCTCCGCCTCAGCGAGTCCAGCCCCGGCCTAGTCGGTCGCCTGCCTTTCTCATAGCCGTTACCCTCAGGCCGCCACAGCCGCCGACCGGGAGAGGCGCGCGCC
ENSMUST00000030252.1	1	23	ENSMUSG00000028527.1	GGCAGGCGAGTCCCCGCGTGCGG**AGGGT**GTCGAGGCAGGGGCTGCTGGGCAAAGTGCGCGGGCTGCCGTCCTGGCCACCGCCAAAGCC
ENSMUST00000030339.1	1	18	ENSMUSG00000028602.1	TTTCACCGCGGGAGAGTC**AGGGT**GCCGGCAGGTGGCCAGGCGCTGGAGACTCGGGAAGCCAAG
ENSMUST00000030372.1	1	190	ENSMUSG00000028626.1	AAGGACCCAGACAAGCTTGCCCGGGGAAAGGATGGGGCTGAGGGCCAGGAGGAAGGCTTTGATCTTGGAGGCAAGGAGGAAAGGGACTTCGAATGGACTTCTGCTCTTCACACAGAAAGTAGTCCCGTACCCCGAGATGCCCCCGGGACTTCCCAGCTGGGGCGTCTGGTCAAACTCAGAATGCAGACCC**AGGGT**GGGCACAGAAGATCCGCCCCTGACCGGGCGGAGCTGGACAGTTCCTCCCCACAGTGCTCTCAGGTGACAGGCCTGCAGGTCCCCGCCCCGGCCCGTCTAGCTGCGTTTTCGGGAGATCCAGTCCGAGGCTCCGAAAGCAGCCCCCGCCATCGGTGCTTGGACCCCCGCTCCAGAACCCGCTGTTCGCC
ENSMUST00000030543.1	1	123	ENSMUSG00000028760.1	GAAGAAAACAAAAGAGCAGACCCGAACCCCAGATGAAGTGTTAGAAGCAGAGGCAGAGCCTAAAGCCGAAGAAGAGCTTGCAGTTGACAGTGTCCTTGAGCCTGAGCAAGAGAAGATGAGCCA**AGGGT**TTCCGTCTGAGAGAGACCCCTCTGCCCTGAAGAGAGGGAAAGCTGAGGAAGGAAACGGAGAAGAGGCTGAGCCTGTGCGAAATGGCGCTGAGAGTGCTTCTGAGGGGGAAGGGGGAGATGGCAACTCAGGCTCTGCTGACAGCTCTGCTGATGGGCTCACCTTCCCGTTTAAAGCAGAGTCCTGGAAGCCTGCAGATACAGAAGGCAAGAAGCAGTATGACCGGGAGTTCCTACTGGACATCCAGTTTATGCCCGCCTGTATCCAAAAACCAGAAGGCCTGCCTCCCATCAGCGACGTGGTCCTTGACAAGATCAACCAGCCCAGATTGTCAATGCGGACCCTGGATCCTCGCATTTTGCCTCGAGGACCTGACTTCACCCCAGCCTTTGCAGACTTTCCAAGGCAAACGCCTGGTGGAAGAGGTGTGCCTCTGTTGAATGTTGGACCTCGGAGGTCTCAACCTGGCCAGAGAAGGGAGCCCAGAAAGATAATCACTGTCTCCGTAAAAGAAGATGTGCACTTGAGAAAGGCGGAGAATGCCTGGAAGCCGAGCCAGAAACGGGACAGCCACGCCGATGACCCCGAAAGCATTAAAACTCAGGAACTTTTCAGAAAAGTTCGAAGTATCTTGAATAAACTGACACCACAGATGTTCAACCAGCTGATGAAGCAAGTGTCGGCTCTTACGGTGGACACGGAGGAGCGGCTAAAAGGGGTCATCGACCTTGTCTTTGAGAAGGCTATCGATGAGCCCAGCTTCTCTGTGGCGTACGCAAACATGTGTCGGTGCCTAGTAACG
ENSMUST00000030551.1	1	172	ENSMUSG00000028766.1	CGCCAGAGTACGCTCCCGCCACTGCGCTCCTTAGGGCTGCCGCTCGCGAGCCGGAACAGACCCTCCCCACGAGTGCCTGCAGGATCGGAACGTCAATTAACGTCAATTAACATCTGACGCTGCCCCCCCCCCCCTCTT

				CCCACCATCTGGGCTCCAGCGAGGGACGAATCTC**AGGGT**ACACC
ENSMUST00000030586.1	1	29	ENSMUSG00000028795.1	GCTCCAGTTCCCCTGAGGAGAGAGAAAGC**AGGGT**GAAGGGAGATTGCAAAGAAGCACTGTTTCACACTCCAGACCCCAAACTTCCAGACCTGAGGTCCAACACACCACCCA
ENSMUST00000030729.1	1	91	ENSMUSG00000028894.1	CGGAGGTGTCCTGCAGGCCCACCGGTGACAGCTCGGGAGCCCCCCGAAGCAGCTCTAATACGGAATGGGAGGTTCCCACCTGCCCTACCCC**AGGGT**TTGACAGCTCAGCATGGACCAGTCTGTGGCAATCCAGGAGACCCTGGTTGAGGGGGAATACTGCGTCATCGCAGTCCAAGGTGTGCTGTGTAAGGGAGATAGCCGGCAGAGCCGCCTGCTCGGGCTGGTGAGGTACCGGCTGGAAAATGACGCCCAGGAGCATGCTCTCTTCCTGTATACACACCGGAGGATGGCCATCACAGGAGACGATGTATCTCTGGACCAGATAGTGCCACTCTCAAAAGATTTTATGCTGGAAGAAGTGTCCCCAGATGGTGAACTCTACATCCTTGGCTCTGATGTGACAGTACAATTGAACACAGCTGAACTCAAGCTTGTATTCCAACTTCCCTTTGGTTCACACACCAGAACGTTCCTCCAGGAAGTGGCCAGAGCCTGTCCAGGTTTCGACCCTGAGACGCGGGATCCCGAGTTCGAGTGGCTGTCAAGACACACATGCGCGGAGCCCGATGCCGAGTCGCCGAAACCGCGCGAGTGGAATTCGGACCCGGGTACCCGGAGTGGGTTCGCGCCCATTGGAGGAAGCAGGCATCAGTCTCGGAATGCACGGCGAGGATTGGAGGATGTCTTGCCTAGGGGCCCTGGCTACATTCTGCTTTGGGGCGGAGCCGCTGAGGAGCCGGAATTTCTATTGGCGGAGGAG
ENSMUST00000054917.1	2	1482,2018	ENSMUSG00000028906.1	GAACTTTATGGAATCGGTACCCGAACCACGGCCCAGCGAGTGGGACAAGCGCTTATCTACACACTCACCCTTCCGGACTCTTAACATCAACGGGCAAGTCCCTACTGGAGATGGAAGTGTAAATGGCATTCGAACAGAGGAGGTGGCTACCGTGACAAAAGGGCCATCCACCTACCCTGCCTCTGAATGGGAGTGCCCCAAACAGTCAGTAGTTCCTAGTCAGAGCCTGATGACCACTCCGCCGGCGTCTCCACAGAGCTTTGGTTCTGGCTCCCTCTCCATAAACAGCAAGGAGGCGGAAGAGAAGGAGCAGGGGGCAGCTGGCTATCTTGATGCTGAAGAGATGCCAACAGGCCCAAGTGGGGAATGCTTAGGAGTGGAGGAACAGGCCAGTGCATTCAGTTTCCCAGTAACTCCAGCTTCCTGCCAGCTGCAACTCGGTGGGGAAAAGGCAGACAGTAGCGAAGAGCTGGGTGCAGCAGCAGAGACCCTTGAGACCCAGAGCGGATCCTTTCTTGACTCACCTGTGGGTAACCAGTTCCCCACCCTCATTCGAAGTTTCCAGCCTCCTCTGGTAAAGACTCAAACTGTCACCATCTCAGATACTGCCAATGCTGTGAAAAGTGAAATCCCAACCAAAGATGTCCCTATTGTCCACACTGAGACCAAGACCATCACCTATGAAGCTGCCCAGACTGAGGACAGCAATGGGGACTTAGACCCTGGAGTCTTGCTGACAGCCCAGACCATCACATCCGAGACCACAAGTAGTACAACCACGACACAGATTACCAAGACTGTAAAAGGTGGGATTTCTGAGACCCGGATCGAGAAGAGAATTGTGATCACAGGAGATGCCGATATCGACCATGATCAGGTCCTTGTACAAGCCATCAAGGAAGCCAAGGAGCAGCATCCAGACATGTCAGTGACCAAGGTGGTCGTCCACCAGGAGACAGAGATCTCTGAGGAGTGAGCTCAGGGACTGTCCTGCCCCACCCCCACCTGTCCC
ENSMUST00000053819.1	2	810,864	ENSMUSG00000028911.1	GAGGAGAGTAGTCAGAGATGATTGCAAGGTTGTTGGGAGTGAATCAGGTGGTCAGGGGTTCTGGAAGAGAGAAATCATGAGGTAGGTTTTCTTCTTTGAAGGTGGGGAAAGATCAAGTGCAGACTGAGCTGTGGCCAACCGTTTGCAGACCAGGAATCCACACTAGCTCTAATGAGAGAGCTCTTGGTGTGCGGGAACTGCCAGTTTGCCGACGTGAAAGAGTCCCAGGCTGGGTAATGGTGAGCCCTGAAGTCGCACCCCAGCTCTGCCACTGAGTGAGCACGGGTAAGTCTTCCACCTTCTCTGGGTGGCCTTGATGGCCCTCCCTCCTCTGAGACTAAAGAAAAAGGGAGGGCAGAAAGCCAAGAGCAGCCTCCTTCCTGTCTCAGAATAGGAAAAGGTCTCAGGAACCTGCTCCTGGAGCAGCAGCTTGCCACTGTGGCTTGTAAACTCCCTCAGTCACTGCGGAAGCCAGCTCACATCCATGGCCATTAAGGTTAAGCAGTTAATGTGCTTTGAGGGCCTGACTGCTGGTGCCCTGGGATGCTGCAGACCTGTGGAATCAGGGCCATTGCACTGTTCTCATTCACAAGCTTCTACAAGTTAGCATCACCTGAGCACGAGAGTTGGCTGTAGAACTGTCTTAGTTCTACAGGTTTCTGTGCACTCGATGCAGCACTCGAGAATTACTCTCTACTGTCCTGTCATTATGCCCTTTTCACCTCTTAAGACCCAAGTTGGTTGAAGCCTAGGATCTACTGAGTGCTTTGAAAGCTGTTTGATTCCTGTTCACTGAATACCATTTCTTTC**AGGGT**AGATTTAAGGGCTCTGCCCTCAAAATACAATGCTACTGGCTCTAGATTG**AGGGT**TCAAGCCACCCTGTGGGTTTACTTCAACAGATGAAAATTTTTCCTTGGCTACAGCAACATCCCTAATCCTGACCAGCCATGGAGAGGTTCGGTTCTTACAAGGAAAATGAGTGAATGTGGGA
ENSMUST00000062981.1	1	41	ENSMUSG00000028937.1	AGAGCTCTTCCTAACAACTTCCCTTTGGCTGCAGCTTCTGC**AGGGT**GCAGCAGAGACAGAAGGAC
ENSMUST00000059610.1	4	1,80,245,321	ENSMUSG00000028960.1	G**AGGGT**CACGTGACCCCTTTCAAAGATGGCCGCCCTGTTGTTTTGATGAATAATTCTTGGTGGGGCGAGGGGGTAAGAGT**AGGGT**TGGAGGGGTAGGAGGATTTACGCTTCCAGCGAGGGCTTCGCCAGTCCCGTCCC

				TCCCCTGCCCCCCACCGGGGTTCTCGCGTGGAGGCGGGGCGAGCCTGGCCTGCTTTTAGAGGGGAGGGGCTTCCCGGTCCGGTGCTGGGCTCTGCCTGGGCTGCTGT**AGGGT**CGCCGCGCCTCGGGGGCATCCAGTGTGCAGTGGAGCTGTTCCCGCCTGGGCCCAGGGGTGGGACCCGGAGC**AGGGT**CTGCGGGAGAAAAAAACGCAGCTGCCGCGTCACCGCCACGAAGACACGGCGCGCAGCGGGCACGAGCCGAGCTGGAGACCGCGCCGCCCGCCCTGGGTAACCTGGGAAGCTGAGGGGAGTCAGTGGCGCCTGGAGAGGACCCCATAGCGGTGGCCGTGGCCAGAGGCGGCAGCTCTGGGCGCTTGCTGCTGGAGGAGGCTGCGGCGGTGCGAGCGGCCGAAGCCAAGGCGATTCAGTGCCTCGTGTTCTTAGTTTTTAACCTCTGACTATGCAATTCTGAAACCTCCCCCATTGGGGGACCAGACAGCCCGATAGATACCTTCCACTCTTCCTTTGCTCCCGCCCTGGTCTCAAGAACTGAAGGATCTCTCTAACGCCTTTCACCATTAAGAGGAAAGCG
ENSMUST00000030801.1	4	119,198,363,439	ENSMUSG00000028960.1	GGAAGAGGGGGTGGGGCAGGGGGCGGGGACAGGATGCAAGCGAAGAGGAAATCGGCGGCGCGACGCCCGCTGCTTATTGGCTGGCGAATCCCAGAGCGAGAAGCCCCGCCTCCCCGGCG**AGGGT**CACGTGACCCCTTTCAAAGATGGCCGCCCTGTTGTTTTGATGAATAATTCTTGGTGGGGCGAGGGGGTAAGAGT**AGGGT**TGGAGGGGTAGGAGGATTTACGCTTCCAGCGAGGGCTTCGCCAGTCCCGTCCCTCCCCTGCCCCCCACCGGGGTTCTCGCGTGGAGGCGGGGCGAGCCTGGCCTGCTTTTAGAGGGGAGGGGCTTCCCGGTCCGGTGCTGGGCTCTGCCTGGGCTGCTGT**AGGGT**CGCCGCGCCTCGGGGGCATCCAGTGTGCAGTGGAGCTGTTCCCGCCTGGGCCCAGGGGTGGGACCCGGAGC**AGGGT**CTGCGGGAGAAAAAAACGCAGCTGCCGCGTCACCGCCACGAAGACACGGCGCGCAGCGGGCACGAGCCGAGCTGGAGACCGCGCCGCCCGCCCTGGGTAACCTGGGAAGCTGAGGGGAGTCAGTGGCGCCTGGAGAGGACCCCATAGCGGTGGCCGTGGCCAGAGGCGGCAGCTCTGGGCGCTTGCTGCTGGAGGAGGCTGCGGCGGTGCGAGCGGCCGAAGCCAAGGCGATTCAGTGCCTCGTGTTCTTAGTTTTTAACCTCTGACTATGCAATTCTGAAACCTCCCCCATTGGGGGACCAGACAGCCCGATAGATACCTTCCACTCTTCCTTTGCTCCCGCCCTGGTCTCAAGAACTGAAGGATCTCTCTAACGCCTTTCACCATTAAGAGGAAAGCG
ENSMUST00000030810.1	1	55	ENSMUSG00000028962.1	GGAGCGGCGGGGGCGCGCCCCGGGGTGGGCACCGGGAAATCGTCGGGAGCGCGCG**AGGGT**TCCGGAGGATCAGGGGAGACCCGGAGACCCCCGGGACACGAAATCTAGAGCTAGCGGGTTATGCCTCCACCTTGTTGCCCTGAAAGCCGAAGCGACAGCGAGAAGGGCTAAGATTTGGCC
ENSMUST00000030830.1	1	59	ENSMUSG00000028980.1	AGAGCTTCATCTGGAAGTGCTGGTCCCCAGATTGGCCATGAGGGGACCAAATGCAGACC**AGGGT**TGACTGACACCAGGTTGTGTTCTTTGCCTGCACTGGCACACAGGCATTTGGAAG
ENSMUST00000030886.1	1	103	ENSMUSG00000029022.1	GATCTCGGGACCACAGAGGCGTGCCTTCGTCCCGCTAGACCGGTAGAGAAGGGGCAAGCGCCTAGGCCCCGGTGTGCACCCTGCCTGAGTGCGCGTGGAACCT**AGGGT**CAGCACCTCTGCAGCCCAGAGACAGTGACATTACTGTGAGAAGCCCGCATGCCCAAT
ENSMUST00000030938.1	1	86	ENSMUSG00000029062.1	CCGGGCGCTGTTCCTTCCCAGACTCCAGGACCGGCTGCGGCGGCTGTAGCGGCGCAGGGGTGAGTAGCGGCGCGGGGGTTCGGAGC**AGGGT**TTACGGCGCCCCTGAAGAATCGCGGCTGGCGACACGCTGCTGCCGCGGAGCAGTCTCGCTCCACACGGAGCTGAGGGCGGTGGAGGCGGCAGGCCTGGCGGCCCCCGGAGCCGGCCCTTGCCTCAGGTTTGCGTGACTGAACCCTCAGAAGTGGGACCCCGCCCCGGAGTCCCGCGCTTGACAGTGCACCTTGATCTTACCTGTCACCCAGGCCTCCCCGCGTCCTGGAGCTTTCTCATACAACCTTTTGACACCTAAGGCAGAGTGTGTTGAGTGCGAGGCACTGAAATGACCTGGATGGTCTTTCATCCTAGAACAGTACCGTTACGTGGATGATGATGGTTGCGTTTTACGGAAAACACTGAGGTAAACTAAGTTACCCAAAACCTTACAGGAATGACAGAAACGACAGTGTATTCAGGCAGAATCCTTCCGACCTACCGGGACTTACTCTGAAACACTAACGATTAGACTTAAGTGTTCGGAAAAGACAGACCGACAGACCGACCGTAGCTTTCTGTGTCCCGAGGTTGCTTGAATTGTTTTTCTTTTTGCAGTGTTTTAACTCAA
ENSMUST00000030987.1	1	100	ENSMUSG00000029104.1	GGCTGAGCGCCTTGGTTCCGCTTCTGCCTGCCGCGCAGAGCCCCATTCATTGCCTTGCTGCTAAGTGGCGCCGCGTAGTGCCAGTAGGCTCCAAGTCTTC**AGGGT**CTGTCCCATCGGGCAGGAAGCCGTC
ENSMUST00000031024.1	3	322,1563,2040	ENSMUSG00000029142.1	GTCGGTCTGAGGCGGCGGCAGGGCCTGCGGCGTGGAGCCGAGGCGGTGACCCGCAGGTCCCGAGGTGGAGCCCGGAGGGGTGGAGGACCTGGCGCGGCGGCTGCCACCCCGCGGCGCGCCTCCGGGTCTGGTGAGAAGGCGGCGGGAGCCCCGTCGCCCTCTGCAGGGGTGTCCGAAGAATGTCTACTGGCCGCTGTGGTATTACCCCGCTGCCTGGCTCCTGGCTGACATCCTGATTAGAGTTAGCATCTCAGGCGACTTTGCTGCAGTCTGTAAAGTTCAAACAAGAGCTGTGTTGCAGTACAAATATTTACACTATAGA**AGGGT**GGGGATAGAGCAGATATTACTTAGAACGATGTTAAGATGGCAGACAACTGTTGATTATACCAAGACAACAACAACAACAAAACATTC

				ATAATTGTGTGGGCCAGACTCACACCAGGAAAAAGTTATTTTAGTGTAAAGTGGGGAATACTTTTAAAGTGTTTTTGGTTACAACTAATGTTGATAAGCACTTCGAATGAAAAAAATAACAACCTTATCTTTTTTCTTTCTTCCAACCTTTACACACACAAGTTGCCAAGAGCAAGTCAAAGTAAGTAAGGTTTTTGTTTTATTGGCCCAGTGTTTGGGTTTGATCTCCCAAGAGTTGATCTGGGGTATTTATTTGGTTAATTATTTTGTTGATGTGAGCACCTTGGGGGAAAAGTCCTTTGATGGTGCTACCATTGACAGTTCGATCCTGGGTTGCAGATACATAAGCTGAGAATGCATCTGATATACCAAAACCACAGATCATGTCGCTTAGCAACCCTGCTTCCTCTTCCCTTTGTGGCTGGTAGGAAGCCGAGGTACCCGTTACTAACTGGGGAAGAGAGCACAGTGGGAAATGTGGCCTCTTGCAAAGCAGTGCATTTGCACTGGGTAAACTGAGGATGTAAGTTGAGGACTGTGCTGTCTCCCTTCTGTCCCAGGGAGTATTCACAGCCTTTGTGTAAAGGAACTTTGCTTC
ENSMUST00000031032.1	1	77	ENSMUSG00000029147.1	GCACCTTGCGTCGACTGCGCAGCCGGGCCCGCTCCTTGCCACGCGCGCCCCCAGGGGCCCCGGCTCCGGCGCCGGCA**AGGGT**CGCGTCCCGCTTACCTGTTCCTCAGGTAGCCAGCCATCCGCCGCC
ENSMUST00000052121.1	1	396	ENSMUSG00000029199.1	AAGCGACGAGTTGTTGGACGCGTCCGGTGCCGGGGGTGCTGTTCCCTCGATCCCTTGACACTCCTGAGACCTAAAAGAGGGGGATGGCTCTACGCTGCTGGGATACAGCTCGCAGCCTGGGGTCCCGGGTGAGCGGCGGGAACGCCATTGCTTATCCTAAGTTCAAAACTAGGGAAATTGTTCCAGATATCCTTTTTTTAAAAGCCCCGACAGCTGTGGCATATCTTAATTATTGCAAACTTGTTGACAACATATTTTAGTACCTGTTTTAGGAATAGAAGACATGAAAACGTGGCATGTTAAGTCACCCACTAAGGTTTTCTAACCTATATTTAGCGGTTAACTTTGATCTGCGTCCCACTTTTTTCCCCCATTTGTCATGGCTGAGCGTGCATC**AGGGT**CTCTGTAATCTAGGCTGGCCTGAAACTAAATTCTTAGACCAAAGACGACTCCTCACTCTGCCTCCTCTGAGAGCTGCATTACGTGTTTGAGCCGCCGTGACTTACGGTTCTTTCACCTTGAGTCTTTTTCAGGTTCTGATCTACGTAGTTTGAGCTCTTAAATCGTTTTACATAATTTCTGAATCAATTTCTTTAGCTTTGGTATTATAATGGGTTAAAACTAAATTATTTCAGAGTCTACTGAGTGAATGTTGTACTGAACCCTTTTTGTAG
ENSMUST00000031105.1	1	14	ENSMUSG00000029203.1	GGAACGCGACGGCG**AGGGT**GGCAGTGGCAGCGTTCGTGTGCTCGGGTCTGAATCGCTGAGGGAGGAGGCGGCGGCGGAGGAAGAGGTGGCAGCGGTGGCGGTGGTCGTAGCGGTGGCGGAGGAGGCGGGTACGAATCAGCTGCGGGCAGAGAC
ENSMUST00000031136.1	1	6	ENSMUSG00000029227.1	CTCTTC**AGGGT**CGCCGCCTCCACCGAGGTTGGCCCCAGATTTGAGTCTCGCGCTCTTCGTTCGCTTACCGGCGGCTTCCCTCCCATTCTCGCGCCCTGGGACGGCGAGGCTGGAAAAAGGGGTTGAGAGAGCTGTTGGCCGCCGCCTTTAACTTGTGCGTGGGGCGGCC
ENSMUST00000031137.1	1	0	ENSMUSG00000029227.1	**AGGGT**CGCCGCCTCCACCGAGGTTGGCCCCAGATTTGAGTCTCGCGCTCTTCGTTCGCTTACCGGCGGCTTCCCTCCCATTCTCGCGCCCTGGGACGGCGAGGCTGGAAAAAGGGGTTGAGAGAGCTGTTGGCCGCCGCCTTTAACTTGTGCGTGGGGCGGCC
ENSMUST00000031190.1	1	414	ENSMUSG00000029265.1	GCAAAGCGTGCCGGGATCAGCTTGCGGCAAACCTCCTTCCCCGGCCCGTAGAGAGACCACCGTTAGCGCCGCTCCTGCTCGCACAGCCTGCTCTCGGCCACACGCTTGGCCGCTGCGGCTCCCGCAGTGTTCGGCCCGGTCCACTTGGTTTCCCAGGCAGCCGGCGTGCGCTCAGCTGCGGCTTCGGCAGACATGTTGTGAGGCGGCGGCGCGGGTGCCTGAAGGATGGTTTGGCCGAGGCGGCTGCAACCGCTGCTGGTGGCGGCGTCCTCGGGGGCTCCGGCTCTGTAGAGCTGACCCTGCTCAGTGTCCGCCCGGGACCGCGGCCGGGCGGGTATTCCTCTGTCTTGCGTGCGCTCCCGTGCCGTTTAGGTTCGGTTAGACGACAGCGCCAGTCCGTTTGAGGCGACACGC**AGGGT**GGTTCTCCAGCCCTGGGAGTGGTGTCCCTAGAACCCTCAGCCCCCTGACCTTTCCTTCATATTCCCACTAAAATCTCTCACACAGTGGGTGTTCCCTGCCCTCCAGCCCTCCTTCCTGGTTTCTGCACTCTCTTCTCTGAGCTTCCCGGACCCCAACATCCCTCTCCAGGGACAGCCTGTTGAGAAATCTTCGTGGAGTGGTGGACCAGAGGCGAGGAGTTTAAAAGTTGGGGCTTGAAAGACAGGAAGATACG
ENSMUST00000002832.1	1	392	ENSMUSG00000029267.1	CCGCTAGTCCGCGGGAAACCAAAATGGCGAAGGGCTGTTGCGAAGTGGTCTGTGTTTGAGGCCGGTGTGAGCACGCACATTCTCCTTCCTAACCCTCGTCCCCAAGGAACTCGGTGTGTGTGTGCGTGTGCGCAGGGCTCCCGCTGGGGCGGGTGCCCAGGGAGTGCCCGGACTCGCGGGGGAGCGCCCACGGGAACGAGATTGCTTCTATTTTCCTGTATGAAGCGGTTGGCACCACTTAAGTGACCGAATGAGAGACTCTACAGGAGCAGGTAATTCACTGGTCCACAAGCGGTCTCCTTTACGTCGAAACCAAAAGACCTCAGCATCCTTGAACAAGCTGTCTTTACAGGATGGACATAAAGCCAAAAAACCAGCATGTAAATTTGAAG**AGGGT**CAAGATGTCTTAGCTAGATGGTCAGATGGCTTGTTTTATCTTGGAACTATCAAAAAGATAAACATATTGAAACAGAGCTGCTTCATCATATTTGAGGACAGTTCCAAATCCTGGGTTCTCTGGAAGGACATCCAAACAGGAGCCACTGGGAGTGG

				GGAA
ENSMUST00000031328.1	1	516	ENSMUSG00000029381.1	GGGACGTCAGTGTGAACGCAGTGGGTAGACCCCACTCAGGACTTCCGCTGAATTCCAGCGGGTGTAGTGGGAGAAGCATCCCCGGGGAGCCGCAGGCTTCGCTGTCCCGACTGAGTTTATCTTGGCCTGAGGGCAGCGTGCTGAGCGATCTAACCCAGCAGGGAAGCTCCTCTTGCCTCCATCTGGGTCAGGCACTTTAAACCGAAGCCGACTTGACCATGCCTCTGGCGCGATGAAGACTCCGGAGAACTTGGAGGAGCCTAGCGCCACGCCAAACCCCAGTAGGACCCCCACGGAGAGATTCGTTTATCTGGAAGCGCTCCTAGAGGGAGGGGCTCCCTGGGGCTTCACCCTGAAAGGTGGCCTGGAGCGTGGAGAACCGTTAATCATTTCCAAGATTGAAGAAGGGGGCAAAGCCGACTCAGTGAGCTCCGGACTGCAAGCTGGGGACGAAGTCATACACATCAATGAGGTGGCGCTGAGCAGTTCCAGGAGAGAGGCTGTCTCCCTAGTGAA**AGGGT**CCTACAAGACCCTGCGGCTGGTGGTGCGCAGA
ENSMUST00000031341.1	1	119	ENSMUSG00000029394.1	GGTCCGGCCCCGGCCCAGCACCGACCGGCTGGGCTCAAAGTTTGCGGCCGCCCCTGCGCCGCGCGCCCGATGTATGGGTGATCTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGC**AGGGT**GAGGGACGGCCATATTTGCCGGCGCGGCCCGAGCCGGCGACAACAAAAAGTGCGCGGGCTCCCGGCGGGCGCTCGGACGGCTGCGGGGACGTGGGGCCGCCCGGCCCGGGCCTCGGCCTCGGCCTCGCCGGCGCGCTCGTGGCCTGGCCCGGCTCTGCCCGGCGCGCCCGCCGCCCGCGGGGATGTCGTACAAGCCGAACTTGACCGCGCACATGCCCGCCGCCGCCCTCAACGCCGGAAGTGTCCACTCACCCTCTACTAGC
ENSMUST00000031426.1	1	46	ENSMUSG00000029469.1	CCAAGGAGCGGTCTCTAAGAACCCGCAAGCGCCCCAGTGCCTCCCG**AGGGT**GGGGAGGTGGTTTCGTGAGGAGGATTTGAGTTTTAAGCTATAACATTAATC
ENSMUST00000031528.1	1	272	ENSMUSG00000029552.1	GCGGCGCCGGAGTTCCCGCAGCGGAGATCGCGGACGCGGGACTGAGCCCCTCCGACGCCCAGTATGGACCTGGAAACCAAAATGAAGAAGTGGAACTATGGACACCAAACAAGGTGATTTATGGGAAATACTTCGAGCTGTGCCTGGCAGTGCAGATGCTTGCTGCTGTTCCCACTACAATCCCTTGTAGACCCATTCCTGTGAAAGCAGTGGACGTTTTGGGGGGCAGGATACTATGTATATAACAGGCAATCTCTCTGCTCTGGATCAAG**AGGGT**CACCTGAATTGTTGCCAGCATATCTGGTTTCTTGACATGATTATGGAGAAATTGGTGCCACTTCCATTTCTAACTCTAAACTAAACAGAGAGAAGAAGCAGGGGCTTGGAGACTCGGGTCATGGAAATATGGGCTTAGGTCATGAGCAAGGATTTGGAGCCCCCTGTCTAAAATGCAAAGAGAACTGT
ENSMUST00000031544.1	1	137	ENSMUSG00000029562.1	GCGGCCGAGCCGGGTGAGAAGCAGCGCGGGCCCATGCAGGACGCTGAGAACGTGGCGGTGCCCGAGGCGGCCGAGGAGCGGGCTGAGCCCGCGAGGCAGCAGCCGGCCTCCGAGTCGCCGCCGACGGACGAGGCGGC**AGGGT**CTGGGGGGTCCGAAGTGGGGCAGACGGAAGACGCCGAAGAAGACGCCGAGGCCGGACCGGAGCCCGAAGTGAGGGCCAAGCCGGCGGCCCAATCCGAAGAGGAAACGGCGACGAGTCCGGCCGCCTCGCCCACGCCGCAGTCGGCGGAGCGGTCCCCGTCGCAGGAGCCCTCTGCTCCCGGGAAGGCAGAGGCCGTTGGCGAGCAGGCCCGGGGGCACCCCTCGGCTGGAGCGGAGGAGGAGGGCGGGTCTGATGGGAGCGCGGCTGAGGCGGAGCCGCGGGCTCTGGAGAACGGAGAGGCAGATGAGCCCTCCTTCAGCGACCCCGAGGATTTCGTAGACGACGTGAGCGAGGAAGAACTACTTGGTGATGTACTC
ENSMUST00000053600.1	1	992	ENSMUSG00000029613.1	AATGGGTGTTCCAGGAGACGCGTCTTTTCCCGAGAGCGGCAGCGCCAACTCTCCCGCGGTGACTGTGACTGGAGGAGTCCTGCATCCATGGAGCAAACCGAAGGCGTGAGGTACAGAATGTGCTAAGGCCATCAAGCCTATTGATGGGAAGTCAGTCCATCAAATTTGTTCTGGGCAGGTGGTACTCAGTTTAAGCACCGCTGTGAAGGAGTTGATAGAAAATAGTGTAGATGCTGGTGCTACTACTATTGGATCTAAGGCTTAAAGACTATGGGGTGGACCTCATTGAAGTTTCAGACAATGGATGTGGGGTAGAAGAAGAAAACTTTGAAGGTCTAGGCTCTGAAACATCACACATCTAAGATTCAAGAGTTTGCCGACCTCACGCAGGTTGAAACTTTTGGCTTTCGGGGGGAAGCTCTGAGCTCTCTGTGTGCACTAAGGTGATGTCACTATATCTACCTGCCACGGGTCTGCAAGCGTTGGGACTCGACTGGTGTTTGACCATAATGGGAAAATCACCCAGAAAACTCCCTACCCCCGACCTAAAGGAACCACAGTCAGTGTGCAGCACTTATTTTATACACTACCCGTGCGTTACAAAGAGTTTCAGAGGAACATTAAAAAGGGAGTATGCCAAAATGGTGCAGGTCTTACAGGCGTACTGTATCATCTCAGCAGGCGTCCGTGTAAGCTGCACTAATCAGCTCGGACAGGGGAAGCGGCAGCCTGTGGTGTGCACAAGCGGCAGCTCTGGCATGAAGGAAAATATCGGGTCTGTGTTTGGCCAGAAGCAGGTTGCAAAGCCTCATTCCTTTTGTTCAGCTGCCCCCTAGTGACGCTGTGTGTGAAGAGTACGGCCTGAGCACTAGGACGCCACAAAACCTTTTCTAGCGTTTCGGGCTTCATTTCACAGTGCACGCACGGCGCCGGGAGGAGTGCAACAGACAGGCAGTTTTTCTTCAT

				CAATCAGAGGCCCTGTGACCCAGCAA**AGGGT**CTCTAAGCTTGTCAA
ENSMUST00000031640.1	1	84	ENSMUSG00000029635.1	TTTAATAACAAATATTTATTTGTGATTTTTTTTTCCTTCTAGTGATAGAACAAATACTGGCAAGTTTTATGGAACAGAGTAGCA**AGGGT**AGGCTGACATGTGATTAGGTGTCGAGCCAGAAGGCCACGGGGTGTAGCCGGAGCTTGAGCACTCCTATGAGAGCCAGTCTTAGAAAGCTCTCAAAGTAATCTTTGTTAGCATTCTTGAGACTAGGAGCCTAGGCAACATAAACATTTATCAATGTATTTCACAGATAAAGATTGGGAAGATATAAAAAAGATGCCCGAACATTCAACATTAATGAAAGATTTCAGAAGAAATACGTATACCAATTGCAGCCTTATCAAGTATATGGAAAAGCATAAAGTTAAACCCGATAGTAAAGCATTCCACTTGCTTCAGAAGTTGCTCACT
ENSMUST00000031664.1	1	57	ENSMUSG00000029657.1	GCTGCGTGAGAGAGGCGGGCGGCGGAGAGCGGTGGCAGAGACTGAGCGCAGTCTTGC**AGGGT**AAGCCGGAGGCATCTTCCCGACTGGTCGGGAGCAGGACGAGCACGCAGCGGACCCGAGGCGGAGGCGGACCGGGCCAGCC
ENSMUST00000006301.1	4	479,899,1213,1683	ENSMUSG00000029703.1	AGCGACCGGACTTCGTGGAGGCGCGGGTTCGGTTGAGCCCTCGGCCACCCATGGCTCCTCTCACGCCGCAACTGCTCCTGCAACGTGGGCGACCCAAGACGGATAAGCTGGGGAAGATTCAGAGTTTGAATCTGTCGGGGCTGCAGCTGCTCTCAGAGCACTTGGATCCCAATCTCCTGGGGCGCCTGAAGAAGCTGAGGGAACTTGACCTCTCTAACAACTTGCTGGAGACGCTGCCTGCTAACCTGGGCCTGTCCCATCTGCGCATCCTTCGCTGTACCAACAACCAGCTCGGGGATGTCACTGCCTTGCACCAGTTCCCAGAACTTGAGGAGCTCAATCTGGAAGGCAACCCCTTCCTGACGGTCAGTGACAACCTCAAAGTCTCCTTTCTCCTGCCCAAGCTTCGTAAGGTGAATGGCAAGGACACGGCCTCCACCTGCTCACAGGTGGAGAATCTAGATCGGGAGCTGATGGAC**AGGGT**AAGGATGATGGCGTGGGGGTGGGGTCCTTGGTCATAGCAATTGGGTACTGAGTGGGACAGAAGTGGAGTTTTGGAGCTGTGTAACAGAGATTCTTGCCCAGACAGCCTCAGGTCTGAGGTGGTGAGTCTGTTTTTTTTTGTTCCTTTCTTTCTGTGTTTGGAGACCCTGTCTCCAAGGTATGCAGCAAGCACAGCAGGACACCAGCGAAGCTAGACTCACAGTGAGCTGGTTTTTGGCACATGCTCTTTCTTGCTTATATAGCCCAGGTGGCCTAGGACTCTTCTGCCTCAGCCCCCCAAGTGTTGGTATCACCACCATGTTCAGTTGAACCAGACTGATTTCAAGTCTAGCTACTAGATATTGAGTAGTTTCTAGAAGGTGGTATAGTCAGTCTACTGTGTGAGCCGGAGGAGTT**AGGGT**GGAGGTGCTGTGTGTAGCCTGGAGACCCAGGCTGGGCGGGGACGGTTCTGGTCTTTCTTACCGCAGGTCACAGCTCACTGGCAGAAGTTCATAGCCACTGTGAGCCCT
ENSMUST00000031740.1	5	35,933,1053,1188,1346	ENSMUSG00000029726.1	CACTCGGGGAAGGAGGGAGTGAGGTGGTCTTAGGA**AGGGT**TACAGGGGGCTTCCCCTTGCTCTCTTCTCAGTACCCTCGCTTGAGAAGGGGAAATTAAACAGGGAGAGGAGATGATCGAGATGGCGGCGGAGAAGGAGCCCTTTCTGGTGCCGGCCCCGCCGCCGCCGCTCAAAGATGAGTCGGGCGGAGGGGGCGGCCCCGAGGTGCAATCGCACCAAGAGGCTGCCTCCGGGGAGCTCCGTGATGGGACAGAACACGGGCCGGGCCCTCGCGCGCACTCGGCCGGGGCCGGCAGCCGAGCGGAGGGGGCGGCCCCCAGGCACAGGCGCACGGGGAGCCCCACGGGCGAGCCGCCGCTCCTGCGGACGTGGGGGAGGAGCGCCGGGGAGGGGGCGGGACGGACCTGGGTCCCCCAGCCCCTCCTCGACCTCGCAATGGCTACCAGCCCCACCGACCCCCTGGGGGTGGTGGGGGCAAAAGAAGAAATAGCTGTAACGTGGGGGGAGGGAGCGGTGGAAGCTTCAAACATCCGGCCTTCAAGAGGCGCCGGCGAGTGAATTCAGACTGCGACTCTGTGTTACCATCCAATTTCCTTCTGGGGGGTAACATATTTGATCCACTGAACCTGAATAGCCTCCTGGATGAGGAAGTGAGTCGCGCACTCAATGCGGAGACCCCAAAGTCATCCCCACTTCCGGCCAAGGGGCGAGACCCTGTGGAGATCCTCATCCCCAAAGATATTACTGACCCGCTCAGTCTCAACACTTGCACTGACGAGGCCCATGTAGTGCTTGCCTCACCACTCAAGATTGGTCGCAAGCGCCATAGACACCGGGGACCGCACCACCAGCAGCAGCAGCAGGCGTCTGGAGGGAATGATAGCAACGCCGCCGTGCTGCCCACTGACCCTCTCACGCCCTCACTCCATGGGG**AGGGT**GCTACGCAGCAGCAGCAAAACAGAGGCCAGAACCGTGATGCCCCTCAACCCTATGAACTCAACACAGCCATCAA
ENSMUST00000061232.1	1	33	ENSMUSG00000029810.1	TCACGGCCCCTTGGTAGCCCCCTTTTGAAGCAT**AGGGT**TCCTTCTTCTCTGGAAGAGTCTCCAAGTCTACTCCTCAAGCTCCATCTTGGCTCAGGATGCTTCTCCTTCCTTCTATCTCTGCTTTCCTGTAGGACTCTGGGGAGGGAGGGATGTGTTGGACAGAGGATGTGACTCTGGAAACAGGGCTGAGGCTGGGGAGGTCAGAGTCTGGCTTTACCTTCCATAGTTATCAGTGCCTCACGCCTGCGTTCTAAGAGCAGGGCCTTTGAGACCACGCAGAGGTGGGACAGCTGTGGGGACACGGGGTGTTCTTTTTCTTTGTTTCTGAACACTGGGAGGAGGGATATCAGAGAGCCACTATCTGGAGCGGTGCCAGAAGTGGTGAGAGGCTTCTTGGTGCCTAGGGCTTTAGTTCCTGCTCTGCAGAGGAAGCAGAGGGATTCTGGGTGGCCAGGGCAGGGATAGCACTGGGGGTCTAGAGGGGGCCAGCACCCAGACAACTGAGACTTTATTCCTGGAACCTCAAGGGAAGGTGTGAACCTGAGGCCTTCATTTGTGTTTCTCTTCGTCCCTCCTGAAAAGTTGTCAGACTCCTGTG

				CTTTCGGCTCTGAGGTGCACGGCAGGAAAG
ENSMUST00000032141.1	1	13	ENSMUSG00000030060.1	CTAGCTGCGAGGA**AGGGT**GGACTAGACCCTCGGGCGGTCTGAGCGGCAGCGCTGAAGT
ENSMUST00000032398.1	1	54	ENSMUSG00000030264.1	TTTCCGGGCTGGCACCTCGGCTTCCGGCGGCGTGCTCGCGGTGCGGAGACCGGA**AGGGT**CTGTGCTTGCTGCCGAGACTGTTGGTCCTTTTAGAAACATCTCCATC
ENSMUST00000032723.1	1	20	ENSMUSG00000030512.1	GCAGGCTGGTGTCGGAGGTG**AGGGT**CCGCGGGCTGCGACAGG
ENSMUST00000032729.1	1	105	ENSMUSG00000030516.1	CGCCTGAGTTGCCCGCGACGGCTCTGCCCGCCGACGGCACGTCTCTCGGCGGCCGCGCGTTCCGGGGAAGTTACGTGCGGGAGCAGGCTTTGGAGGAGACGCCCG**AGGGT**GTAGGGGACAGCCGGAGGCCCGGGTACTGCGGAGCGGCGAGCCGGCGGAGGGCGGCGGAGGCCGAGCAGGCGGCCGGGTGTGCCCCGCGGAGAAGCCCGGGCGGGGCGGACGCTTCCCGGACTTTTGTCCCACTTGAATCCCCTCCCCGTGGGCCGGGCCTTTCCGGCCTCCCCCGCCCCTGCCCCGCTCGTCCCCGGGAGATGTTTATGCGGACGGTGGCGTGAGGAGCGGGCGGGCCGGCGGCGCGGAGTTTCGGGTCCGAGGAGCTTCGCGCGGCGCGGAGAGAGACAAGATGTCCGCCAGGGCCGCGGCCGCTAAGAGCACAGCAATGGAGGAAACAGCTATATGGGAACAGCACACAGTGACGCTTCACAGG
ENSMUST00000032826.1	1	606	ENSMUSG00000030605.1	GAGAGCAGAGTGCTCCTTACACTCTCCTCAGAAAGCTGCTGAGGGGGATTCTACAAAGTACCATGGAGAGGCAGGTGCGATGCCAAAAGCCTCTAATTGGGGCCAAGGCAGGAGAACTCACAGGTCCAAGGCTAGCATGGGCAACTGGGAGTGTCCCTGTCTCAAAGCAGTAAGGACTGGGGATGTAGCTCAATGGTAGAAGCCTCACCTAGCTTGTTCAAGTTTAGTCCCCAGTACTACACACGCGCTAAGAAGATGACGAAAAGCCTGCTTTGTGTGGAGTTACCTTCGCTGTTCCGTACTGTCCAAGGCCACTCTGCTCCCAAAGCCACTCCTCCTGGGCGAGCCAGGGCTAGGGATGTGGAAGAAGAGGTCATCCTGCTTTTCTCTCCTACCAGAGACCAACTACTACAACCTGGATGGAGAATACATGTTCACCACAGCCGTCCCCAATACTGCCGTCCCCACCCCGGCCCCCACCCCCGATCTTTCCAACAACCTAGCCTCCCGTGAGTTAACTCTGCTGGCTCCTTGTCTCCCGTGTCTCCCGTGATGTCTTCTCTTCCATCTGCTGTCGGTGTCCCTTGGTGTTATCTGCTCTGAGTG**AGGGT**CTGAGGTTCTCTCTGTCTCTAGGTCCTCATCAGAGGCCACGTTGTTTTTTCTCCTCTTGTCCCGTGGACATAACCGGGCCGTGGAACTTTGGATTAGGCTCCCGATGGTCACTGTCTCCCTGCAGGTTGTTCTACACAGCTGGGC
ENSMUST00000032840.1	1	33	ENSMUSG00000030611.1	TGGTGCTGGCTCGAGCTAAGCCAAGCGCCGCGG**AGGGT**CAATTTCAGTC
ENSMUST00000032851.1	2	13,63	ENSMUSG00000030620.1	AAGTTAGGAAGGA**AGGGT**CAGAGGTCGCCGGCCCAGATGCGTTCCTGTGTTGTTATGTAGTGG**AGGGT**CACGTTCCTTCCTGCAAATTCTGGAAGGTTCTTGAGTTCAATTAGGACAGTGGCTGCGGAATTCCTGGTGTCCGGCCTGAGGTGCCCGCTGGCCTAGCAGAGGCGCCGAGGGCGCTGCC
ENSMUST00000057491.1	2	27,77	ENSMUSG00000030620.1	CCGGAGAGGCGTGCAAGTTAGGAAGGA**AGGGT**CAGAGGTCGCCGGCCCAGATGCGTTCCTGTGTTGTTATGTAGTGG**AGGGT**CACGTTCCTTCCTGCAAATTCTGGAAGGTTCTTGAGTTCAATTAGGACAGTGGCTGCGGAATTCCTGGTGTCCGGCCTGAGGTGCCCGCTGGCCTAG
ENSMUST00000032989.1	1	437	ENSMUSG00000030738.1	CCAGAGATGTGGCAGATGTGCCTAGACTGCATCAATGAACTGATGGATACGTTGGTTGCACATTCCAACATCTTTGTTGGAGAGAACATTTTGGAAGAGAGTGAGAACTTACACAACTTTGATCAGGTCACTGCGTGTACGAGGCTGCATCCTAACTTTGGTGGAGCGAATGGATGAAGAATTTACCAAAATAATGCAAAATACTGATCCTCACTCCCAAGAGTATGTGGAGCACCTGAAGGATGAGGCACAAGTGTGTGCCATCATTGAGCGAGTGCAGCGCTACCTGGAGGAGAAAGGTACCACTGAGGAGATCTGCCAGATCTACTTAAGGCGCATCCTGCACACGTACTACAAGTTTGACTACAAGGCCCATCAGCGGCAGCTTACTCCTCCTGAAGGATCCTCAAAGTCTGAGCAAGACCAGGCAGAAAATG**AGGGT**GAGGACTCAGCTGTGCTA
ENSMUST00000033068.1	1	221	ENSMUSG00000030800.1	AGAACAGGTCCACGCTGGTCACTGCAGAGAGACTAAAGGTGTGTCCCGTCTTCCCCCTGGCCATTTTCTGCCGAGAAGCCTGCTTCACCTTCCCAGCCTAGATCCTGGGATTCCTCACTCTGATCCCACACCTAGATCCTGCCTTCAAAACCAGCCTTCTGGTTCTTCCCTTTCTACCTAGGGGCTCCTTCGGGGGGCCCTTGTCCTAGGCCATGGCCCTA**AGGGT**GGGCCTGGGACTTGGGCAGCTGGAAGCTGTGACCATTCTGCTCCTTCTCGGATTGCTCCAGTCGGGAATCCGAGCTGACGGGACTGAAGCCTCCTGTGGTGCCGTCATCCAGCCACGCATCACCGGTGGTGGCAGTGCAAAGCCCGGTCAGTGGCCCTGGCAGGTCAGCATCACCTACGATGGCAACCATGTTTGTGGCGGGTCGCTCGTGTCAAATAAATGGGTGGTGTCTGCTGCTCACTGCTTCCCCAGA
ENSMUST00000051220.1	1	603	ENSMUSG00000030868.1	GGCCGATCAACCGGAAGTAGCTGGAATCACCGTCTGCCTGAGCTACTGACAGGATCCTGAGGTTCAGAGAGGGGGAAGCCATGGAGTTGGGC

				GAACTGCTGTACAACAAGTCGGAGTACATCGAGACGGTGCGCGTGTGGCGACCCTGCCGCCGCTGGCAGTCACGGGACCCTCGAGGACTGGACGGTCGCCCCTCCCGTCCCGGCTGCACTGGTTCCCGTTCCCTCAGTCCCTTCCTTGGATGACTTAGAGATGCTTCGTGTTTCATCTGATTGTTATTTAGTCGGTGCATGCATGCATTAGGCTCTCTTCTCCTTCATCTCGTGTGTGTGGGTGTGCTGTGTAGCGGGGGAGGAAAGTGTGGATGTGGGAGAGTTTCTATGCATATATATCTATGTGTGTGCATATACACACGCCTGAGTTTCCTGTTAAATAATGTCTTCCAGAGGAATACACAGTACAGCCTATTCATTCTGTATATAAATTACATTTTCAGACTCCGGGCCCTTTTTAAAAATAATATTTCACAGTCTGCTTACGTGCTAAGACGTTATTGTTTCTATTCGTCAACTCATAATACAACATATGTAAACTGCCCCCGTT**AGGGT**TACTATCATTATTTTTTCTGTGTGTCTGTGATCATGGAAAAGTAATTTTCCTCACTGAAGGCTATGAAACCGTAATATGGAAGTGGGGTCTGAATGCACATCAGTCATTAGACCGCTCATTAGATACCGATCCTGAATTCATTTCTTGAGCTCTCAGTTCCTGATCTACCCTTGCTCTTTTGATAGATTGGATTCAGTTCCTGAGTGCTCTTATCACGGAGCCGTGCCCACAGCCTTCCCCCCCCCCCCCCAGTGCATTCCTTCTCCAGTTTGTTTTTGTTTGTTTGTTTGGTGATGGAGTCTCACTTCATAGTTTAGTCTAACCCCAAATTCACAGTCACCCCACCCAGAGCTGGGACAGTAGGGGTGCAGTATACATTCAGGCCTCATTCATTTTTAGACTG
ENSMUST00000033169.1	1	127	ENSMUSG00000030878.1	TTGGGCCGGGCAGCAGGCGTGAGGAGCCGGCTCCCGGCGCCACCCGGGGCGCGCTCGCTAGGGCGCCGGCCTTTGGGCGGCGCGGGATAGCGGCGAGAGCTGCTGCGGGACCTGCGTGTCCCGCCCC**AGGGT**GGCTCTGGCTGAGGGCGGCGAC
ENSMUST00000033321.1	1	182	ENSMUSG00000031012.1	CGCGGATCAGCCGCCACCACCTCCCTTCGCGACGATCCTCCCTCCATGGTGCTGCCGCGGCCCCCCCTGTAGCCCGAGCTGCCCCGCGCCGCGCCGGAGCCGGTCTCGGGCAGAGGGAGCGGTCGCGGCCTCGCGGCCCGCGCGGGCTGACGAGCGGAGAGTGCGGCGCTTCGCGGTCCCCG**AGGGT**CCGCACGCCCCGGCAGCGCGGTCGCCAGCCACCGCGCGAGGAGCAGCGGGCGGGCGGGCGGCGCCGGGCCCGGGCCGCCCTCGCTCCCACGCCCCGGCCCCGCCGCCCGCGCCGGGGCGGCAGCCGGCAGAGGAAAGGCGCTGCAGTCTCCGGGCCTCACGGCCCCAGTCGAGCTTCCTCAGCACCGAGGGCTTGCGGGTCCTGAGTGGAGGACACGAGCCCGGAGCCGGGCACTGAGCTCTTGGGCGCCCCCAACCCAGTTTTCAGAACCCTCCACGCTGCGGCCGCTGTCCCCTTCGGACC
ENSMUST00000057655.1	1	182	ENSMUSG00000031012.1	CGCGGATCAGCCGCCACCACCTCCCTTCGCGACGATCCTCCCTCCATGGTGCTGCCGCGGCCCCCCCTGTAGCCCGAGCTGCCCCGCGCCGCGCCGGAGCCGGTCTCGGGCAGAGGGAGCGGTCGCGGCCTCGCGGCCCGCGCGGGCTGACGAGCGGAGAGTGCGGCGCTTCGCGGTCCCCG**AGGGT**CCGCACGCCCCGGCAGCGCGGTCGCCAGCCACCGCGCGAGGAGCAGCGGGCGGGCGGGCGGCGCCGGGCCCGGGCCGCCCTCGCTCCCACGCCCCGGCCCCGCCGCCCGCGCCGGGGCGGCAGCCGGCAGAGGAAAGGCGCTGCAGTCTCCGGGCCTCACGGCCCCAGTCGAGCTTCCTCAGCACCGAGGGCTTGCGGGTCCTGAGTGGAGGACACGAGCCCGGAGCCGGGCACTGAGCTCTTGGGCGCCCCCAACCCAGTTTTCAGAACCCTCCACGCTGCGGCCGCTGTCCCCTTCGGACC
ENSMUST00000033509.1	2	166,354	ENSMUSG00000031168.1	TGCCTACTGGTCCGTAGGTAATAATTAAAATGACAGTTTGAGATGATCAATATTCTGACTAAATGCTGACGAGGTCTGTTTGCCAACTTGTTTACCGTCATGCCTTCTGTTTGGCTTTTAAGAACTGGCACTGTTGAGAGTCTACACCAACTGCTCAGCAGGAGTG**AGGGT**TTGAAGGTGACCGATGCTGTTAGGACTGGAGAGTTCTGAGCTCTGGTGGGCGCTAGGTTTGTTTGTACTGAATGTAATCCACCTGTCGTATTCTCTGCATTTGGGCTAAGAATGGGTCCGGGAACTGATTGGTTGCCTAGAAAACTTAGAAGACCACGCAACTCCGGTCACTAGCAAATGTTG**AGGGT**TTCAAATTTCAGCCTCATCTTGTGCGATTGATAAGAGGGCAGGGAAATTGAAGCTCAGAATAGCATAGATTTGCTATCGGGAGAAAGCGCCCACAGACCTTGGAGGTCTCCACCCTACTCCTGACTTGGTCTCAGCCAACAGGGAAGATGACACCATAGGCGAGGACAGGGCCTGCGACATTCGGAGGACTCCTATTGGCAGAAGCCACCTTCTCCACTTCACTATTGGTCCGCTCCATCGGGCGGGGAAGCGCTAGAGCTGAGCGGAACTGGGGCTATTAGGGAGCCTGCAGGTCTTCCTGGAAAGTCGCAAGCCTGTGTTAGGAAGTCGCCCTGCGATCGCGCCGCCTGGGGTTTTTCTGTCCCTTTGTCCTCGTTTATGTACGAAGCTGCCAGCGGGCCATAGAAAC
ENSMUST00000033582.1	1	17	ENSMUSG00000031231.1	TTTCAGGACGCTTTGCA**AGGGT**AGCTGGGGTGAATTTGCACCAAGGCAGCAGCATAGTCGCCGCAGTTCCATCTTCGTCTCCGCG
ENSMUST00000033604.1	1	52	ENSMUSG00000031252.1	CGGAAACTCTCGCGCCTGGCAAGCTCGAGCCGATCGCCCGGTGCATAGGCGC**AGGGT**CTCCGGGTAGTC
ENSMUST00000033673.1	1	137	ENSMUSG00000031311.1	CGGTCGCGCGCTCTTTTCTCGGGACGGTGGAGGCCGTGCAGCGTCGCCCATACTCCGAGCAAAGAACTGTGGCCAGAGGCAGTCGAGGTTAGTGAGGACTGCGAGGCAGACACTTTGCTGTGTTCAAATCCAAGTCA**A**

				GGGTACAAAA
ENSMUST00000052229.1	1	102	ENSMUSG00000031311.1	GTGCAGCGTCGCCCATACTCCGAGCAAAGAACTGTGGCCAGAGGCAGTCGAGGTTAGTGAGGACTGCGAGGCAGACACTTTGCTGTGTTCAAATCCAAGTCA**AGGGT**ACAAAA
ENSMUST00000033715.1	1	92	ENSMUSG00000031349.1	GAGCGTCAATTGGTTGCGCCAGAGCCAAGCTAGACCAATCAACATTATGAAGGAAGCTCTGCTGATTGTGGGCTCATATCTATCAGTAGAAA**AGGGT**GGCGGGTGTTCAGCCAGACTTCTCTGGTTGCCGGTTGTCTGCAAGCTGAGGTCGATCATTTGAGTGTCTAAACCGGGAAGAAGAGTTGATTGCAAACGAAACCATACTTTGAGCCATA
ENSMUST00000033797.1	1	88	ENSMUSG00000031422.1	ATTCCCACTTCATCTTTCCAGACCATCCTAGGAAATACTAGGAATCCTTGGAAGGGAAAGAAGGAACATTGTTGGTTGGAATAAAAAC**AGGGT**TGA
ENSMUST00000033824.1	1	79	ENSMUSG00000031447.1	TCCACGGGCTCTCGCGAGACCCTCGGCTCACGTGACCGGCGGGCGCGGCACTGCTCACGTGACAGGCGCTGCCGGCCGC**AGGGT**CCTCTCCGTGCCGGCGCCGCAGCTGCGGGGCCTCTCGAGTCGGTGGACGCGCCCTCCCGCCGGCCTCGCCGCCCGCGCAACCGCCGTCCTCCGGCCTCGGCTGCGTCGCGCC
ENSMUST00000033899.1	1	89	ENSMUSG00000031503.1	AGCAGAGCCAGGCCGGCCTGGCCGCCGGTGTGCCACGGGCCAACGCTTCTTCAGGGGCCCATGCGCGCGGGCAGCAGCTCCTGACCCTG**AGGGT**TAGGAAGGGATCGAGCCGAGTCTAGAGCTCAAAGACTGGGATC
ENSMUST00000034166.1	1	26	ENSMUSG00000031730.1	CTCCTCCTCACGGTTGCACCGAAGGA**AGGGT**GCGCGACTTCAGAGCAGCGTCCCTTAGGAGGCGCGACAGCGACAAGACAGAAAGTAGGCACGTCCCGCCACGGAGCCTGACTCCGGGCAGAGCGCACGCGTTCGGCTGTCCAATCAACGTCTAGGGGCGGGCCGGCTGGTGGGGCTTGGGAGATAGGTGGAGCCGAGCCCACATTCTCCAATGGGATGCAGGCAGAGGCGGGCTTAATGGCAGAAGGAGCATGGCGTGGAGACAGCTGAGA
ENSMUST00000034226.1	1	28	ENSMUSG00000031774.1	TGTGGCTGTAAGGAACAGGAAGCCCCGA**AGGGT**CAAAAGGAATACAATAGCGAAGTGTGTTTTCTTCCTTTAAGCCGTCGTTCTTTTCTTGGTTTCTTTTCTAGTTTTTTAAGAGCGAGAGTGGCCTTGGCGGCGACGGTTTACGGTAGGCGCCGCGGAGGTGAGGGCGGCTCGCCTCCCGCGCTCTCGTAGATCTGCCACCTCCCTCCTTCATAGACGGGACTTGACTGCTAAAGCGCCTTGAGTACCTGAGAGTCTCCATTAGAATCTGCTTTGGAAGCAAGAACAGACTGTACCATT
ENSMUST00000034277.1	1	93	ENSMUSG00000031819.1	GGTAGCAGCTGCTTTCCGGCAGACGTTTTCCGGCCGACCGGCTGAGGCGGGAGGCCGCGGCCGGAGGTGCGAGAGCGTCACGGCGTGCAGCGG**AGGGT**CGTGGCGGAGGACCGCGGTGCGTGGGTCGCG
ENSMUST00000034329.1	1	129	ENSMUSG00000031865.1	TGGATGAAGCAAAAGGCAAAAATGATGGCACTGTCCAGGGAAGGAAGTATTTCACATGTGATGAAGGCCACGGCATCTTTGTACGCCAGTCCCAGATCCAAGTATTTGAAGATGGAGCAGATACTACTTCCCCAGAGACTCCTGATTCTTCTGCTTCAAAGGTCCTCAAGAGAGAGGGAGCCGATGCAGCTGCAAAGACCAGCAAACTGCGGGGACTGAAGCCTAAGAAGGCACCGACAGCCCGAAAGACCACAACTCGACGGCCCAAGCCTACTCGCCCAGCCAGCACTGGGGTGGCTGGGCCCAGTAGCTCCCTTGGCCCCTCTGGCTCAGCGTCAGCCGGGGAACTAAGCAGCAGTGAGCCCAGCACCCCAGCTCAGACTCCGCTGGCAGCACCCATCATCCCCACACCGGCCCTCACCTCTCCTGGAGCAGCACCCCCACTTCCATCTCCCTCTAAGGAAGAGGAAGGGCTGAGGGCTCAGGTACGGGACCTGGAGGAGAAGCTGGAGACCCTGCGCCTAAAACGCTCAGAAGACAAAGCAAAGCTGAAAGAGCTGGAGAAGCACAAGATCCAGCTGGAGCAGGTGCAGGAATGGAAGAGCAAAATGCAGGAGCAGCAGGCAGACCTGCAGCGGCGCCTCAAGGAGGCTCGGAAGGAAGCCAAGGAGGCGCTAGAGGCAAAGGAACGCTACATGGAGGAGATGGCCGACACAGCCGACGCTATCGAGATGGCCACTCTGGACAAGGAGATGGCTGAAGAGCGCGCTGAGTCTCTGCAGCAAGAGGTGGAGGCACTGAAGGAACGGGTAGACGAGCTCACCACAGACCTGGAGATTCTCAAGGCTGAAATCGAAGAGAAAGGCTCTGATGGGGCCGCATCAAGCTACCAGCTCAAGCAGCTGGAGGAGCAGAATGCCCGCCTGAAGGATGCCCTGGTGAGGATGCGAGACCTCTCTTCCTCAGAGAAGCAGGAGCACGTGAAGCTGCAGAAACTCATGGAAAAGAAAAA
ENSMUST00000051662.1	1	136	ENSMUSG00000031904.1	AGGCCATACTAAGCACAGGTGTACAGGAACCATTTACCATGGAAGCACAGGAGCTTGGGAGCCCCACACCCACCTACCATCTTCTCCCCAAAGCCAACCAGCACACTGTAAAAGAAGATGCCGGCTCACCATCTCA**AGGGT**CTCCA
ENSMUST00000034441.1	1	1744	ENSMUSG00000031960.1	GGGCTCCGGGCAAGGAAGGACCTGGGGACCCGGACCCTCGGGAAAAAAAGCAAGTGAGCCCCGAGAGCTCTACGAGAAGAGCCGGCGCTTGGAGGGGGAGGGGCAGCTGCAGCGGGCTGCCGGGCGGTCCCGCCCCTGGCCTGGGTCAGGACCCGGTCTCCGCAGGAGCCGGATCTCGAGAGTAGCTTTTGCTATTCCCTCGGAGCACTGAGAGTGGTGTGGTTTCTGGTGGACTTGCAGAGGACCAAGACCTTGGGAAGATCGCGGTTGCTCTTCAGTCGCCACCCAGAGCTAAGGTTCCCGAGGAGACTTTCCGAAATGG

				ATGCCACTTTAACAGCACGAGAGATCCGAGAGCGGTTTATAAATTTCTTCAGACGAAATGAGCACACCTATGTCCACTCTTCCGCCACCATCCCTCTGGATGACCCCACTCTGCTCTTCGCCAACGCTGGCATGAACCAGTTCAAACCCATCTTCCTAAACACAATCGACCCATCTCACCCTATGGCGAAGCTGAGCAGAGCTGCCAATACCCAGAAATGCATCCGAGCTGGGGGCAAGCACAACGACCTGGATGACGTGGGCAAGGATGTCTACCACCACACTTTCTTTGAGATGCTGGGCTCCTGGTCTTTTGGGGACTATTTCAAGGAATTGGCATGTAAGATGGCCCTGGAACTTCTTACCCAGGAGTTTGGTATTCCAGTTGAAAGACTCTATGTCACTTACTTTGGTGGTGATGAGGCGGCCGGCCTAGAGCCAGATCTGGAGTGCAGACAGATTTGGCAAAATTTAGGACTGGATGAAGCCAGAATCCTCCCTGGCAACATGAAGGACAACTTCTGGGAGATGGGTGACACAGGCCCCTGTGGTCCCTGCAGCGAGATCCACTATGACCGCATTGGTGGCAGGGACGCCGCACACCTTGTCAACCAGGATGACCCCAATGTGCTGGAGATCTGGAACCTCGTGTTCATCCAGTATAACAGGGAGTCGGATGGTGTTCTGAAAC
ENSMUST00000001520.1	2	125,213	ENSMUSG00000031967.1	GCTGGTGGGGTCGACGGGCAGTCGAGCCCTGGCCTGGCCTTTCTCCAAGCTGTGGCGATGTGGCGGATGCGCAGGGAGCGGCGGTACGGTCTGGAGCAGCGTGAGGGCCTGTGGCATTGCTCTGC**AGGGT**CATCTGGGGAGATGCTCGCAGCAGCTGGCTCTGCAGGGAAAACTGACTTCATTTTCCCCGAGGCTGTATTCAAAACCTCCCAG**AGGGT**TTGAGAAGTTTTTTAAGAATAAGAAGAACAGAAAAAGTGCAAGCCCAGGAAATTCAGTACCTCCAAAAAAAGAACCAAAAAATGCTGGCCCTGGAGGAGATGGAGGCAACAGAGGAGGGAAAGGAGATGATTTTCCCTGGTGGAAACGGATGCAAAAG
ENSMUST00000034552.1	1	85	ENSMUSG00000032051.1	GTGTAGCCCTCTCGCAGCCGGACACGCGGGACCTACCCGACCCTCAGCACTGCGCAGGACTCCGCGGGACCCGGAACCTTCCGAC**AGGGT**T
ENSMUST00000056684.1	1	219	ENSMUSG00000032117.1	CCGGCTCTTATCTGCACTGAAGAGTTGCGGAGTTGCCTGGCATTCGAAATGAAATTTTGCCGGAGTAGTTGGAGTGATCAGCGCCATACACCTTGCGATTTCAGCGCCTCTGGTCTTGTTTTCAGACTGGACTCAGGCTGGCCTTGAACTCCCAGTGTAGCTGAGGATGACCTTTCGCTCATGGACTTCCTGTTTCCACTTCCTAAGTGCTGGGATTCC**AGGGT**GACAGAGTGCCACTGTCCACTGAAATTCATCAGCTGCACTAAAGCAAAGCTTGCCTCAGTGAAAGGAGTATTCATGCAGACTTCTGTGTTACAGG
ENSMUST00000054708.1	2	35,185	ENSMUSG00000032123.1	GTTGCTTCCTAAGAGCTTCTTGCTGGTCAGGAGGG**AGGGT**CAGGTCCTAGCGTCCTAGCTGGGTTTTGTTCCCGCTGGCGCCGGAATCCTCTGCGGGTTGGGAGCCGCACTGCCGGCTGCCGAGGCCACGGGATTGTTCCTGGCTTACCAGTTAGCTGAGTAGGCGGCGGGGCGGCGGCCACCGG**AGGGT**CACC
ENSMUST00000034639.1	2	7,157	ENSMUSG00000032123.1	AGGAGGG**AGGGT**CAGGTCCTAGCGTCCTAGCTGGGTTTTGTTCCCGCTGGCGCCGGAATCCTCTGCGGGTTGGGAGCCGCACTGCCGGCTGCCGAGGCCACGGGATTGTTCCTGGCTTACCAGTTAGCTGAGTAGGCGGCGGGGCGGCGGCCACCGG**AGGGT**CACCATGTGGGCCTTCCCGGAGTTGCCCCTGCCGCTGCCGCTGCTGGTGAATTTGATCGGCTCGCTGTTGGGATTCGTGGCTACAGTCACCCTCATCCCTGCCTTCCGTAG
ENSMUST00000048674.1	1	47	ENSMUSG00000032295.1	GTCATGGATTACCATCTAGAGACACGGTACTTCTTGGGCAGGACCTG**AGGGT**GGCTGTGTATGCACGCTTCTCTGGCTTAG
ENSMUST00000034865.1	1	39	ENSMUSG00000032315.1	CTGAAGGTGGTAGTTCTTGGAGCTTCCCCGATCCTCCCT**AGGGT**CCTAGAGAACACTCTTCACTTCAGTCCCTCCTTACAGCCCAAGCAGCCACCTAGATC
ENSMUST00000034878.1	1	32	ENSMUSG00000032328.1	GTAGCGGCAGCGGTGACTGCGCGTCTCCTGTC**AGGGT**CGGCGGCACGCAAGTCCCCTGGGCGGCCCAGCTGGACGTGGCCGAGCCGAAGCCCGGGGGCCG
ENSMUST00000034997.1	2	118,273	ENSMUSG00000032424.1	TTCTTTTACGACGGAGCCTAAGATATTCTTTGTCTTGTCGGTGAGTGAGTTACAGTCGGATGACCAAGTGAAATATAGGGGTGCAACGAGGATTTGGAGGCTTCTGAGACTTGAACTT**AGGGT**ACTGGTGTAAACTTCCTCGGAGAAGTGCGCAGCAGCTAATGATATTTCGGGATTGGAGTCTGGGCCCCAGTGAGATTCGTACTAAGCGGCCTGACTGAAGGCCGCATGCGTTCTAGTTCCTGAGTCCCCGCGTGGGTAGGTTTTTACAGC**AGGGT**TTGCAGCCTTTTGTGCTGTTCCGAAGGTACTAGAGTCACCGAAAGAGACATCCTATTATATGCACGTTCACAAGGACA
ENSMUST00000035205.1	1	179	ENSMUSG00000032586.1	AAAAGATTTCATTCTGTCTTCCCCGGCTGGAGCAGACCTACTTTATAAAGTTATGTATGCTTCTTCTGAGGGAGTAATACTGCTAACGATACCGTAAAAATCGCTAAGGAGCCTCGCTTCAACTCAAGATGGCCTTTCTCAGGGAGGACCTTAAATTATCTGATGTGGGAATAATAAAG**AGGGT**TTGTTATTTCCTGGTCTTTGAAGCATCTGTACCTCCAAAATCACCATCCTACAGTCTCAGCTGGTTCCCTGGGCTGCTTGAGTCGAGCCATC
ENSMUST00000041081.1	1	56	ENSMUSG00000032771.1	GAAGCTAGGGGAGCGCGGCTATTGCCGCTGCCGCTTCCACCGCAGTGTGAAGAAAA**AGGGT**CTGAAACAAAGTCTTACCAACGTCTGCTTTTGAACACAGTGACTGCTGGATCTTTAAACATCAAGTTCAGCTTTGTC

				TGTCAACCTGTCTGAC
ENSMUST00000050950.1	4	219,329,509,766	ENSMUSG00000032806.1	GCCGGCCCGGGCCACTACTTGTGAGGAGCTCTGTGGCCGCGGAAGCAAGTGAGAGATTTCGACCAGTTACCTTACTCTGGTTTTCCTGCCTCCCTCTTCATCAGCGAGATTCAAGGCTGGACCAGGGCCCCCAGGGAAAAAATCCTGCTATCAAGGAAGAAAATATAGGACCAGGACCTTCCCATGGACCCTTCTCAGGACATTCCAACAGCACAAGCA**AGGGT**GTCTCCCTAAGACACAAGAGGCCTGAAAAAACTATCCTTTGTGAAGTGCCATGGTGGTCAAGAAAAGCAGAGGTAGCTCCCAGCAGTTGCCTGGCCTGGGAGGAC**AGGGT**GGTTGTACAGGTTTTGTAGGCATGCTTGGAACTGCCCTGCTGTTCATCAGCCTACCATGGGGAGCTCAAGTGATGGCCAGTGCCAACATCAGCACTGCTCTGGGCCACACAAGTGGTCACTATTTGAGTATTGGGGATGGCTCAGTGACAGAATTTGATTTCCCTGAGAAGAGTG**AGGGT**ATCATTGTGATCTCTAGCCAATACACTGGACAGACCAATGGGACAGGCCCCAGCCCCATACTTAAGGTTATATCCCTGGACACAGAGGTGCTGACCATTAAGAATGTGAGTGCCATAACCTGGAGCAGTGGAGGTGGCTTTGTGGTAGGCATCCACTCAGGTCTAGCTGGGCTGGCCCCACTCCACCTCCAGCTCATGGATTTCTATGAGGCCCCACCCCTGCTGATCGAAGAACGGAGAGATTTCTGCATC**AGGGT**GTCACCTGCTGAAGACCTCCCTTCTGCTCTCAACACCAACTTGGGCCACTTCTCAGAGAACCCAATACTCTACTTGCTTCTGCCTCTTATCTTTGTCAACAAGTGTTCATTTGGTTGCAAAGTGGAACTTGAAGTTTTGAAGGAGCTCCTACAGAGCCCCCAACCCATGCTGTTGGGCCTCTTGGGCCAGTTTCTGGTCATGCCTTTCTATGCTTTCCTGATGGCCAAAGTCTTCATGCTA
ENSMUST00000037967.1	1	188	ENSMUSG00000032806.1	CGAGGCCCGGGCAGGACGGGCCTCACTTGCCGGCGTTTGCCGGCCCGGGCCACTACTTGTGAGGAGCTCTGTGGCCGCGGAAGCAAGTGAGAGATTTCGACCAGGAAAAAATCCTGCTATCAAGGAAGAAAATATAGGACCAGGACCTTCCCATGGACCCTTCTCAGGACATTCCAACAGCACAAGCA**AGGGT**GTCTCCCTAAGACACAAGAGGCCTGAAAAAACTATCCTTTGTGAAGTGCC
ENSMUST00000062098.1	1	21	ENSMUSG00000033006.1	TCAGTCTCGGCTGTCCAGCC**AGGGT**GTTTGGTGGTGAGGATTCAGGCTCCGTCCAGACAAGGCAGTGGCCTGAGGCTCAGGGCCCCCCAGCCCCTCCCTCCCAGTCCATCAGCGTCACTCCCCAGCCCCGAGCTGGACCGCACACCTTGGGACACGGTTTTCCACTTCCTCAGGACGAGCCCCAGACTGGAGGAGAGGTCGGAGGAGGTGGGCGTTGGGCTCTTCACGAGGACCCCGGCGGCGGGCCCGGGGGAGGCGGCCGAAGCGGCGGCGGCCGGGAGCGAC
ENSMUST00000040019.1	1	85	ENSMUSG00000033006.1	CAGGACTGGGTCTCCTTTCCAGGGAGAGGAAGAGCCCTTCATGGAACCGTCTGCAGCGGCTCAGTCAGTCTCGGCTGTCCAGCC**AGGGT**GTTTGGTGGTGAGGATTCAGGCTCCGTCCAGACAAGGCAGTGGCCTGAGGCTCAGGGCCCCCCAGCCCCTCCCTCCCAGTCCATCAGCGTCACTCCCCAGCCCCGAGCTGGACCGCACACCTTGGGACACGGTTTTCCACTTCCTCAGGACGAGCCCCAGACTGGAGGAGAGGTCGGAGGAGGTGGGCGTTGGGCTCTTCACGAGGACCCCGGCGGCGGGCCCGGGGGAGGCGGCCGAAGCGGCGGCGGCCGGGAGCGAC
ENSMUST00000050006.1	1	151	ENSMUSG00000033545.1	TGCTTTTTCCACCCCGCGGATTTTTTTTGAGGATTCCCCCCCTCACCTTTTTTCATTTTTCTCCCCTCGGGGCTCTTTTGTGACTCTCCCCAACCCCAACCCTCCGCCTTTATGTTCGCCCAGACCTCCACCCGCTTCTGAGTAGTGGGGG**AGGGT**TTCAGCCTCCACGTTCCCGCCCCACCGGGGCCCCGGCGAAC
ENSMUST00000042012.1	1	129	ENSMUSG00000033732.1	CGCCGGCGGATCGGCAGTGGCGGTGGCTTAGGCCTTGAAGCGATTCAGCATCCGTCGGGTACCGAAGCCATCCTTCTTGCAGCAGGTCTGCTTTGCCTTGAAACCGTTGCTGTAACCAAGAGTTGACTG**AGGGT**CACAGCTTTGCTTGTCACC
ENSMUST00000054613.1	1	129	ENSMUSG00000033732.1	CGCCGGCGGATCGGCAGTGGCGGTGGCTTAGGCCTTGAAGCGATTCAGCATCCGTCGGGTACCGAAGCCATCCTTCTTGCAGCAGGTCTGCTTTGCCTTGAAACCGTTGCTGTAACCAAGAGTTGACTG**AGGGT**CACAGCTTTGCTTGTCACC
ENSMUST00000044369.1	1	105	ENSMUSG00000033793.1	CACGGAGTCGCCTTCGTTCTGCTCTGGGTCTCCCGTGGCCACTGAGACCTCGGAGCTCGACCGGCGCCTGCCCGCCCGTGCGGCCCTCACTCCCCGAGGCTATCC**AGGGT**CTGTGGGAAACATTCAAAGTCATAAAGTTTAG
ENSMUST00000036996.1	1	42	ENSMUSG00000033938.1	AGTGCTTCCAGGTGGGAGCGAGGTGACCCCGGCTACTAAAGA**AGGGT**AAGGCAGAGTAGCC
ENSMUST00000042664.1	1	41	ENSMUSG00000033965.1	GGACAGGCTGGCCAGCTCGGGCGCTGGGAGGAGGAGGAGGC**AGGGT**CTCAGGCAGCCGCGGCGGCAGTGCTCGGAGCGGCAGGAGCAGTAGCAGCAGAAACAAGTACCAGCCAGACAACAGCTCCTCCGGCAAGCCACAGTCAGTCCCCTAGCCGCG
ENSMUST00000048082.1	1	88	ENSMUSG00000034053.1	GTGTGCGGCCGAGGGGACTCCGCGGCGGACGCAGCTCCCGGCTGAGGCTGCGTGAAGGATCCGCTTCCGGCGGCCGCCTACTGCGACC**AGGG**

				TGGTGTGCGCTGTCACCCACGGGCTCAGCGCGGCGTCCCGCGACGGCCTTTCGCTGAGCTGGCCCGGCGGCTGCGATCCCTGCGCGTGCAAGCCGAGGCCCCGCGGCC
ENSMUST00000035840.1	1	73	ENSMUSG00000034075.1	ATCACCTTTCCCCCTCCCATGTGCTTTCCTTCATTTGAGATCTTTTGACCTTCATTTTTATTTGGGAGGGGGA**AGGGT**GATAATTATACATTTTCTGTTTTCCCCAGTTTCTTTCCTCTCTGTTTCCCTCATCCCATTTTCTTGTCTGTTCTGCCGCTGTGTGGGCCTGGGCTATGCGGCAGGGCACATCTTTCATCAGAGCTCCAAC
ENSMUST00000040721.1	1	26	ENSMUSG00000034118.1	CGGCACGGCTGCGCCTCCGCCATCGT**AGGGT**GCCGATCCCCTTGCCACAGTCGAGTCTCCATGGCCTGACCGTGTCTTGACAATAATTTTGAGCAAAATCTATGTCTAATAAGAAGATAACCACATCAAG
ENSMUST00000051232.1	1	119	ENSMUSG00000034120.1	CGTCAGGTTCGGGTGCTCTGCGGCGGCCTTGCGGCTCCCTCCCTACCCACGAGGACTGTAGCTACCGAGCGCCTGACGGAGCTGCGTTTCCGGAGAGCGAGGGCCTGTCCGGGGCGTT**AGGGT**CTCGGCGCCGCTTCGCAGCC
ENSMUST00000047473.1	1	129	ENSMUSG00000034120.1	CTCAGGCGTCCGTCAGGTTCGGGTGCTCTGCGGCGGCCTTGCGGCTCCCTCCCTACCCACGAGGACTGTAGCTACCGAGCGCCTGACGGAGCTGCGTTTCCGGAGAGCGAGGGCCTGTCCGGGGCGTT**AGGGT**CTCGGCGCCGCTTCGCAGCC
ENSMUST00000039679.1	1	24	ENSMUSG00000034558.1	ATTCCTCAGGGAAAGCTGTGTGG**AGGGT**TGGAGGGAGGGAAGATTGGATGCCTGAGCCCTGTGAGAGCCCAGGGATGTGATTGGGGTCTATTAACTGGCTCCAACATCCAAGGTTTTATCTGTGCAACCATTCTCTGAGG
ENSMUST00000058094.1	1	4	ENSMUSG00000034681.1	AAG**AGGGT**GGGAGGCGAGGTCGATGTCTGTGGCCGGAGCGGACGGTGCAGATTGCGAGCCGGCCTAAAAGTGCTCTTTGGCGTAAATTGCAATCGATTAGGGATCGTTTCTCAGACTCAAGTTAGAAGTGAGAGTTCAGATAAGTGAGGCCGACATTGCTGCCTTGAAGAAGGGGAGA
ENSMUST00000040344.1	1	841	ENSMUSG00000034707.1	CACCCTGACGTCCACAGAGGCAGCACGGAGTGGCGAAACTCGGTTCCAGCCTGTCGTCGGCAGTGAGCGGGTTTAGCTTTACACAGCCTCTGCCCAGCTTTAACTTGTAAGACAGCTATGAGTCACTTTGAGAATTCCAGAGGCCATGTTGGGGGGACAGCCATTGAGTTTATTCCTTTACCTCATGTGACCCCAGCAACTTTGGTGATACTGAGAGGCCAGCAGGCAGTAGAGTGGACACCTCGGCCGTGGCCACTTTAGAGGGGGAAAAGTTTAAGTTTTAAACTAAAAGTTACAGAATTGAATGTGGATACCGGCTTCATTCACCCCCACTTGGATTCTAAACATGACCAGTGAAATAGTGAAAGCTGACCACAGTTGTTCCCAAATAAAGGTCGGCAGCTCCTACCAGGTCTGGGATTGAGATGTTAGAGTCTTCAGTTTTATAGCCGGCTCCTGAAAGCAGGCGACATCAGAGTGGTAACAGTCAGTAGGCTGCAGTAGGTGTCCTACCTCGAGGCCCTCAGATGGAGGTAACACATTAGGATTGTGGGACACAAGATCCTCTCTGAACCTCCTGGTTAAGGAACGTTCCTGCAAACATTCAAGTAGACCTTCTATAACAGACTGCAGCGTGCATGGCCTCTACCCACAAGAGATGCACTGCAGGAGGCCGGCCCTGTTCTCTGTACTCAGCATTTTGACATCTCCTTTGAAGGCCAGGTATATGTGTACCAGTGCTCTTCAAAGGGAGAACCATTAAAACCAACATGGAATGCAGGGACTTCGCCTTATAAGATTTCCAGTTTTAAAACTGCCCCTCAGATACAATTTCAAAGT**AGGGT**ACACATTAGAGTGTCTTTGAGTTCAACAAGTTGGTACTGTTGCAAACACCTTCTGAATTGCCAGCGCCCGGGTTTTTATGTAAAAATAGAGTGGCT
ENSMUST00000038488.1	3	530,1113,1406	ENSMUSG00000034908.1	GCTCCTGGTAGCTCCGAGTTCTGCGCCGCGTCCGCCGCCCTTAAAGGGCCCGCGTCCGGGAAGCCTTCGGGCCAGGGCCACCGCCGCCTCGGCTCTCCGGGCGCGAGCGGACGCCGGGTCTCCAGCCGGGCTGGGCCGGGCTGGGCCGGGCTGGGGTAGCGGGTCGCGGTGCCGCCCTCGCGAGCCGGGATCCGCGCGAGGCCCAGGAGCGGCTCCAGGGAGGGGACGCGTCCTATCTGAGGCCGGGGTTAAAGTTCTGGTCCCGGTGAGATGCTGGAAGCTGCTGCGGCAGCCGCAACGCGCCCGGTCGCCGTCCCGTCGCCAATCCCCGCCGTCCCGGGCCATGATCGCCTGGCGTCTGCCCTTGTGCGTGCTCTTGGTGGCCTCCGTCGAGAGCCACCTGGGGGCCCTGGGGCCCAAGAACGTCTCGCAGAAAGACGCGGAGTTTGAGCGCACCTACGCGGACGACGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCACACCGTGACCCGCAACCGGACCG**AGGGT**GTGCGAGTGTCTGTGAATGTCCTGAACAAGCAGAAAGGGGCGCCTTTGCTGTTTGTGGTCCGCCAGAAGGAGGCTGTTGTGTCCTTCCAGGTGCCCCTAATCCTTCGAGGACTATATCAGCGGAAGTACCTCTACCAAAAAGTGGAACGAACTCTGTGTCAGCCCCCCACCAAGAATGAGTCTGAGATCCAGTTTTTCTATGTGGACGTGTCTACCCTGTCACCCGTCAATACCACTTACCAGCTCCGAGTCAACCGTGTGGACAATTTTGTGCTCAGGACTGGAGAGCTGTTTACTTTTAATACCACTGCAGCCCAGCCCCAGTACTTCAAATACGAGTTTCCTGATGGTGTGGACTCGGTAATTGTCAAGGTGACCTCCAAGAAGGCCTTCCCCTGCTCAGTCATCTCCATCCAAGATGTCCTGTGCCCTGTCTATGATCTGGACAACAATGTAGCCTTCATTGGCATGTACCAG

ENSMUST00000048250.1	1	139	ENSMUSG00000035476.1	ATATGTGGATACACTGAAAAAGATAACAATAATCATGTCTCAAGAAGAGCATGATTATGTAACTATCTCTCACACAACTGCGACAAAACTGTGAAAATCGTAATGGTGGGAAAACAGGCGCAAACCCATGGACTTGGAA**AGGGT**GAAAGGCTTGTAAGGTGGGTTTCCTGTCGATCCCCAGAAGCAGTCTAGCAGTCCTACTGTTCTTAAAGGTGCCCTTGCCTTTGTGTAGTTTTTGTCTCCCTTAGAGATGGACAACTCCACTTGCTATTATGAGACAAGTTAGGAGGAACATATACACTACTTGACATATCTGACTAAAGGTGTCCCAGTGTTCGTAATAAGATGCTGAAATACCGACAGCATGACACTTGTCAGTTGACCATGAAAGAAGCATGTGTGAAAAGTCTGATGCTTTATTAAAACTATTGCATGAAAACTCACCAAGGTCAATAAGCTGTTAACATACAGTAGATGC
ENSMUST00000038384.1	1	64	ENSMUSG00000035851.1	CAGGATGCAAGATTTTTCCTCATAAAGAGTAATAACCATGAGAATGTGTCTCTTGCCAAAGCAA**AGGGT**GTATGG
ENSMUST00000049411.1	1	27	ENSMUSG00000035960.1	AGGCAGACTCCATTCTTTGTGCCGTG**AGGGT**CTCTGGCTTCGTTGGGAGGCAGCGCAGTAAACACTGCTTCGGTGCTCCAGGAGCCTAAGGGCTTTCGTCACAGCG
ENSMUST00000047766.1	1	38	ENSMUSG00000036106.1	GTGCAGGCCTCCGCCAAGGTCACAGGCAGACAGGCCA**AGGGT**ACCCCTTCCCTCGCCCACCCTGCAGCTTCTGGCTCCTGAGCAAGGTTGAAGTTC
ENSMUST00000035496.1	4	387,421,622,1577	ENSMUSG00000036180.1	CCGGGCTCCATGTGTGCGGCCGAGGGGCGCATTATCTGGCCGGCGGCGCGGGCGGGCGGAGCGGCGGAGCGAGCGCCGCGGGCCCGGGCGGCCCCTCAGGCGCAGCGAGCACGCGCGGCCGGCGCCCCCCGCCCCCAGCCCTGTGGACACGCGCGCTGCCCCTGGGCCCGGTCGGCGCGCGGCCGGGTTGGCCAGCACATTGAGCCAGCACATCCACATAAGTTGCCTTTTGACAGAACTGTGGCCATGGCAGCATGGTAGGATCCGTGTCCCGGACCCTGAGGCCAGAATGAGTGAAGAAGCATGCCGAACCCGCAGTCAGAAGCGCACCCTTGAACCTGACCTAACGGAGGATGATGTGGAGAACAAGAAAATGAAAATGGAGAA**AGGGT**CATCAGAGCTGACAGTGGACGGAGACAGC**AGGGT**GATGCCAGAGCCGAGTGCAGGCTCAGCCCAGGGGTTGCTGAGGACAACAGAGGCCATGGGCACAGGATCTGGCGAGGGGCTGTTAGGAGACGGGCCTGTGGACATGCGCACTTCACACAGTGACATGAAGTCTGAGAAGAGACCTCCCTCGCCTGATGTGATTGTGCTCTCTGACAGTGAGCAGCCATCGAGCCCA**AGGGT**GAATGGCCTGACCACAGTAGCCTTGAAAGACACCAGCACTGAGGCGCTCTTGAAAAGCAGCCCAGAAGAACGAGAGCGGATGATCAAGCAGCTGAAGGAGGAGCTGAGGCTAGAGGAAGCAAAACTGGTCTTGTTGAAGAAGCTGCGGCAGAGTCAGATACAGAAGGAAGCCACCGCACAGAAGCCTACAGCTTCCTCAGGGAGCACTGTGACCACCCCTCCCCCACTCGTGCGGGGTACCCAGAACATTCCTGCTGGCAAGACCTCACTTCAGACCTCCTCCACTCGAATACCCGGCAGCATCATCCCACCACCACTGGTCCGAGGTGGGCAGCAGGTGTCTGCCAAACTGGGACCACAGGCCAGCTCTCAAGTAGTCATGCCA
ENSMUST00000040299.1	1	48	ENSMUSG00000036315.1	ATCAGTTTTCCGCCTACGTCGGACCTAATGAGGTTCCCCAGCAGCTG**AGGGT**CCTACCTAGCACTCCAAACTCTTGCTGTCAGAGGACCCAGTGGGAAGAAGACTCAGCTCTCATCCGCC
ENSMUST00000036509.1	1	3	ENSMUSG00000036352.1	GCA**AGGGT**ACAGCTCCTGCCCCTTCAGTGACGGGCGGCGGAGCTGACAGGAGCCGGGGCGGGGCGGCGGCGGCCAGCGAAGGAGCGCACGGCGGCCCGGCCCCGCCCCTGGTCCTCCCGCCAGCCTCAGTGACCTTCACTGGTTCGGGCGGCGGGTGCAGGCCCGGGCGGCGGCGCG
ENSMUST00000043098.1	1	76	ENSMUSG00000036390.1	CAGTGGCCCCGAGGCAGCAGTGCAGAGTTCCCCAGCGAGGCTAGGCGAGCAGCCGGCCGGCCGGAGCGGAGAAGGG**AGGGT**GGGAGCGAGGCGCAGAGCCGGCGCCGCGCACTGTGGGGGCCAGGAGCAGCCCGCGCGCCGAGGGAGGGACTCGCACTTGCAAT
ENSMUST00000040506.1	1	243	ENSMUSG00000036501.1	CCCGCTCGCCGTTAGGGAGGCTCTGCGCCTCAGCCGCCACCGCCTCCGCCTCCGCCTCCGCCGCTCCCGCCCACTTCTCCGCGTCTGCCGCCGCCGCTGCCCGGGGTCTCCGGGGGGTCGCTACCGGGCTGGCCCCGCGCCACTGCAGTCGCTTCAGCCTCGCGCTAGAGGCCGCTTCAGGAGGAGACCCGCCGGCCGCCGTGCCACTTAGGGCCTCAGTTCTCGCCTCGTCGACGTCGCCA**AGGGT**TCTGGAAAAGCGGCCAAGGCCGGGGAACGGGGCTTCGCGGTTCCAACGATTAAGTTCTGAAGTACTGATCGAGTTCTGCGTTTCTTCAATGAGGAACTACAGGCTGATCTTCTGCCATAATCTCAAACAGCCATAAATGACAGAACGATGCTTGCTCAGTGAGGGAAGCTGGTGCAGAAGCCGTGTTTTAAACTTAGGTGTTTAAGTACTCAAAGAAAAGACAGCTTTGATTTCTGGCTGCAAAAAAGCT
ENSMUST00000042858.1	1	1593	ENSMUSG00000036606.1	AAGATAGAAGCCAACCGTAACGCCTGCTACACAGGTGCCCGAGAGGCAGGCCGCACTATCTTCTACAAGCCCTTCCACGGAGAAATCCAGTGTGGCGGCCATCTGATAGGTGCCAGCGAGAGCTTCCCATGCGGCTCGGAGCATCTGCCCTATCCACTGGGCAGTCGTGATGGACTCGTCGCCACAGCCGTGCTGCACCGCGGGGGCCTGAATCTGACAGCAGTGACAGTAACTGCCGAGAATGACCACACTGTTGCGTTCCTGGGCACCTCAGATGGCCGGATCCTTAAGGTGTACCTTGCTCCAGACGGCACTTCTGCAG

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ENSMUST00000045604.1	1	99	ENSMUSG00000036850.1	CAGGGAGGACCTTGCTGTGCCTTGGAAGGAGTGACCGGTCAGGCGGTGTTTTAAACGGCTCAGGCTGGGGAAACCGTGTCTGAGCTGTCTCAGGTCGAA**AGGGT**TCTCCCTTTCTCCCTTGCGGGCCGAGCTCTAGAGCCGTCAGCCCAGAGCTGATTTATCCAGAGCCCAGC
ENSMUST00000050641.1	1	166	ENSMUSG00000036965.1	GCTTGGATCCCAGAGCCCAGCCTGGGAGGAACCGGGGCTGCTGGTGTACCACCATCATCCCCAACACTCCTGTTCAGAAGATGGGTGGGGAAATCAGCCGATGACCAGTGGGAAAAATGAGCTACAAGATCACCTGATCTTCATCAGTGAGAAAGCTTTGCACAAG**AGGGT**GTGCTAGAAAT
ENSMUST00000061519.1	1	367	ENSMUSG00000036965.1	CCGTGTCCCTGCGCTCCGTCGGTCAGCGGGCGCGGGCCGGCAGGATGGAGCCGCAGCACGTGCGCCCCGTGCTTGGATCCCAGAGCCCAGCCTGGGAGGAACCGAAAATCTTCAGTACTCGTCTCGCAACATGAACGTTTAAAGCTAAAACCTTCACAGAGATGTGAGATGGAGCAGGAGCAGTGGCTAAATGTTGAACTCTTCAAAACTTGGCGTATGGGCTGCTGGTGTACCACCATCATCCCCAACACTCCTGTTCAGAAGATGGGTGGGGAAAGTGGAAAGTCTAATCAGTCAGCCGATGACCAGTGGGAAAAATGAGCTACAAGATCACCTGATCTTCATCAGTGAGAAAGCTTTGCACAAG**AGGGT**GT
ENSMUST00000000506.1	1	9	ENSMUSG00000037017.1	GATTTCGAG**AGGGT**GGGACGGGTTTAGCGACTGTGGTTCTGGTTCGGGGAGTTCCTCCATGGTGGTTCTGGGAGATTGAGGAGGAGCGCCCCGCCCAGCCGTCGTCGGCGCCCGCTCTAAGGAAAGGCTTTTCCACCCCCGAGGGCTCCCTGGAACAAAACCCTGATTCTTTTGCTTCCGGAATCGCATTTCTAGTCTCTCCGTTATTGTCTGTTACCTGACGGAAACTGCCCTCTTTCTTCCCCAGCAAGAGCCCTGAGATCTAAACTCAGAACTAATTGTTAAGAATAAGCCCAAGTGTAGAAACCTCTGAAAACCCGAATCTCCTCAGTCTTGAGTCTTGTCCAGTCCAGGCGGGGAATTGGTCCCGGTGGGCTTTGTGCGCACTGGACAAGGATTTGCTCAAGTCTGGAAAGATTTTTAGACGATCGTTTGTAAAACGCGTATAGGATAGAAAGGTGATTGATTTATTTGGTGGCTGACATAGTTGGAAATCTGTTGAAAGGGGACACTTAAAGAATTGTGAACAACAACAACAAAATCAATACAGGAAAATTGTTTTTCAAGTGGTGGAAGGCTTCTGAAGAGAGACTGAGTATTGGTTCAGGGCTATTGAAATGATGCAGAATTTGGCTCACTCTGAGCTACTAGATCTGCCCAGTAGTTATGCTCTTCAGAATTATTGGCCTGCCTGGAAGCTTTTTGAAAATTAGTTTGCTCGGTTTGAGACGGGGTCTTACTGTATGGCCTACACTGGTGTATAATTGGTGATCCTCCTGTCTCTGTTCTCTTCAGTGCTGTAATTACAGGTATGCACCACCACGACTTCAGCTTGGAGTTTCCAAGTGCAGAGTGTCTTAAGGGCATTATCTACTACAAGGTTTGAAGAGTGGCACTTTAAGAACCAGAAACCCAAAGGTACCAGGTCTACTCCTAAAAGTCCTGCTGGCTCGGGAATCTGTG
ENSMUST00000046983.1	1	17	ENSMUSG00000037049.1	TCAGTCAACCACAACGA**AGGGT**AATCAGGTGTCTCCAGCGTTACCCGGGCCCCGAGGGCCAGCCAGGGCTTCGGCCTGTGGGGCCTGGAGGGGCAAGCCAGTCCTGTCTACGAGCCTGGCA
ENSMUST00000042512.1	1	41	ENSMUSG00000037262.1	GAGCCAGTTCCGCTTCCGACCGCTTTGTAGTTGTAGCGCTC**AGGGT**CGCC
ENSMUST00000041418.1	1	1172	ENSMUSG00000037286.1	AGCAGAGGGCGGTCGGGACCCGAGTCTGCAGCGGCGCCATTGGCGTGTGGAAAATGCCACCAGATGGCGGGTTAGGATTGCAGCTCCGTTGAAGGCGCGGCCCCCGCTCCCGAACCCCCGGCGACCACCCCGTAACCACCCCCCCACCTCGGGAATAACACACCGGAGACTTTTGGGGGGAAACTAGGTCGACGGCCGACAGCGCCCGGATGGGCAGCTGAGGTGTGACTTTGAGGTTGAATAACCAGTTTGAATTATACAGAAATTTCTGTACTGTGGAATAGCTTCTCCAGCAATGATTACTTCAGAGTTACCAGTGTTACAGGATTCAACTAATGAAACTACTGCCCACTCTGATGCTGGCAGCGAACTTGAAGAAACAGAGGTCAAAGGAAAAAGAAAAAGGGGTCGTCCTGGCCGGCCTCCATCAACAAATAAGAAACCTCGAAAATCTCCAGGAGAAAAGAGCAGAATTGAAGCTGGAATTCGAGGAGCAGGTCGTGGAAGAGCCAATGGGCACCCCCAACAGAACGGCGACGGGGATCCTGTCAC

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ENSMUST00000043296.1	1	218	ENSMUSG00000037544.1	AGTTTATAGTGTGTCGCTGCCACGCCTAGCGGGTTTACCGCCTCCCTCCTCCCCCTCGCCCTCCCGCTCCCAACCCTTTGCCTTCCAAACAATTTAAATGTCGCACAGAACCAACCTATCGCAAGCCTCGTTCGAGGGGAAGGGGCGGGAGCTTCCGGAAGTGTTGGCAAAAGTCCCTCCAATCAGCGGCTGGCAGCGGGAAATTTCAGTTCCGTGA**AGGGT**CGGTCCGGGAGTTCCTTCTGCGGATCGGTGGAGTTTTCTGTGTTGCGACATTGTTGTGGATCCAGAAACTGCTTCAGG
ENSMUST00000045457.1	1	16	ENSMUSG00000037677.1	AGTACCTTCCCGGCAA**AGGGT**TACTGGGCATTCTGGACCGTAACCCTCGCTTGCA
ENSMUST00000047074.1	1	145	ENSMUSG00000037777.1	ACTCCTGCTCCCGGGCCCTTCTTTGTTTTCTCCCTGGGTTTGTTTTTCTTCTACCTGGCTTGGCTGTTTCTTCATTCACTTTTGAGAAGAGCCCGTCTCCAAATCGCCCAGTTACACAAGTGCCCGGGGCTCTCTGGACTTGTG**AGGGT**CCCTGCTACTCTGACTGCCCTGGTATCAAGTTACTGAAAGTCTACACCCAGGCAGTCCTCATATTTACATACAAATAACTCCTGGGTTTGCTTTTATGTCACTATTGGGTCCTGCAAGAGGCTTGCCAGAGCGTCCTTAATCCAATCAGGAGGCACTTTGAAAGGATGTCTGTTGAGCGGTCAGAAGGATGTTCGTCGCTATTAAGTGTTGCCACACAAAATTTTTCGCATGTTTCGGTCTGAGTTTTTTTTTTTTTTTAAATCTTCGGAGTTAAAAAAGTGAGGAATGATGTACAGCTGCTCAGTTGCCTTCGACAGCTTGGAGATGCTGAGGGAAACGCTGCAGCCCTGGTGAAGAAGATCTGACTAGGGACGGGTTTGGATCCATACCAGGCTGGTGTGGATTGGGGCTGGTGTGGACGGCTTACTCTAAACCCCTGCTTAAGGAATTCCTGGAAGCCTCGGGAAAGTACTCCCCAACCAGTCGTGGTGGAAATGGCTTTGCCACACAGTAAGATGCCATCACAGGGGACACTGACAAGTATCTCGGGCCACAGGACCTTAAGGAGCTAGGTGATGACTCCCTGCCAGCAGAAGGTTACGTAGGCTTCAGTCTTGGAGCCCGTTCTGCCAGCCTCCGCTCCTTCAGTTCGGATAGGTCCTACACCTTGAACAGAAGCTCCTACGCAAGGGACAGCATGATGATAGAGGAACTTCTGGTACCATCCAAAGAGCAGCACCTGACGTTCACGAGGGAGTTTGATTCTGACTCCCTCAGACACTACAGTTGGGCAGCGGACACGTTAGATAATGTGAACCTGGTCTCAAGCCCGGTGCATTCTGGGTTTCTGGTTAGCTTTATG
ENSMUST00000049974.1	1	1051	ENSMUSG00000037805.1	CGGGTAAGGCTTGCCGCTCCCTGCCATGCGTTCAGATCTAGCGGGATGGCCAGCGCCGACCATGACCTGTTCTGTTTTCTCCCCTCCCAAACGCAGGCTCAAGTCCACCCCACGCCCCAAGTTCTCGGTGTGCGTTCTGGGGGACCAGCAGCACTGTGATGAAGCCAAGGCCGTGGATATCCCCCACATGGACATCGAGGCGCTCAAGAAGCTTAACAAAAACAAGAAGTTGGTCAAGAAGCTGGGTAGGTGGGGCTCACTAGGGCTGAACACAACCCATGACCCCCTGCCCAGGAGTGGCAGCACACATTGGGCTTCACAACCAGTTAGAAAATGCCCCACAGGCTGGTCTGATACTCCCCTCTCGCCAGTGTGTGCAGTTGACTCATAGCCAGCTATTGGTTTGGGTTTCAAGTCTTTTCAGTTAACAACCTATCGAGGGAGGGGTCACAAGTGTCTCCCACGTGTTAGCCTCCATGGTAGCCCCTGTCTCCGCATACATTTTGGGAATAGTTATCCACTGTGAGCTAGGCAGTTGTCATGCCTGCTTTTATAGATAGAAGGTTTCTCCATCTGTCTTAAGATTTGGAGTAATACTGAGTCTTACTGATGTTGCCAGCCTGGGGTCTAAGGTTATCCTCTAGAAGTGCTCAGGACTGTGCCCTGTCACTGAGCTGTGTTCTCAGGTGACATTATGGTTCCCAGGCCTGCTTGAGGCTTCTCAGATAGCTGGCCTTGGTCCACCTTTGACAGATAATGAGACAGCTTTTTTCTTAAGATTTTATTTTATGTATATGAGCAGGCTGATGAGAGCCTCAGATCCCATTACAGGTGGCTGTGAGCCACCATGTGGCTGCTGGAAATTGAACTCAGGACCTCTGGAAGGCAGCACTCTTAACTGCTGAGCCATCTCTCCAGTCCATAGTTTGAGGCAATTTAAATGCAGGCTTACAGTGAATCCAAGGGGTGGGGGCCATCACAGCCCCTCAGTTCTATGCAGCACACCAGGGAT
ENSMUST00000042891.1	1	41	ENSMUSG00000038146.1	CGTGCCCGGAGCCCTGGGAAAGAGGGAGGAGGGAGGAGGG**AGGGT**CGTGGCCGGCCGCC
ENSMUST00000046893.1	1	622	ENSMUSG00000038390.1	CAAGACTGGTCAGCGGCTCCCTAACCCCGGGCTCGCAGGCTGATGACCCTGGGAGACAGGGGCCTCGAGGGGCCGCAAACTAGCGCGCCGCGGGCTGAGCCCGAGAGGCCAGGCTGGGGGGAGGGAGGCCCGGAGGGAGGGAGTGAAGGAAGGAGGAGGGCTGGCGAGCTGGAGCCGGCAGGCGGCGGGAGCCCGGGCGAGCCTCGTCGGGAGTGCGTCTCCTCGGCAGA

				GCAGGACGCAGCCAGAGCTTGTCCAGGTGACTGAGCTCCACCCCTGTGCACCAAGACACCCACCCCACCCCCCACTGGTCAAGCCTCGCTGGAGAAAGAGACCGGGAAGTCCCAGCATGAGAATCAGAGCTGCCCAGCCAGCTTCATAGATGGGGAAGCAGCCTGCTTGCCTCCCCCATCAATTACAGGGATAACTGAGAAAAAGCCCCACCCAATATGGAGGCTGAGGACTACCGCCTCTATTAATTCCCTGCCTTCTCCCCTGCCCTGCCCACCTGGCCTTAGCTGGGTCACTCATGCAATGCTGAGAAGTAAGCAAGACTTGGGGTCAGCTTGCCTGGCTACCAGGCAAGGACTGTGGGCATCATGGGGGTGTGTGTGAGCGGGGCTCC**AGGGT**GAGACCTAGCCCCCGCCCCCAGGAATTCAAGGGGGTGGGGGTGGGGCCGAGGATAGA
ENSMUST00000038681.1	1	93	ENSMUSG00000038503.1	CGGATGAGGTCCGGACAGGAGGAACCAGAACGAGGCGGGGTGCGGTAGGCTACGGACTCCTCGGAGGCGGAGCCATTGGGACTTGAGTCCGCG**AGGGT**GGGACGGGGTCAAGTACTGGGTTTAGTTCTGCGCAGAACACGCTTAGGGACTGGATTGGAAGGCCGGGGGCGGGGTGGGGGCGAGGCCCCGGCGTCCGGACTCCGCACGCTGTCTGCGCAGGCTCATTGTGCCTTACGCTGGGCAGTCCGTTACGCTAGGCTGCTAAC
ENSMUST00000052687.1	2	44,145	ENSMUSG00000038525.1	AAAATGAGAGGGCTGGACGGGAGAGTGAGTGTTGGGGCGGAGCT**AGGGT**CTGTGTTCAACGCGCCGCAGTCCCGGTCTTGGTCCAGGAAAAAGCTGCTTGCACTAGGGGCATCCCGCCTGCCTGGTGAAAGGAACCGCAGCACAC**AGGGT**GGGAGGGCTTCCGATTTTAG
ENSMUST00000060173.1	1	597	ENSMUSG00000038605.1	ACACTGGCTGCCTGGTGCTCCGCGAGGGGCGTGTGCCCGAGCCGCACATCCGCGGGCTCCATGTTCACCGAGCTGCGGTCCAAGCTGAGCCCCCCGCGAGCTCGCGCCGGGGCTGTGCGTCCGGGCTTCGGGGAGCGTCCGGATGTGGACGGCCGAGCTCTGCTTCGACTGAATGCAGATAAGCTGCAGAGAATGGGGTTGACCCAAGAGGCTCAGAGGCAGGAGGTGCTGCAGCAGGTACTCCACCTGCAGGTTCGTGAGGAGGGGCGGAGCCTGAAGCTGCTCAGCCAAGCTTCCTTCGGAAACATGTCCTAGCTGCTGCCTATACTTGGACCCCAGACCCCAACACTGTGACCAGAGCCCACAGCCAAGAATGAGTCAGAATTGGCCCTACAGCCCCTTTGGATCCTGCAGGATACCCTAGTGGCTAAACCTAGCCCAGTGATCAGGGAGGAGCAAGACTTCCACCTCCAGGTGTCTCTGGAGAGGCACTACAGGTTCTGCCCTGTGGCTGGGTGGGTGGTTGTTGCCTGCTTATAGACCCTTCTTCTGAGATCCAAGCCCAGGTCCCATCCCCTGGTGCTGCTGGCAGCAAAC**AGGGT**AGCTGCCTGGAACTAGAATGGGGTTTGAATGTCCCCAGACTCCCAGGGAGTCTGTTTATTTATTCTCCCTCCAACATGTGACCATCCCCCATCTGAGTCATGAGTCTTCCCCTTAAATCTTAGTTCTGTGTCTTTCCCGGGCACCCCCAGATCAGCCACACAGTGGGCCAAGCTGTCTTGGCTCTCTTTCAAGTATATCTGTCCCCTAGCTCTCCTAGAGTACAGCAGGCCCAACCTGCTGTCCATACTA
ENSMUST00000049343.1	1	8	ENSMUSG00000038644.1	GCGCGCAG**AGGGT**TCAGGGGTCACGGCGGCGTATCTTGTGGCGGGAAAAGCTGTTTGAGGCG
ENSMUST00000049666.1	1	119	ENSMUSG00000038683.1	ATTTCCCAAGGCCGGCGGAGCCCACGGCTTCCCAGGACTTGCCTGCTTGACACAACTTTTCTTTCTCTCTGCTCTGAGAGCCTCCTCCCGCGGCTTCCTTCCTTAAGCTCGTCGCAGA**AGGGT**CACGTGACGTCCCACGTAACGGAGGACGGAGCGCGTCCTCCGTTATTGCCATTTGCAGGCGCCTAAAAGGTGCCCCCGGGCGGTGACGTATAACTCGCGCGCCGGCTGAGGAAGGGAAGGGCCAGCCTCCGCAGCCATCGGGTCTCCACGCCGGCGTCTCTTGCCCGGCACGAGTGCTGCGGA
ENSMUST00000046951.1	1	119	ENSMUSG00000038683.1	ATTTCCCAAGGCCGGCGGAGCCCACGGCTTCCCAGGACTTGCCTGCTTGACACAACTTTTCTTTCTCTCTGCTCTGAGAGCCTCCTCCCGCGGCTTCCTTCCTTAAGCTCGTCGCAGA**AGGGT**CACGTGACGTCCCACGTAACGGAGGACGGAGCGCGTCCTCCGTTATTGCCATTTGCAGGCGCCTAAAAGGTGCCCCCGGGCGGTGACGTATAA
ENSMUST00000052650.1	1	924	ENSMUSG00000038721.1	AAGCTTTAAATATGACTACCTCGTTTGTTTGAAAATATGTTTAGGAGAGGAAGCTGTATGATTTGATAACTTGTATTAAAATACCAATTACATTTATAGGACCTTTTAAAACTCGGTGCAATTAAACCGTGTTCTTTTACATTTTTCCGAAGCGACCCTGACATTTAGAAAGACTCCAATTGCCTCGTTAAAATCGCGAAATTAACAGCGTGCCTACGCCAGGCTCAGCGTTGTGGATGTGTGTGTATGGTGTTTTTCCGTGACTCCCCCACATCAGTCTTTGGGGGTGGTCTGCGAAGGTATTTGATTTGTTGTGAGGCAAGAGATATCTCATTAATGTAGGTAGTTAAACAGATTTAATCCGTATTCGTTCTCTCTCTCTCCCCCCTCCCTCTCCCCCCCTCTCCCCCTCTTTCTCCCTGGGTGTTTTTTTCTCTTCCCCTCCTTTTTTTCTGCCCTCTCCTCACTCCCTGGCGCTCTCTCGCTCTAGCTCTCTCTCGCACTCGCTCTCTCTCGCTCTCACCCTCGCTCTGCGTTCTGTCCGGGAGGAGTACCCAGAAGCCAATAGGATGCGGGGTCTCTAATGGATGCAAATGATGGTGAAAAGACGGGGCAAAATATGAAACAACTCATTTGGAGGGAAGTAAATCACCGAAAACTGTTTATGAACTGGCATCCCTTCTTCGAAATGTAAAGCGAGGACCTCTTTAAGTGGCGGTATATTTTTGTTTGGGGGGTGGGGGGTGGGGGGAGGGCGAGCGAGCCGCGGCTGCCATGCAGGC

				TTAGACTTTTGCAGGCTTCGCTCTTCTATTCCTGGAAATCACAAAA AGTGTGGCGGCTTTGAGATCTTCTTCGTCTTTTCTTTCTTTTCCTT CCTTCCTTCTTTTTTTTCCCCTCCTCCCTTTTCCTCTCCTTTCCTG GCG**AGGGT**GACTAGGAGCCGGCGAATCCGCGTTTTTTTTTCTCTCT CTCTCCCTCCCTTTTCCCCCTCCCCACCCCCTCCCCAACAGCCCCC
ENSMUST00000049352.1	1	194	ENSMUSG00000038721.1	GAGCTCCGGCCCCGCGAGCGGAGCCAGGAGCTGGGCCTCCCACAGC AGCGTCCCCCGCCGCGCCAGTCCCCGCTAGTGGTAGTATCTCGTAA TAGCTTCTGTGTGTGAGCTACCGTGGATCTCCTTCCCTTCTCTTGG GGGTCCGGGGGGAAAAAAAGAAAAGGATTTTAAGCAAGGACTCCCT CGTCCTGCG**AGGGT**GATCGACTGCGGCCTGGCAGAACCCCCTCGCC CCCGCCCCATGTAAAAAAGCCTCCTTGTGCAATGGTCTGTTTCCTT TGAACGTGCTTCTTTGTAATGACCGAGGTACCGATTTCTGCTAAGT TTTCCCAACAACATGAAACTGCCTATTCACGCCGTAATTCTTTCTG TCTCCCGCTCACTTTCTCTCTTTCTCTCGCTCTCTTTCTCTCACCG CGTCCCCATCTTTCCTCGCAACCCCCTCTCCCCGCTGCCCTCCCTA GCTGGCTTTCTCTCTTGCTTCTCTCTTTTCCTCCTGTCCCCCCACC CCCACCCCCTTTGGTTTGACAATTTTGTCTTAAGTGTTTCTCAAAA GAGATTACTTTAGTTAGCATGCGCGCTGTGAGCATTGTTAAAAGTG TTCTTAGGTTTACTGTGAAGAGAATGTATCCTGTATCTGTGAATTG CTTTATGGGGGGGAGGGAGGGCTAATTATATATTTTGTTGTTCCTC TATACTTTGTTCTGTTGTCTGCGCCTGAAAAGGGCGGAAGAGTTAC AATAAAGTTTACAAGCGAGAACCCGAGACTGGCCCGGGCCGCCGCT CCTCATTCGCTCCTAGGCGCCTTGCAGGGCTGGGGGTGGGGGGGAG CTGGTCAGCAGGCTCCTGGGCTGGCCTAGGCTAGGTCGCTGAGAGG AGGGGGCGGGGGCGGGGGCTGGAAGCAGGTGGTGCGAGTCCCTGGG CCCAGGGGCGCAGGGGGTGAGGGAGGCGGCTGAACGTGATTGGAGG AGAGAGGATCGAGGGAGGGGAGCCAAGAGAAACCCCCTCCCCTTGC
ENSMUST00000043775.1	1	664	ENSMUSG00000038773.1	GTGGAAGCGAGCAGTGCGTGGAGTTCGGGAGATGTGTGATGTGTGT GAGACAACCCTCTTCAATATCCACTGGGTCTGTCGGAAATGTGGAT TTGGGGTCTGCCTTGACTGTTACCGGCTCAGGAAAAGCCGTCCAAG GAGTGAGACAGAAGAAATGGGGGATGAGGAAGTTTTCTCCTGGCTG AAGTGTGCAAAGGGGCAGTCCCACGAACCAGAAAACCTCATGCCCA CCCAGATCATCCCTGGCACAGCGCTTTACAATATTGGAGACATGGT ACACGCTGCCCGGGGAAAGTGGGGGATTAAAGCTAACTGCCCTTGT ATAAGTCGGCAAAGCAAATCTGTTTTGAGACCTGCTGTCACCAATG GGATATCACAGCTTCCCAGTGTAACCCCTAGTGCCTCTTCTGGAAA CGAAACTACCTTCTCAAGCGGAGGCGGAGCTGCAGCGGTCACAAAT CCAGAGCCAGACCAAGTTCCCAAAGGTGCTGGCACTGACGGCAGAT CTGAGGAGCCCCTAAAAGCAGAAGGTTCTGCGTCAAATAGCAATAG TGAACTAAAAGCCATCAGGCCCCCGTGCCCGGACACAGCCCCTCCT TCCTCTGCTCTGCATTGGTTGGCCGACTTAGCAACTCAGAAGGCGA AAGAAGAAACGAAAGATGC**AGGGT**CCCTGCGGTCGGTGCTCAATAA GGAGTCTCATTCACCCTTTGGGCTGGACTCATTCAACTCTACTGCA AAAGTCTCTCCATTG
ENSMUST00000045372.1	1	132	ENSMUSG00000038871.1	GAGCGTTGATGCCGGCTGTAGCGATGAATCCTCACTGGCGTCTGCA GCACGGCGTTACCGAGGACCGGCTGCTACTGGTAGTTTCCTTGCAG ATATACTGCTGTTCTTGAACATCATCCCATTGAGAACCCC**AGGGT**A GTTCAGCCACCAGC
ENSMUST00000047558.1	1	29	ENSMUSG00000038943.1	CCGTTCTCCGTCCCGCGCGTGGCAAGTGG**AGGGT**CTCGATTCTGGA CAGCTTGGAGCGTCCACC
ENSMUST00000035301.1	1	40	ENSMUSG00000039105.1	AGAGTCTGGGTGGTGGATCAGGTGATCCGAGGGGCTTCGG**AGGGT**G TTTGAGCAGTTGACTTAGGCCGTTCTCTCAGCCCAAAGTCCCCTCA GCA
ENSMUST00000048657.1	1	53	ENSMUSG00000039367.1	GTTCGGCTCCTCTGTGAGGAGCTCAAGTCACTCTTAGACTACCTAC CTAGGG**AGGGT**GGAGCAGAAGAGTCAGCAATCCGAGTTGGCTTTGT CACCTATAATAAAGTGCTCCACTTCTACAATGTGAAAAGCTCCTTG GCTCAGCCACAGATGATGGTTGTATCTGATGTAGCTGACATGTTTG TGCCACTGCTGGATGGCTTCCTAGTCAATGTCAGTGAGTCTCGGGC TGTTATCACCAGCTTATTGGATCAGATTCCAGAAATGTTTGCAGAT ACAAGAGAGACAGAGACAGTGTTTGCTCCAGTTATCCAGGCCGGGA TGGAAGCTCTGAAGGCTGCTGAGTGTGCAGGAAAGCTGTTTCTGTT CCACACATCCTTGCCCATTGCAGAGGCCCCAGGGAAGCTGAAGAAT AGA
ENSMUST00000035672.1	2	1712,3211	ENSMUSG00000039457.1	CACCTGCGCCCGCCGCCCGCTTTCGGTGCGCGCCGGGTCCGTCGCC GCGTTCCAGGTCCCTCTGTCCCAAGCGCCACCATGCACTCGCTCTT CAGGAAGAGAAACAAAGGCAAATACAGCCCAACGGTGCAGACGCGG AGCATCTCCAACAAGGAACTCTCAGATCTGATTGAGCAGCTGCAGA AGAATGCAGACCAGGTGGAAAGGAACATTGTGGACACCGAGGCCAA GATGCAGAGCGACTTGGCCCGGATGCAAGAGGGGCAGCTCCCTGAG CACCGGGACGCGGCCCTGCAGAACGTGTCTGACTCAGAAAAGCTGC

				TGTACGTGCTGGAGGCAGATTCGGCCATCGCCAAGCACATGAAGCACCCACAGGGGGACATGATCGCCGAGGACATCCGCCAGCTGAAAGAGCGCGTGACCAACCTGCGGGGGAAACACAAGCAGATGTACAGCCTGGCAGTGAAAGAGGCCGACCCGAGAGTCAACTGGGACACACTGGTGGACGAGAAGCTGGACAAGCTGAGCAGCCAGAGCTTTGGGACTGACCTTCCTCTGGTGGATAGCCAGGTGGAGCAACACAACATCTTCCACAATGAAGTCAAAGCCATCGGGCCCCACCTGGCCAAGGACAAGGAGCAGAACAGTGAACTCCAAGCCAAGTATCAGAAGTTGCTGACAGCATCACAGGCACGGCAGCAGCACCTGAGCTCGCTGCAGGATTACATGCAGCGCTGCACCAATGAGCTGTACTGGCTGGACCAGCAAGCCAAGGGCCGCATGCAGTATGACTGGAGCGACCGCAACCTCGACTACCCCAGCCGCCGCCGCCAGTACGAGAATTTCATCAACCGGAACCTGGAGGCCAAAGAAGAAAGAATCAACAAACTGCACACTGAAGGTGACCAACTGCTGACAGCTGAGCACCCAGGGAGGAACTCCATTGAGGCACACATGGAGGCTGTGCATGCTGAGTGGAAGGAGTACCTGAACCTGCTCATCTGTGAGGAGA
ENSMUST00000044911.1	1	274	ENSMUSG00000039615.1	GGCCGCAGGCAGCTCCTCCCGATTCCCGAGGAAGCCCCTCGAGAGCGGTCTGATCTGCGGGCCTCTCTTCTACCCTCAATTCCGCCTTCCTACCGGCGGTCCAGACGTTCCCAGGCTGTCGCGTGAGCCCGTGTGTGCCCTGGTGGTGCGCTAGGACCCGGGCCTAGTGACCGGCCCTCGGAAGGCCACTTCTCAATGACCGCTGCCACGTTCGCCCAGCTTGGGGCCGGAGGGCGGGGCTTGAGCGCCGATGGGCGGAGCCTTGGTCTGAGC**AGGGT**AGGTCTCGGTTACTGTAGGGCGGGGCCTGTAGAGCGCGGCGGAAGCTTCTCAGAGCTAAGGGAACTGGCTCAATCCACGAGGCTCCGCCTTTGCTCACGTGTCCCCATGCCAGCTCCGCCCCACACCGGAAGTTCCGGTGGCGGATCGCCGACCGGGCGGAGCTGATCGCTGCGCGGGCTGCGAGATCTAGGTGGCCGGGCGCGGAGCCCAAGCCGTGCCGCGCGGCGCC
ENSMUST00000044268.1	1	81	ENSMUSG00000039660.1	AACTGGCAGGCGCGCGGTGGGCCTGGAAACATGGCGGAGCGCCCGAGGAAGCGTCCGTGTGGTCCGGGTGAACATGGCCAA**AGGGT**TGAATGGCGAAAATGGAAACAGCAGAGTAAGTAAAAAGCTGAGGCCGGGTTGGGCAAGCGCACTGAGCCCTCCCTTTCCACAAACCAGCTAATGGCCCGACGAGCCCTCTTTGGGTCTCAGTGTATCCAAGTGAGTGGTGGCAGCCTCTCCAGAGCCTAGGCTAGCCCAGCGAGAAGGAACTCTCCTCCCCATGTCAAGTCCTTTCCCTCCAATAATTCTCCAGAAAAAGAGGAGAAAAAGAAGTGGAAGGACCTCAAGATA
ENSMUST00000048724.1	4	295,301,1112,1360	ENSMUSG00000039807.1	CCTGTGCCACAGCAAAGGCACGGGAAAATGGAGAGGGGGGCAGCTGGATCTGGTAGACGAGACAAAGCTTTTATTGCTACTAGTACTGAAGGGACGGACAAAGGCATCATGTTAAACACAGTCAAGACTGGAGATGCCACCACCACTTCATCAGAAGTGGGAGAGAAGGGGACAGCCTTACCTTGCACCAGTATTGAGGCGGACGAAGGCTTCATGATGGGTGCTTGCCCTAAAAAACATCCCCTCCAGGTTGGGGCAGAAGCCAGTGAATGCACTGTTTTTGCTGCAGCTGAAG**AGGGT**A**AGGGT**GTTGTCACAGAAGGATTTGCTGAAAGTGAGATTTTGCTTACAAGCTCCAAGGAAGGAGAAAGTGGAGAATGTGCTGTGGCTGAGTCAGAAGACAGAGTAGCAGGTCCCTTGGCTGCTCATACAGTTCAAGCTGAAGCCAATGTGAACAGTATTACAACAGAGGAAAAAGACGATGCAGTAACCAGTGCAGGCTCTGAGGAAAAGTGTGGTGGATCTGCATGTACAGTTGAGGGGACGGCTACTTTTATTGGTGAAGTTGAAAGTGATGGAGCTGTTACAAGTGCTGGAACGGAAATAAGAGCAGGATCTCTGAGCAGTGAAGATGTTGATGGGTCCCAAGAAAATAGGATACAAGTTGGTCCTAAAAAAGAAACAGAAGGCACTGTGACATGTACTGAAACCAAAGGAAGAAATGATAACTTCATTTGCTTGGTAACTAGAGTAGAAACCCAAGAGCAACGTGTAGTTACAGGTGCAGATGTGGTCCAAGTAAATGCTGCTAAACCCCAAGAGGCAAATGCCAATCAAGGAGATGGTTCTGGAACTGATGGTGCAGAAGGTGAGAGTGCAGTCACCAGCACAGGCATTACTGAAGAAGATGGGGAAGCATCAGCAAATTGCACAGGCTCAGAAGACAACAGGGAAGGCTGTGCCATAAGTTCTGAAACAGAAGAAAGTGCAGAGAGTGCCATGGACAGCACAGAAG
ENSMUST00000049149.1	2	205,399	ENSMUSG00000040249.1	GCCAGTGCACTGAGGAGGCGGAAACGGGGGAGCCCCTAGTGCTCCATCAGGCCCCTACCAAGGCACCCCCATCGGGTCCACGCCCCCCACCCCCCACCCCGCCTCCTCCCAATTGTGCATTTTTGCAGCCAGAGGCGGCTCCGAGATGGGGCTGTGAGCTTCGCCCTGGGAGGGGGAGAGGAGCGAGGAGTAAAGCAGGGGTGA**AGGGT**TCGAATTTGGGGGCAGGGGGCGCACCCGCGTCAGCAGGCCCTTCCCAGGGGGCTCGGAACTGTACCATTTCACCTATGCCCCTGGTTCGCTTTGCTTAAGGAAAGGATAAGAATAGAAGAGTCGGGGAGAGGAAGATAAAGGGGGACCCCCCAATTGGGGGGGGCGAGGACAAGAAGTAACAGGACCAG**AGGGT**GGGGGCTGCTGTTTGCATCGGCCCACACC
ENSMUST00000062861.1	1	6	ENSMUSG00000040472.1	GTGCA**AGGGT**CCACGGGACGGACGGACGGGCGGGCGGGCACTGCTCTCTATATGCGCGGCGTGTGCCTCGGCCCTGACGGGTGGGGCTTCGGAAAGATCCGTGGGGACGGAGGCCGTGGTTGTGGTGAGCGCTTCCTCCTGACCTCACAGTGCCAGCCGCCGGCCCCCTTTTAACTCACGGGGA

				TCCTTATCCTGGGCCTGCTGGCAGCTTCCGGGAAACACCTGGGGGGCGGGGCCGTGTGGGCGGGGTTCTGTGATTGACATCTCTTTCGGCAGATTGAACGGGCTGCCTCCGGACCCCTCCCCTATCGCCAACGCTGA
ENSMUST00000002393.1	1	6	ENSMUSG00000040472.1	GTGCA**AGGGT**CCACGGGACGGACGGACGGGCGGGCGGGCACTGCTCTCTATATGCGCGGCGTGTGCCTCGGCCCTGACGGGTGGGGCTTCGGAAAGATCCGTGGGGACGGAGGCCGTGGTTGTGGTGAGCGCTTCCTCCTGACCTCACAGTGCCAGCCGCCGGCCCCCTTTTAACTCACGGGGATCCTTATCCTGGGCCTGCTGGCAGCTTCCGGGAAACACCTGGGGGGCGGGGCCGTGTGGGCGGGGTTCTGTGATTGACATCTCTTTCGGCAGATTGAACGGGCTGCCTCCGGACCCCTCCCCTATCGCCAACGCTGAGCCGAAACCATG
ENSMUST00000045141.1	1	11	ENSMUSG00000040472.1	AGGGGGTGCA**AGGGT**CCACGGGACGGACGGACGGGCGGGCGGGCACTGCTCTCTATATGCGCGGCGTGTGCCTCGGCCCTGACGGGTGGGGCTTCGGAAAGATCCGTGGGGACGGAGGCCGTGGTTGTGATTGAACGGGCTGCCTCCGGACCCCTCCCCTATCGCCAACGCTGAGCCGAAACCATG
ENSMUST00000049228.1	1	16	ENSMUSG00000040476.1	GGCGGTGTGGTTGATT**AGGGT**GCTGCTTTCAATCGTGTGGCCTTTGGGAACCCCGCGTAGCCACTGCCGCCTCCTTCTGTCCTCGCC
ENSMUST00000045035.1	1	29	ENSMUSG00000040564.1	CATGGGCCTCCTGAGAGATCCTTAGATCC**AGGGT**GCCCCTCCAACCAGG
ENSMUST00000046478.1	2	148,171	ENSMUSG00000040644.1	CTTCATCCTTCAGGTACCAGCCATCTGGGCAGAACTTAAGCTGTGGAGACTGAGACCACCCCTCCAAGGATCTCGTCTGAGCATCTCTAGTGACCTTCTCTGCATTAACTGTCAGTGCTACGGATATTTTTAGCTCCAAGTCCTGGC**AGGGT**GGGGCACCTATCTGAGGC**AGGGT**TTGGTGCCCCCTCCCCACTGACCCTACATCCCTGGCTGCCGCTGCTGTTACTTCAGG
ENSMUST00000040428.1	1	52	ENSMUSG00000040904.1	TCGCTCTGCGCCGCGCAAGTCCCCAAATCCAGCTCCTGTCCTAGCATTTCC**AGGGT**TCCCTCTCCCGGCTTCTGTG
ENSMUST00000047013.1	1	187	ENSMUSG00000041012.1	GCAGTCCACTGCCACCGGTCGCCAGCGATCCCGTTCCCGGGTCTCCGAGCAGACCCAGAGTGCGCTCGCCGAGGTGTTGGGACACTTGCGGACCTGACCCTGGAGATCACCCGGGTTTGCCCGCCTCCCATCATCCGCGATTCCCTGGCCCGCGATCCTGAGCCCAGGGAACTCATTGGGTGGGGGT**AGGGT**CCTCGGGGACCCGGGCCAGCTCCCGGGGCGACG
ENSMUST00000035875.1	1	41	ENSMUSG00000041431.1	GGAACGGCTGTTAGTGTTTAGCTGTGGATAGCCAGAGGTT**AGGGT**GTCTTCTCGAATCGGGGAACCTCTGATTTTGGAGGAGCC
ENSMUST00000047629.1	1	939	ENSMUSG00000041438.1	AGGTCGGATTCTCAGTCTCTGCTGGCACCCTGCGGGTACCCACGTCGCAGCTGGTTCCTTAGACTACATTAGCGTGTTTGATGTCAAATCAGGGAGCATAATTCGTAAGATGGTTTTAGATAGGCAACACCTGGGAGTGACTAAGTCCAGGTGCATAGTGTGGGGTGTTGCCTTCTTGTCCGACGGCACTGTCATAAGTGTGGACTCTGTTGGAAAGGTGCAGTTGTGGGACTCTGCTACTGGGACACTCGTTAAGAGTCATCTCGTCGCAAATGCTGATGTGCAGTCTATTGCTGTTGCTGATCAAGAAGACAGTTTTGTGGTGGGCACCGCCGAGGGCACGGTATTCCATTTCCAGCTGGTGTCCATGACTTCCAACAGCAGTGAGAAGCAGTGGGTGCGGACGAAACCGTTCCAGCATCACACTCATGACGTGCGTGCTGTGGCCCACAGCCCAACAGCCCTGATCTCAGGAGGCACCGACACCCACCTGGTTATTCGGCCTCTCATGGAGAGAGTGGAGGTAAAGAATTACGATGCTGCTCTCCGAAAGATCACGTTCCCCCATCGGCGTCTCATTTCCTGTTCAAAAAGAAGGCAGCTTCTCCTTTTCCAGTTCGCGCATCACTTGGAACTGTGGAGACTAGGATCCACATCTGCAACAGGCAAGAACGGAGATACTCTTCCACTCTCTAAAAACGCAGATCATCTCCTGCACCTCAAGACAAAGGGCCCTGAGAACATTATCTGCAGCTGTGTCTCCCCGTGTGGAAGCTGGATAGCCTATTCTACAGCGTCTCGCTTTTTTCTCTATCGATTGAAATATGAACGCGATAACATAAGCCTCCAAAGAGTTTCCAAATTGCCATCATTCCTGCGCTCTGCCCTTCATATTCTGTTTTCTGAAGATTCAACAAAGCTCCTTGTGGCATCCAATCA**AGGGT**CTCTGCATATTGTTCATCTGTCGGAAGGAAGCTTCAAGCACTTGCATACTTTCCAGCCGCAGTCAGGT
ENSMUST00000041997.1	1	286	ENSMUSG00000041598.1	AACAATCGGCGGCGGTCGCCCCGAGGGGGGCGTGTGCGCACAGACTTCTCCATGAATAACCGCTGAGTTCGTCGGTAGTGGTAGAGGGGTGTACGCGTGCTCTCCCGTGTACACACACTGCTTTAGGCGCCACCCGGTGTCGCCCGGCCGGGGAGAAAGGAGGGCAAGAGCCGGCTGGAAGGCAATAGCCTAAAGAGCAAATACTCCCCGCCCGTCGGAGCCCTTCCTTCTCCCGCCCCGCCCGCCTCCCTTGGAAGACTTGGAGGCCAAGGCCGCAAGAGGCGC**AGGGT**GGGGCTGGGCCGAGCTGGCGGTCCCTTAGAAACCTGGGACGAGGCTTTACGCGGGGGGACCTGCGCGCGCGCCCGGTACGTCCGAAGCATGGGGCTCGAGGCTTTTTCAGGGGCGAGTAGGTAGCGGTTGGTTAATGATTTAACCGCTGGCTTGGGACGTTGAAGGCTGCGATCCTGATCTCTGGCTCCTCCCCATTCCTGGAGCGCCCCCAGCCGGAGGAACAAATCTGCCCTCCTGTGTCTGTGGCGTCGTCTGCTGGAGCTGCCTTTCCCCTTTGGGGGACCCCTGGTTGCTGTGGCCCTCTGAT

				TGCCCTGTCTACCCTTTGCATTGCTGGACTTCAGATCTGACCCCATACCTGCCTGTTGCCTTGGGAGTGCCCAGCTCCCCCGCAGCCAGCACG
ENSMUST00000048046.1	1	71	ENSMUSG00000041732.1	CTGACAAGGAGATCTGTGGAGTTTTTCTCCAAGTGAACCAATCCCCTGTGTCCTGGCTCACACTGTGGTT**AGGGT**GGGCACATCCACTCTGCCATCTTTAACACACAGAAACCAAACATCAGTGCTCCAGTAGCTTACTA
ENSMUST00000038945.1	1	132	ENSMUSG00000041801.1	GAGCGGTGGAACATGTAAGGGCACATCCCGCCAGCAGCCGCCCAGCTCGCAGACGGAGCGCAGGGGAGCGGGCGTGCGGGCGGCGAGGCGCAGGGCACCGGGTAGAGGCTCGGGGAGGTCGAAGCGGCGCGC**AGGGT**TCCAAGCCGGCGGCGAGAGAGTAGCATCGCACGAGCCTCCCGGTACCCGCTGTCTGCGAGGCGGCCCGGGCCGCAGGCTCGACCGCACAGGGAGCAAGGCCAACCAGCTCCAGGGCGCGAGAAGCCGGCGCTGTAGAGCCGGGACAGCCGGGATCGCCGCAGCCTCCAGAGCTGTGGGAACCTCGGGGTGCCC
ENSMUST00000048966.1	4	426,585,1874,2505	ENSMUSG00000041852.1	TGAGAGGAGAAACTGCCCCCTTTCCTTTTTCTTCCCGGTTTCTCGCTTTCCCTTCCTCCCTGCCTCCGCGGGGGGTTGTTTTCCTGCCGGCCTGCATGCTGTGGGCTGTCAAGGGGTTTGGGGGCAAGTGCCAGGGGAGGATGCAGCTGCAAAGGAGGGCTGCTGGCCTGCTGCTGTGCTGCTGAACAGTATGCAGTCGTTTCGGGAGCAAAGCAGTTACCACGGAAACCAGCAGAGCTACCCACAGGAGGTGCACAGCTCATCCCGCATAGAAGAGTTCAGCCCTCGCCAGGCCCAGATGTTCCAGAATTTTGGGGGAGCAGGTGGTGGTAGTAGTGGCACTGGCAGCAGCAGTAGCGGTCGACGAGGAACAGCTGCTGCAGCGGCAGCAATGGCTAGTGAGACCTCTGGCCATCAAGGCTATC**AGGGT**TTCAGGAAAGAAGCTGGAGATTTTTACTACATGGCAGGCAACAAAGACACAGTGGCAGCAGGAACCCCACAGCCTCCTCAGCGAAGGCCTTCTGGGCCTGTACAGAGCTATGGACCTCCCCAGGGGAGCAGCTTTGGCAATCAGTATGCGAGTG**AGGGT**CATGTGAGCCAATTTCAAGCACAGCACTCTGCCCTTGGTGGTGTGTCTCATTATCAGCAGGATTACACAGGGCCTTTCTCTCCTGGGAGTGCTCAGTATCAACAGCAGGCCTCTAGCCAACAACAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCAGCAACAGCAGCAGCAAGTACAGCAGTTGAGACAACAGCTTTACCAATCCCATCAGCCTCTGCCACAAACCACTGGACAGCCAGCCTCTGGCTCATCGCATCTACAACCAATGCAGCGGCCCTCAACTCTGCCATCTTCTGCTGGTTATCAGTTAAGAGTAGGTCAGTTTGGACAGCACTACCAGTCTTCTGCTTCCTCCTCTTCCTCCTCCTCCTTCCCTTCTCCACAGCGTTTCAGTCAGTCTGGACAAAGCTATGATGGC
ENSMUST00000036160.1	1	149	ENSMUSG00000042275.1	GCTGAGTCGGCCAACTTTGGATTCTGGGATTCCCAGGACATCAATCAGGTCAAGCTACATAGAGGTCCACCAGGGGTACATTCCACGCATTCCACTGCTCTCTCTGGGCTCTGTCCTTTAACATCTGGGTTAACTGGATCGTGCAAAC**AGGGT**AACAGGCGCAGAAAACAGCTGGACACGTTGCTGAGCCCAGACTGTACGTGACTAGTTCTTAGAAACCGCTTCTGGATCTCTCTGAGCCAACAAGCTCGTCGGTCTGA
ENSMUST00000046532.1	1	20	ENSMUSG00000042367.1	GAGATGCCTCCTTAATGAGT**AGGGT**AGAAAGGAAGAGCATTCCAGGCGGGAGGAATCAAGGCCAGGTCTGAGCAGAGAGAGGCAAGGTGGGCACAGCCCCCCGAACCCTGAGCAGGCACC
ENSMUST00000044156.1	1	176	ENSMUSG00000042406.1	GGCTAGGTGTCCCACCCCGCCTTGTAAGACACCGGAAATTCGTCAACGAGCGATCCCTCCGCGCTCCGGAACCAGACCGCGGCTGGTCGTCAACCTATAAAGTAGTGCACTTTTCTCTCATGGGGCCTTTAGGACGATCTCTAACGCCACAGTTACCCCCCGAGCACAGCGGAGA**AGGGT**TGGGGCGGGCGAGGGCGTCAGTGAGAGGCGGTTTGGTGGCGCTGCGGTAGGATCACGTGACCACAGTGGGAGGATACGCGGTGTGCTGCGTCCCTGGCCGAGGCTATAAAGGGCGGGTTTAGGGCGTGCCGCCGCCATTTCTGCTTGCTGTCTGCCGGTTTAAGTTGTGTGCTCGGGTGTCCCTTTCCTCTTCCCCTCCCGCAGGGCTTGCGGCCACCATGGCGTATTAGAGGCAGCAGTGCCTGCGGCAGCGTTGGCCTTTGCAGCGGCGGCAGCAGCACCAGGCTCTGCAGCGGCAACCCCCACCGGCCTAAGCCATGGCG
ENSMUST00000030630.1	1	102	ENSMUSG00000042446.1	AAGACGAAGACACAGAGATGGATTCCCCCAGCCCAGACGGCGAGGGAGGAAGAAGTCTGTGGTACCTGTGGAACCCAGAAGTCTTATTCAAGGAGCCTTGCA**AGGGT**GCTCAGTGTCTGGAATGACACTGAAGTATATGTATGGGGTAAATGCCTGGAAGAACTGGGTTCAGTGGAAAAATGCCAAGGATGAACAAGGAGATCTGAAGTGCGGGGGAGGTGAACTTGCCTCTGCTAGTCCGTGTTCTGACTCCTTAGGAAGTGCTCAAGACCATGCCCTCTCTCAAGAATCCTCAGAGCAAGGCTGTAAAGCCCGCTCTGTGAAACTGAAGGAAGATATTCTGTCCTGCACTTTTTCTGAGTTGAGTTTGGGCTTATGCCAGTTTATCCAAGAGGTGCGGAGACCAAATGGTGAAAAGTATGACCCAGACAGTATCTTATACCTGTGCCTTGGAATTCAGCAGTACCTATTTGAAAATGGTAGAATAGATAACATTTTTACGGAGCCCTATTCCAGATTTATGATTGAACTTACCAAACTCTTGAAAATATGGGAACCTACAATACTTCCTAATGGTTACATGTTCTCCCGCATTGAA

				GAAGAGCAT
ENSMUST00000057427.1	1	197	ENSMUSG00000042590.1	CACATTGGCTGTAGAGGAACCAGTGTGAAGAGTGGCGTTTCCTGCATAGCCATGGCTTTAAAATTCAAAAAACGGTGGAGTGCTGGCGGTCAGCAGTGCCCAGAGGAACTGAGTTAAAGAACGGAGCTCTGCAGAGTTAAAACAAAGCCTTAAAGCCACGTGATGATACGAGTCCCGTATCCTTGAATTACATCCA**AGGGT**CCCTAAGCCATTGTCTTCATTGACTCCTCTTCAGGCAAATTCCAATTTTGAGAATACAAACTTTTGGGTCTTCAAGAGTGGCTAGCCTCGTCAGCCCTTGCTGTAAACATCTGTTATCAGAATCCCATATCTATGTGTGGCAGAACATTATGTTATATTAAATGGACTAACATTACAAATTGCCTTTACCTTGGACCAATATATCCAGAACTTGGGCTGTAAAATCTCTTCTATTCATCACACGACCACTGCACTA
ENSMUST00000042141.1	1	73	ENSMUSG00000042699.1	GCCGTTCTCGTGGAAGGTTGGCGCTGCGAACTCGCCTAAGAAGGCTGTGCTCTCGGGCACGGAAAAGCGGAGG**AGGGT**GTGAAGAAGACACCTGAATC
ENSMUST00000049668.1	1	248	ENSMUSG00000042936.1	AACTCAGCTGCCGACCCACCAGGCCCAAGCCTCTGGCTTGCAGGCAGAACTGCCTTCAGTGCAGCTGCAGCCTTCTTGGCAAGGCCCACTGCCCATGTTGCAGGCCCAGCCTGGAGCCTCTGCCACACTGGCAAACTTTCCCCGGGGCTCCACTCGATCACGTATGGCTCCATCAGGAGAACCTGGCCCCTCTTCTCTAGAACCTCGGGGCCCTCCTAGGGAACGTAGGGCACCTGCAAGGGACAAAA**AGGGT**CCTCCAAAAGAGCGC
ENSMUST00000050897.1	1	2	ENSMUSG00000043065.1	C**AGGGT**CAGTTTTAGTTCCCGGTGAACCTAGCGCGTTTGGCTCCACTGGGAGGTAGCAAGACATATTTCTAAGCAAACGATCAAAAGTTAAGGCAAGGAAGTGCGGTATGTGGAGGTTGGTGTGCAAGTTTCTTTTGGAGACTTCTAGAGGCTTATGACAGGCGCGCCATTTGGCCCTTTGGGTGAGAACTGCAGAGCCCCACGCCAGTACCGCCTCTGGGTCGCCTCGGAGGAGCTCGCCGGATGTACGCAAAGGCGTGGGGGCGGAGCTCTGGTAACCCAGGCAACGGCCCGGAAGCCACTTTCCGCGTTCCCCCGTGGCGGGCTCTGTGGTTCTGGAGGCTGAACTTTTAGTCGGGGCGGAGGCACAGTCGGCCAGCGGCAAG
ENSMUST00000058150.1	1	36	ENSMUSG00000043165.1	TCACCTCCTTCCCTCACTCATCTTCCCTGGTGCTTC**AGGGT**AACCCTTCTCCTTAAACAAG
ENSMUST00000062888.1	1	12	ENSMUSG00000043848.1	GAGGGGCTTCGG**AGGGT**GTTTGAGCAGTTGACTTAGGCCGTTCTCTCGGCCCAAAGTCCCCTCAGCA
ENSMUST00000055995.1	1	19	ENSMUSG00000044123.1	GCCTGGGGTCGTGATTGCT**AGGGT**GGATCTTCGGTTTGCTCAGAAGCCGCTGTGGTCGAGA
ENSMUST00000050516.1	1	34	ENSMUSG00000044475.1	GCCTTTGCATACGGCCGGCGCGGGCGAGCCTCC**AGGGT**CTCTTCCTACGCTCCCAGTTAGTCCTGGCAGGACTTTCCTGGAACGTCATTTGTC
ENSMUST00000061392.1	1	4	ENSMUSG00000044539.1	GCG**AGGGT**ATCTGGGGTCCTGCTTAGAATTTGGACCGCTTGACCTGTGAGTCCCTGTGGCTCTTCGGCCATTCTGATGTGAAC
ENSMUST00000053864.1	1	41	ENSMUSG00000044573.1	AGTGCGCATGCGCCTCGTCCCGACGCGGTTTCTGGGCGCC**AGGGT**CTGCACCGAAAC
ENSMUST00000058733.1	1	609	ENSMUSG00000044600.1	TTTCCGGTTTGACGGACGCCTTGGGTGTAAGGATGATCGGAGACATACTGCTGTTCGGGGACGCTACTGATGAACGCCGGGGCTGTGCTCAACTTTAAACTGGAAAAAGAAGGACACACAAGGCTTTGGGGAAGAATCGAAGGAACCCAGCACAGGGAGACAACATCCGAGAGTTTTTACTAAGCCTGAGGTATTTCCGGATCTTCATCGCACTGTGGAATGTGTTCATGATGCTCTGCATGATCGTGACTGTTCGGCTCTTGAGTCCTGCGTGGAACCCAGAGATCACCTGCTGGACATCAAGGCTCTATTTCTGTTTCTGATGACTTCAAGAATCTTCTCAATGGAAAACCAGGGACCTTCCCAGAAGGCCCAAGCTCATTTGGGTGGAGAATGTCCATTTCCCAGCTCCCTGACCCTCGTCAGCCACAGTGACAAAGTCAGACTTTATTAGGAGAAAGACCTAGGTCTTTACCTTGTGCTGGCATTCTATCTTCTCCTGGCCCAGCTTCTCCAGAAACCTGACCTGGGCTATTTCTTGGTTGAATTGATGGTGATTGTTTTGGTTTGATTTGGGTGTCTTTGTCTGTTTTTTTGTTTTTTTGAGAC**AGGGT**TTTTCTGGTTAGCCCTGGCTATTCTGGAACTCACACACCAGACGGGCCTCAAACTCATAGAGATCCGCCTGTCTCTGCCTCTCAAGTGCTGGGATTAAAGGTGT
ENSMUST00000050410.1	1	122	ENSMUSG00000044627.1	GCCTGACGTGGGGCGGTTGGTGGTCTCCGTCGTCGGTTTCTAGTTCCCTGAAGCAGCCGTTTAACCCCAACCCTGGACCCTTCCGAGTTTAAGCCCACCCCACTCCGGGTGCCCCGGACCTT**AGGGT**TCAGGAGGGGTGAGTCAGAATTCAGCCGACTTTACCATGGCGGCTACCGATCACCGCAACGGCCATTCCCC
ENSMUST00000061681.1	1	126	ENSMUSG00000044645.1	GGCCGCGCGCTCCGCCGCCCGCCAGTCTGGTCGGCGCGCGCTCAGCGGCGGCGGCGGCGGCCCGACGACGCAGCAGCGGCGCTCGCGCTCGGCTCCCCGGCCACGGGACGCGGTCGCACCCGGCG**AGGGT**GCAGCCCCCGGAGCGGCGGCGGCGGCGGGAAAA
ENSMUST00000058776.1	1	416	ENSMUSG00000044980.1	TTTTTTGTTTTTTTTTTTTTTCTTAACCCACCTCCTTTTTTTTATTTTCTTCCTCTTCCTGATATGCAAGTGATGTGGCTTGTGACCATAGC

				CTTGGGCAATCCTACAATCACGAGAGTTGCTATGCTGCTTTCCAAAAAAAAGATGAAAAATGGAGGAAAAGTGAAAAACAACAAAAACAAACCAAAAAAAAAAAATGATAAAAAGCCAGACTTTTTGTTTTTGTTTTTAAACCATTTTGGAAAGAAGCGGGTTTTGAAAAATAGTTCTGTTAATTTGGGACAAATTATATTCTAGAAGCTTTGTGTGACCTCATGGCTGTTTCCAAAGACTGTCATCAACCTGTTTCGAAGTGAAACAGTTGGGACTCATTGGACCACAGTGGAAGTGACAACTCCTTAACCCAGTCCTGGGGTG**AGGGT**GTGGTGTCCTTCTGTGGTGACTAATGCGGGTAAATGTAGGGACCTGGTTTTATGCCTCCCGACCCTGTCTTCATCCTCTGTTTTTTTTTTTTTGTTTTTGATTTTGTTTTTTTTAAATGTACTTTAAGAGAAAAGGAGAAGAGAATGCCAGAAAACTAAGATGGTTCAATTAATCCACTTCCTTCAGCCTTATGCCCTTGGATAGGACATCCTCCATACACCGGCC
ENSMUST00000060985.1	1	8	ENSMUSG00000045553.1	GGCTGA**AGGGT**AGCAGACGTTTCCACAGCCGCCGACCCGCAGCTTGAGTGTCCTGCACCACCTTTCGTGGAAATCTGAGCCGGCTGTACAGCTTTCCTCCTTGTTCCTGCAGCC
ENSMUST00000055258.1	1	38	ENSMUSG00000045671.1	CTCCACACCCACAGTTGCCACTTGGGGTGCACAGATA**AGGGT**AGGTCACCAACTGATTATGCCTGTCTCTGAGCCATGCAAGAGGCTCCTAATGTGCTGGGGGGGGGAGCACATATGCATATATATAT
ENSMUST00000055744.1	1	19	ENSMUSG00000045748.1	AGACGGTTGCGGGCGCAG**AGGGT**TGGTAGTTGTCGCTGTGGGCCTTCGCTGCCGCTTCTGCATCGTGAATCGGGGGACCTTGGCAGCCAGACCTCGTTCCTCTTACAGTAGCTCTCATCTAGTCGCCACAACTCCGCCACC
ENSMUST00000060433.1	1	114	ENSMUSG00000045752.1	GGGCGCTGAAGCCACGAAAATCTGATCGCCCGAGACTCGGTTTCCCAGGAACCCGAGCGAGACTGGACAGGACCGAATCCCGGGGAACTGGCGGGACGCTGCGAGAAAGGCGGC**AGGGT**ATTGAGGCGTGTACGGACGCTGGAACGCTCCTGTATCTGTGCGCGCTAGGATACCCTTTAACCACCCAGCTTCGCGAGGCCTCCCGTCCGGCTGTGAGTAGAGGCACTTGACACATAGTGGAGGTGGGACGGGTGTCAGGTCGT
ENSMUST00000060630.1	5	13,1804,2315,2338,2535	ENSMUSG00000046268.1	TGGACAGTTGGC**AGGGT**TCCTGATGCAGATGGACAGGTTCATGATTTTTCAAGCCTCCCGCTTCCCCGGTGAAGCCGAGAGAGTGGCCTTCCTGGTATCCCGTCTGACTGGGGAGGCGGAGAAGTGGGCCATCCCCCACATGCAACCAGACAGCCCTTTGCGAAACAATTACCAGGGGTTTCTGGCTGAGCTCCGCAGAACCTACAAGTCCCCGCTGAGGCACTCAAGGCGAGCACAAATCCGGAAGACATCCGCGTCCAATAGGGCTGTGCGGGAGCGAGAGCGGGAGCGCCAGATGTTGTGTCGCCAACTGGCCGCAGCTGGCACAGGATCCTGCCCGGTGCATCCAGCCTCCAACGGGACCAATCCCGCACCAGCCTTGCCCTCTCGTGGCCGGAACCTTTAAGGACTTGCCACCACCCTGGTAGTCTGTGTCCACCCAGGTAGCTAGACTCCGTTGTTGAGAGTTGTCAATTCAGTAGCTTTGCCCTGTTTGAGGCACCCTTCACGCCTCTCTGGTCTACGGGAGACCATCCTGTCATCGGCATTGGTCACCCACCCCGCTGTGCGGCGTGTATTTGTTTTGTTAGCGTTACCCGCGACTCAGTGCATGCTCCCCCTTTCTGTTGCTTGCAATCCCAGCTTCTCCAGCAATCACAACACAGCCCCTTGGGCATGTGCCTGCCCAGGAACCATTTAGGCTGACCACCTCTGCGAGCTCAGCTCACGGATACTCAGCTCCTGGAACACTCCCTACAGCTCTTGCTGCCCCAGGCTGAAGAACTGGCGAGGAGTGGCCAACTGCTTCGGGTCTCATGTGGACACATGTTCCAGTCCCAAGGAGCAGAGCCTCACAGGAGGATGACCTCTCAATCAGACTCAGCCAAGCCTCTGGACCATGACATCATCTGTCATTTCAATGCCAAATGAACTGTGTTTACATACCTACCTGGCCCCTTTGGGGAGATGGGTTACCTCTCCTGGGTTTTCCTGCCCTCCTCTGCATGGTCTT
ENSMUST00000051734.1	4	8,161,1933,3161	ENSMUSG00000046700.1	GTATACTG**AGGGT**GTATGTAAAATCACAAAGAAGAAACTGTGTCAGGTAAGGAAATATACATTCAAAATAATATATATATATTTAAAATTAAGTCTTCTACTTGACTTTTAACAATTCTTGAAGAGAAGTCGAGAATGTAAGTAATATTTTTATTTAAGTA**AGGGT**TTAAGGAAAGGGCATGCTACCCTGAATGGCAGTCATGAGCAGAACAGATGCTGTTTAAATTTAATGGAAACATAAGCTTAATATTTTAGCCATAGAAAGCTAAATTTGAATTTATCTATACCGCATAATAATCAACCTGAGGAAAATGATTTGATTTTTCAAAAGCTTAATTTCTTTATTCTAGAAAATTCAAGTGATGTATTGTCTTCCCATTGTTATATTCATTCACGTTAATCATGCAATCATTAGGTGTCTACTTCTGCTATACTACTAACAGTGGCCAGCTCACTAGACACATACCTGAACAAAAACAGTAAACATTTTTAAAAACTTACTTTATTTGAAAATTCAGATACTTTTATATCATTGAGTCATTTACTGCTGTAAAGTTTTTACTAAGAAAAGGCAGAGAAATCAACCTTAGCATCCTGTTATAAACTGTCCATTTATTTGCTCATTTCTTCAGGATACTCTTATTCCTTTCTGTTATAAAGAAAACAAATTCTGAAGAATCCAACTTTTCATTCCAGAGTTCCTATCTTAATTAGCATACAAGGTAGGTAAGGTTTAAACAATTTCCTCAAAGCTGTGACTTTAGGTTGCCATCCTTAGCTTATAGTTTTCCAGTTGGGTGATGCTCATCTACAGGGCTCTTGTAAATAAACACAGTTTCGGAATTATAGGCTCAGGTTAAGGGAATAGTTTCAG

				AAAACTTTGAGTGTGAAGATGTTTGAAAATTATTTAGAACTATCTGAATAATCTCTGGATGATGTTTGTGATATTCCGAGGAGCTGCTGAGGACACAGGTCTTACTGCTTTGTGAGAATCAGTGCAAAAAATAGCTCT
ENSMUST00000058928.1	1	1	ENSMUSG00000046710.1	C**AGGGT**CTGCACCGAAAC
ENSMUST00000053872.1	1	239	ENSMUSG00000046722.1	CTCAACTCCCCGCCGTGCCGAGAAGCAGCCAGGGGACCCGGAGTGGCGGAGCCCCCGCCCGCAGTGGGGACGCCGGGGAGCCGCAGGATTCCACATCTAAAGAAGACAGGACCTTGTGCCTGCCTGCCCAAGCCTCTTGCCAGTGCCCCACCAGTCAGAGACTCCGACCTTCACCGAAAGGCCACTTGTTGGTGTCTAGGATTTCTACCTTTTCCCACCCCATCCGGTTGACTGAACCC**AGGGT**GTTGTTACACCTGCCTGTGAGGACTGGTTGGTTAGCAACAAACACGAGCCCCCTGGGGCCTCTGGCAGCGGCCTGAAGCTGGAACCATCAGGGAAC
ENSMUST00000062238.1	1	239	ENSMUSG00000046722.1	CTCAACTCCCCGCCGTGCCGAGAAGCAGCCAGGGGACCCGGAGTGGCGGAGCCCCCGCCCGCAGTGGGGACGCCGGGGAGCCGCAGGATTCCACATCTAAAGAAGACAGGACCTTGTGCCTGCCTGCCCAAGCCTCTTGCCAGTGCCCCACCAGTCAGAGACTCCGACCTTCACCGAAAGGCCACTTGTTGGTGTCTAGGATTTCTACCTTTTCCCACCCCATCCGGTTGACTGAACCC**AGGGT**GTTGTTACACCTGCCTGTGAGGACTGGTTGGTTAGCAACAAACACGAGCCCCCTGGGGCCTCTGGCAGCGGCCTGAAGCTGGAACCATCAGGGAAC
ENSMUST00000050490.1	1	309	ENSMUSG00000047213.1	GGAAGTGGGGCTGAGGCGCCTGTCCGCCATTGTGGGCCCGAGGATCGGAGGACGAGCGGGGACGAGCAGTGTGCAGGCGGCGAGCTCGGGCCCCTTCCGCGACTCCCGAGCGTGAGCCCTCTCCCTGGAGCCTGCGAGAGCGGCGGCGGCGGAGGCCGGAGCAGAGCTTCGCGAGGGCGGTAGTCGACTGCTGTGAGTGCTCTCGGCGAGGCCCAGGCAGCGGCGGCGGCGGCGGCGGTTCCTCTCGGGTTACGGTGAAGAATGTCAGCCACTAGCGTGGATCAGGAGACCTAAAGGGCAAGGAAATAA**AGGGT**GGGAAAACATGATGCACACATCTGTTGACTTTCCTAACTTGATGTAGTCAGGACCAGAGCAGAGACCCACCTGGCTTCTAAGGCCC
ENSMUST00000061794.1	1	318	ENSMUSG00000047245.1	GTGTTTGCAAAAAGGGAAAAGTACTTTGCTGCCTCTTTAAGACTAGGGCTGGGAGAAAGAAGAGGAGAGAGAAAGAAAGGAGAGAAGTTTGGAGCCCGAGGCTTAAGCCTTTCCAAAAACTAATCACAACAATCGCGGCGGCCCGAGGAGGAGAGCGCCTGTTTTTTCATCCCAATTGCACTTCGCCCGTCTCGAGCTCCGCTTCCCCCCAACTATTCTCCGCCAGATCTCCGCGCAGGGCCGTGCACGCCGAGGCCCCCGCCCGCGGCCCCTGCATCCCGGCCCCCGAGCGCGGCCCCCACAGTCCCGGCCGGGCCG**AGGGT**TGGCGGCCGCCGGCGGGCCGCGCCCGCCCAGCGCCCGC
ENSMUST00000055486.1	1	4	ENSMUSG00000047249.1	GTC**AGGGT**GAAGCCATGTTCC
ENSMUST00000058161.1	1	42	ENSMUSG00000047350.1	GAGTGACGAGAGGCTTTGTCCGGTTCGGCGGTCTTTCTGTG**AGGGT**GTTTCGACGCGCTGGGCGGTTTGTGCTTTCATCACATTTGTTAACAGGTCAAAATGCAGATCTTCGTGAAGACCCTGACCGGCAAGACCATCACCCTAGAGGTGGAGCCCAGTGACACCATCGAGAACGTGAAGGCCAAGATCCAGGATAAAGAGGGCATCCCCCCTGACCAGCAGAGGCTGATCTTTGCCGGCAAGCAGCTGGAAGATGGCCGCACCCTCTCTGATTACAACATCCAGAAGGAGTCAACCCTGCACCTGGTCCTCCGTCTGAGGGGTGGC
ENSMUST00000058023.1	2	492,561	ENSMUSG00000047614.1	GTCTTTACGCTTCAGCTCTCTGGGTCACGTGGTTCCCAGTGGTTCCCAGTAGCTCCCCAGACACCCTAACGCCCTGGGCACCTTTGAGCATCCCTGATTGGGAAAGGGATGCAGGCTTTAGAAAGCGGCTGACGGGTAAAATCGCTGCATACTCTGCACAAGCCTCAAGGTGCACGGGCACAGGGAAGATGCGAGCCTGCCAATGAGCAGCCCTCTTCTCTCTCCTGAATGGTCTGGAGCAGGAGGCCCAGAGGCTGCACAGACTCCTTACATAGCCCTGCATCATCAGCCTACTGAAGGCCCCTCCCCTACCCCTGCTGCTTTTCATTTGCCTAATTACCAAGTCAAAGTTGCAGTCCAATTTGCTTTATTTTTGTAAGTGAAATGACCCCCCTACGCCCCCTGTAGGTCGTGTCCTGTAAGCGCACCCTTCCCTCCTACTTGTCAGGAACTAGGAGTGGGTGAGTCCTGGGTCTTGGGTTTTGAGATGG**AGGGT**TGGCATCCATCCCTGCTGTGGTTCTTGCCCTGATCTAAGTCAGTCCCTCTGTGAAAGGCTGGAC**AGGGT**GGCAAGGCAGCATGAAGCACTACAGGTGCCCAGCCTGAGGGGGCAAAATGAGCCTCCCTCCCCAACTTCAGAGGGAGCTGGTGGATCAGAGGGCGTTGCCTCGTTTCAAAGGAGGCTGAGATACTTCACTGGAGTATGGAGGCTTCAGAGCCCAGGCTGGCCTGGCATTTAAAGGGAAATGTGGGACTCTTGACTGGCCATGGCAGAAACAAGGTCAGTCAAGGATGGACTGGCCTCTGGGGACCTAAGAGGGCACCCCCACCTTTTCTCCTTACTTTTCTGGTTGGTTCGGGTTTTCGGGGTTTTTTTGTTTGTTTGTTTTATTCTTGTTTTTTGCACTTAATGG
ENSMUST00000055747.1	1	7	ENSMUSG00000047858.1	GGGCTGA**AGGGT**AGCAGACGTTTCCACAGCCGCCGACCCGCAGCTTGAGTGTCCCGCACCGCCTTTTCGTGGAAATCTGAGCCGGCTGTACAGCTTTCCTCCTTGTTCCTGCAGCC

ENSMUST00000059828.1	1	75	ENSMUSG00000048354.1	GGGCAGGGACCGCCAGGGCCGGACCTCCGGGCCGGCGCCTCCGCGCCCCCGAGATGAGTACGGTTTCTTCTGTGG**AGGGT**ACGCAGTTAAAGTCTTGATTTCCTGGATCTGGTAACATGGCAAAAGATGTGTGGTATCTCTTGTAGCCGTCCACCCGTCCACAGTCAACACACTTGGGAAGCAGCTTTTGCCAAAAACCTTCGGACAGTCC
ENSMUST00000054634.1	5	363,1436,1551,2018,2322	ENSMUSG00000049237.1	GGGATTTTAAAGTGGAAATCACCTTTTCAAGATTATTACCATTTCTGTTGTGGTACTGGAGGCTCTAAAATCTCTGCATGATGTAGTTCAGTTGAAGTGTTTTGGGTATTCTTAGTGATTTTAGAAAAGCCTCATTTTGTAAAAGTAAAATATCAGTAAATATCCCAAGATAATTTTCAGATATTTTACTGTATTATGTGTAAACGATTGAACGTAAAGGGAAATATAAACAGACTTAAAAGTCCAGGCTTAGGAGGGCACATAATTATTTTAATCCCAACACTCAGAAACCAGAGAGGCAGGCTTCTGTGAGGTCCAGGCTAGTCTGCTCTACATAGCAGAGAAGGAGCAGCTGGAACTAC**AGGGT**TTATCAAAAAGAAAGCAGTAGCTCCTCCCGCCATTGTGAGTGCCAAGTGTGACACTGCTGCAGGTCACAGTGGTGTTTTGGAGATGTGTTTAGTTAAGAAGTAATCTTAAAGCTTTCTAATGTCCTAGCAAGTCCTGCTTAGCTGAGGGAATTTTATTTGCATATAATAAATTTTATTCCTGACCGGTGGTCTCAGGGGGCTAATATTAAAGTATTTATCCTTCTTGTCTTTTTAATCCTAGGTAGAGAGGTAGCAAGAGTGCTAAGCACGATATTACAAGTAATGAAAATTCTTTCATTTGGCAATTATATATTCTTGTCAGATCTCAAAAATTCGTGGCTGTTTAGAAGAGAGTGGCTGGAGGATGAAGAGATTCTTCTAAAATTAAAGGGAAATGGTTTCCTAAACTACACAGCAGAGAAGGCGGTGGCCAAGCATATAGCAACATGTGGGATACATTTTCACAGTGTCCTTAAGAAAGGGCAGGACACTCGGGGCTAGTGCAGGGGCATTTGAAGCACACTTCCATTTCTGGGATCTCGTATTTCATTGTGTGTAATAAGGACCTGAGAACACAGGCAGATGCAGCTCTTCAGTTTCATCTTGAGTTTATTTTCCAAATAAAAAGGGCCTGCTCTTACGGC
ENSMUST00000059580.1	1	612	ENSMUSG00000049327.1	AAAGGGAAATGAATTTTTTTTTACACACACACACGCACACACACACACATACACACACACTCACACTCACTCTTAGCTAATTACTTCTAAATGTTTTTAAAAAGTATATTAAAGATGCCTTTTCATGTAGTATTTAAATATCTGTTACAGGTTTCCAAGGTGGACTTGAACAGATGGCCTTATATTACCAAAACTTTTATATTCTAGTTGTTTTTGTACCTTTTTGCATACAAGCTGAACGTTTGTGCTTCCCGCGCAGTGTAAGACTCGGCACAGGTTTTAGAGAATGGAGTTGAACATGAACTAGGAAGCCGGGCTCTGCCCAAGATGAAAGCCAGGACTCCCCCACACCCCACGTCCAAGGACAGGCCGGTGTGAGGGCGCTGCCCCCCCACGCACAGCCTGGACGGGATGTCTCCAAGCTCTTGTTCTCCTCAGCATCCTGACAGGCGTACACACTGTCGTGTATGAATATTTTTTAGCAAAAGTTTCACAGTAAGCTAGTCTTCCCCTCTGCTTTCTCCAAAGCTTACTGAGCCCGGGGCTGGGAGGCCCGGCCAGGAACAGACCTCTTCCACAGGCTTACGGCTTTTCCAGGCACCTTGAAGCATC**AGGGT**GGACAGTCAGATTAGAGGCGGGCCGGGAAAAGCACTGTTCTCCTGCTCAAGAAGGGCAGGTCTCCTGAAACTGCATTAATTCTTTATAGAAATGTGAACACTGAATTTATTTTAAAAAATAATAAAAACAAAACATTTTAAAAAAATCAAAAAAAGAAAAAATGGAAAAAAAAACCCACAGAAAACAACTTAACGTGTATATAGGTTTTGAAGGGAGTGAAATGAATGCGGTTTTCTTTTCTTCTGGGGTTTATTTTTTTTCTTTTTGGCTTGGCTGGTTGGTTTGTGTAGAGAAGATTTGAGATGGTACTCTATTCTAATCAAAAGTGAGGTTTTGTAGTGGGACCAGAAATTACTAAGCCCACACCCCCTCCCTAACCCCAATTCTGCTGC
ENSMUST00000054168.1	1	107	ENSMUSG00000050441.1	TGGCGGCCGAGCCGTGTGTCTCCTCCTCCGCCGCCGCCATATTGTCTGTGTGAAGCTAGGGGAGCGCGGCTATTGCCGCTGCCGCTTCCACCGCAGTGTGAAGAAAA**AGGGT**CTGAAACAAAGTCTTACCAACGTCTGCTTTTGAACACAGTGACTGCTGGATCTTTAAACATCAAGTTCAGCTTTGTCTGTCAACCTGTCTGAC
ENSMUST00000051517.1	1	17	ENSMUSG00000050490.1	GGCGGTGTGGTTGATT**AGGGT**GCTGCTTTCAATCGTGTGGCCTTTGGGAACCCCGCGTAGCCACTGCCGCCTCCTTCTGTCCTCGCC
ENSMUST00000056704.1	1	181	ENSMUSG00000050560.1	GGCGAGAGGAGGAGGAAGCCCGGAGCGGAGCGGGGCGGCTGGGGGGGTGGACCCGCCGCGGCTGCTGCTGCCACCGCCGCCGCCGCCACCACCGCTCGTGGGGCTCGTGGCGTGAGGAAGGAGGACGAGTGAGACCCCGGGGCGAGCGGGCGGCGGCGCCGCTGCTGCTGCTGCTGCGGG**AGGGT**CGGCGGCGGGACGGCG
ENSMUST00000060404.1	1	195	ENSMUSG00000050565.1	GGAAATGAAACCGAGCGCAGAGTAGTTTGGGGCTCCGACAATGGCTTAGCCGCCGACCTCTAGCAAAAGCCTACAGAAAGAGGAGACCTAGACCCCCCAAACTGAAGCTCCAGGACTAGGCAGAGCTGCCCGCCTCCGCTCGGGTCACTTCGCACCACCACCTTCCCGCGCGGCCCACTGCGTCCTTCCCTCTTG**AGGGT**CCGGGTGGACTCAATCCGGGAGTGCGCGCCCAAAGGGCCGCAGAAATCACCAGGACCCAGGCGGGGCCGGAGCGGGGCCGGCCTCCACGGGGGCGCGCCTGCCGCCGCGTGCCCGCCGCCGCGCGCGCTCCCGAGCCCGCAGCCGAGACTGTTACCTTCGCGGTCCTCACTGGAGGACGGAGAGTCCCGTAACCCTCGGCCGCTCGTGGCCGGA

				GACAGCTGCGGCTGCTGTGAGTGCTGCTCAAGGCGAGCAGACCTCCGCGTCTTCATCTCCTCGGCTTCCTGGGCTCGCCGCTGCCTCCGTGGTCGAGAGCGAAGGTTGTAAGCGCTTTCTCTCACTTCCTCTCCCGCAGAAGCCGGCCGGAACTTTTCTGGCGGGGTTCGTCTCCCCCCCGGAGACCTTTCTTTGGCCGCCCGGGGCTCGAAGTCGCCGTACACTTCTGCCGGCTCCTCTGAAAACCTCACTTCCCGTCGTCCGCGGCGCGACGGGTGAGCTCCGTACGCAGGTCTTTGAGAAAGGATCCCTCCCCACCCCCACCTCCCCTACGGCACAAACAGAAATCGAGGTGTGTGACGCATTCCCAGACCATCCTGCAAACTCAACACCAGCGACTTCTCTGTGACTGGGTCCAGATAAAGGTCCTTTCAAGACTGACTTCAGTGGATCTACTCCACCAGGTCTTCCCGACCTTACTACATCACTGCCAAGTGCTATTGGCGAGACTGCCTGCACCAGCAGAAGACTCACCGGATCCATCAGAGCGTCGGTTTTACCAGAGCAAAGCAAGAGCCTGTGTGGTTCTGCCTCCCGC
ENSMUST00000053254.1	1	1279	ENSMUSG00000050620.1	CAGGATGGGTTTGATCCGTCAAGCCAAGGAATGAGGAAGAAAACATATACTCGGTGCCCCACGACAGCACCCAGGGCAAGATCATTACCATTCGGAACATCAACAAAGCCCAGTCCAATGGCAGTGGTAATGGTTCTGACAGTGAGATGGACACAAGTTCCCTAGAGCGAGGCCGCAAGGTATCTGCAGTGAGTAAGCCTGTGCTGTACAGGACAAGATGCACTCGCCTGGGGCGGTTTGCTAGTTACCGTACCAGCTTCAGTGTCGGGAGTGATGATGAGCTGGGACCCATCCGAAAGAAAGAGGAGGACCAGGCATCCCAAGGTTATAAAGGGGACAATGCTGTCATTCCATATGAAACAGATGAGGACCCCAGGAGGAGGAATATCCTTCGAAGTCTAAGAAGGAACACCAAGAAACCAAAGCCCAAACCCCGGCCATCCATCACAAAGGCAACCTGGGAGAGTAACTATTTTGGGGTGCCCTTAACAACAGTGGTGACTCCAGAGAAACCGATACCCATTTTCATTGAAAGATGCATTGAGTACATCGAAGCCACAGGACTAAGCACTGAAGGCATCTACCGGGTCAGTGGAAACAAGTCAGAAATGGAAAGTTTGCAAAGACAGTTTGATCAAGACCACAATCTGGACCTGGCAGAGAAAGACTTCACTGTGAACACTGTGGCAGGGGCCATGAAGAGTTTTTTCTCAGAGCTACCAGACCCCCTGGTACCATACAGCATGCAGATTGACTTGGTGGAAGCTCACAAAATCAACGACAGGGAACAGAAGCTGCATGCTCTGAAGGAAGTGCTGAAGAAGTTCCCGAAGGAAAACCATGAAGTCTTCAAATATGTCATCTCCCACCTGAACAAAGTCAGCCACAACAACAAGGTGAATCTTATGACCAGTGAGAACCTGTCCATCTGCTTCTGGCCCACGCTGATGCGGCCTGACTTCAGCAGCATGGACGCGCTCACAGCCACGCGCTCCTACCAGACCATCATCGA
ENSMUST00000051412.1	1	85	ENSMUSG00000050904.1	CATTAGCAGAGACATGTTTCTGAGACAGCCGACTATGTGACACTCTGATTTCACAGCCCTGACTTCCCCACCTGTGGAACGTGT**AGGGT**TATTTGCCTAAGATGCGACC
ENSMUST00000053256.1	1	27	ENSMUSG00000051141.1	CGGACGTCCGCACGTGGTTGCCGGTTT**AGGGT**GCTGCTGTAGTGGCGATACGTCCCGCCGCTGTCCCGAAGTGAGGGATCCGAGCCGCAGCGAGAGCC
ENSMUST00000051112.1	2	24,51	ENSMUSG00000051256.1	CGAGGTAGCAGGGAAGGGGTTCGC**AGGGT**GCTTGGCTGGGTGTGTGAGCAG**AGGGT**CGGCGTTAGGGGCCTTAGTTCTGTACA
ENSMUST00000062200.1	2	37,64	ENSMUSG00000051256.1	GTGAAAGCCGGGCCGAGGTAGCAGGGAAGGGGTTCGC**AGGGT**GCTTGGCTGGGTGTGTGAGCAG**AGGGT**CGGCGTTAGGGGCCTTAGTTCTGTACA
ENSMUST00000049640.1	1	120	ENSMUSG00000051303.1	GGTCCGGCCCCGGCCCAGCACCGACCGGCTGGGCTCAAAGTTTGCGGCCGCCCCTGCGCCGCGCGCCCGATGTATGGGTGATCTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGC**AGGGT**GAGGGACGGCCATAGTTGCCGGCGCGGCCCGAGCCGGCGACAACAAAAAGTGCGCGGGCTCCCGGCGGGCGCTCGGACGGCTGCGGGACGTGGGGCCGCCCGGCCCGGGCCTCGGCCTCGGCCTCGCCGGCGCGCTCGCGGCCTGGCCCGGCTCTGCCCGGCGCGCCCGCCGCCCGCGGGGATGTCGTACAAGCCG
ENSMUST00000058162.1	1	5	ENSMUSG00000051510.1	TCTC**AGGGT**CCTGACCTATGCTCTGTGTCTTGCAGAGTGCCTGCTCACTGTGTCCCCCGGGTT
ENSMUST00000053054.1	1	13	ENSMUSG00000051612.1	GGGAGGCTGCCAG**AGGGT**TTGTCACTGCTGTTGCTCCTCCGCCTCAGCGAGTCCAGCCCGGGCCTAGTCGGTCGCCTGCCTTTCTCATAGCCGTTACCCTCAGGCCGCCACAGCCGCCGACCGGGAGAGGCGCGCGCC

Genes with an annotated 5′-UTR in the ENSEMBL database and expressed at late-gastrulation stage according to our U74Av2 Affymetrix wild-type data set were searched for high-affinity Grsf1-binding sites (5′-AGGGU-3′). Genes with binding sites are listed with their ENSEMBL transcript ID, total number of matches, locations of the matches, ENSEMBL gene ID and the 5′-UTR sequence.

Table S4. Bioinformatic prediction for Grsf1 and β-catenin co-regulated genes (intersection of Tables S1 and S3)

Probe Set ID	Gene symbol	wt-mut	het-mut	Total matches	Locations	Gene ID	Sequence
99561_f_at	Cldn7	0.6	0.7	1	383	ENSMUSG00000018569.1	GCCCGCACCTGCCGCCGCACCGCCAGCTCCCTGTGCCGCGCACCGCAGCCTGGGGCCCAAGGGCCCGCATACTTTCTGGGGGCCACGCCCTAACGGCCCCTCCACTTCTTTGGGTAGTCTCGGAGCACGCCGGTAGGAACCGCCCGGCCTTCGGGGACCGCTTTTGTCTGGAACCAGTCCTTCGGGCGAAGCCGGTTCCCTCTGCTGTGAGAGTGTCGCTTCACCGGAGGGGACGATTTGTGTTTACCTCGGTTAACAAGATTTGTAGTTACCCGGTCCAAAAAAAAATCTTTTTCTCCTTTGGGTGACTTAAATCTCTATCCAAATTTTCTTGTGTTGCTGCTCCCCGGATTTTTGTTTTTTTGTTTTTTTGCTTTACTGTAGGGTCGCCCTCCCGGCGCGTCCCGTCTTTTCTGAGACAAGGAA
94036_at	Cdc42ep4	-0.6	-1	1	286	ENSMUSG00000041598.1	AACAATCGGCGGCGGTCGCCCCGAGGGGGGCGTGTGCGCACAGACTTCTCCATGAATAACCGCTGAGTTCGTCGGTAGTGGTAGAGGGGTGTACGCGTGCTCTCCCGTGTACACACACTGCTTTAGGCGCCACCCGGTGTCGCCCGGCCGGGGAGAAAGGAGGGCAAGAGCCGGCTGGAAGGCAATAGCCTAAAGAGCAAATACTCCCCGCCCGTCGGAGCCCTTCCTTCTCCCGCCCCGCCCGCCTCCCTTGGAAGACTTGGAGGCCAAGGCCGCAAGAGGCGCAGGGTGGGGCTGGGCCGAGCTGGCGGTCCCTTAGAAACCTGGGACGAGGCTTTACGCGGGGGACCTGCGCGCGCGCCCGGTACGTCCGAAGCATGGGGCTCGAGGCTTTTTCAGGGGCGAGTAGGTAGCGGTTGGTTAATGATTTAACCGCTGGCTTGGGACGTTGAAGGCTGCGATCCTGATCTCTGGCTCCTCCCCATTCCTGGAGCGCCCCCAGCCGGAGGAACAAATCTGCCCTCCTGTGTCTGTGGCGTCGTCTGCTGGAGCTGCCTTTCCCCTTTGGGGGACCCCTGGTTGCTGTGGCCCTCTGATTGCCCTGTCTACCCTTTGCATTGCTGGACTTCAGATCTGACCCCATACCTGCCTGTTGCCTTGGGAGTGCCCAGCTCCCCCGCAGCCAGCACG
94449_at	protocadherin gamma subfamily B, 1	-0.5	-0.6	2	47,62	ENSMUSG00000024463.1	CCTGTCAGATCACCATCCCATATCGTCACGTGCATTCTACTGTCAAAGGGTACAGTGGCTGAGGGTCTGTGCCCTGCTCCACGGCAGCCCCCGAATGGTGCCCACCATGGCACCTGATATCTTAGGTTTCTGGGTTCCACCCACAATGCTGTCACTCGTGAACCTCAGTGTGAGTCATTGGCAAGTCCTGGGTCTTCCTTCTCCCCAGAGTAATCACACAGAGCGCTCACACTCTCTCCTCCTGGGAGCCTGTGTGAGAATTAATTACCAGCACATCCCCGAAACTGGTGAAGTCGTGGCTGTAGGAGAATGTGTGGTGGGATACATCTCCTGGAAGGGACCTGCGGAAGTTAGAAATTAAGCGGTGGCTGGCGAGCCCTGCACATTGAGCTGGTTGGGAGAGGGCTACGGATCAGTTGGCTCTGTCTGGAGCCTGTAGAAT
164467_f_at	Gjb3	1.8	0.8	1	20	ENSMUSG00000042367.1	GAGATGCCTCCTTAATGAGTAGGGTAGAAAGGAAGAGCATTCCAGGCGGGAGGAATCAAGGCCAGGTCTGAGCAGAGAGAGGCAAGGTGGGCACAGCCCCCCGAACCCTGAGCAGGCACC
97013_f_at	Cyba	0.5	0.5	1	48	ENSMUSG00000006519.1	GACTTGCGAAGTGGGCTGCAGAGTTGGACCGGGCTGCTGCGTGTGCGCAGGGTCCTCGTC
93941_at	T	-1.4	-1.4	1	95	ENSMUSG00000023865.1	GGCTCCGCAGAGTGACCCTTTTTCTTGGAAAAGCGGTGGCGAGAGAAGTGAAGGTGGCTGTTGGGTAGGGAGTCAAGACTCCTGGAAGGTGGAGAGGGTGGCGGGAGG
100009_r_at	Sox2	1.3	1.3	1	318	ENSMUSG00000047245.1	GTGTTTGCAAAAAGGGAAAAGTACTTTGCTGCCTCTTTAAGACTAGGGCTGGGAGAAAGAAGAGGAGAGAGAAAGAAAGGAGAGAAGTTTGGAGCCCGAGGCTTAAGCCTTTCCAAAAACTAATCACAACAATCGCGGCGGCCCGAGGAGGAGAGCGCCTGTTTTTTCATCCCAATTGCACTTCGCCCGTCTCGAGCTCCGCTTCCCCCCAACTATTCTCCGCCAGATCTCCGCGCAGGGCCGTGCACGCCGAGGCCCCCGCCCGCGGCCCCTGCATCCCGGCCCCCGAGCGCGGCCCCCACAGTCCCGGCCGGGCCGAGGGTTGGCGGCCGCCGGCGGGCCGCGCCCGC

							CCAGCGCCCGC
100479_at	Dnmt3a	0.7	0.8	1	62	ENSMUSG00000020661.1	CCACAGGCAGAGCCGCCTGAAGCCCAGCGCTGAGGCTGCACTTTTCCGAGGGCTTGACATCAGGGTCTATGTTTAAGTCTTAGCTCTTGCTTACAAAGACCACGGCAATTCCTTCTCTGAAGCCCTCGCAGCCCCACAGCGCCCTCGCAGCCCCAGCCTGCCGCCTACTGCCCAGCA
104672_at	Frzb	-1.1	-1	2	10,105	ENSMUSG00000027004.1	GTGGGGACCAAGGGTTCGTCTATGGATCCAGAGCCGGGGGTGGAGTGGGGAAAGGTGTGCGGCTCCTGTCGGGAGCTGCCTGGGGCTACAGCATCACAGATAGACAGGGTCTCACACTCCAGTCCCCTGAAAACTCAAAGCCTTCTCGGAAGGAGGAGCCGGAGGGCAGGGGACCGCGGGGCGGAGCTCTTGTCGGCCGAGGTGGGAAGGCGCAGCTGCGAGCCAAGGCGCTGACCTCCTCTGAGCTCCTCTGGCCGCTCGCAGGATCTTCCCGACCCTGCAGGACTTGGCAAACTCCCACCTCCGCTCCCATTAGTCCTCCCACCCCCACCAAATCTCCTCCCTCGGAGGTCCCCTATCCATCTCACTTTGCAGAATTTATCGCTTCTTCCAACACCTTTTTGCAACACCCCAGAACTCCGAGTCCCTTAACTGAATTTGACTTTTGTTTTTATTTCTCTCTGGCTTCCTCTTCTGCCCCCTCATCTGATTGATGTGCTAAGGCTGATGTCTCTGCCAGAGCGAGAGGAATAAATAGATGCTGCCTCGCCTAGAGGCTTAGACGCTTGGGAAGAGCAGCCGGCGCAGCGAGGCACCGGGCTCCGCCAAGCTAGTGGACCGGACCTGGGAGCACTTGGATCCAAGAGAACTGTGATTGTCCCAGGGGTGGGGGCAGCTCCCCAGGTCGTTGGGATCACCCCTCGGAACCGCAGGGGGAGACTTCGGAACGAAAGTGTCTCCCGCGTCCGTCGCTCGGCTGCGCCCTGCCCCATCCTGCTGGGACC
93543_f_at	Gstm1	0.7	0.7	2	14,72	ENSMUSG00000004038.1	CTGCCTTCCGCTTTAGGGTCTGCTGCTCTGGTTACAGACCTAGGAAGGGGAGTGCCTAATTGGGATTGGTGCAGGGTTGGGAGGGACCCGCTGTTTTGTCCTGCCCACGTTTCTCTAGTAGTCTGTATAAAGTCACAACTCCAAACACACAGGTCAGTCCTGCTGAAGCCAGTTTGAGAAGACCACAGCACCAGCACC
93888_at	Hoxb1	-1.7	-1.8	1	31	ENSMUSG00000018973.1	TGACATACTGCCGAAAGGTTGTAGGGCAAGAGGGTGTCTCCCCCAAACGGCCCGACCCTCCTTCGGCCTCTAC
98419_at	Meox1	-1	-0.7	1	14	ENSMUSG00000001493.1	CACTCATTCACTCAGGGTCCCCGGGAAGGGCTTGTCAGTATGGGTGGGTCCAAGGTAGGACAGTCAAAATGTTCAGCATGGTAGGAAACAACTCCGTGCCCGATAGTCAGCGTGTGTCGGGGGCAGGAAGGCAGACGTGAAGCCTAGACAGGTGTGGACACGCACATGTGTGTTCCTGGCCACGTGTTTGTGGAATTTGAGGCAAAATTTTTGTTTTGGTTCCTGGGGTAAAGTTTCCATTCAACATTTTCCTCTACTGTTTAATTTTTTTTTTTAATTTTAAATTACAAAACTCTGACTAGAAAAAGCGCAATACCTTTGAAAGGACTGGGGCAGGCAGTGGACAGCAG
93953_at	Prss12	0.7	0.6	1	2	ENSMUSG00000027978.1	CGAGGGTGGGGTGGAGGTCGGACTCCGGGCTACAGAGCTCCTGGCGCTCATCGCCTCTGGCGCTCCAGCCTTTGCTTCGCGGGGCTGACCCTTTGGGTCCCGGTGTGA
98427_s_at	Nfkb1	-1.3	-1.1	2	206,229	ENSMUSG00000028163.1	CGCGGGCCGGTTCTAGCAGCGCAGGCCGGAGCTCAGGGCCCCGCCGCGCCCGGCCCGCCCCGCGCTTCTCCGCCCGCGCCGCAGCCATGGCGCGCCGCTGAGCCGCCCGCCCGCCCGCCCGCGCCCCGACCCGGCTCGGGCTCCCGCCGGTCCGCGCCGCTCCGCAGCGGGAGCCCGCAGGCGAGGAGAGGCCGCGCCGCATCTCCAGGGTACCCTCAGAGGCCAGAAGAGGGTGTCAGAGCCCTTGTAACTGGAGTTTGACGGTCGTGAGCTGCGCATCTTCACC
103818_at	Slc7a7	0.6	0.6	2	43,187	ENSMUSG00000000958.1	AGCAAATCAGCAAAAAGAGGATCTAGCGAATCAGTTGGTTTCAGGGTTGGTTCCTCATACAGGCATCTCAGCGCAGGGACATTTGAAACTGAAATCAGAGGGGAGAGACTTTGGGGGTCAGGGGGAGGCAGAAAAAAGTTTTACCAAACTGCCTCATTCATGCCTGTCCTGTGTCATAACAGGTTGAGGGTTCAGCTGTCTGATAAATAAGAGGGCAATGCGAGCAAGCTGGTGAAGGTCTTCCTTCTCTTCGCC

92997_g_at	Sox17	-0.8	-0.7	2	733,1020	ENSMUSG00000025902.1	CCCATTTAGTGAAGAAACTGAAATATGGCCCACTCACACTGCTGGCGGGTCTGAAGTGCGGTTGGCCCCAACACTCCTCCCAAAGTATCTATCAAGAGAATGGTCAGCAGAAGTTAGATCTAGTTTTTAGAGAAATCAACCAAGACAGGGAAGACAGAGAAAATGCATTCTGGACCCGCTACTGTTTTCAATCGTCATTTCAAACAAAACCCGTAGTTTATTTAAAAAAAAAAAAAACACGGAAAGAGAAAATTAGGCCCTGAGATCTTTGAAAAGATGCCCATTACTAGATACAAAAGAGAAGAGTCACTGTGGAGGTGAGGGACTGCGTCCCTGCTTCTGAGAGGCAGGAGAGCTACATGGGGAGACTGTCTCAAAACTAACAACAGAAGAGATAGAATTTTTTTTTTCTTAAAGAGCACCTGGCTAGAGAATCGATTTGTAAAATTGCTATTTCTACCCTTAGAGTTTCCTTGATTAAACATCTGAAATGCATTTTTTTTGTTTTACTTTCAAGCTAATGTTTTTCAGAAAAAAATAAAAAGCTTTGAGGAAAAGCACATTATCAGTTAGATTTAAGACCAATTGCTTTTAAATTACCAATTTAAAATATCATTTTTTTTTATTTCTTAAAGCAGATTTAATTTTACCCCCTTTGTATGAATCTTACAGACCTGGAGTTTTAACTACTATCACTGATCTCTACACACAACCTCCAGCTTTAAATGGGAGGGAGGGTCACCACTGCTTTATAACATAACAAATTAGAGAAAAGCTGGCTTCTGTATGAGTTCTTTGGAGACAAAGTAGCTCCAGAAACTGCAGACCAGAAGCTATCAAAATCTCTGTGCTTTTTTGGAACCTCCAGTAAGCCAGATTTGGTCTCTGAAATAATACAGGAAAACCTCAGCATGTCACCTCATGGATACAATGAGCAGCACCTCCAGACATCTGAATTTCAGCCTTCCTATTTCCCCAAGAGGTCTTGGCGCCAGCGCCCGGCTCCAGCCAGi
96771_at	Erbb3	1	0.8	1	57	ENSMUSG00000018166.1	GCACCGTGAGACACTGGGACCACAGCTGCTGCTCAACTGGGGAGTACAAATTGCCAAGGGTATGTATTACCTCGAGGAACACAGCATGGTG

Highlighted are those transcripts that showed a significant β-catenin-dependent deregulation and contained a *Grsf1* consensus-binding site in the 5′ UTR.