Clpx Cas9-CKO Strategy

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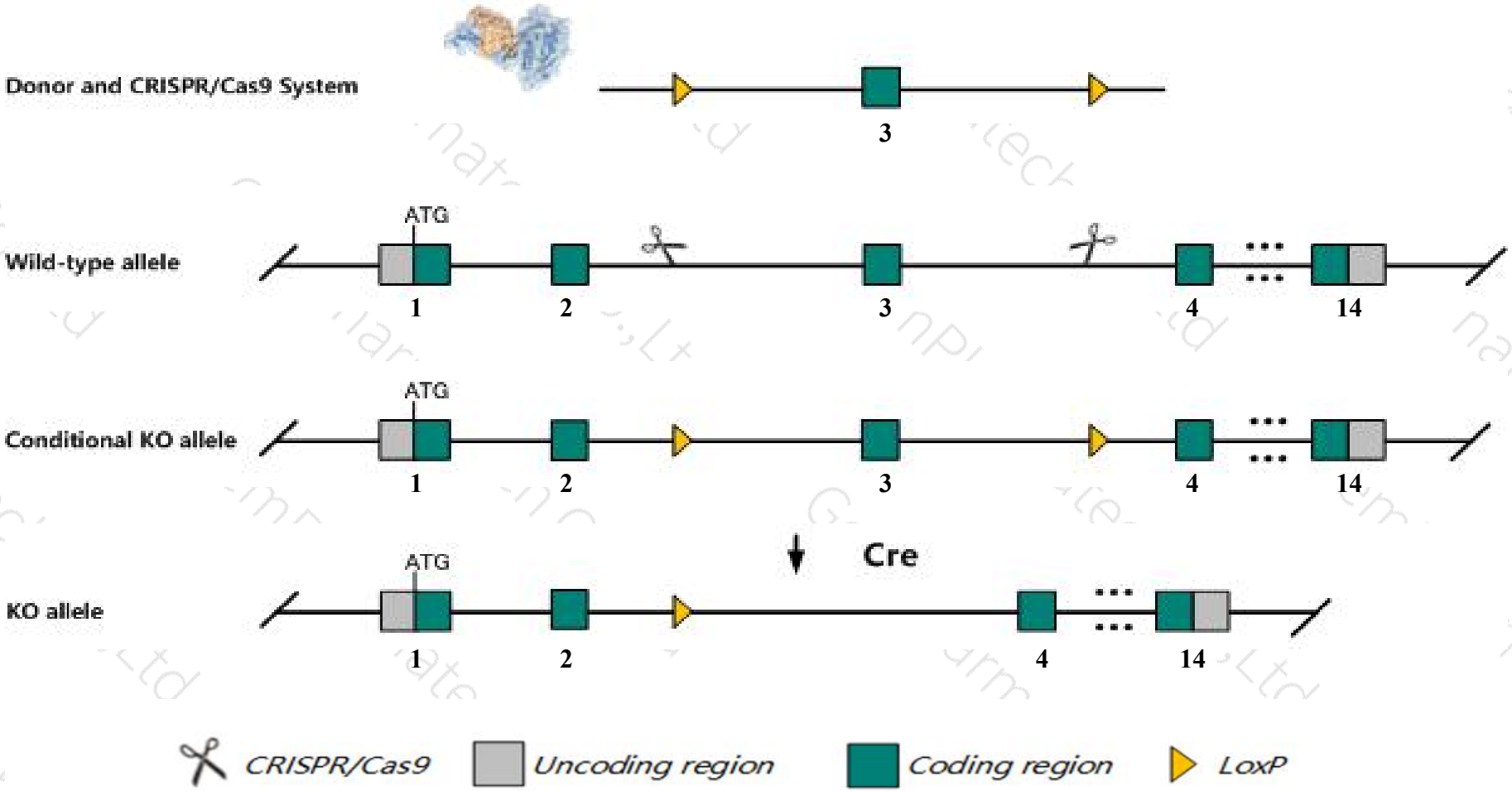
Project Overview

Project Name	***Clpx***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Clpx* gene. The schematic diagram is as follows:



Technical routes

- The *Clpx* gene has 4 transcripts. According to the structure of *Clpx* gene, exon3 of *Clpx-201* (ENSMUST00000015501.10) transcript is recommended as the knockout region.The region contains 118bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Clpx* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ The *Clpx* gene is located on the Chr9. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.

➢ This Strategy is designed based on genetic information in existing databases.Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

集萃药康 GemPharmatech

Clpx caseinolytic mitochondrial matrix peptidase chaperone subunit [Mus musculus (house mouse)]

Gene ID: 270166, updated on 7-Apr-2019

Summary

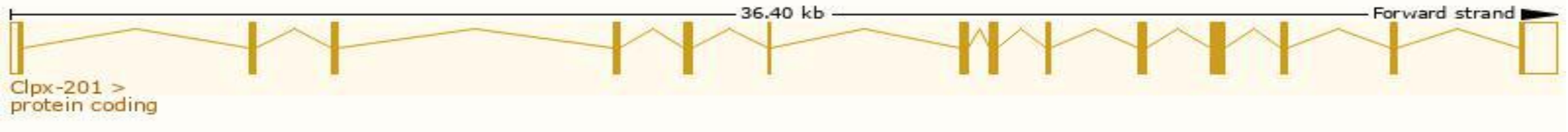
Official Symbol	Clpx provided by MGI
Official Full Name	caseinolytic mitochondrial matrix peptidase chaperone subunit provided by MGI
Primary source	MGI:MGI:1346017
See related	Ensembl:ENSMUSG00000015357
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU014732, E330029I21
Expression	Ubiquitous expression in liver E18 (RPKM 23.0), testis adult (RPKM 18.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

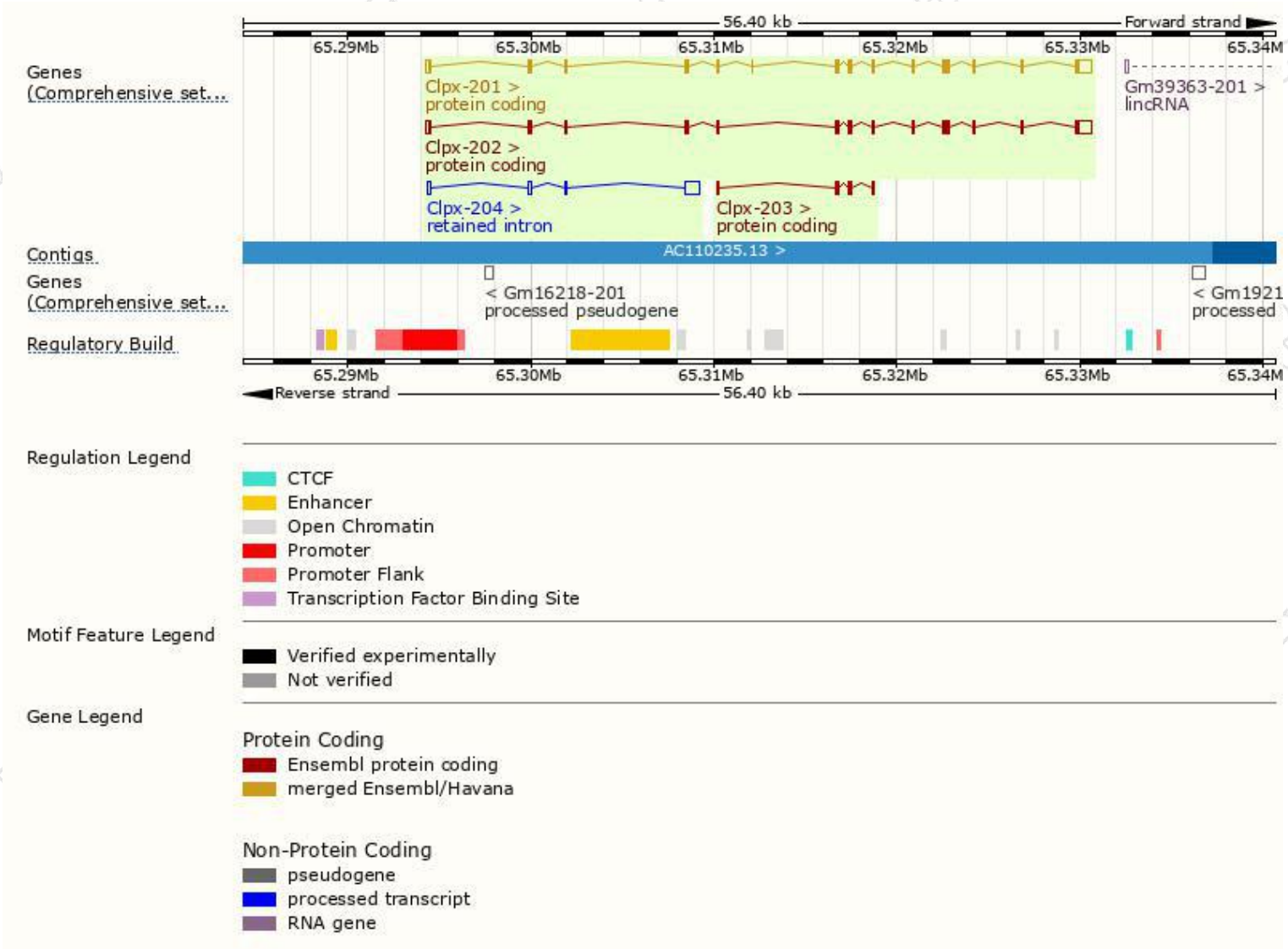
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Clpx-204	ENSMUST00000148632.1	1279	No protein	Retained intron	-	-	TSL:1
Clpx-203	ENSMUST00000147279.1	577	192aa	Protein coding	-	F7BB92	CDS 5' and 3' incomplete TSL:2
Clpx-202	ENSMUST00000113824.7	2809	620aa	Protein coding	CCDS40669	Q6P8N8	TSL:1 GENCODE basic APPRIS ALT1
Clpx-201	ENSMUST00000015501.10	2885	634aa	Protein coding	CCDS23288	Q9JHS4	TSL:1 GENCODE basic APPRIS P3

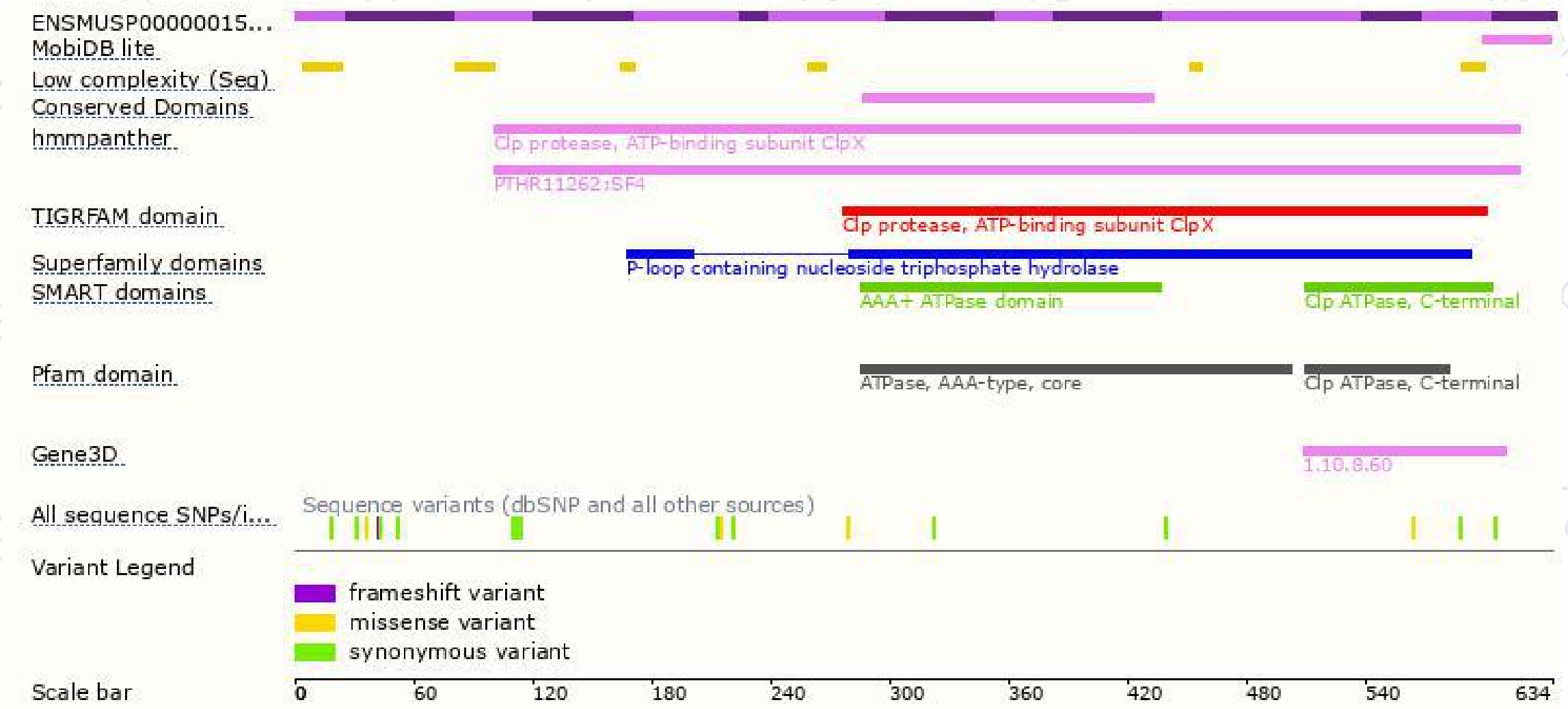
The strategy is based on the design of *Clpx-201* transcript,The transcription is shown below



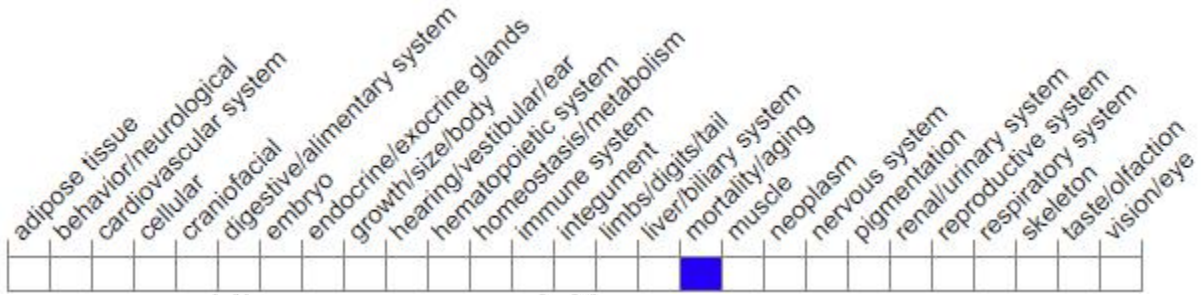
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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If you have any questions, you are welcome to inquire.

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