Prpf31 Cas9-CKO Strategy

Designer:	**Ruirui Zhang**
Reviewer	**Huimin Su**
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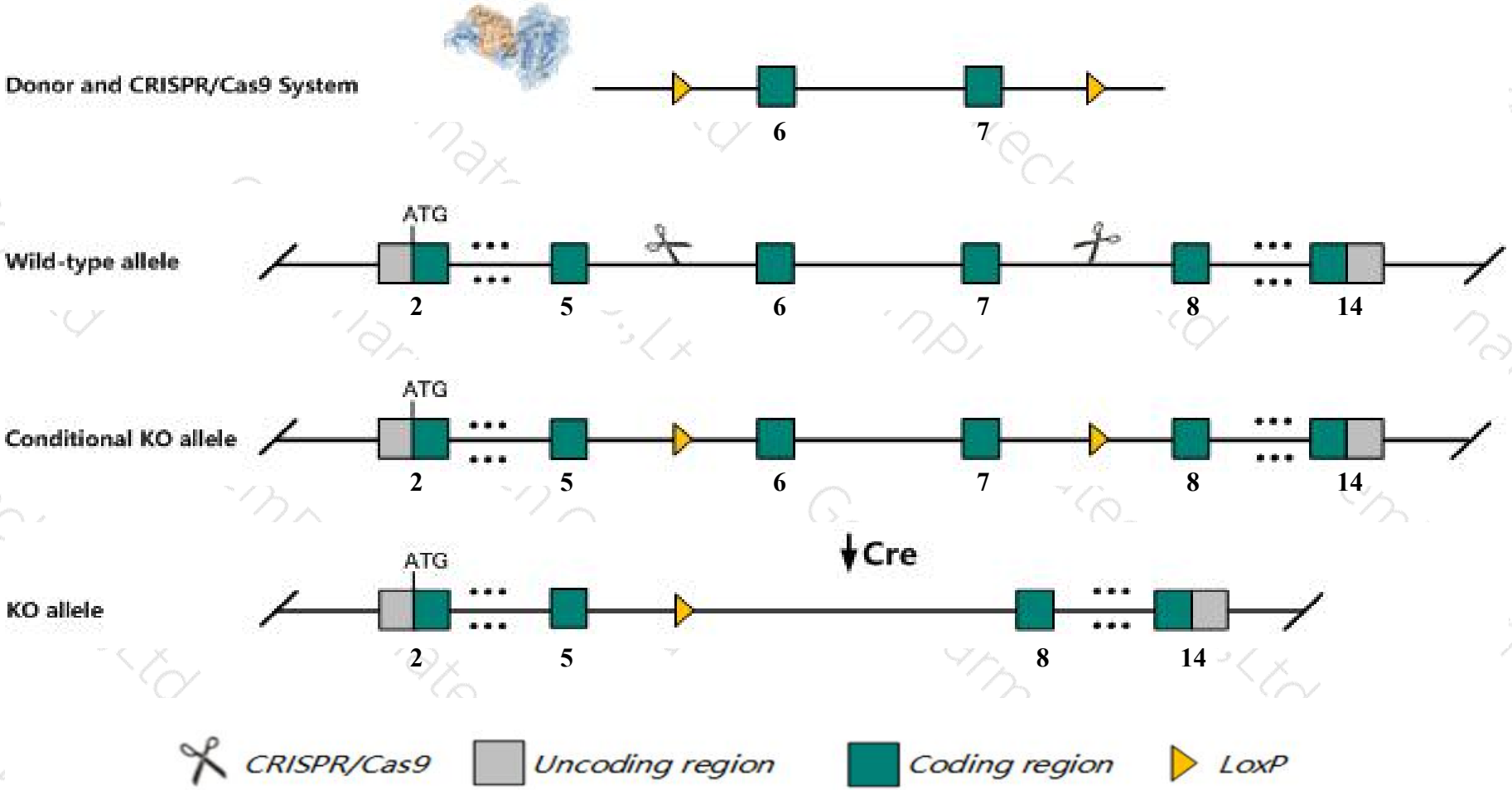
Project Overview

Project Name	***Prpf31***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prpf31* gene. The schematic diagram is as follows:



Technical routes

- The *Prpf31* gene has 6 transcripts. According to the structure of *Prpf31* gene, exon6-exon7 of *Prpf31-201* (ENSMUST00000008517.12) transcript is recommended as the knockout region.The region contains 277bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Prpf31* 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

- According to the existing MGI data,mice homozygous for a knock-in allele die prior to E10. Mice homozygous for a knock-out allele are not produced.
- The KO region contains functional region of the *Gm15927* gene. Knockout the region may affect the function of *Gm15927* gene function.
- The distance of *Tfp4* gene from exon6 of *Prpf31* gene is about 4.1kb, this strategy may affect the regulation of the 5-terminal of *Tfp4*.
- The *Prpf31* gene is located on the Chr7. 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）

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Prpf31 pre-mRNA processing factor 31 [*Mus musculus* (house mouse)]

Gene ID: 68988, updated on 12-Aug-2019

Summary

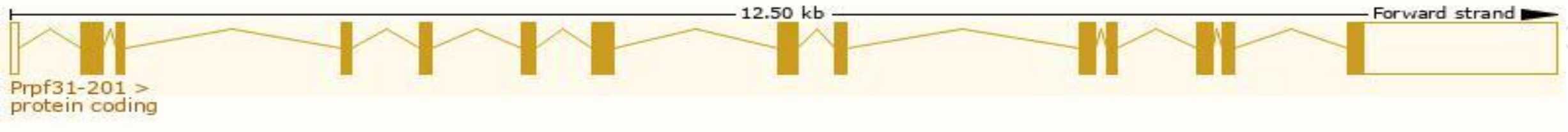
Official Symbol	Prpf31 provided by MGI
Official Full Name	pre-mRNA processing factor 31 provided by MGI
Primary source	MGI:MGI:1916238
See related	Ensembl:ENSMUSG00000008373
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	RP11; PRP31; AW554706; 1500019O16Rik; 2810404O06Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 27.4), CNS E14 (RPKM 16.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

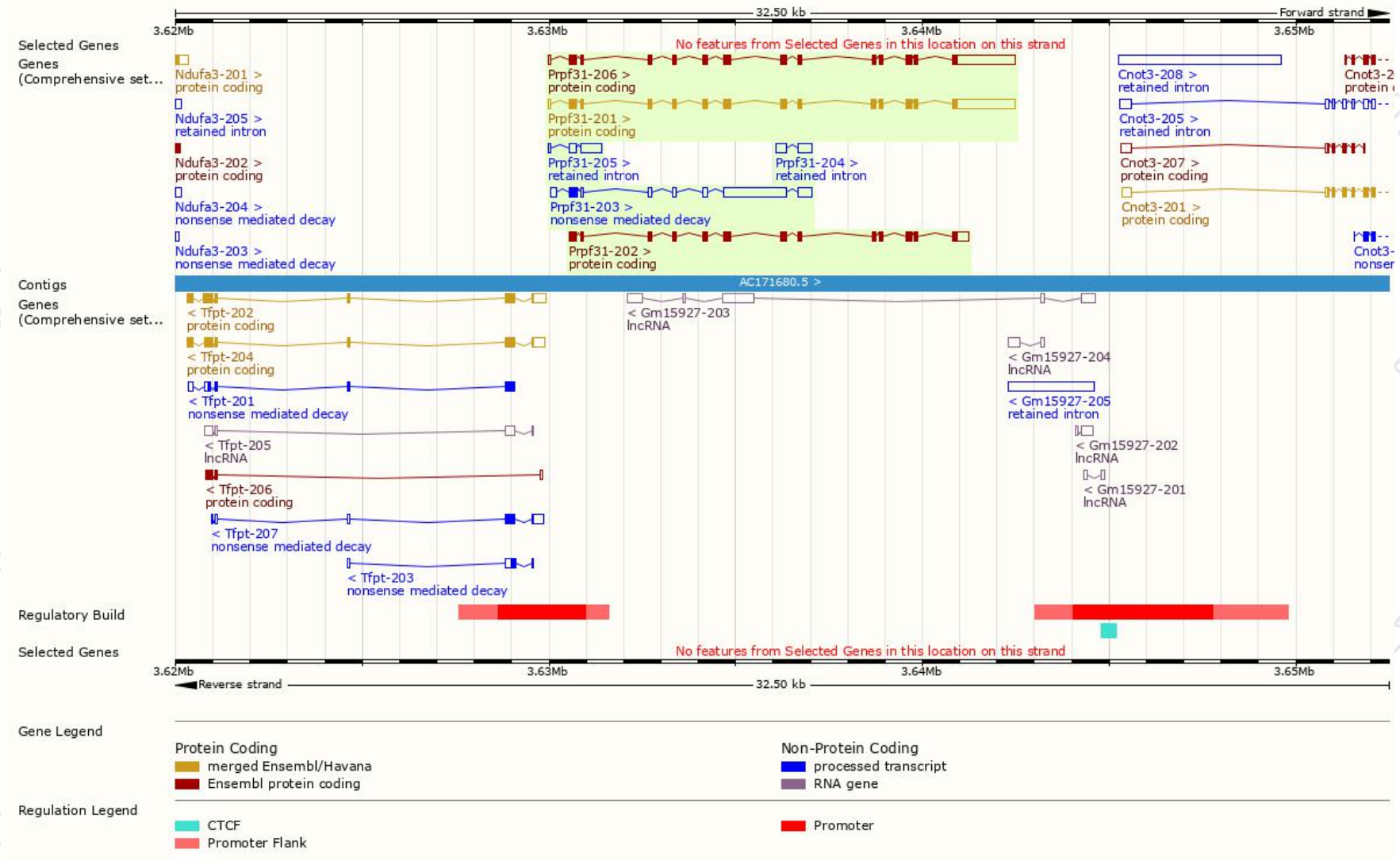
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prpf31-201	ENSMUST00000008517.12	3144	499aa	Protein coding	CCDS39729	Q8CCF0	TSL:1 GENCODE basic APPRIS P1
Prpf31-206	ENSMUST00000179769.7	3125	493aa	Protein coding	CCDS51965	Q8CCF0	TSL:1 GENCODE basic
Prpf31-202	ENSMUST00000108636.1	1798	493aa	Protein coding	CCDS51965	Q8CCF0	TSL:5 GENCODE basic
Prpf31-203	ENSMUST00000125782.7	2731	65aa	Nonsense mediated decay	-	Q8CCF0	TSL:2
Prpf31-205	ENSMUST00000143231.1	827	No protein	Retained intron	-	-	TSL:1
Prpf31-204	ENSMUST00000134047.1	660	No protein	Retained intron	-	-	TSL:3

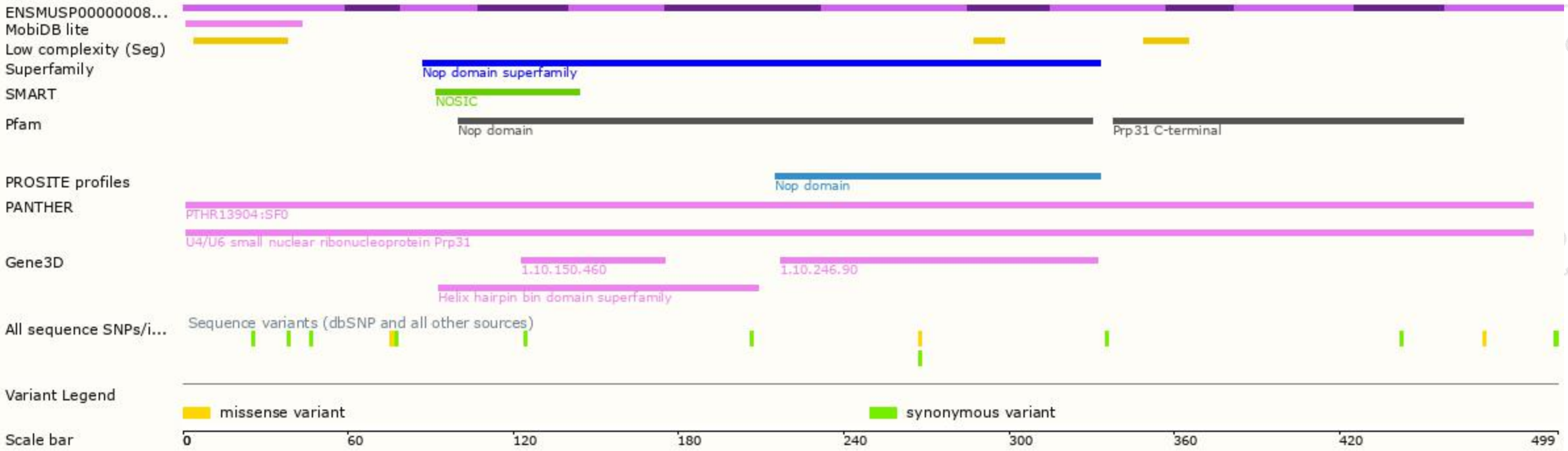
The strategy is based on the design of *Prpf31-201* transcript,The transcription is shown below



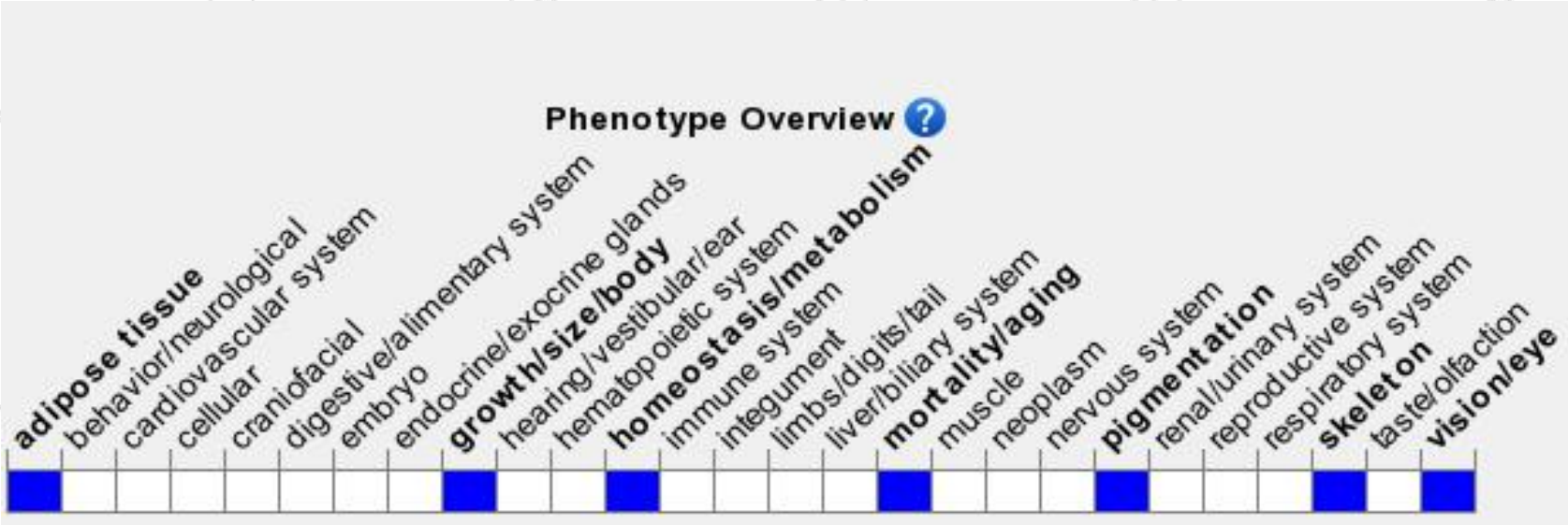
Genomic location distribution



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/).

According to the existing MGI data,Mice homozygous for a knock-in allele die prior to E10. Mice homozygous for a knock-out allele are not produced.

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd