Ptcd2 Cas9-CKO Strategy

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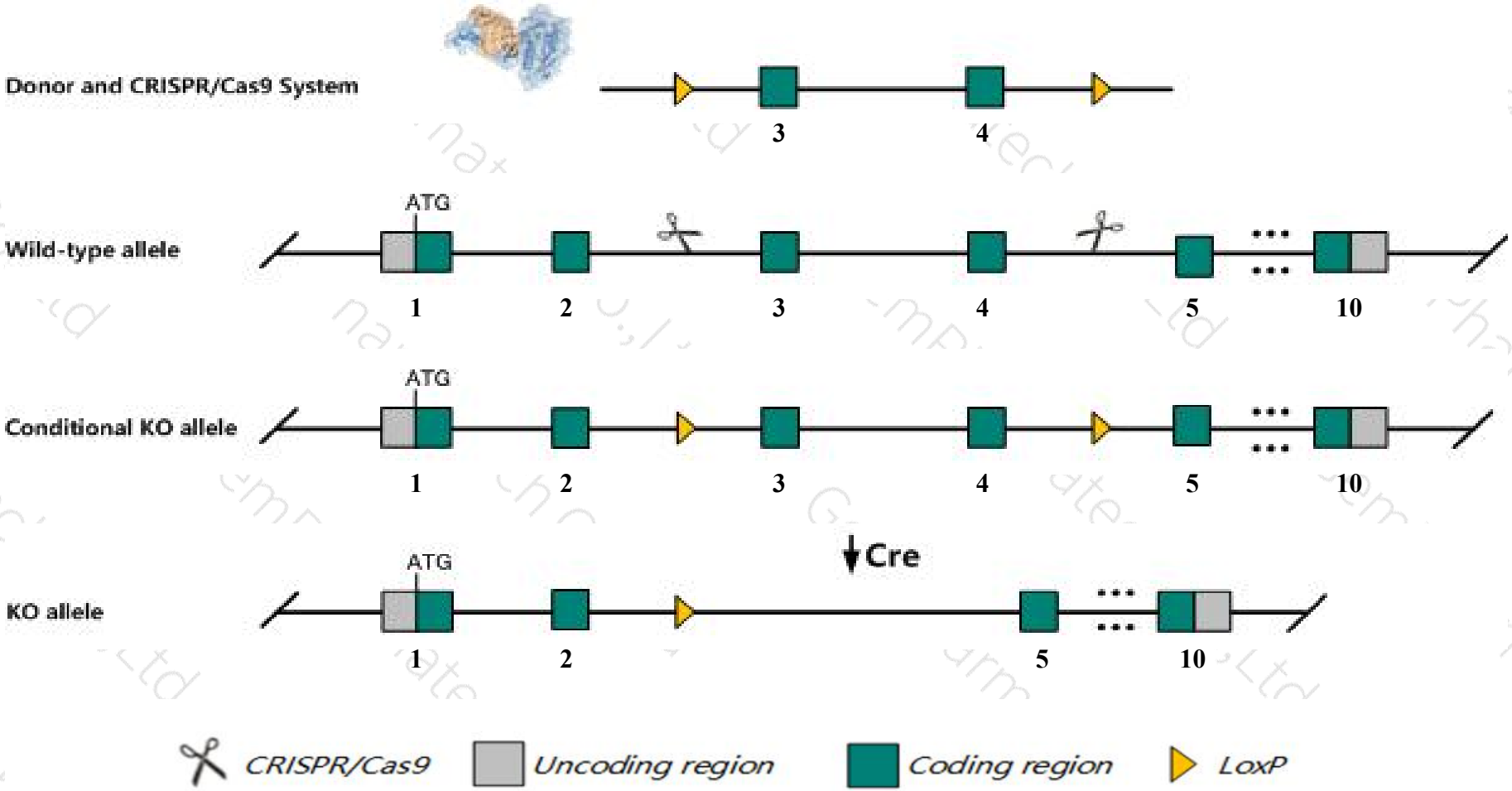
Project Overview

Project Name	***Ptcd2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ptcd2* gene. The schematic diagram is as follows:



Technical routes

- The *Ptcd2* gene has 1 transcript. According to the structure of *Ptcd2* gene, exon3-exon4 of *Ptcd2-201* (ENSMUST00000022153.7) transcript is recommended as the knockout region.The region contains 248bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ptcd2* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J 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 gene trapped allele exhibit abnormal mitochondrial morphology and physiology, especially in the heart, liver, skeletal muscle and kidney.
- The floxed region is near to the N-terminal of *Mrps27* gene,this strategy may influence the regulatory function of the N-terminal of *Mrps27* gene.
- The *Ptcd2* gene is located on the Chr13. 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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Ptcd2 pentatricopeptide repeat domain 2 [Mus musculus (house mouse)]

Gene ID: 68927, updated on 13-Mar-2020

Summary

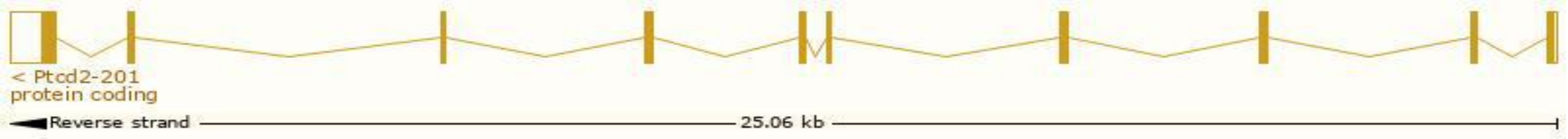
Official Symbol	Ptcd2 provided by MGI
Official Full Name	pentatricopeptide repeat domain 2 provided byMGI
Primary source	MGI:MGI:1916177
See related	Ensembl:ENSMUSG00000021650
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1190005P08Rik
Expression	Ubiquitous expression in heart adult (RPKM 13.1), CNS E18 (RPKM 11.0) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

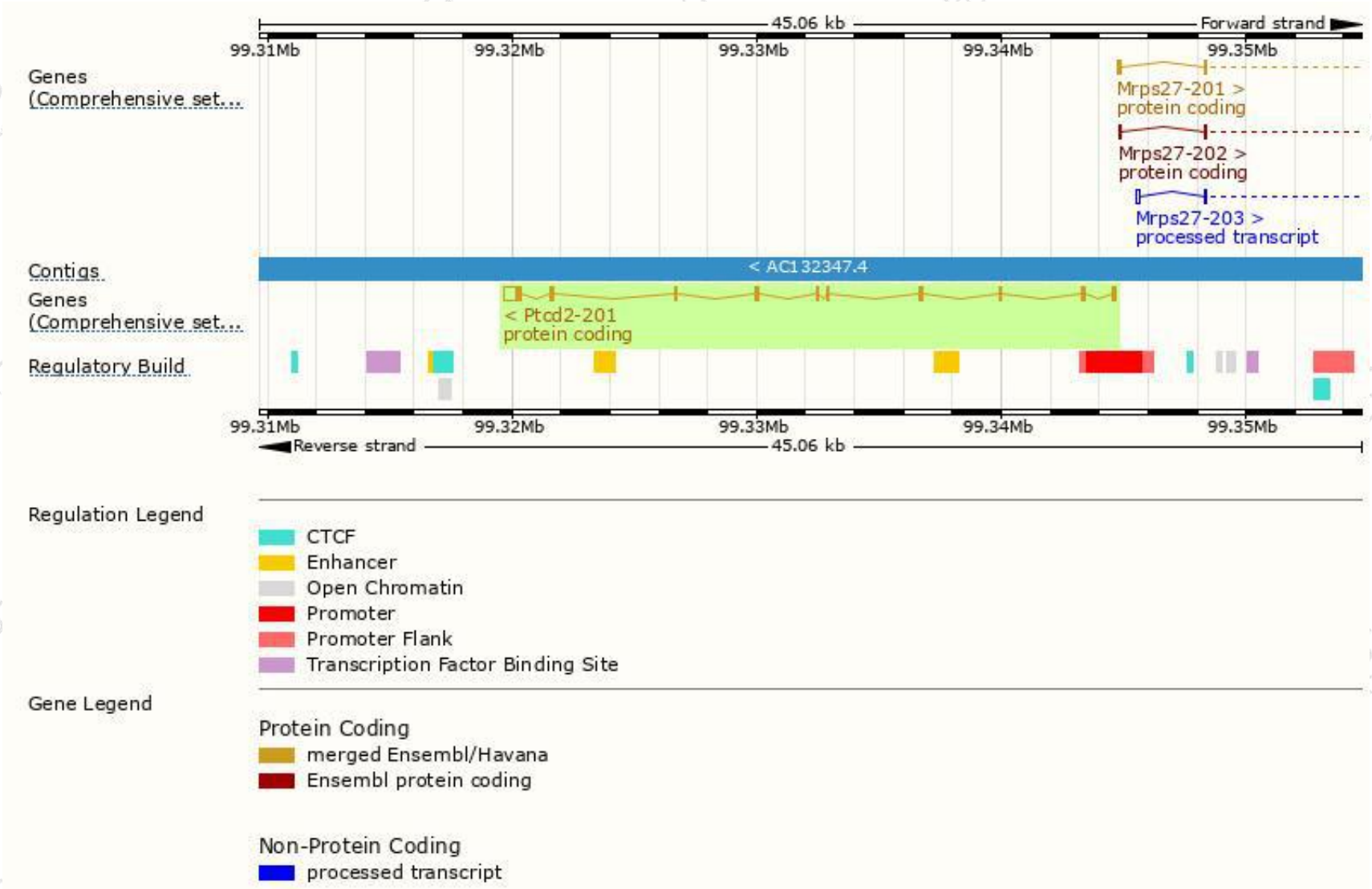
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptcd2-201	ENSMUST00000022153.7	1704	381aa	Protein coding	CCDS26721	Q8R3K3	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

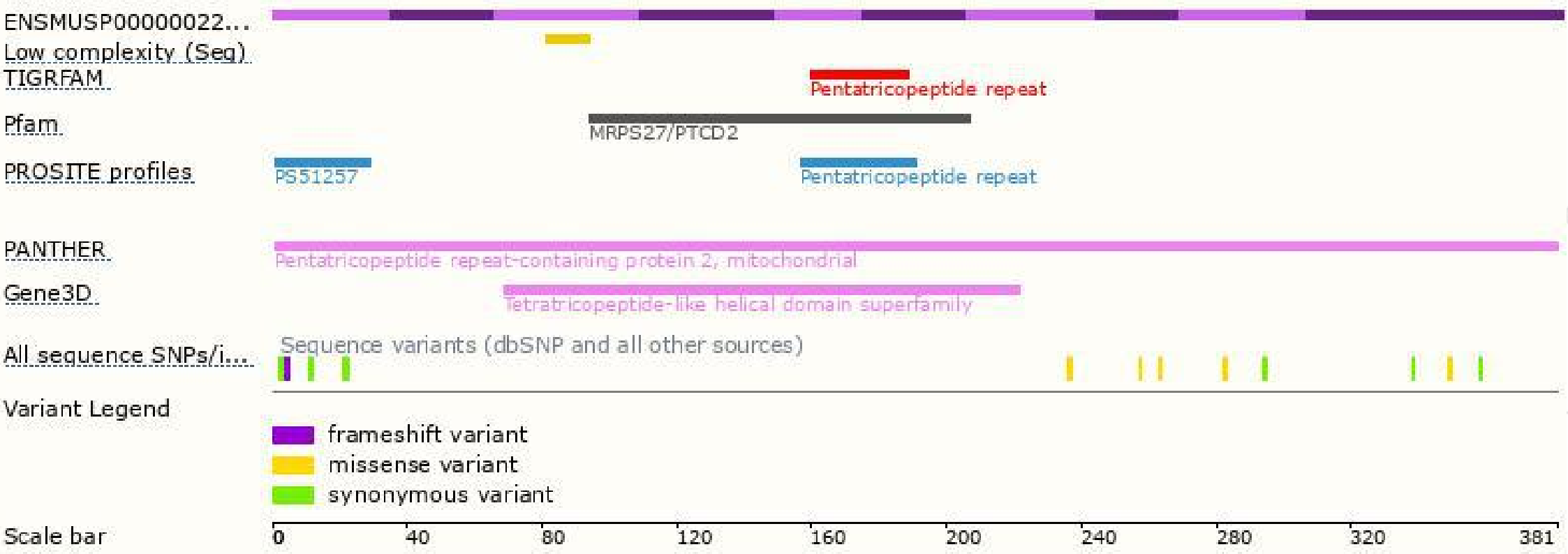
The strategy is based on the design of *Ptcd2-201* transcript,the transcription is shown below:



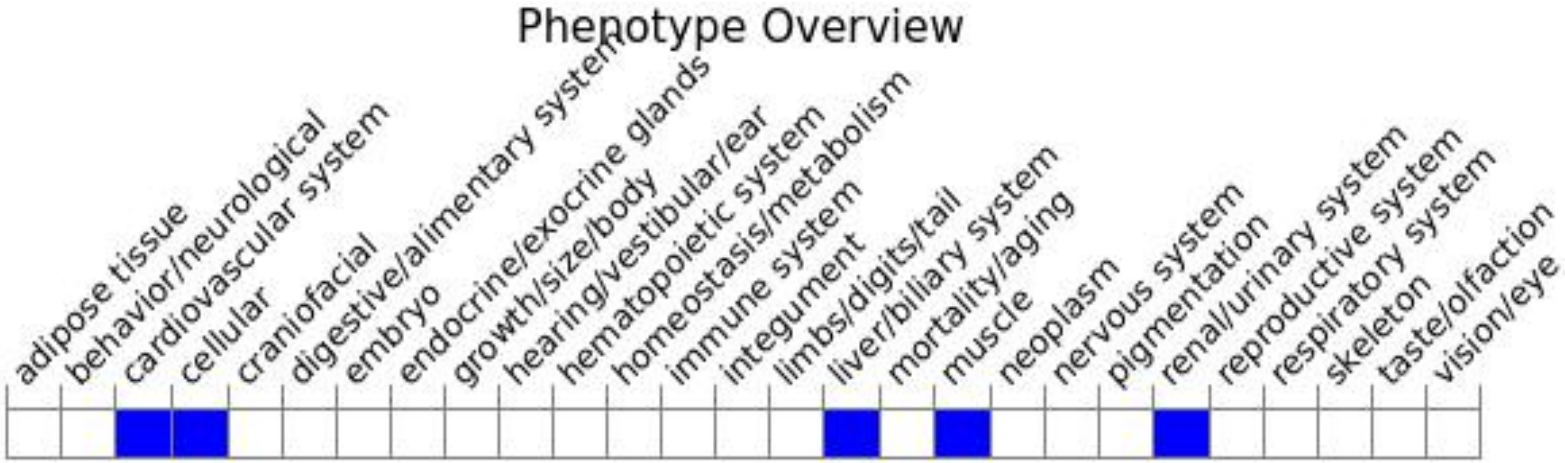
Genomic location distribution



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 gene trapped allele exhibit abnormal mitochondrial morphology and physiology, especially in the heart, liver, skeletal muscle and kidney.

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

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