Stmn1 Cas9-CKO Strategy

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Project Overview

Project Name	***Stmn1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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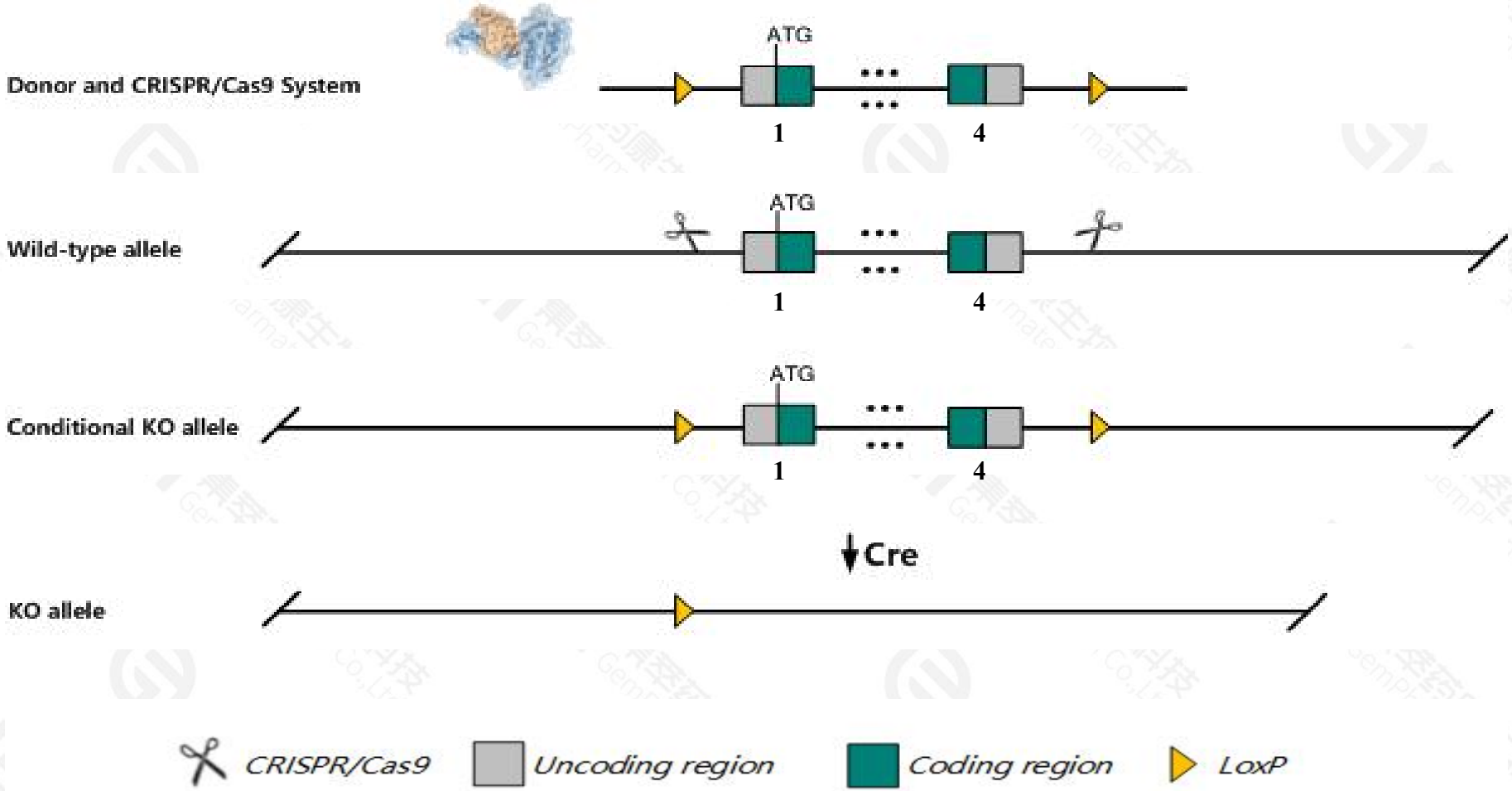
This model will use CRISPR/Cas9 technology to edit the *Stmn1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Stmn1* gene has 5 transcripts. According to the structure of *Stmn1* gene, exon1-exon4 of *Stmn1-203*(ENSMUST00000105868.2) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Stmn1* 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 was 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 targeted null mutation appear normal as young animals, but develop a late-onset appearance of axonal lesions in the central and peripheral nervous systems.

➢ The KO region contains functional region of the ENSMUSG00002075520 gene.Knockout the region will affect the function of ENSMUSG00002075520 gene .

➢ The *Stmn1* gene is located on the Chr4. 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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Stmn1 stathmin 1 [Mus musculus (house mouse)]

Gene ID: 16765, updated on 13-Mar-2020

Summary

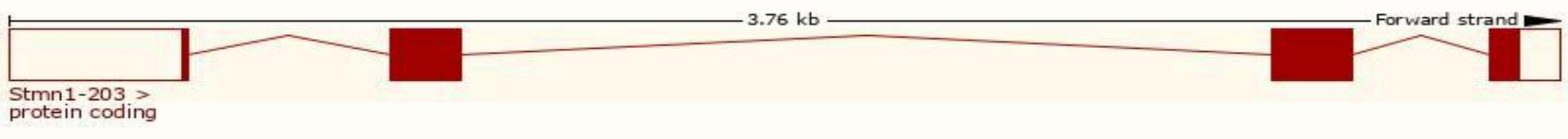
Official Symbol	Stmn1 provided by MGI
Official Full Name	stathmin 1 provided by MGI
Primary source	MGI:MGI:96739
See related	Ensembl:ENSMUSG00000028832
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	19k, Lag, Lap18, Op18, P18, P19, Pig, Pp17, Pp18, Pp19, Pr22, Smn
Expression	Biased expression in CNS E18 (RPKM 553.0), CNS E14 (RPKM 443.2) and 11 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

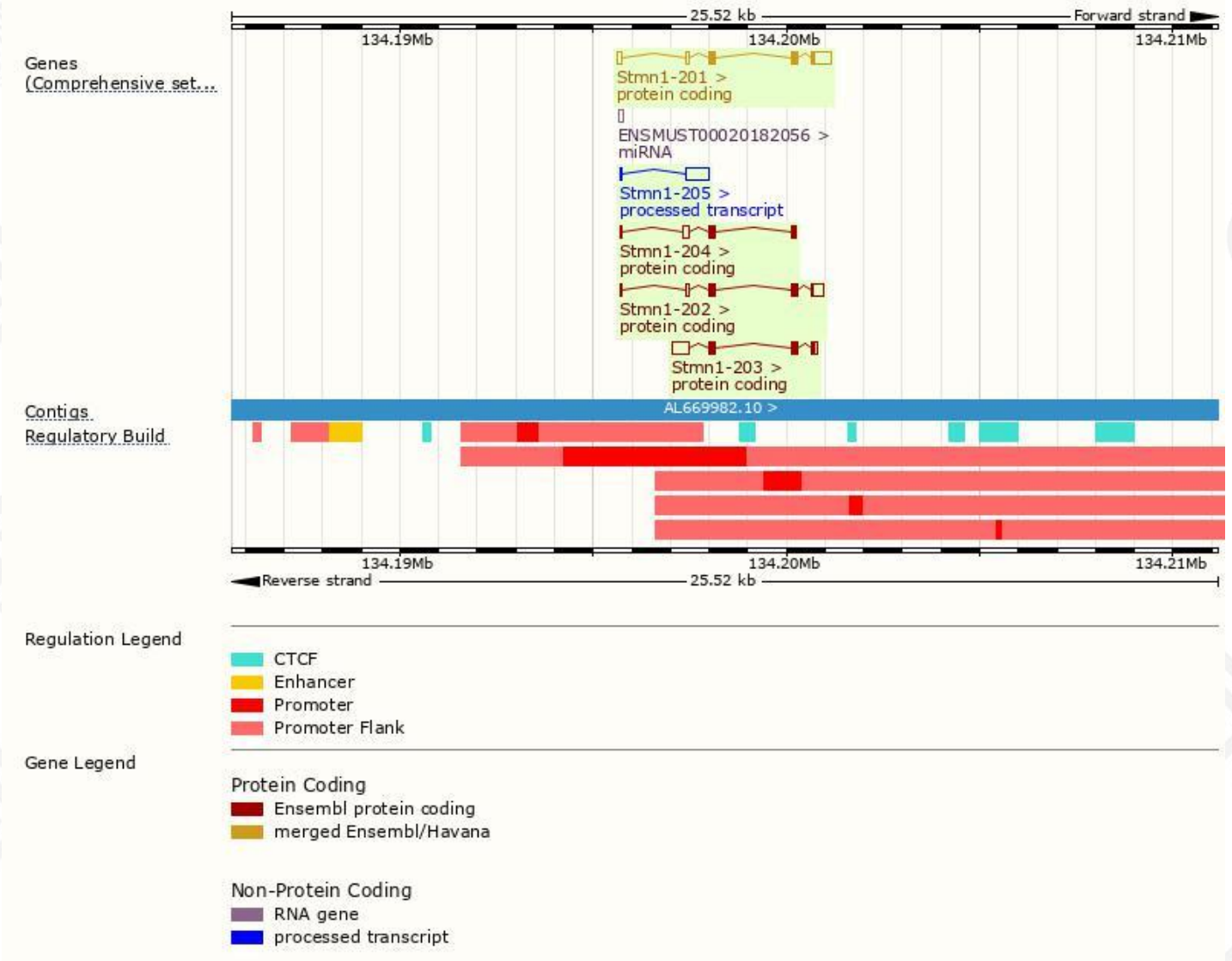
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stmn1-201	ENSMUST00000030636.10	1060	149aa	Protein coding	CCDS18772	P54227 Q545B6	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
Stmn1-203	ENSMUST00000105868.1	967	149aa	Protein coding	CCDS18772	P54227 Q545B6	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
Stmn1-202	ENSMUST00000105867.7	802	147aa	Protein coding	-	D3Z5N2	TSL:5 GENCODE basic
Stmn1-204	ENSMUST00000127279.7	474	102aa	Protein coding	-	D3Z1Z8	CDS 3' incomplete TSL:5
Stmn1-205	ENSMUST00000130253.1	612	No protein	Processed transcript	-	-	TSL:3

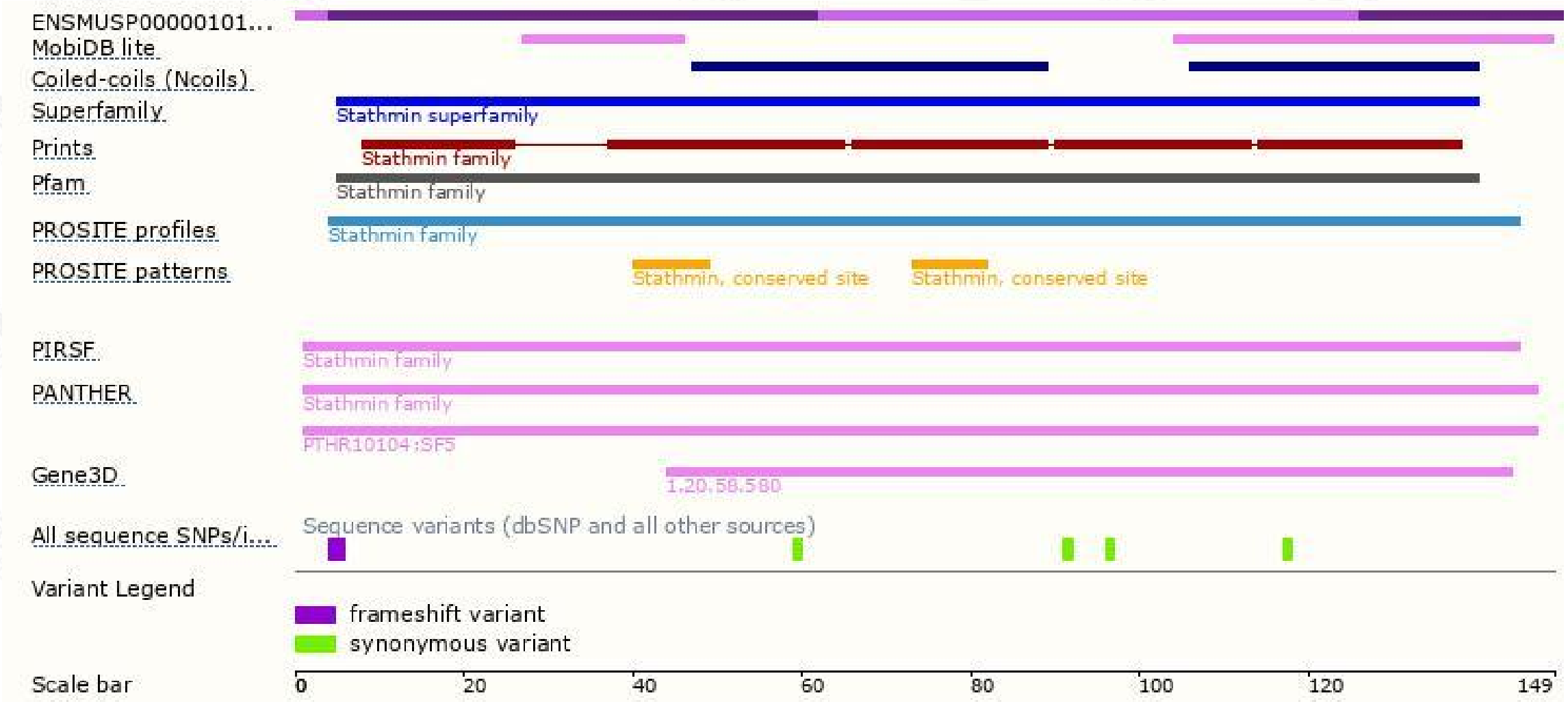
The strategy is based on the design of *Stmn1-203* transcript,the transcription is shown below:



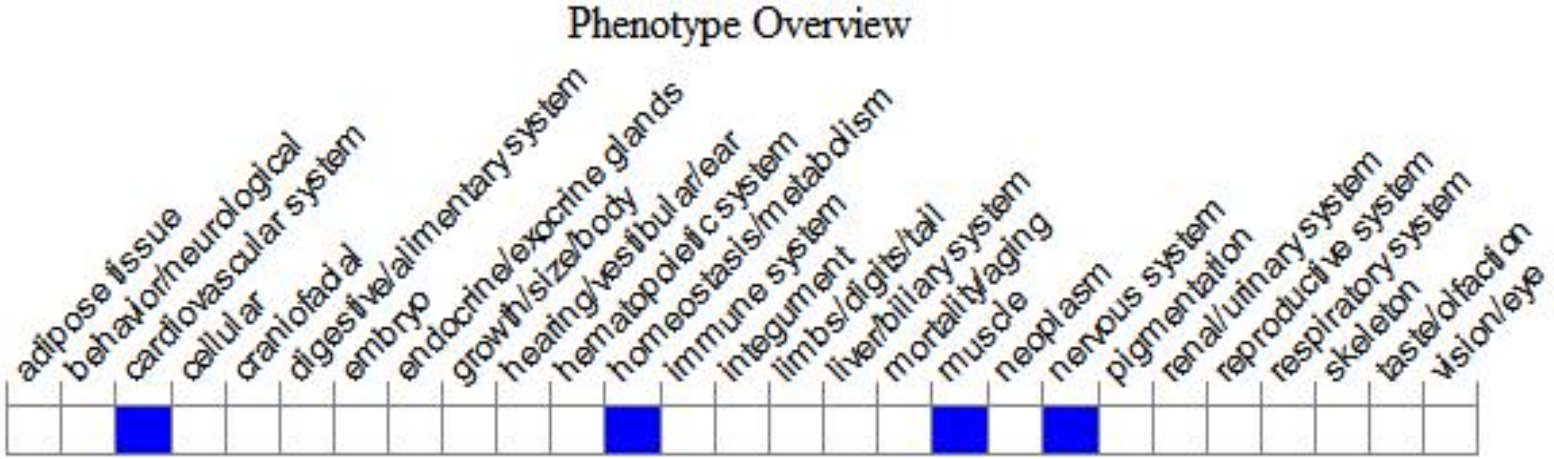
Genomic location distribution



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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