Snai1 Cas9-KO Strategy

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Reviewer: Daohua Xu

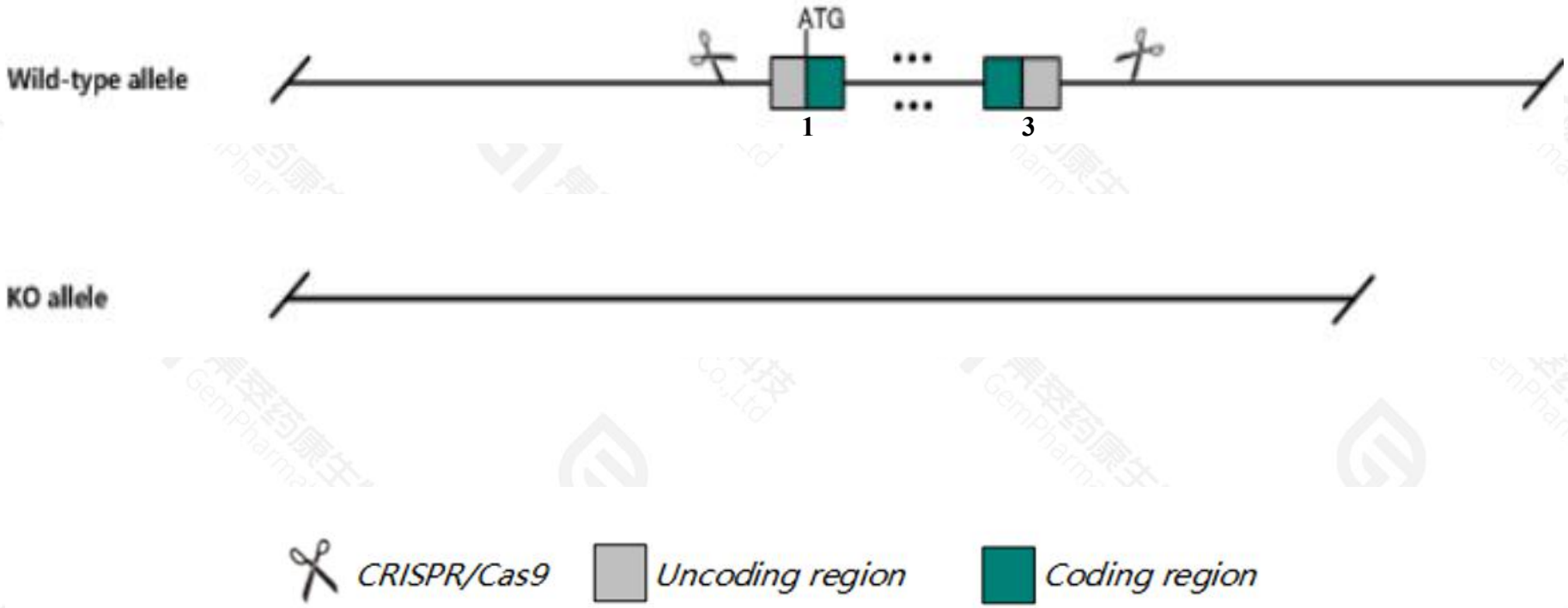
Design Date: 2021-3-3

Project Overview

Project Name	***Snai1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Snai1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Snai1* gene has 1 transcript. According to the structure of *Snai1* gene, exon1-exon3 of *Snai1-201*(ENSMUST00000052631.7) 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 *Snai1* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele exhibit lethality by E8.5, reduced size, and abnormal mesoderm development.

➢ *Gm11474* gene will be deleted together in this strategy.

➢ The *Snai1* gene is located on the Chr2. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

集萃药康 GemPharmatech

Snai1 snail family zinc finger 1 [Mus musculus (house mouse)]

Gene ID: 20613, updated on 13-Mar-2020

Summary

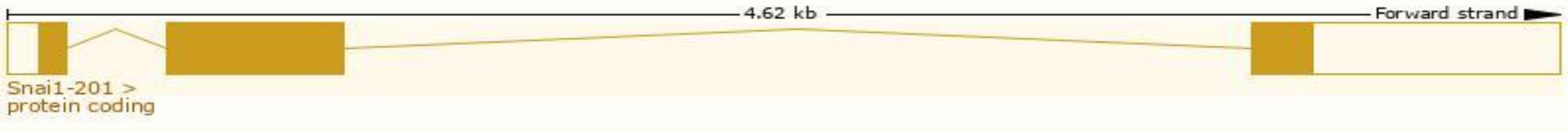
Official Symbol	Snai1 provided by MGI
Official Full Name	snail family zinc finger 1 provided byMGI
Primary source	MGI:MGI:98330
See related	Ensembl:ENSMUSG00000042821
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Sna, Sna1, Snail, Snail1
Expression	Broad expression in limb E14.5 (RPKM 49.3), lung adult (RPKM 33.6) and 20 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

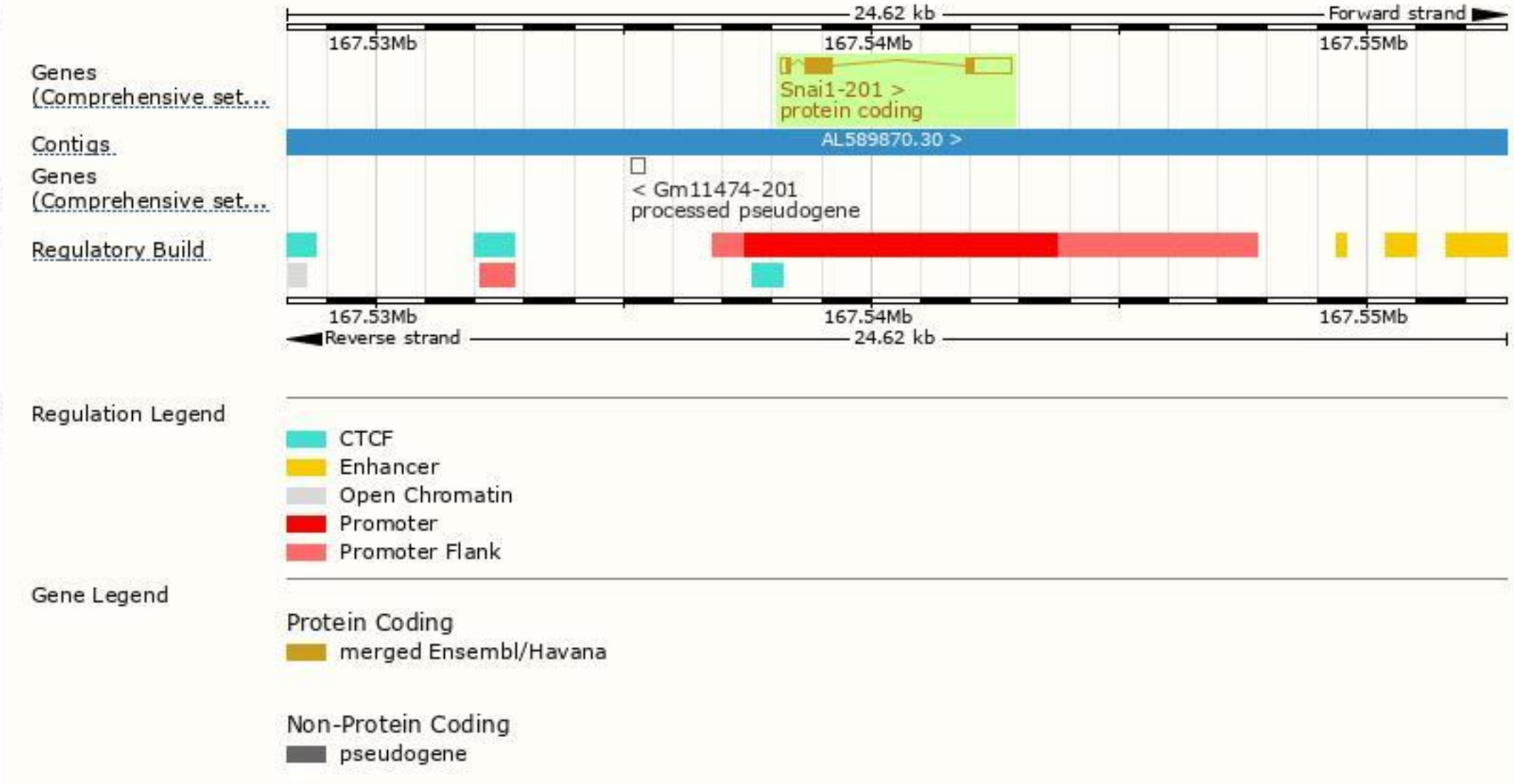
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snai1-201	ENSMUST00000052631.7	1621	264aa	Protein coding	CCDS17102	Q02085 Q4FK48	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

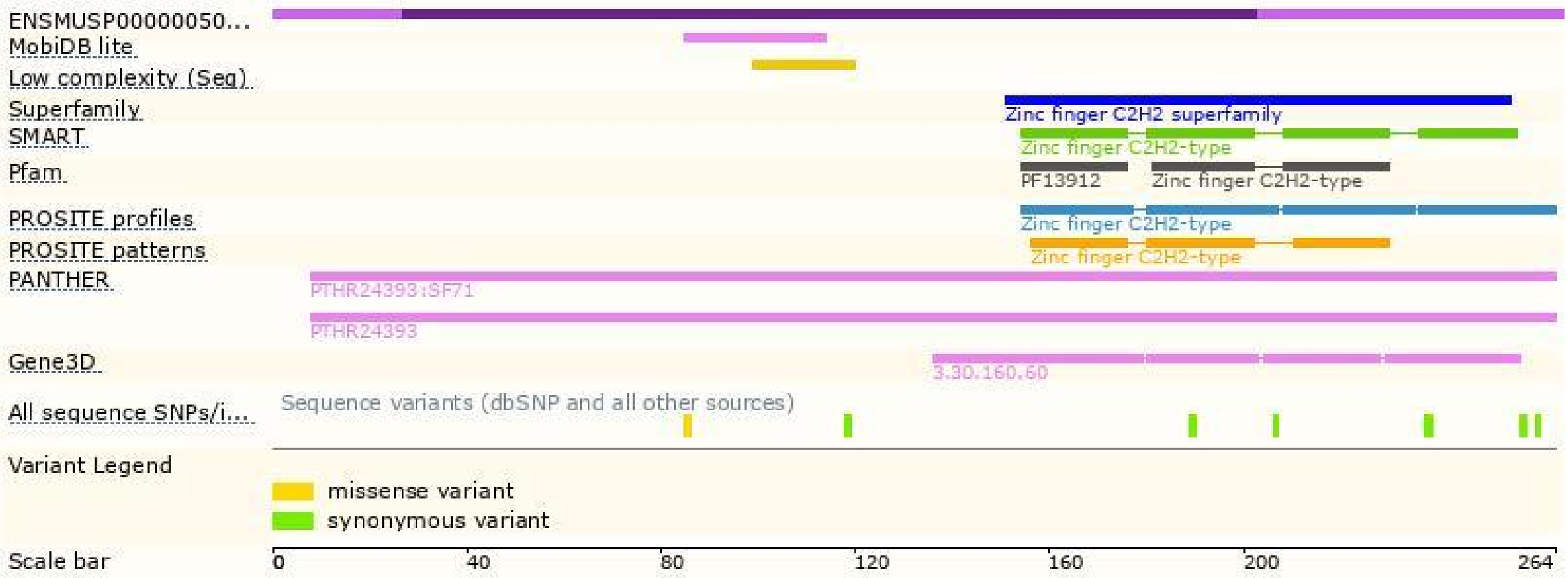
The strategy is based on the design of *Snai1-201* transcript,the transcription is shown below:



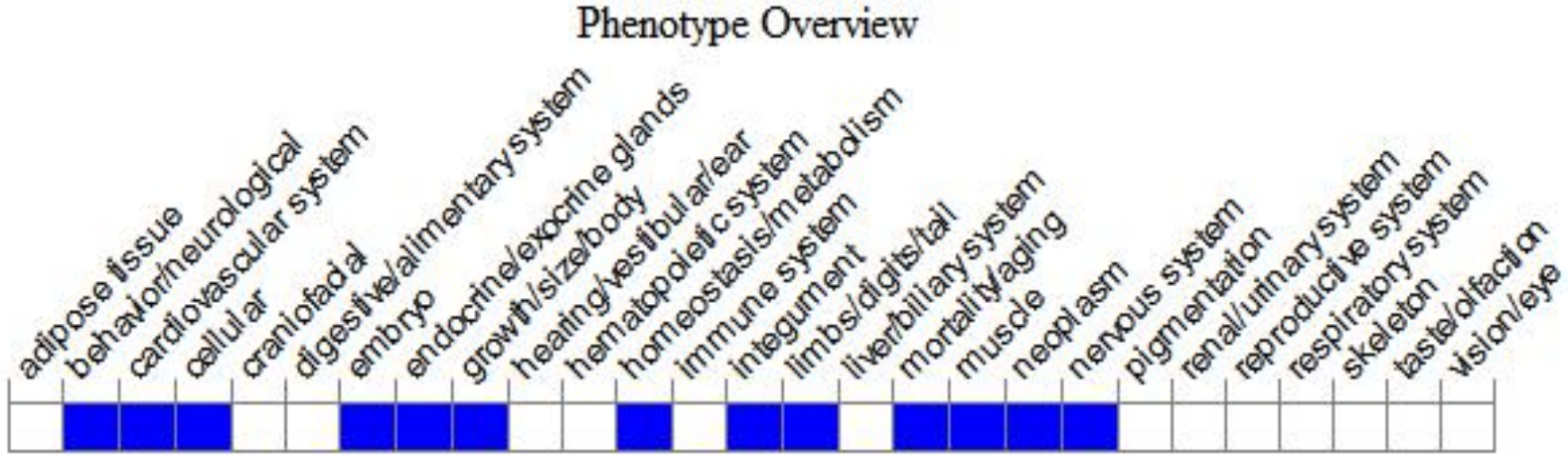
Genomic location distribution



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-out allele exhibit lethality by E8.5, reduced size, and abnormal mesoderm development.

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