

Prmt9 Cas9-CKO Strategy

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Design Date:	2020-5-22

Project Overview

Project Name

Prmt9

Project type

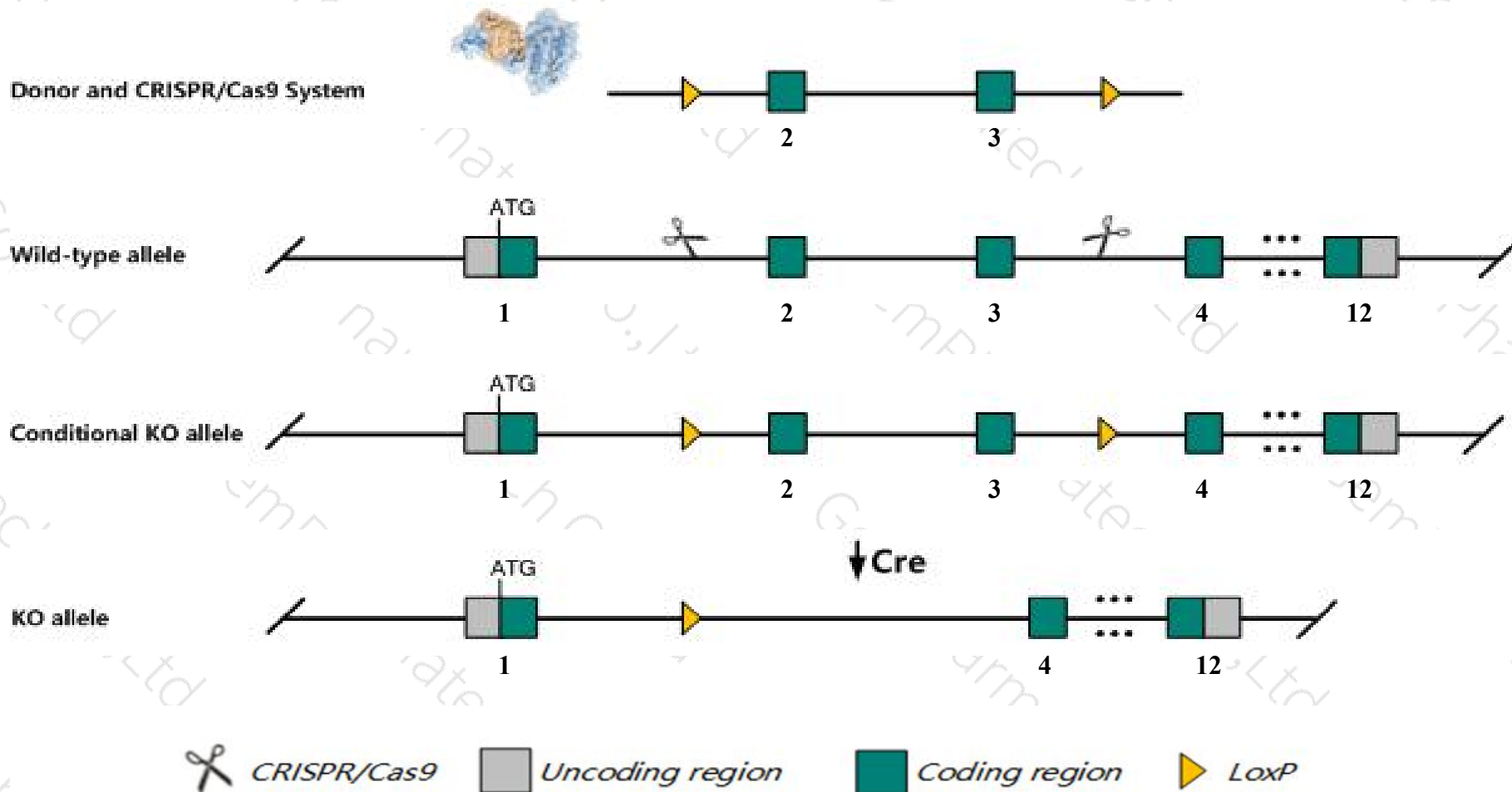
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prmt9* gene. The schematic diagram is as follows:



Technical routes

- The *Prmt9* gene has 5 transcripts. According to the structure of *Prmt9* gene, exon2-exon3 of *Prmt9*-201 (ENSMUST00000056237.14) transcript is recommended as the knockout region. The region contains 386bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Prmt9* 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 *Prmt9* gene is located on the Chr8. 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)

Prmt9 protein arginine methyltransferase 9 [Mus musculus (house mouse)]

Gene ID: 102182, updated on 13-Mar-2020

Summary



Official Symbol Prmt9 provided by [MGI](#)

Official Full Name protein arginine methyltransferase 9 provided by [MGI](#)

Primary source [MGI:MGI:2142651](#)

See related [Ensembl:ENSMUSG00000037134](#)

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 AI931714, Prmt10

Expression Ubiquitous expression in CNS E11.5 (RPKM 7.2), CNS E18 (RPKM 6.7) and 28 other tissues [See more](#)

Orthologs [human](#) [all](#)

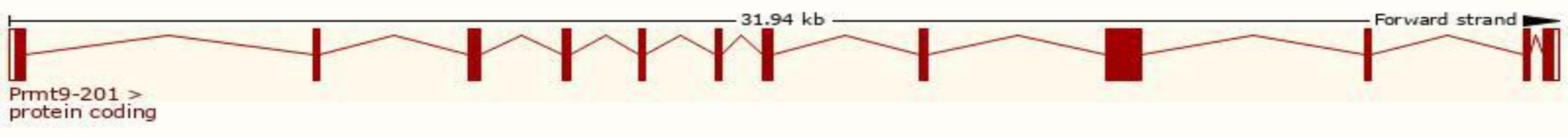
Transcript information (Ensembl)



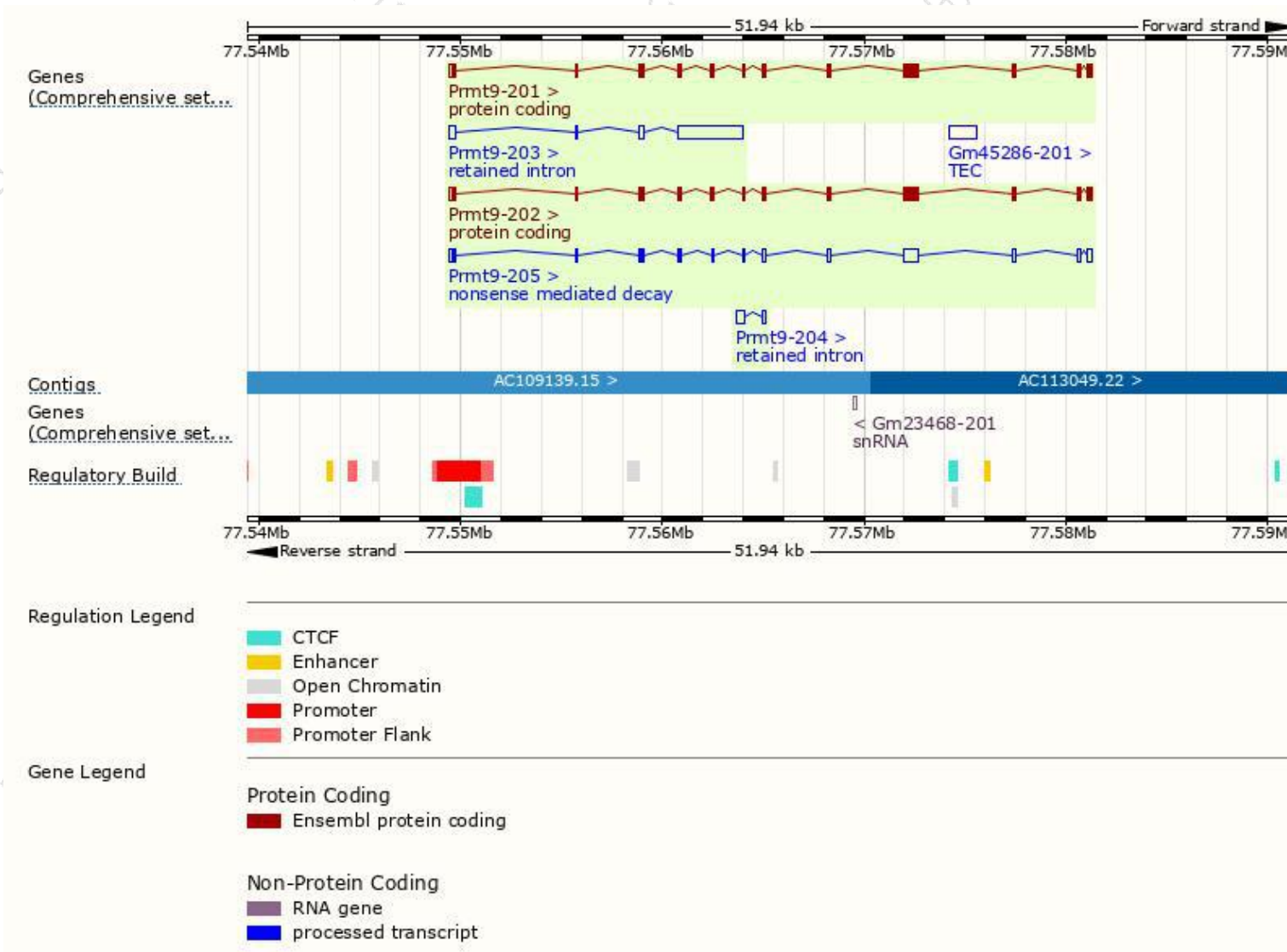
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prmt9-201	ENSMUST00000056237.14	2781	846aa	Protein coding	CCDS40394	F8WIU7	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 P2
Prmt9-202	ENSMUST00000118622.1	2768	846aa	Protein coding	-	Q3U3W5	TSL:5 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 ALT2
Prmt9-205	ENSMUST00000210040.1	2688	305aa	Nonsense mediated decay	-	A0A1B0GT44	TSL:1
Prmt9-203	ENSMUST00000142824.1	3888	No protein	Retained intron	-	-	TSL:1
Prmt9-204	ENSMUST00000156753.1	561	No protein	Retained intron	-	-	TSL:3

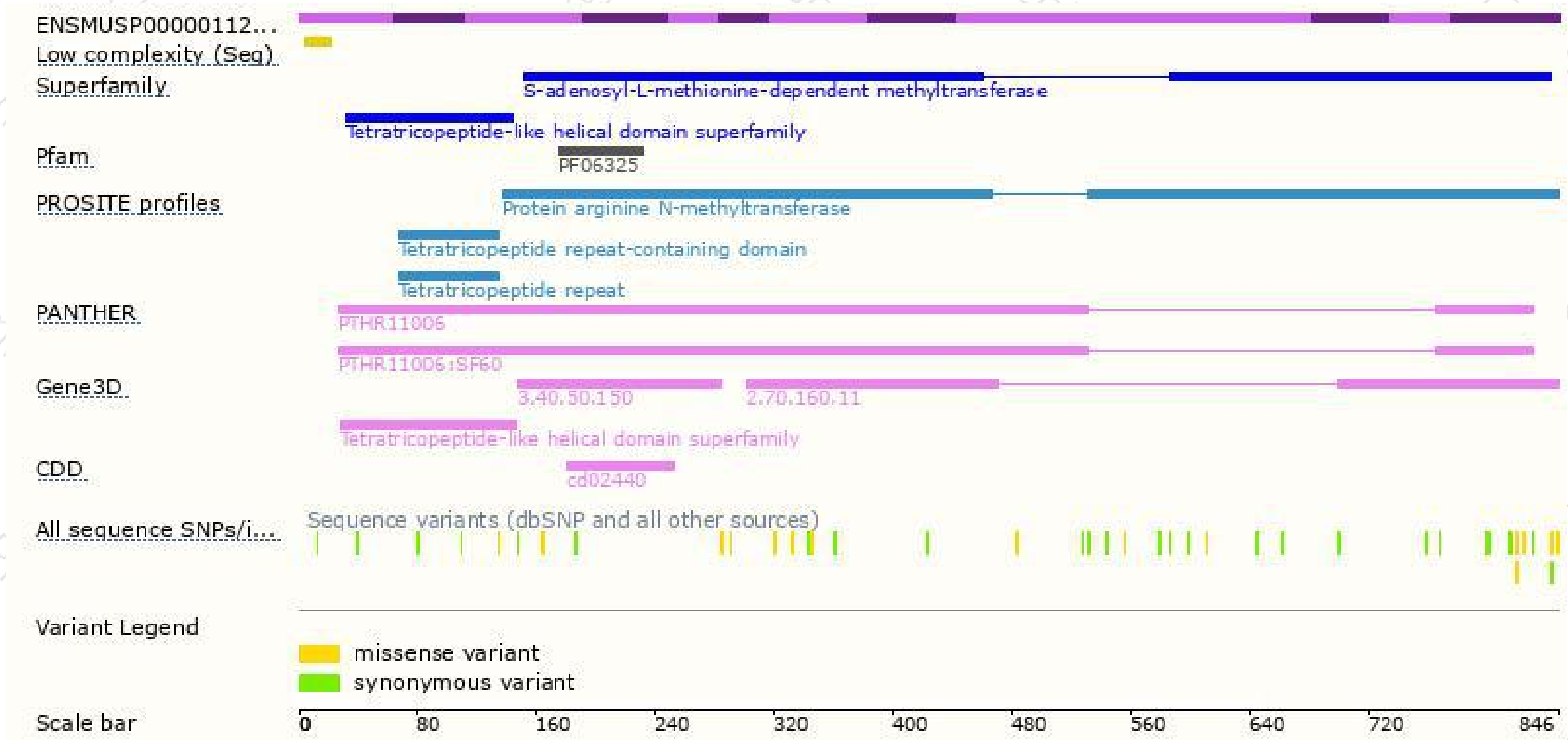
The strategy is based on the design of *Prmt9-201* transcript,the transcription is shown below:



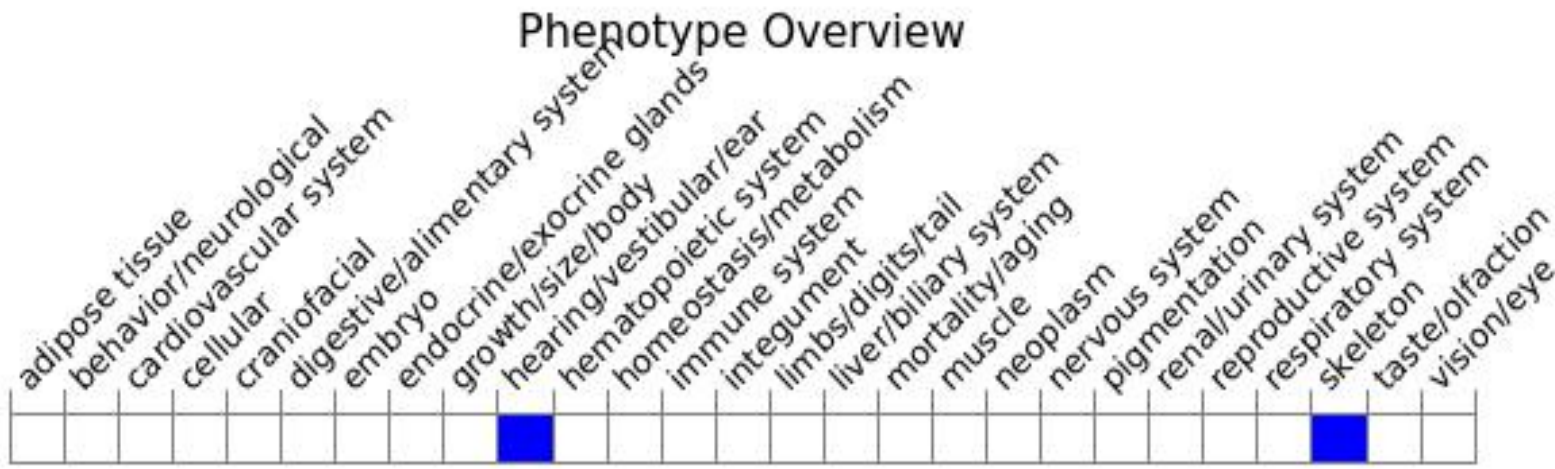
Genomic location distribution



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/>).

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

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