

Prmt3 Cas9-CKO Strategy

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Project Overview

Project Name

Prmt3

Project type

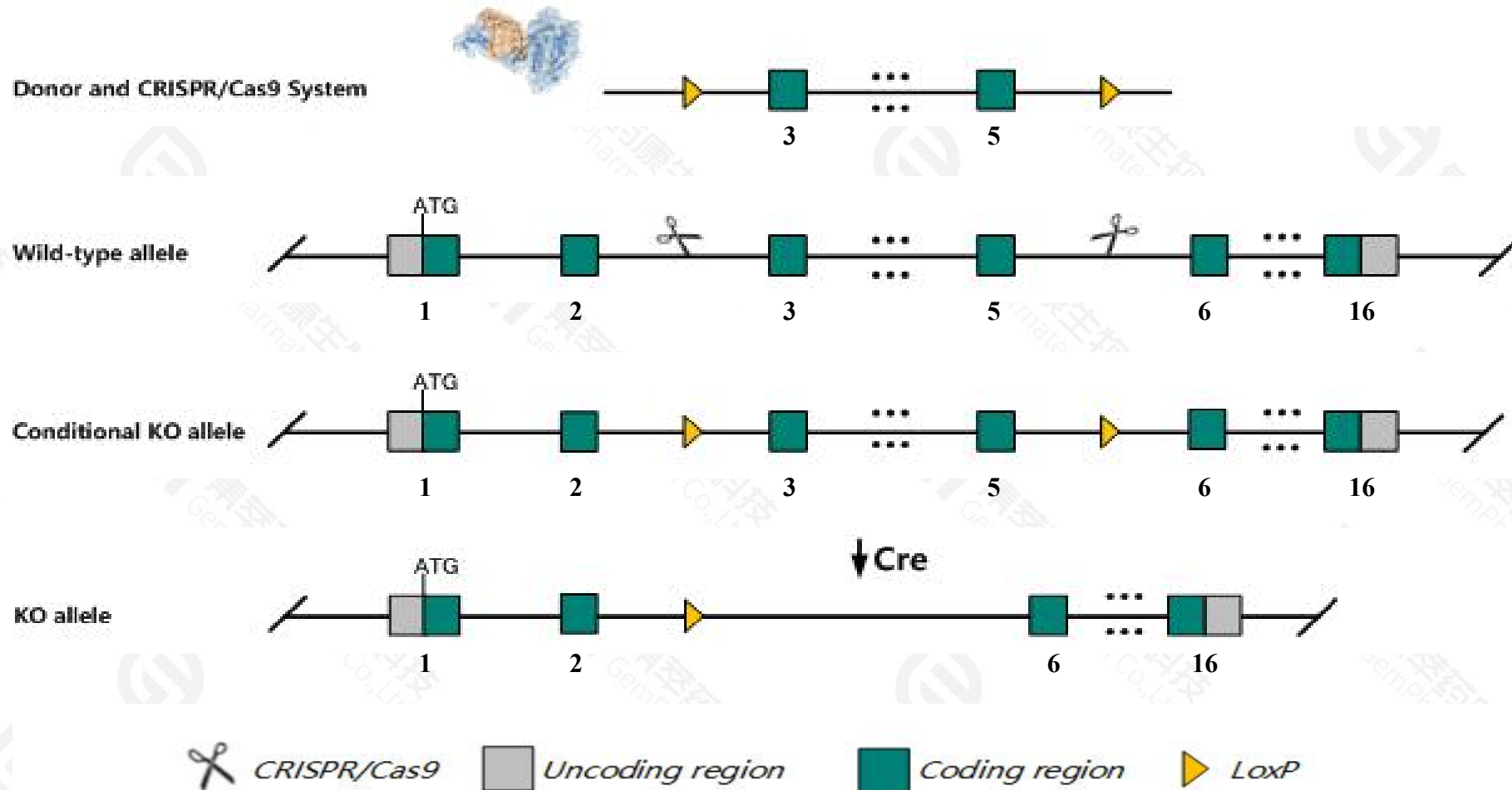
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prmt3* gene. The schematic diagram is as follows:



Technical routes

- The *Prmt3* gene has 9 transcripts. According to the structure of *Prmt3* gene, exon3-exon5 of *Prmt3*-201(ENSMUST00000032715.13) transcript is recommended as the knockout region. The region contains 236bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Prmt3* 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.

- According to the existing MGI data, mice homozygous for a hypomorphic gene trap allele exhibit a reduced embryonic size but survive birth and attain a normal size in adulthood.
- The *Prmt3* 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)

Prmt3 protein arginine N-methyltransferase 3 [Mus musculus (house mouse)]

Gene ID: 71974, updated on 25-Sep-2020

Summary



Official Symbol Prmt3 provided by [MGI](#)

Official Full Name protein arginine N-methyltransferase 3 provided by [MGI](#)

Primary source [MGI:MGI:1919224](#)

See related [Ensembl:ENSMUSG00000030505](#)

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 2010005E20Rik, 2410018A17Rik, AL033309, Hrmt1, Hrmt1l3

Expression Ubiquitous expression in ovary adult (RPKM 18.2), CNS E11.5 (RPKM 14.1) and 28 other tissues [See more](#)

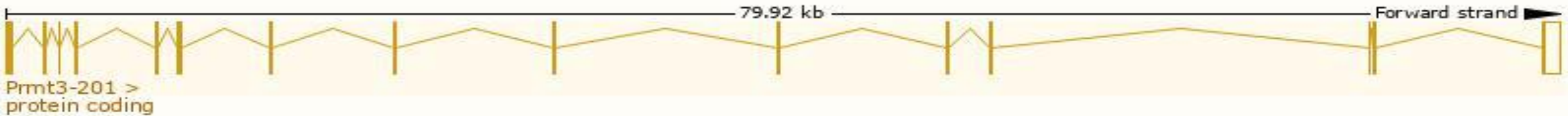
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

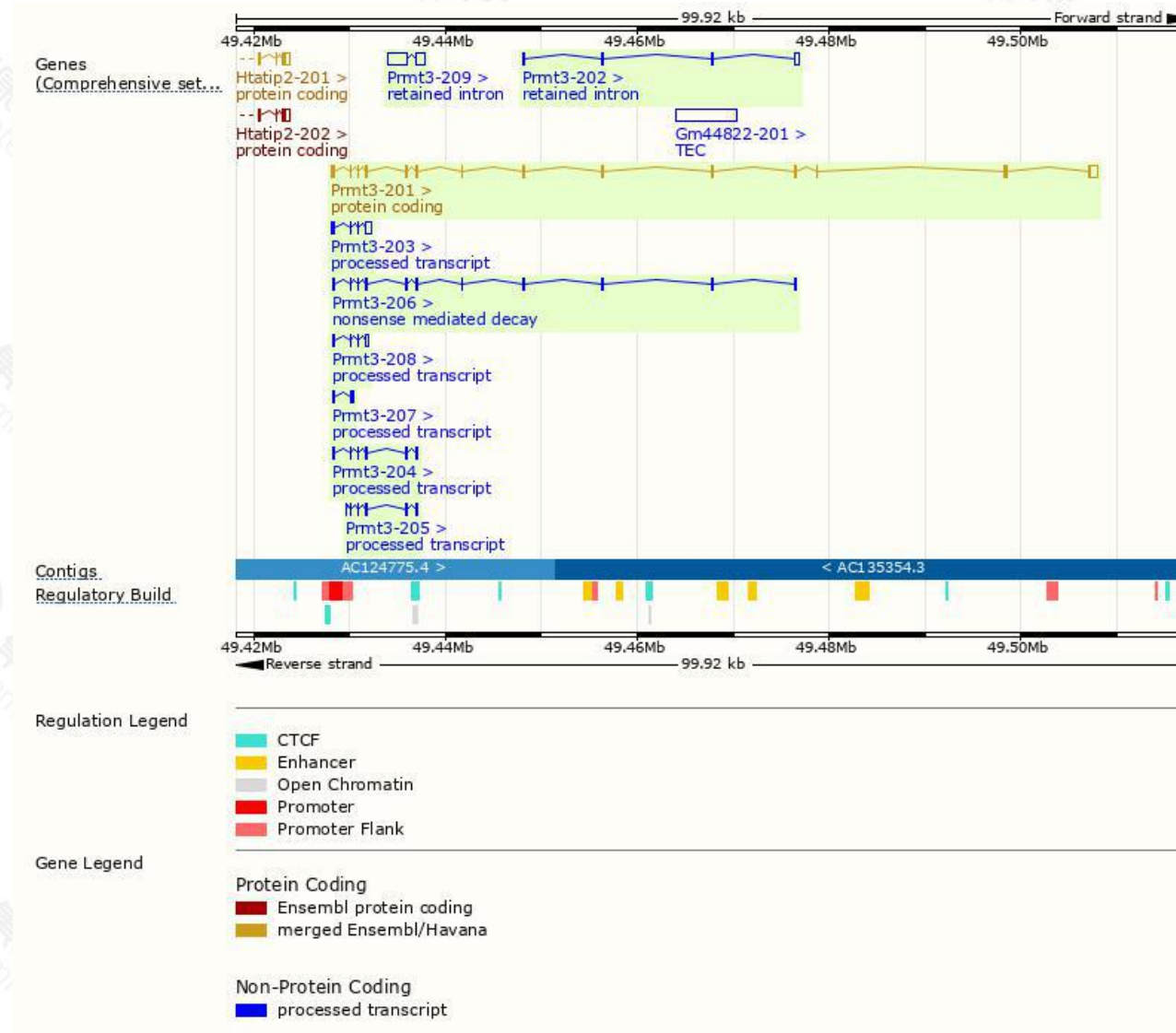
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prmt3-201	ENSMUST00000032715.13	2507	528aa	Protein coding	CCDS21307		TSL:1 , GENCODE basic , APPRIS P1 ,
Prmt3-206	ENSMUST00000147401.8	1242	64aa	Nonsense mediated decay	-		TSL:5 ,
Prmt3-203	ENSMUST00000140656.8	986	No protein	Processed transcript	-		TSL:1 ,
Prmt3-204	ENSMUST00000145666.2	600	No protein	Processed transcript	-		TSL:3 ,
Prmt3-205	ENSMUST00000146052.2	544	No protein	Processed transcript	-		TSL:5 ,
Prmt3-208	ENSMUST00000152127.8	504	No protein	Processed transcript	-		TSL:3 ,
Prmt3-207	ENSMUST00000148996.2	404	No protein	Processed transcript	-		TSL:3 ,
Prmt3-209	ENSMUST00000207216.2	2937	No protein	Retained intron	-		TSL:1 ,
Prmt3-202	ENSMUST00000130907.2	600	No protein	Retained intron	-		TSL:2 ,

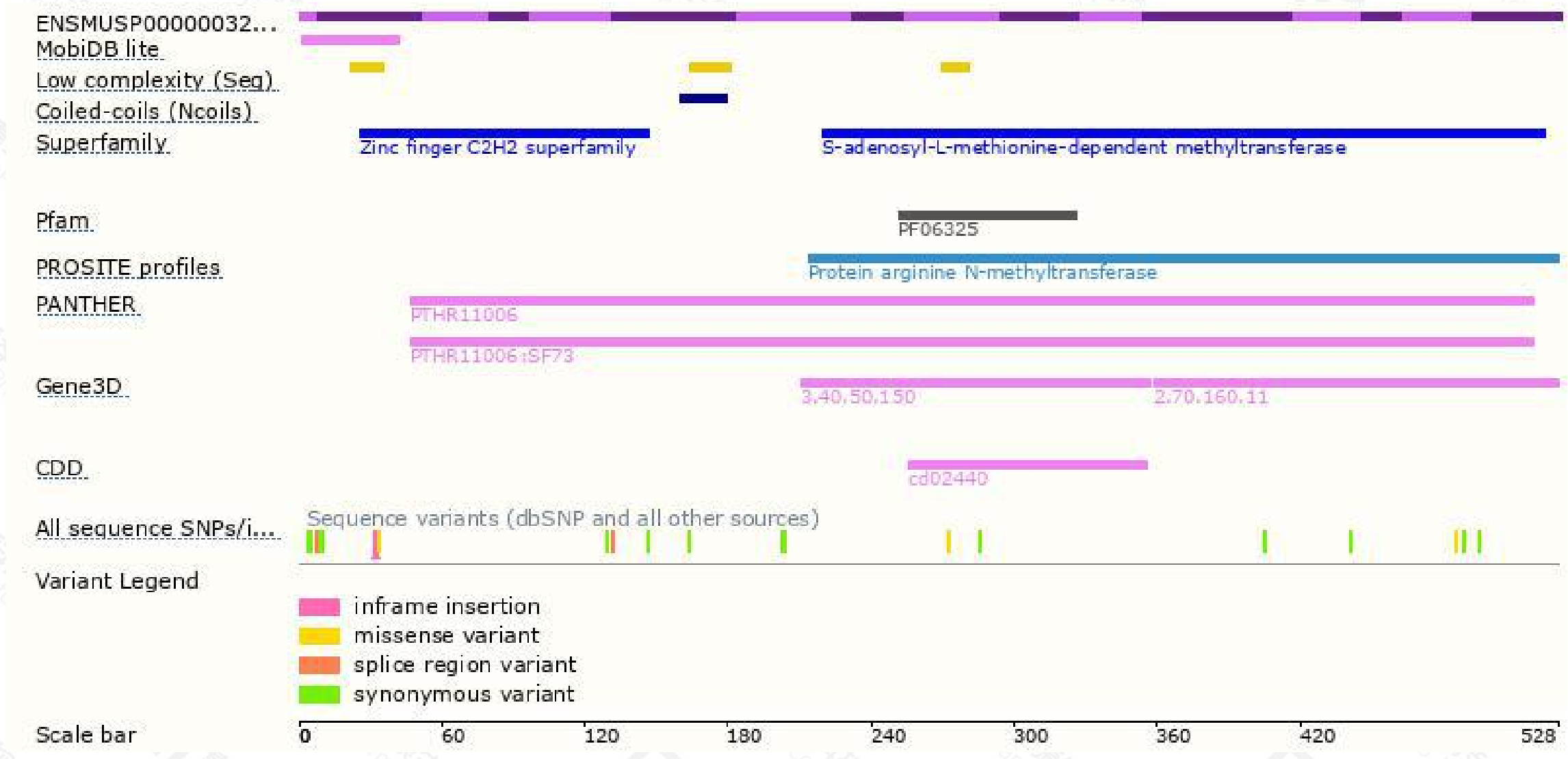
The strategy is based on the design of *Prmt3-201* transcript,the transcription is shown below:



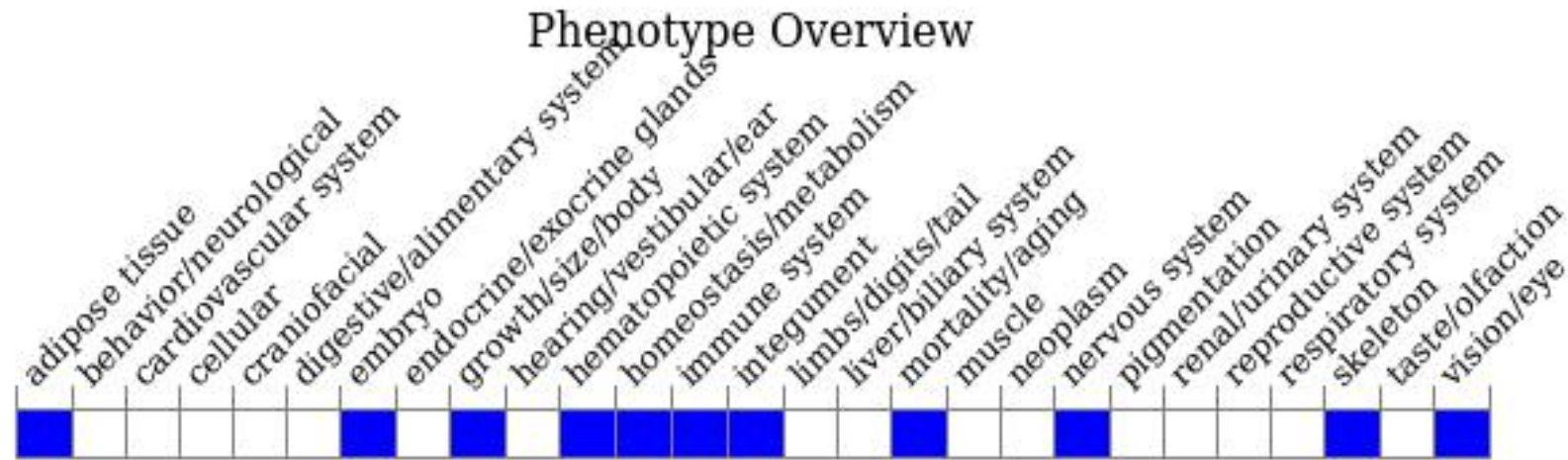
Genomic location distribution



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 hypomorphic gene trap allele exhibit a reduced embryonic size but survive birth and attain a normal size in adulthood.

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