

***Rnmt* Cas9-CKO Strategy**

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Reviewer:

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Project Overview

Project Name

Rnmt

Project type

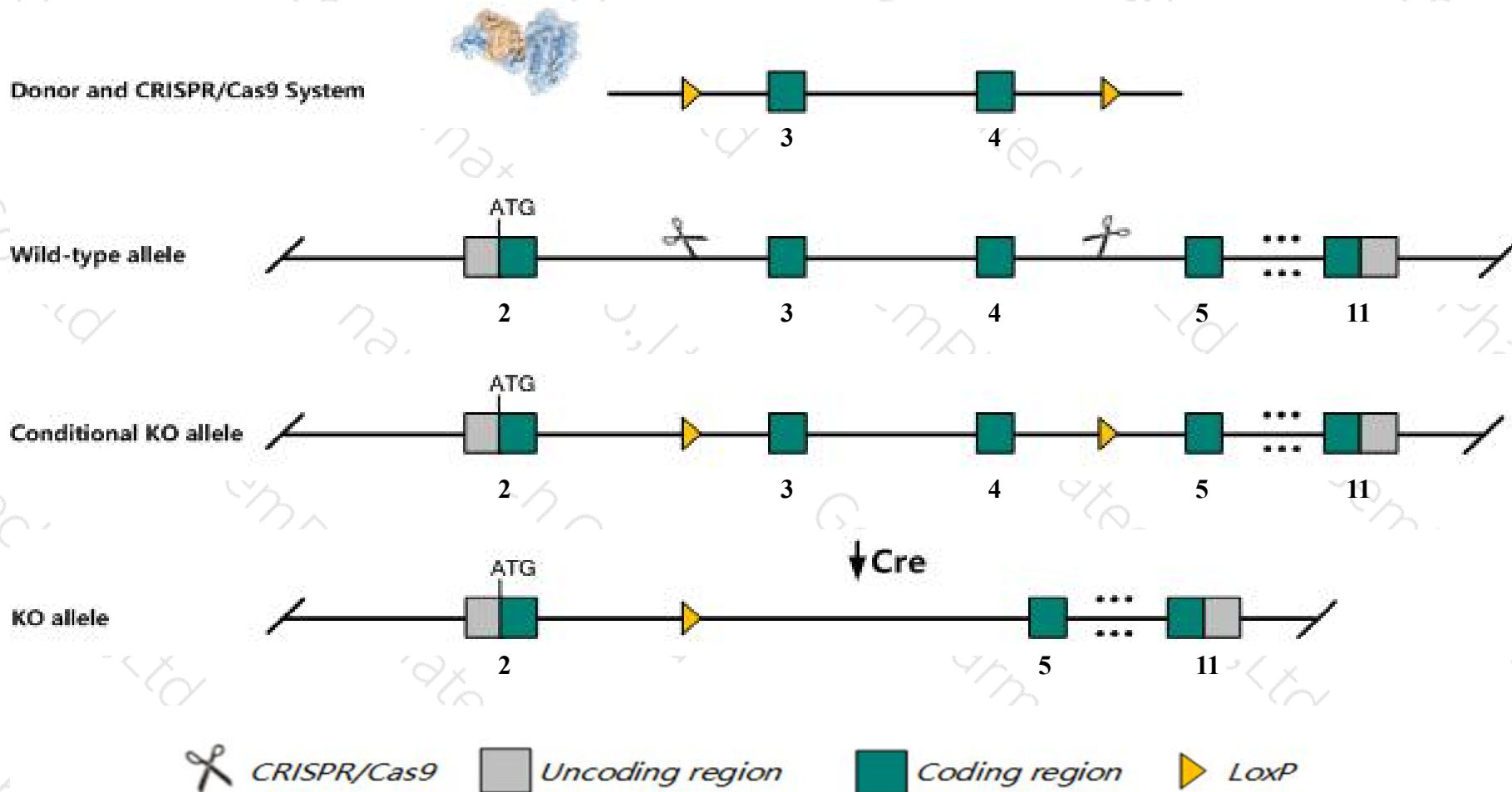
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Rnmt* gene has 8 transcripts. According to the structure of *Rnmt* gene, exon3-exon4 of *Rnmt-201* (ENSMUST00000009679.10) transcript is recommended as the knockout region. The region contains 268bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rnmt* 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.

- Transcripts 206,207 may not be affected. The effect of transcripts 203,204 is unknown.
- The *Rnmt* gene is located on the Chr18. 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)

Rnmt RNA (guanine-7-) methyltransferase [Mus musculus (house mouse)]

Gene ID: 67897, updated on 13-Mar-2020

Summary



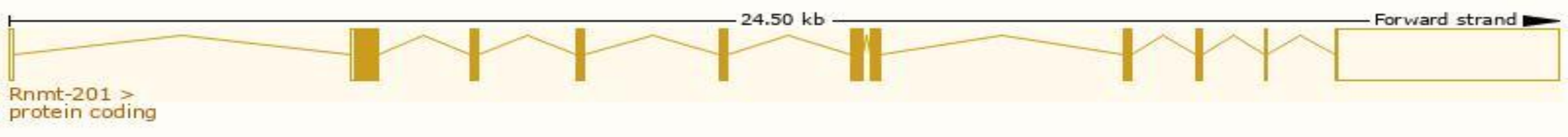
Official Symbol	Rnmt provided by MGI
Official Full Name	RNA (guanine-7-) methyltransferase provided by MGI
Primary source	MGI:MGI:1915147
See related	Ensembl:ENSMUSG000000009535
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610002P10Rik, A1848273, Rg7mt1, mKIAA0398
Expression	Broad expression in CNS E18 (RPKM 9.2), CNS E14 (RPKM 8.1) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

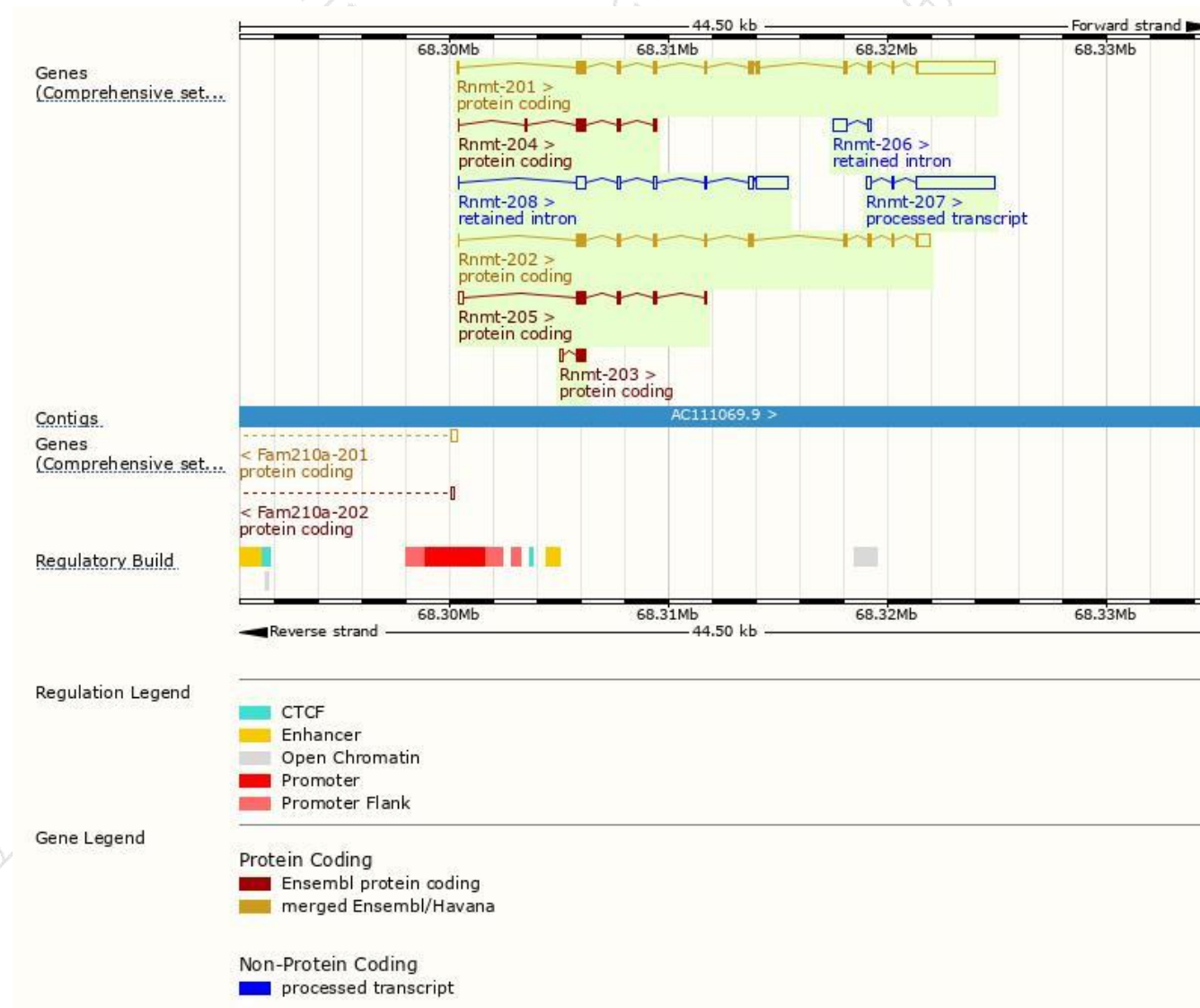
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnmt-201	ENSMUST00000009679.10	5008	465aa	Protein coding	CCDS37852	Q9D0L8	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
Rnmt-202	ENSMUST00000025427.13	1852	410aa	Protein coding	CCDS50314	Q9D0L8	TSL:1 GENCODE basic
Rnmt-205	ENSMUST00000139111.1	965	240aa	Protein coding	-	D3YYS7	CDS 3' incomplete TSL:3
Rnmt-204	ENSMUST00000131075.7	757	205aa	Protein coding	-	D3Z478	CDS 3' incomplete TSL:5
Rnmt-203	ENSMUST00000129849.1	537	124aa	Protein coding	-	D3Z4K1	CDS 3' incomplete TSL:2
Rnmt-207	ENSMUST00000148937.1	3791	No protein	Processed transcript	-	-	TSL:1
Rnmt-208	ENSMUST00000151833.1	2474	No protein	Retained intron	-	-	TSL:1
Rnmt-206	ENSMUST00000139554.1	748	No protein	Retained intron	-	-	TSL:3

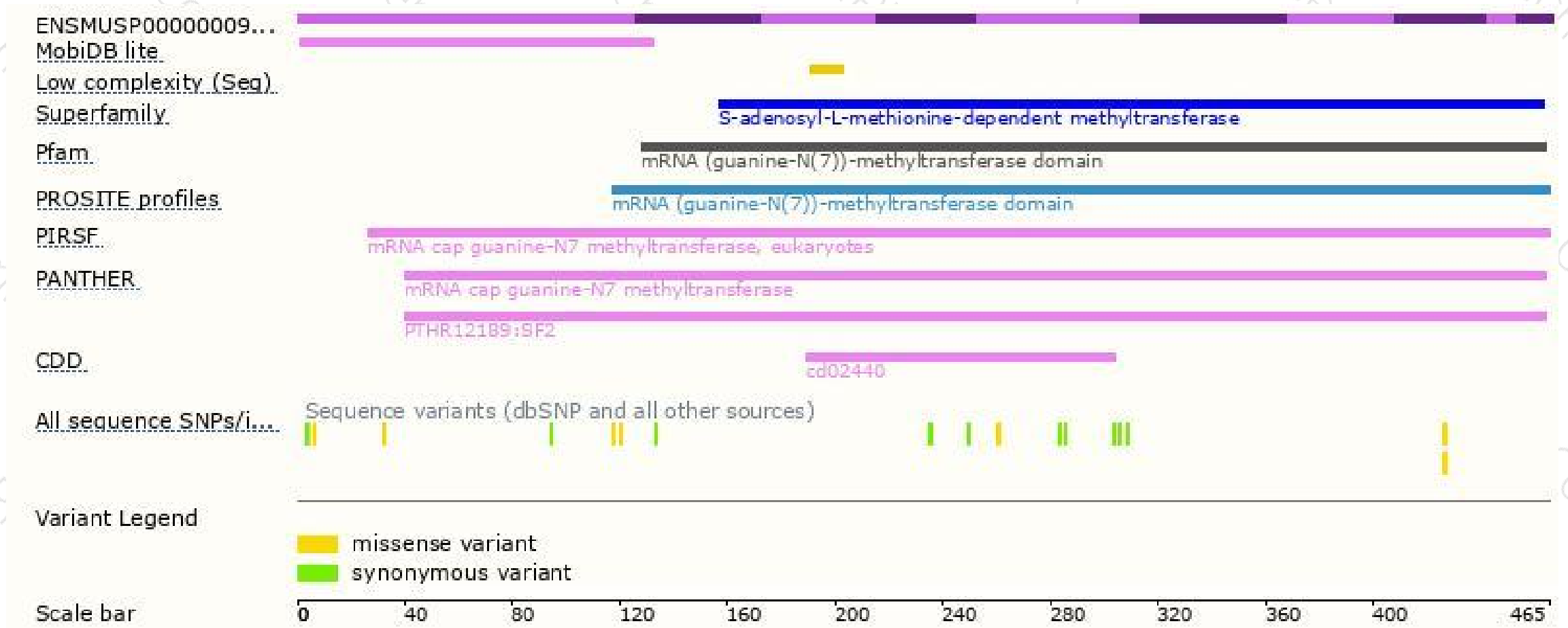
The strategy is based on the design of *Rnmt-201* transcript,the transcription is shown below:



Genomic location distribution

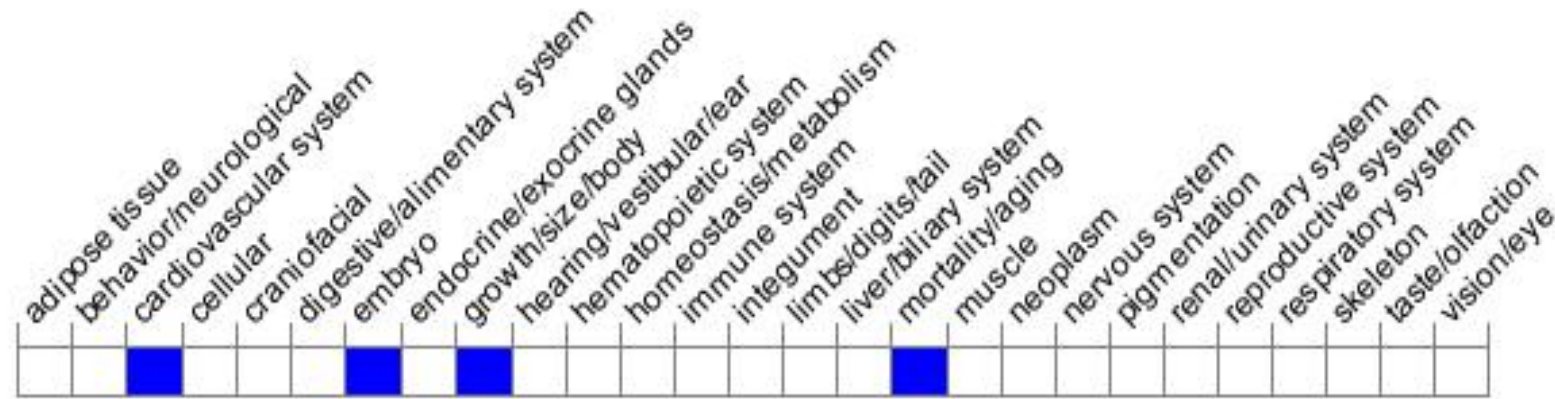


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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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