

# ***Sec24d* Cas9-CKO Strategy**

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# Project Overview

**Project Name**

***Sec24d***

**Project type**

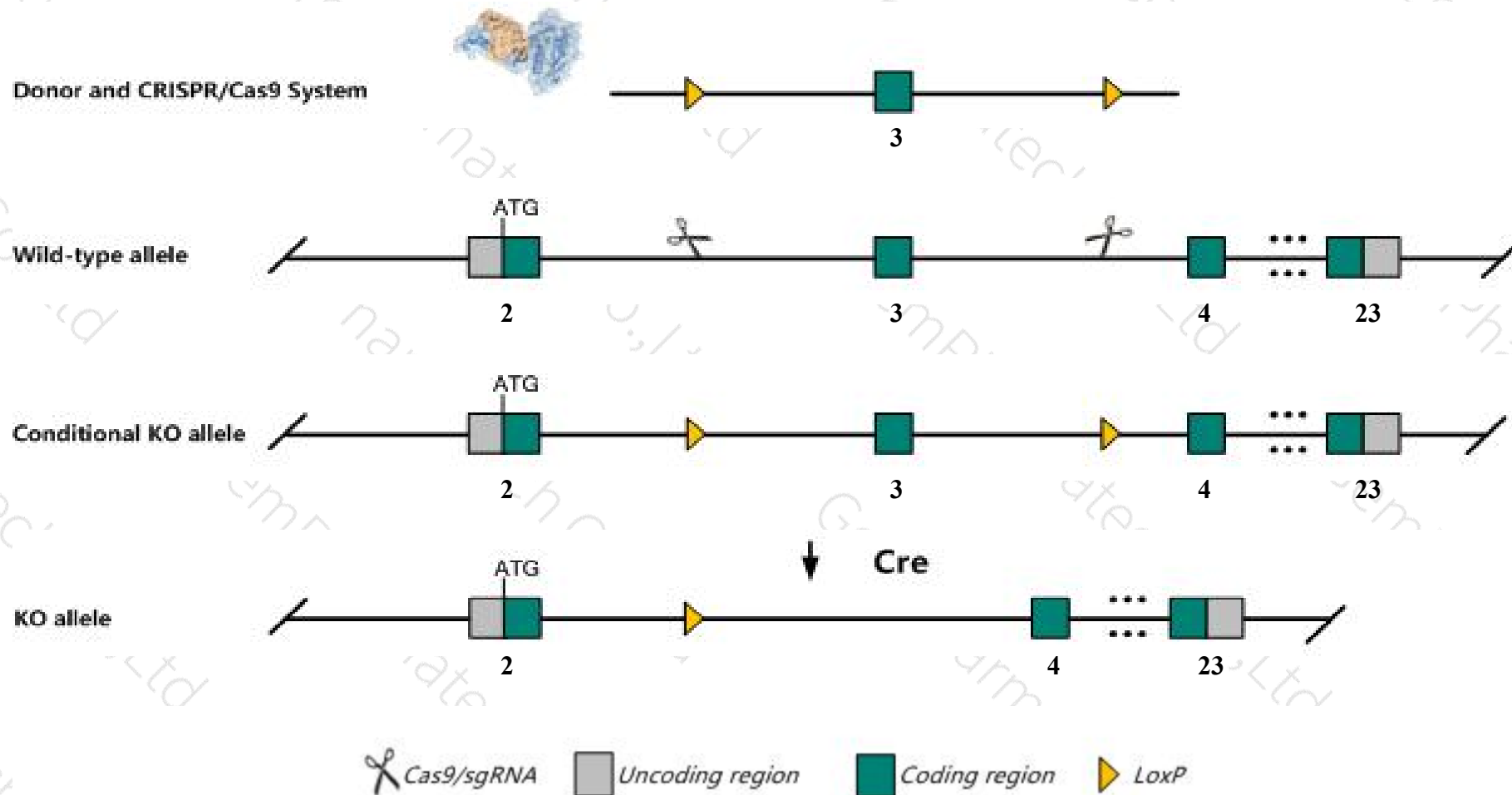
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sec24d* gene. The schematic diagram is as follows:



# Technical routes

- The *Sec24d* gene has 8 transcripts. According to the structure of *Sec24d* gene, exon3 of *Sec24d-201*(ENSMUST00000047923.11) transcript is recommended as the knockout region. The region contains 124bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sec24d* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit early embryonic lethality. A hypomorphic gene trap allele results in lethality during organogenesis.
- The transcript of *Sec24d*-202&203&204&205&207&208 may not be affected.
- The *Sec24d* gene is located on the Chr3. 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)

## Sec24d Sec24 related gene family, member D (*S. cerevisiae*) [*Mus musculus* (house mouse)]

Gene ID: 69608, updated on 13-Mar-2020

### Summary



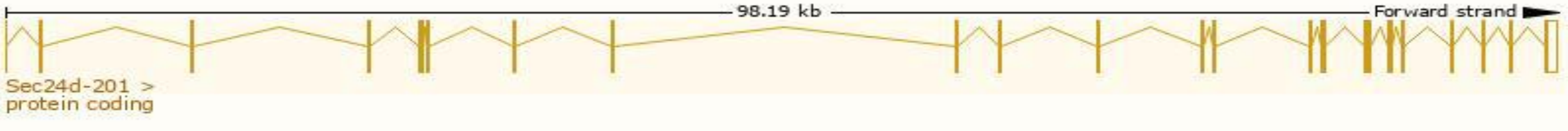
<b>Official Symbol</b>	Sec24d provided by <a href="#">MGI</a>
<b>Official Full Name</b>	Sec24 related gene family, member D ( <i>S. cerevisiae</i> ) provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1916858</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000039234</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	2310020L09Rik, Gm1349
<b>Expression</b>	Broad expression in adrenal adult (RPKM 64.8), duodenum adult (RPKM 50.4) and 24 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

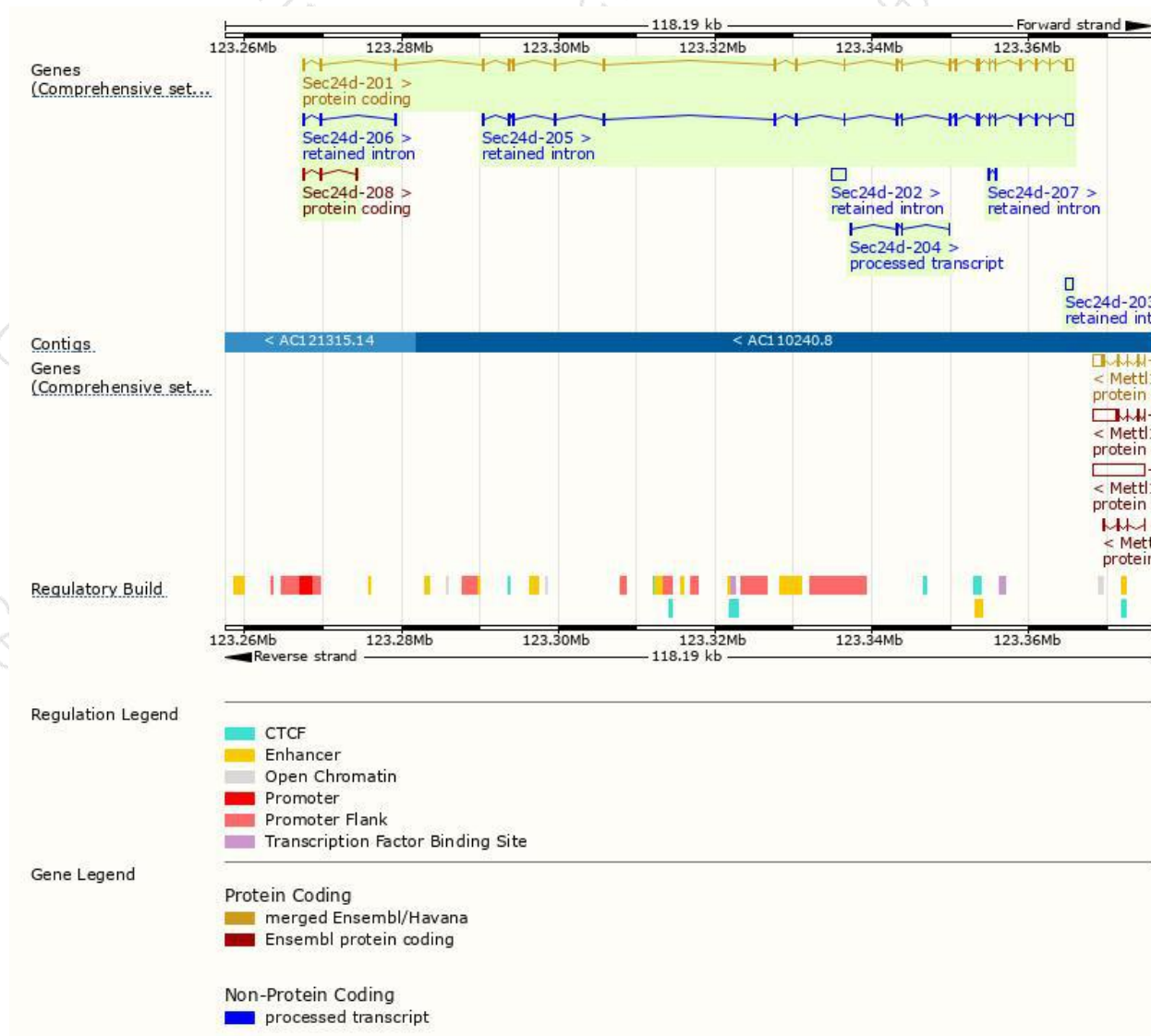
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sec24d-201	<a href="#">ENSMUST00000047923.11</a>	3903	<a href="#">1032aa</a>	Protein coding	<a href="#">CCDS38621</a>	<a href="#">Q6NXL1</a>	TSL:1 GENCODE basic APPRIS P1
Sec24d-208	<a href="#">ENSMUST00000200333.1</a>	307	<a href="#">47aa</a>	Protein coding	-	<a href="#">A0A0G2JGJ5</a>	TSL:1 GENCODE basic
Sec24d-204	<a href="#">ENSMUST00000196631.1</a>	376	No protein	Processed transcript	-	-	TSL:3
Sec24d-205	<a href="#">ENSMUST00000197291.4</a>	3649	No protein	Retained intron	-	-	TSL:5
Sec24d-202	<a href="#">ENSMUST00000196167.1</a>	1947	No protein	Retained intron	-	-	TSL:NA
Sec24d-203	<a href="#">ENSMUST00000196482.1</a>	923	No protein	Retained intron	-	-	TSL:NA
Sec24d-207	<a href="#">ENSMUST00000200309.1</a>	421	No protein	Retained intron	-	-	TSL:2
Sec24d-206	<a href="#">ENSMUST00000198210.1</a>	409	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Sec24d-201* transcript,the transcription is shown below:

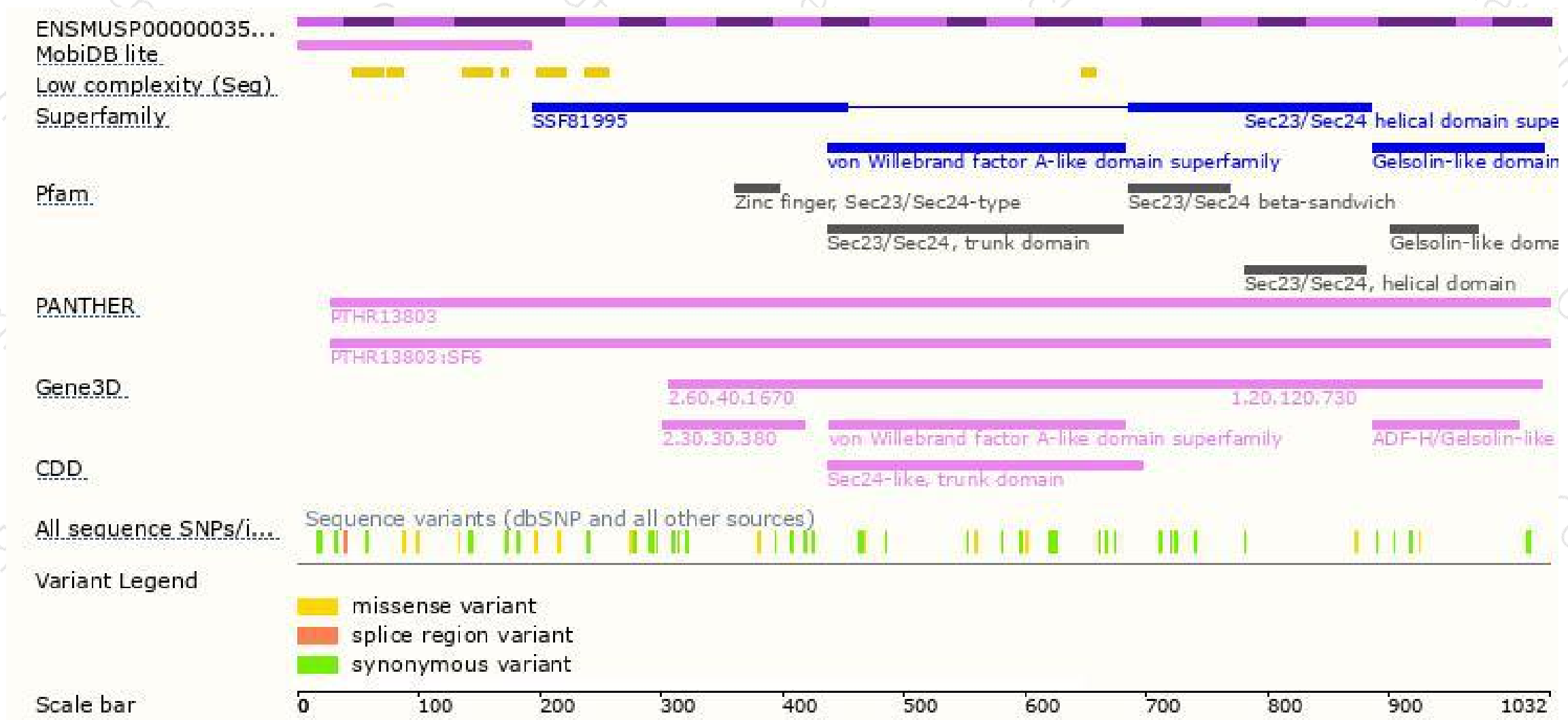


# Genomic location distribution

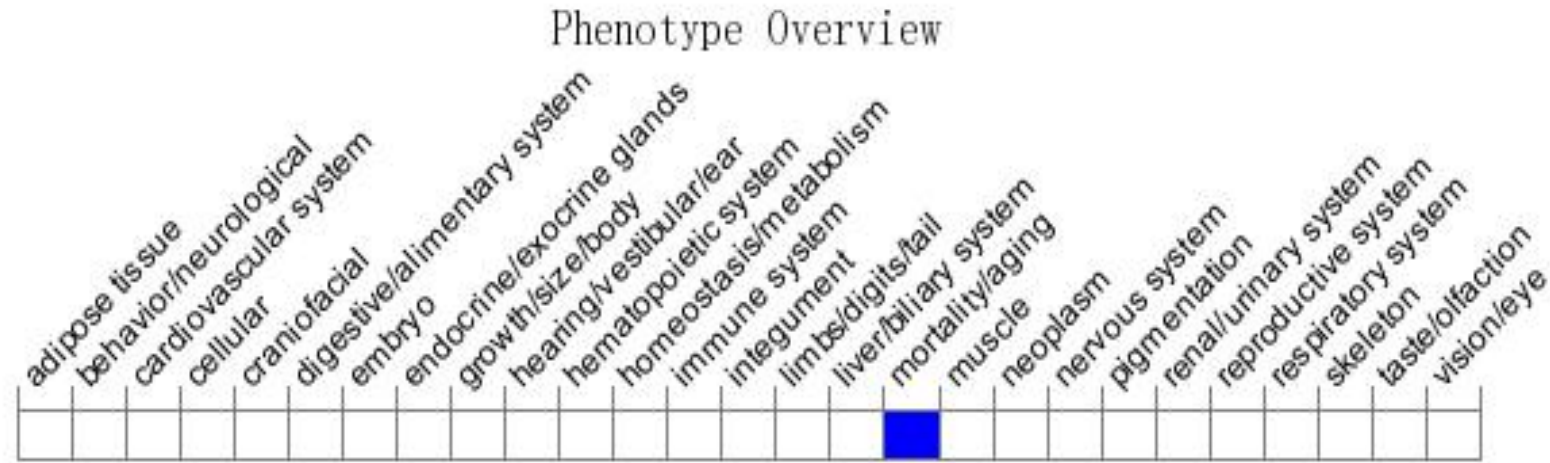




# Protein domain



# 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 early embryonic lethality. A hypomorphic gene trap allele results in lethality during organogenesis.

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

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