

# *Pdlim7* Cas9-CKO Strategy

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**Reviewer: Xueting Zhang**

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# Project Overview

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**Project Name**

*Pdlim7*

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**Project type**

**Cas9-CKO**

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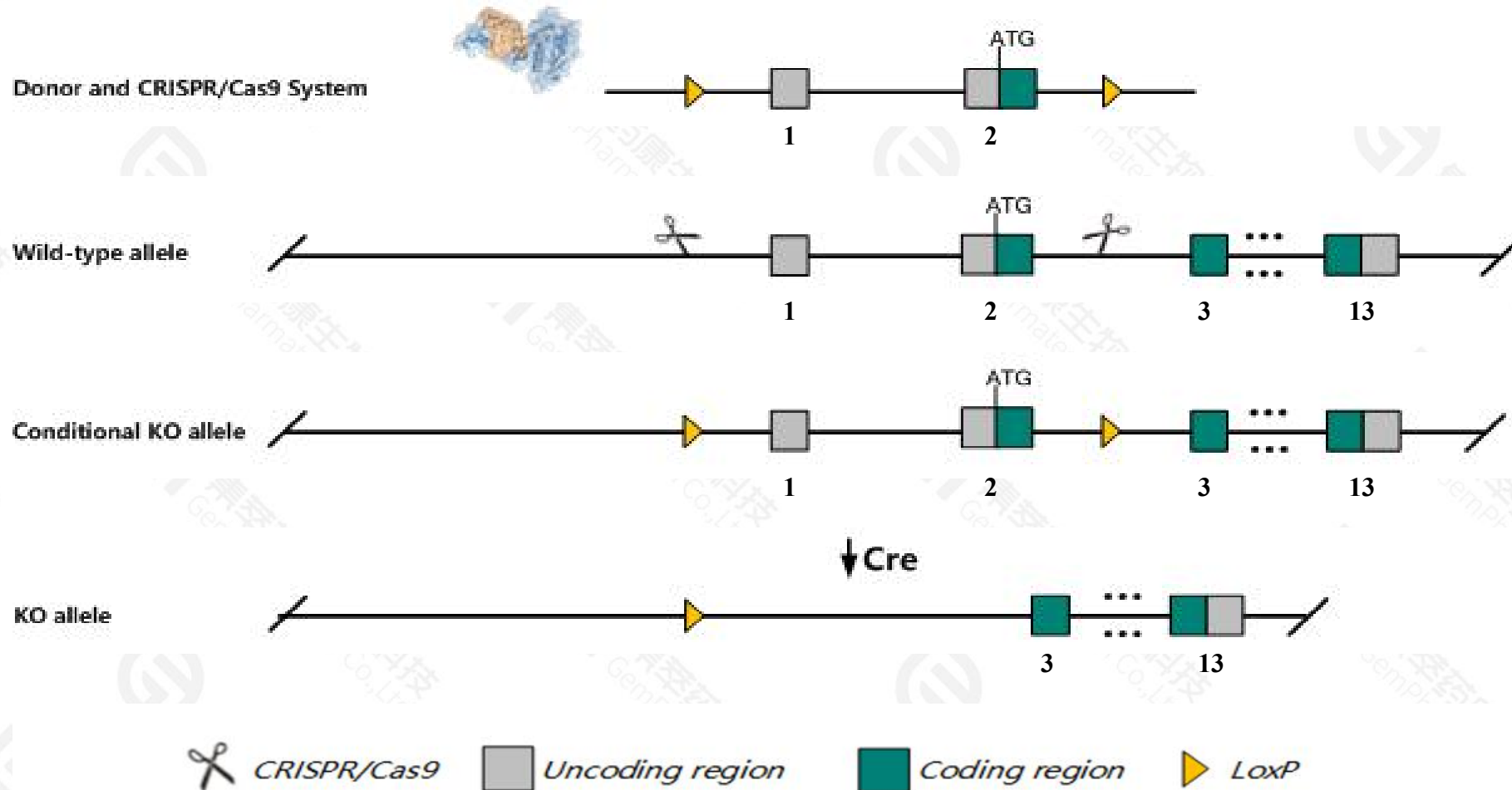
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pdlim7* gene. The schematic diagram is as follows:



- The *Pdlim7* gene has 11 transcripts. According to the structure of *Pdlim7* gene, exon1-exon2 of *Pdlim7*-201(ENSMUST00000046246.13) transcript is recommended as the knockout region. The region contains start codon ATG coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pdlim7* 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 gene trap allele exhibit heart defects and hemostatic dysfunction.
- KO region is close to the 5-terminal of *Mir6945* gene, which may affect the 5-terminal regulation of *Mir6945* gene.
- The *Pdlim7* gene is located on the Chr13. 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)

## Pdlim7 PDZ and LIM domain 7 [Mus musculus (house mouse)]

Gene ID: 67399, updated on 31-Jan-2019

### Summary



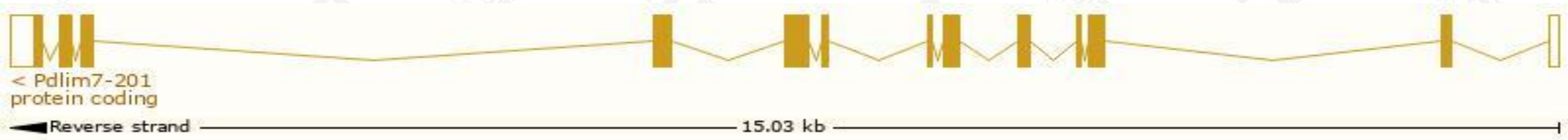
<b>Official Symbol</b>	Pdlim7 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	PDZ and LIM domain 7 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1914649</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000021493</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</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>	LMP
<b>Expression</b>	Broad expression in bladder adult (RPKM 74.8), ovary adult (RPKM 59.7) and 26 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

The gene has 11 transcripts,all transcripts are shown below:

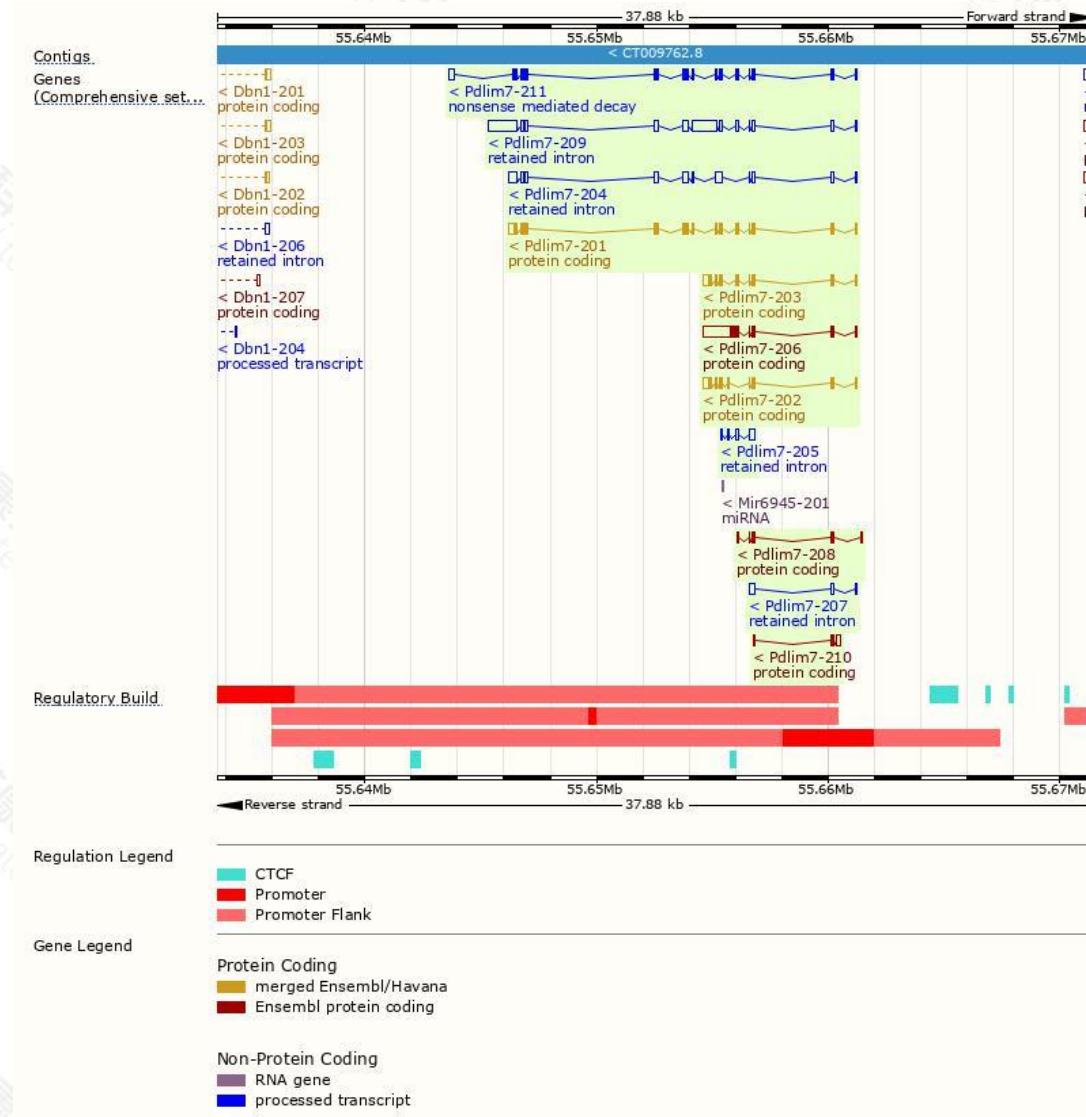
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pdlim7-201	<a href="#">ENSMUST00000046246.12</a>	1697	<a href="#">457aa</a>	Protein coding	<a href="#">CCDS49275</a>	<a href="#">Q3TJD7</a>	TSL:1 GENCODE basic APPRIS P1
Pdlim7-203	<a href="#">ENSMUST00000069968.12</a>	1006	<a href="#">222aa</a>	Protein coding	<a href="#">CCDS49276</a>	<a href="#">Q8BVJ7</a>	TSL:1 GENCODE basic
Pdlim7-202	<a href="#">ENSMUST00000069929.12</a>	899	<a href="#">188aa</a>	Protein coding	<a href="#">CCDS26547</a>	<a href="#">Q3TJD7</a>	TSL:1 GENCODE basic
Pdlim7-206	<a href="#">ENSMUST00000131306.7</a>	1915	<a href="#">219aa</a>	Protein coding	-	<a href="#">B8JJB3</a>	TSL:2 GENCODE basic
Pdlim7-208	<a href="#">ENSMUST00000144288.7</a>	457	<a href="#">124aa</a>	Protein coding	-	<a href="#">B8JJB2</a>	CDS 3' incomplete TSL:5
Pdlim7-210	<a href="#">ENSMUST00000153426.1</a>	365	<a href="#">58aa</a>	Protein coding	-	<a href="#">B8JJB1</a>	CDS 3' incomplete TSL:3
Pdlim7-211	<a href="#">ENSMUST00000155098.7</a>	1756	<a href="#">457aa</a>	Nonsense mediated decay	<a href="#">CCDS49275</a>	<a href="#">Q3TJD7</a>	TSL:1
Pdlim7-209	<a href="#">ENSMUST00000153230.7</a>	3573	No protein	Retained intron	-	-	TSL:2
Pdlim7-204	<a href="#">ENSMUST00000128910.7</a>	1694	No protein	Retained intron	-	-	TSL:2
Pdlim7-205	<a href="#">ENSMUST00000128911.1</a>	450	No protein	Retained intron	-	-	TSL:3
Pdlim7-207	<a href="#">ENSMUST00000136583.1</a>	396	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Pdlim7-201* transcript,the transcription is shown below:



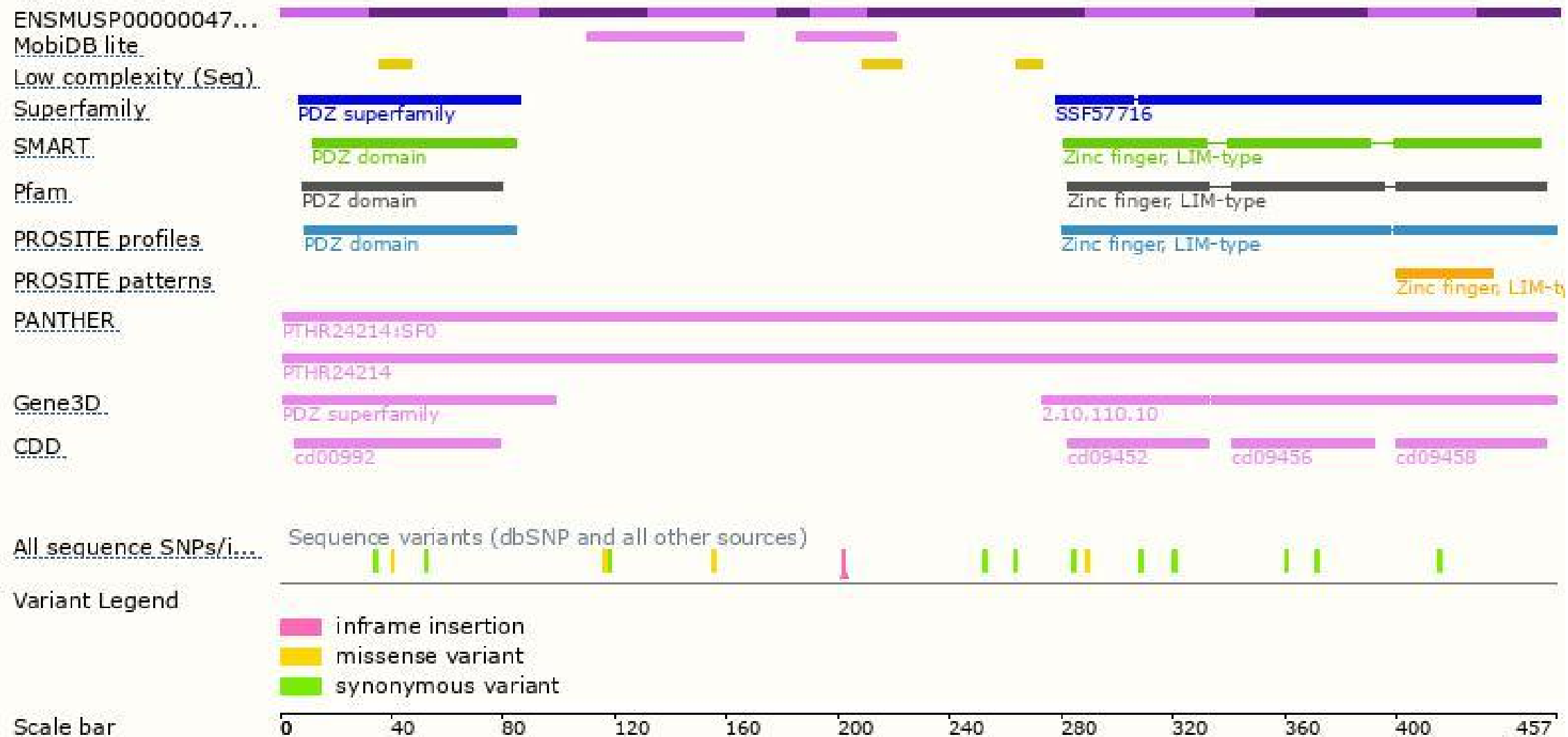


# Genomic location distribution

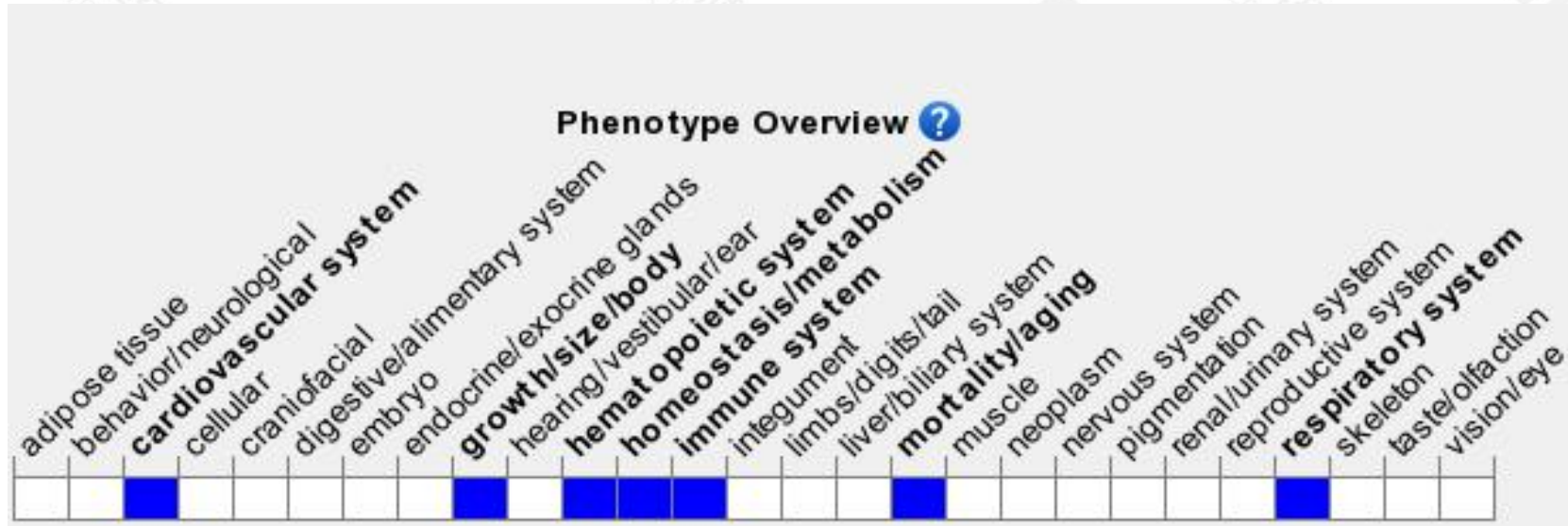




# Protein domain



# 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 gene trap allele exhibit heart defects and hemostatic dysfunction.

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