

# *Masp1* Cas9-CKO Strategy

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**Reviewer: Daohua Xu**

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# Project Overview

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**Project Name**

*Masp1*

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**Project type**

**Cas9-CKO**

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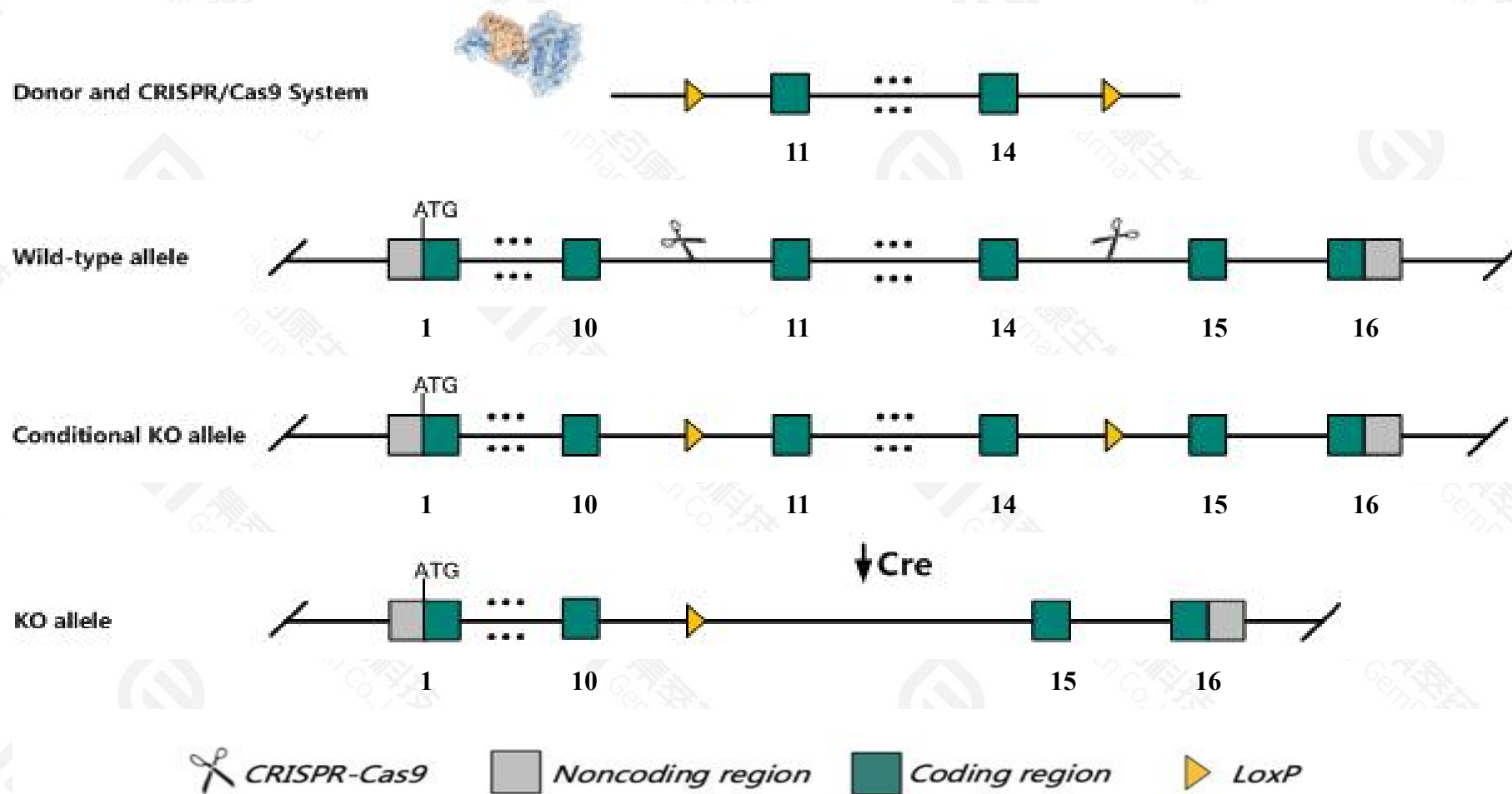
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Masp1* gene. The schematic diagram is as follows:



- The *Masp1* gene has 4 transcripts. According to the structure of *Masp1* gene, exon11-exon14 of *Masp1*-201(ENSMUST00000089883.7) transcript is recommended as the knockout region. The region contains 506 bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Masp1* 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 knockout allele display decreased survivor rate, reduced body weight, and impaired activation of the lectin and alternative complement pathways.
- The *Maspl* gene is located on the Chr16. 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)



## Masp1 mannan-binding lectin serine peptidase 1 [ *Mus musculus* (house mouse) ]

Gene ID: 17174, updated on 24-Apr-2022

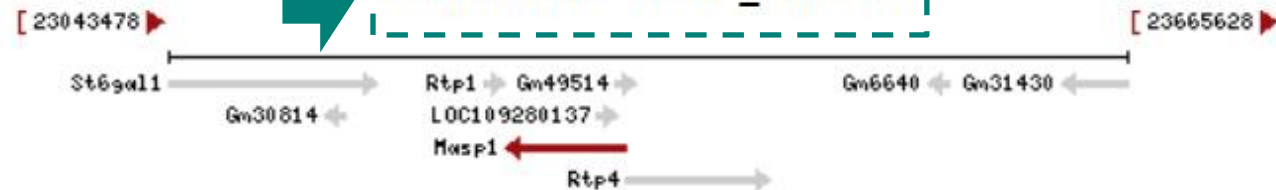
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### Summary

<b>Official Symbol</b>	Masp1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	mannan-binding lectin serine peptidase 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:88492</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000022887</a> <a href="#">AllianceGenome:MGI:88492</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>	CCPII; Crarf; Masp1/3; AW048060
<b>Summary</b>	Enables serine-type endopeptidase activity. Involved in complement activation, lectin pathway. Located in extracellular space. Is expressed in several structures, including alimentary system; brain; genitourinary system; liver; and spleen. Human ortholog(s) of this gene implicated in 3MC syndrome 1. Orthologous to human MASP1 (MBL associated serine protease 1). [provided by Alliance of Genome Resources, Apr 2022]
<b>Expression</b>	Broad expression in adrenal adult (RPKM 13.8), liver adult (RPKM 12.9) and 16 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>
<b>NEW</b>	Try the new <a href="#">Gene table</a> Try the new <a href="#">Transcript table</a>



### Chromosome 16 - NC\_000082.7

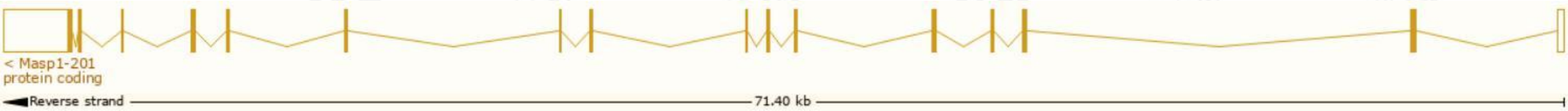


# Transcript information (Ensembl)

The gene has 4 transcripts,all transcripts are shown below:

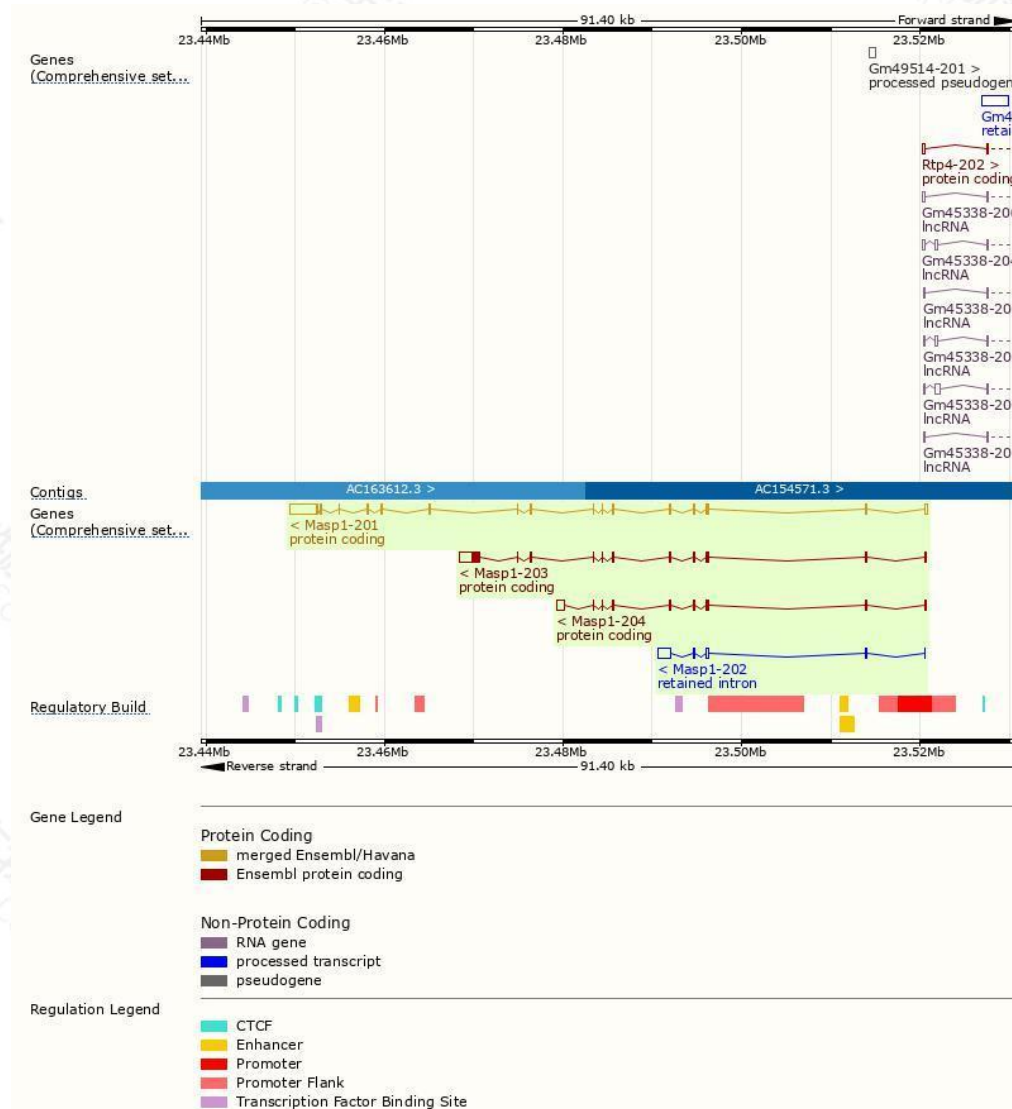
Show/hide columns <span>Filter</span>								
Transcript ID	Name	bp	Protein	Translation ID	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000089883.7</a>	Masp1-201	5345	<a href="#">704aa</a>	<a href="#">ENSMUSP00000087327.6</a>	Protein coding	<a href="#">CCDS37303</a>	<a href="#">P98064-1</a>	GENCODE basic APPRIS P1 TSL:1
<a href="#">ENSMUST00000229152.2</a>	Masp1-202	2093	No protein	-	Retained intron		-	-
<a href="#">ENSMUST00000229619.2</a>	Masp1-203	3786	<a href="#">733aa</a>	<a href="#">ENSMUSP00000155665.2</a>	Protein coding		<a href="#">P98064-2</a>	Ensembl Canonical GENCODE basic
<a href="#">ENSMUST00000230040.2</a>	Masp1-204	2035	<a href="#">385aa</a>	<a href="#">ENSMUSP00000155343.2</a>	Protein coding		<a href="#">A0A2R8VHR3</a>	GENCODE basic

The strategy is based on the design of *Masp1-201* transcript,the transcription is shown below:



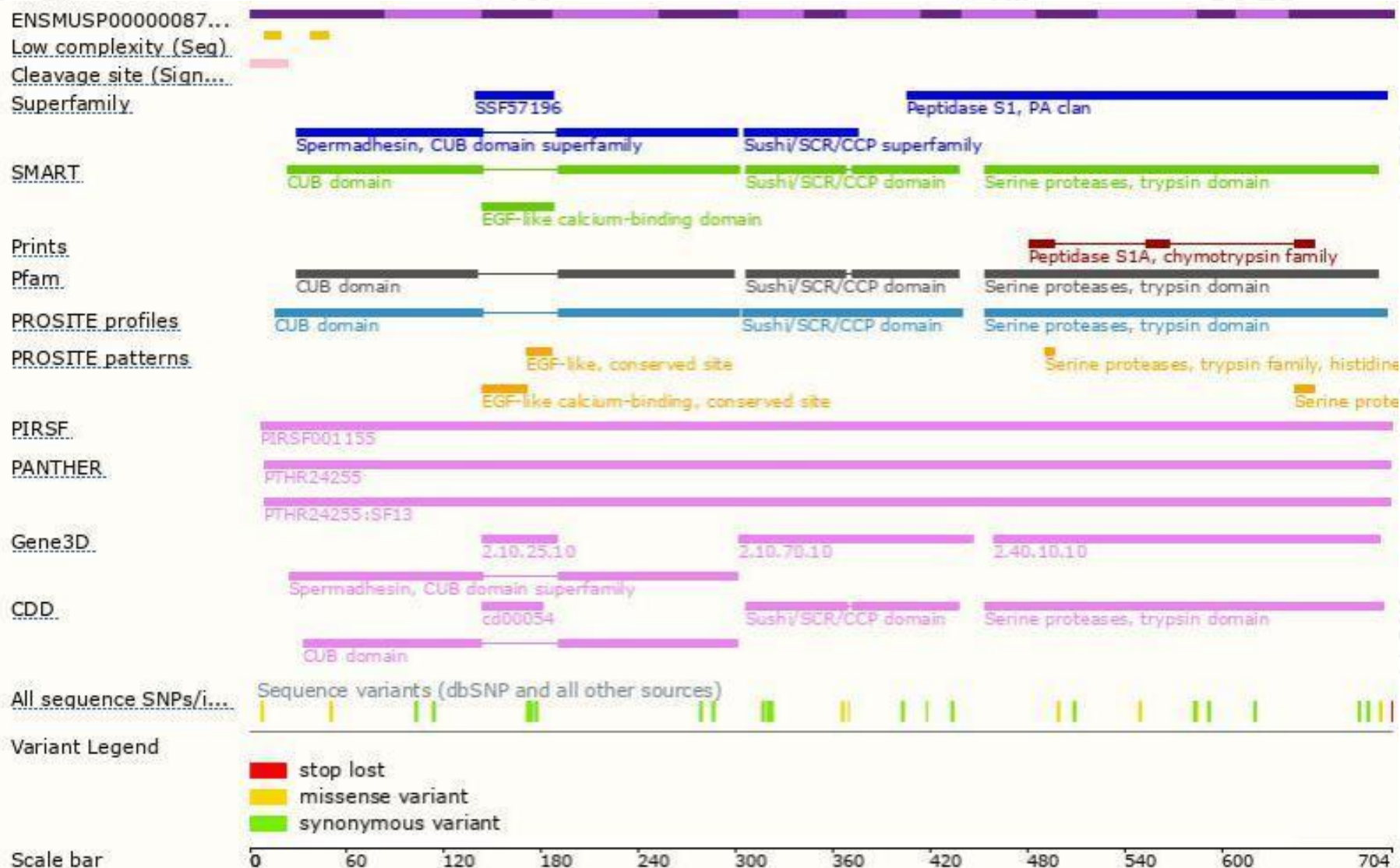


# Genomic location distribution

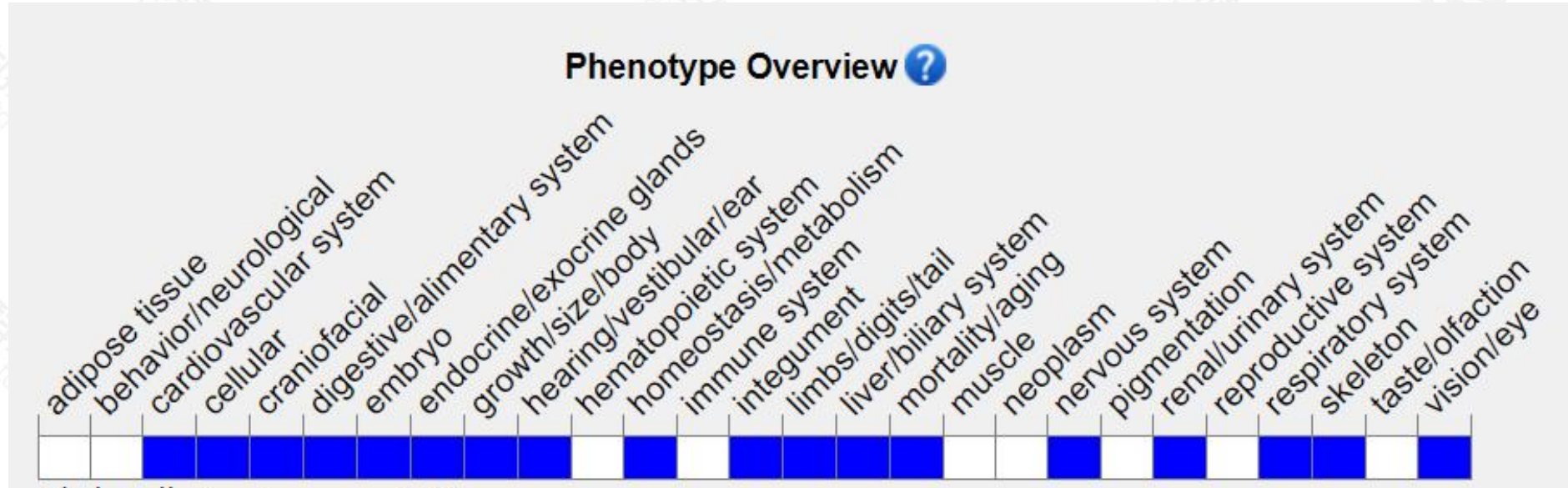




# Protein domain



# Mouse phenotype description(MGI)



<http://www.informatics.jax.org/marker/MGI:88492>

Mice homozygous for a knockout allele display decreased survivor rate, reduced body weight, and impaired activation of the lectin and alternative complement pathways.

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