

# *Plaur* Cas9-CKO Strategy

**Designer:**

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**Design Date:**

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# Project Overview

**Project Name**

*Plaur*

**Project type**

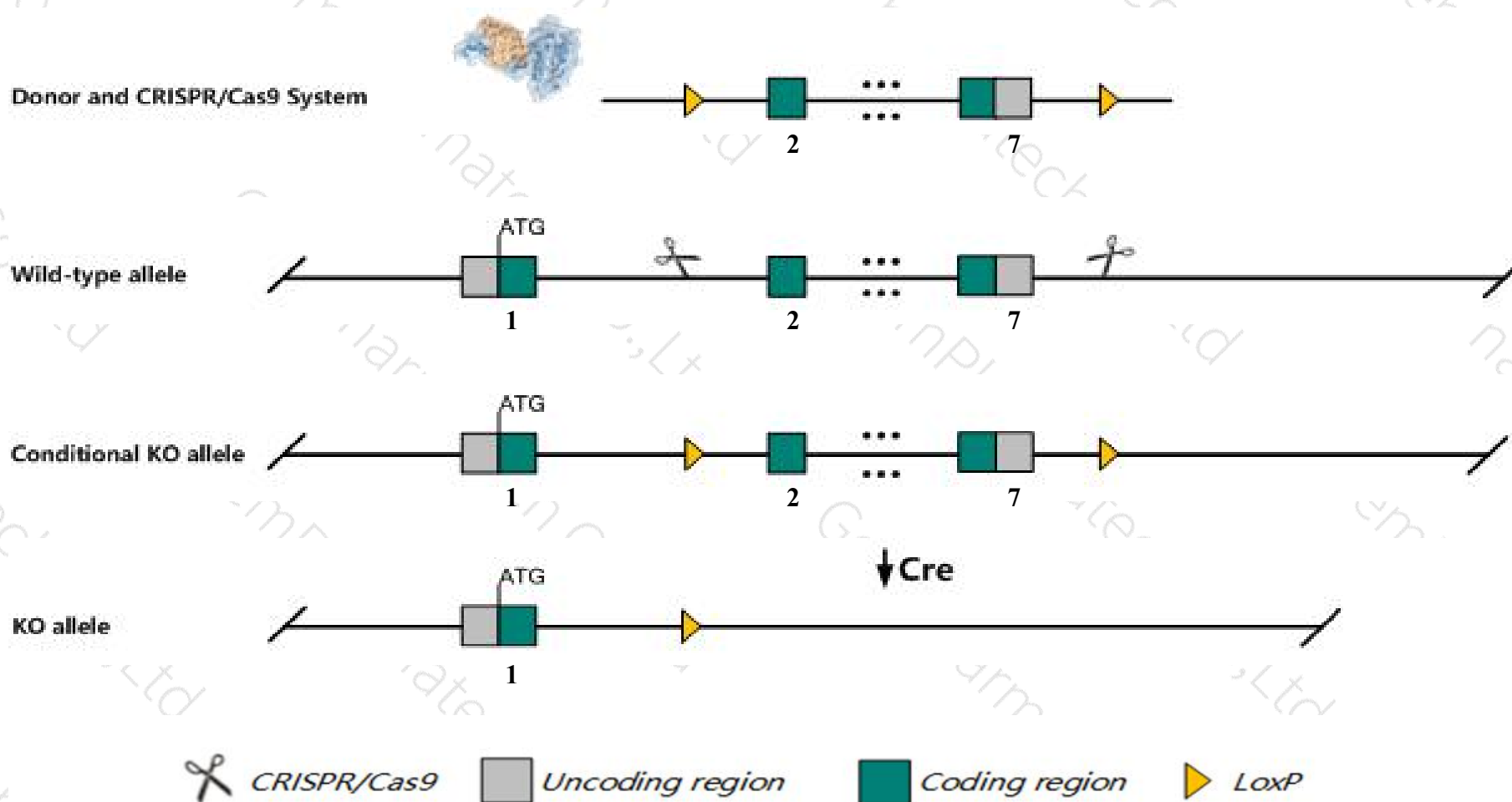
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



- The *Plaur* gene has 6 transcripts. According to the structure of *Plaur* gene, exon2-exon7 of *Plaur-201* (ENSMUST00000002284.10) transcript is recommended as the knockout region. The region contains 926bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Plaur* 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, Homozygotes for a null allele exhibit chronic inflammation, macrophage dysfunction, and reduced angiogenesis. Homozygotes for another null allele show neutrophil dysfunction, increased anxiety, loss of GABAergic neurons, myoclonus, and susceptibility to bacterial infection and PTZ -induced seizures.
- The *Plaur* 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)

## Plaur plasminogen activator, urokinase receptor [Mus musculus (house mouse)]

Gene ID: 18793, updated on 31-Jan-2019

### Summary



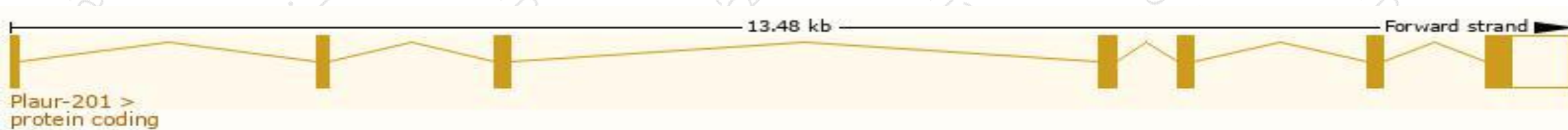
<b>Official Symbol</b>	Plaur provided by <a href="#">MGI</a>
<b>Official Full Name</b>	plasminogen activator, urokinase receptor provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:97612</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000046223</a>
<b>Gene type</b>	protein coding
<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>	Cd87, u-PAR, uPAR
<b>Expression</b>	Broad expression in lung adult (RPKM 24.3), spleen adult (RPKM 16.2) and 16 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

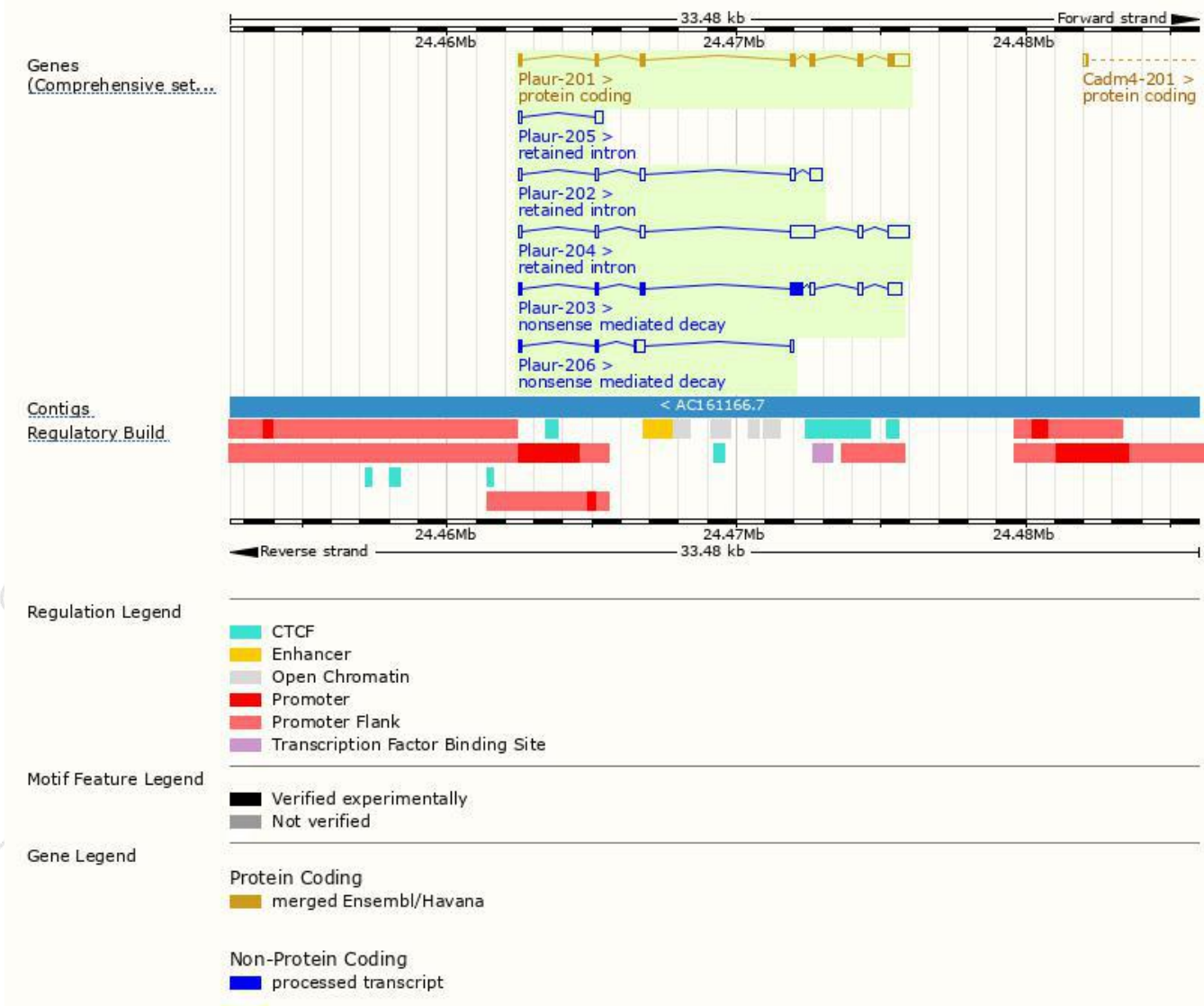
The gene has 6 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plaur-201	<a href="#">ENSMUST00000002284.10</a>	1506	<a href="#">327aa</a>	Protein coding	<a href="#">CCDS20950</a>	<a href="#">P35456 Q545X5</a>	TSL:1 GENCODE basic APPRIS P1
Plaur-203	<a href="#">ENSMUST00000206514.1</a>	1456	<a href="#">222aa</a>	Nonsense mediated decay	-	<a href="#">A0A0U1RNN0</a>	TSL:1
Plaur-206	<a href="#">ENSMUST00000206935.1</a>	604	<a href="#">74aa</a>	Nonsense mediated decay	-	<a href="#">A0A0U1RNF3</a>	TSL:3
Plaur-204	<a href="#">ENSMUST00000206636.1</a>	2009	No protein	Retained intron	-	-	TSL:2
Plaur-202	<a href="#">ENSMUST00000205877.1</a>	872	No protein	Retained intron	-	-	TSL:2
Plaur-205	<a href="#">ENSMUST00000206693.1</a>	347	No protein	Retained intron	-	-	TSL:3

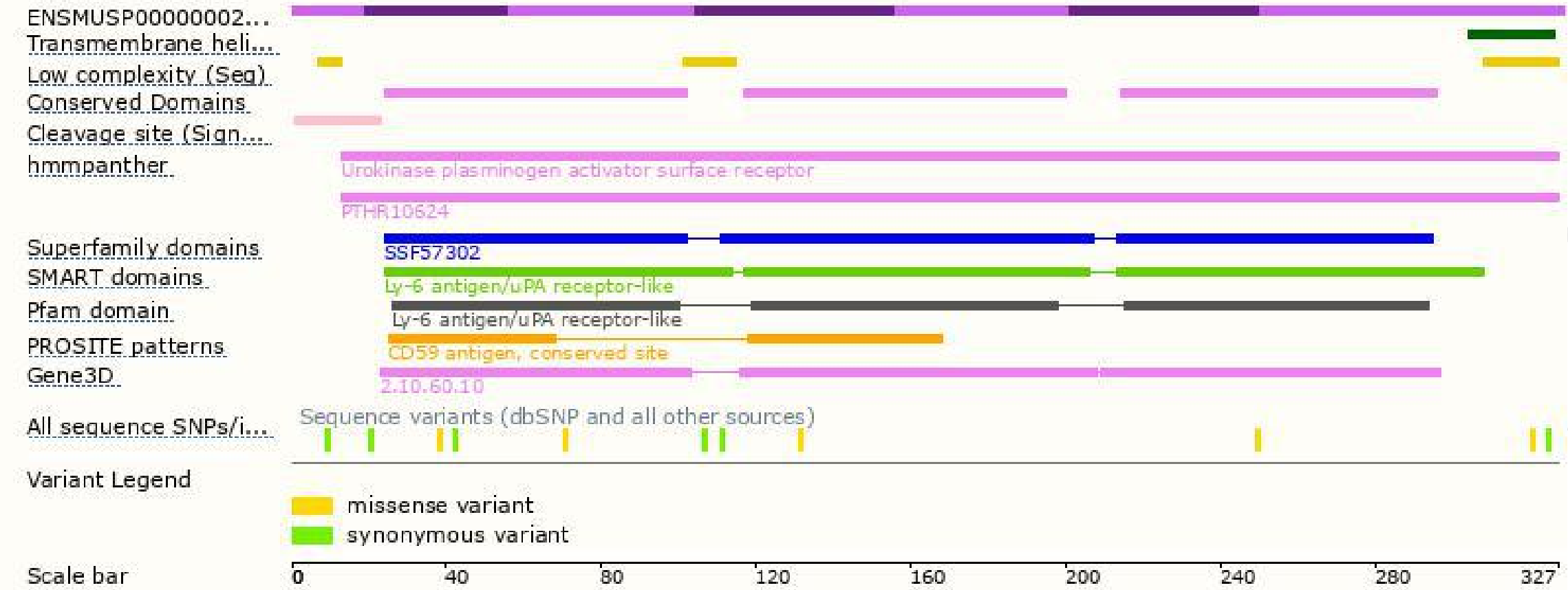
The strategy is based on the design of *Plaur-201* transcript, The transcription is shown below



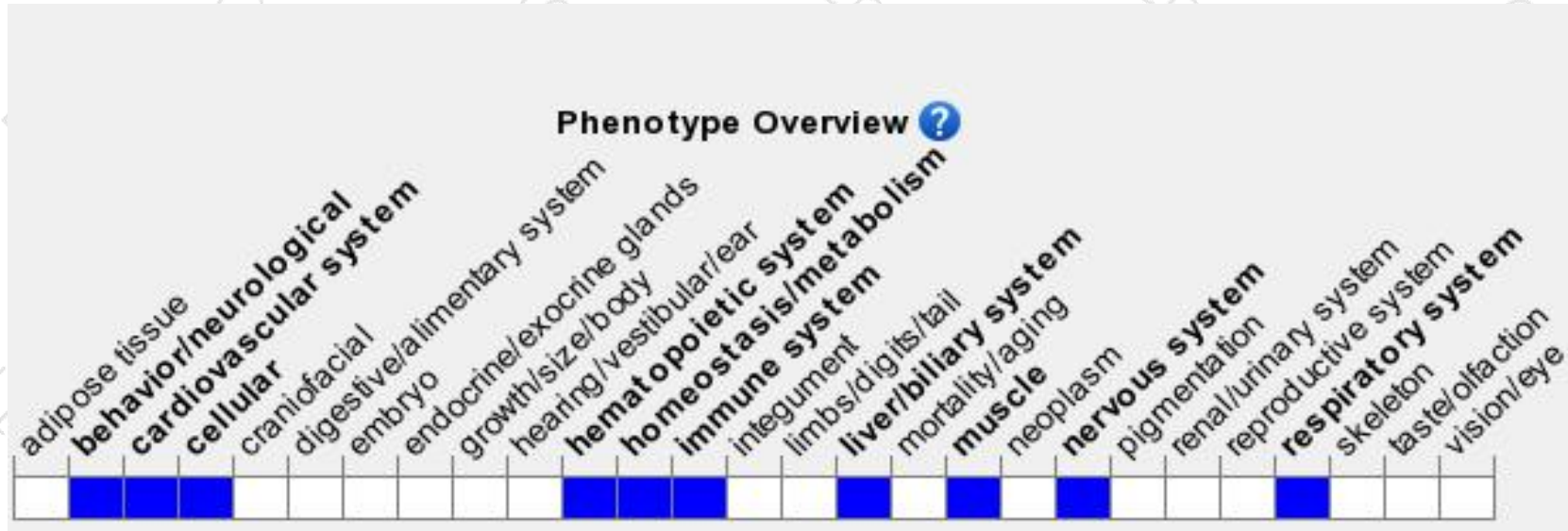
# Genomic location distribution



# 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, Homozygotes for a null allele exhibit chronic inflammation, macrophage dysfunction, and reduced angiogenesis. Homozygotes for another null allele show neutrophil dysfunction, increased anxiety, GABAergic neurons, myoclonus, and susceptibility to bacterial infection and PTZ -induced seizures.

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

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