

# *Mapk3* Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Mapk3*

**Project type**

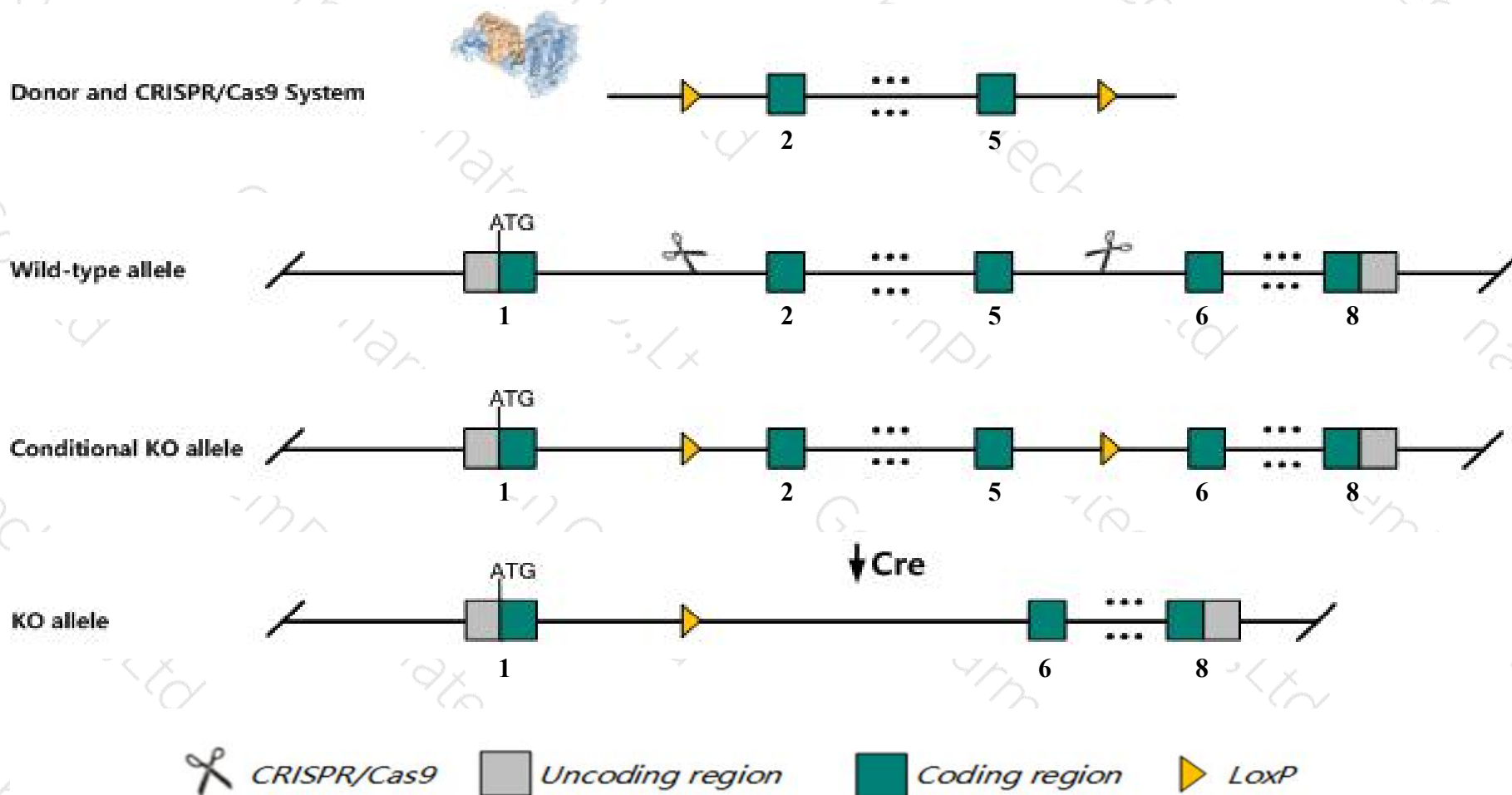
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mapk3* gene. The schematic diagram is as follows:



- The *Mapk3* gene has 8 transcripts. According to the structure of *Mapk3* gene, exon2-exon5 of *Mapk3-202* (ENSMUST00000057669.15) transcript is recommended as the knockout region. The region contains 605bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mapk3* 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 targeted null mutation are hyperactive with impaired T cell maturation and proliferation. Mice homozygous for a knock-out allele on a CD-1 background exhibit normal Mendelian ratios, growth, and no obvious abnormalities.
- The floxed region is near to the N-terminal of *Gdpc3* gene, this strategy may influence the regulatory function of the N-terminal of *Gdpc3* gene.
- The *Mapk3* 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)

## Mapk3 mitogen-activated protein kinase 3 [Mus musculus (house mouse)]

Gene ID: 26417, updated on 19-Mar-2019

### Summary



<b>Official Symbol</b>	Mapk3 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	mitogen-activated protein kinase 3 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1346859</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000063065</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>	Erk-1, Erk1, Er12, Esrk1, Mnk1, Mtap2k, Prkm3, p44, p44erk1, p44mapk
<b>Expression</b>	Ubiquitous expression in colon adult (RPKM 245.8), large intestine adult (RPKM 217.1) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

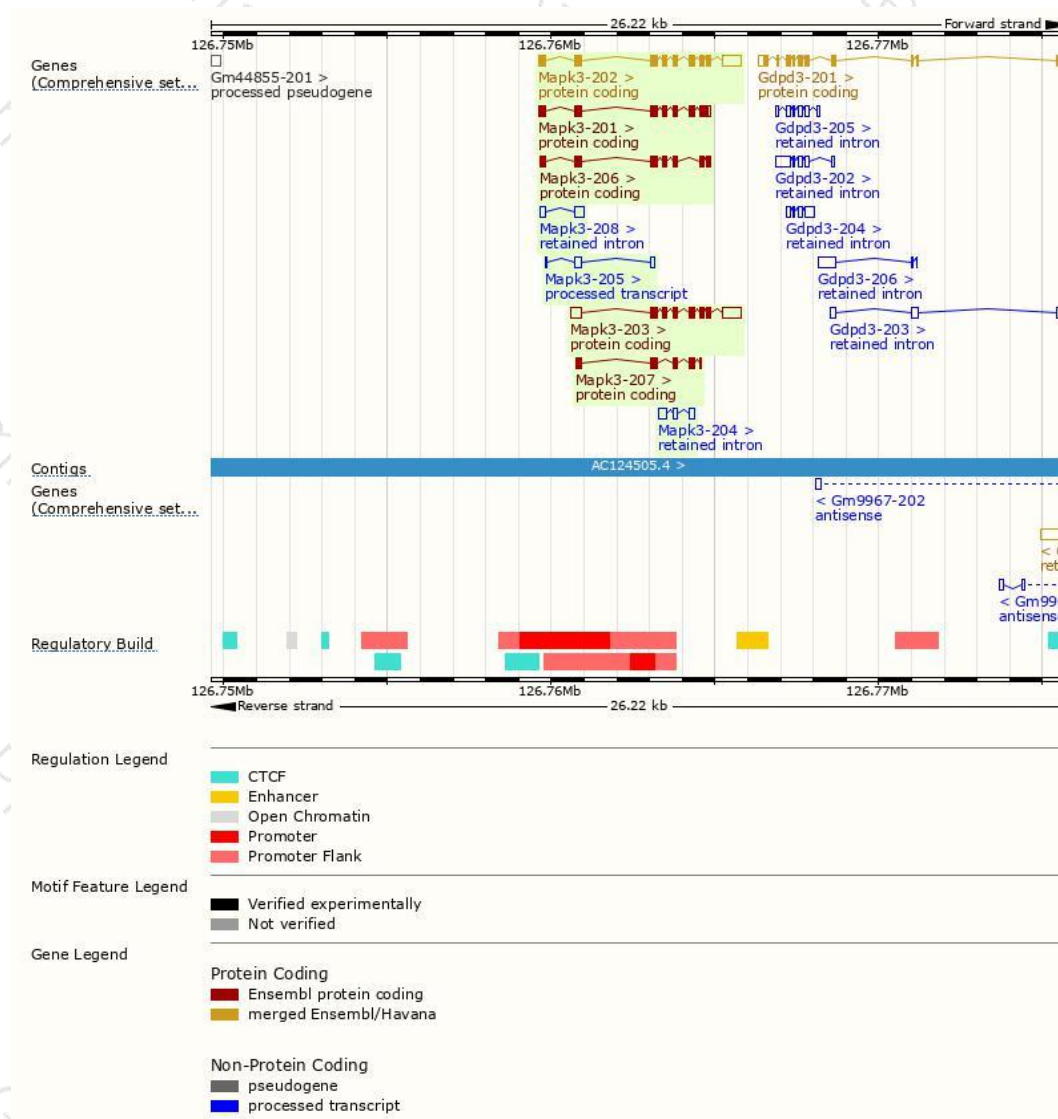
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mapk3-202	<a href="#">ENSMUST00000057669.15</a>	1800	<a href="#">380aa</a>	Protein coding	<a href="#">CCDS21841</a>	<a href="#">Q63844</a>	TSL:1 GENCODE basic APPRIS P2
Mapk3-203	<a href="#">ENSMUST00000091328.3</a>	1716	<a href="#">265aa</a>	Protein coding	-	<a href="#">D3Z6D8</a>	TSL:1 GENCODE basic
Mapk3-201	<a href="#">ENSMUST00000050201.10</a>	1267	<a href="#">380aa</a>	Protein coding	-	<a href="#">D3Z3G6</a>	TSL:3 GENCODE basic APPRIS ALT2
Mapk3-206	<a href="#">ENSMUST00000205657.1</a>	1005	<a href="#">335aa</a>	Protein coding	-	<a href="#">A0A0U1RPX4</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 APPRIS ALT2
Mapk3-207	<a href="#">ENSMUST00000206272.1</a>	641	<a href="#">214aa</a>	Protein coding	-	<a href="#">A0A0U1RPZ0</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Mapk3-205	<a href="#">ENSMUST00000145965.1</a>	337	No protein	Processed transcript	-	-	TSL:5
Mapk3-204	<a href="#">ENSMUST00000135649.1</a>	480	No protein	Retained intron	-	-	TSL:3
Mapk3-208	<a href="#">ENSMUST00000206875.1</a>	436	No protein	Retained intron	-	-	TSL:2

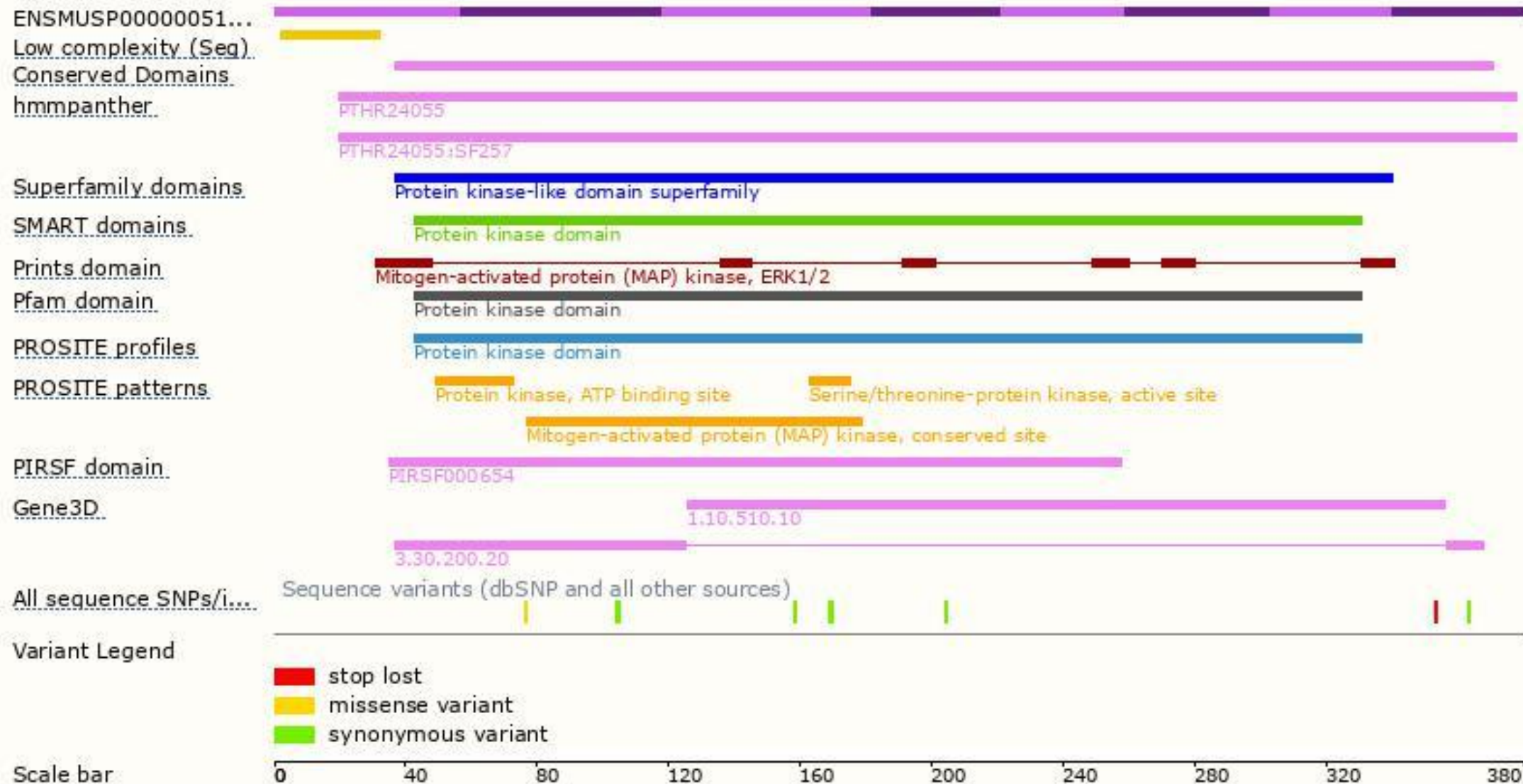
The strategy is based on the design of *Mapk3-202* transcript,The transcription is shown below



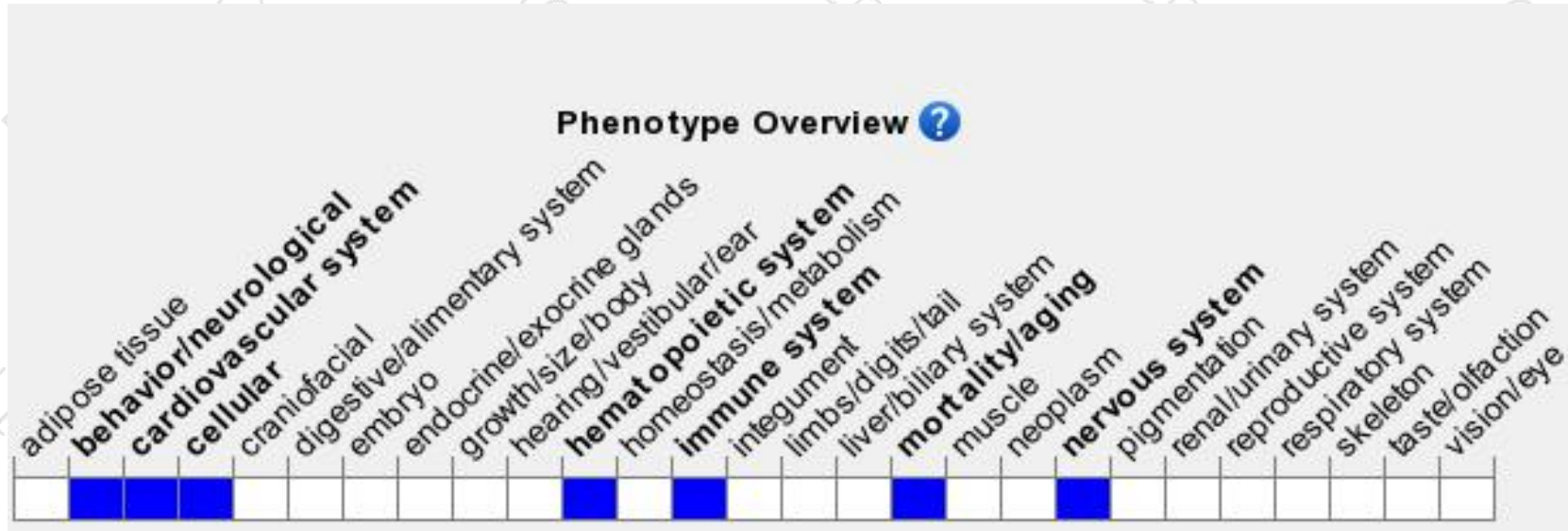
# Genomic location distribution



# 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 targeted null mutation are hyperactive with impaired T cell maturation and proliferation. Mice homozygous for a knock-out allele on a CD-1 background exhibit normal Mendelian ratios, growth, and no obvious abnormalities.

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

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