# *Mpz* Cas9-CKO Strategy

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**Reviewer: Shuang Zhang**

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# Project Overview

| | |
|---|---|
| **Project Name** | ***Mpz*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

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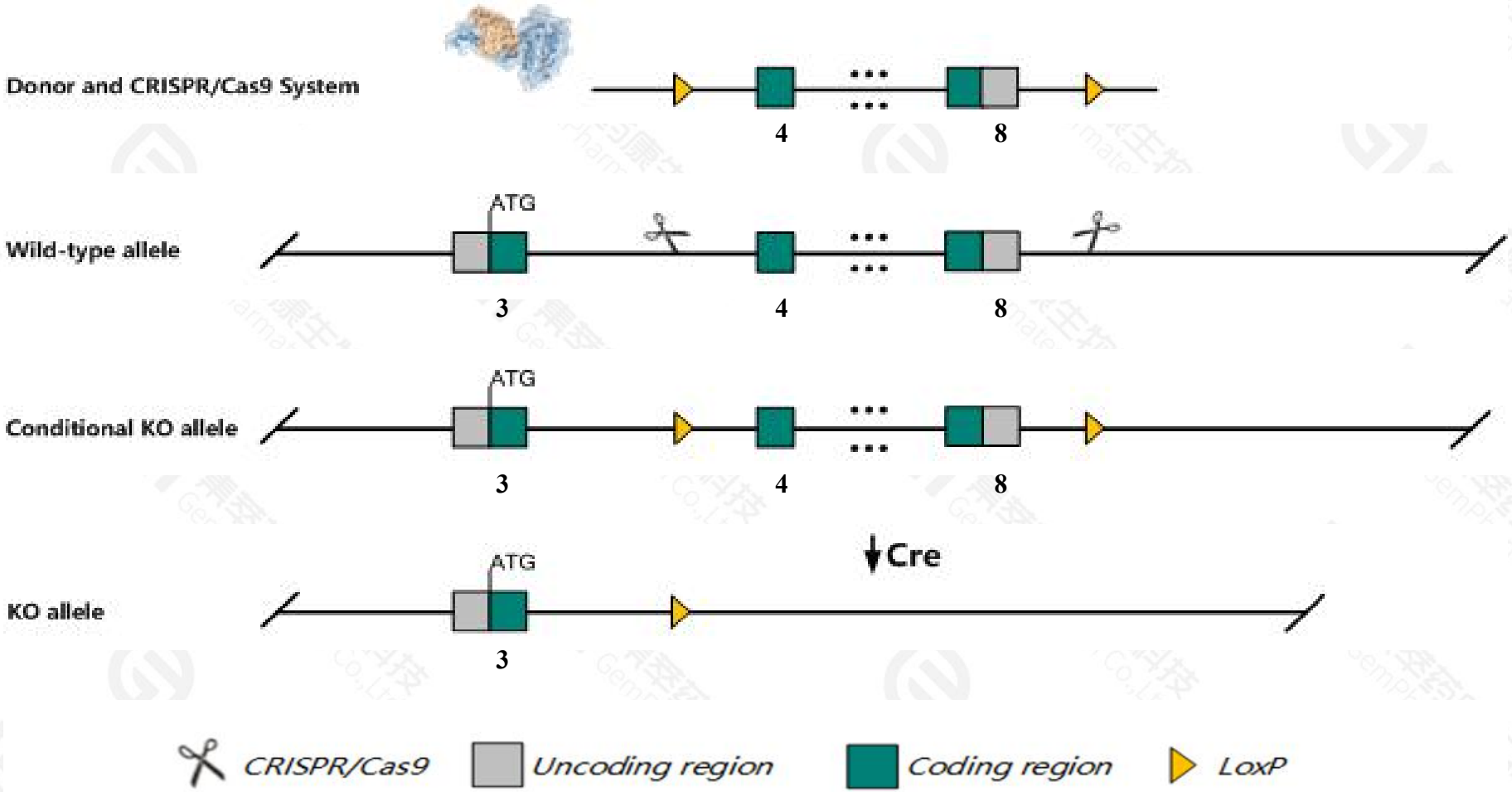
This model will use CRISPR/Cas9 technology to edit the *Mpz* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Mpz* gene has 6 transcripts. According to the structure of *Mpz* gene, exon4-exon8 of *Mpz-201*(ENSMUST00000070758.10) transcript is recommended as the knockout region.The region contains 680bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mpz* 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.

# Notice

➢ According to the existing MGI data,mice homozygous for a spontaneous mutation exhibit premature death, infertility, neurological behavior defects, and demyelination. Mice homozygous for a knock-out allele exhibit abnormal myelination and neurological behavior defects.

➢ The *Mpz* gene is located on the Chr1. 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）

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## Mpz myelin protein zero [Mus musculus (house mouse)]

Gene ID: 17528, updated on 14-Feb-2021

### Summary

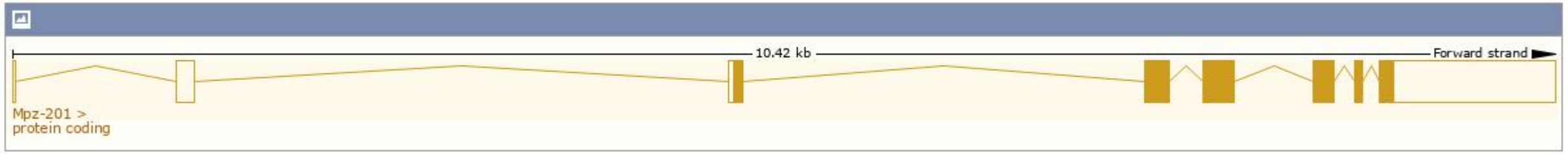
| | |
|---|---|
| **Official Symbol** | Mpz provided by MGI |
| **Official Full Name** | myelin protein zero provided byMGI |
| **Primary source** | MGI:MGI:103177 |
| **See related** | Ensembl:ENSMUSG00000056569 |
| **Gene type** | protein coding |
| **RefSeq status** | REVIEWED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | M, Mpp, P, P-zero, P0 |
| **Summary** | This gene is specifically expressed in Schwann cells of the peripheral nervous system and encodes a type I transmembrane glycoprotein that is a major structural protein of the peripheral myelin sheath. The encoded protein contains a large hydrophobic extracellular domain and a smaller basic intracellular domain, which are essential for the formation and stabilization of the multilamellar structure of the compact myelin. Mutations in the orthologous gene in human are associated with myelinating neuropathies. A recent study showed that two isoforms are produced from the same mRNA by use of alternative in-frame translation termination codons via a stop codon readthrough mechanism. Alternatively spliced transcript variants have also been found for this gene. [provided by RefSeq, Oct 2015] |
| **Expression** | Biased expression in mammary gland adult (RPKM 51.2), bladder adult (RPKM 7.6) and 2 other tissuesSee more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

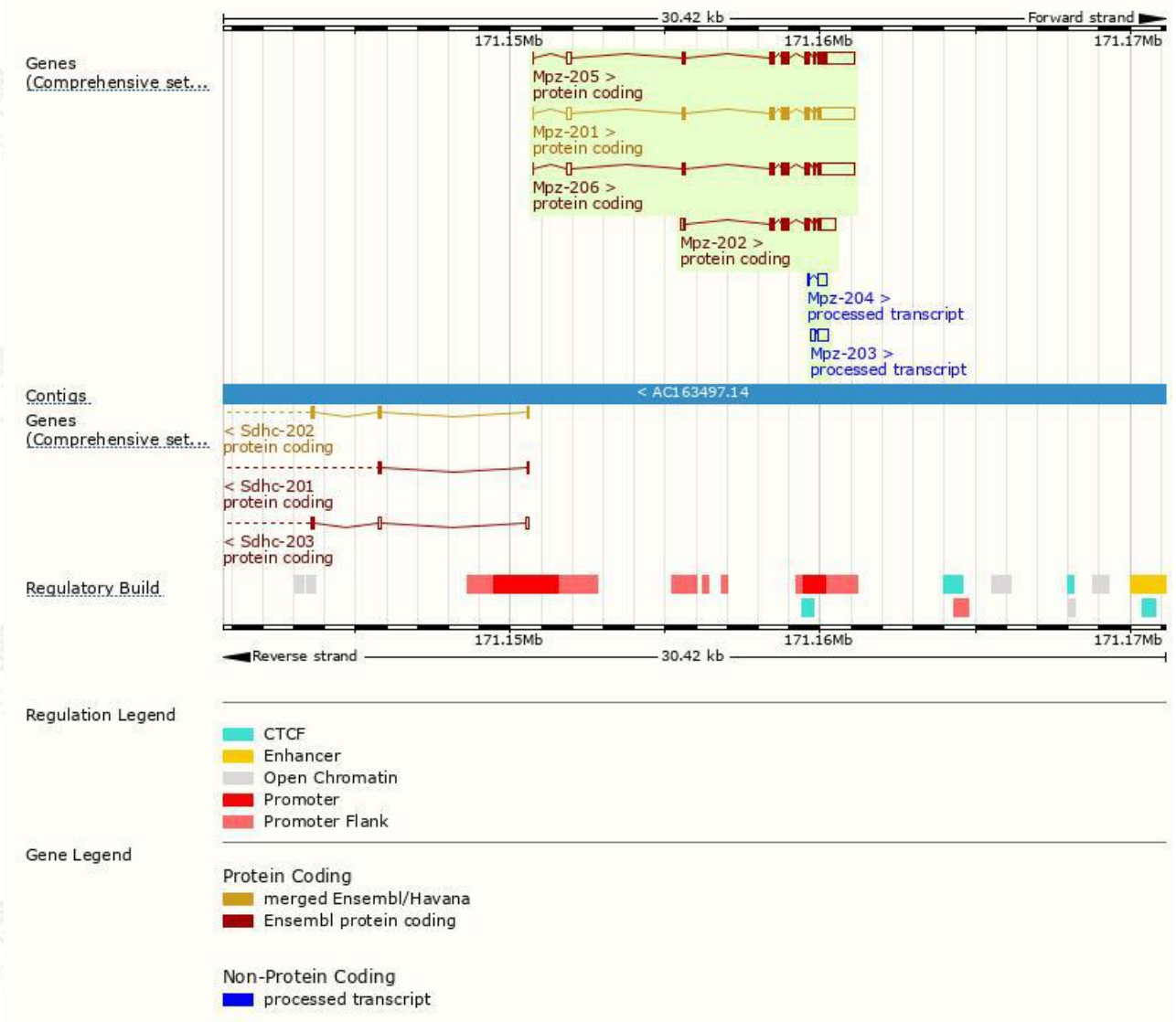
The gene has 6 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| **Mpz-201** | ENSMUST00000070758.10 | 2002 | 248aa | Protein coding | CCDS15479 | | TSL:1 , GENCODE basic , APPRIS P2 , |
| **Mpz-206** | ENSMUST00000238940.2 | 1993 | 248aa | Protein coding | CCDS15479 | | GENCODE basic , APPRIS P2 , |
| **Mpz-202** | ENSMUST00000111334.2 | 1278 | 248aa | Protein coding | CCDS15479 | | TSL:1 , GENCODE basic , APPRIS P2 , |
| **Mpz-205** | ENSMUST00000238908.2 | 2002 | 312aa | Protein coding | - | | GENCODE basic , APPRIS ALT2 , |
| **Mpz-203** | ENSMUST00000125565.2 | 436 | No protein | Processed transcript | - | | TSL:2 , |
| **Mpz-204** | ENSMUST00000149352.2 | 322 | No protein | Processed transcript | - | | TSL:3 , |

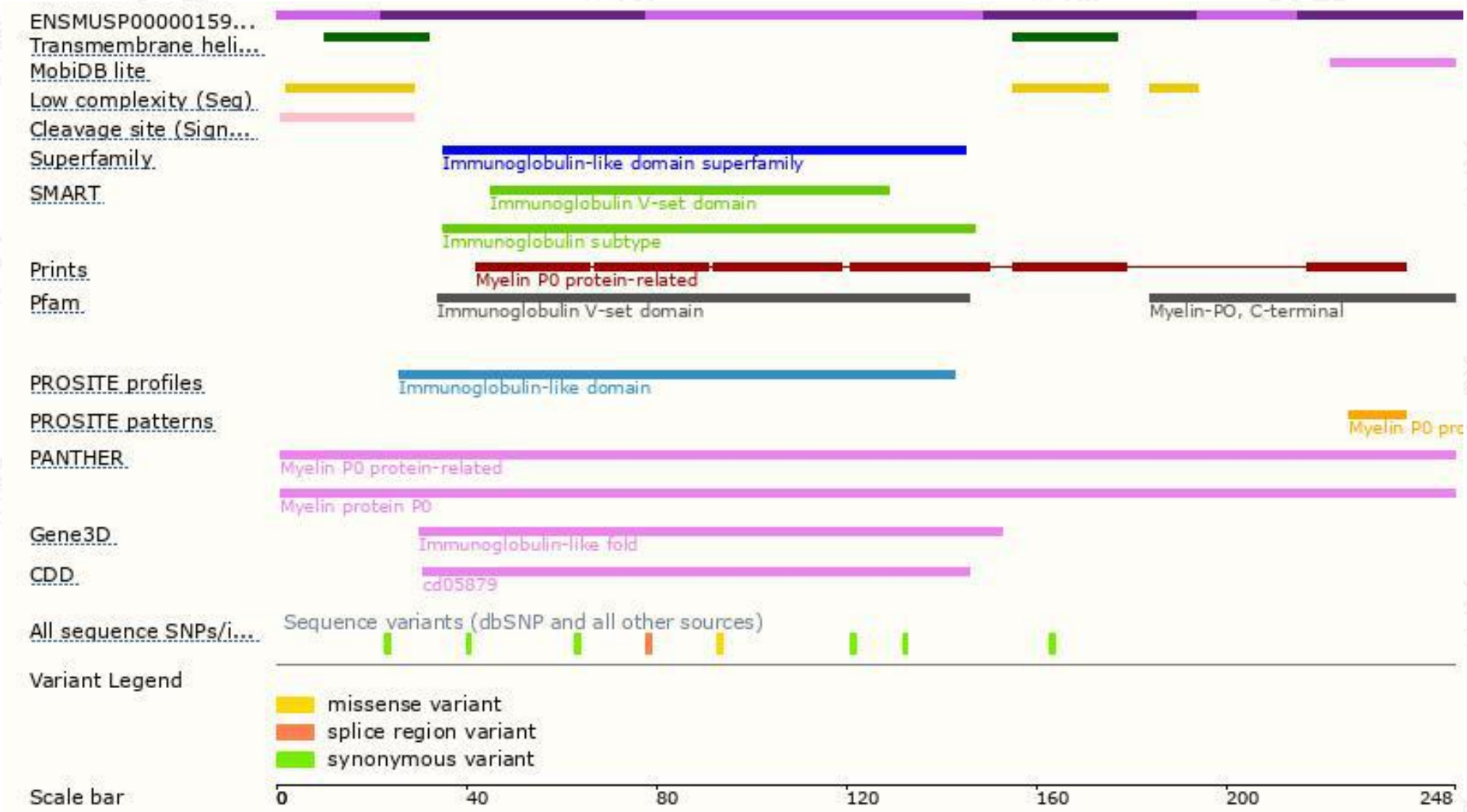
The strategy is based on the design of *Mpz-201* transcript,the transcription is shown below:



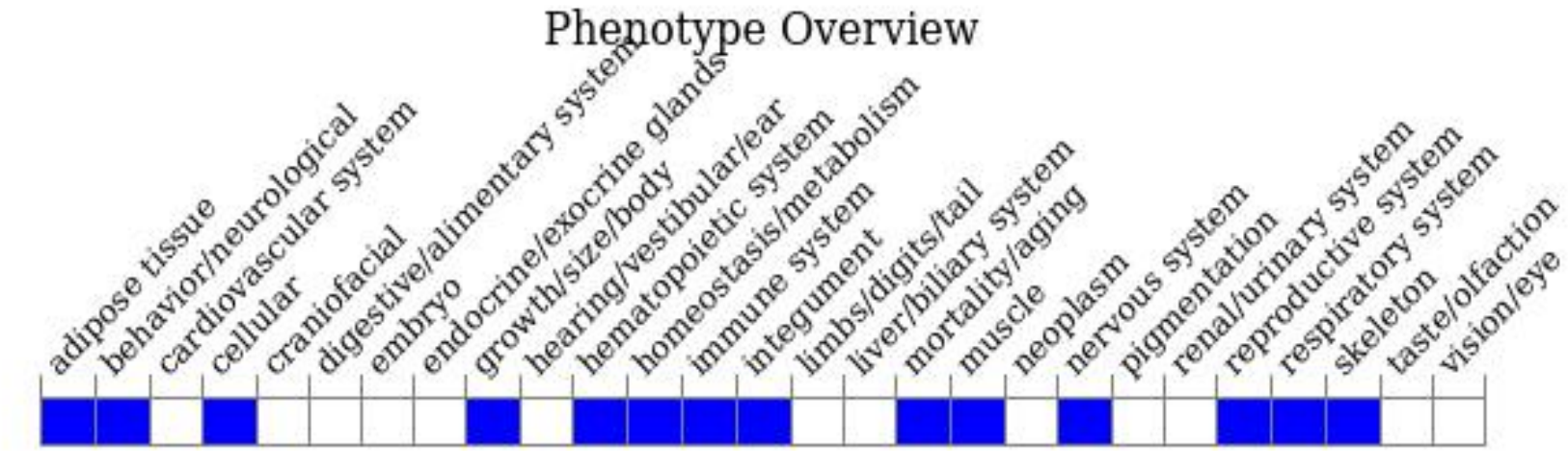
# Genomic location distribution



# 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/).*

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