

# ***Trdmt1* Cas9-KO Strategy**

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<b>Design Date:</b>	<b>2020-5-15</b>

# Project Overview

**Project Name**

***Trdmt1***

**Project type**

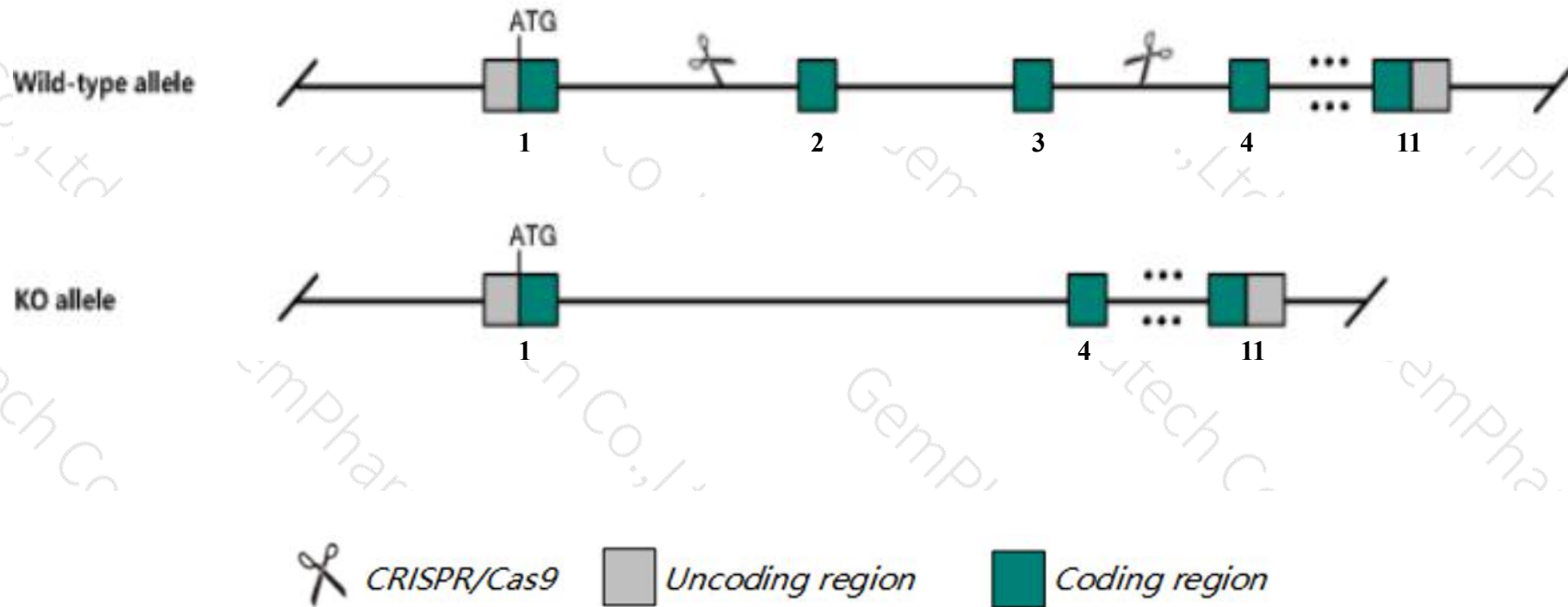
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Trdmt1* gene. The schematic diagram is as follows:



- The *Trdmt1* gene has 3 transcripts. According to the structure of *Trdmt1* gene, exon2-exon3 of *Trdmt1*-202 (ENSMUST00000124488.6) transcript is recommended as the knockout region. The region contains 187bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Trdmt1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for disruptions in this gene have a decreased proportion of natural killer cells in the peripheral blood.
- The *Trdmt1* gene is located on the Chr2. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Trdmt1 tRNA aspartic acid methyltransferase 1 [Mus musculus (house mouse)]

Gene ID: 13434, updated on 13-Mar-2020

### Summary



**Official Symbol** Trdmt1 provided by [MGI](#)

**Official Full Name** tRNA aspartic acid methyltransferase 1 provided by [MGI](#)

**Primary source** [MGI:MGI:1274787](#)

**See related** [Ensembl:ENSMUSG00000026723](#)

**Gene type** protein coding

**RefSeq status** VALIDATED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** Dnmt2, Rnmt2

**Expression** Ubiquitous expression in CNS E18 (RPKM 2.1), bladder adult (RPKM 2.0) and 27 other tissues [See more](#)

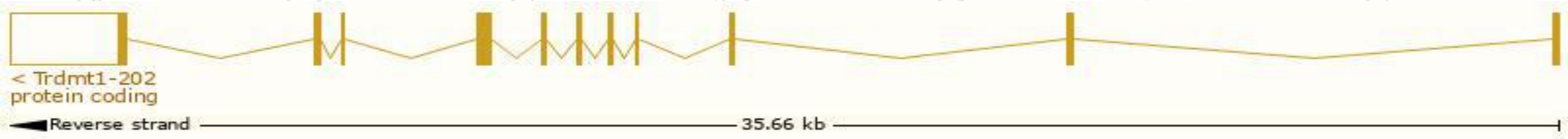
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

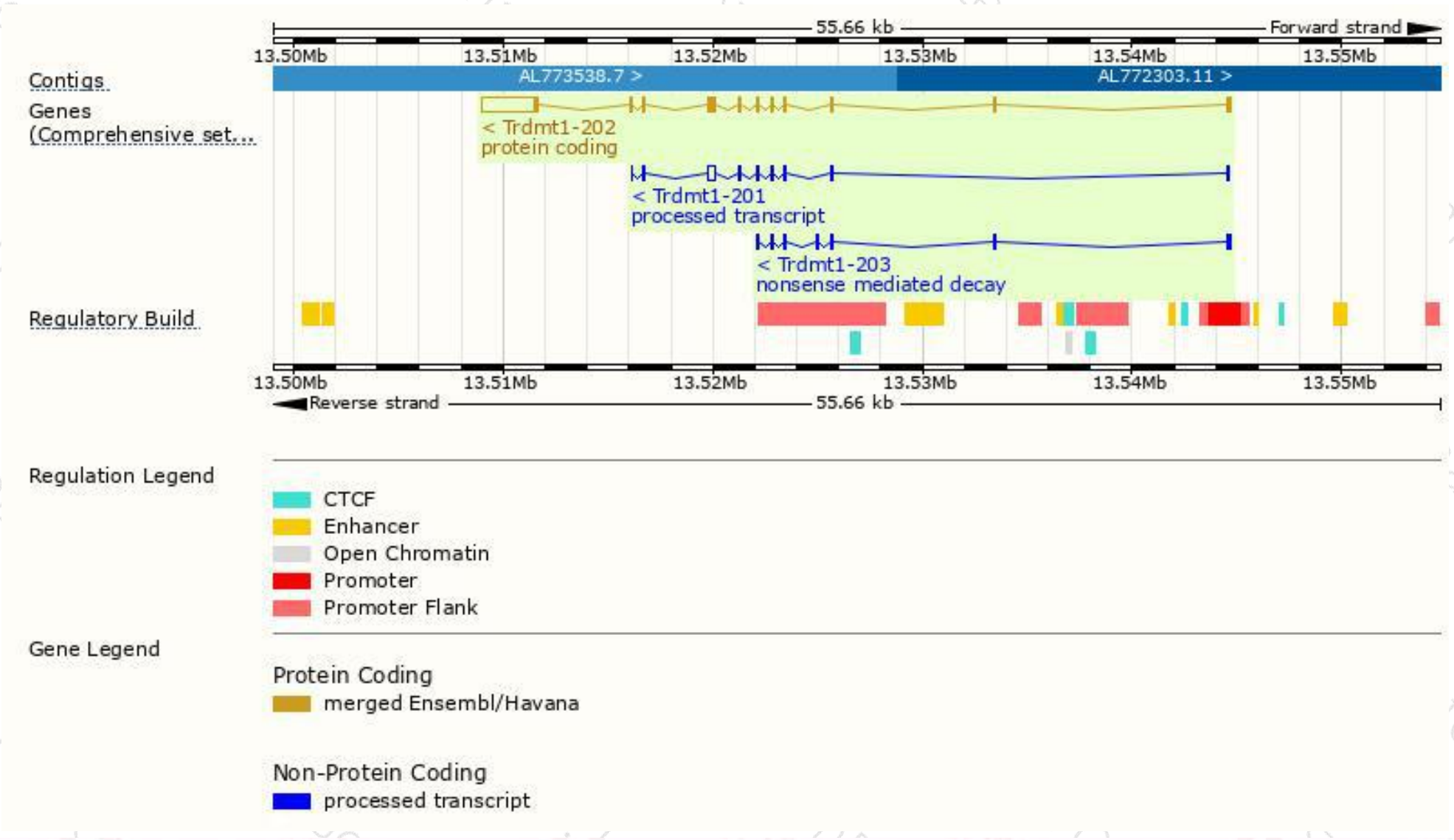
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trdmt1-202	<a href="#">ENSMUST00000124488.6</a>	3788	<a href="#">415aa</a>	Protein coding	<a href="#">CCDS15695</a>	<a href="#">Q55055 Q5I0V6</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Trdmt1-203	<a href="#">ENSMUST00000144957.2</a>	495	<a href="#">84aa</a>	Nonsense mediated decay	-	<a href="#">A0A0A6YWY7</a>	TSL:5
Trdmt1-201	<a href="#">ENSMUST00000028055.10</a>	879	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Trdmt1-202* transcript,the transcription is shown below

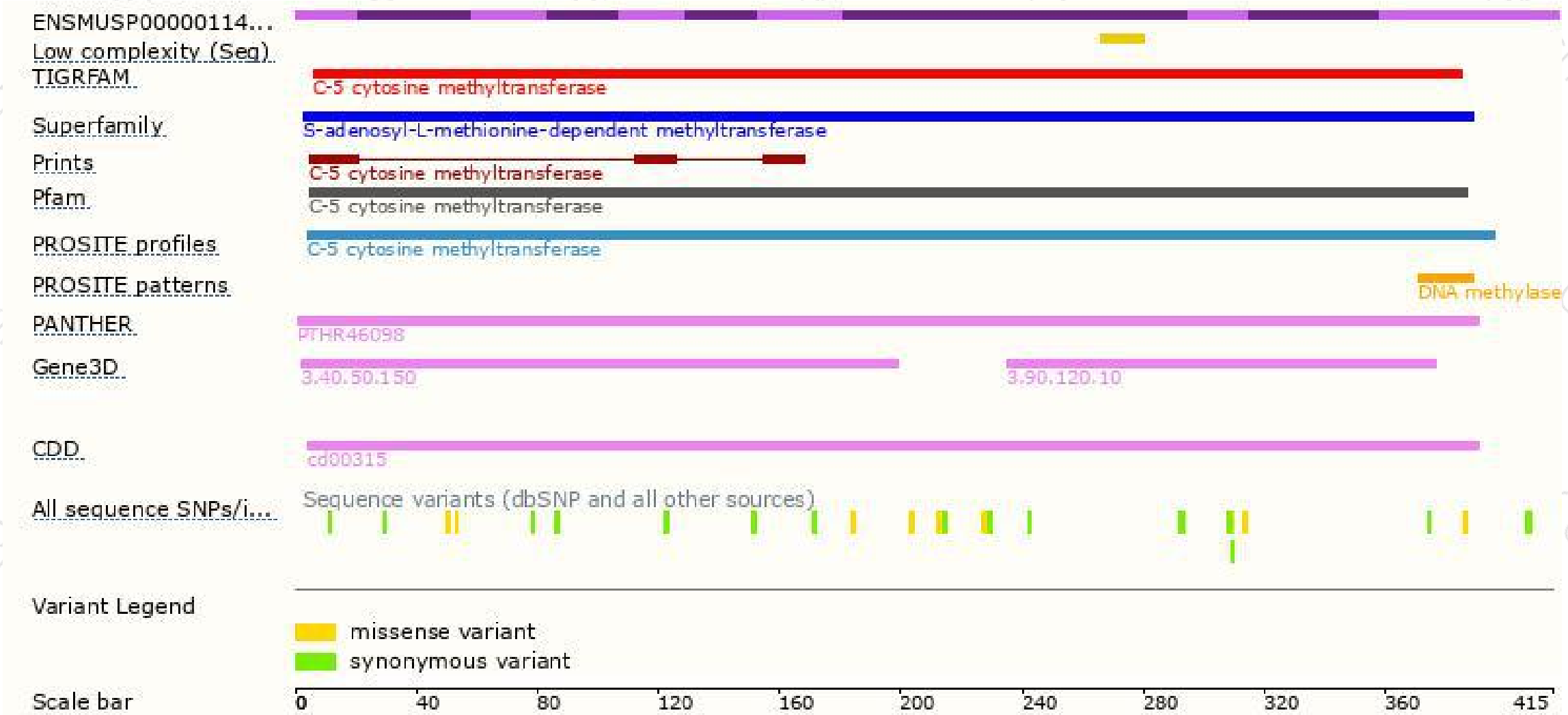


# Genomic location distribution

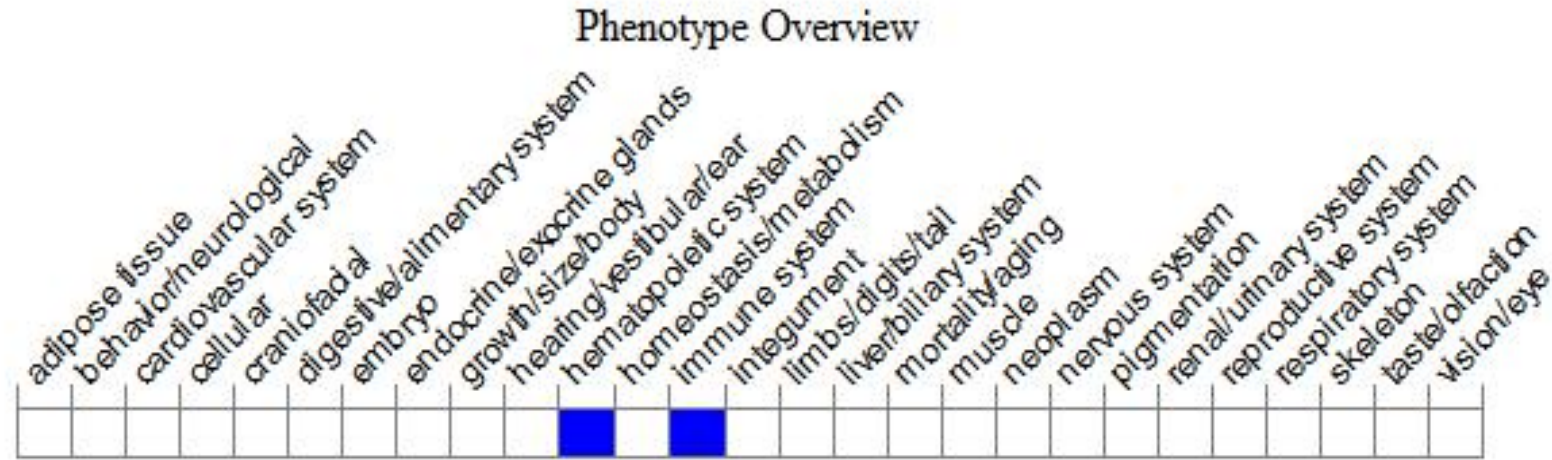




# Protein domain



# 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 disruptions in this gene have a decreased proportion of natural killer cells in the peripheral blood.

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

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