

Hepacam Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Hepacam

Project type

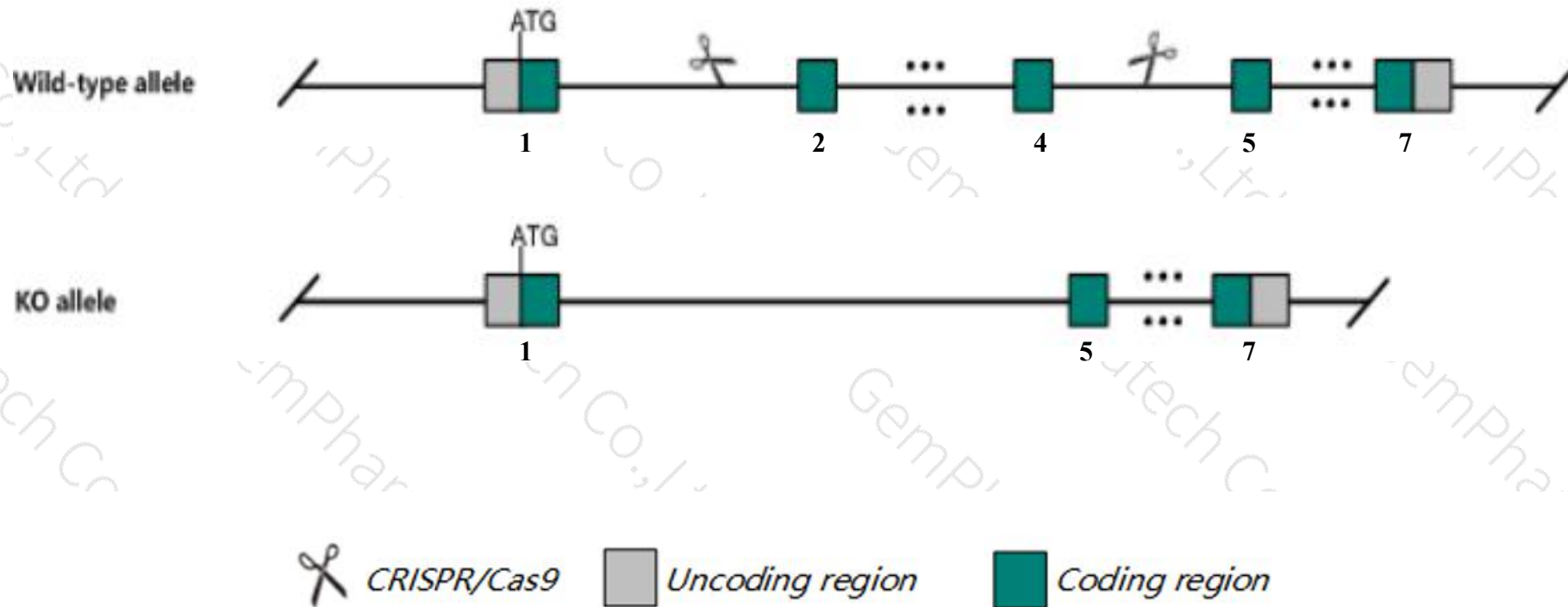
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Hepacam* gene has 2 transcripts. According to the structure of *Hepacam* gene, exon2-exon4 of *Hepacam*-201 (ENSMUST00000051839.8) transcript is recommended as the knockout region. The region contains 724bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hepacam* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele display myelin vacuolization that progresses with age.
- The *Hepacam* gene is located on the Chr9. 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)

Hepacam hepatocyte cell adhesion molecule [Mus musculus (house mouse)]

Gene ID: 72927, updated on 13-Mar-2020

Summary



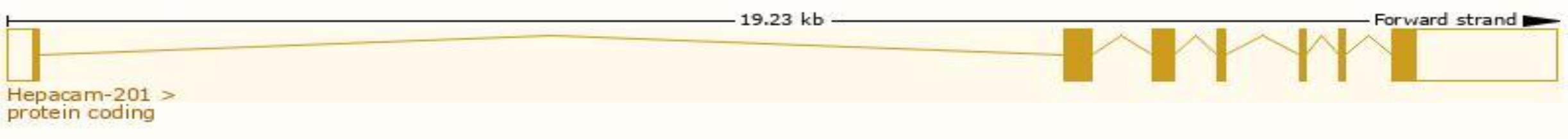
Official Symbol	Hepacam provided by MGI
Official Full Name	hepatocyte cell adhesion molecule provided by MGI
Primary source	MGI:MGI:1920177
See related	Ensembl:ENSMUSG00000046240
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2900042E01Rik, Glialcam, Hepn1
Expression	Biased expression in cerebellum adult (RPKM 30.4), cortex adult (RPKM 23.5) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

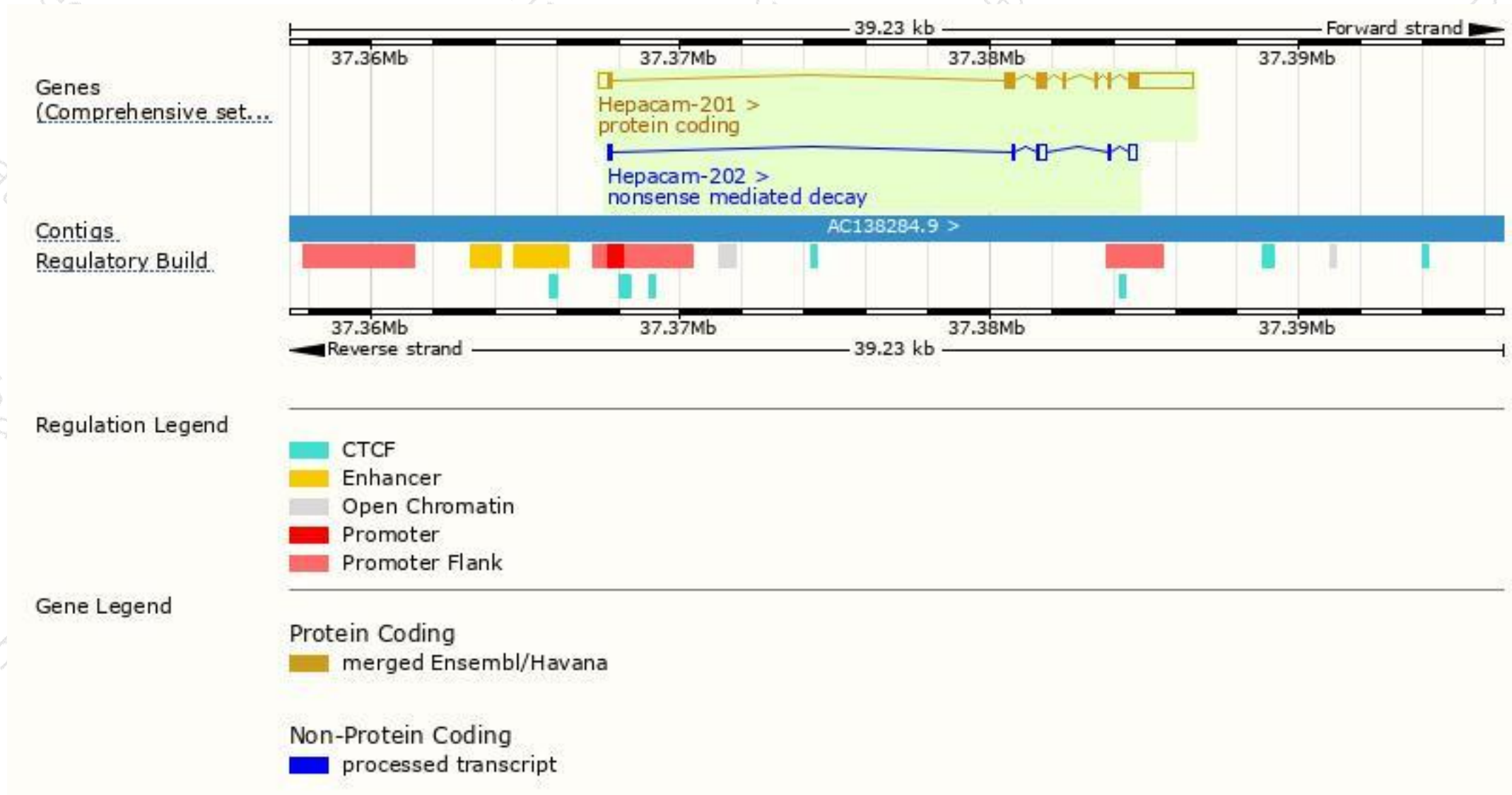
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hepacam-201	ENSMUST00000051839.8	3347	418aa	Protein coding	CCDS22976	B2RSY3 Q640R3	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
Hepacam-202	ENSMUST00000215951.1	800	69aa	Nonsense mediated decay	-	A0A1L1SUR4	TSL:3

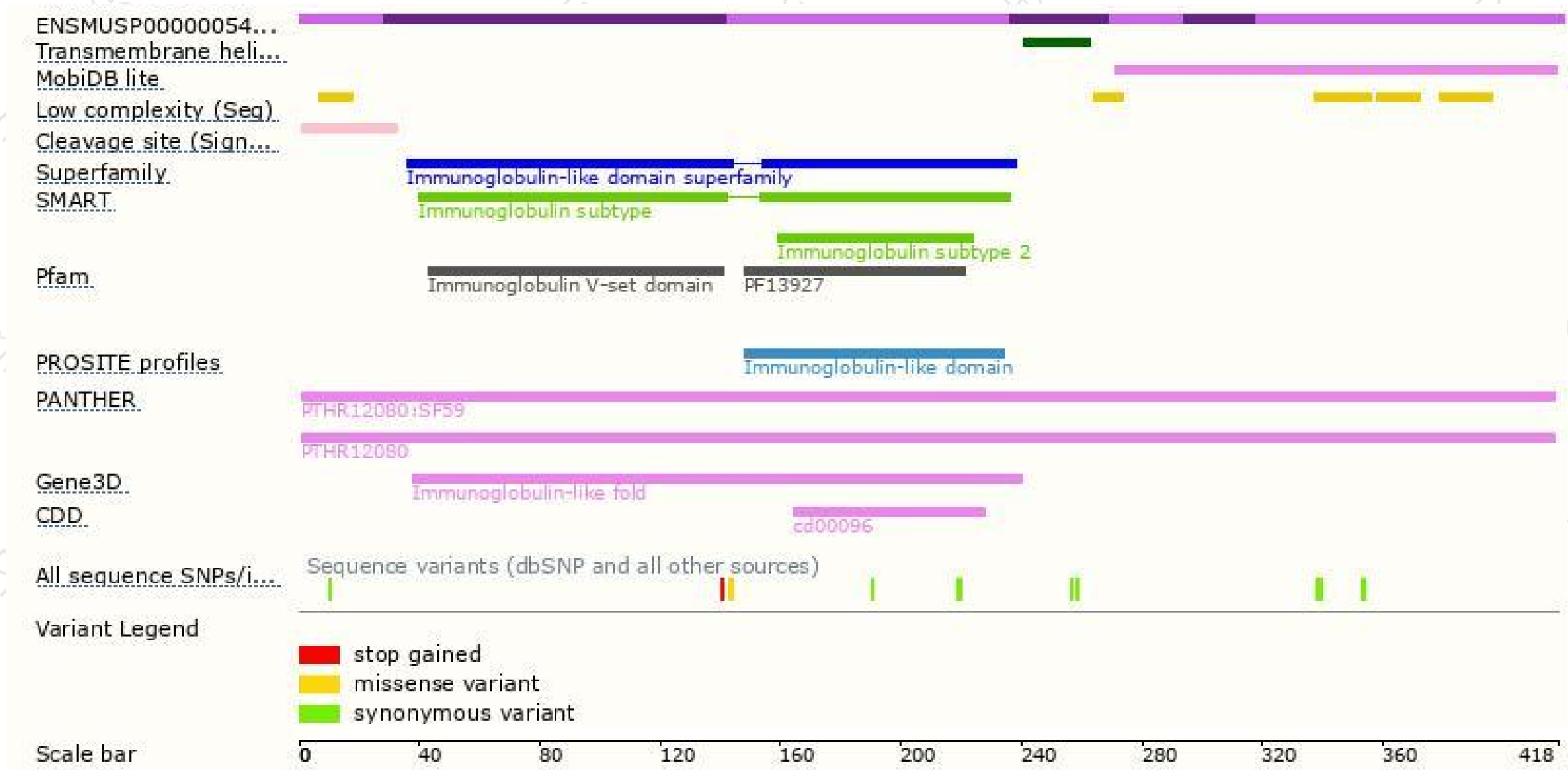
The strategy is based on the design of *Hepacam-201* transcript,The transcription is shown below



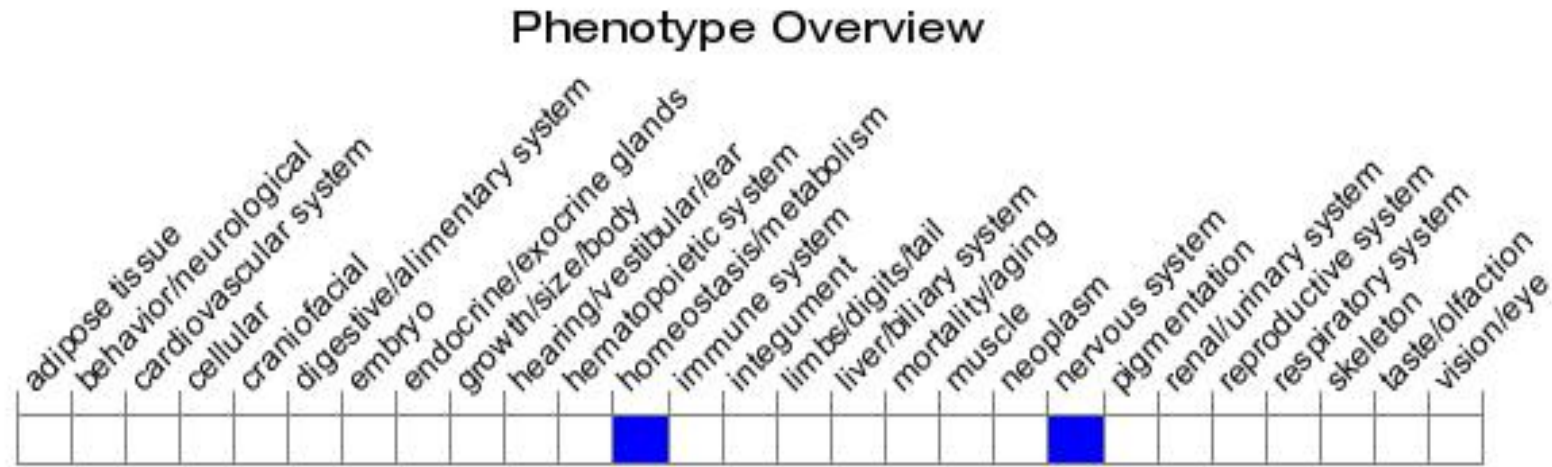
Genomic location distribution



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, Mice homozygous for a null allele display myelin vacuolization that progresses with age.

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

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