Cmtr1 Cas9-KO Strategy

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Reviewer: Lu Chen

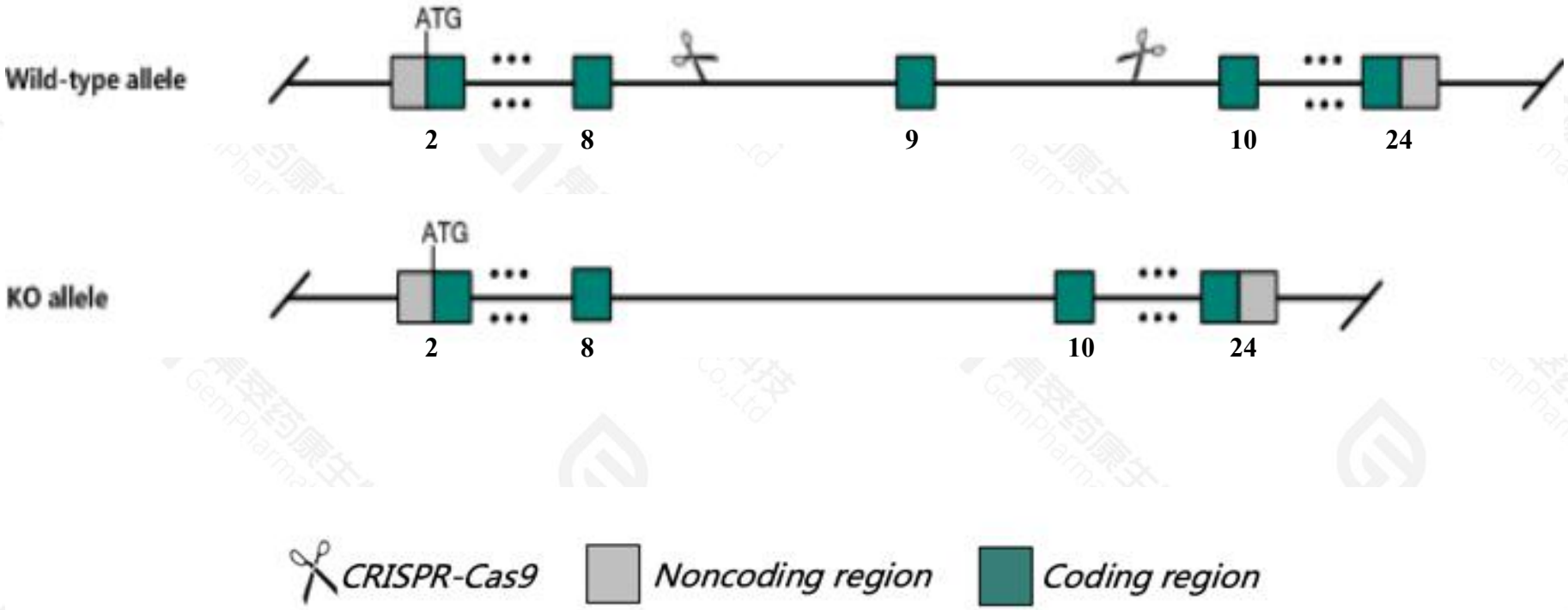
Design Date: 2022-4-6

Project Overview

Project Name	***Cmtr1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Cmtr1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Cmtr1* gene has 17 transcripts. According to the structure of *Cmtr1* gene, exon9 of *Cmtr1-201*(ENSMUST00000024816.13) transcript is recommended as the knockout region.The region contains 199bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR-Cas9 technology to modify *Cmtr1* gene. The brief process is as follows: CRISPR-Cas9 system 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.

Notice

➢ According to the existing MGI data,homozygous knockout is early embryonic lethal. Conditional homozygous KO in neurons leads to reduced neocortex size and neurite dysmorphology.

➢ The transcripts of *Cmtr1*-204 and *Cmtr1*-206 are not affected and their effects are unknown.

➢ This strategy will destroy *Gm28043* gene while knocking out the target gene, and the effect is unknown.

➢ This strategy may affect the 3-terminal regulation of *Ccdc167* gene.

➢ The *Cmtr1* gene is located on the Chr17. 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）

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Cmtr1 cap methyltransferase 1 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 74157, updated on 3-Apr-2022

Summary

Official Symbol	Cmtr1 provided by MGI
Official Full Name	cap methyltransferase 1 provided by MGI
Primary source	MGI:MGI:1921407
See related	Ensembl:ENSMUSG00000024019 AllianceGenome:MGI:1921407
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	MTr1; Ftsjd2; AI451264; 1300018I05Rik
Summary	Predicted to enable mRNA (nucleoside-2'-O-)-methyltransferase activity. Predicted to be involved in 7-methylguanosine mRNA capping and cap1 mRNA methylation. Predicted to act upstream of or within mRNA processing. Predicted to be located in nucleoplasm. Predicted to be active in cytoplasm and nucleus. Is expressed in central nervous system; olfactory epithelium; and retina. Orthologous to human CMTR1 (cap methyltransferase 1). [provided by Alliance of Genome Resources, Nov 2021]
Expression	Ubiquitous expression in cerebellum adult (RPKM 14.8), CNS E14 (RPKM 12.4) and 28 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

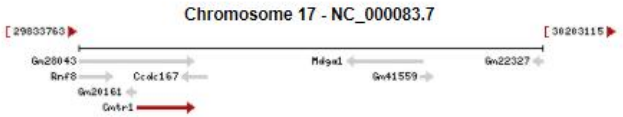
Genomic context

Location: 17; 17 A3.3

See Cmtr1 in Genome Data Viewer

Exon count: 24

Annotation release	Status	Assembly	Chr	Location
109	current	GRCm39 (GCF_000001635.27)	17	NC_000083.7 (29879569..29924953)
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	17	NC_000083.6 (29660595..29705979)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	17	NC_000083.5 (29797546..29840304)

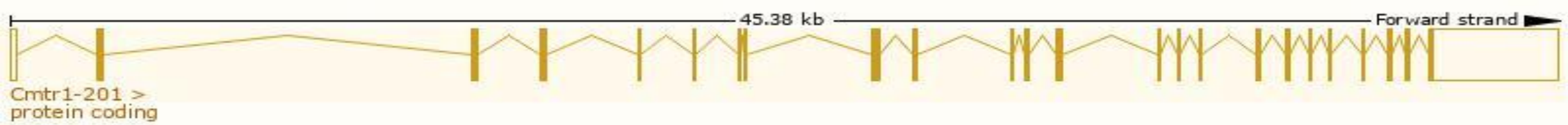


Transcript information（Ensembl）

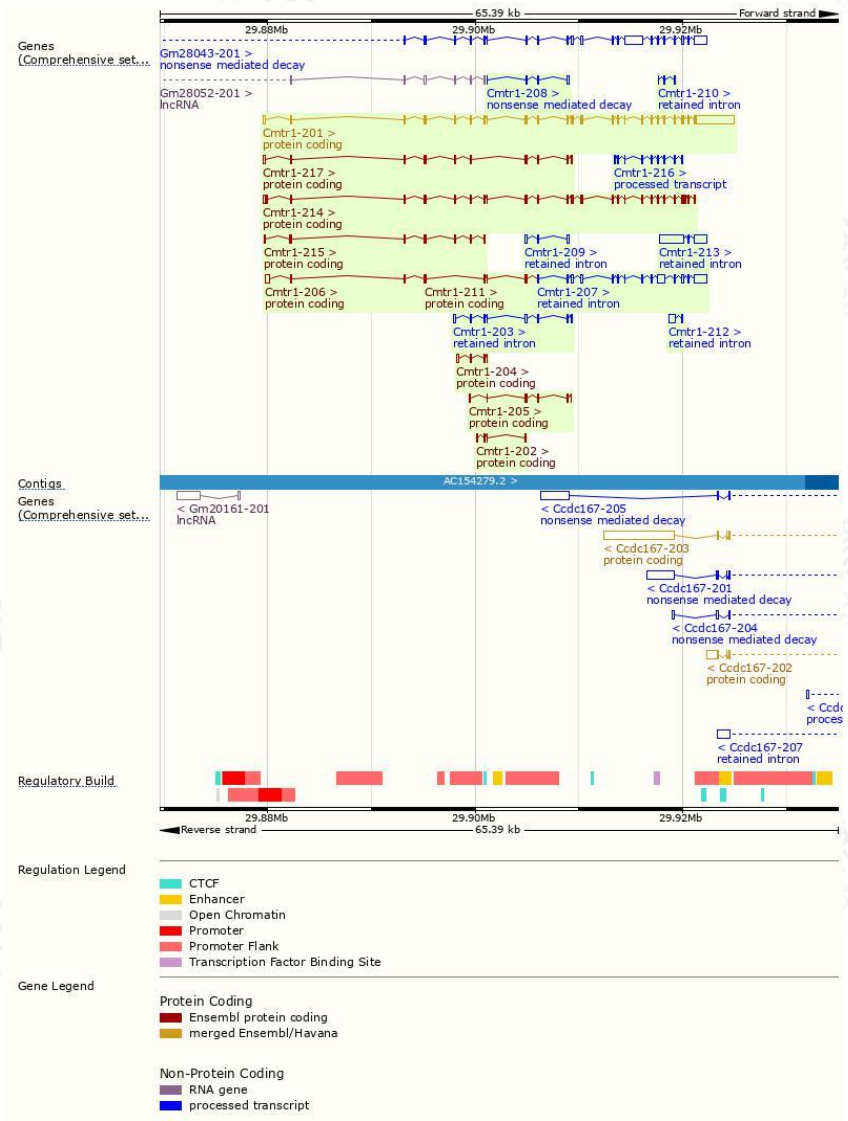
The gene has 17 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cmtr1-201	ENSMUST00000024816.13	6380	837aa	Protein coding	CCDS37539		TSL:1 , GENCODE basic , APPRIS P1 ,
Cmtr1-214	ENSMUST00000234911.2	2815	844aa	Protein coding	-		CDS 3' incomplete ,
Cmtr1-217	ENSMUST00000235031.2	1271	369aa	Protein coding	-		CDS 3' incomplete ,
Cmtr1-215	ENSMUST00000235014.2	771	225aa	Protein coding	-		CDS 3' incomplete ,
Cmtr1-206	ENSMUST00000130423.4	655	99aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Cmtr1-205	ENSMUST00000130052.9	615	165aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Cmtr1-211	ENSMUST00000234388.2	440	147aa	Protein coding	-		CDS 5' and 3' incomplete ,
Cmtr1-202	ENSMUST00000127695.2	375	72aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Cmtr1-204	ENSMUST00000129864.2	367	68aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Cmtr1-208	ENSMUST00000172516.9	495	37aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:3 ,
Cmtr1-216	ENSMUST00000235028.2	792	No protein	Processed transcript	-		
Cmtr1-213	ENSMUST00000234716.2	3600	No protein	Retained intron	-		
Cmtr1-207	ENSMUST00000138939.2	3075	No protein	Retained intron	-		TSL:2 ,
Cmtr1-203	ENSMUST00000128410.8	959	No protein	Retained intron	-		TSL:5 ,
Cmtr1-212	ENSMUST00000234666.2	702	No protein	Retained intron	-		
Cmtr1-209	ENSMUST00000172610.2	557	No protein	Retained intron	-		TSL:2 ,
Cmtr1-210	ENSMUST00000234278.2	232	No protein	Retained intron	-		

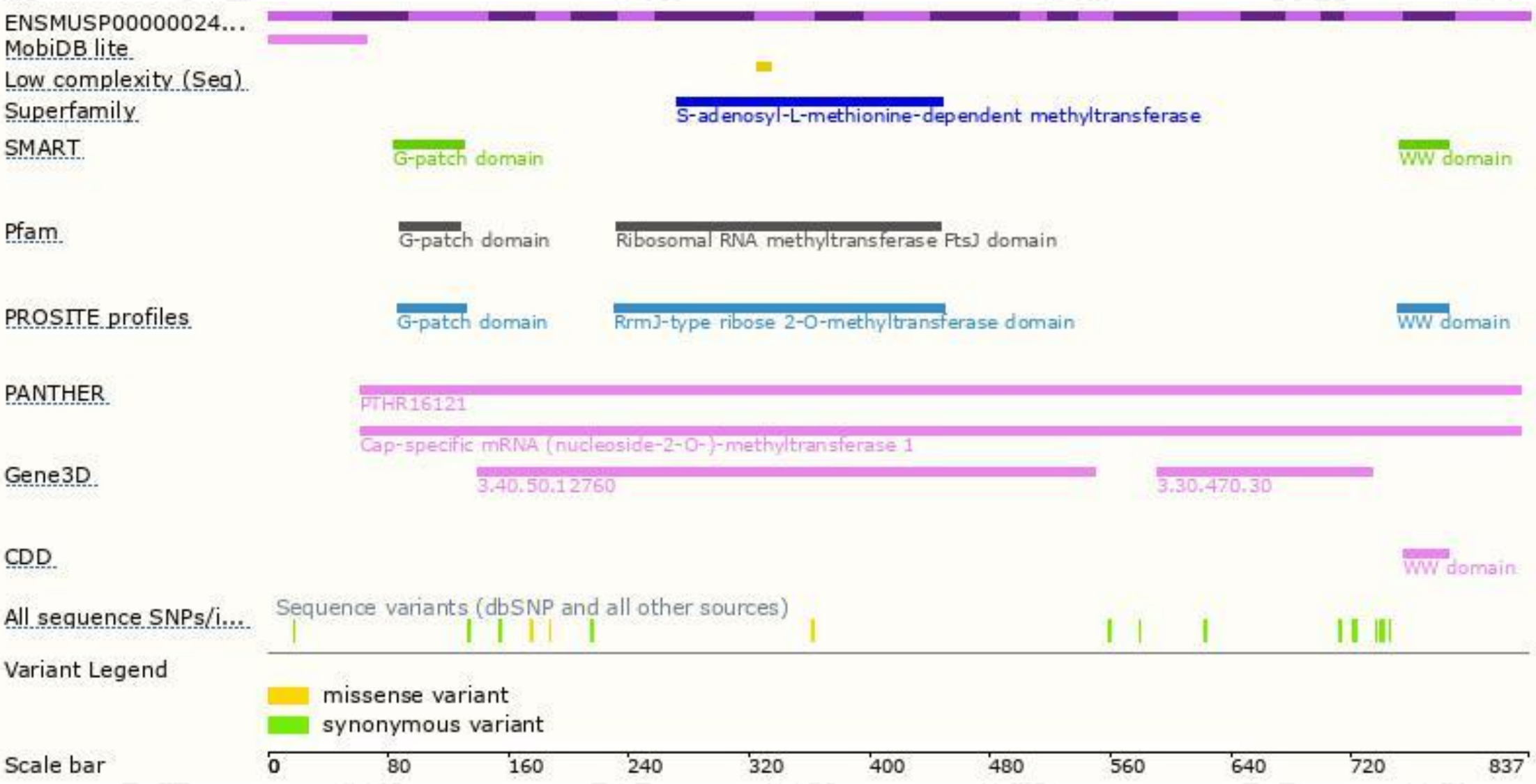
The strategy is based on the design of *Cmtr1-201* transcript,the transcription is shown below:



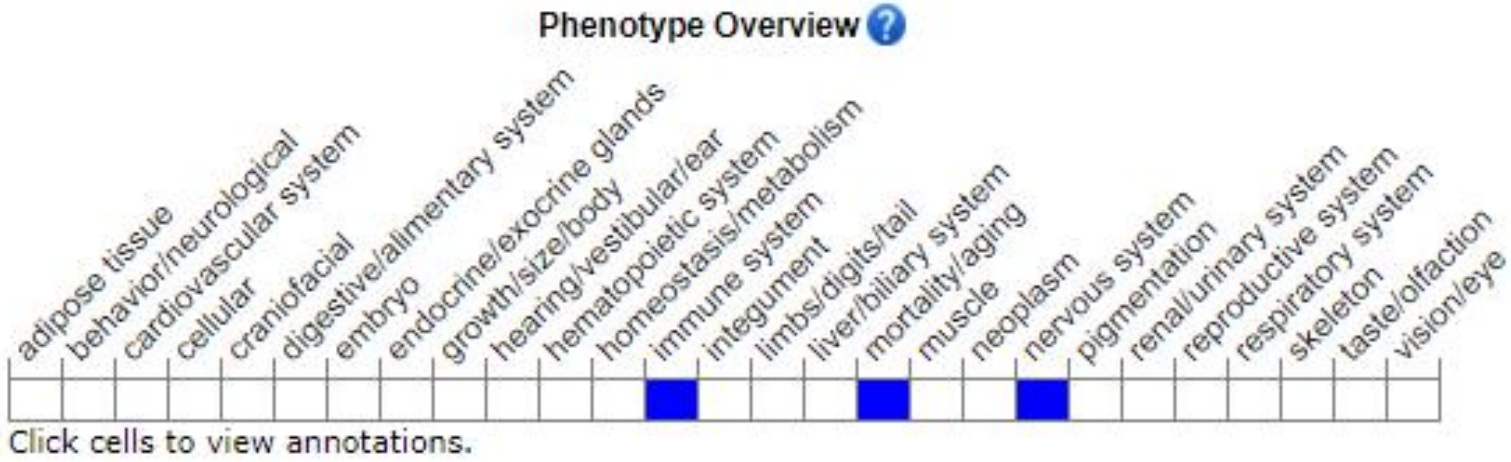
Genomic location distribution



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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