Cacnb4 Cas9-KO Strategy

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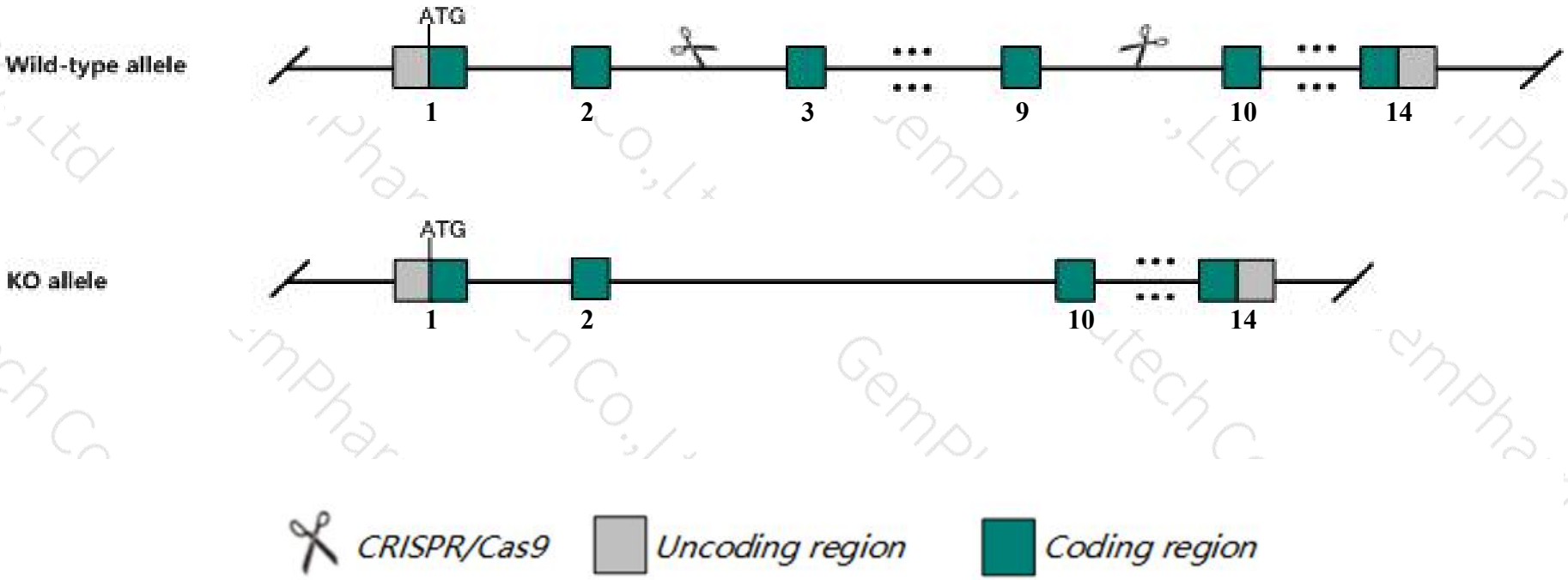
Project Overview

Project Name	***Cacnb4***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cacnb4* gene. The schematic diagram is as follows:



Technical routes

➢ The *Cacnb4* gene has 6 transcripts. According to the structure of *Cacnb4* gene, exon3-exon9 of *Cacnb4-201* (ENSMUST00000078324.6) transcript is recommended as the knockout region.The region contains 611bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cacnb4* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Homozygous mutants have lethargic behavior, unstable gait and seizures, with peripheral motor nerves showing reduced conduction velocity and prolonged distal latency.

- The *Cacnb4* 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）

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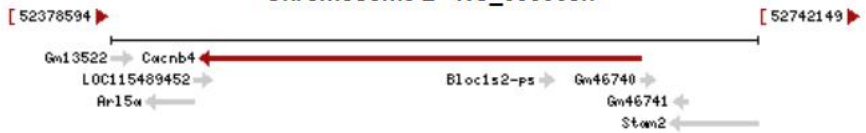
Cacnb4 calcium channel, voltage-dependent, beta 4 subunit [*Mus musculus* (house mouse)]

Gene ID: 12298, updated on 12-Aug-2019

Summary

Official Symbol	Cacnb4 provided by MGI
Official Full Name	calcium channel, voltage-dependent, beta 4 subunit provided by MGI
Primary source	MGI:MGI:103301
See related	Ensembl:ENSMUSG00000017412
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	lh; Cchb4; 3110038O15Rik
Expression	Biased expression in cerebellum adult (RPKM 13.8), cortex adult (RPKM 11.2) and 4 other tissues See more
Orthologs	human all

Chromosome 2 - NC_000068.7

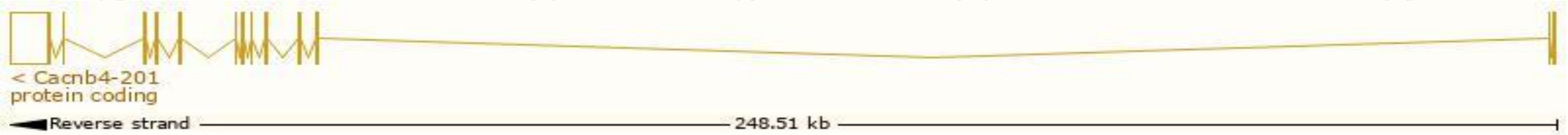


Transcript information（Ensembl）

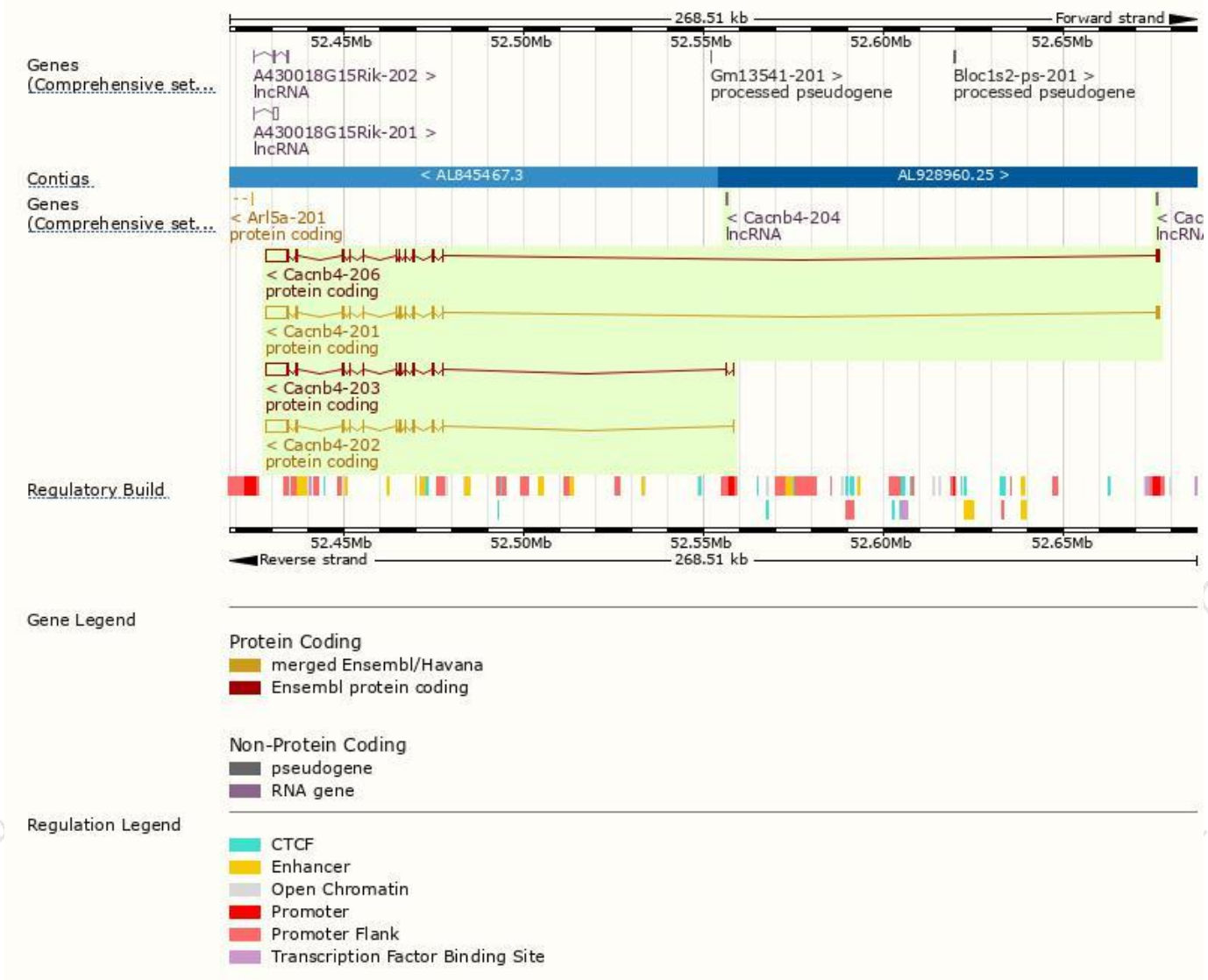
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Cacnb4-201	ENSMUST00000078324.6	8225	519aa	ENSMUSP00000077438.6	Protein coding	CCDS16034	A2ATZ8 Q8R0S4	TSL:1 GENCODE basic APPRIS P4
Cacnb4-203	ENSMUST00000102761.8	8039	473aa	ENSMUSP00000099822.2	Protein coding	CCDS71052	Q8R0S4	TSL:1 GENCODE basic APPRIS ALT1
Cacnb4-202	ENSMUST00000102760.9	7872	486aa	ENSMUSP00000099821.3	Protein coding	CCDS16035	Q8R0S4	TSL:1 GENCODE basic APPRIS ALT1
Cacnb4-206	ENSMUST00000178799.7	7981	519aa	ENSMUSP00000136811.1	Protein coding	-	J3QK20	TSL:5 GENCODE basic APPRIS ALT1
Cacnb4-204	ENSMUST00000132322.1	290	No protein	-	lncRNA	-	-	TSL:3
Cacnb4-205	ENSMUST00000148837.1	208	No protein	-	lncRNA	-	-	TSL:3

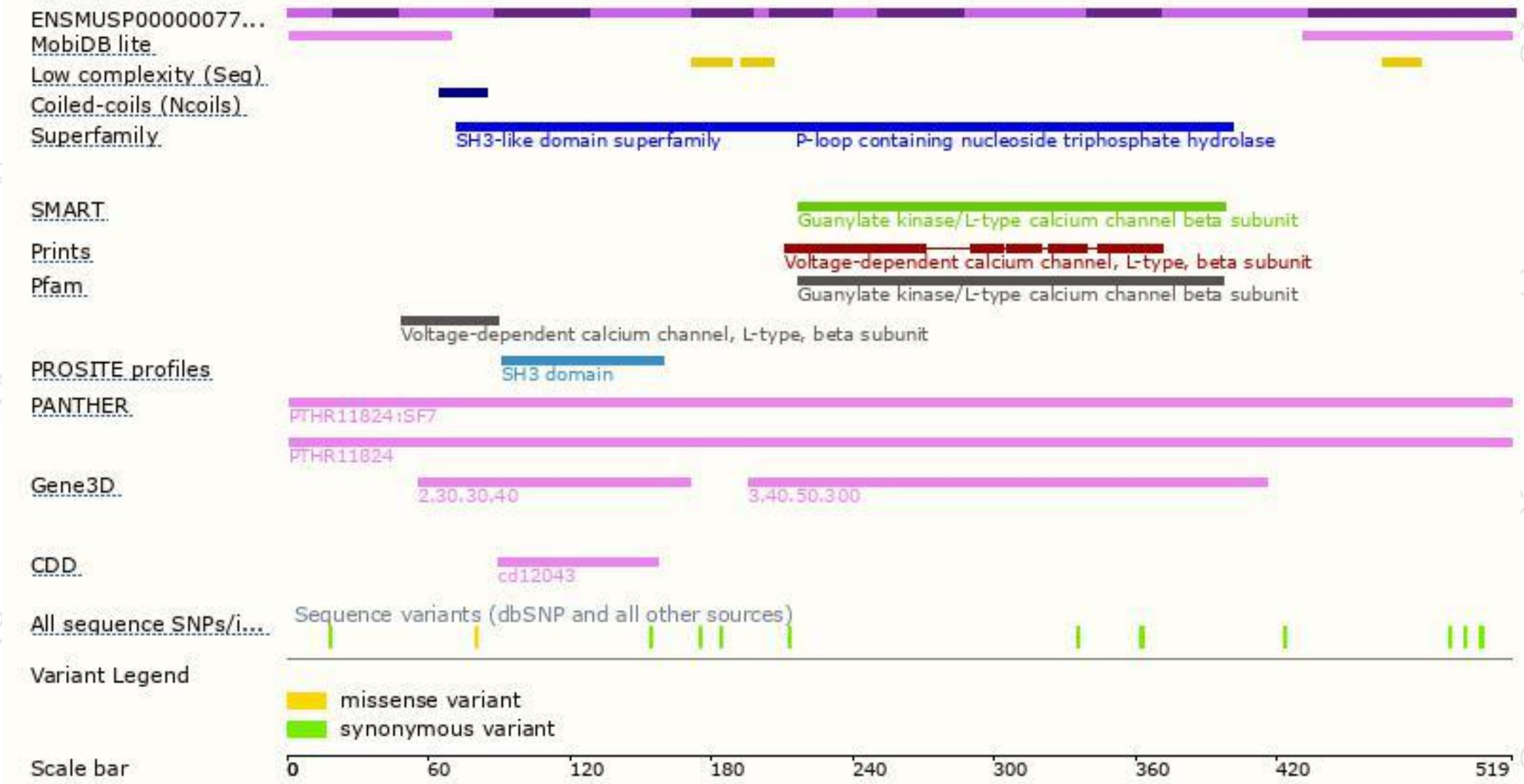
The strategy is based on the design of *Cacnb4-201* transcript,The transcription is shown below



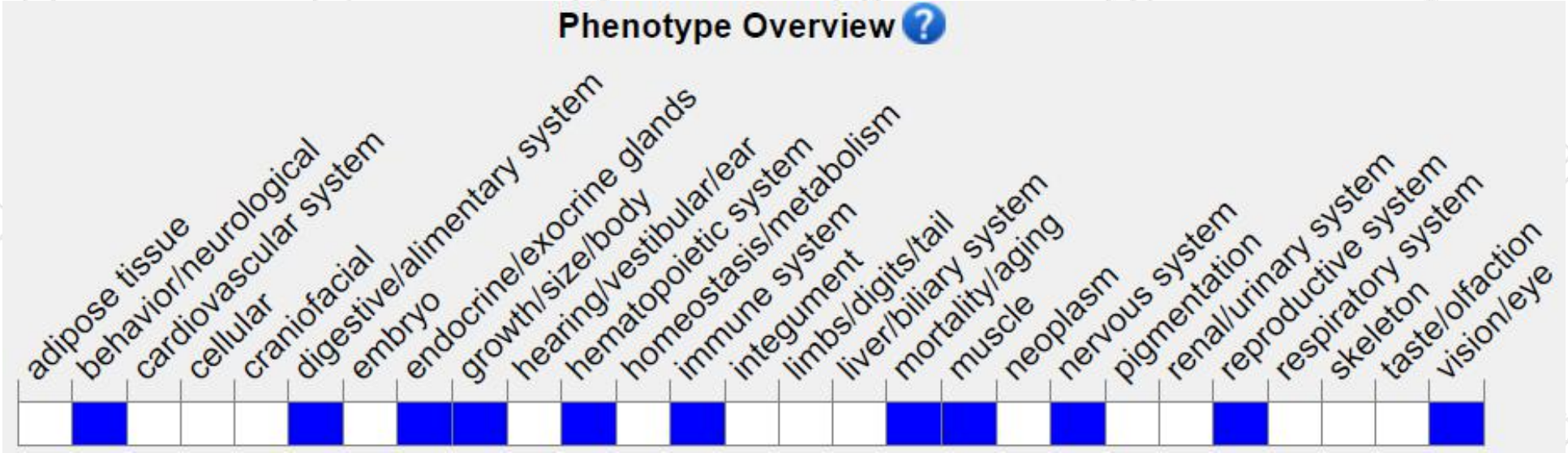
Genomic location distribution



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,Homozygous mutants have lethargic behavior, unstable gait and seizures, with peripheral motor nerves showing reduced conduction velocity and prolonged distal latency.

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

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