Slc1a3 Cas9-KO Strategy

Designer: Daohua Xu

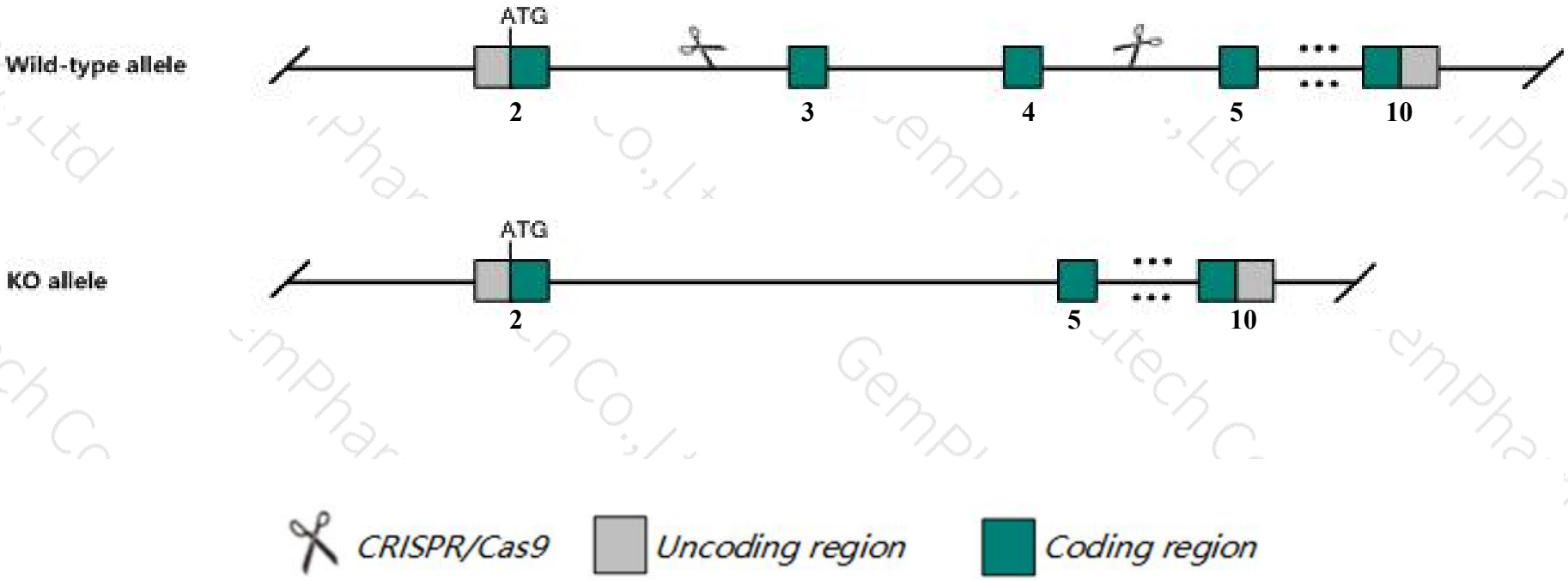
Design Date: 2019-7-18

Project Overview

Project Name	***Slc1a3***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc1a3* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc1a3* gene has 8 transcripts. According to the structure of *Slc1a3* gene, exon3-exon4 of *Slc1a3-201* (ENSMUST00000005493.13) transcript is recommended as the knockout region.The region contains 343bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc1a3* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for disruptions in this gene display no abnormalities with respect to appearance or survival but do display functional abnormalities related to the central nervous system.

- The *Slc1a3* gene is located on the Chr15. 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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Slc1a3 solute carrier family 1 (glial high affinity glutamate transporter), member 3 [Mus musculus (house mouse)]

Gene ID: 20512, updated on 9-Apr-2019

Summary

Official Symbol	Slc1a3 provided by MGI
Official Full Name	solute carrier family 1 (glial high affinity glutamate transporter), member 3 provided by MGI
Primary source	MGI:MGI:99917
See related	Ensembl:ENSMUSG00000005360
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	AI504299, B430115D02Rik, Eaat1, GLAST, GLAST-1, GLU-T, GluT-1, Gmt1, MGluT1
Expression	Biased expression in frontal lobe adult (RPKM 107.1), cerebellum adult (RPKM 104.8) and 8 other tissues See more
Orthologs	human all

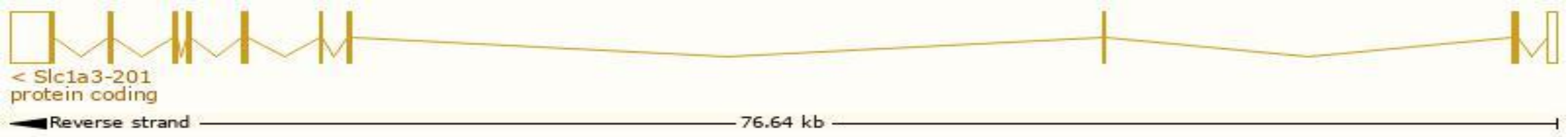
Transcript information（Ensembl）

The gene has 8 transcripts,all transcripts are shown below:

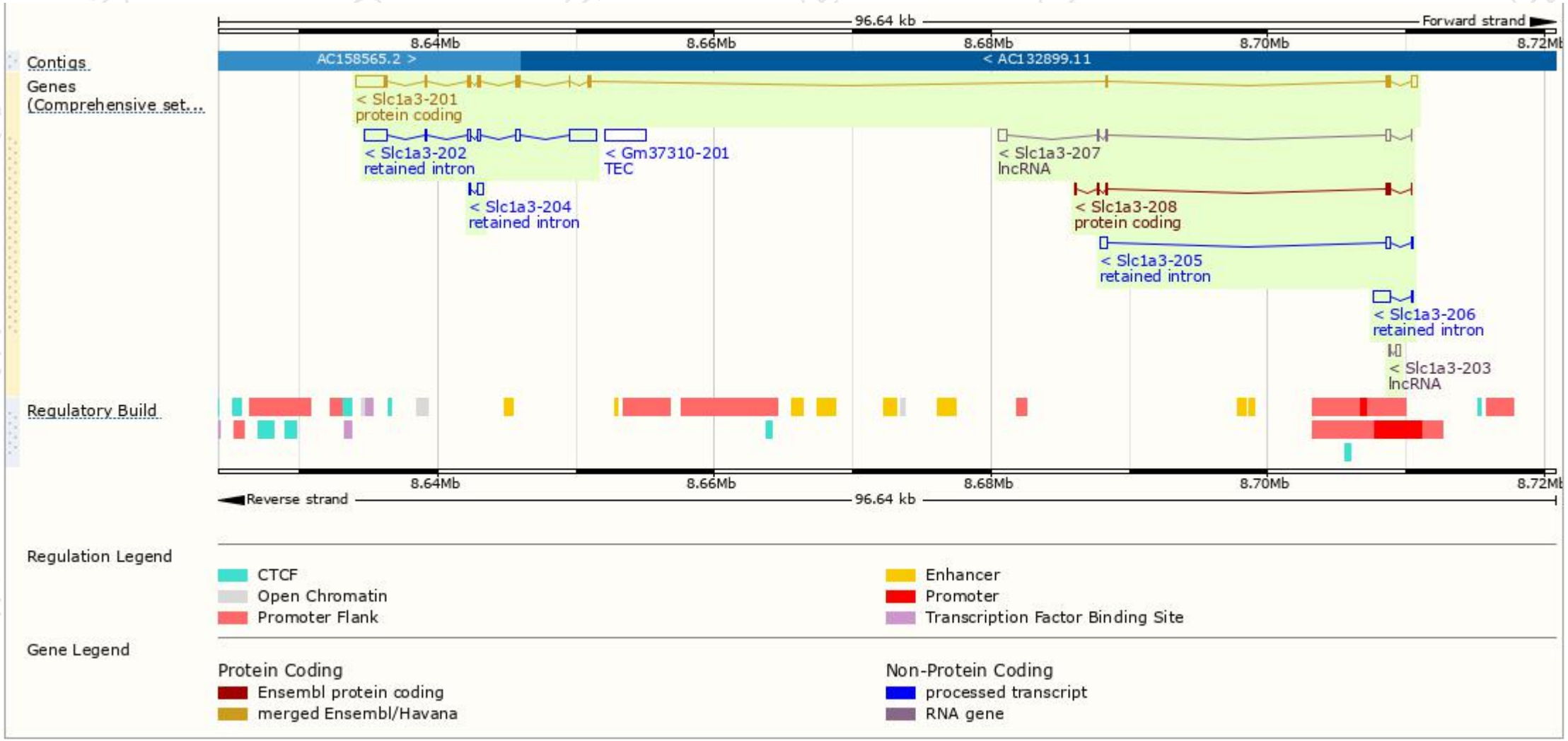
Show/hide columns (1 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc1a3-201	ENSMUST00000005493.13	4163	543aa	Protein coding	CCDS27373	P56564 Q543U3	TSL:1 GENCODE basic APPRIS P1
Slc1a3-208	ENSMUST00000157065.1	728	129aa	Protein coding	-	D3YY51	TSL:1 GENCODE basic
Slc1a3-202	ENSMUST00000125997.1	4435	No protein	Retained intron	-	-	TSL:2
Slc1a3-206	ENSMUST00000133309.1	1373	No protein	Retained intron	-	-	TSL:1
Slc1a3-205	ENSMUST00000129325.1	964	No protein	Retained intron	-	-	TSL:2
Slc1a3-204	ENSMUST00000128879.1	469	No protein	Retained intron	-	-	TSL:2
Slc1a3-207	ENSMUST00000153455.7	1252	No protein	lncRNA	-	-	TSL:1
Slc1a3-203	ENSMUST00000126747.1	402	No protein	lncRNA	-	-	TSL:5

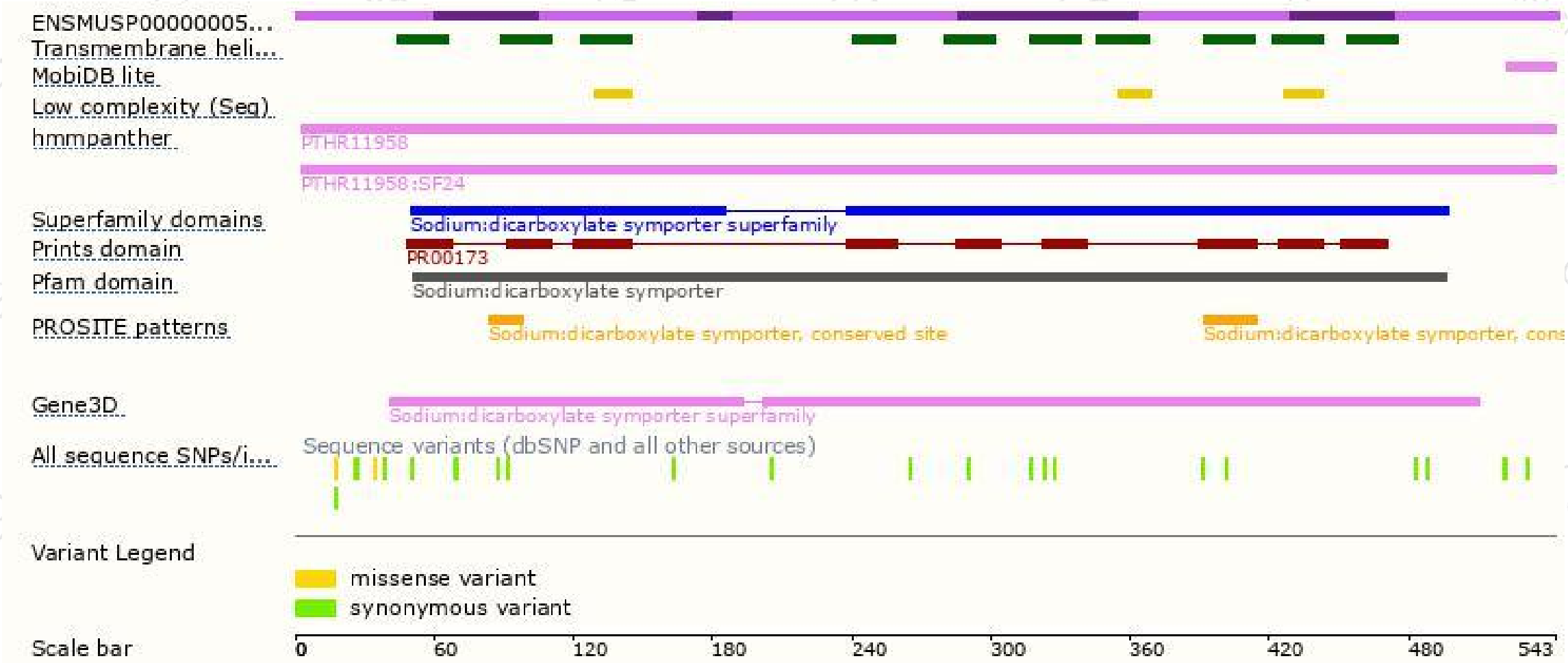
The strategy is based on the design of *Slc1a3-201* transcript,The transcription is shown below



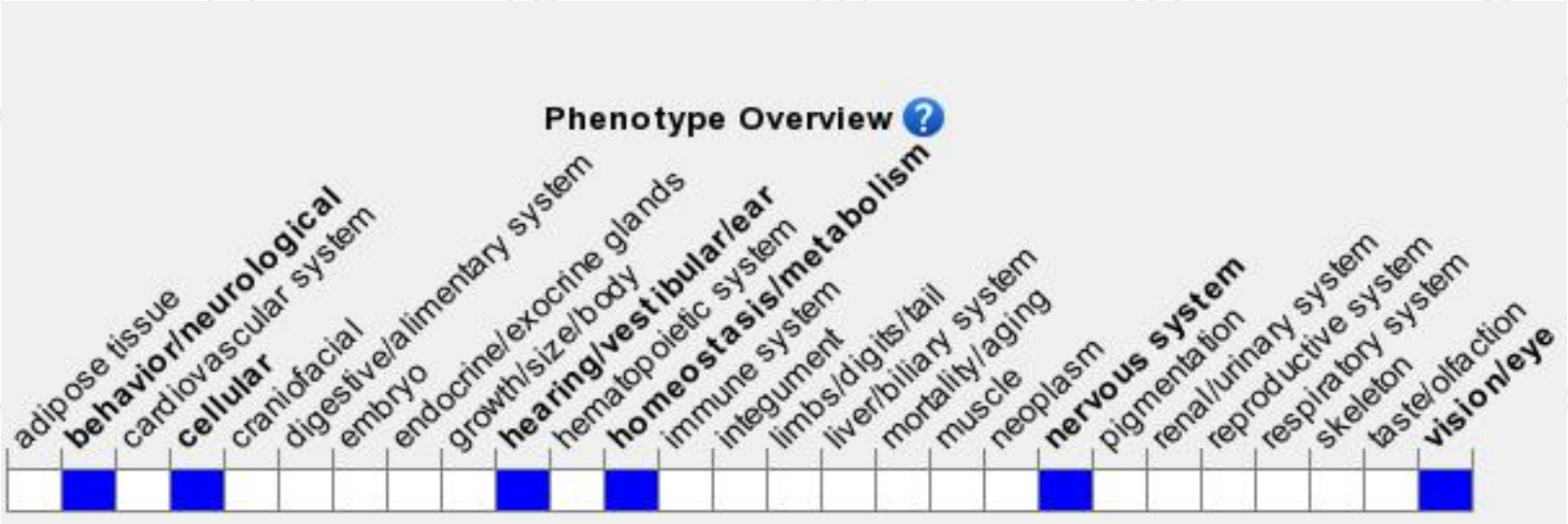
Genomic location distribution



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 disruptions in this gene display no abnormalities with respect to appearance or survival but do display functional abnormalities related to the central nervous system.

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

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