

Slc17a5 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

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Project Overview

Project Name

Slc17a5

Project type

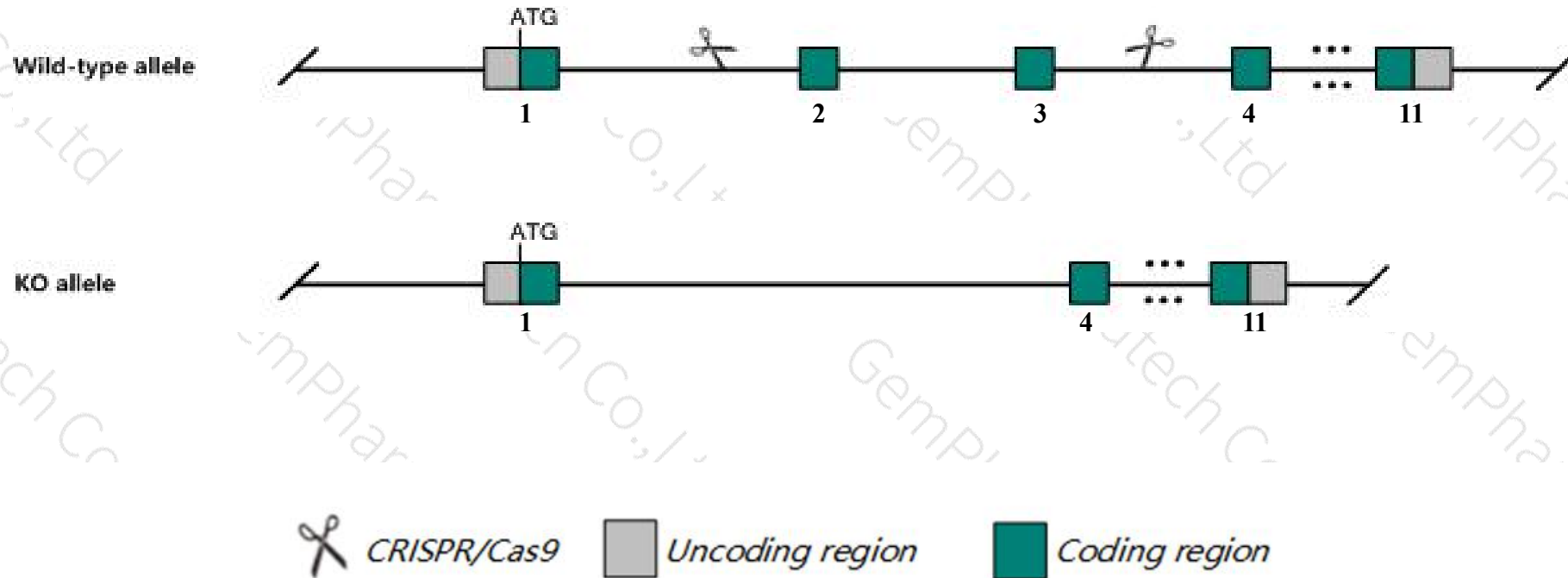
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc17a5* gene. The schematic diagram is as follows:



- The *Slc17a5* gene has 3 transcripts. According to the structure of *Slc17a5* gene, exon2-exon3 of *Slc17a5-201* (ENSMUST00000052441.11) transcript is recommended as the knockout region. The region contains 431bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc17a5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutant mice exhibit numerous neurological abnormalities, including impaired exploratory and locomotor activity, hearing deficits, and an increased depressive-like response.
- The *Slc17a5* 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)

Slc17a5 solute carrier family 17 (anion/sugar transporter), member 5 [*Mus musculus* (house mouse)]

Gene ID: 235504, updated on 10-Oct-2019

Summary

- Official Symbol** Slc17a5 provided by [MGI](#)
- Official Full Name** solute carrier family 17 (anion/sugar transporter), member 5 provided by [MGI](#)
- Primary source** [MGI:MGI:1924105](#)
- See related** [Ensembl:ENSMUSG00000049624](#)
- 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** SD; AST; NSD; SLD; ISSD; SIASD; SIALIN; 4732491M05; 4631416G20Rik
- Expression** Ubiquitous expression in kidney adult (RPKM 12.0), genital fat pad adult (RPKM 7.5) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 9; 9 E1 [See Slc17a5 in Genome Data Viewer](#)

Exon count: 12

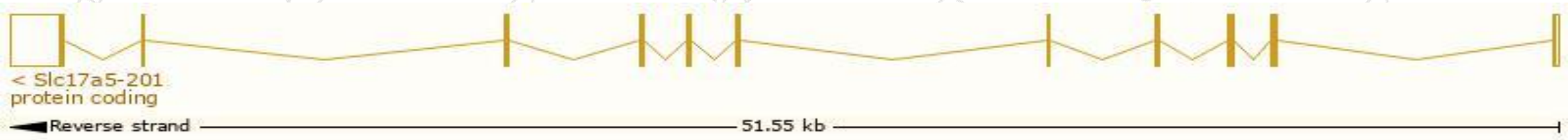
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	9	NC_000075.6 (78536487..78588045, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	9	NC_000075.5 (78384316..78435834, complement)

Transcript information (Ensembl)

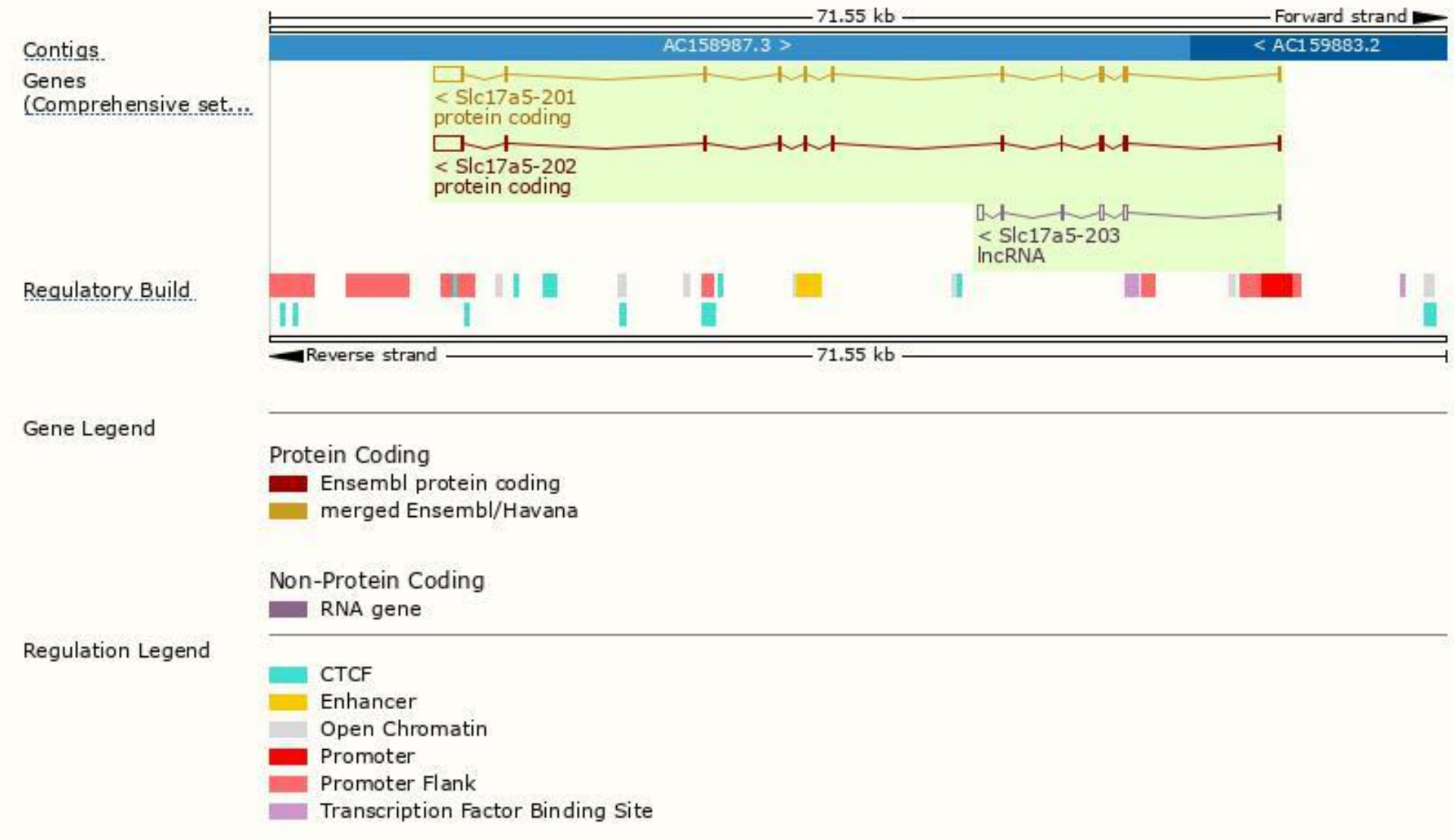
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc17a5-201	ENSMUST00000052441.11	3236	495aa	Protein coding	CCDS23364	Q8BN82	TSL:1 GENCODE basic APPRIS P3
Slc17a5-202	ENSMUST00000117645.7	3114	469aa	Protein coding	CCDS72283	Q8BN82	TSL:1 GENCODE basic APPRIS ALT2
Slc17a5-203	ENSMUST00000119213.2	1151	No protein	lncRNA	-	-	TSL:1

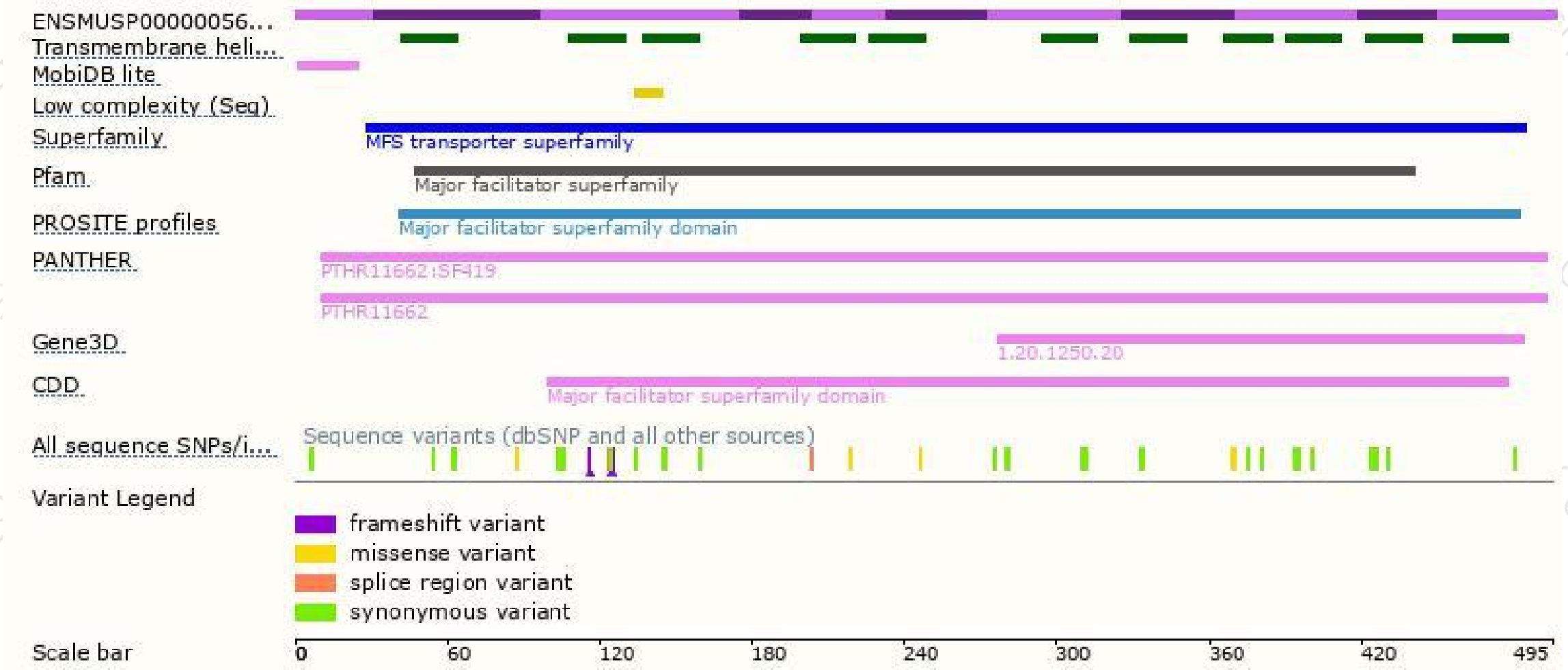
The strategy is based on the design of *Slc17a5-201* transcript,The transcription is shown below



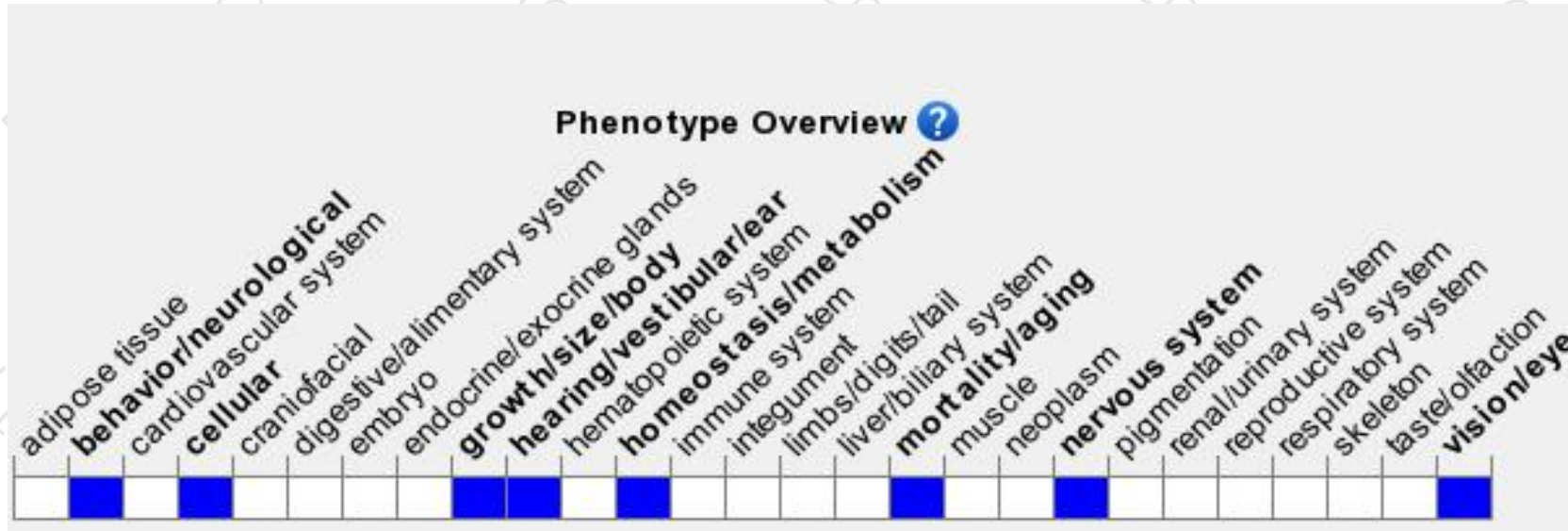
Genomic location distribution



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 mutant mice exhibit numerous neurological abnormalities, including impaired exploratory and locomotor activity, hearing deficits, and an increased depressive-like response.

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

Tel: 400-9660890

