

Nat8l Cas9-CKO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

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Project Overview

Project Name

Nat8l

Project type

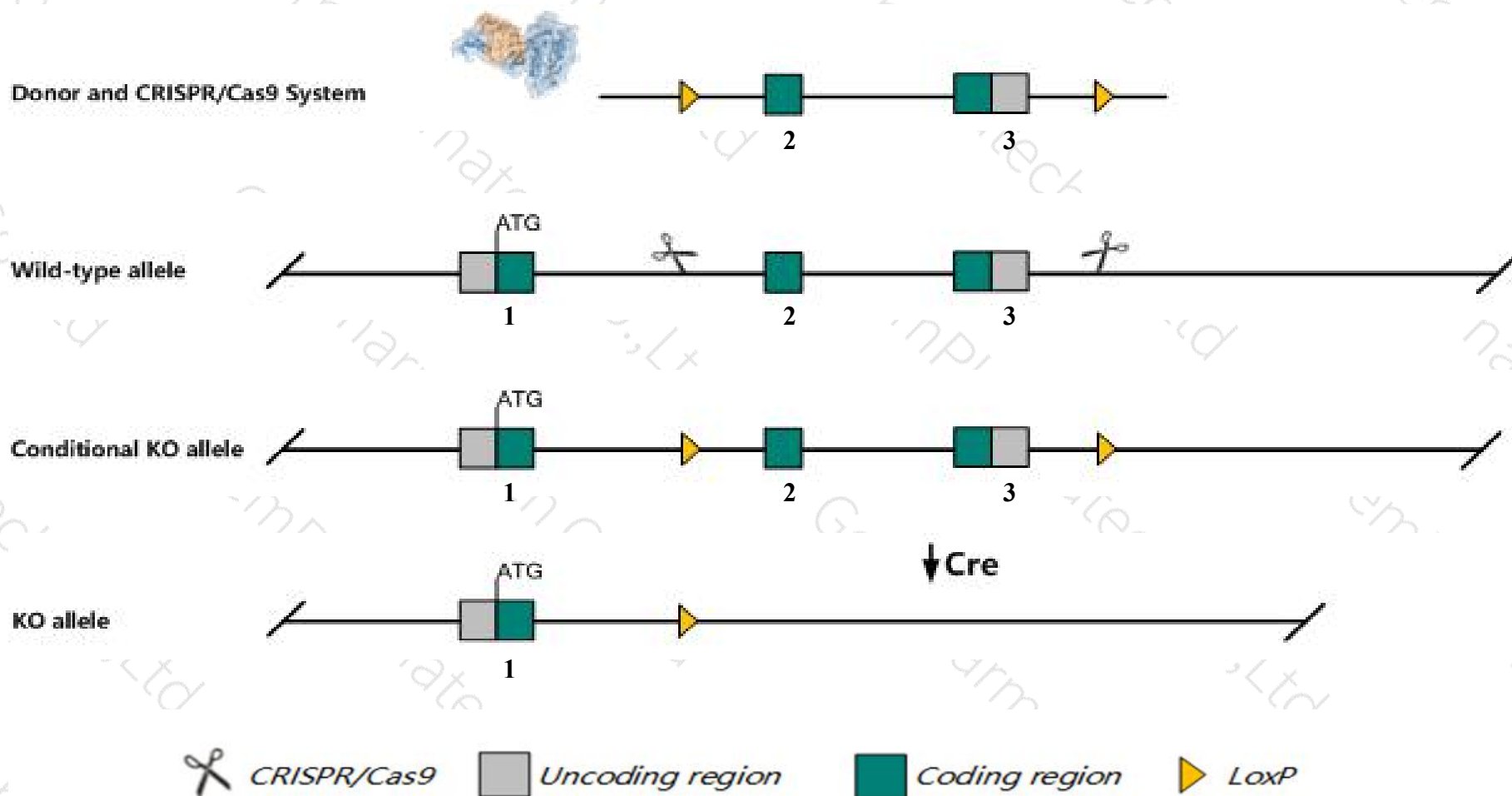
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nat8l* gene. The schematic diagram is as follows:



Technical routes

- The *Nat8l* gene has 2 transcripts. According to the structure of *Nat8l* gene, exon2-exon3 of *Nat8l-201* (ENSMUST00000056355.8) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nat8l* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a null mutation display abnormal responses to novelty and decreased social investigation in a novel environment.
- The floxed region is near to the N-terminal of *Gm42847* gene, this strategy may influence the regulatory function of the N-terminal of *Gm42847* gene.
- The *Nat8l* gene is located on the Chr5. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Nat8l N-acetyltransferase 8-like [*Mus musculus* (house mouse)]

Gene ID: 269642, updated on 10-Dec-2019

Summary

- Official Symbol

Nat8l provided by [MGI](#)
- Official Full Name

N-acetyltransferase 8-like provided by [MGI](#)
- Primary source

[MGI:MGI:2447776](#)
- See related

[Ensembl:ENSMUSG00000048142](#)
- 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

Shati; 1110038O08Rik
- Expression

Biased expression in cerebellum adult (RPKM 48.7), cortex adult (RPKM 39.5) and 11 other tissues [See more](#)
- Orthologs

[human](#) [all](#)

Genomic context

Location:

5; 5 B2

See Nat8l in [Genome Data Viewer](#)

Exon count:

3

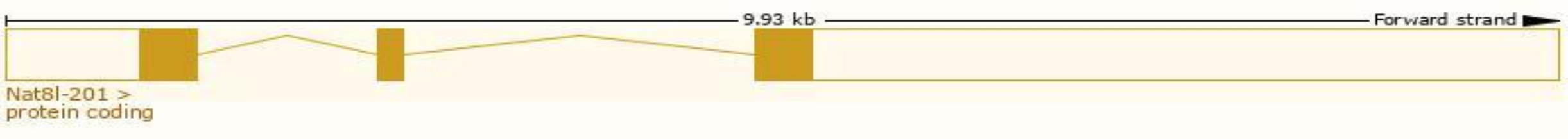
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	5	NC_000071.6 (33995984..34005916)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	5	NC_000071.5 (34338633..34348565)

Transcript information (Ensembl)

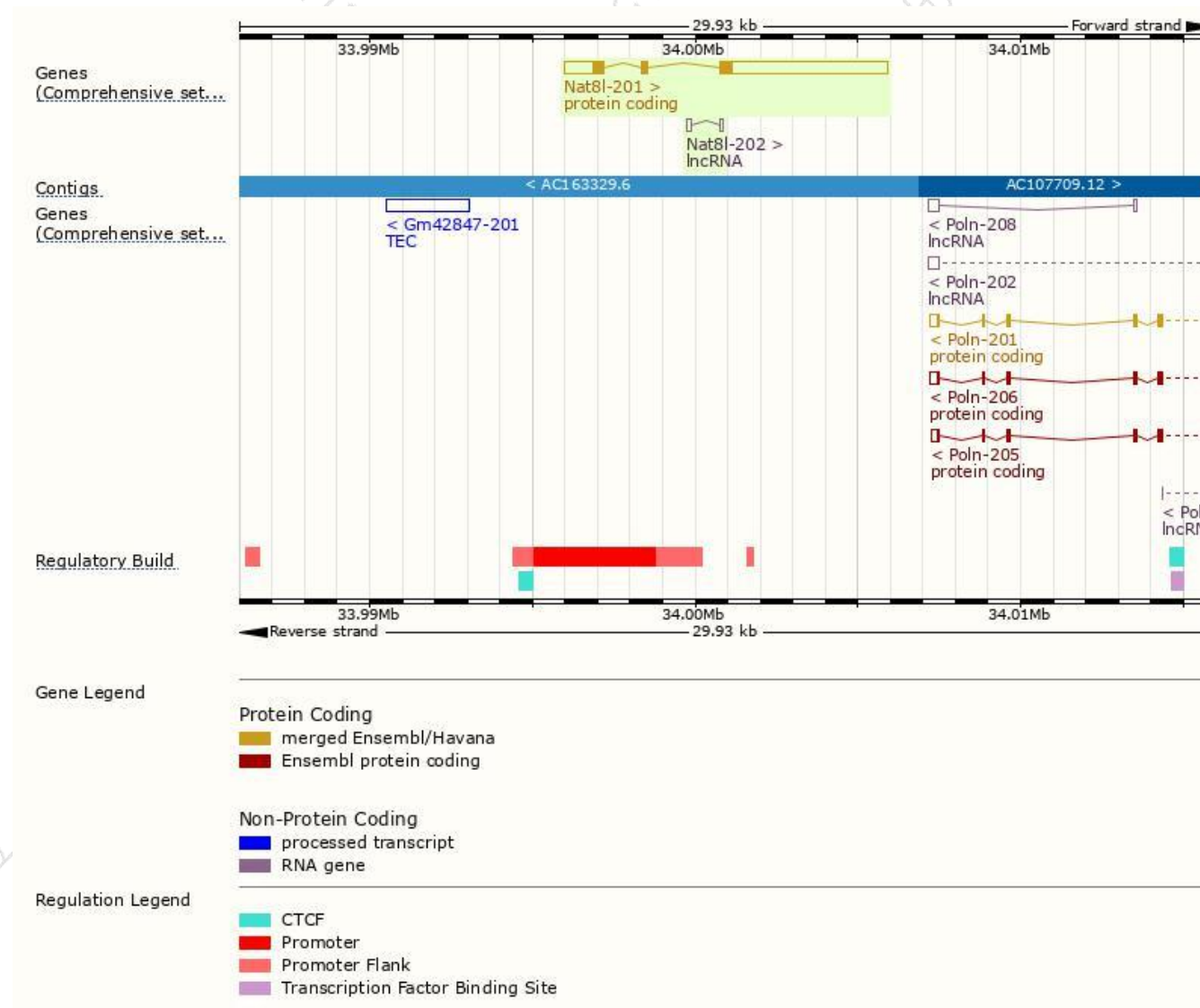
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nat8l-201	ENSMUST00000056355.8	6529	299aa	Protein coding	CCDS19210	A0A0R4J0R4	TSL:1 GENCODE basic APPRIS P1
Nat8l-202	ENSMUST00000201041.1	205	No protein	lncRNA	-	-	TSL:5

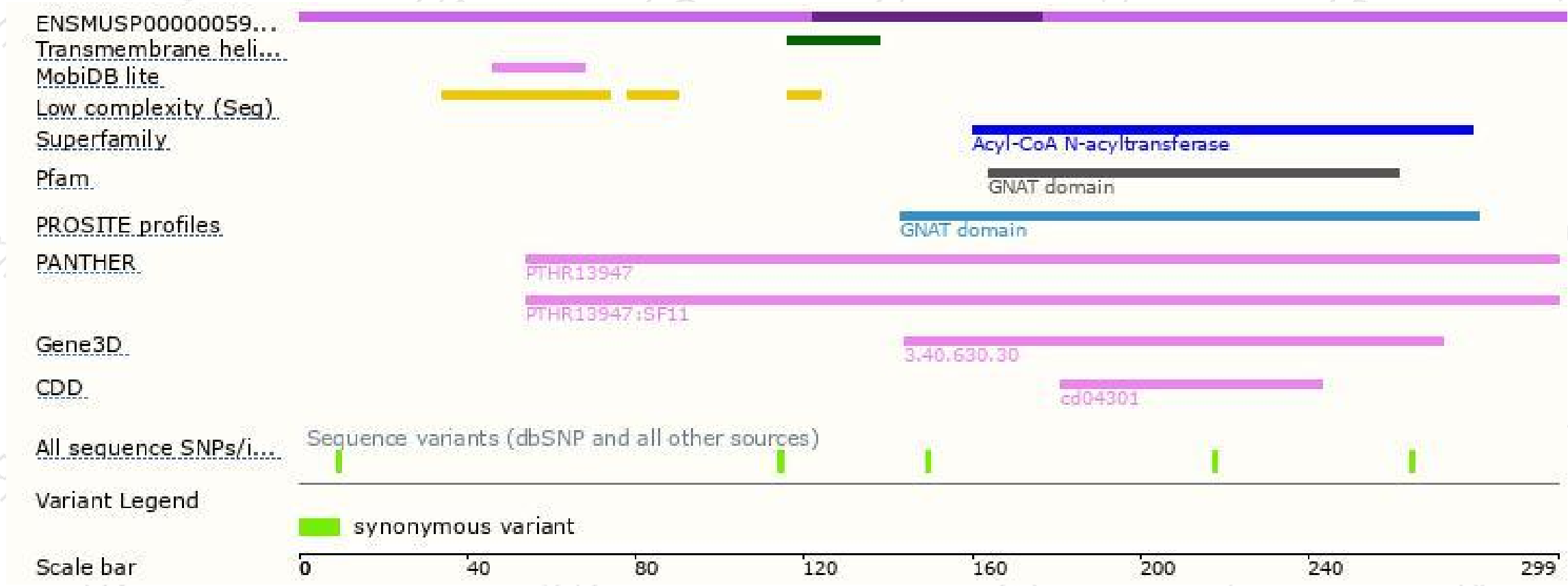
The strategy is based on the design of *Nat8l-201* transcript,The transcription is shown below



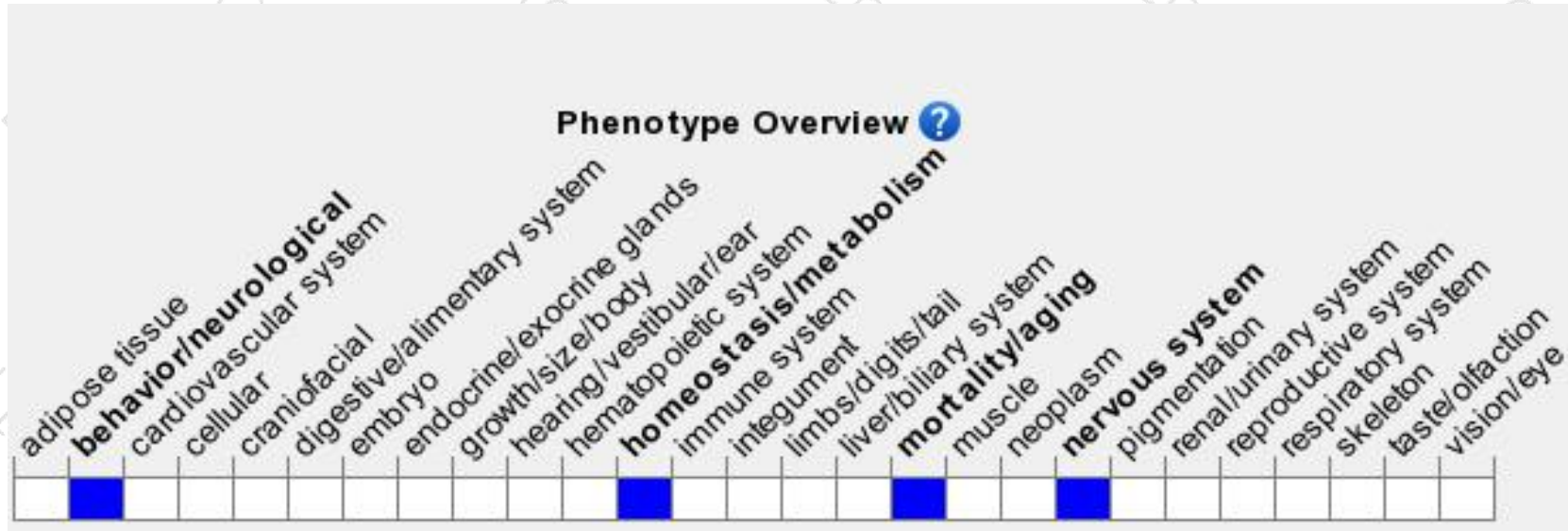
Genomic location distribution



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 mutation display abnormal responses to novelty and decreased social investigation in a novel environment.

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

Tel: 400-9660890

