Snta1 Cas9-CKO Strategy

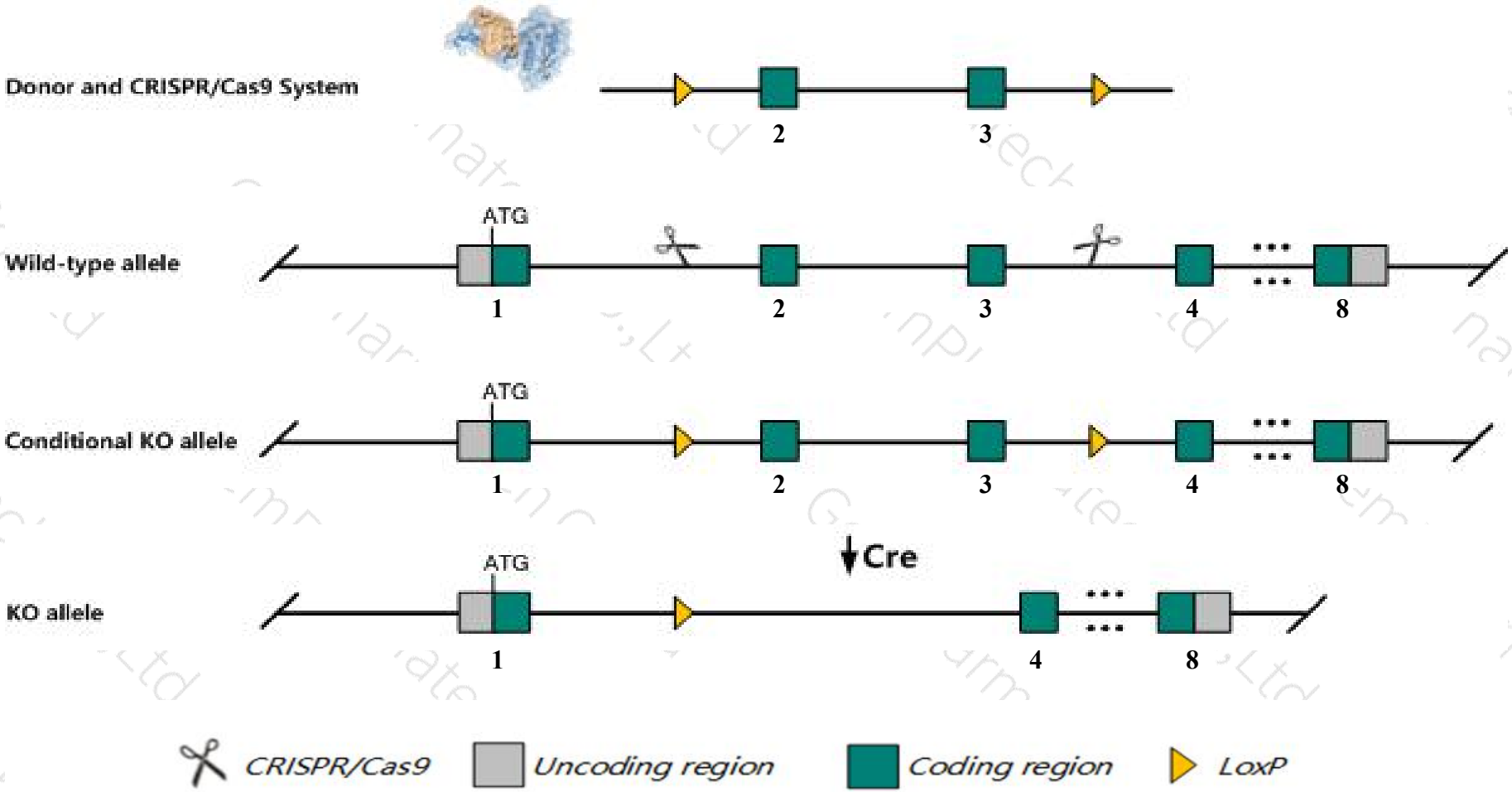
Designer:Xueting Zhang
Reviewer:Yanhua Shen
Date:2019-11-18

Project Overview

Project Name	***Snta1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Snta1* gene. The schematic diagram is as follows:



Technical routes

- The *Snta1* gene has 3 transcripts. According to the structure of *Snta1* gene, exon2-exon3 of *Snta1-202* (ENSMUST00000109728.7) transcript is recommended as the knockout region.The region contains 391bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Snta1* gene. The brief process is as follows:gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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.

Notice

- According to the existing MGI data,Mice homozygous for a targeted null allele display impaired astrocyte and neuromuscular synapse morphology. Mice homozygous for another targeted null allele show neither gross histological abnormalities in skeletal muscle nor significant changes in muscle contractile properties.

- The *Snta1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Snta1 syntrophin, acidic 1 [*Mus musculus* (house mouse)]

Gene ID: 20648, updated on 10-Oct-2019

Summary

Official Symbol	Snta1 provided by MGI
Official Full Name	syntrophin, acidic 1 provided by MGI
Primary source	MGI:MGI:101772
See related	Ensembl:ENSMUSG00000027488
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	Snt1; AW228934
Expression	Ubiquitous expression in adrenal adult (RPKM 25.8), kidney adult (RPKM 24.0) and 26 other tissues See more
Orthologs	human all

Genomic context

Location: 2 H1; 2 76.52 cM

See Snta1 in Genome Data Viewer

Exon count: 8

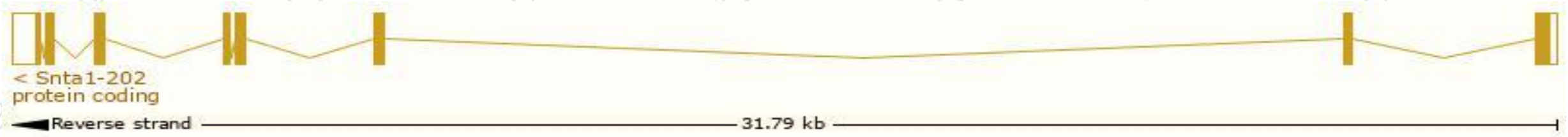
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (154376313..154408107, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (154202050..154233820, complement)

Transcript information（Ensembl）

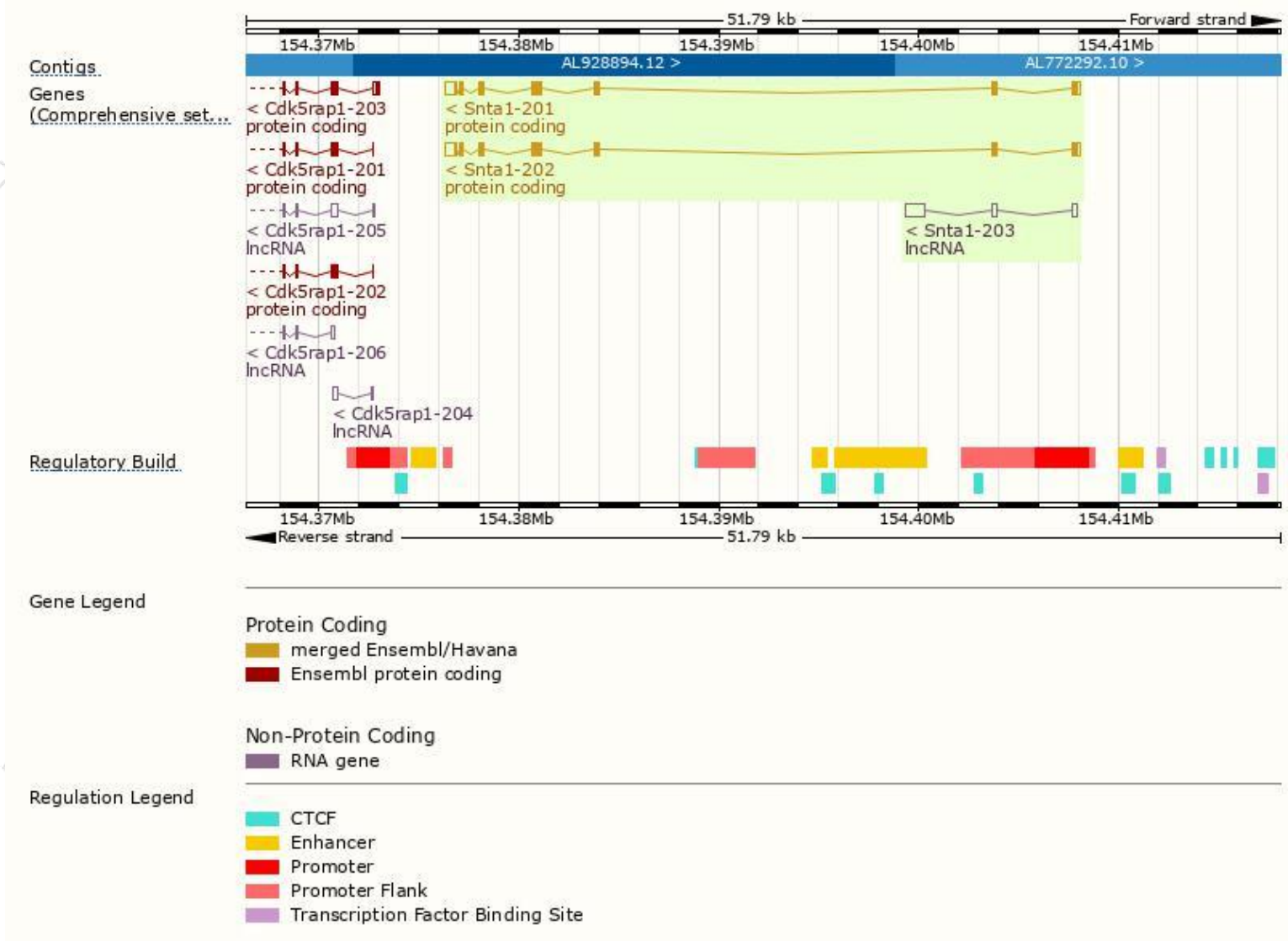
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snta1-202	ENSMUST00000109728.7	2131	499aa	Protein coding	CCDS50763	A2AKD7	TSL:1 GENCODE basic APPRIS P2
Snta1-201	ENSMUST00000028991.6	2125	503aa	Protein coding	-	Q61234	TSL:1 GENCODE basic APPRIS ALT2
Snta1-203	ENSMUST00000133018.1	1438	No protein	lncRNA	-	-	TSL:1

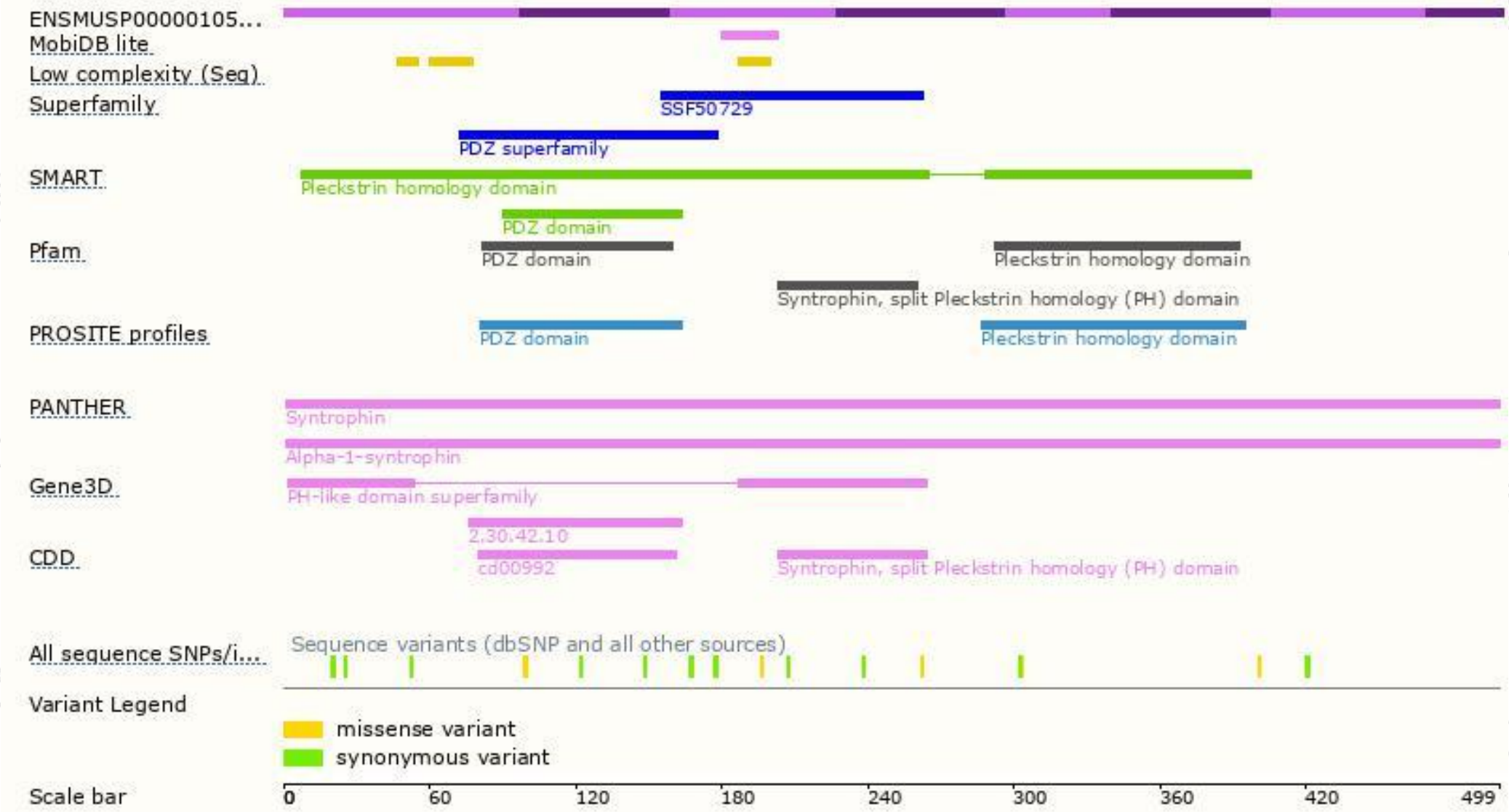
The strategy is based on the design of *Snta1-202* transcript,The transcription is shown below



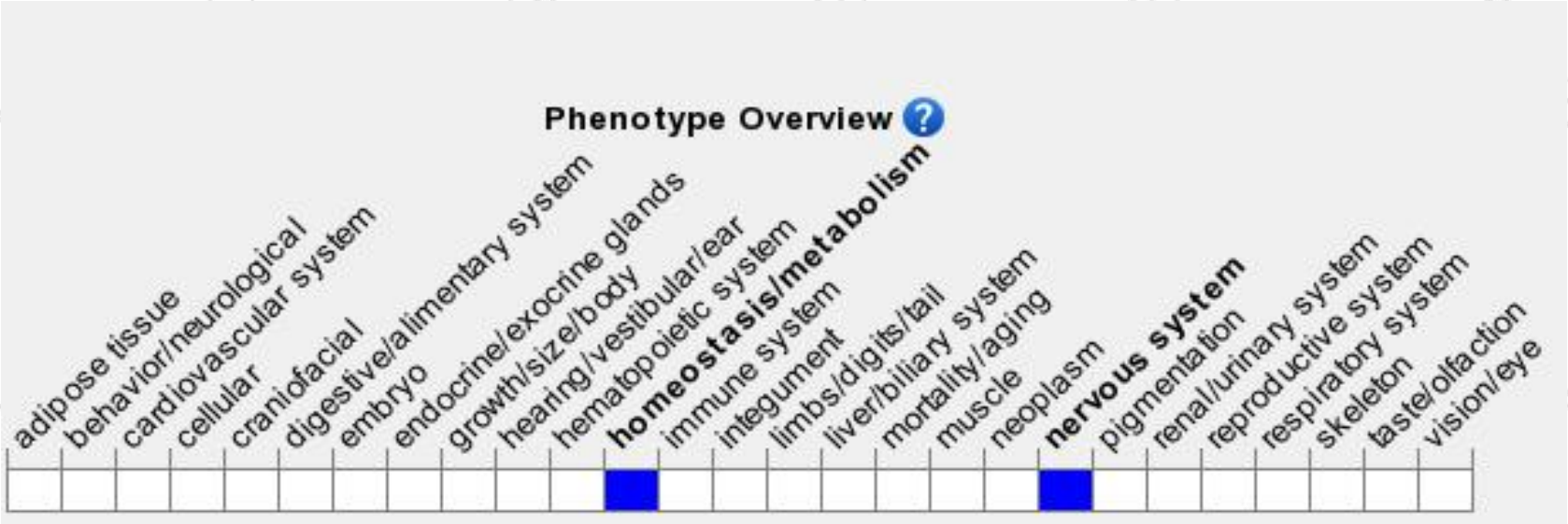
Genomic location distribution



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.

Tel: 400-9660890

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GemPharmatech Co.,Ltd