Slc12a1 Cas9-KO Strategy

Designer:Xueting Zhang
Reviewer:Yanhua Shen
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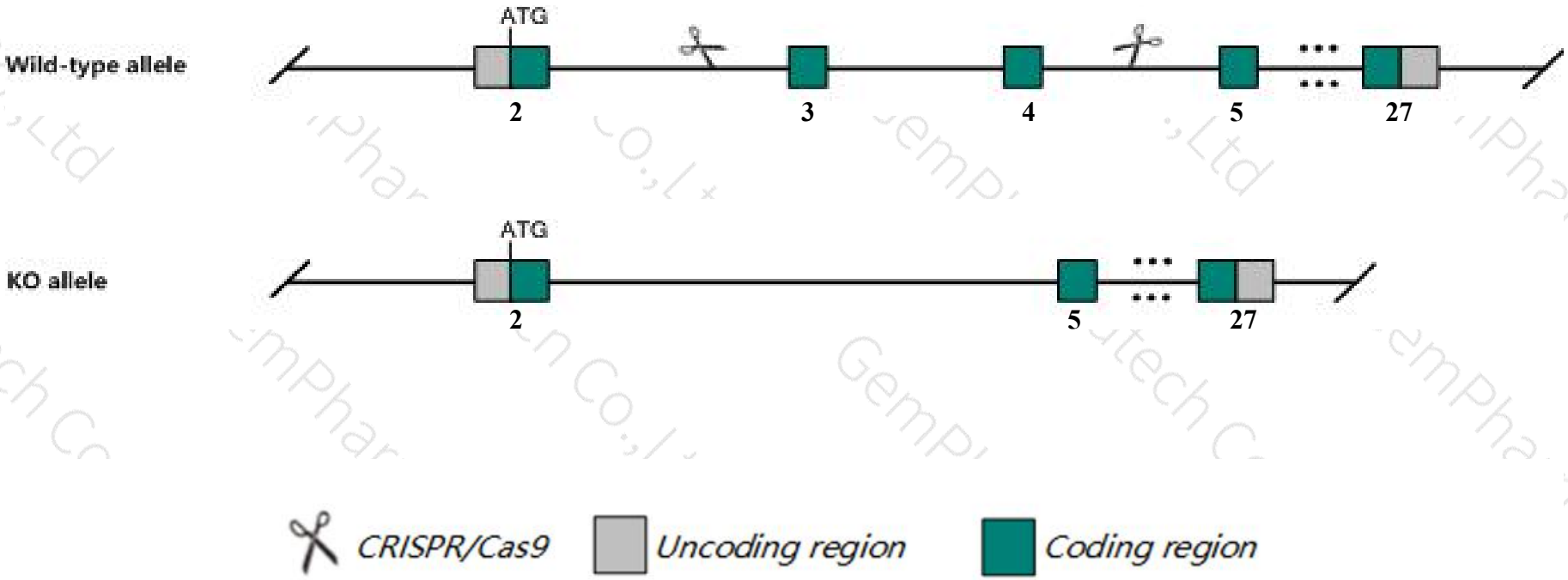
Project Overview

Project Name	***Slc12a1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc12a1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc12a1* gene has 4 transcripts. According to the structure of *Slc12a1* gene, exon3-exon4 of *Slc12a1-201* (ENSMUST00000028630.8) transcript is recommended as the knockout region.The region contains 208bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc12a1* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ According to the existing MGI data,Mice homozygous for disruptions in this gene do not survive to weaning and suffer from various metabolic abnormalities related to kidney function. Mice homozygous for an ENU-induced allele exhibit kidney disease, impaired urinary excretion of metabolism products, polyuria, and kidney alterations.

➢ The *Slc12a1* 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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Slc12a1 solute carrier family 12, member 1 [*Mus musculus* (house mouse)]

Gene ID: 20495, updated on 10-Sep-2019

Summary

Official Symbol	Slc12a1 provided by MGI
Official Full Name	solute carrier family 12, member 1 provided by MGI
Primary source	MGI:MGI:103150
See related	Ensembl:ENSMUSG00000027202
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	Nkcc2; mBSC1; urehr3; AI788571; D630042G03Rik
Expression	Restricted expression toward kidney adult (RPKM 70.5) See more
Orthologs	human all

Genomic context

Location: 2 F1; 2 61.23 cM

See Slc12a1 in Genome Data Viewer

Exon count: 29

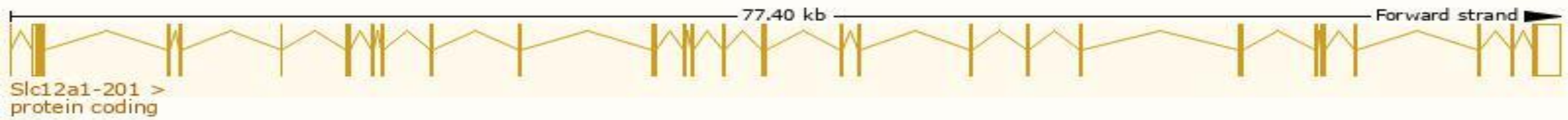
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (125152510..125230002)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (124978336..125055738)

Transcript information（Ensembl）

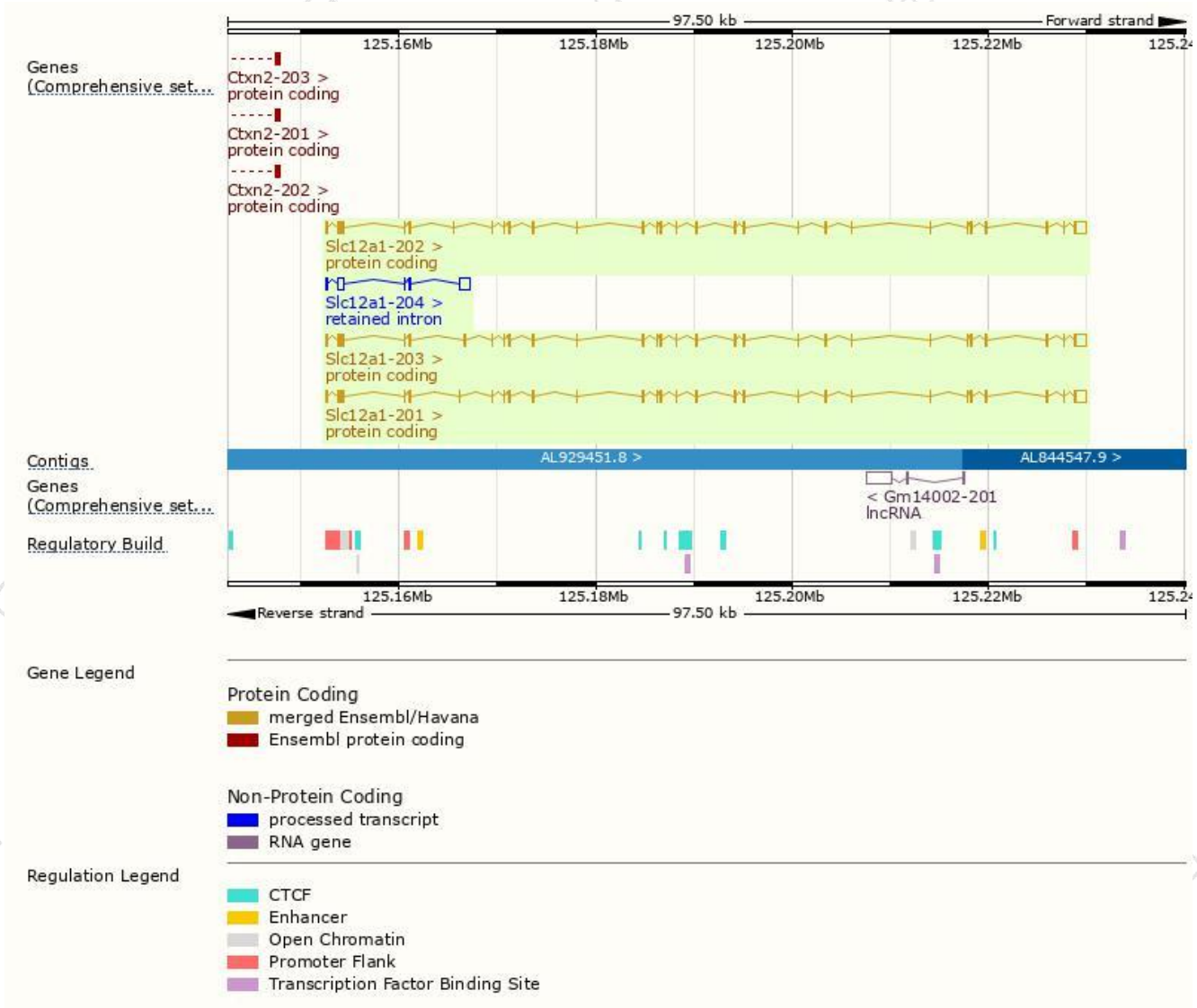
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc12a1-201	ENSMUST00000028630.8	4645	1090aa	Protein coding	CCDS50693	A2AQ50	TSL:1 GENCODE basic
Slc12a1-203	ENSMUST00000110495.2	4642	1090aa	Protein coding	CCDS50694	A2AQ51	TSL:5 GENCODE basic APPRIS P2
Slc12a1-202	ENSMUST00000110494.8	4740	1090aa	Protein coding	-	A2AQ52	TSL:5 GENCODE basic APPRIS ALT2
Slc12a1-204	ENSMUST00000147095.1	1876	No protein	Retained intron	-	-	TSL:1

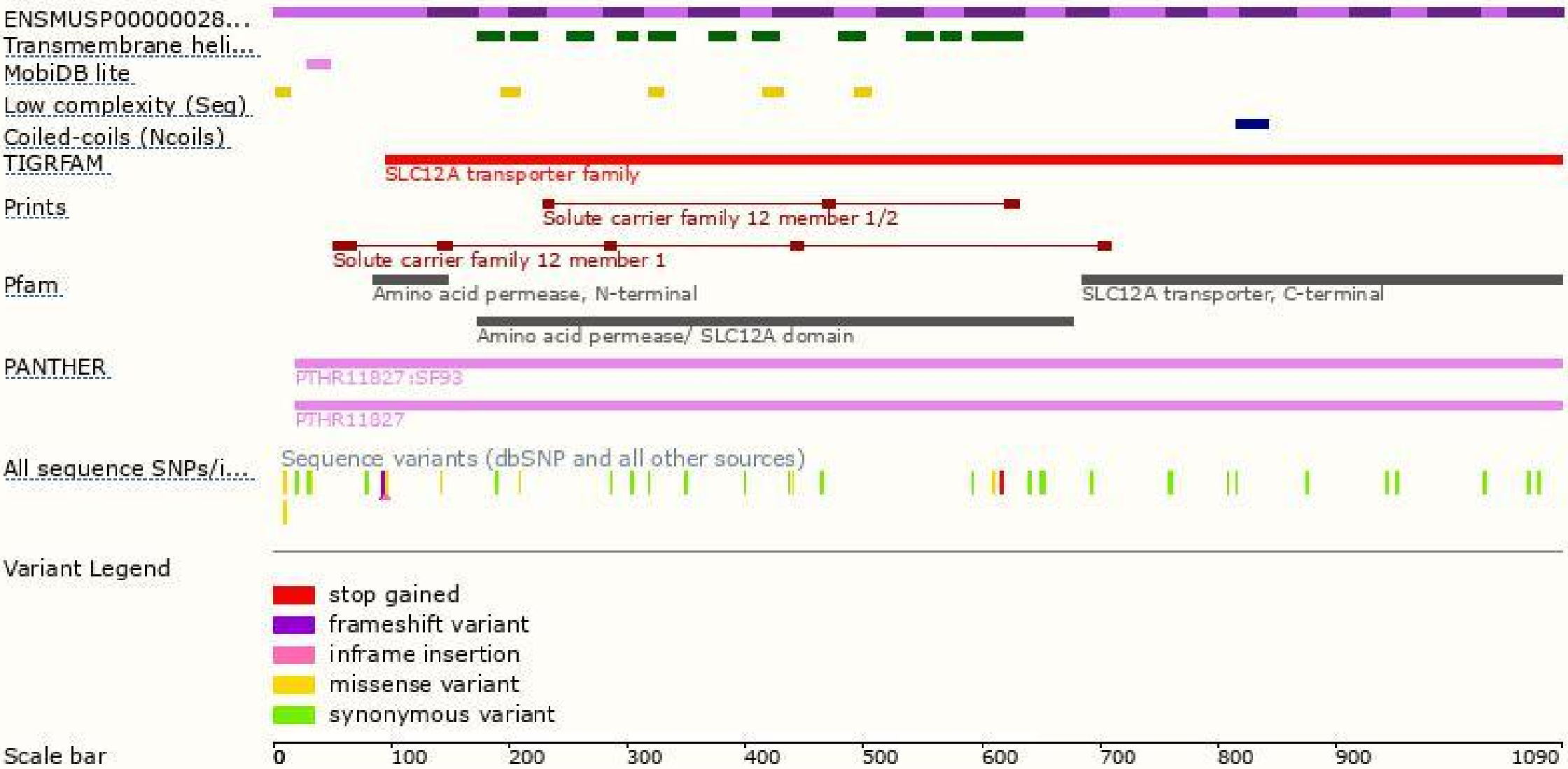
The strategy is based on the design of *Slc12a1-201* transcript,The transcription is shown below



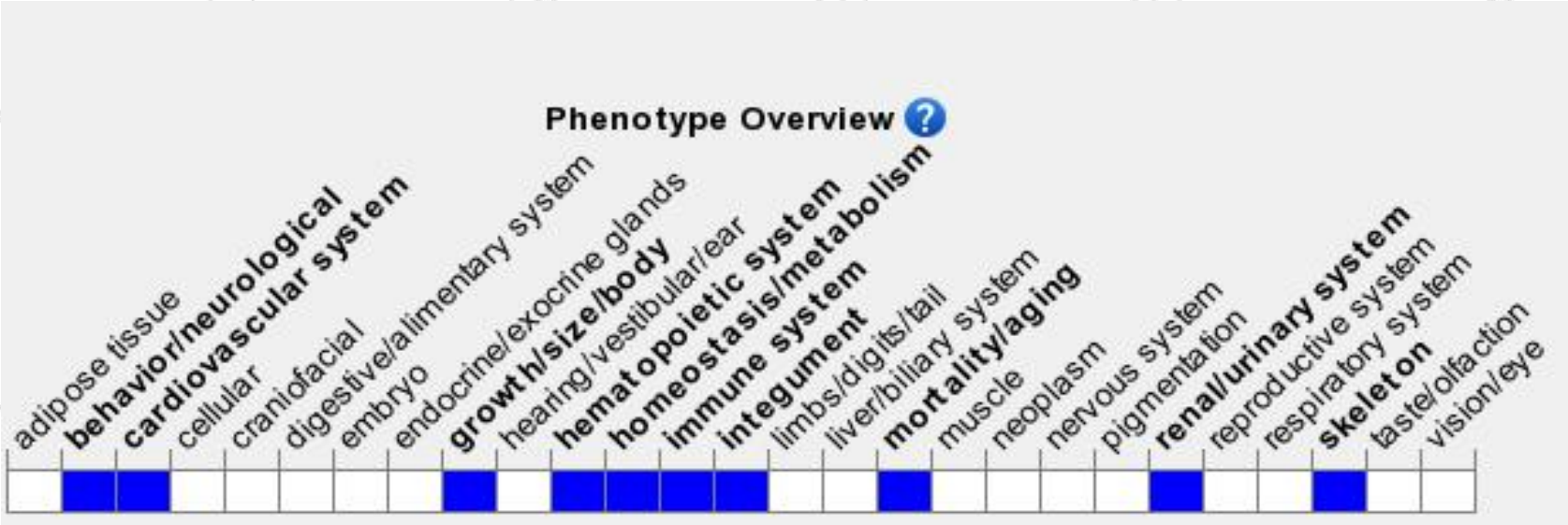
Genomic location distribution



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 do not survive to weaning and suffer from various metabolic abnormalities related to kidney function. Mice homozygous for an ENU-induced allele exhibit kidney disease, impaired urinary excretion of metabolism products, polyuria, and kidney alterations.

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GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd