Slco1c1 Cas9-KO Strategy

Designer:Xueting Zhang
Reviewer:Yanhua Shen
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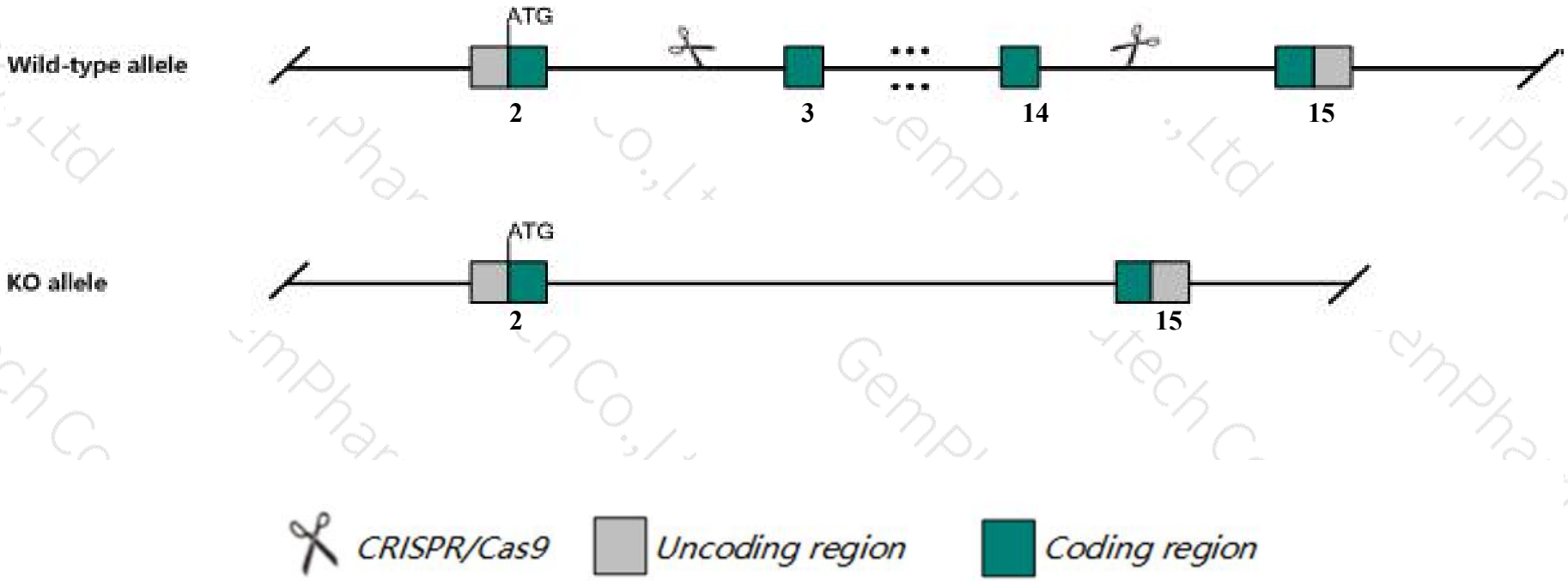
Project Overview

Project Name	***Slco1c1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slco1c1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slco1c1* gene has 6 transcripts. According to the structure of *Slco1c1* gene, exon3-exon14 of *Slco1c1-201* (ENSMUST00000032362.11) transcript is recommended as the knockout region.The region contains 1796bp coding sequenc Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slco1c1* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit decreased thyroxine and triiodothyronine levels in the forebrain, in the absence of overt growth, reproductive or neurological abnormalities.

- The *Slco1c1* gene is located on the Chr6. 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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Slco1c1 solute carrier organic anion transporter family, member 1c1 [*Mus musculus* (house mouse)]

Gene ID: 58807, updated on 5-Oct-2019

Summary

Official Symbol	Slco1c1 provided by MGI
Official Full Name	solute carrier organic anion transporter family, member 1c1 provided by MGI
Primary source	MGI:MGI:1889679
See related	Ensembl:ENSMUSG00000030235
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	Oatp2; Oatpf; OATP-F; OATP-14; Slc21a14
Expression	Biased expression in frontal lobe adult (RPKM 12.2), cortex adult (RPKM 11.8) and 4 other tissues See more
Orthologs	human all

Genomic context

Location: 6; 6 G2

See Slco1c1 in Genome Data Viewer

Exon count: 15

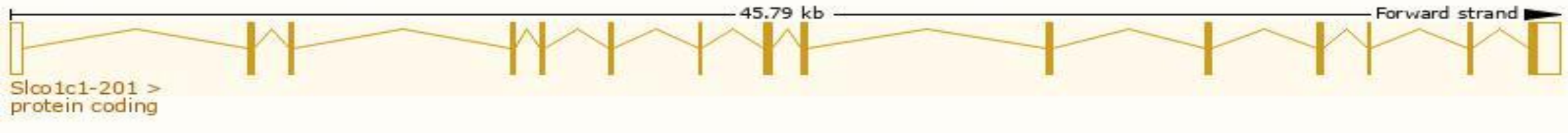
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	6	NC_000072.6 (141524354..141570177)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	6	NC_000072.5 (141472907..141518698)

Transcript information（Ensembl）

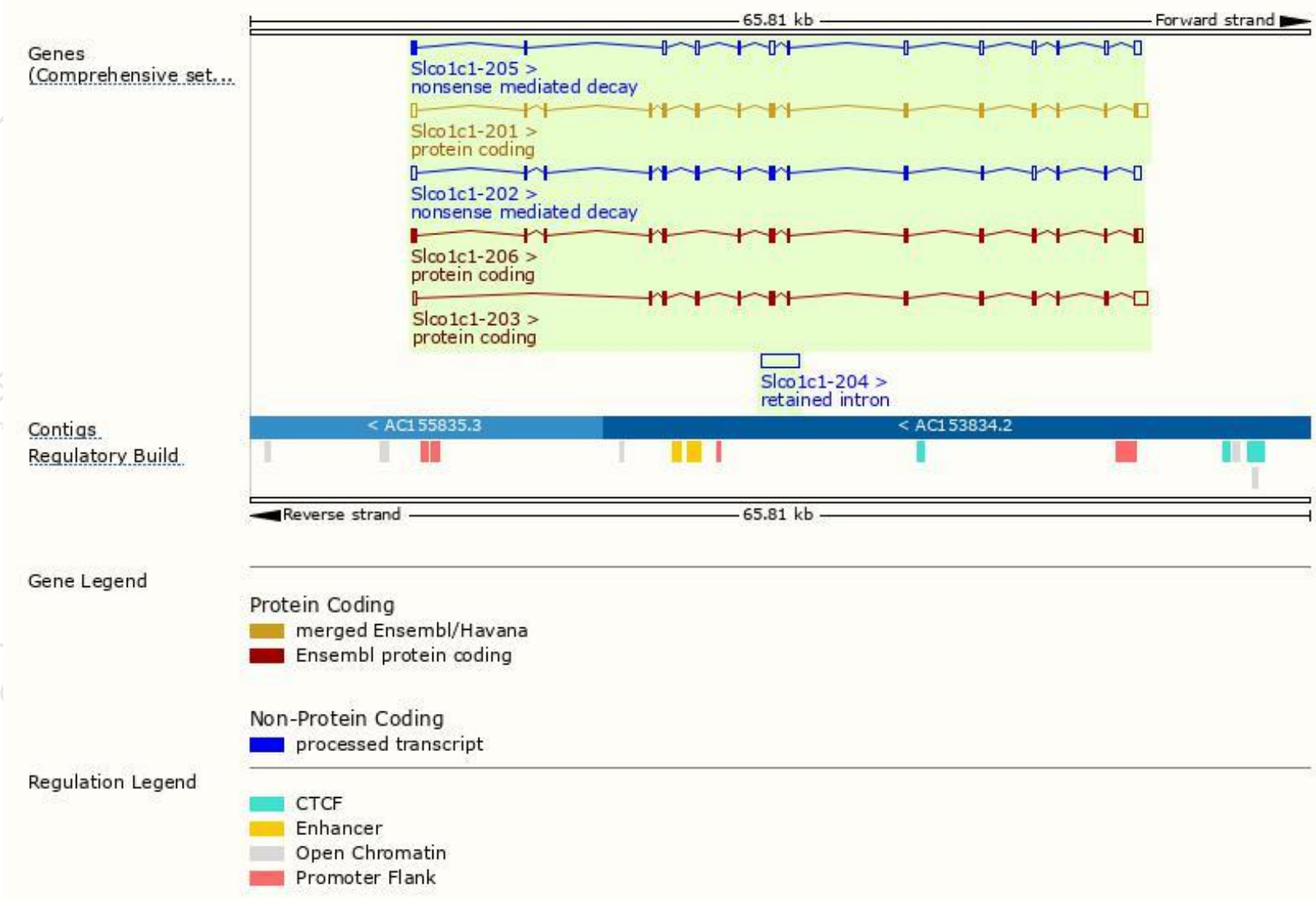
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slco1c1-201	ENSMUST00000032362.11	3178	715aa	Protein coding	CCDS20677	Q9ERB5	TSL:1 GENCODE basic APPRIS P2
Slco1c1-203	ENSMUST00000203140.1	2771	544aa	Protein coding	-	A0A0N4SVD7	TSL:5 GENCODE basic APPRIS ALT2
Slco1c1-206	ENSMUST00000205214.2	2515	666aa	Protein coding	-	A0A0N4SUZ6	TSL:5 GENCODE basic
Slco1c1-202	ENSMUST00000135562.7	2680	469aa	Nonsense mediated decay	-	Q66L38	TSL:1
Slco1c1-205	ENSMUST00000204998.2	2427	46aa	Nonsense mediated decay	-	A0A0N4SW25	TSL:5
Slco1c1-204	ENSMUST00000203755.1	2300	No protein	Retained intron	-	-	TSL:NA

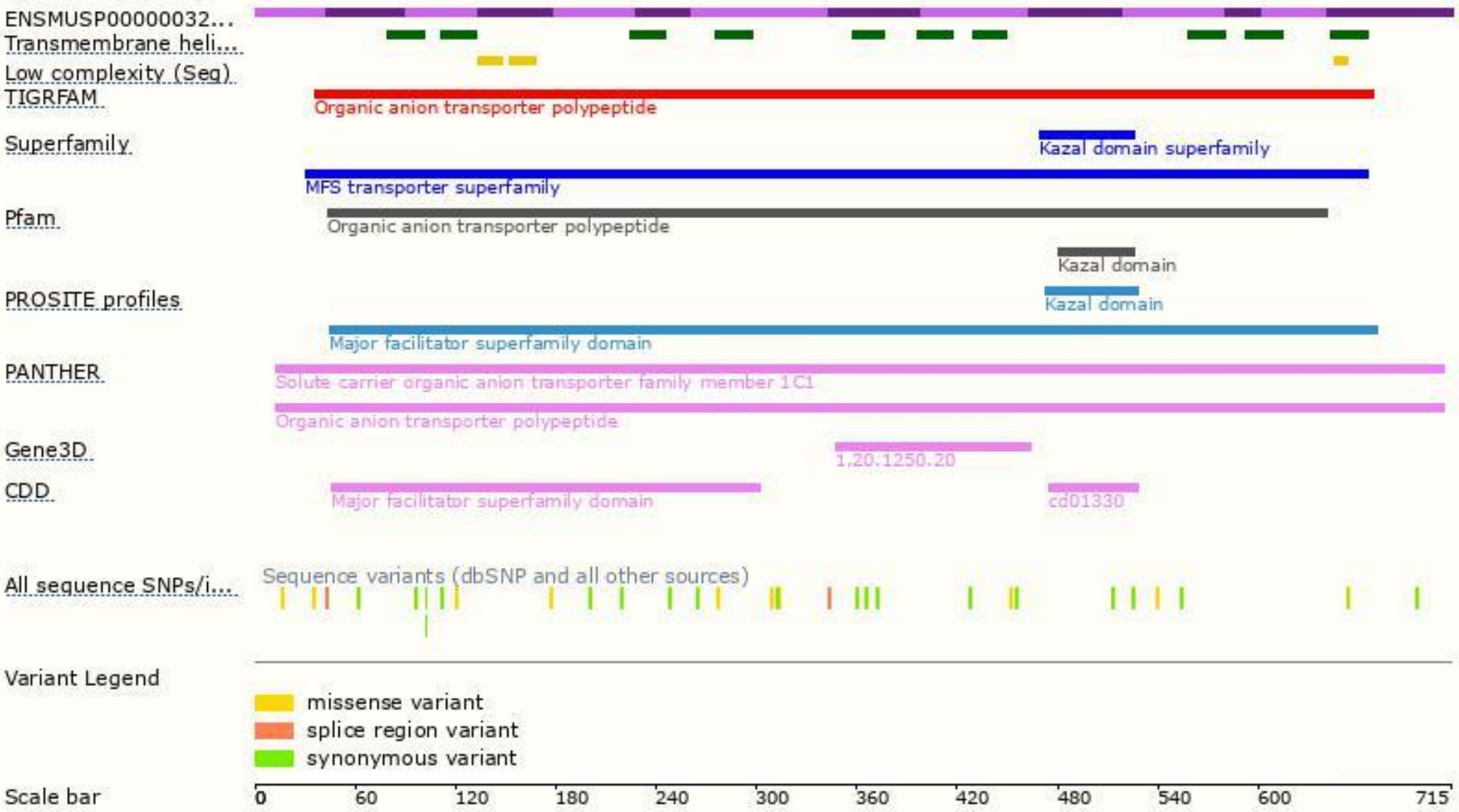
The strategy is based on the design of *Slco1c1-201* transcript,The transcription is shown below



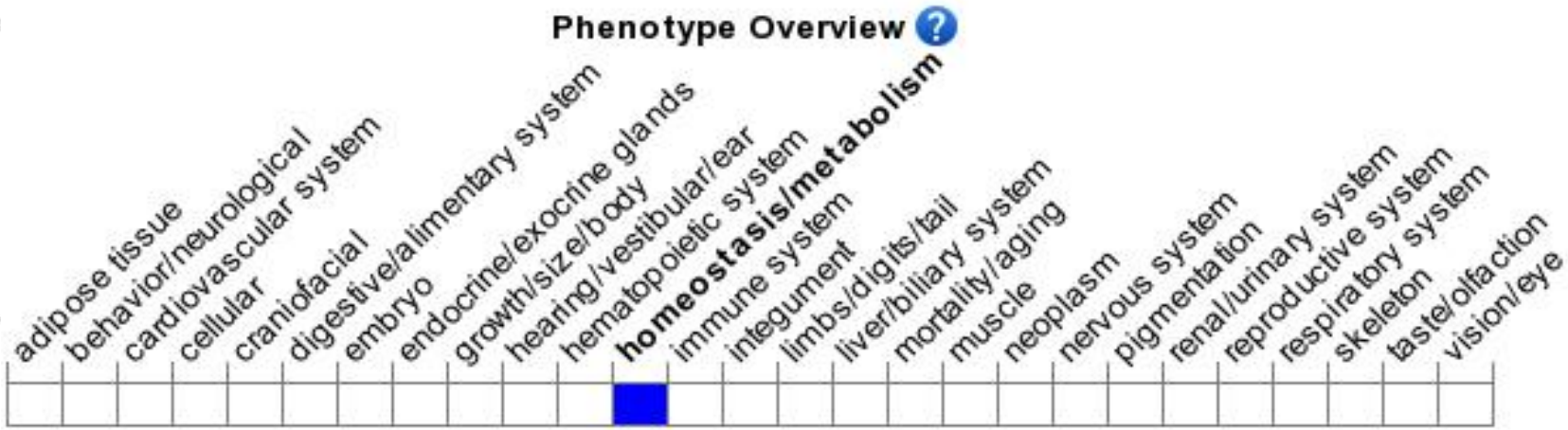
Genomic location distribution



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/).

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集萃药康
GemPharmatech

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

Tel: 400-9660890

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GemPharmatech Co.,Ltd