Slc22a5 Cas9-KO Strategy

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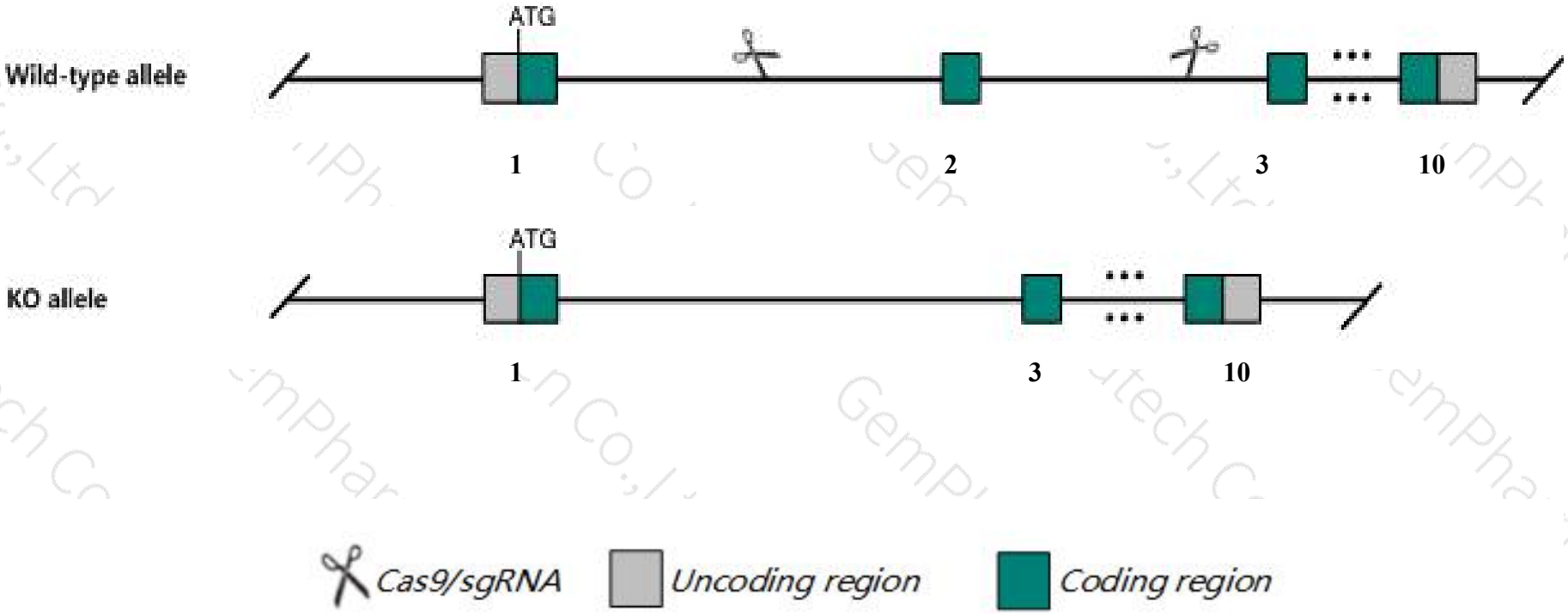
Project Overview

Project Name	***Slc22a5***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc22a5* gene. The schematic diagram is as follows:



Technical routes

- The *Slc22a5* gene has 3 transcripts. According to the structure of *Slc22a5* gene, exon2 of *Slc22a5-201* (ENSMUST00000019044.7) transcript is recommended as the knockout region.The region contains 104bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc22a5* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

Notice

- According to the existing MGI data,Homozygotes for a spontaneous missense mutation exhibit systemic carnitine deficiency, cardiac hypertrophy, impaired Na-dependent carnitine transport, fatty liver, hypoglycemia, high postnatal mortality, and male infertility.

- The *Slc22a5* gene is located on the Chr11. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information（NCBI）

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Slc22a5 solute carrier family 22 (organic cation transporter), member 5 [Mus musculus (house mouse)]

Gene ID: 20520, updated on 29-Mar-2019

Summary

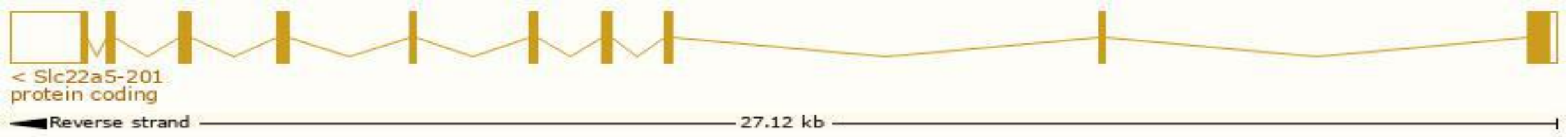
Official Symbol	Slc22a5 provided by MGI
Official Full Name	solute carrier family 22 (organic cation transporter), member 5 provided by MGI
Primary source	MGI:MGI:1329012
See related	Ensembl:ENSMUSG00000018900
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Lstpl, Octn2, jvs
Expression	Broad expression in kidney adult (RPKM 72.8), placenta adult (RPKM 29.8) and 24 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

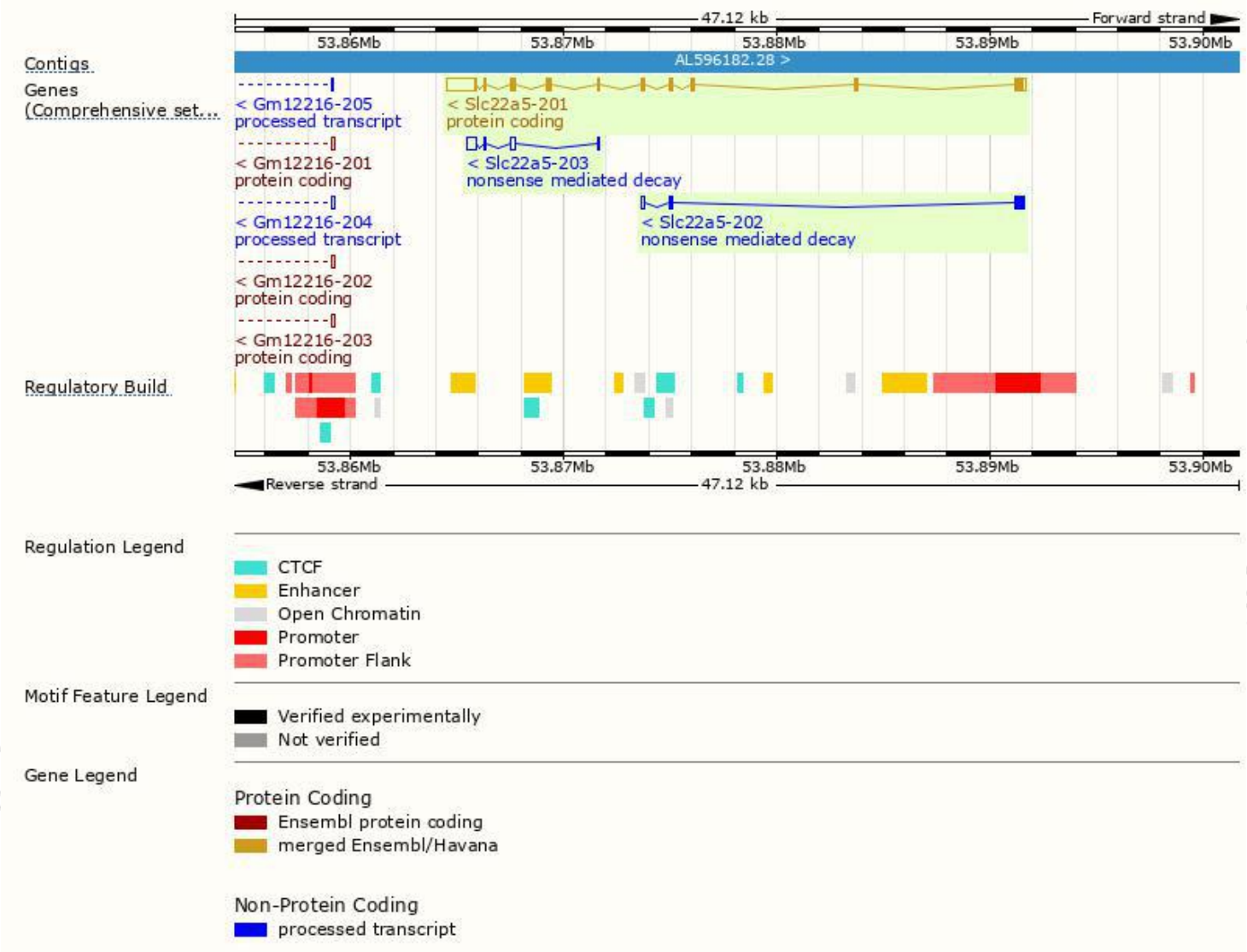
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc22a5-201	ENSMUST00000019044.7	3062	557aa	Protein coding	CCDS24687	Q5SX17 Q9Z0E8	TSL:1 GENCODE basic APPRIS P1
Slc22a5-203	ENSMUST00000152084.1	861	36aa	Nonsense mediated decay	-	F6TNN8	CDS 5' incomplete TSL:5
Slc22a5-202	ENSMUST00000136307.1	737	146aa	Nonsense mediated decay	-	D6RH54	TSL:2

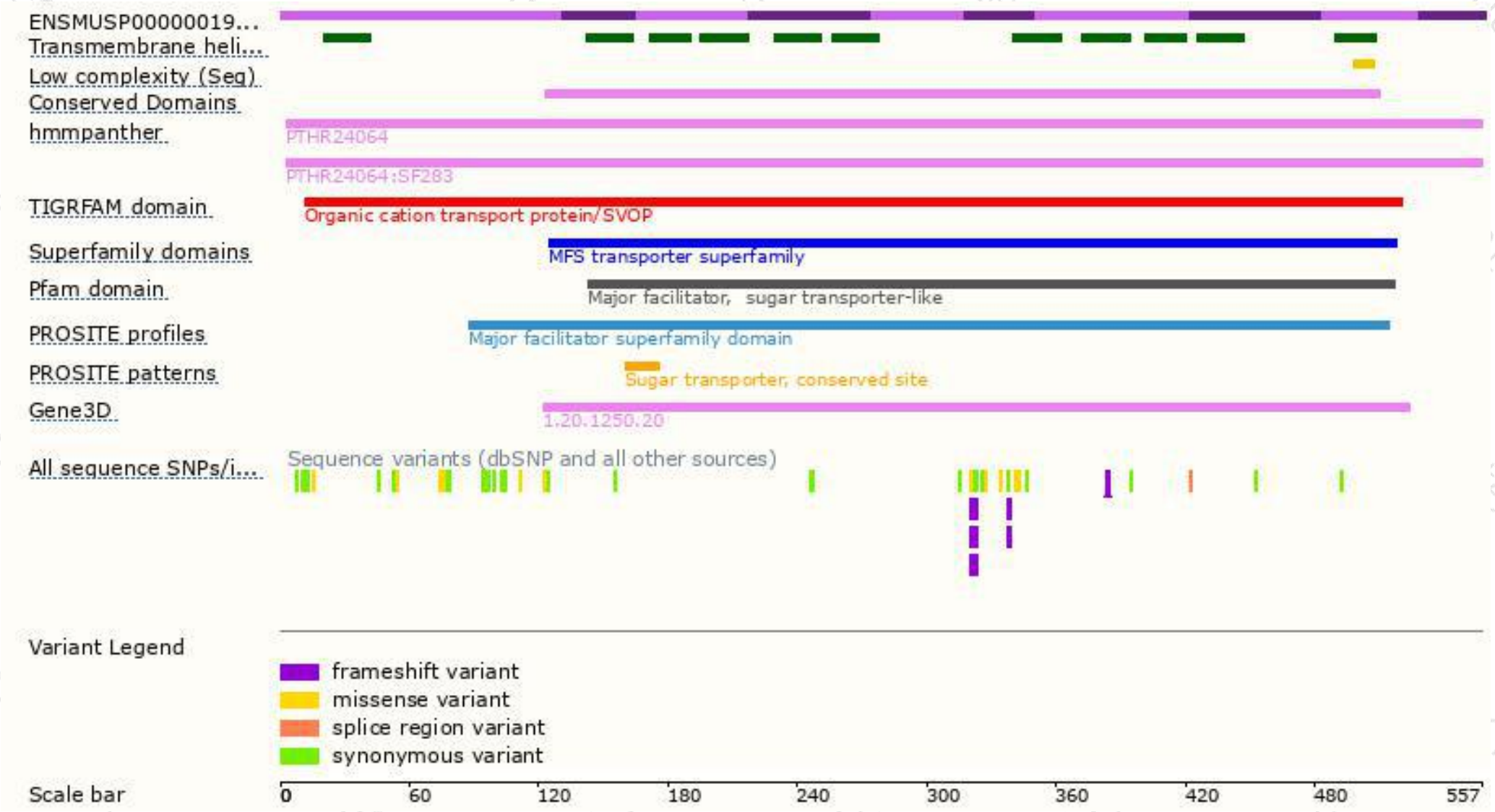
The strategy is based on the design of *Slc22a5-201* transcript,The transcription is shown below



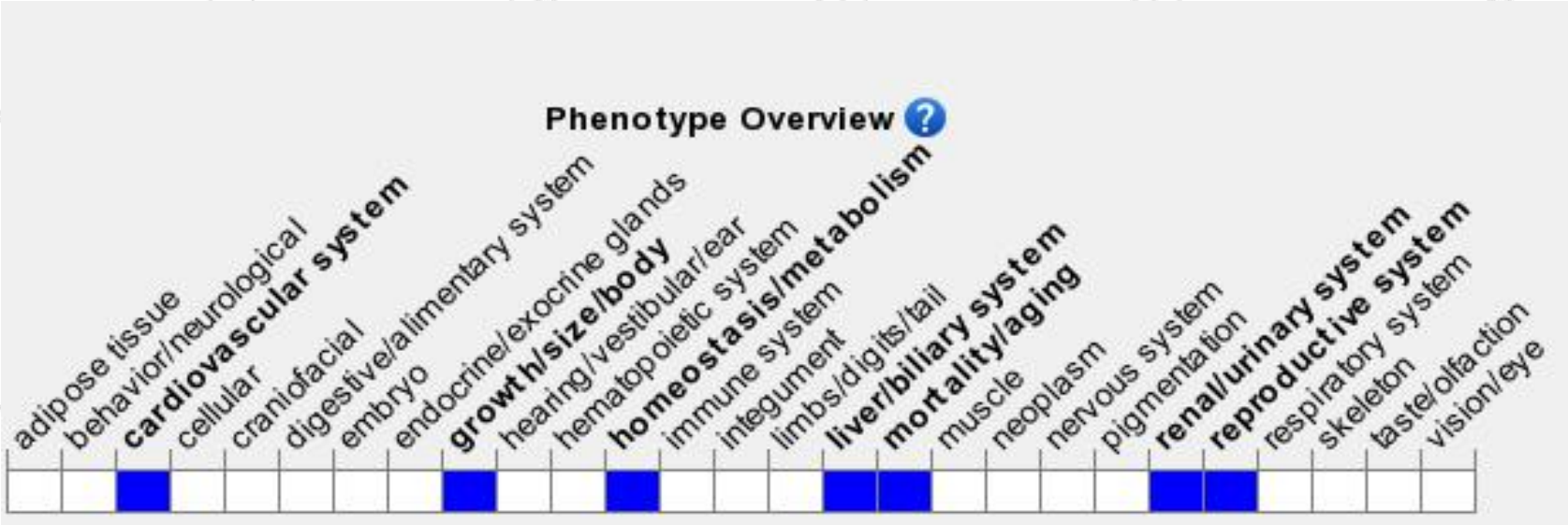
Genomic location distribution



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,Homozygotes for a spontaneous missense mutation exhibit systemic carnitine deficiency, cardiac hypertrophy, impaired Na-dependent carnitine transport, fatty liver, hypoglycemia, high postnatal mortality and male infertility.

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

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