Slco3a1 Cas9-CKO Strategy

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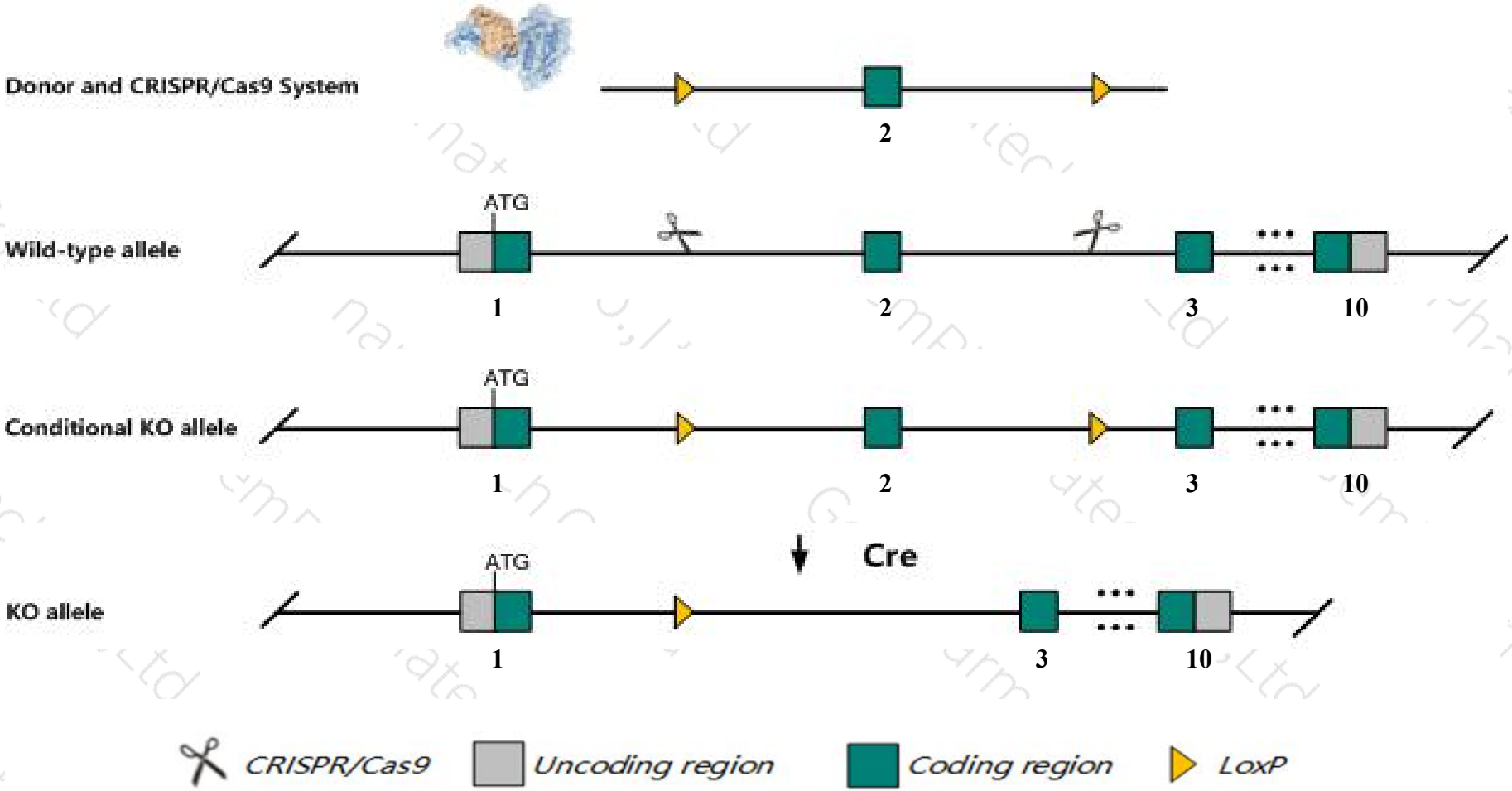
Project Overview

Project Name	***Slco3a1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slco3a1* gene. The schematic diagram is as follows:



Technical routes

- The *Slco3a1* gene has 8 transcripts. According to the structure of *Slco3a1* gene, exon2 of *Slco3a1-201* (ENSMUST00000026897.13) transcript is recommended as the knockout region.The region contains 466bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slco3a1* 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.

Notice

- According to the existing MGI data,mice for a null endonuclease-mediated mutation exhibit shorter survival times, increased hepatic levels of bile acid, and develop more liver injury after induction of cholestasis.
- The *Slco3a1* gene is located on the Chr7. 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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Slco3a1 solute carrier organic anion transporter family, member 3a1 [Mus musculus (house mouse)]

Gene ID: 108116, updated on 13-Mar-2020

Summary

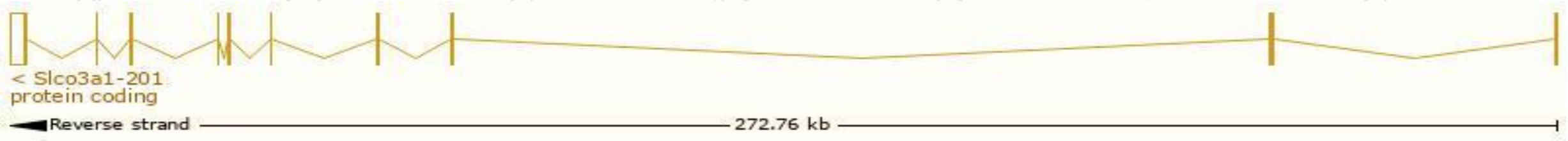
Official Symbol	Slco3a1 provided by MGI
Official Full Name	solute carrier organic anion transporter family, member 3a1 provided by MGI
Primary source	MGI:MGI:1351867
See related	Ensembl:ENSMUSG00000025790
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5830414C08Rik, Anr1, MJAM, OATP-D, R75096, Slc21a11
Expression	Broad expression in lung adult (RPKM 34.1), ovary adult (RPKM 22.9) and 24 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

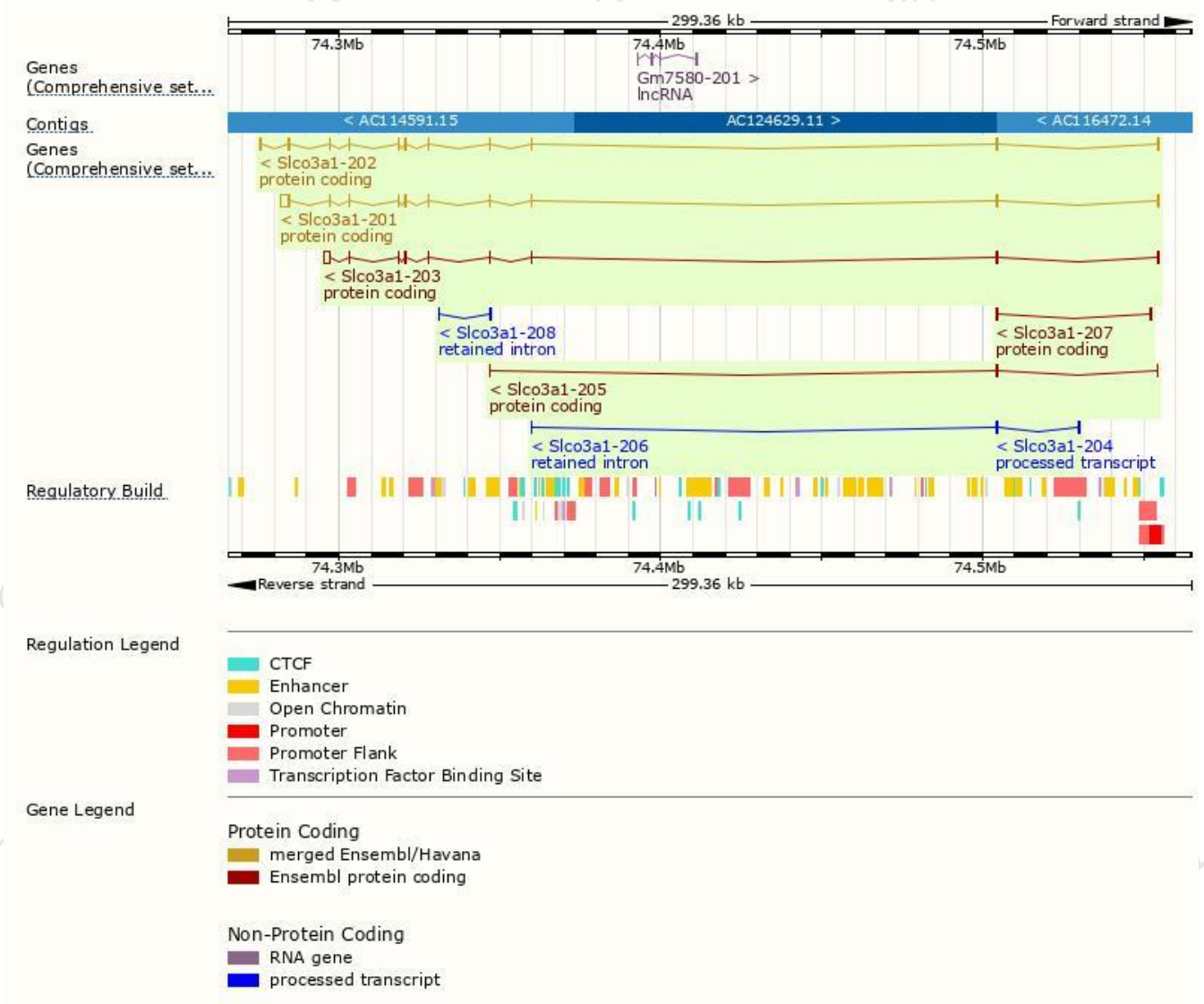
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slco3a1-201	ENSMUST00000026897.13	4589	710aa	Protein coding	CCDS21367	Q8R3L5	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P4
Slco3a1-202	ENSMUST00000098371.8	2709	692aa	Protein coding	CCDS21366	Q8R3L5	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Slco3a1-203	ENSMUST00000107453.7	3793	602aa	Protein coding	-	D3YXA8	TSL:1 GENCODE basic
Slco3a1-207	ENSMUST00000138099.1	887	165aa	Protein coding	-	D3YUC4	CDS 3' incomplete TSL:2
Slco3a1-205	ENSMUST00000134539.1	656	219aa	Protein coding	-	F7B851	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Slco3a1-204	ENSMUST00000129292.1	442	No protein	Processed transcript	-	-	TSL:3
Slco3a1-208	ENSMUST00000142175.1	628	No protein	Retained intron	-	-	TSL:3
Slco3a1-206	ENSMUST00000136389.1	425	No protein	Retained intron	-	-	TSL:2

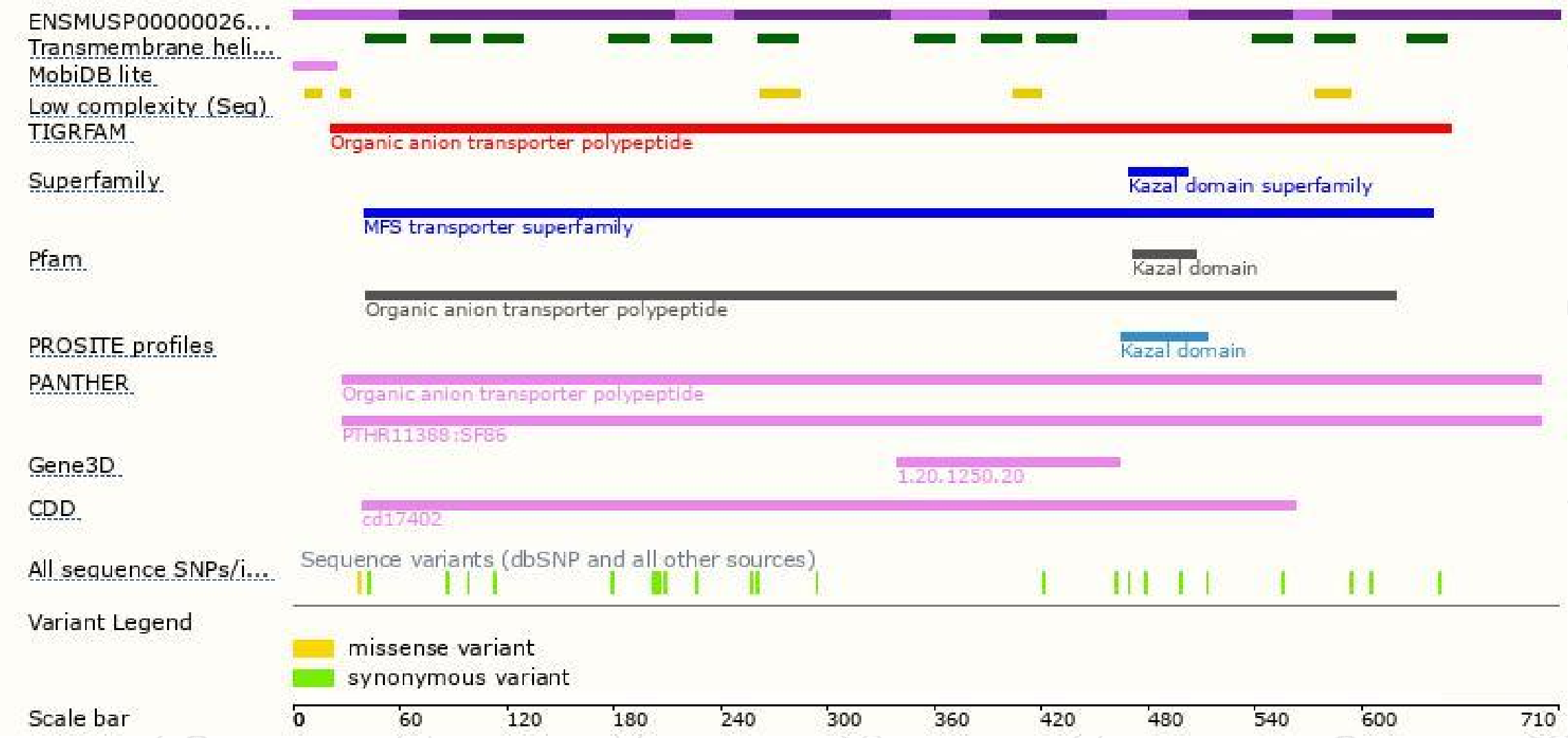
The strategy is based on the design of *Slco3a1-201* transcript,the transcription is shown below:



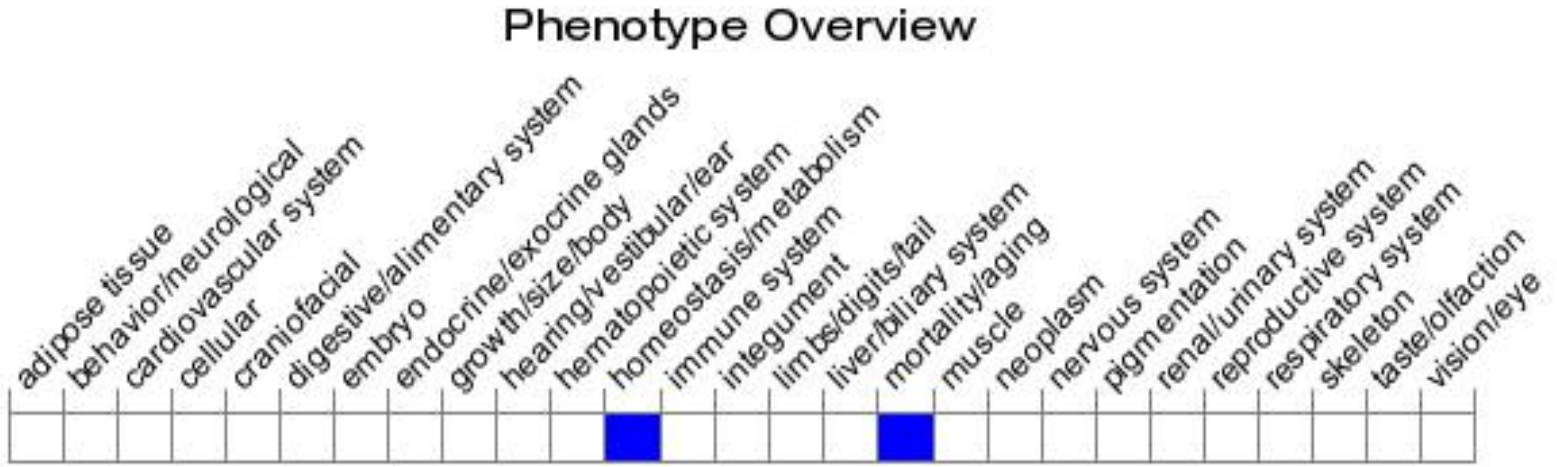
Genomic location distribution



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 for a null endonuclease-mediated mutation exhibit shorter survival times, increased hepatic levels of bile acid, and develop more liver injury after induction of cholestasis.

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

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