

Stard3 Cas9-CKO Strategy

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Reviewer:

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Design Date:

2020-2-13

Project Overview

Project Name

Stard3

Project type

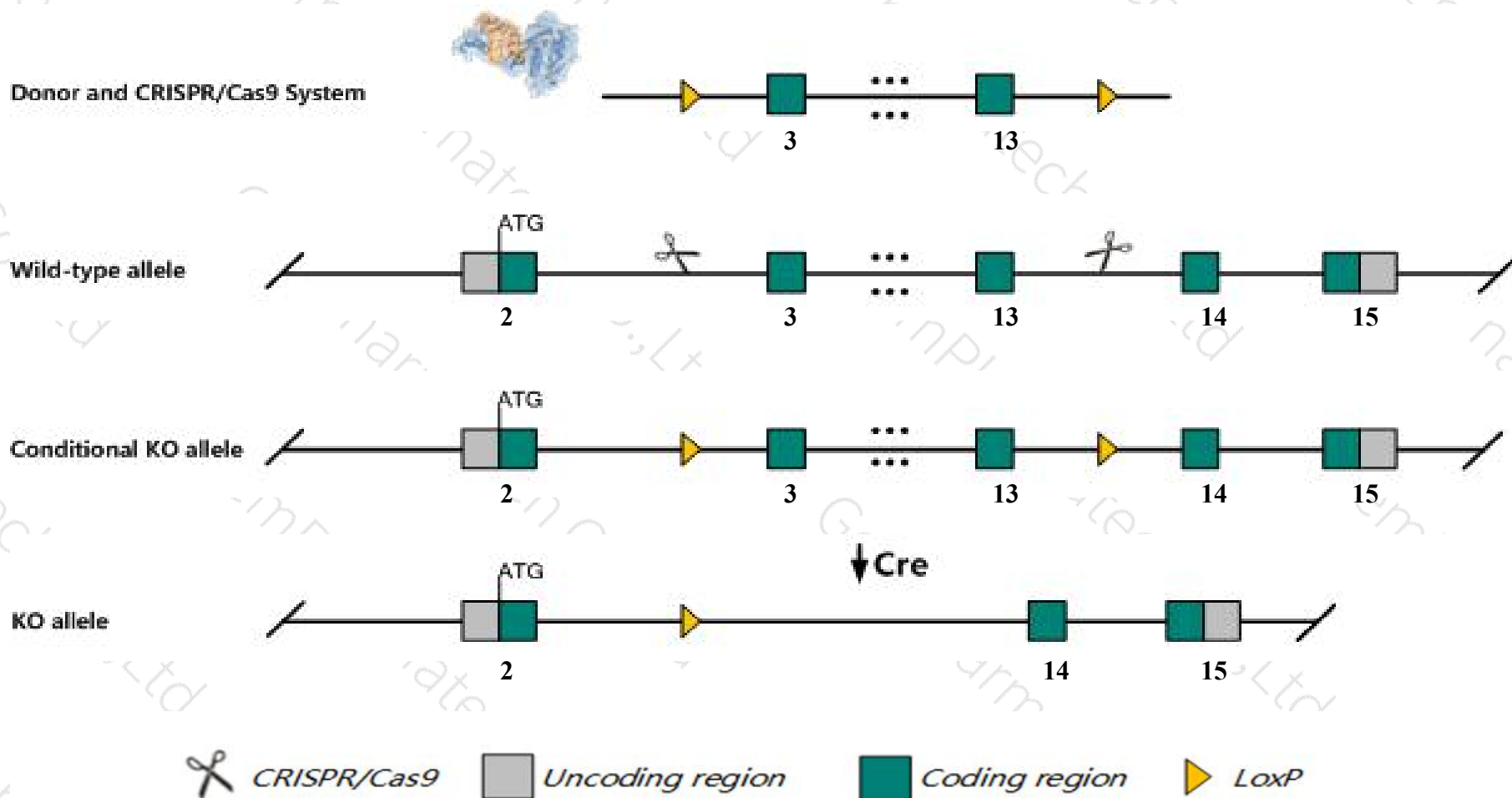
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stard3* gene. The schematic diagram is as follows:



Technical routes

- The *Stard3* gene has 7 transcripts. According to the structure of *Stard3* gene, exon3-exon13 of *Stard3-201* (ENSMUST00000018311.4) transcript is recommended as the knockout region. The region contains 920bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stard3* 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.

- According to the existing MGI data, mice homozygous for a truncated allele are viable and fertile and display mild defects in cholesterol metabolism.
- The *Stard3* 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 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)

Stard3 START domain containing 3 [*Mus musculus* (house mouse)]

Gene ID: 59045, updated on 10-Oct-2019

Summary



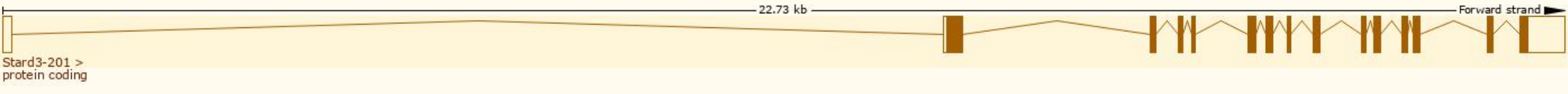
Official Symbol	Stard3 provided by MGI
Official Full Name	START domain containing 3 provided by MGI
Primary source	MGI:MGI:1929618
See related	Ensembl:ENSMUSG00000018167
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	es64; Mln64
Expression	Ubiquitous expression in thymus adult (RPKM 38.5), colon adult (RPKM 38.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

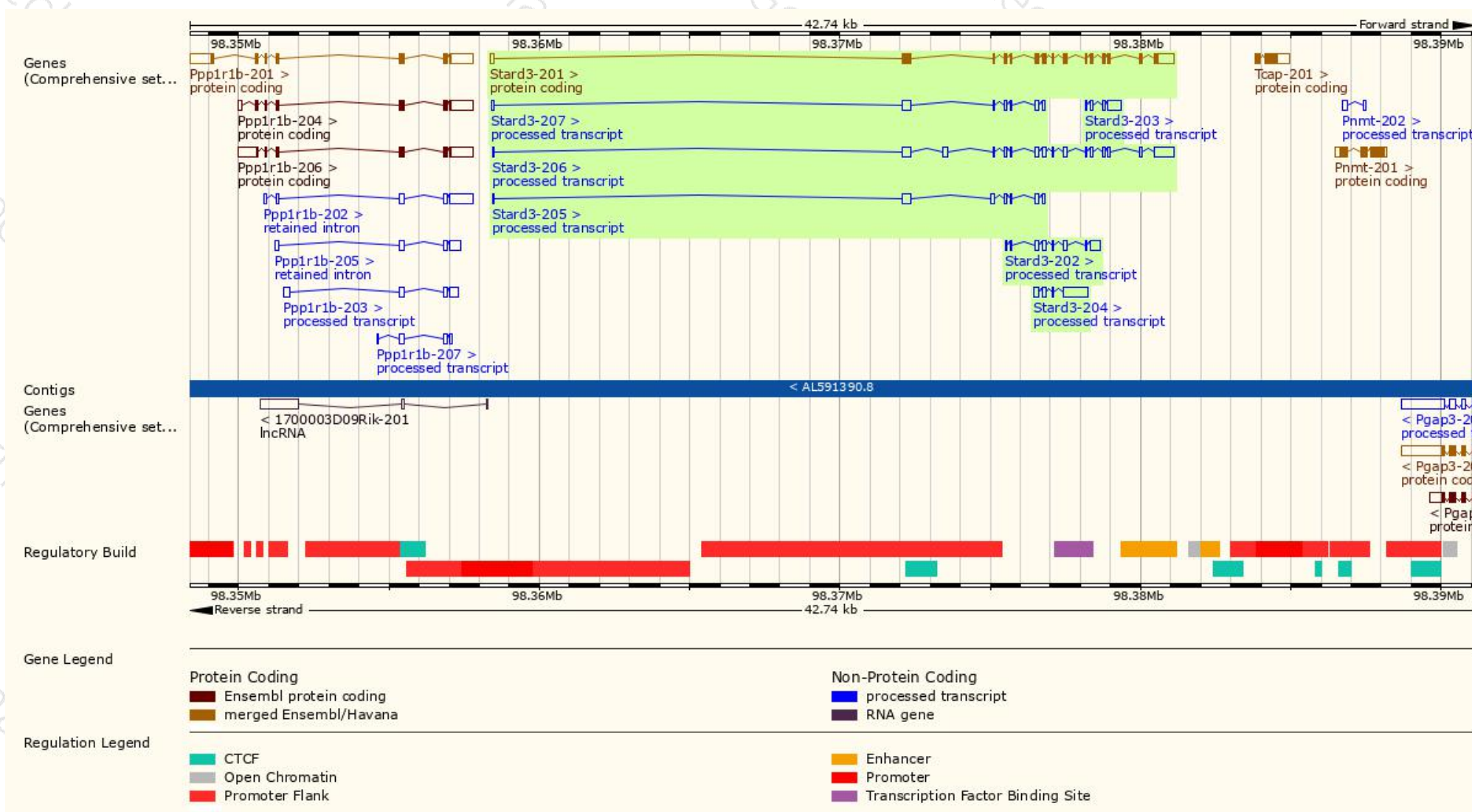
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stard3-201	ENSMUST00000018311.4	2070	446aa	Protein coding	CCDS25345	Q544C3 Q61542	TSL:1 GENCODE basic APPRIS P1
Stard3-206	ENSMUST00000154960.7	2170	No protein	Processed transcript	-	-	TSL:1
Stard3-204	ENSMUST00000148738.1	1096	No protein	Processed transcript	-	-	TSL:3
Stard3-202	ENSMUST00000130323.7	831	No protein	Processed transcript	-	-	TSL:3
Stard3-205	ENSMUST00000152559.7	813	No protein	Processed transcript	-	-	TSL:3
Stard3-207	ENSMUST00000155063.7	751	No protein	Processed transcript	-	-	TSL:3
Stard3-203	ENSMUST00000143243.1	694	No protein	Processed transcript	-	-	TSL:3

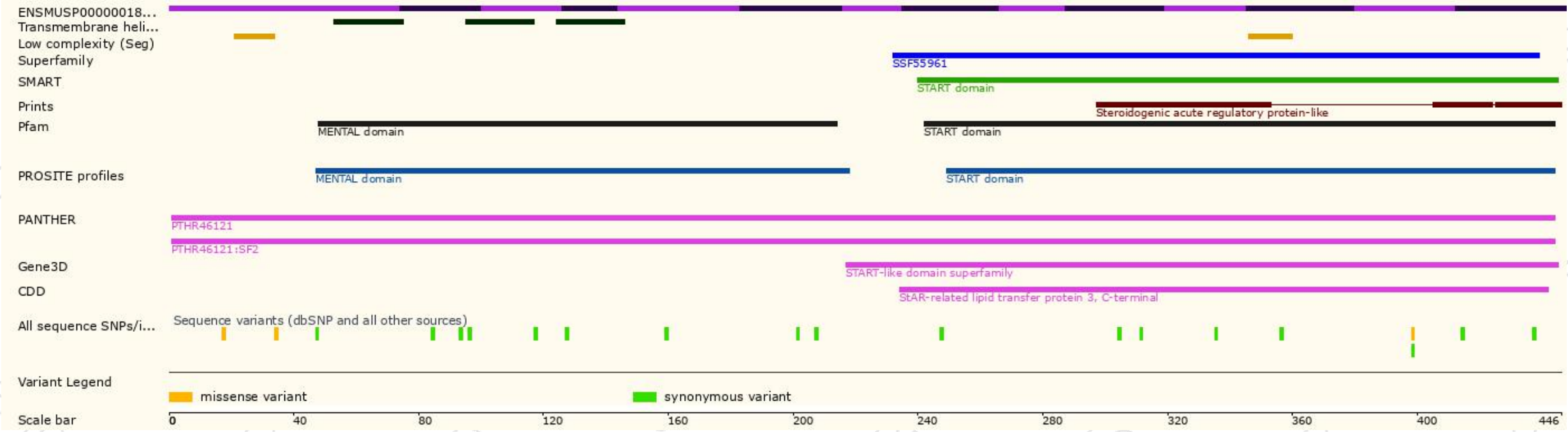
The strategy is based on the design of *Stard3-201* transcript, the transcription is shown below:



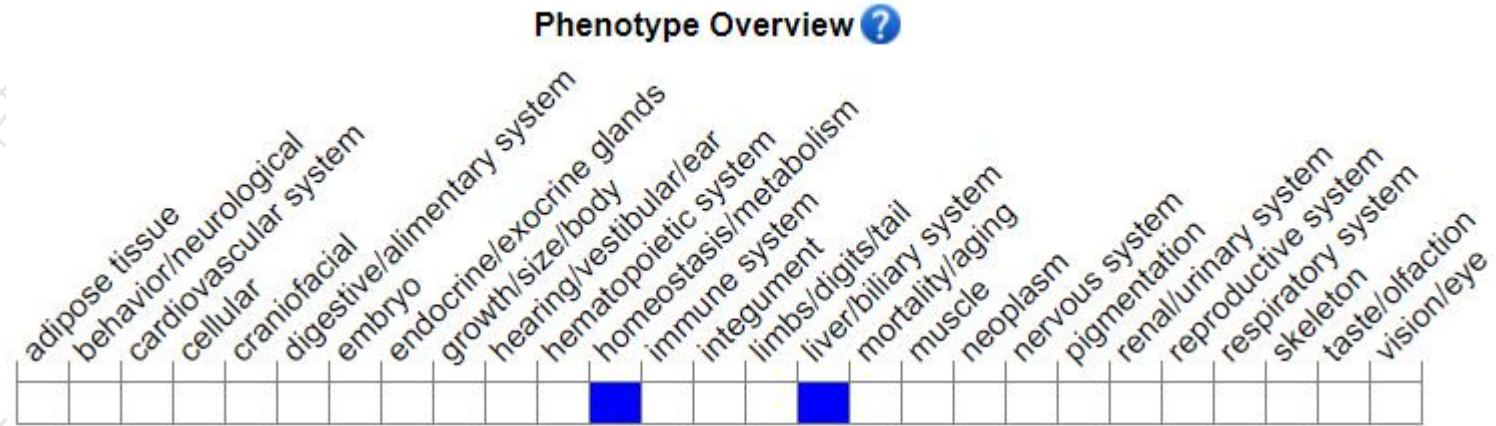
Genomic location distribution



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 a truncated allele are viable and fertile and display mild defects in cholesterol metabolism.

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

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