

Colec11 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Colec11

Project type

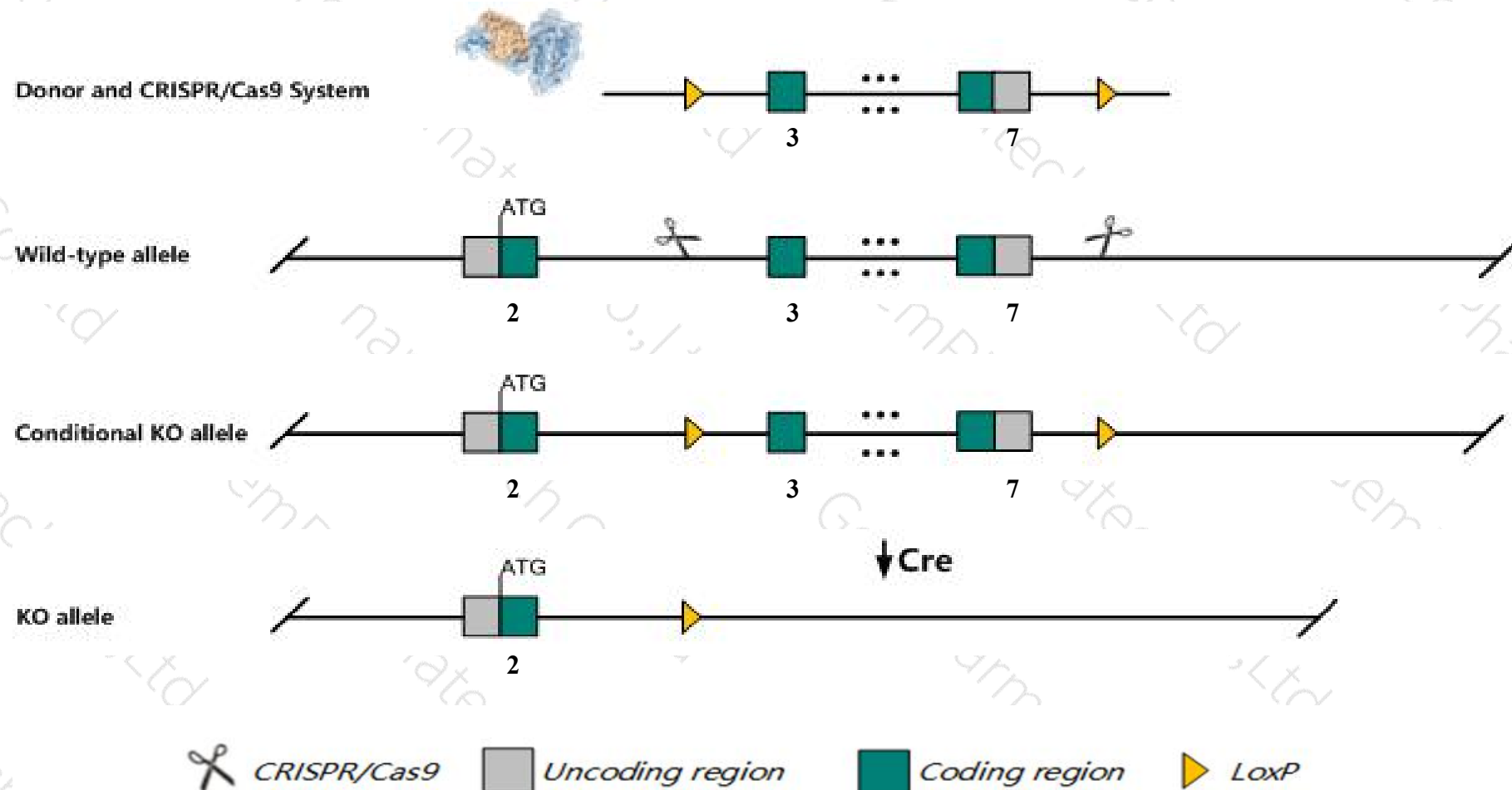
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Colec11* gene. The schematic diagram is as follows:



- The *Colec11* gene has 3 transcripts. According to the structure of *Colec11* gene, exon3-exon7 of *Colec11-201* (ENSMUST00000036136.8) transcript is recommended as the knockout region. The region contains 686bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Colec11* 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 knockout allele exhibit decreased susceptibility to kidney reperfusion injury.
- The *Colec11* gene is located on the Chr12. 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)

Colec11 collectin sub-family member 11 [*Mus musculus* (house mouse)]

Gene ID: 71693, updated on 13-Mar-2020

Summary

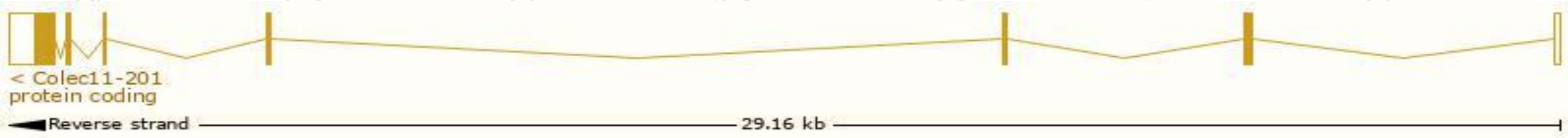
Official Symbol	Colec11 provided by MGI
Official Full Name	collectin sub-family member 11 provided by MGI
Primary source	MGI:MGI:1918943
See related	Ensembl:ENSMUSG00000036655
Gene type	protein coding
RefSeq status	REVIEWED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CL-K1
Summary	This gene encodes a member of the collectin family of C-type lectins that possess collagen-like sequences and carbohydrate recognition domains. Collectins are secreted proteins that play important roles in the innate immune system by binding to carbohydrate antigens on microorganisms, facilitating their recognition and removal. The encoded protein binds to multiple sugars with a preference for fucose and mannose. Mutations in the human gene are a cause of 3MC syndrome-2. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Sep 2015]
Expression	Biased expression in liver adult (RPKM 12.7), liver E18 (RPKM 9.2) and 11 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

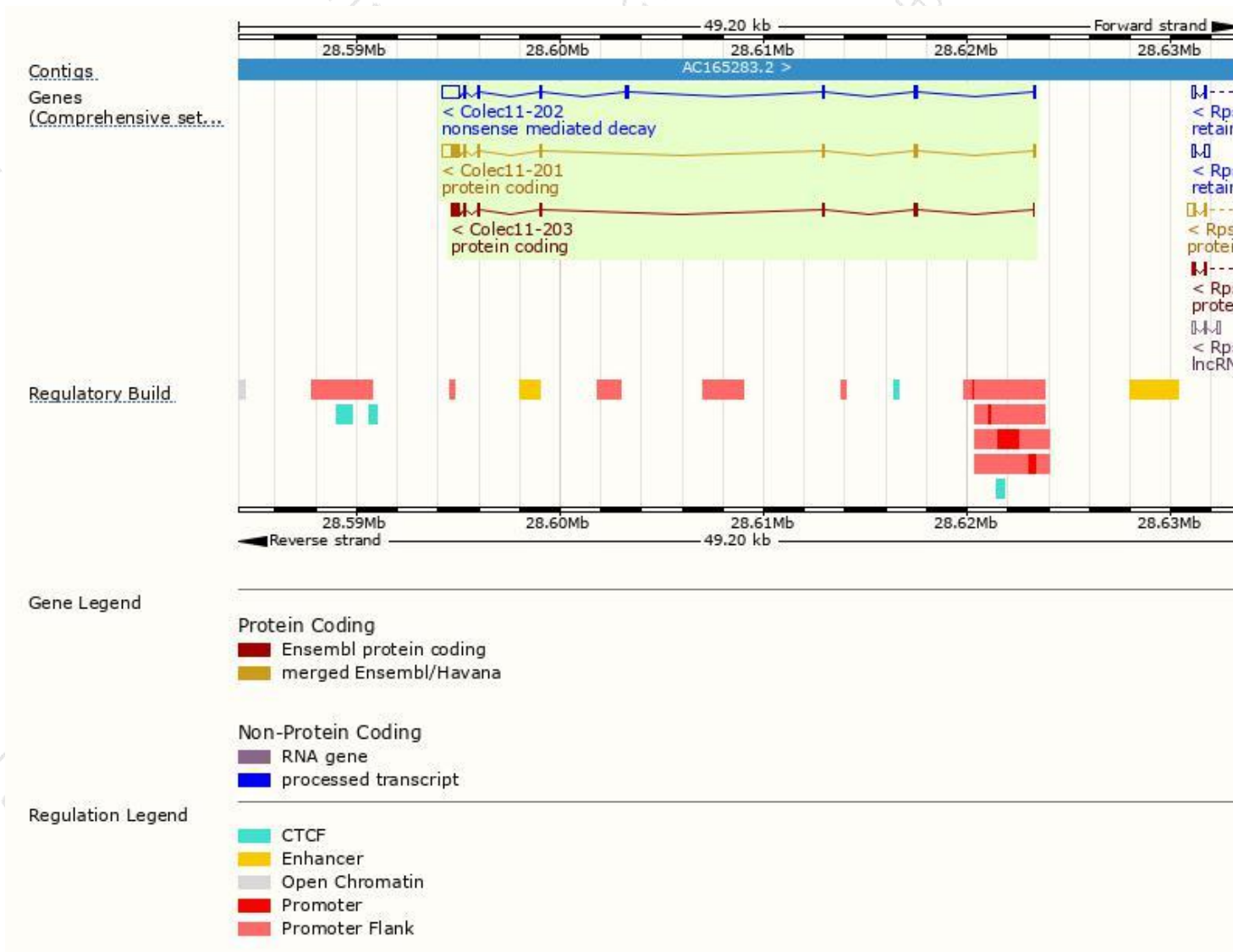
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Colec11-201	ENSMUST00000036136.8	1423	272aa	 Protein coding	CCDS36426	A0A0R4J0M6	TSL:1 GENCODE basic APPRIS P1
Colec11-203	ENSMUST00000220836.1	887	278aa	 Protein coding	-	A0A1Y7VKG6	TSL:1 GENCODE basic
Colec11-202	ENSMUST00000220655.1	1603	91aa	 Nonsense mediated decay	-	A0A1Y7VLI6	TSL:5

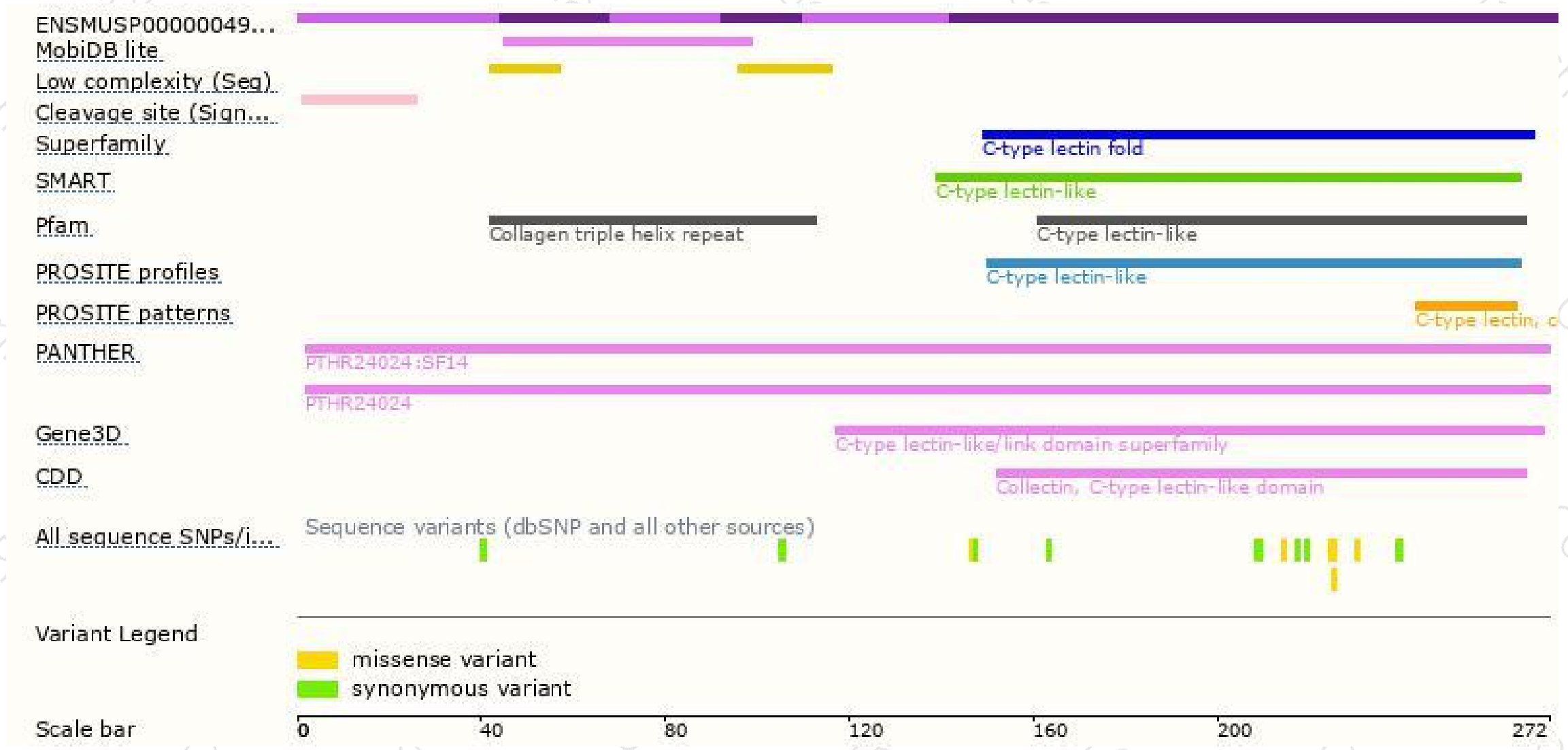
The strategy is based on the design of *Colec11-201* transcript,The transcription is shown below



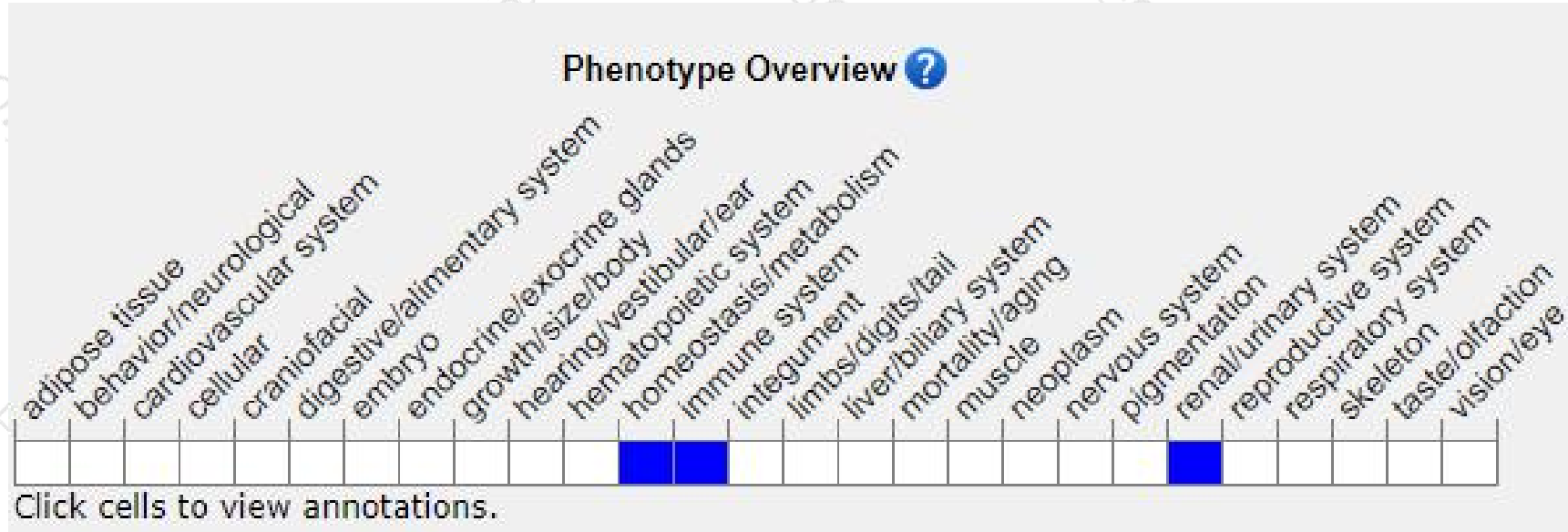
Genomic location distribution



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 knockout allele exhibit decreased susceptibility to kidney reperfusion injury.

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

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