

Havcr2 Cas9-CKO Strategy

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Project Overview

Project Name

Havcr2

Project type

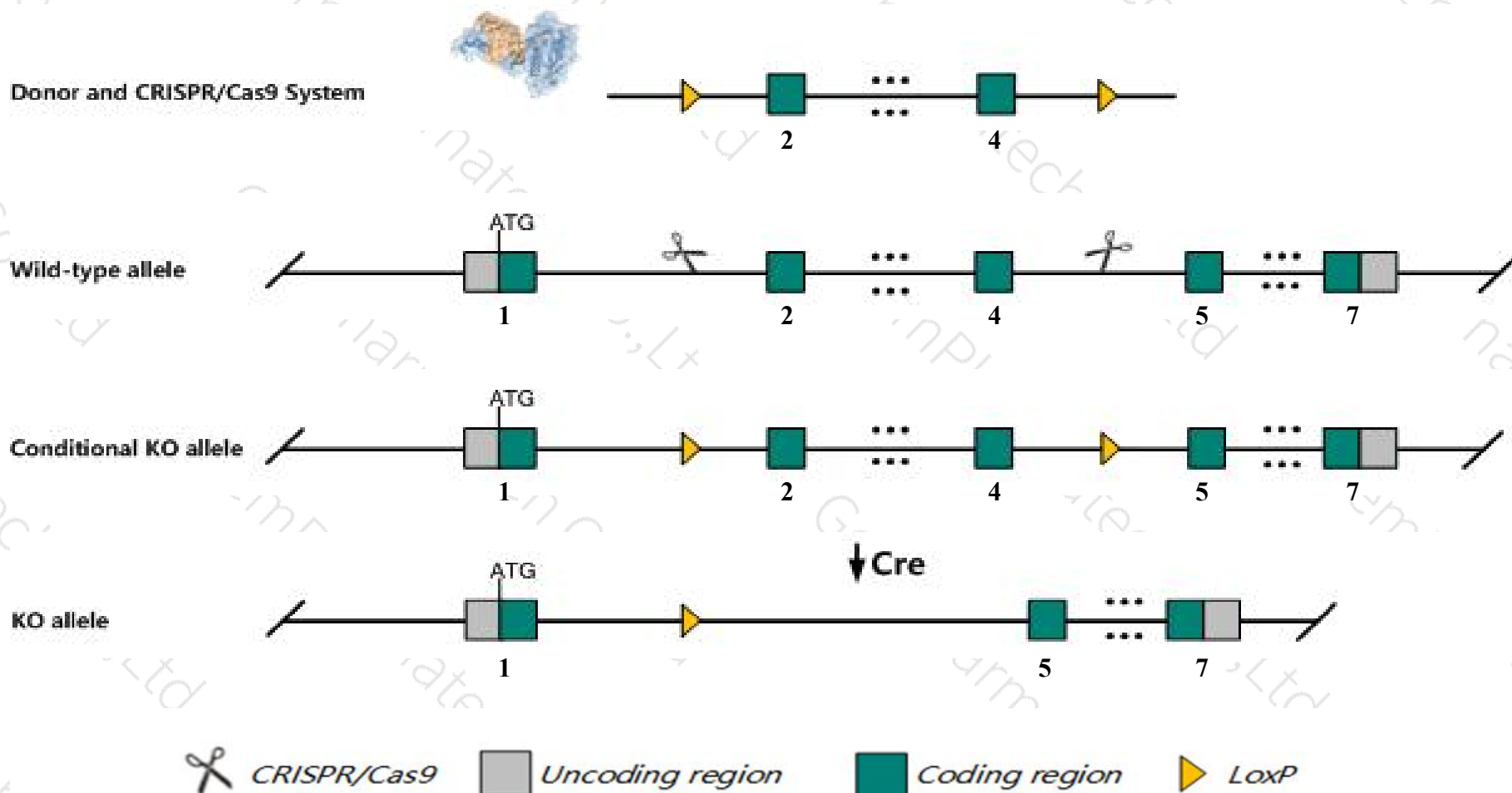
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Havcr2* gene. The schematic diagram is as follows:



- The *Havcr2* gene has 2 transcripts. According to the structure of *Havcr2* gene, exon2-exon4 of *Havcr2-201* (ENSMUST00000020668.14) transcript is recommended as the knockout region. The region contains 464bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Havcr2* 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 knock-out allele exhibit normal thymic development and show no evidence of autoimmunity or lymphoproliferation. Mice homozygous for a different targeted allele exhibit improved survival following influenza infection.
- The *Havcr2* 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)

Havcr2 hepatitis A virus cellular receptor 2 [Mus musculus (house mouse)]

Gene ID: 171285, updated on 12-Mar-2019

Summary



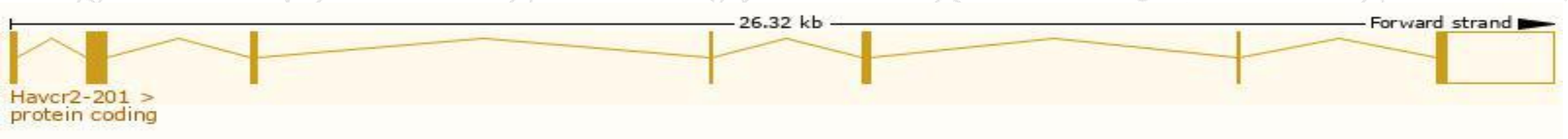
Official Symbol	Havcr2 provided by MGI
Official Full Name	hepatitis A virus cellular receptor 2 provided by MGI
Primary source	MGI:MGI:2159682
See related	Ensembl:ENSMUSG00000020399
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	TIM-3, Tim3, Timd3
Expression	Broad expression in spleen adult (RPKM 1.3), lung adult (RPKM 0.8) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

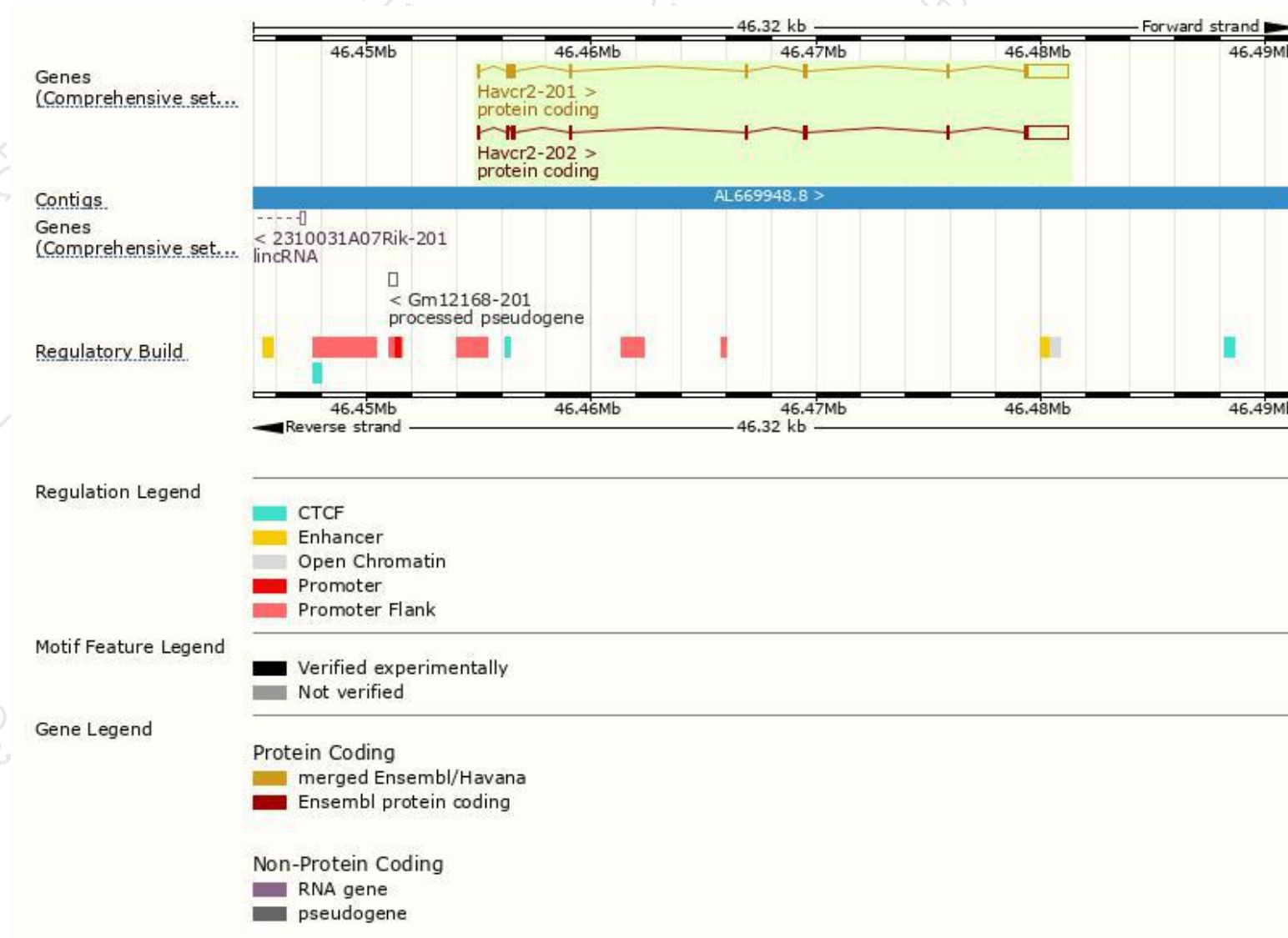
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Havcr2-201	ENSMUST00000020668.14	2721	281aa	Protein coding	CCDS36135	Q8VIM0	TSL:1 GENCODE basic APPRIS P1
Havcr2-202	ENSMUST00000109229.1	2531	232aa	Protein coding	-	D3Z3I4	TSL:1

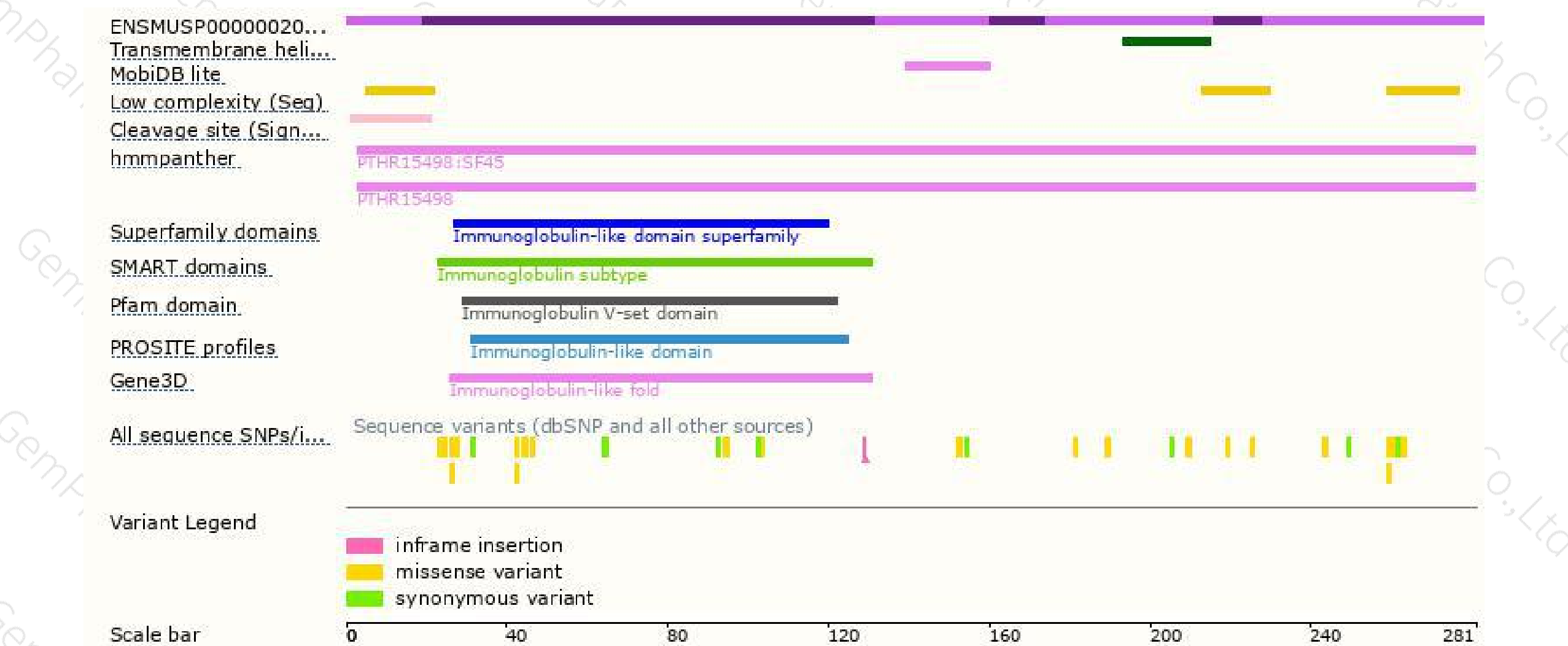
The strategy is based on the design of *Havcr2-201* transcript,The transcription is shown below



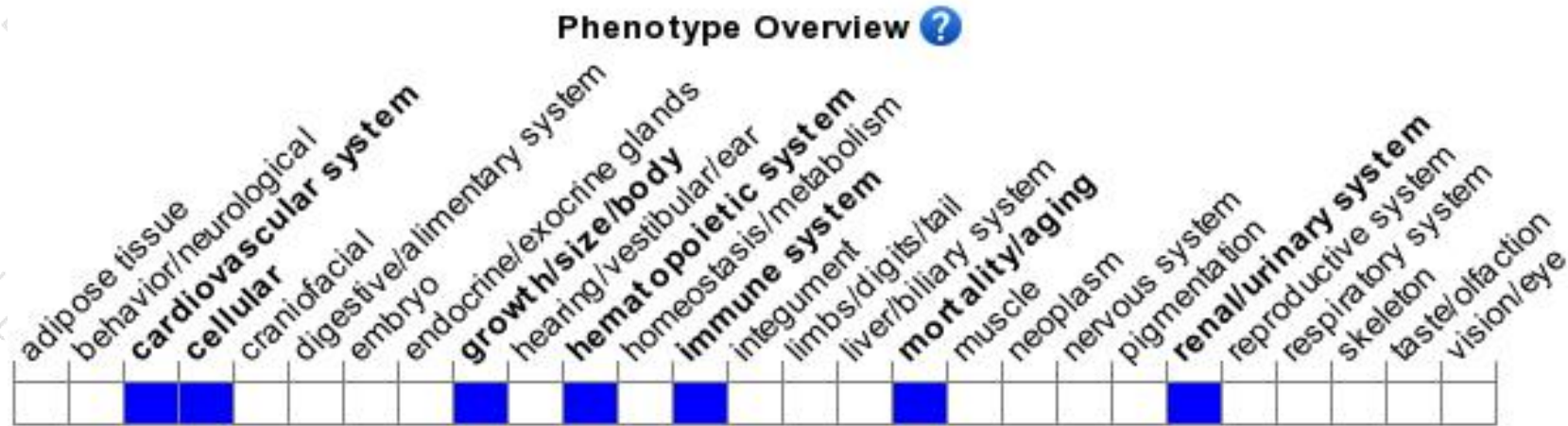
Genomic location distribution



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 knock-out allele exhibit normal thymic development and show no evidence of autoimmunity or lymphoproliferation. Mice homozygous for a different targeted allele exhibit improved survival following influenza infection.

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

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