

Crtam Cas9-KO Strategy

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Project Overview

Project Name

Crtam

Project type

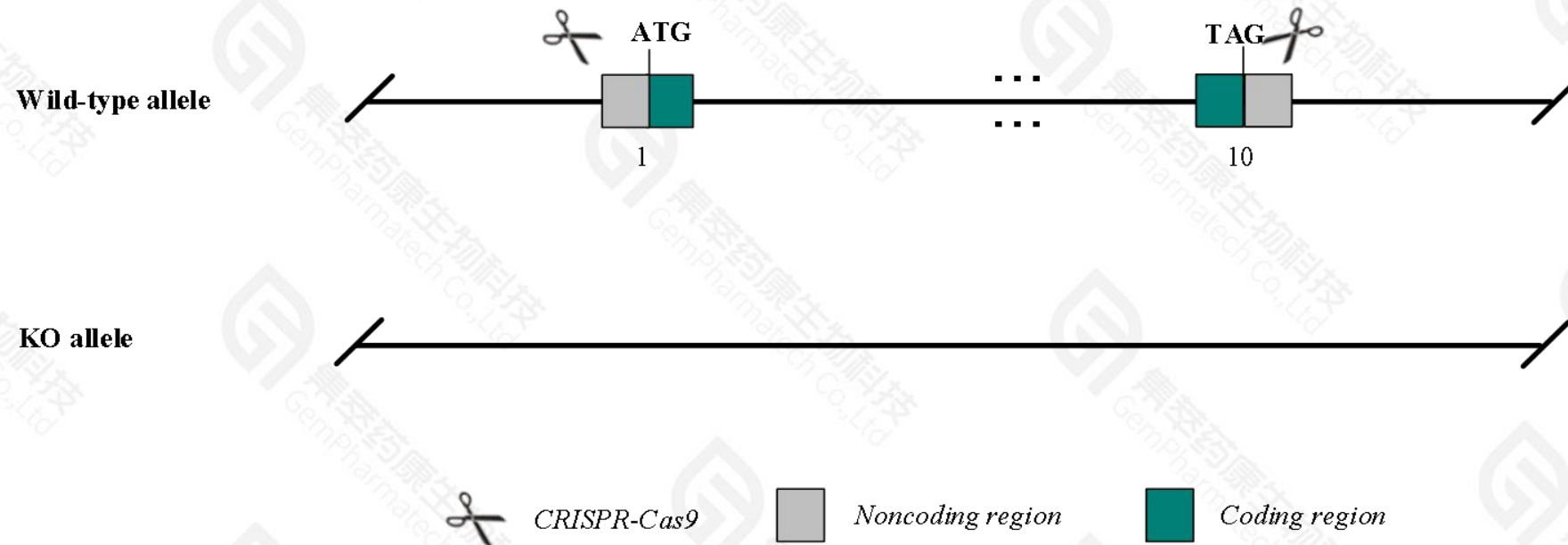
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Crtam* gene has 4 transcripts. According to the structure of *Crtam* gene, exon1-exon10 of *Crtam*-202(ENSMUST00000180384.3) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Crtam* gene. The brief process is as follows: CRISPR-Cas9 system 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.

- According to the existing MGI data, homozygous null mice have defects in late stage T cell activation that leads to less production of inflammatory cytokines, higher proliferation, and an increase in T cell number with age.
- The *Crtam* gene is located on the Chr9. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Crtam cytotoxic and regulatory T cell molecule [*Mus musculus* (house mouse)]

Gene ID: 54698, updated on 25-Jan-2022

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Summary

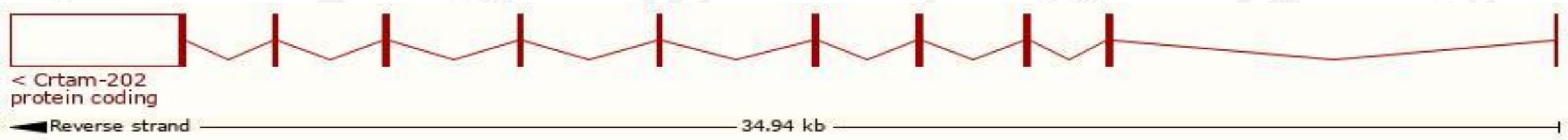
Official Symbol	Crtam provided by MGI
Official Full Name	cytotoxic and regulatory T cell molecule provided by MGI
Primary source	MGI:MGI:1859822
See related	Ensembl:ENSMUSG00000032021 AllianceGenome:MGI:1859822
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	Enables signaling receptor binding activity. Involved in several processes, including detection of tumor cell; establishment of T cell polarity; and regulation of T cell activation. Located in immunological synapse. Orthologous to human CRTAM (cytotoxic and regulatory T cell molecule). [provided by Alliance of Genome Resources, Nov 2021]
Expression	Biased expression in cerebellum adult (RPKM 7.1) and testis adult (RPKM 4.5) See more
Orthologs	human all
NEW	Try the new Gene table
	Try the new Transcript table

Transcript information (Ensembl)

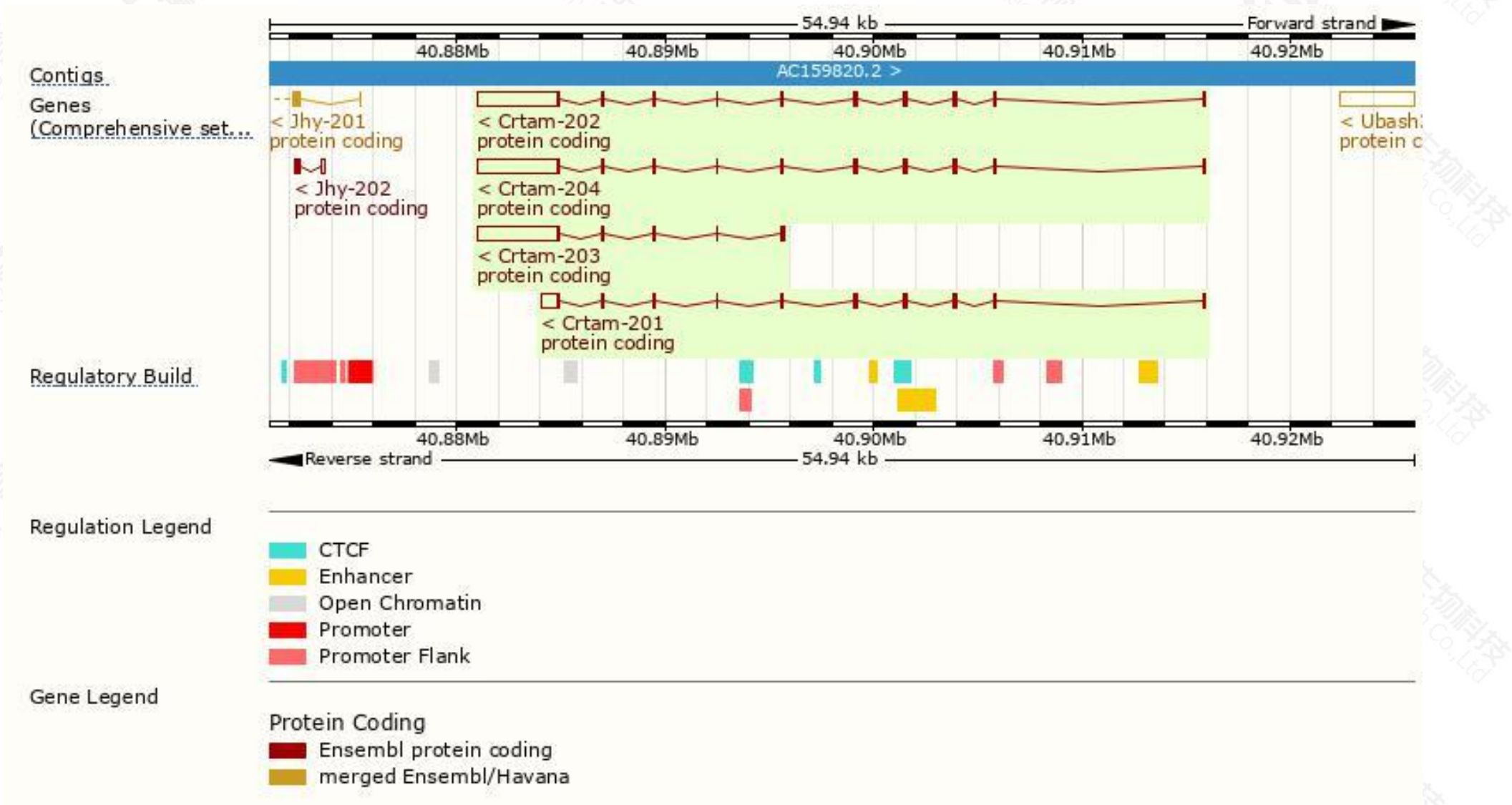
The gene has 4 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden) Filter							
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000180872.9	Crtam-203	4443	196aa	Protein coding	-	Q149L7-2	GENCODE basic TSL:1
ENSMUST00000034519.13	Crtam-201	1876	386aa	Protein coding	-	E9QPS7	GENCODE basic APPRIS ALT1 TSL:5
ENSMUST00000188848.8	Crtam-204	5001	392aa	Protein coding	CCDS40593	Q149L7-3	GENCODE basic APPRIS P3 TSL:1
ENSMUST00000180384.3	Crtam-202	5046	393aa	Protein coding	CCDS72216	Q149L7-1	GENCODE basic APPRIS ALT1 TSL:1

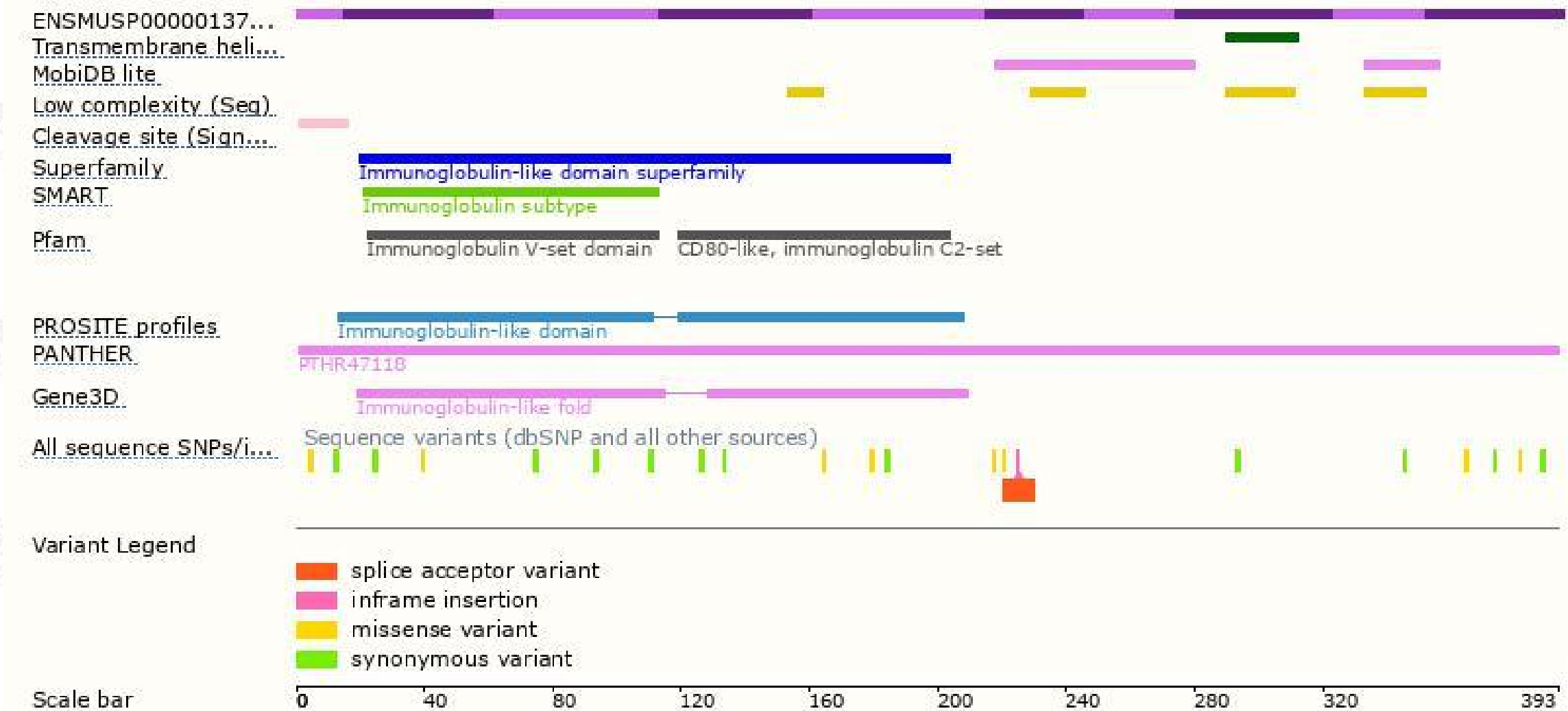
The strategy is based on the design of *Crtam-202* transcript,the transcription is shown below:



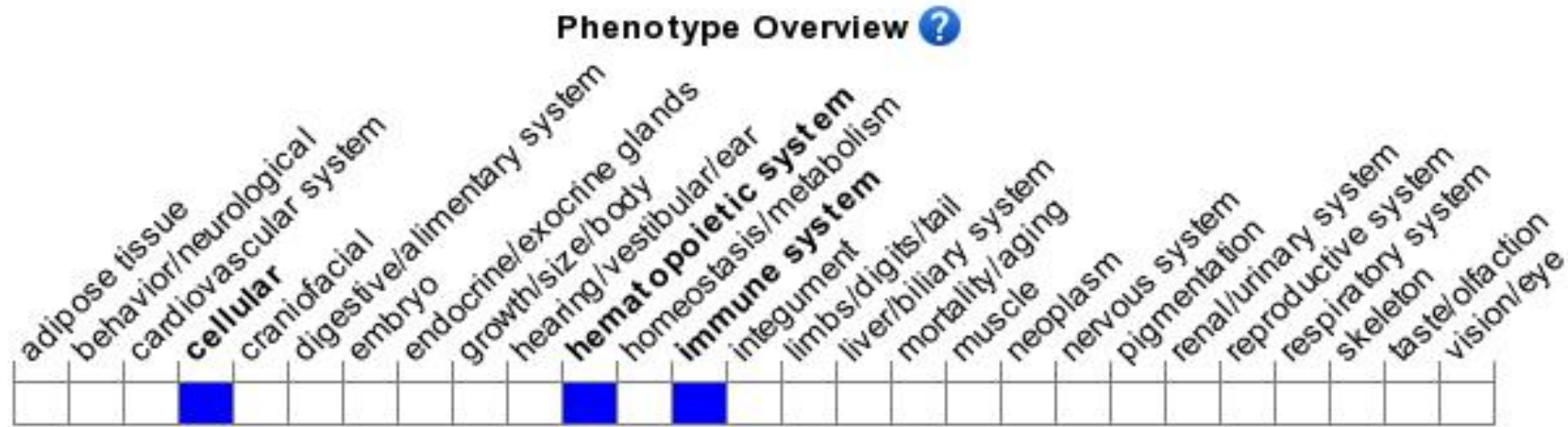
Genomic location distribution



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, homozygous null mice have defects in late stage T cell activation that leads to less production of inflammatory cytokines, higher proliferation, and an increase in T cell number with age.

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