

Mr1 Cas9-CKO Strategy

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Project Overview

Project Name

Mr1

Project type

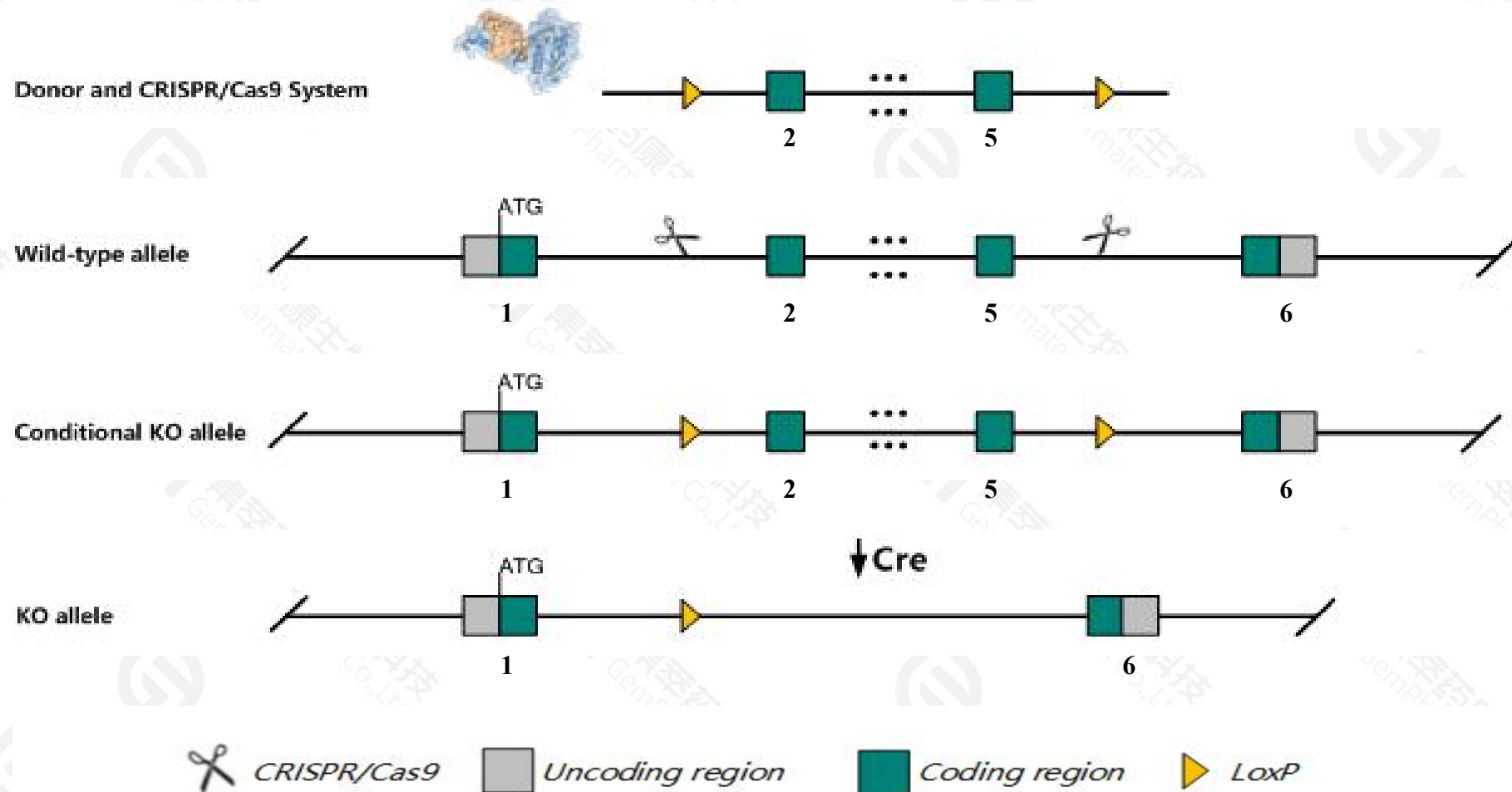
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mr1* gene. The schematic diagram is as follows:



Technical routes

- The *Mr1* gene has 5 transcripts. According to the structure of *Mr1* gene, exon2-exon5 of *Mr1*-201(ENSMUST00000027744.10) transcript is recommended as the knockout region. The region contains most 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 *Mr1* 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, null homozygotes lack mucosal-associated invariant T cells that express the canonical mVa19-Ja33 rearrangement of the Tcra gene.
- The *Mr1* gene is located on the Chr1. 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)

Mr1 major histocompatibility complex, class I-related [Mus musculus (house mouse)]

Gene ID: 15064, updated on 13-Mar-2020

Summary

Official Symbol Mr1 provided by [MGI](#)

Official Full Name major histocompatibility complex, class I-related provided by [MGI](#)

Primary source [MGI:MGI:1195463](#)

See related [Ensembl:ENSMUSG00000026471](#)

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 H2Is

Expression Broad expression in bladder adult (RPKM 9.5), thymus adult (RPKM 9.3) and 19 other tissues [See more](#)

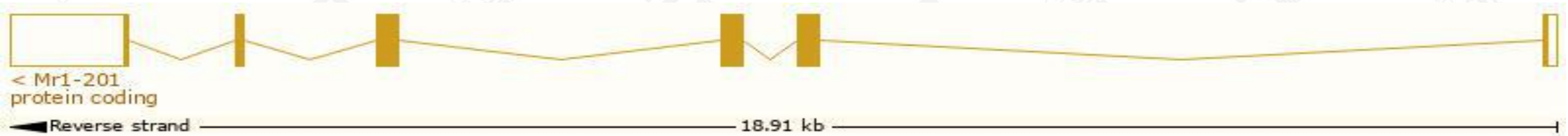
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

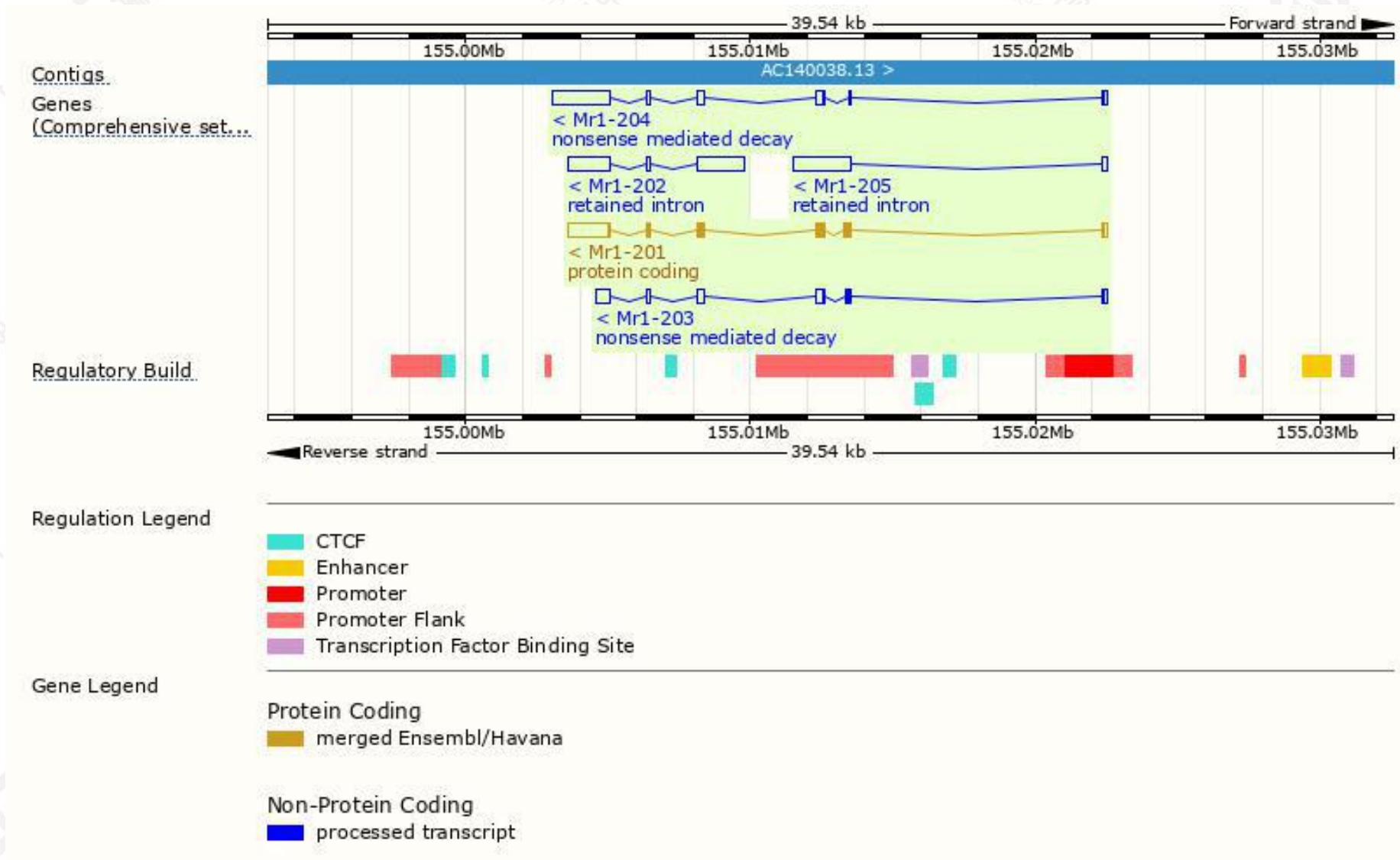
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mr1-201	ENSMUST00000027744.9	2512	341aa	Protein coding	CCDS15383	Q8HWB0	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 P1
Mr1-204	ENSMUST00000194612.5	2949	54aa	Nonsense mediated decay	-	A0A0A6YXY6	TSL:1
Mr1-203	ENSMUST00000192410.1	1500	89aa	Nonsense mediated decay	-	A0A0A6YWB2	TSL:1
Mr1-202	ENSMUST00000191773.5	3214	No protein	Retained intron	-	-	TSL:1
Mr1-205	ENSMUST00000195579.1	2170	No protein	Retained intron	-	-	TSL:1

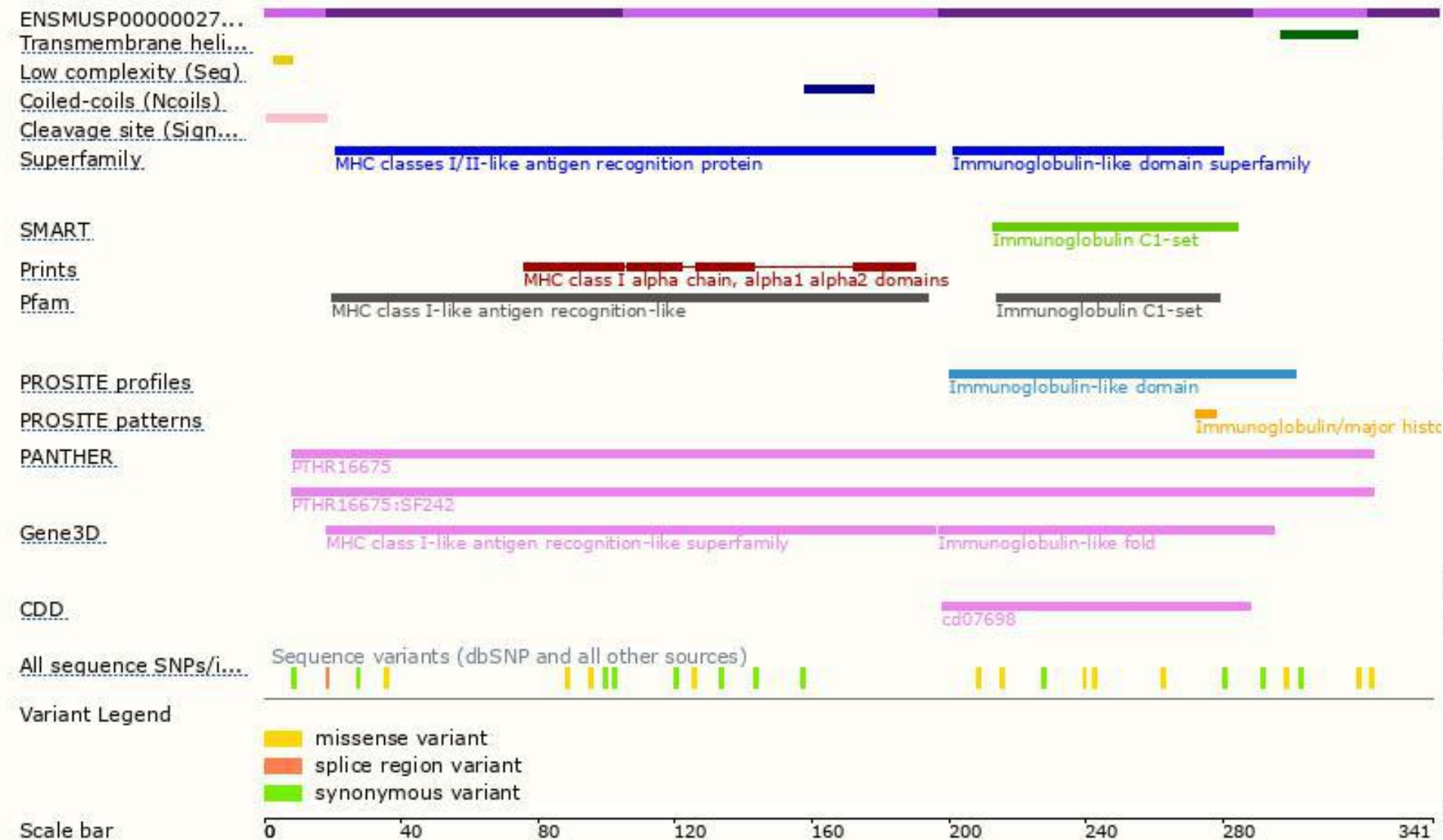
The strategy is based on the design of *Mr1-201* transcript,the transcription is shown below:



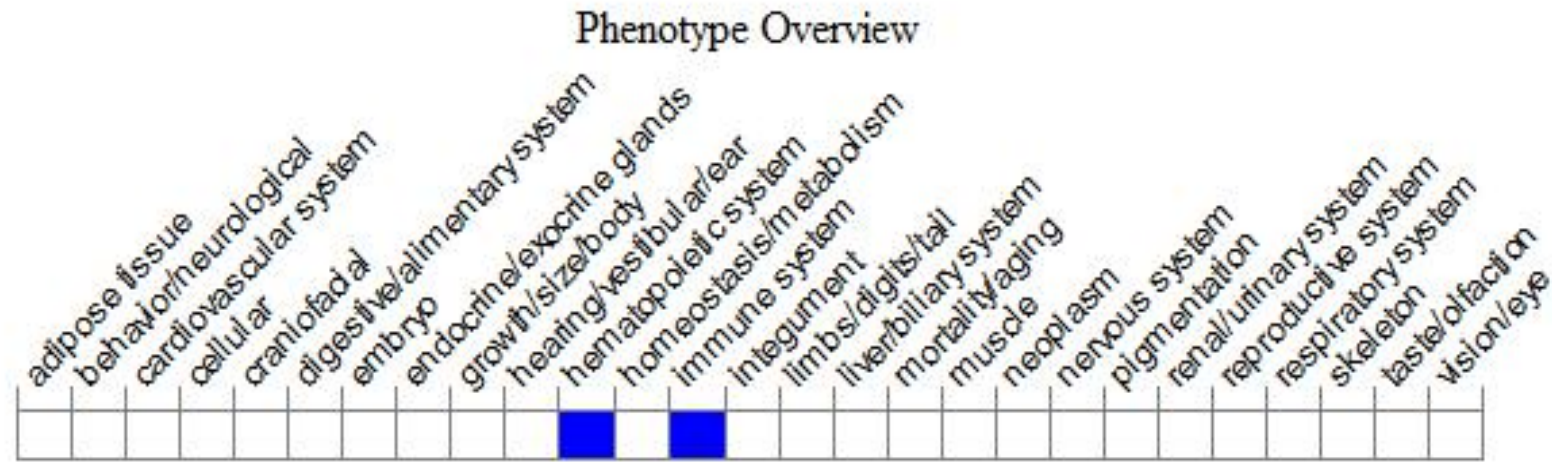
Genomic location distribution



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, null homozygotes lack mucosal-associated invariant T cells that express the canonical mVa19-Ja33 rearrangement of the Tcr α gene.

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