

***Batf3* Cas9-CKO Strategy**

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Project Overview

Project Name

Batf3

Project type

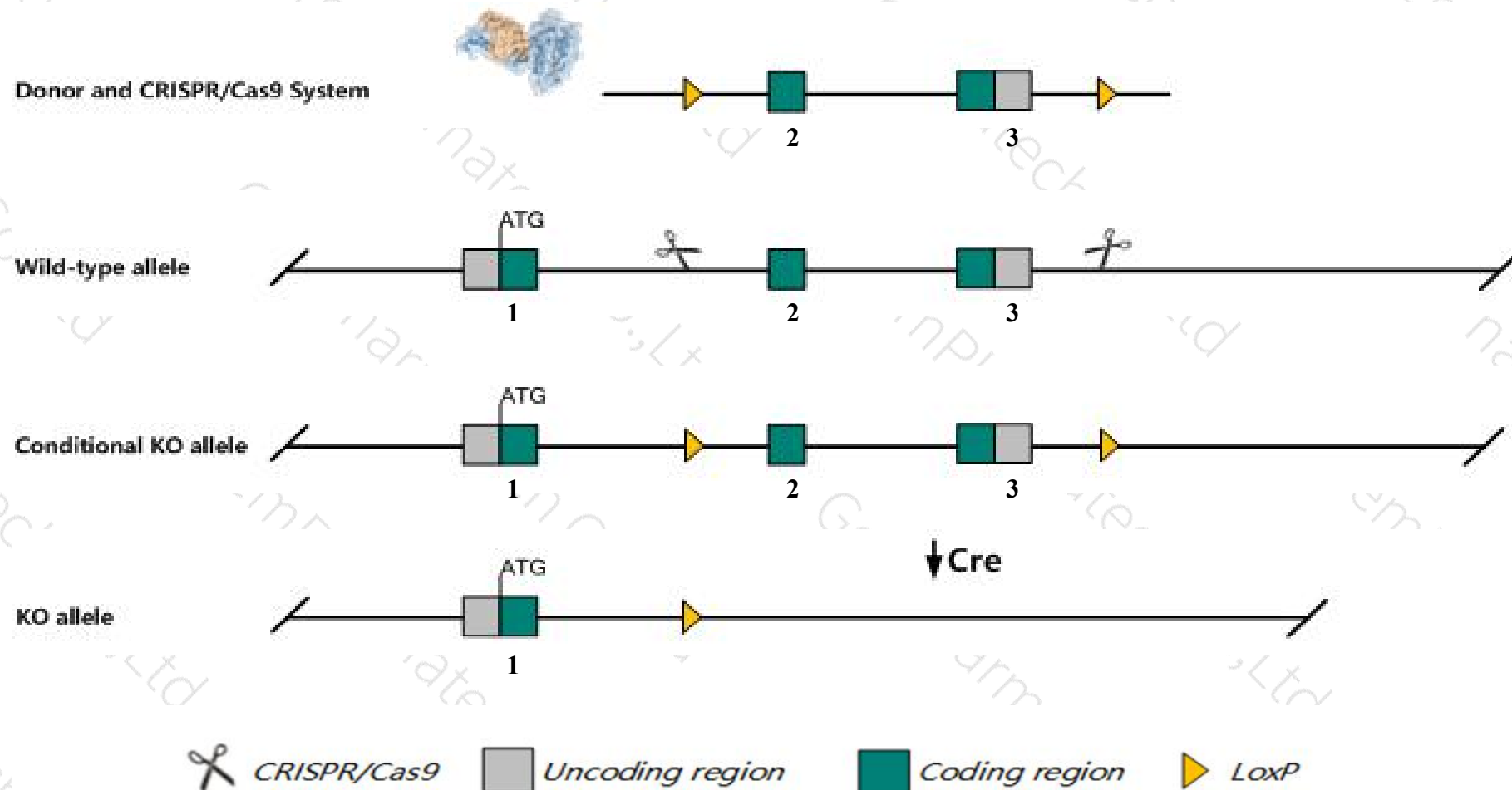
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Batf3* gene. The schematic diagram is as follows:



Technical routes

- The *Batf3* gene has 5 transcripts. According to the structure of *Batf3* gene, exon2-exon3 of *Batf3-201* (ENSMUST00000027943.5) 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 *Batf3* 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 null mutation lack CD8alpha⁺ dendritic cells, have dysfunctional cross-presentation of antigens, and generate lower numbers of memory CD8⁺ T cells in response to infection.
- The *Batf3* 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)

Batf3 basic leucine zipper transcription factor, ATF-like 3 [Mus musculus (house mouse)]

Gene ID: 381319, updated on 9-Apr-2019

Summary



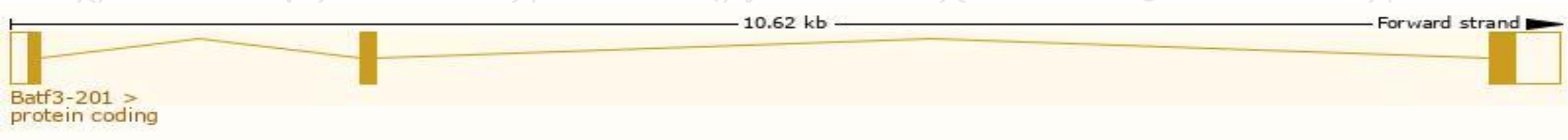
Official Symbol	Batf3 provided by MGI
Official Full Name	basic leucine zipper transcription factor, ATF-like 3 provided by MGI
Primary source	MGI:MGI:1925491
See related	Ensembl:ENSMUSG00000026630
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9130211I03Rik, Snft
Expression	Broad expression in spleen adult (RPKM 8.6), mammary gland adult (RPKM 6.6) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

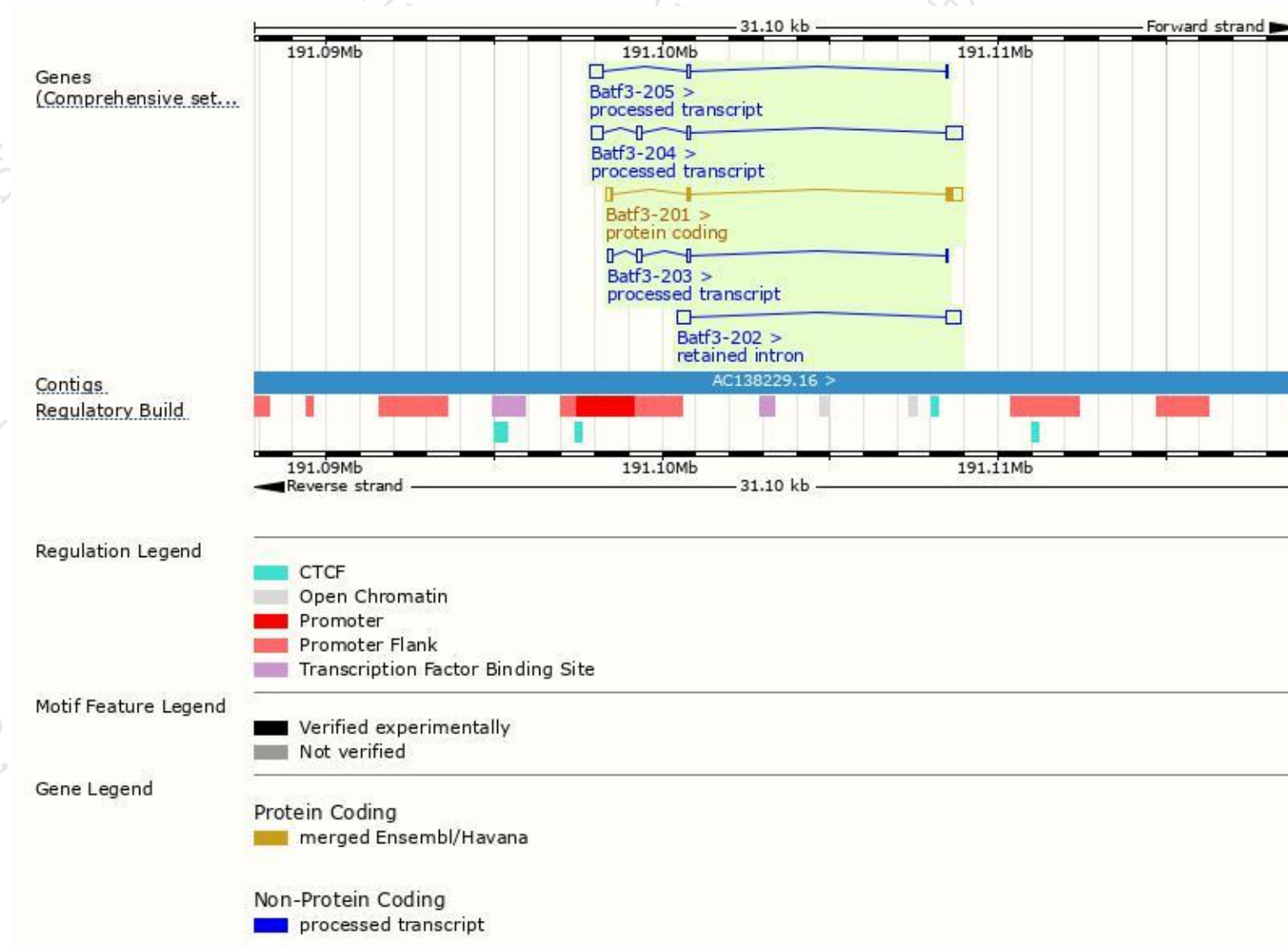
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Batf3-201	ENSMUST00000027943.5	801	118aa	Protein coding	CCDS15615	Q9D275	TSL:1 GENCODE basic APPRIS P1
Batf3-204	ENSMUST00000193771.5	1110	No protein	Processed transcript	-	-	TSL:1
Batf3-205	ENSMUST00000194833.5	532	No protein	Processed transcript	-	-	TSL:3
Batf3-203	ENSMUST00000192268.1	438	No protein	Processed transcript	-	-	TSL:5
Batf3-202	ENSMUST00000191621.1	815	No protein	Retained intron	-	-	TSL:3

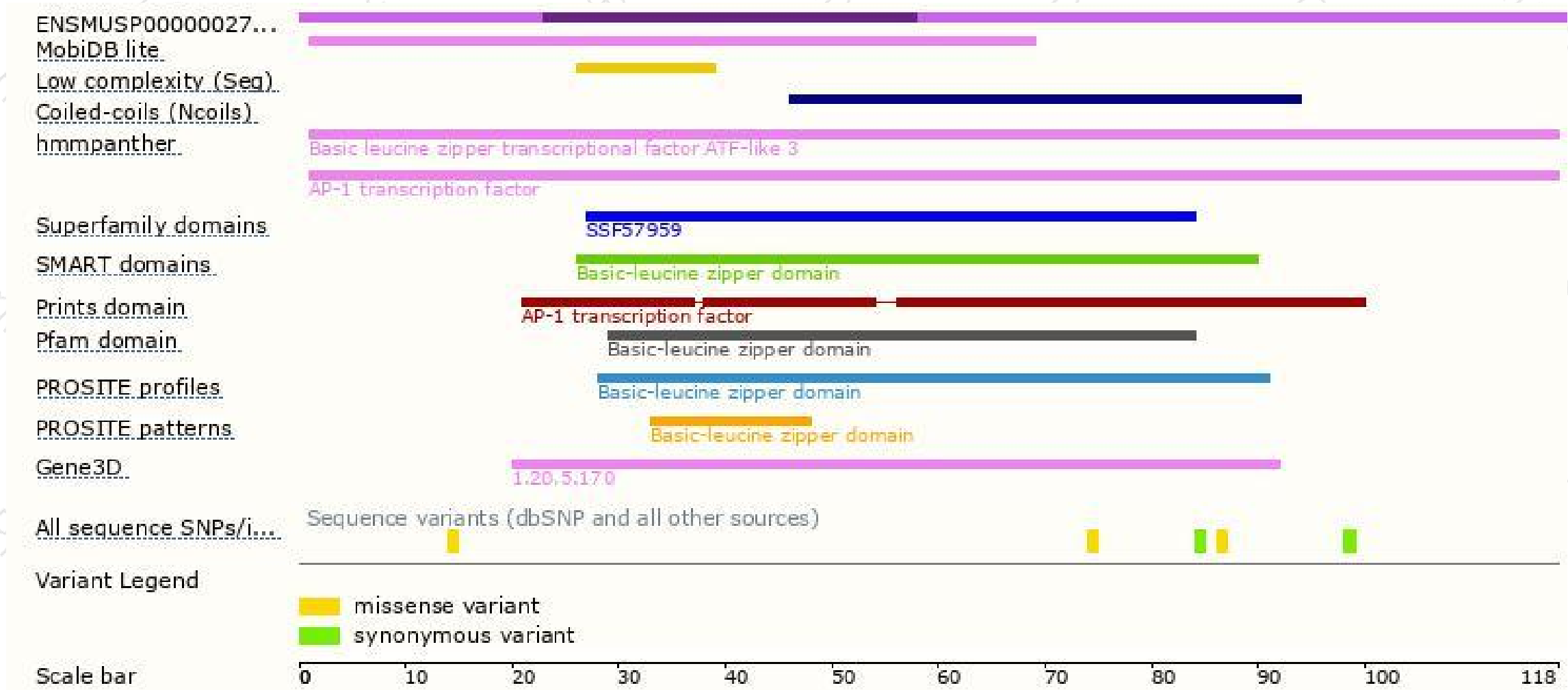
The strategy is based on the design of *Batf3-201* transcript,The transcription is shown below



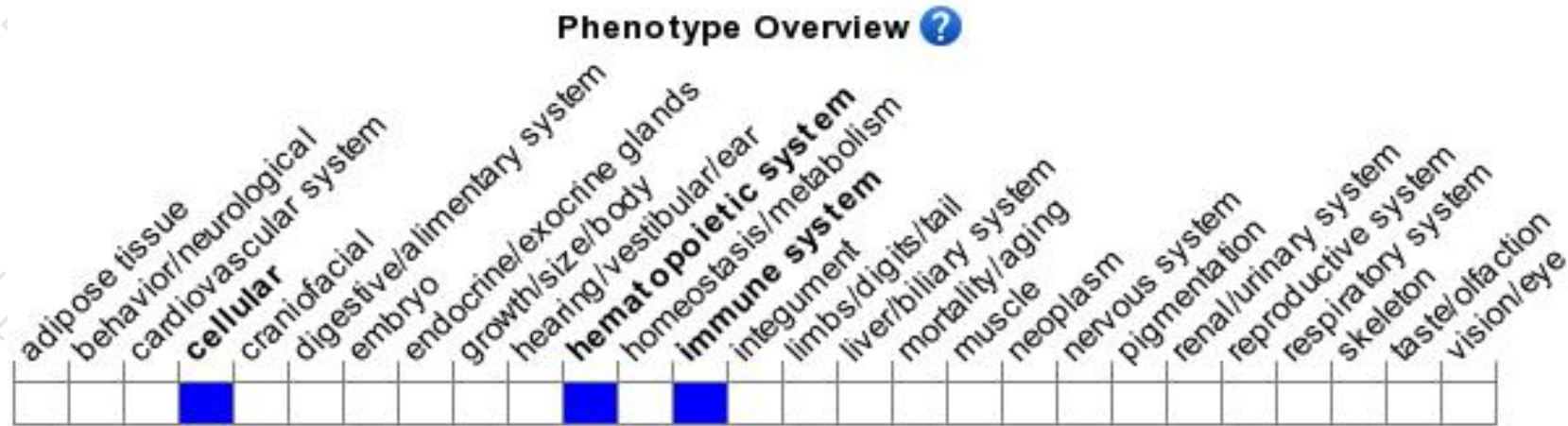
Genomic location distribution



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 null mutation lack CD8alpha⁺ dendritic cells, have dysfunctional cross-presentation of antigens, and generate lower numbers of memory CD8⁺ T cells in response to infection.

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

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