

***Gzmb* Cas9-KO Strategy**

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Project Overview

Project Name

Gzmb

Project type

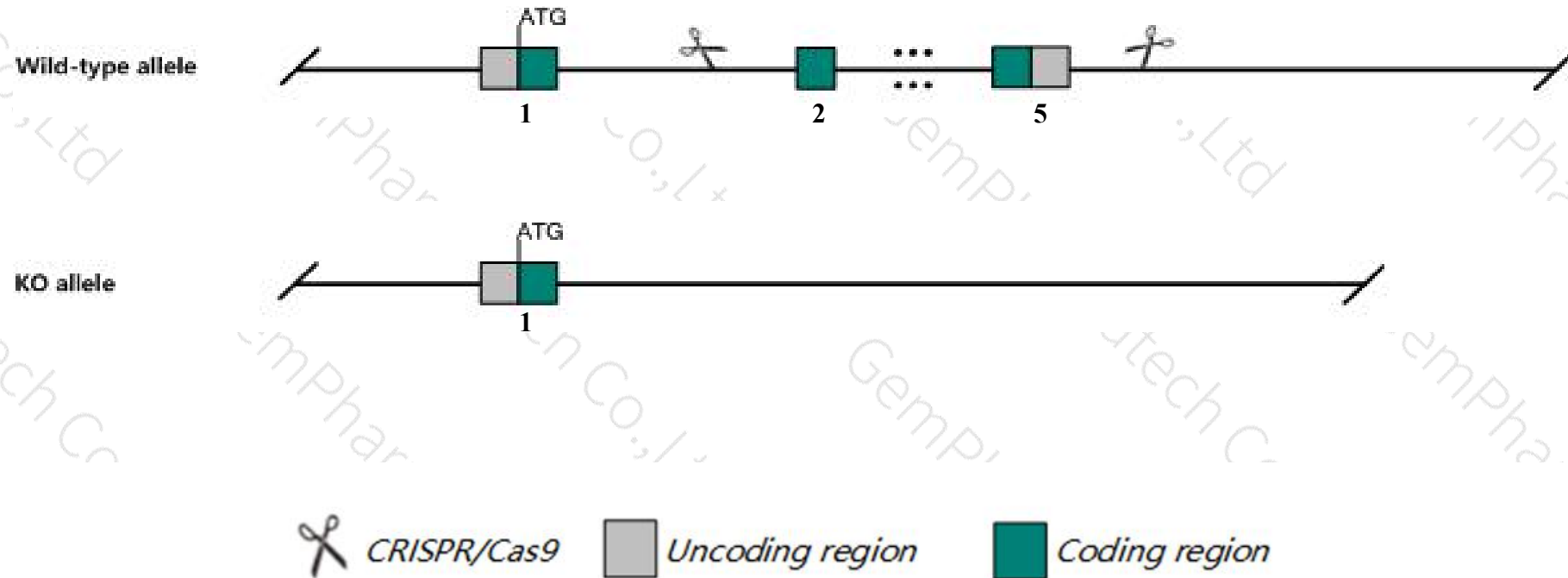
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Gzmb* gene has 1 transcript. According to the structure of *Gzmb* gene, exon2-exon5 of *Gzmb*-201 (ENSMUST00000015581.5) transcript is recommended as the knockout region. The region contains 689bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gzmb* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for a null allele show impaired CTL and NK cell cytotoxicity, and enhanced clearance of allogeneic and syngeneic tumor cells. Homozygotes for another null allele have defective CTL cytotoxicity and show impaired clearance of allogeneic tumor cells only if the selection cassette is retained.
- The *Gzmb* gene is located on the Chr14. 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)

Gzmb granzyme B [Mus musculus (house mouse)]

Gene ID: 14939, updated on 19-Mar-2019

Summary



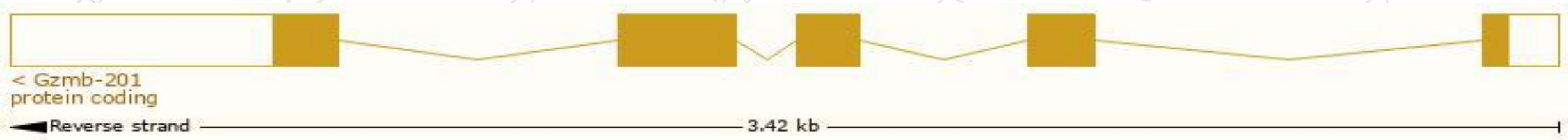
Official Symbol	Gzmb provided by MGI
Official Full Name	granzyme B provided by MGI
Primary source	MGI:MGI:109267
See related	Ensembl:ENSMUSG00000015437
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI553453, CCP-1/C11, CCP1, Ctla-1, Ctla1, GZB
Summary	This gene encodes a member of the granzyme subfamily of proteins, part of the peptidase S1 family of serine proteases. The encoded preproprotein is secreted by natural killer (NK) cells and cytotoxic T lymphocytes (CTLs) and proteolytically processed to generate the active protease, which induces target cell apoptosis. This protein also processes cytokines and degrades extracellular matrix proteins, and these roles are implicated in chronic inflammation and wound healing. Mice lacking a functional copy of this gene exhibit impaired immune cell-mediated cytotoxicity. [provided by RefSeq, Sep 2016]
Expression	Biased expression in large intestine adult (RPKM 11.7), small intestine adult (RPKM 4.9) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

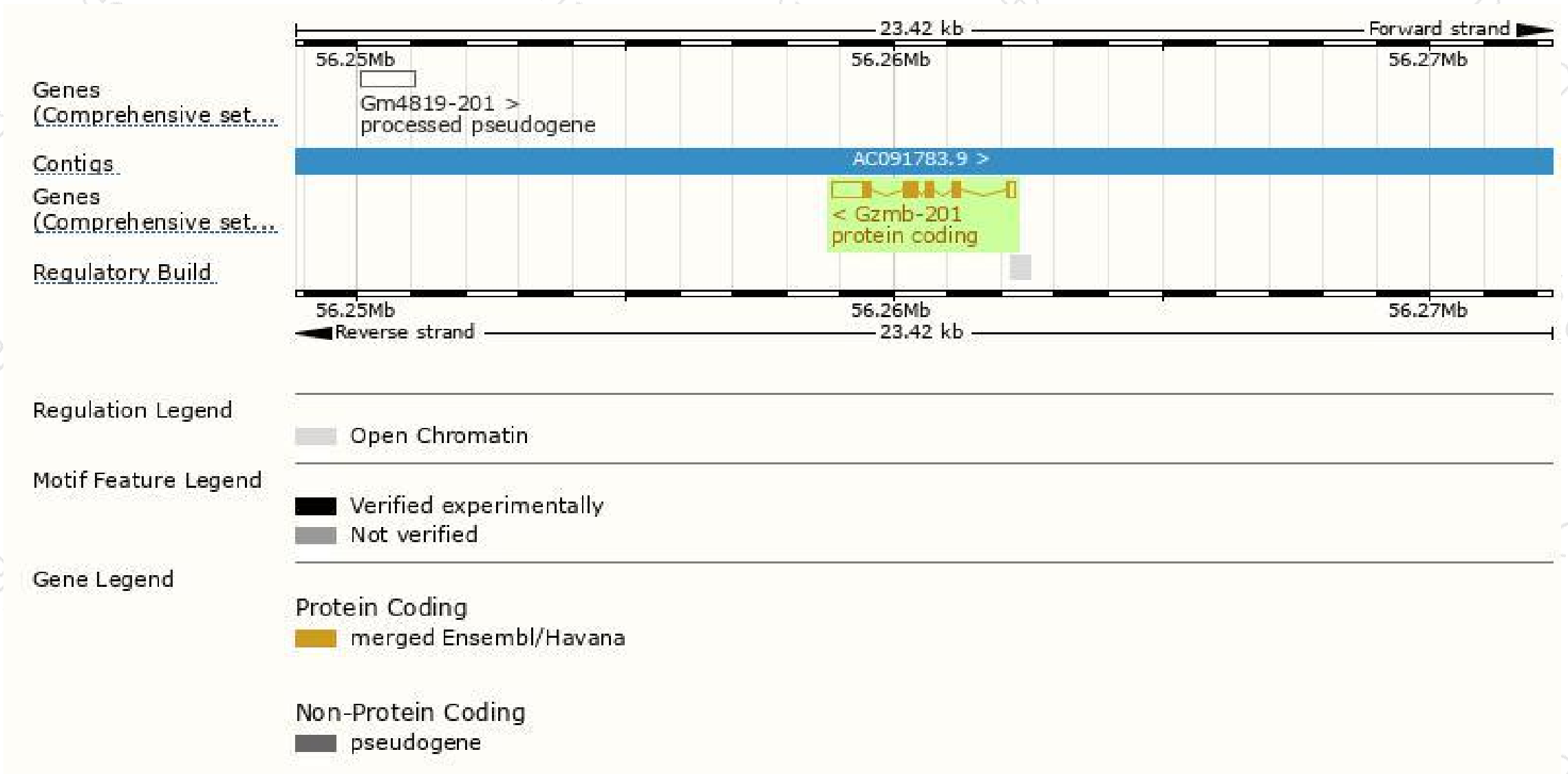
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gzmb-201	ENSMUST00000015581.5	1436	247aa	Protein coding	CCDS27147	P04187 Q3TZH4	TSL:1 GENCODE basic APPRIS P1

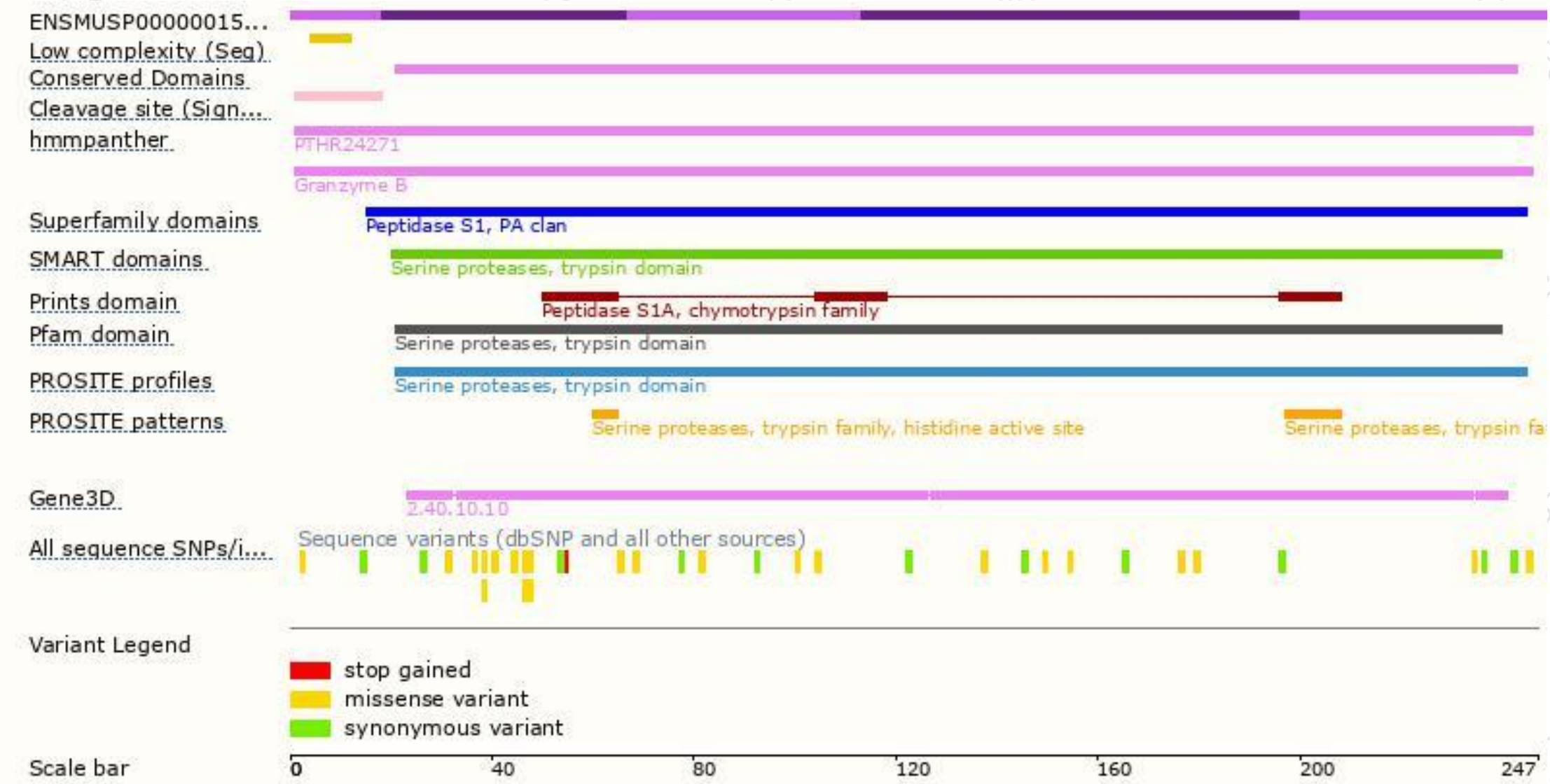
The strategy is based on the design of *Gzmb-201* transcript, The transcription is shown below



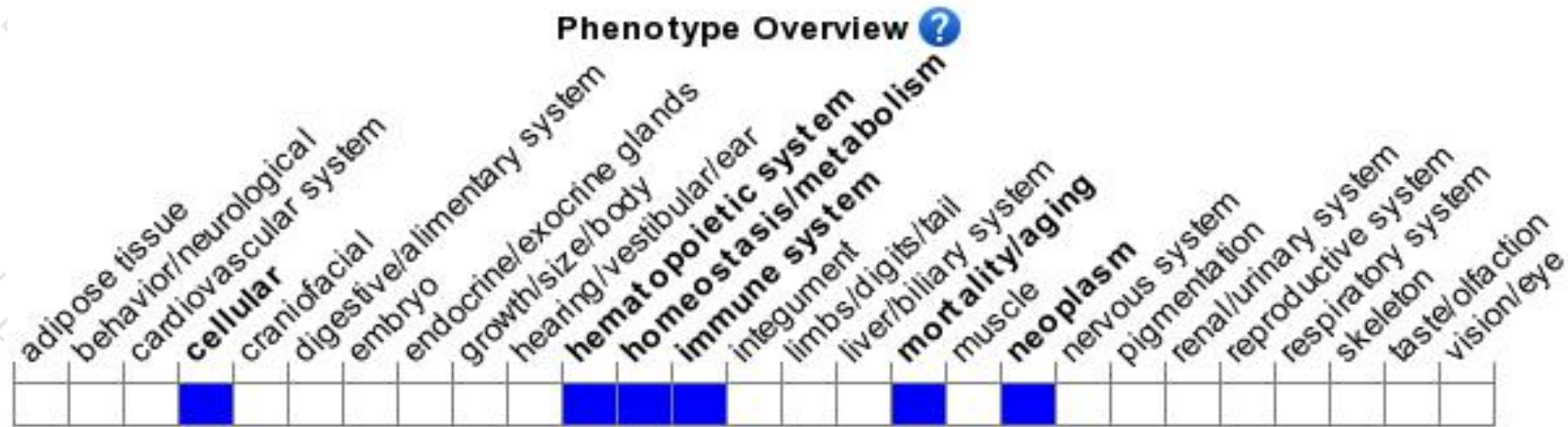
Genomic location distribution



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, Homozygotes for a null allele show impaired CTL and NK cell cytotoxicity, and enhanced clearance of allogeneic and syngeneic tumor cells. Homozygotes for another null allele have defective CTL cytotoxicity and show impaired clearance of allogeneic tumor cells only if the selection cassette is retained.

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

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