

Serpinb9 Cas9-KO Strategy

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Project Overview

Project Name

Serpinb9

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Serpinb9* gene. The schematic diagram is as follows:



- The *Serpinb9* gene has 2 transcripts. According to the structure of *Serpinb9* gene, exon4-exon5 of *Serpinb9-202* (ENSMUST00000063191.13) transcript is recommended as the knockout region. The region contains 256bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Serpinb9* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice show defective CTL immunity and clearance of LCMV. Following infection with LCMV or L. monocytogenes, mutant CTLs display a breakdown of cytotoxic granule integrity, increased cytoplasmic granzyme B, and reduced survival due to increased granzyme B-mediated apoptosis.
- The *Serpinb9* gene is located on the Chr13. 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)

Serpina9 serine (or cysteine) peptidase inhibitor, clade B, member 9 [Mus musculus (house mouse)]

Gene ID: 20723, updated on 31-Jan-2019

Summary



Official Symbol Serpina9 provided by [MGI](#)

Official Full Name serine (or cysteine) peptidase inhibitor, clade B, member 9 provided by [MGI](#)

Primary source [MGI:MGI:106603](#)

See related [Ensembl:ENSMUSG00000045827](#)

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 BB283241, CAP-3, CAP3, PI-9, PI9, Spi6, ovalbumin

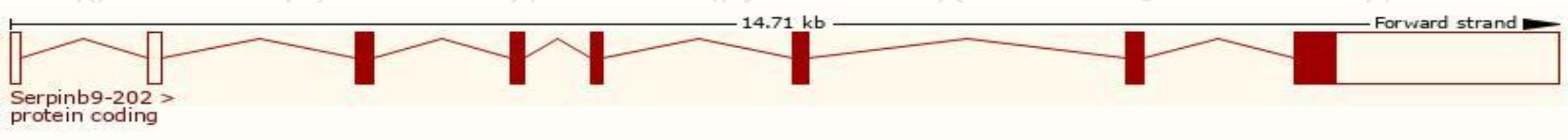
Expression Broad expression in lung adult (RPKM 6.6), placenta adult (RPKM 6.0) and 21 other tissues [See more](#)

Transcript information (Ensembl)

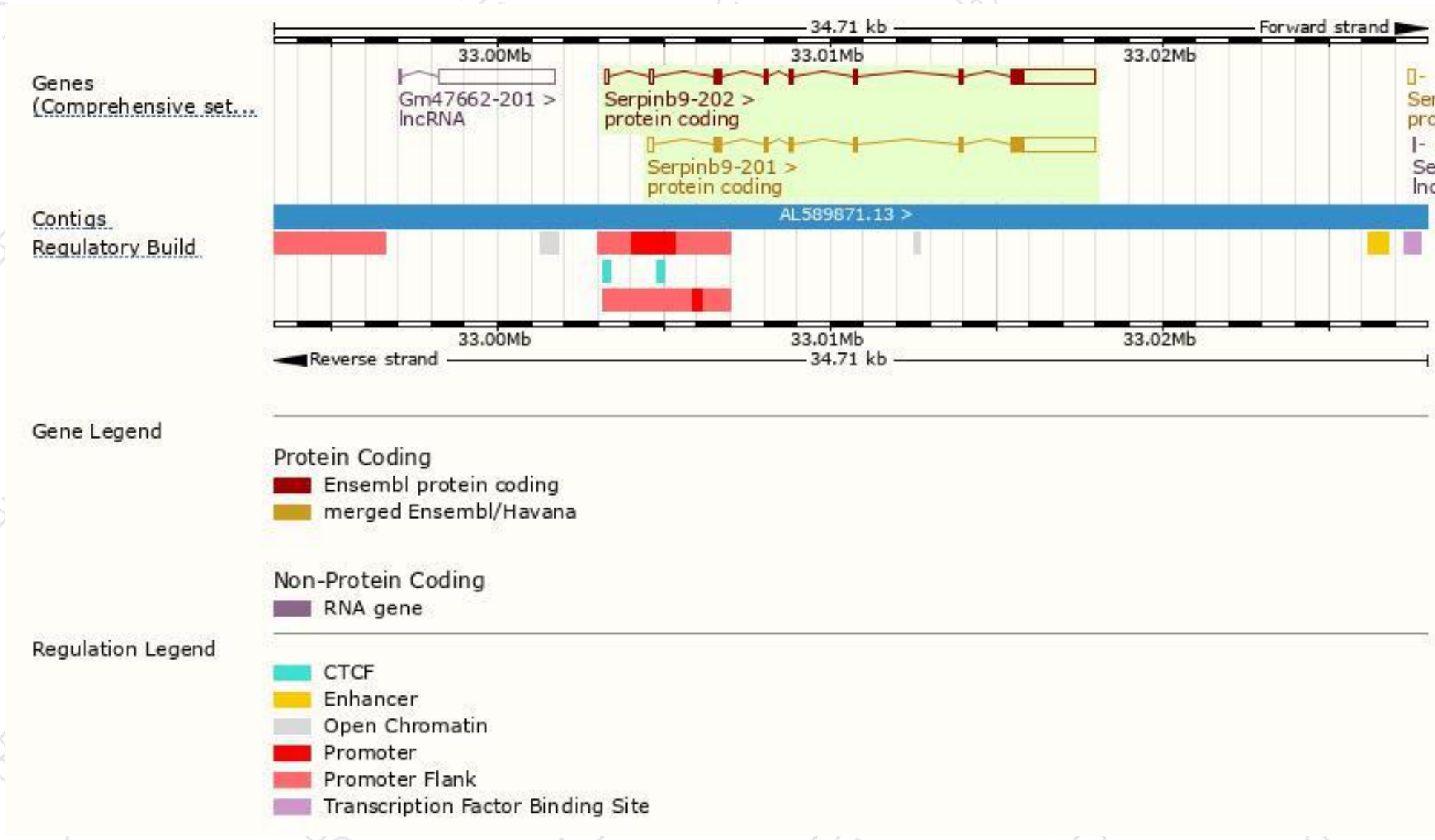
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Serpib9-202	ENSMUST00000063191.13	3472	374aa	Protein coding	CCDS26431	Q08797	TSL:5 GENCODE basic APPRIS P1
Serpib9-201	ENSMUST0000006391.4	3397	374aa	Protein coding	CCDS26431	Q08797	TSL:1 GENCODE basic APPRIS P1

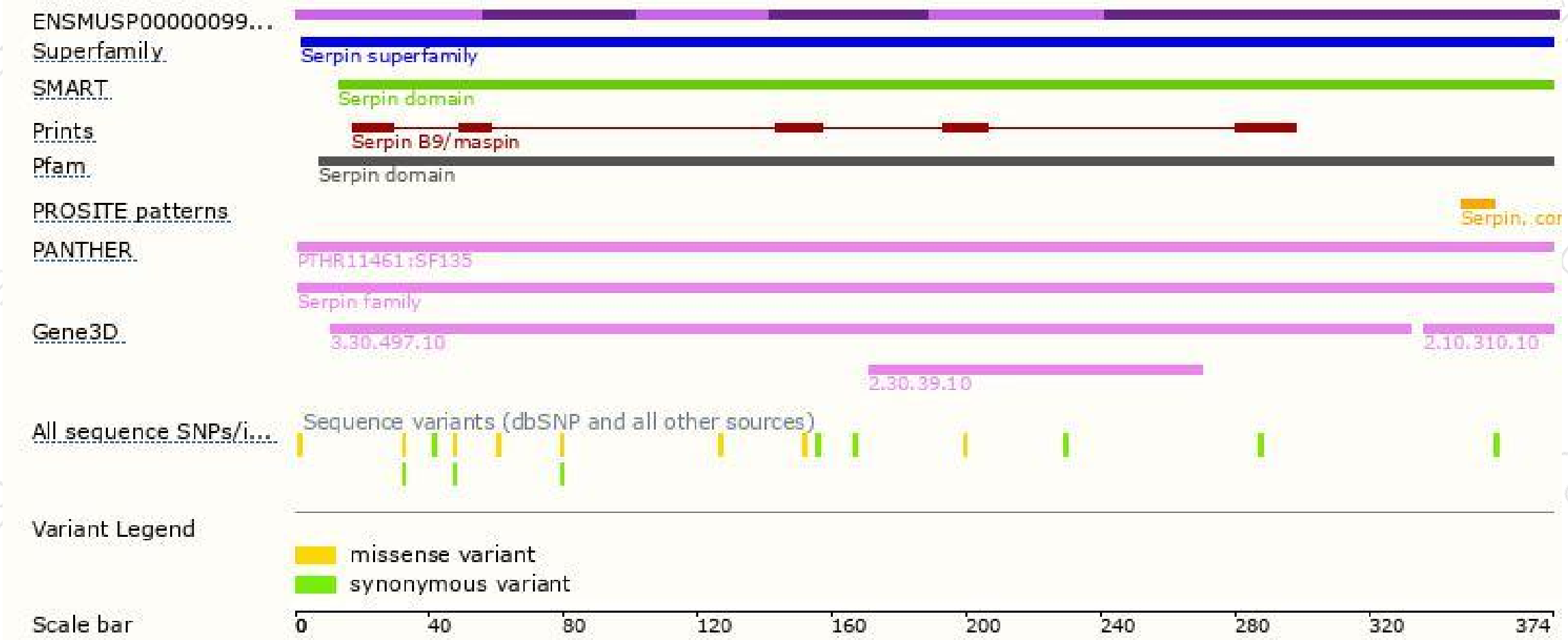
The strategy is based on the design of *Serpib9-202* transcript,The transcription is shown below



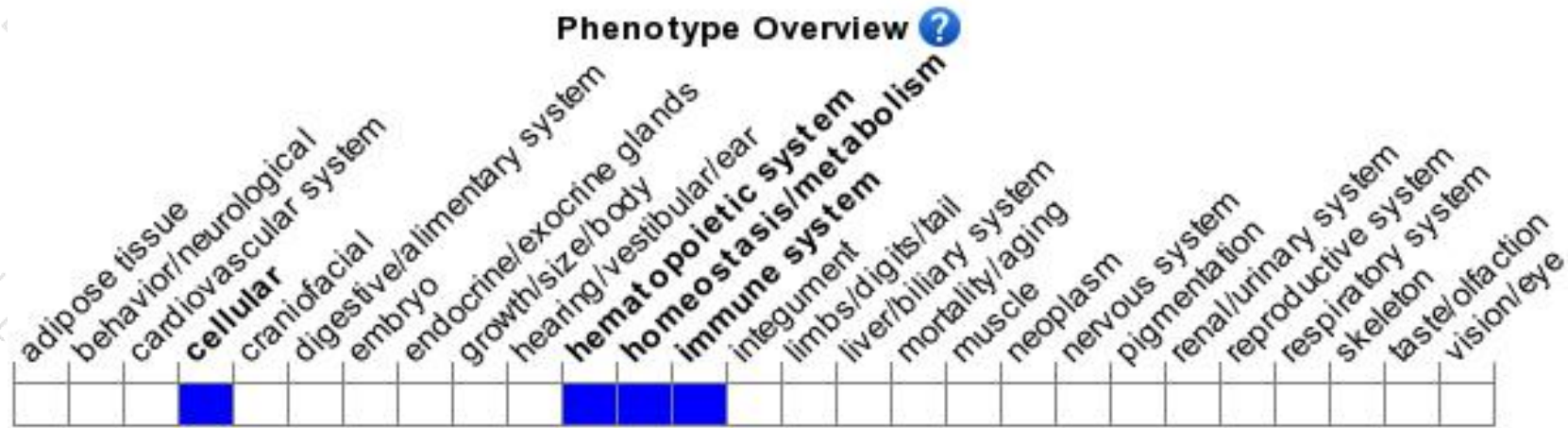
Genomic location distribution



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 show defective CTL immunity and clearance of LCMV. Following infection with LCMV or L. monocytogenes, mutant CTLs display a breakdown of cytotoxic granule integrity, increased cytoplasmic granzyme B, and reduced survival due to increased granzyme B-mediated apoptosis.

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

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