

Serpine1 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Serpine1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Serpine1* gene. The schematic diagram is as follows:



- The *Serpine1* gene has 3 transcripts. According to the structure of *Serpine1* gene, exon3-exon5 of *Serpine1-201* (ENSMUST00000041388.10) transcript is recommended as the knockout region. The region contains 628bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Serpine1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Although mice homozygous for disruptions in this gene display an essentially normal phenotype, a mild blood clotting defect does exist. Mice homozygous for an allele with amino acid substitutions exhibit decreased sensitivity to LPS-induced lethality.
- The *Serpine1* gene is located on the Chr5. 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)

Serpine1 serine (or cysteine) peptidase inhibitor, clade E, member 1 [Mus musculus (house mouse)]

Gene ID: 18787, updated on 31-Jan-2019

Summary



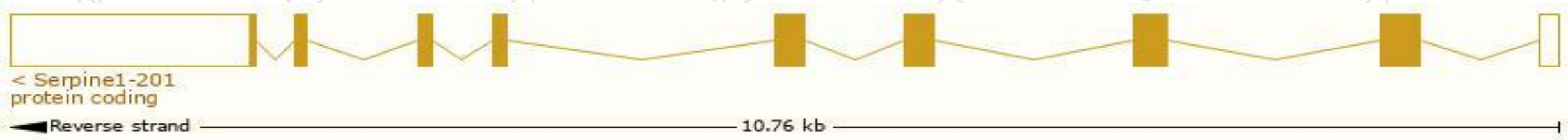
Official Symbol	Serpine1 provided by MGI
Official Full Name	serine (or cysteine) peptidase inhibitor, clade E, member 1 provided by MGI
Primary source	MGI:MGI:97608
See related	Ensembl:ENSMUSG00000037411
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	PAI-1, PAI1, Planh1
Expression	Biased expression in placenta adult (RPKM 80.4), liver E18 (RPKM 11.4) and 3 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

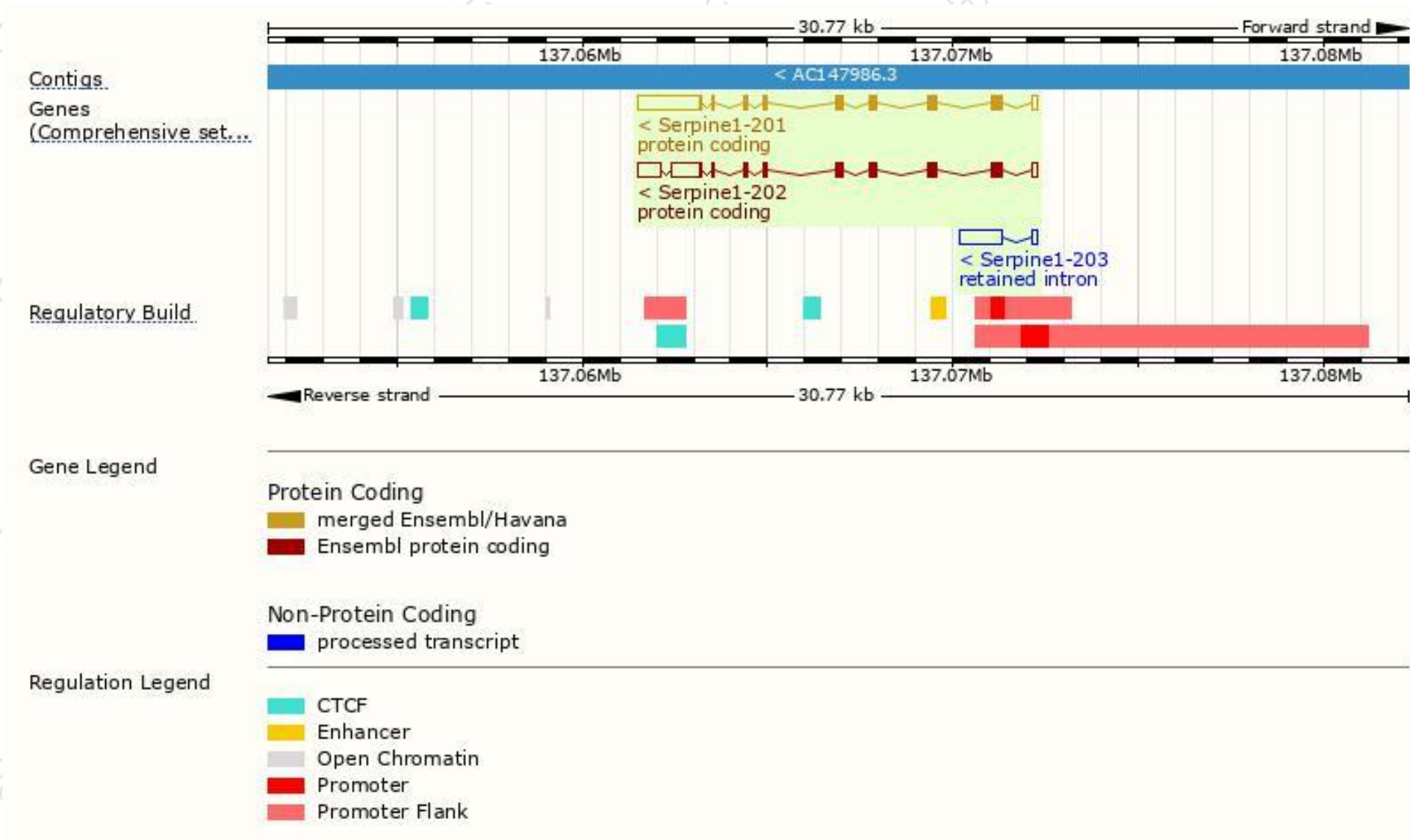
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Serpine1-201	ENSMUST00000041388.10	3011	402aa	Protein coding	CCDS19761	G5E899	TSL:1 GENCODE basic APPRIS P1
Serpine1-202	ENSMUST00000077523.3	2697	402aa	Protein coding	CCDS19761	G5E899	TSL:5 GENCODE basic APPRIS P1
Serpine1-203	ENSMUST00000199832.1	1268	No protein	Retained intron	-	-	TSL:1

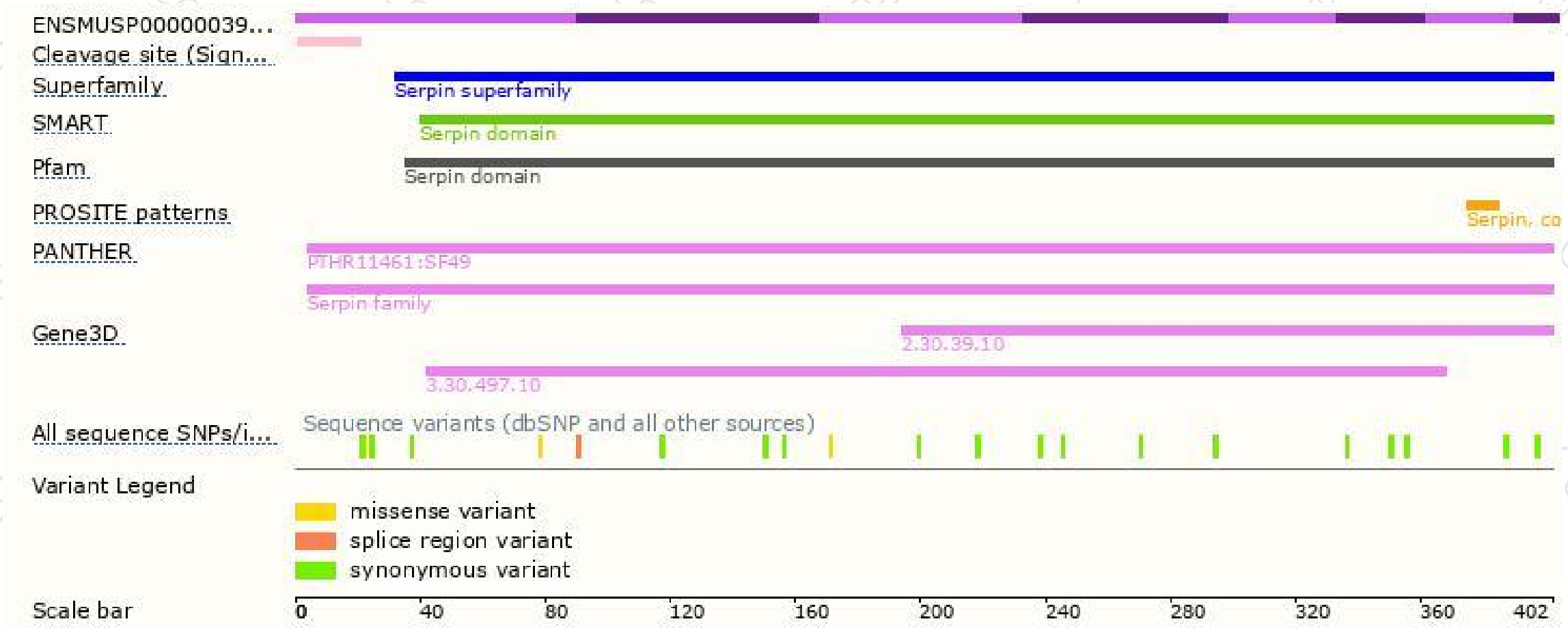
The strategy is based on the design of *Serpine1-201* transcript,The transcription is shown below



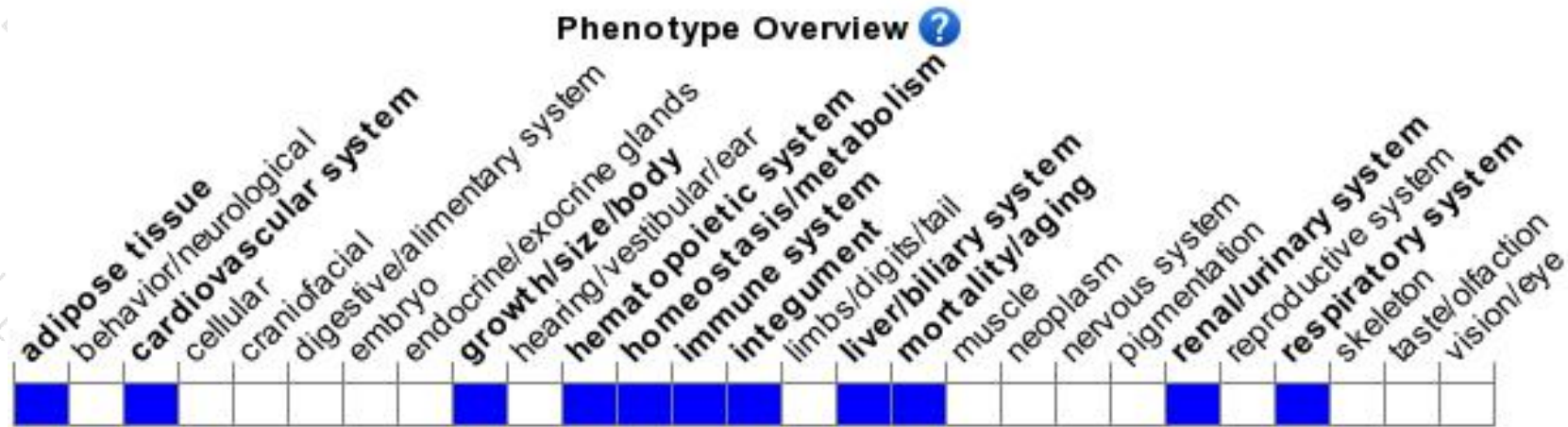
Genomic location distribution



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, Although mice homozygous for disruptions in this gene display an essentially normal phenotype, a mild blood clotting defect does exist. Mice homozygous for an allele with amino acid substitutions exhibit decreased sensitivity to LPS-induced lethality.

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

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