

Serping1 Cas9-KO Strategy

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Overview

Target Gene Name

- Serping1

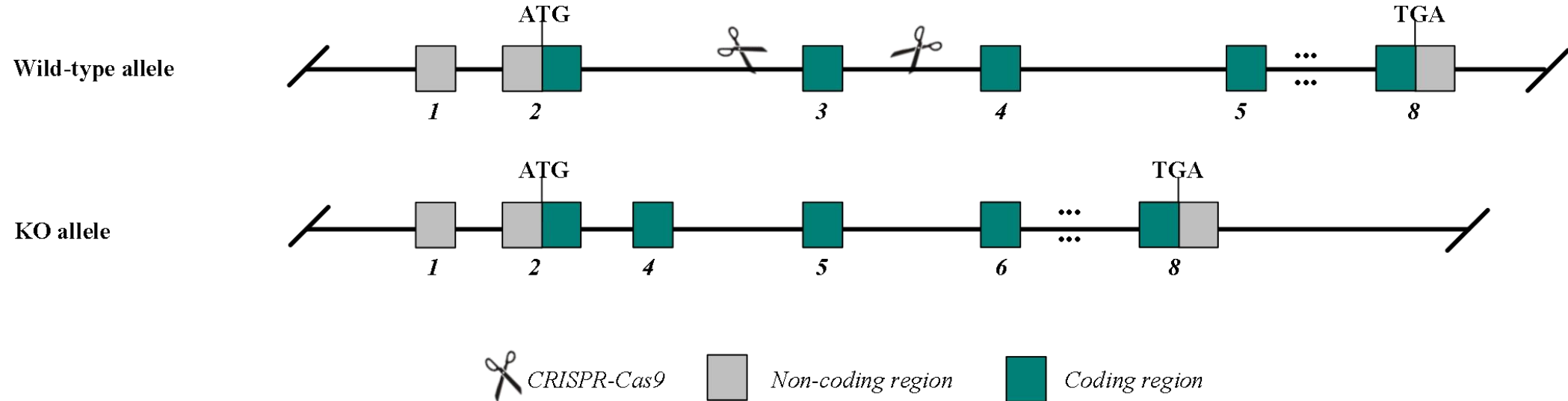
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Serping1* gene.

Technical Information

- The *Serping1* gene has 3 transcripts. According to the structure of *Serping1* gene, exon3 of *Serping1-201* (ENSMUST00000023994.10) transcript is recommended as the knockout region. The region contains 514bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Serping1* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Serping1 serine (or cysteine) peptidase inhibitor, clade G, member 1 [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 12258, updated on 4-Apr-2023

Summary

Official Symbol Serping1 provided by [MGI](#)
Official Full Name serine (or cysteine) peptidase inhibitor, clade G, member 1 provided by [MGI](#)
Primary source [MGI:MG1:894696](#)
See related [Ensembl:ENSMUSG00000023224](#) [AllianceGenome:MG1:894696](#)
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 C1nh; C1Inh; C1 Inh; C1INH.
Summary Enables complement binding activity and serine-type endopeptidase inhibitor activity. Predicted to be involved in negative regulation of complement activation, lectin pathway and negative regulation of endopeptidase activity. Predicted to act upstream of or within several processes, including complement activation, classical pathway, fibrinolysis, and negative regulation of peptidase activity. Located in extracellular space. Is expressed in several structures, including genitourinary system; neural ectoderm; notochord; pancreas mesenchyme; and visceral pericardium. Human ortholog(s) of this gene implicated in several diseases, including COVID-19; angioedema (multiple); cerebral infarction; pancreatitis; and toxic shock syndrome. Orthologous to human SERPING1 (serpin family G member 1). [provided by Alliance of Genome Resources, Apr 2022]
Expression Broad expression in liver adult (RPKM 378.2), lung adult (RPKM 269.8) and 18 other tissues [See more](#)
Orthologs [human](#) [all](#)
NEW Try the new [Gene table](#)
Try the new [Transcript table](#)

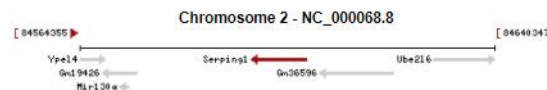
Genomic context

Location: 2; 2 D

See Serping1 in [Genome Data Viewer](#)

Exon count: 8

Annotation release	Status	Assembly	Chr	Location
109	current	GRCm39 (GCF_000001635.27)	2	NC_000068.8 (84595704..84605778, complement)
108.2020622	previous assembly	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (84765360..84775444, complement)



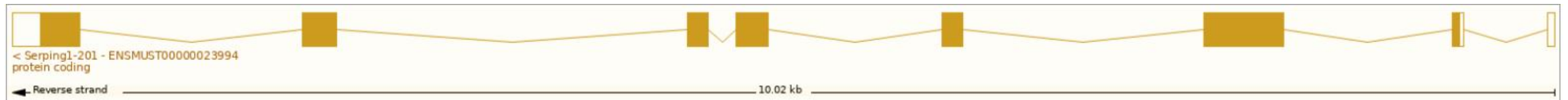
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

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

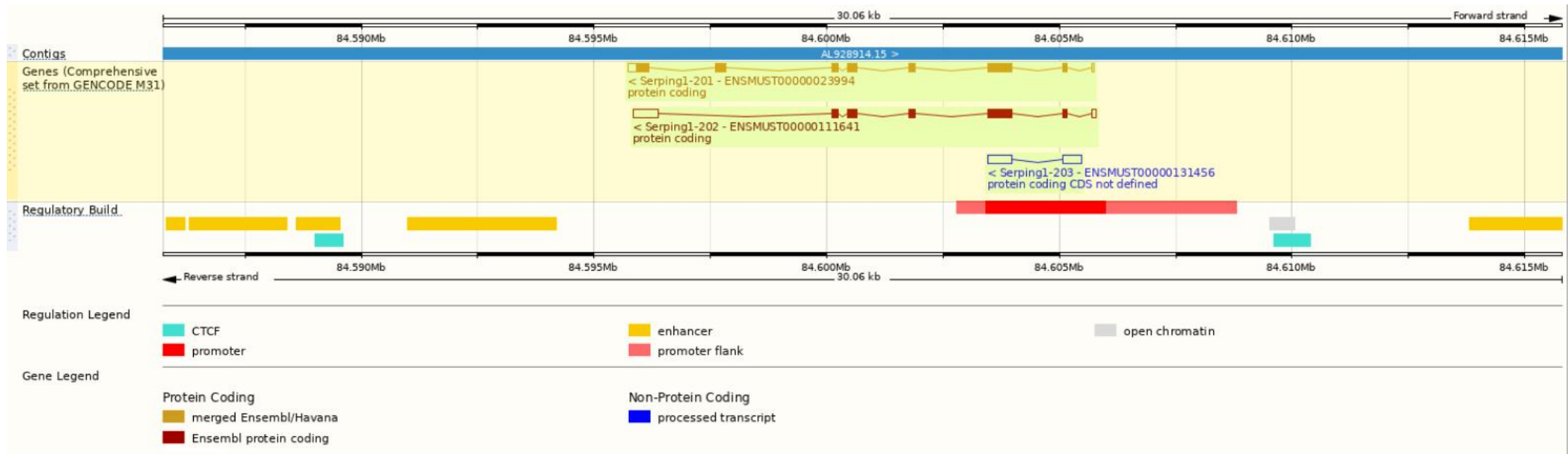
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000023994.10	Serping1-201	1768	504aa	Protein coding	CCDS16193	P97290	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000111641.2	Serping1-202	1665	347aa	Protein coding		A2ATR8	GENCODE basic TSL:5
ENSMUST00000131456.2	Serping1-203	903	No protein	Protein coding CDS not defined		-	TSL:2

The strategy is based on the design of *Serping1-201* transcript, the transcription is shown below:

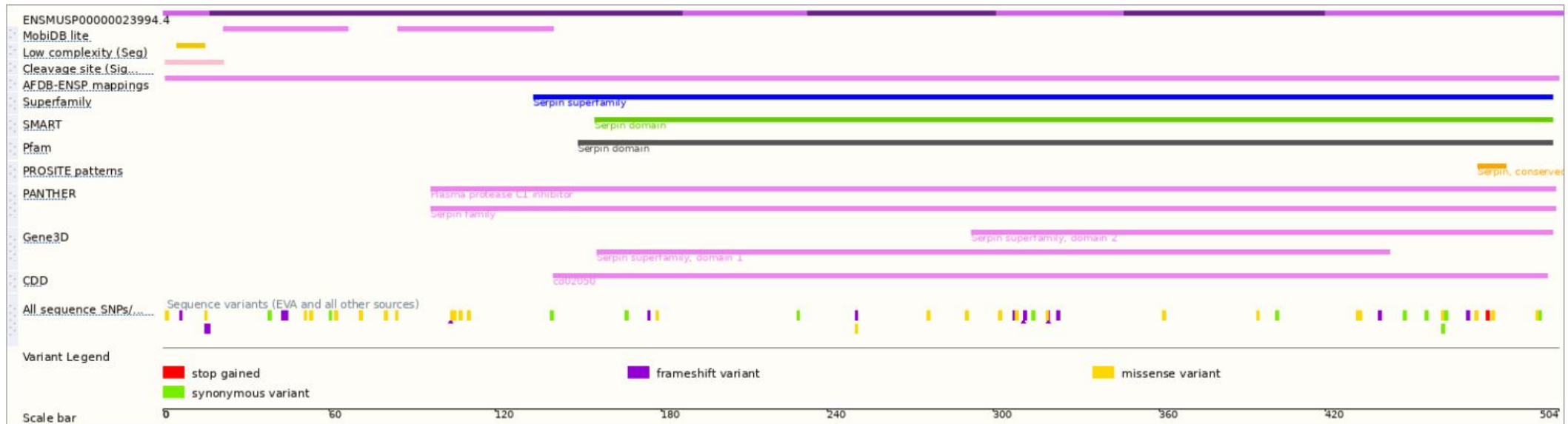


Source: <https://www.ensembl.org>

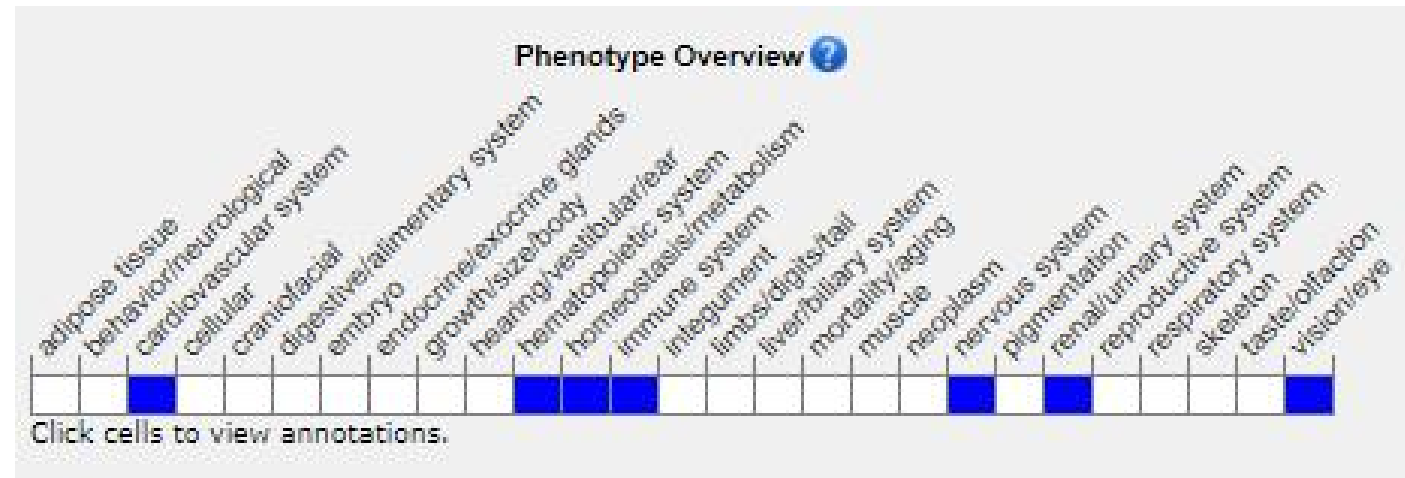
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Mutant mice exhibit an increased vascular permeability compared to controls.

Important Information

- According to the MGI data, mutant mice exhibit an increased vascular permeability compared to controls.
- *Serping1* is located on Chr2. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.