

Serpinh1 Cas9-KO Strategy

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Design Date: 2021-8-23

Project Overview

Project Name

Serpinh1

Project type

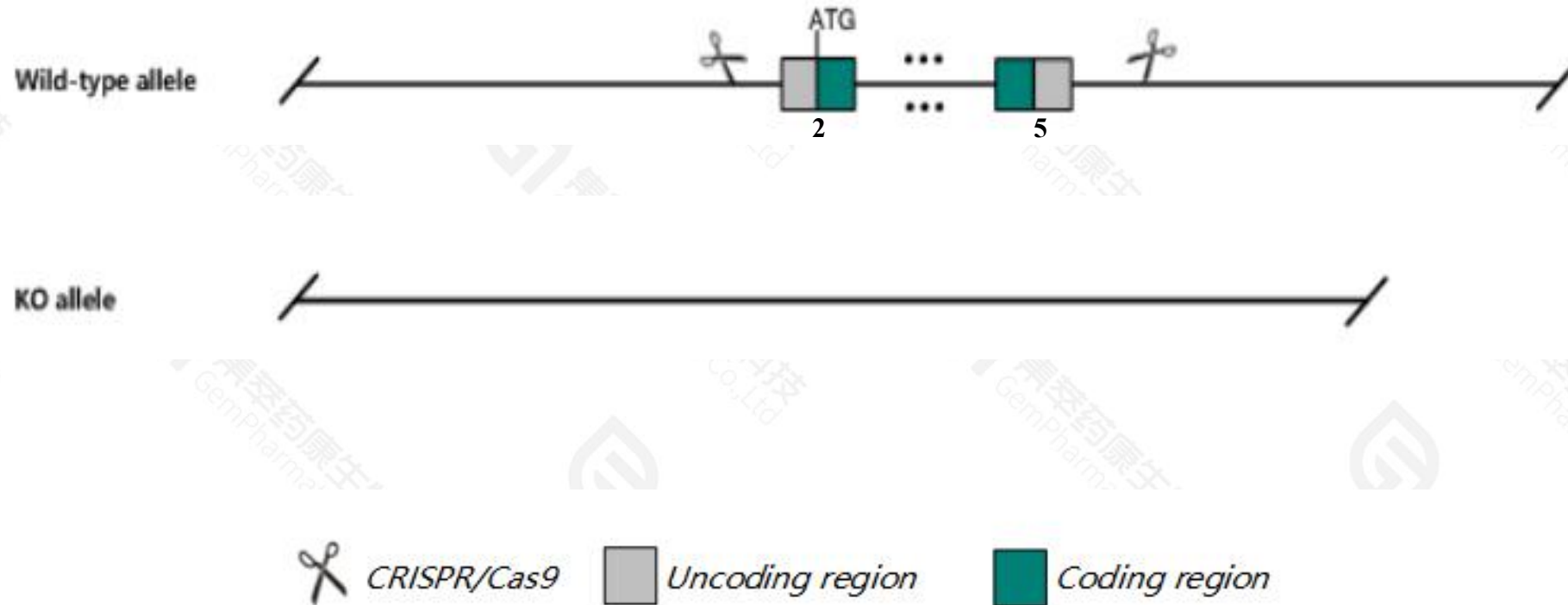
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Serpinh1* gene. The schematic diagram is as follows:



- The *Serpinh1* gene has 7 transcripts. According to the structure of *Serpinh1* gene, exon2-exon5 of *Serpinh1*-202(ENSMUST00000169437.9) transcript is recommended as the knockout region. The region contains all 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 *Serpinh1* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for disruptions in this gene die as embryos before E11.5. Mice homozygous for a conditional allele activated in chondrocytes exhibit complete perinatal lethality, cleft palate, respiratory distress, abnormal chondrocytes and bone formation.
- The *Serpinh1* gene is located on the Chr7. 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.

Serpinh1 serine (or cysteine) peptidase inhibitor, clade H, member 1 [Mus musculus (house mouse)]

Gene ID: 12406, updated on 13-Mar-2020

Summary



Official Symbol Serpinh1 provided by [MGI](#)

Official Full Name serine (or cysteine) peptidase inhibitor, clade H, member 1 provided by [MGI](#)

Primary source [MGI:MGI:88283](#)

See related [Ensembl:ENSMUSG00000070436](#)

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 BERF-1, Cbp1, Cbp2, Hsp47, J6, Serpinh2, gp46

Expression Broad expression in limb E14.5 (RPKM 483.4), ovary adult (RPKM 448.6) and 19 other tissues [See more](#)

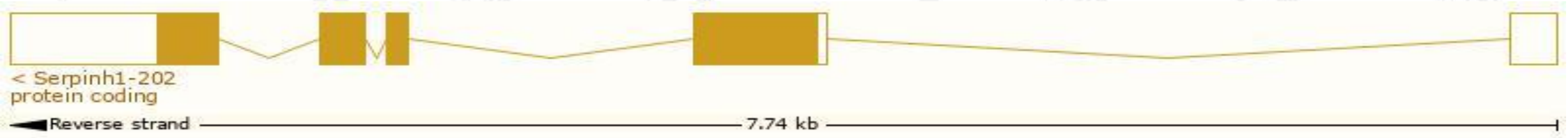
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

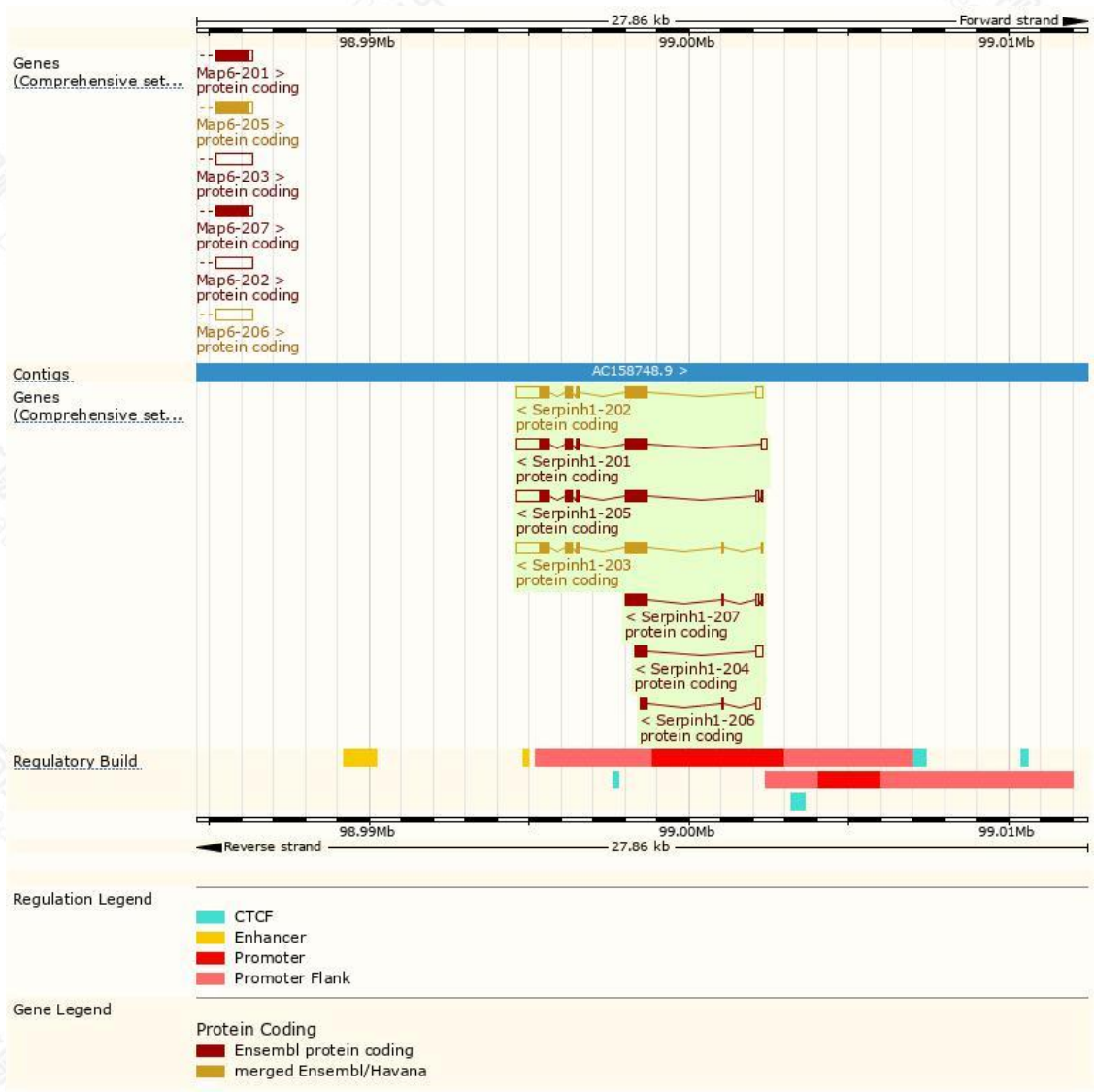
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Serpinh1-202	ENSMUST00000169437.8	2274	417aa	Protein coding	CCDS21480	P19324	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Serpinh1-201	ENSMUST00000094154.5	2215	417aa	Protein coding	CCDS21480	P19324	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Serpinh1-205	ENSMUST00000208119.1	2173	417aa	Protein coding	CCDS21480	P19324	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Serpinh1-203	ENSMUST00000207849.1	2128	417aa	Protein coding	CCDS21480	P19324	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Serpinh1-207	ENSMUST00000208749.1	828	203aa	Protein coding	-	A0A140LHR4	CDS 3' incomplete TSL:5
Serpinh1-204	ENSMUST00000207989.1	592	115aa	Protein coding	-	A0A140LHK0	CDS 3' incomplete TSL:2
Serpinh1-206	ENSMUST00000208292.1	358	53aa	Protein coding	-	A0A140LHD6	CDS 3' incomplete TSL:3

The strategy is based on the design of *Serpinh1-202* transcript,the transcription is shown below:



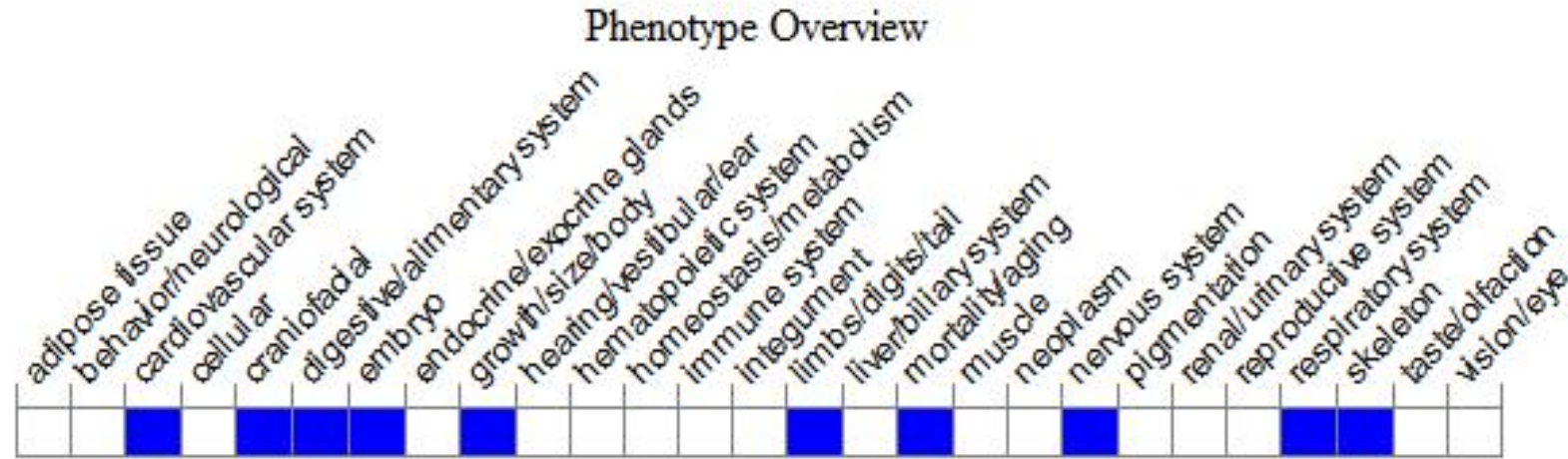
Genomic location distribution



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, mice homozygous for disruptions in this gene die as embryos before E11.5. Mice homozygous for a conditional allele activated in chondrocytes exhibit complete perinatal lethality, cleft palate, respiratory distress, abnormal chondrocytes and bone formation.

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