Serpinh1 Cas9-CKO Strategy

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Project Overview

Project Name	***Serpinh1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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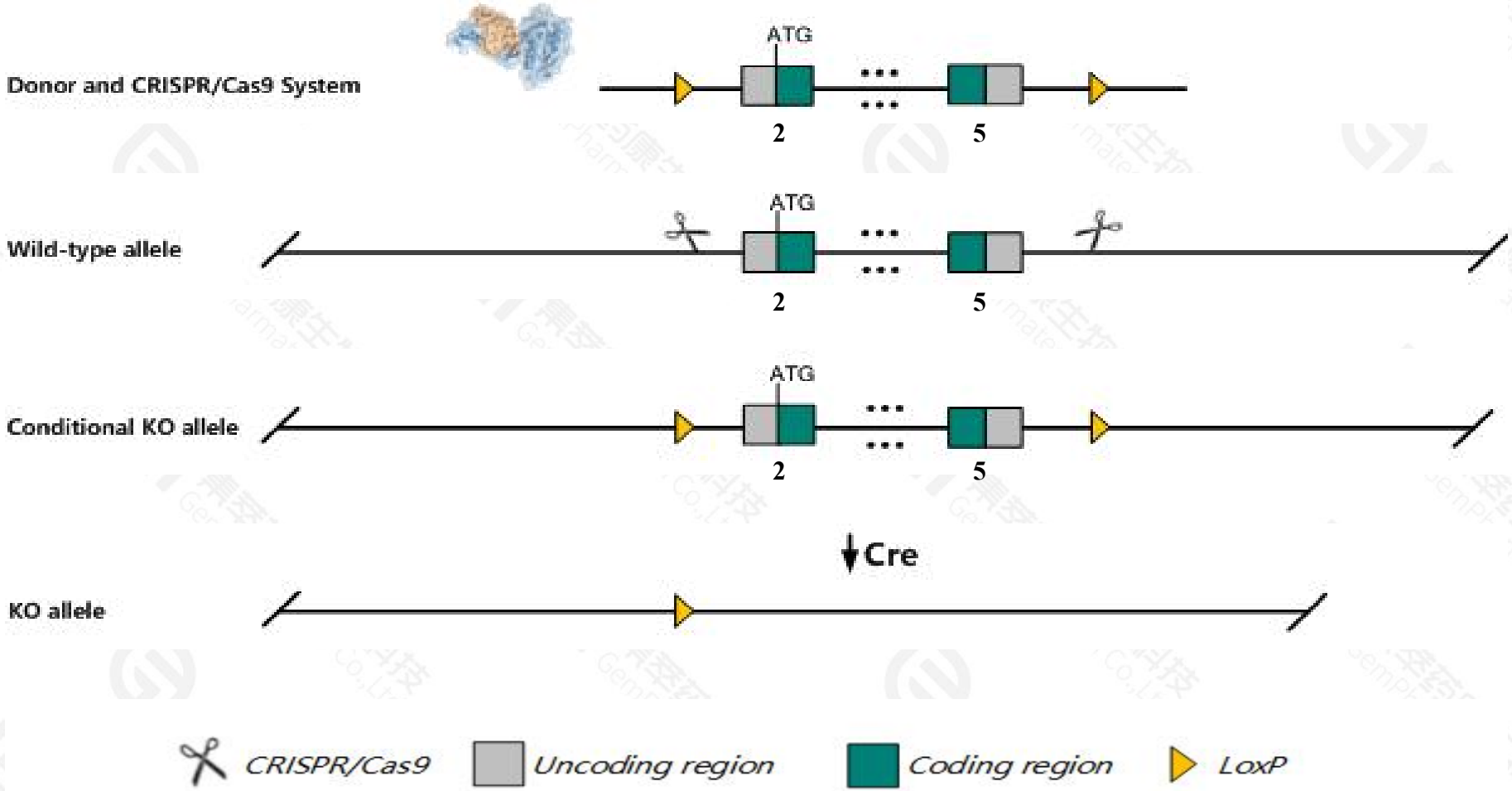
This model will use CRISPR/Cas9 technology to edit the *Serpinh1* gene. The schematic diagram is as follows:



Technical routes

➢ 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 and Donor 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.

➢ The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ 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 chondocytes 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information（NCBI）

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

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

Summary

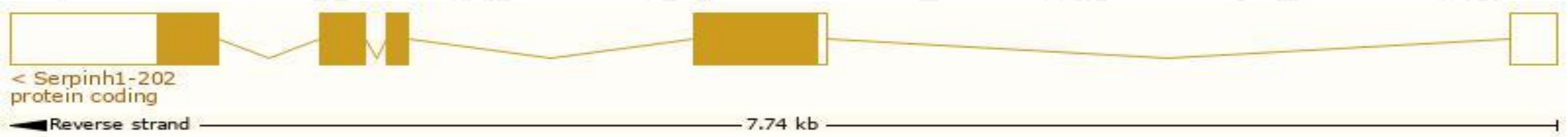
Official Symbol	Serpinh1 provided by MGI
Official Full Name	serine (or cysteine) peptidase inhibitor, clade H, member 1 provided byMGI
Primary source	MGI:MGI:88283
See related	Ensembl:ENSMUSG00000070436
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; 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 tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

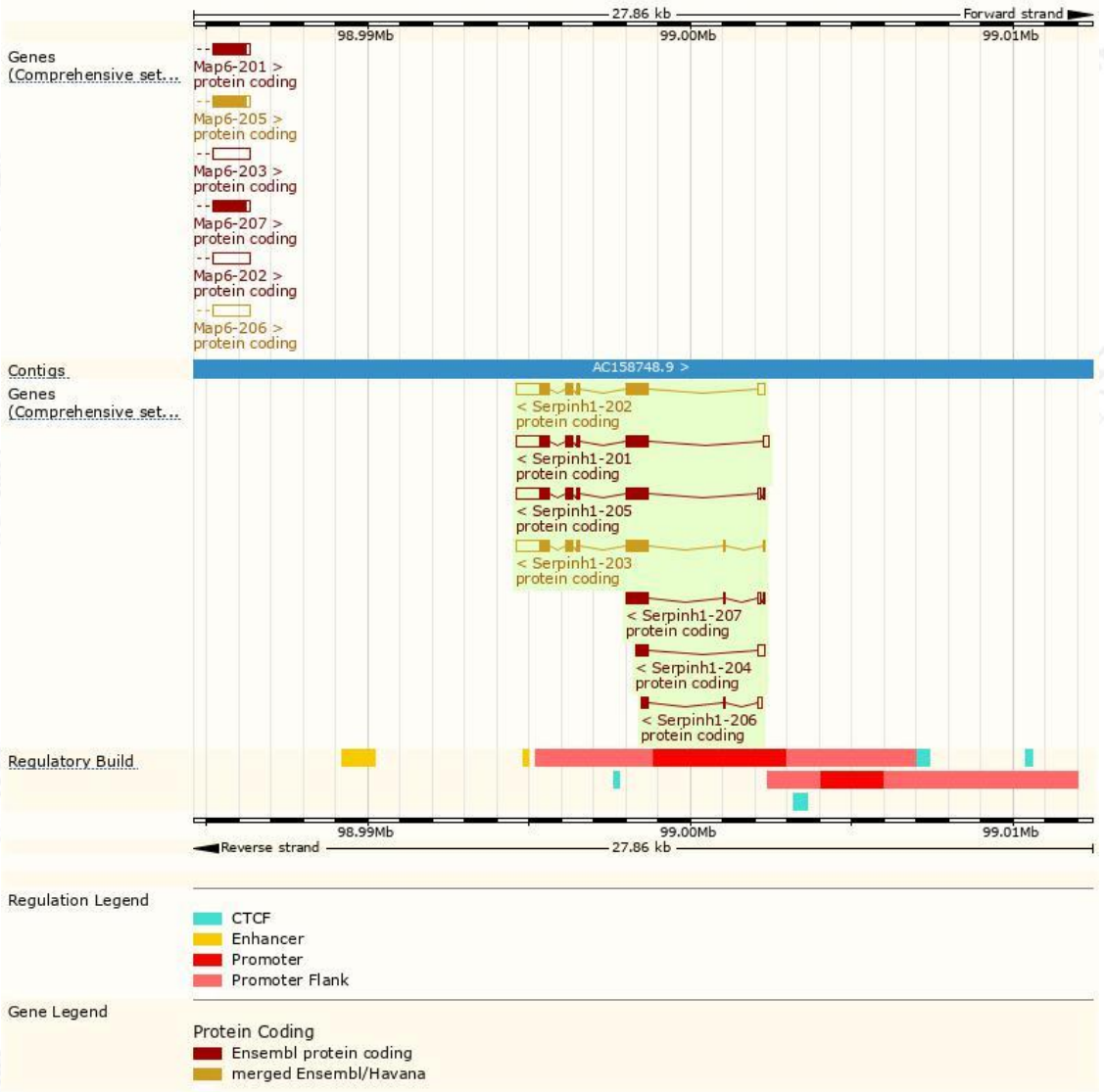
The gene has 7 transcripts,all transcripts are shown below:

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:

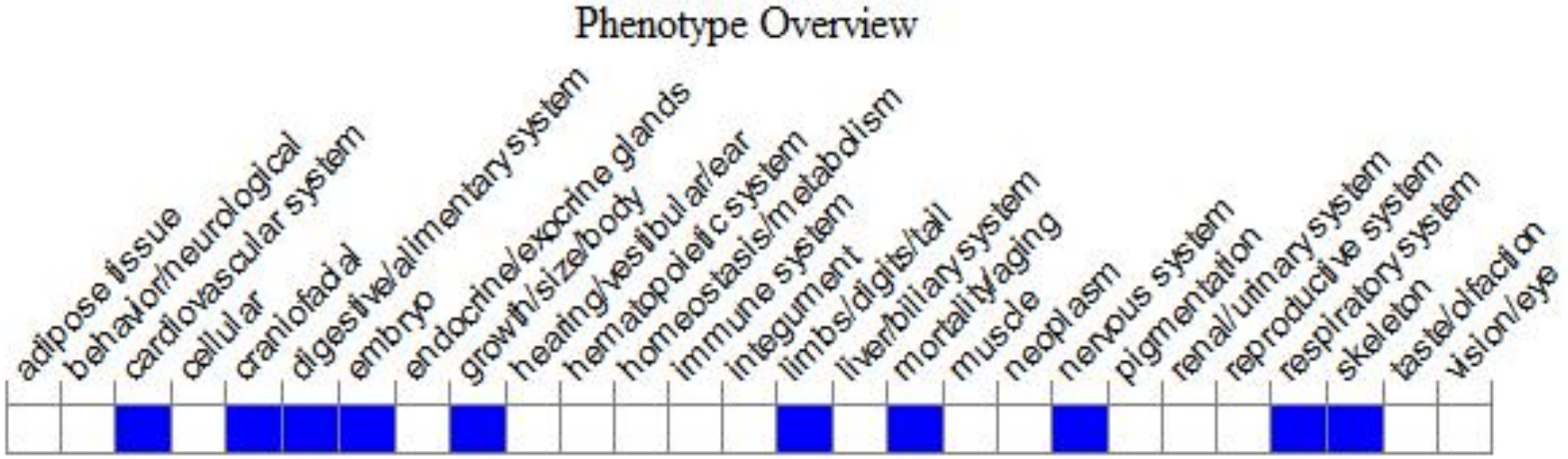


Genomic location distribution



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 chondocytes and bone formation.

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