

Serpinb10 Cas9-CKO Strategy

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Overview

Target Gene Name

• Serpinb10

Project Type

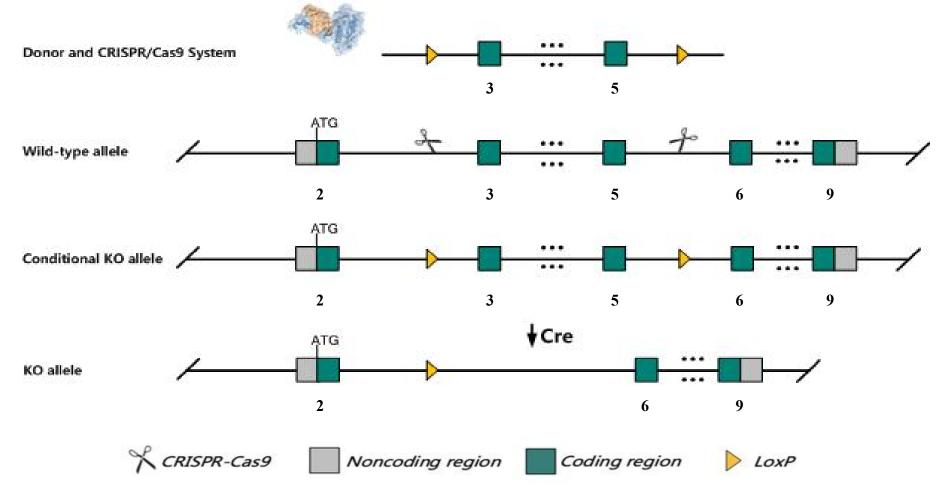
• Cas9-CKO

Genetic Background

• C57BL/6JGpt



Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Serpinb10 gene.



Technical Information

- The Serpinb10 gene has 5 transcripts. According to the structure of Serpinb10 gene, exon3-exon5 of Serpinb10-XM_006529597.4 transcript is recommended as the knockout region. The region contains 322bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Serpinb10* 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 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.
- 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.



Gene Information

Serpinb10 serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10 [Mus musculus (house mouse)]

Gene ID: 241197, updated on 5-Mar-2024



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



Transcript Information

The gene has 5 transcripts, all transcripts are shown below:

| Gene ID | Gene symbol | Transcript | Length (nt) | Protein | Length (aa) | Protein name | Isofo | |
|---|--|--|-----------------|----------------|-----------------------|--|-------|---|
| 241197 | Serpinb10 | XM_006529597.4 | 2845 | XP_006529660.1 | 382 | serpin B10 | X1 | |
| 241197 | Serpinb10 | XM_006529598.4 | 2669 | XP_006529661.1 | 345 | serpin B10 | X2 | |
| 241197 | Serpinb10 | XM_006529599.1 | 1821 | XP_006529662.1 | 268 | serpin B10 | Х3 | |
| 241197 | Serpinb10 | NM_198028.3 | 3490 | NP_932145.3 | 357 | serpin B10 | 1 | |
| 241197 | Serpinb10 | NM_001160307.1 | 3314 | NP_001153779.1 | 320 | serpin B10 | 2 | |
| RefSeg Ann | otation GCF 00000 | 01635.27-RS 2024 02 | | GAS CHE | | | | ± 0 : |
| | | f | ox region | Serpinb10 | | | | 2.0 |
| XM_00652959 XM_00652959 | 97.4 | 01635.27-RS_2024_02 | ox region | | | <u>; </u> | | XP_006529660.1 XP_006529661.1 |
| XM_00652959 XM_00652959 XM_0065295 NM_19802 | 97.4 98.4 99.1 28.3 | - f | ox region | | XP_00652966 NP_93; | 2145.3 | | XP_006529660.1 |
| XM_00652959 XM_00652959 XM_00652959 | 97.4 98.4 99.1 28.3 97.1 | | ox region | | NP_932 | | | XP_006529660.1 |
| XM_00652955 XM_00652955 XM_00652955 XM_0065295 NM_19802 NM_00116030 | 97.4 98.4 99.1 28.3 97.1 | NCBI RefSeq Annotat | ion GCF_0000016 | Serpinb10 | NP_932 | 2145.3 | | XP_806529660.1 XP_806529661.1 Gm18249 |
| XM_00652955 XM_00652955 XM_00652955 NM_19802 NM_00116036 NP_001167641.1 NP_035241.1 ogical regi | 97.4 98.4 99.1 28.3 97.1 | ************************************** | ion GCF_0000016 | Serpinb10 | NP_932 | 2145.3 | | XP_006529660.1 XP_006529661.1 Gm18249 |
| XM_00652955 XM_00652955 XM_00652955 NM_19802 NM_00116036 NP_001167641.1 NP_035241.1 ogical regi | 97.4 98.4 99.1 28.3 97.1 1 ons, aggregate, l | NCBI RefSeq Annotat | ion GCF_0000016 | Serpinb10 | NP_932 | 2145.3 | | XP_006529660.1 XP_006529661.1 |



Transcript Information

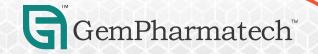
The strategy is based on the design of *Serpinb10*-XM_006529597.4 transcript, the transcription is shown below:

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1. XM_006529597.4 → XP_006529660.1 serpin B10 isoform X1

Conserved Domains (1) summary

cl38926 | serpin; SERine Proteinase INhibitors (serpin) family

Location:1 → 277
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Important Information

- Serpinb10 is located on Chr1. 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 risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

