

Spp1 Cas9-CKO Strategy

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Overview

Target Gene Name

• Spp1

Project Type

• Cas9-CKO

Genetic Background

• C57BL/6JGpt



Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Spp1 gene.

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Technical Information

- The *Spp1* gene has 7 transcripts. According to the structure of *Spp1* gene, exon2-8 of *Spp1*-202 (ENSMUST00000086833.13) transcript is recommended as the knockout region. The region contains all of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Spp1* 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

Spp1 secreted phosphoprotein 1 [Mus musculus (house mouse)]

Gene ID: 20750, updated on 21-Dec-2023

Summary

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Official Symbol	Spp1 provided by MGI						
Official Full Name	secreted phosphoprotein 1 provided by MGI						
Primary source	<u>MGI:MGI:98389</u>						
See related	Ensembl:ENSMUSG0000029304 AllianceGenome:MGI:98389						
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	OP; 2AR; Bsp; Eta; Opn; Ric; BNSP; BSPI; OpnI; ApI-1; ETA-1; Spp-1						
Summary	Enables extracellular matrix binding activity. Acts upstream of or within several processes, including cellular ion homeostasis; cellular response to leukemia inhibitory						
	factor; and neutrophil chemotaxis. Located in apical part of cell and cytoplasm. Is expressed in several structures, including alimentary system; brain; metanephros;						
	reproductive system; and skeleton. Human ortholog(s) of this gene implicated in several diseases, including autoimmune disease (multiple); biliary atresia; coronary						
	artery disease (multiple); disease of cellular proliferation (multiple); and hepatitis. Orthologous to human SPP1 (secreted phosphoprotein 1). [provided by Alliance of						
	Genome Resources, Apr 2022]						
Expression	Biased expression in kidney adult (RPKM 580.4), liver E18 (RPKM 36.2) and 1 other tissue See more						
Orthologs	human all						
NEW	Try the new Gene table						
	Try the new Transcript table						
* Genomic context							
- Genomic context							
Location: 5 E5; 5 50.66	See Spp1 in Genome Data Viewer						
European C	.nlm.nih.gov/						
Exon count: 8	0 /						
1000000000000							
G D1 1							
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Transcript Information

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

Transcript ID 💧	Name 🍦	bp 🍦	Protein 🖕	Biotype 🍦	CCDS 🍦	UniProt Match	Flags 🖕
ENSMUST0000086833.13	Spp1-202	1411	<u>295aa</u>	Protein coding	<u>CCDS57367</u> &	F8WIP8 &	Ensembl Canonical GENCODE basic APPRIS ALT2 TSL:5
ENSMUST00000112747.2	Spp1-204	1507	<u>294aa</u>	Protein coding	<u>CCDS19486</u> ൽ	P10923 & Q547B5 &	GENCODE basic APPRIS P2 TSL:1
ENSMUST00000112748.8	Spp1-205	1456	<u>294aa</u>	Protein coding	<u>CCDS19486</u>	P10923 & Q547B5 &	GENCODE basic APPRIS P2 TSL:1
ENSMUST0000031243.15	Spp1-201	1410	<u>294aa</u>	Protein coding	<u>CCDS19486</u> &	P10923 & Q547B5 &	GENCODE basic APPRIS P2 TSL:1
ENSMUST00000112746.8	Spp1-203	669	<u>164aa</u>	Protein coding		<u>D3Z4N2</u> &	TSL:5 CDS 3' incomplete
ENSMUST00000145084.8	Spp1-207	634	<u>152aa</u>	Protein coding		<u>D3Z513</u>	TSL:5 CDS 3' incomplete
ENSMUST00000132457.8	Spp1-206	354	<u>48aa</u>	Protein coding		<u>D3Z116</u> 교	TSL:3 CDS 3' incomplete

The strategy is based on the design of *Spp1*-202 transcript, the transcription is shown below:



Source: https://www.ensembl.org



Genomic Information

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

Protein Information



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

Important Information

- According to the existing MGI data, two alleles determine natural resistance/susceptibility to the lethal effects of the Gilliam strain of Rickettsia tsutsugamushi. Mice homozygous for a knock-out allele exhibit abnormal osteoclast physiology, macrophage recruitment, wound healing, response to injury, and inflammatory response.
- Gm42793 gene will be deleted.
- Insertion of loxp at both ends may affect the regulation of this gene.
- *Spp1* is located on Chr5. 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.

Mouse phenotype description(MGI)



Two alleles determine natural resistance/susceptibility to the lethal effects of the Gilliam strain of Rickettsia tsutsugamushi. Mice homozygous for a knock-out allele exhibit abnormal osteoclast physiology, macrophage recruitment, wound healing, response to injury, and inflammatory response.

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