

Acsn3 Cas9-KO Strategy

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Project Overview

Project Name

Acsn3

Project type

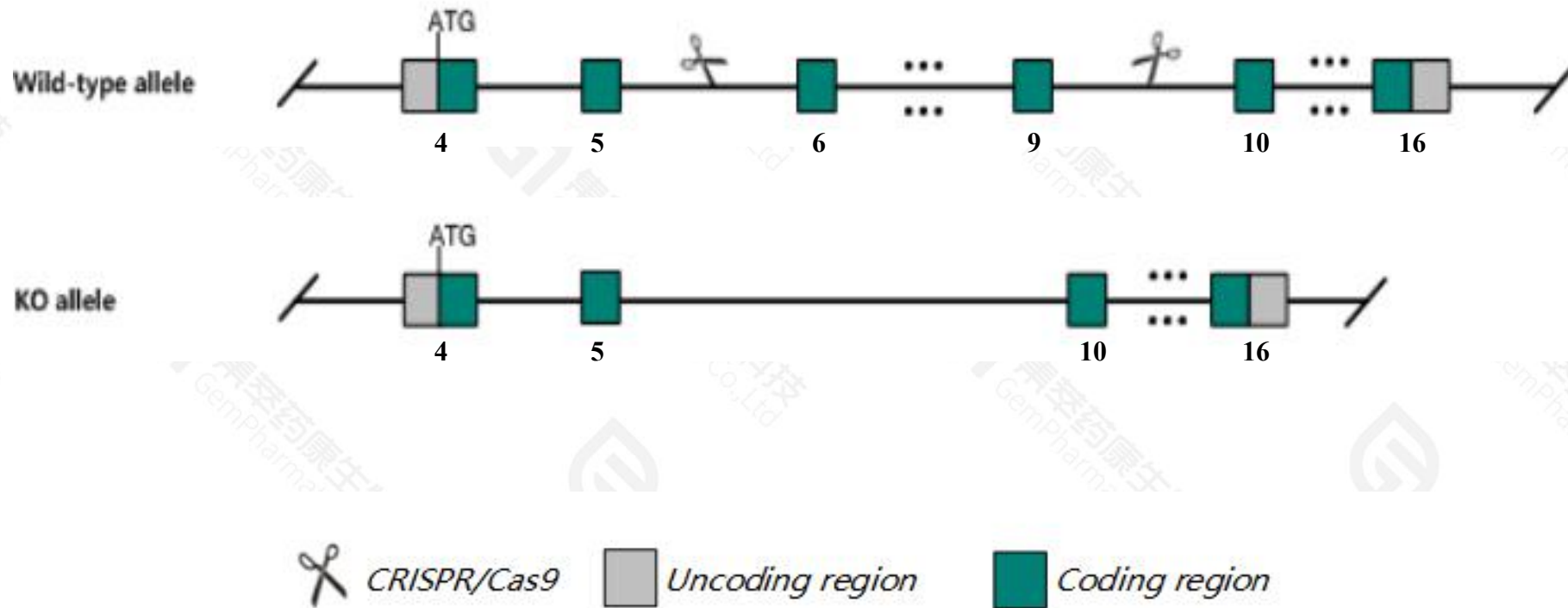
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Acsn3* gene. The schematic diagram is as follows:



- The *Acsn3* gene has 8 transcripts. According to the structure of *Acsn3* gene, exon6-exon9 of *Acsn3*-204(ENSMUST00000106528.8) transcript is recommended as the knockout region. The region contains 589bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Acsn3* 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, homozygous null mice are viable and fertile with normal kidney function and morphology and blood pressure similar to wild-type on either a regular or high salt diet.
- Knockout the region may affect the function of *LOC118567502* and *Eri2* gene.
- The *Acsn3* 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.

Acsn3 acyl-CoA synthetase medium-chain family member 3 [Mus musculus (house mouse)]

Gene ID: 20216, updated on 4-Feb-2021

Summary



Official Symbol Acsn3 provided by [MGI](#)

Official Full Name acyl-CoA synthetase medium-chain family member 3 provided by [MGI](#)

Primary source [MGI:MGI:99538](#)

See related [Ensembl:ENSMUSG00000030935](#)

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 S, Sa, Sah

Expression Broad expression in liver E18 (RPKM 13.3), liver adult (RPKM 7.2) and 18 other tissues [See more](#)

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

Transcript information (Ensembl)

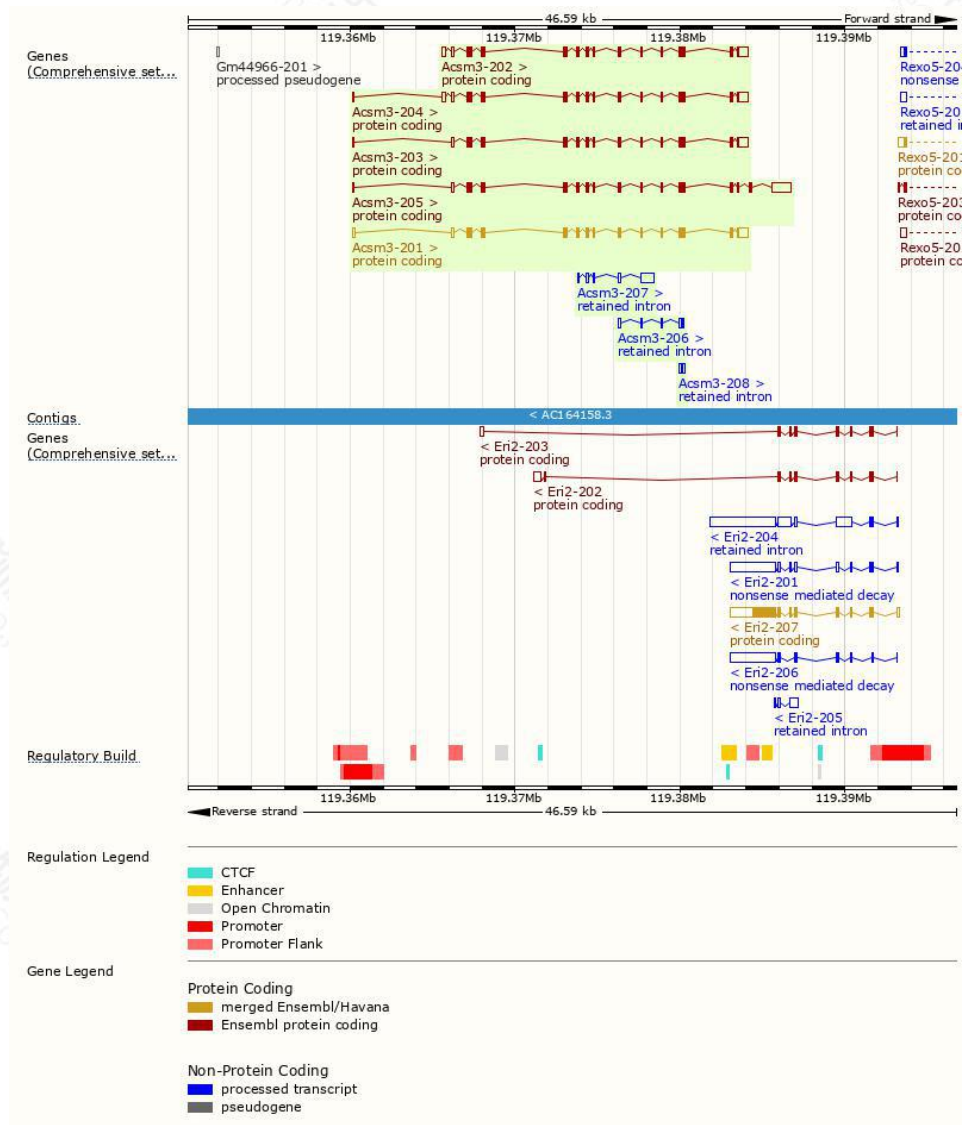
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Acsm3-204	ENSMUST00000106528.8	2755	580aa	Protein coding	CCDS21786		TSL:1 , GENCODE basic , APPRIS P2 ,
Acsm3-202	ENSMUST00000106526.2	2704	580aa	Protein coding	CCDS21786		TSL:5 , GENCODE basic , APPRIS P2 ,
Acsm3-201	ENSMUST00000063770.10	2651	580aa	Protein coding	CCDS21786		TSL:1 , GENCODE basic , APPRIS P2 ,
Acsm3-203	ENSMUST00000106527.8	2557	580aa	Protein coding	CCDS21786		TSL:1 , GENCODE basic , APPRIS P2 ,
Acsm3-205	ENSMUST00000106529.8	3295	622aa	Protein coding	-		TSL:1 , GENCODE basic , APPRIS ALT2 ,
Acsm3-207	ENSMUST00000149766.2	1325	No protein	Retained intron	-		TSL:1 ,
Acsm3-206	ENSMUST00000149598.2	488	No protein	Retained intron	-		TSL:2 ,
Acsm3-208	ENSMUST00000154828.2	229	No protein	Retained intron	-		TSL:5 ,

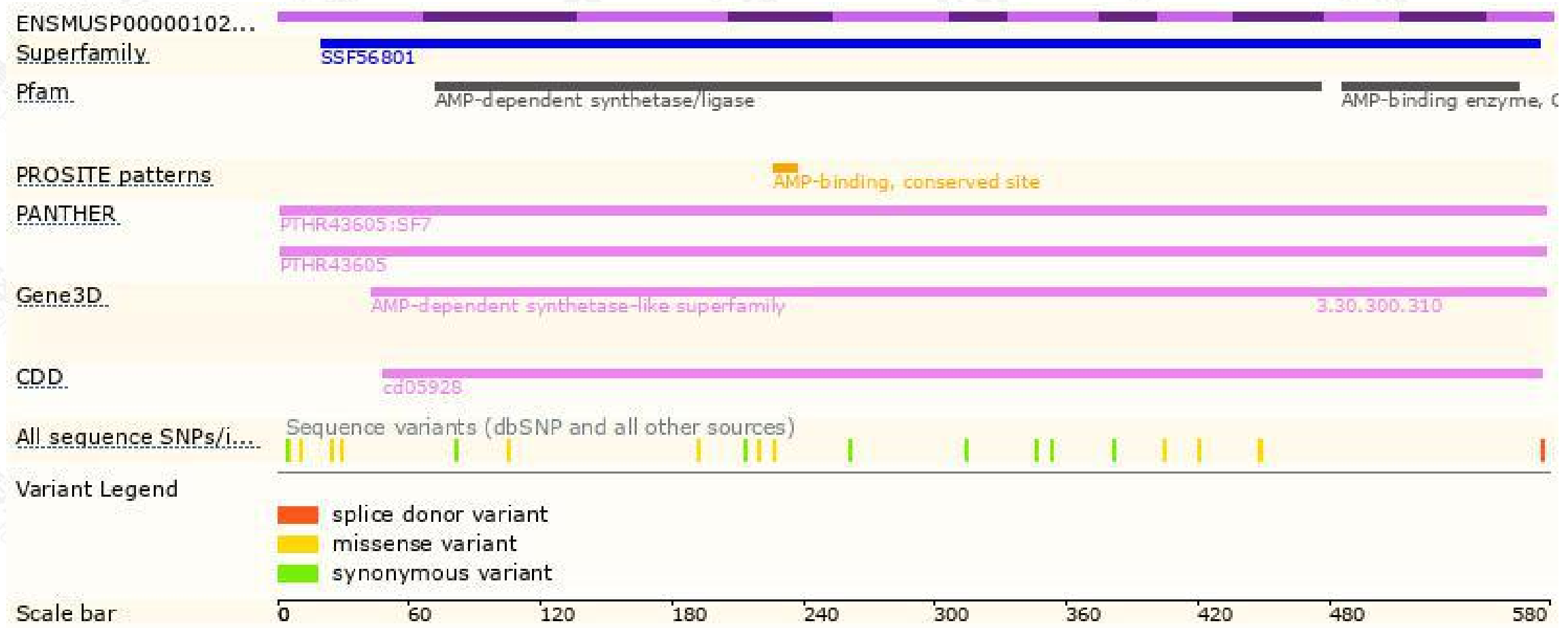
The strategy is based on the design of *Acsm3-204* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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