

# AcsM2 Cas9-KO Strategy

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# Overview

## Target Gene Name

- Acsn2

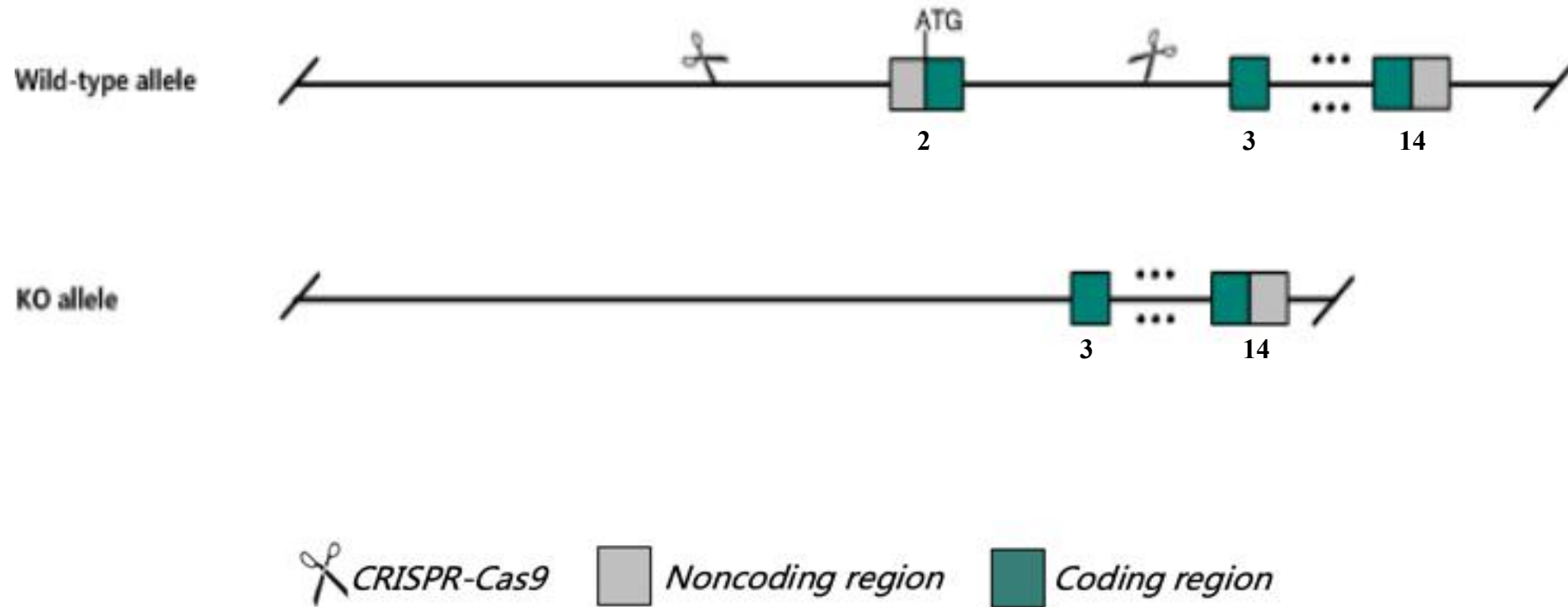
## Project Type

- Cas9-KO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



# Technical Information

- The *Acsm2* gene has 10 transcripts. According to the structure of *Acsm2* gene, exon2 of *Acsm2*-207 (ENSMUST00000167935.10) transcript is recommended as the knockout region. The region contains start codon ATG. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Acsm2* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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.

# Gene Information

## Acsm2 acyl-CoA synthetase medium-chain family member 2 [Mus musculus (house mouse)]

Gene ID: 233799, updated on 31-Jan-2019

### Summary

<b>Official Symbol</b>	Acsm2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	acyl-CoA synthetase medium-chain family member 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2385289</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000030945</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	AI315615, BC031140
<b>Expression</b>	Restricted expression toward kidney adult (RPKM 70.4) <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

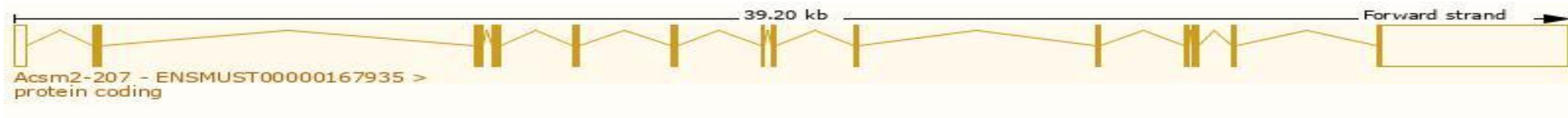
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

The gene has 10 transcripts, all transcripts are shown below:

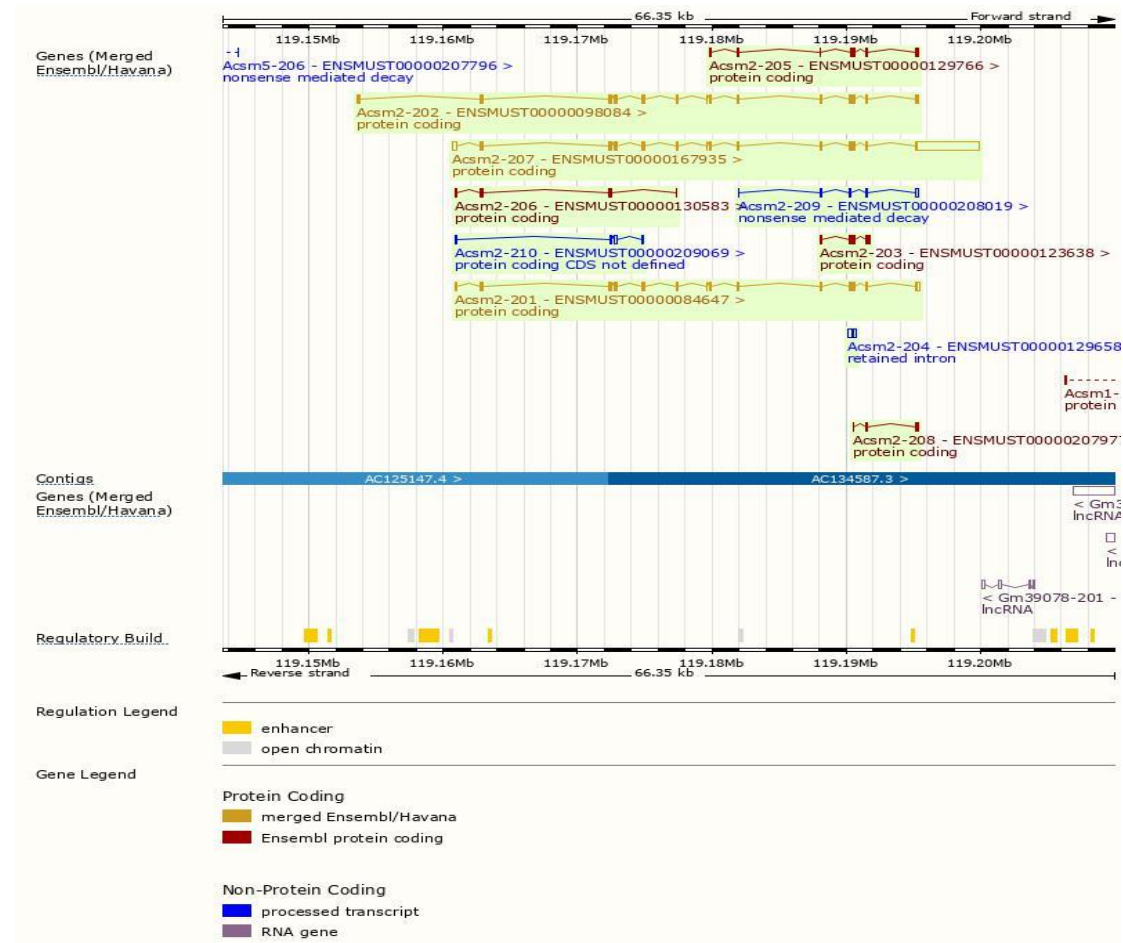
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Acsm2-207	<a href="#">ENSMUST00000167935.9</a>	6738	<a href="#">575aa</a>	Protein coding	<a href="#">CCDS21782</a>	<a href="#">Q8K0L3</a>	TSL:1 GENCODE basic APPRIS P3
Acsm2-202	<a href="#">ENSMUST00000098084.10</a>	2099	<a href="#">600aa</a>	Protein coding	<a href="#">CCDS52379</a>	<a href="#">Q8K0L3</a>	TSL:1 GENCODE basic APPRIS ALT2
Acsm2-201	<a href="#">ENSMUST00000084647.12</a>	2051	<a href="#">580aa</a>	Protein coding	<a href="#">CCDS52380</a>	<a href="#">Q8K0L3</a>	TSL:1 GENCODE basic APPRIS ALT2
Acsm2-205	<a href="#">ENSMUST00000129766.8</a>	810	<a href="#">216aa</a>	Protein coding	-	<a href="#">F6V4U2</a>	CDS 5' incomplete TSL:5
Acsm2-203	<a href="#">ENSMUST00000123638.1</a>	631	<a href="#">163aa</a>	Protein coding	-	<a href="#">F6XLJ8</a>	CDS 5' incomplete TSL:3
Acsm2-206	<a href="#">ENSMUST00000130583.1</a>	557	<a href="#">149aa</a>	Protein coding	-	<a href="#">D3YXB1</a>	CDS 3' incomplete TSL:3
Acsm2-208	<a href="#">ENSMUST00000207977.1</a>	429	<a href="#">86aa</a>	Protein coding	-	<a href="#">A0A140LHG2</a>	CDS 5' incomplete TSL:3
Acsm2-209	<a href="#">ENSMUST00000208019.1</a>	566	<a href="#">83aa</a>	Nonsense mediated decay	-	<a href="#">A0A140LIB0</a>	CDS 5' incomplete TSL:5
Acsm2-210	<a href="#">ENSMUST00000209069.1</a>	550	No protein	Processed transcript	-	-	TSL:5
Acsm2-204	<a href="#">ENSMUST00000129658.1</a>	482	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Acsm2-207* transcript, the transcription is shown below:



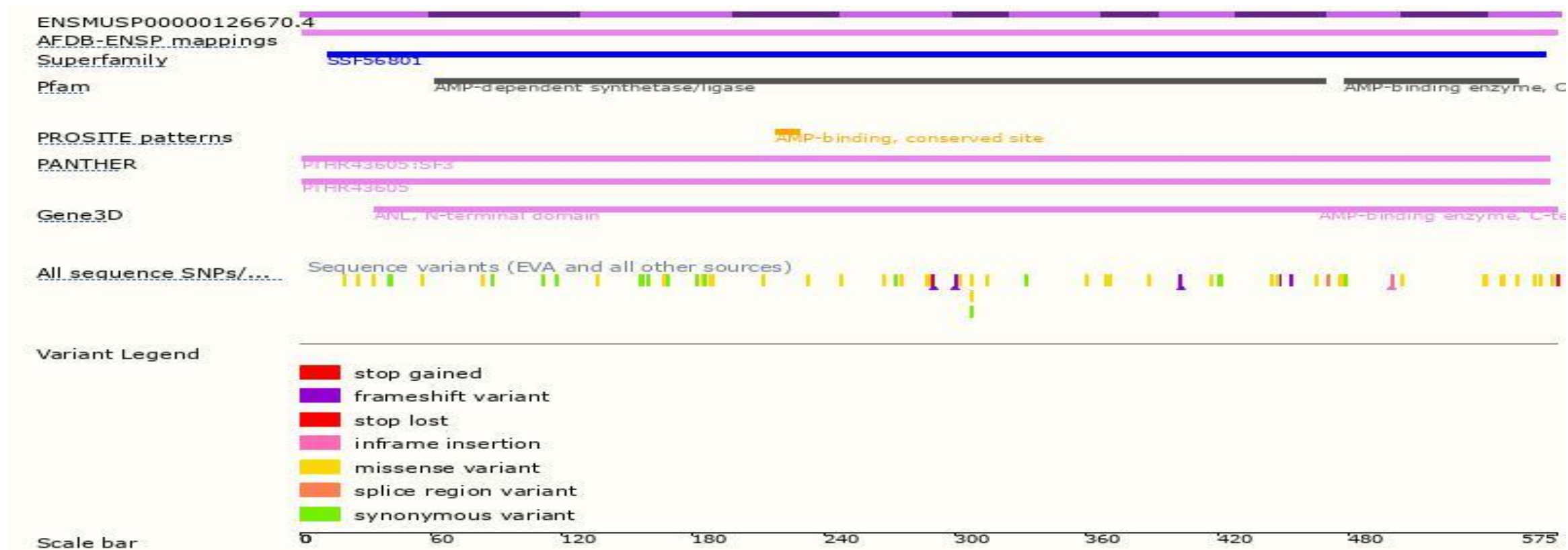
Source: <https://www.ensembl.org>

# Genomic Information



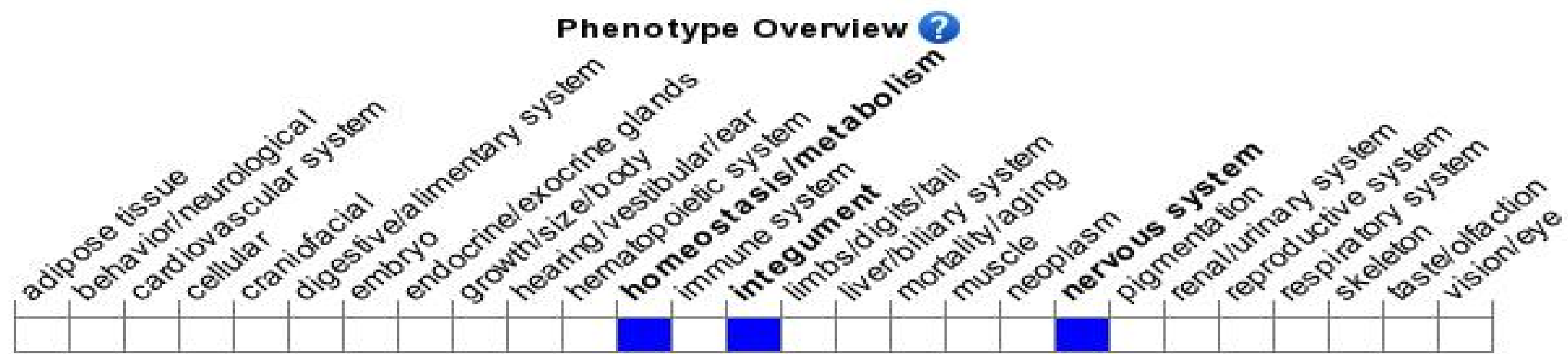


# Protein Information





# Mouse Phenotype Information (MGI)



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# Important Information

- *Acsm2* is located on Chr7. 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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.
- Transcript 203,205,208 CDS 5' incomplete the influences is unknown.