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Srrm2 Cas9-KO Strategy

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Reviewer: Yanhua Shen

Design Date: 2022-09-27

Overview

Target Gene Name

- Srrm2

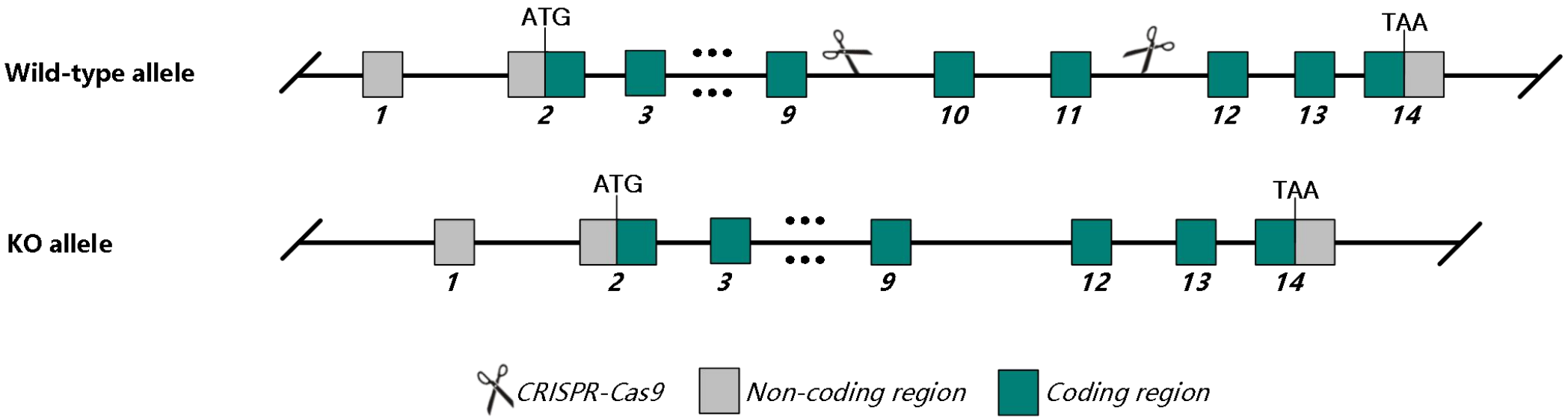
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Srrm2* gene.

Technical Information

- The *Srrm2* gene has 12 transcripts. According to the structure of *Srrm2* gene, exon 10-exon 11 of *Srrm2*-201 (ENSMUST00000088621.11) transcript is recommended as the knockout region. The region contains 6857 bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Srrm2* 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

Srrm2 serine/arginine repetitive matrix 2 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 75956, updated on 30-Aug-2022

Summary

Official Symbol	Srrm2 provided by MGI
Official Full Name	serine/arginine repetitive matrix 2 provided by MGI
Primary source	MGI:MGI:1923206
See related	Ensembl:ENSMUSG00000039218 AllianceGenome:MGI:1923206
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	SRm300; mKIAA0324; 5033413A03Rik
Summary	Predicted to enable C2H2 zinc finger domain binding activity; mRNA binding activity; and protein N-terminus binding activity. Predicted to be involved in mRNA splicing, via spliceosome. Predicted to act upstream of or within RNA splicing and mRNA processing. Predicted to be located in Cajal body and nuclear speck. Predicted to be part of U2-type catalytic step 2 spliceosome and U2-type precatalytic spliceosome. Orthologous to human SRRM2 (serine/arginine repetitive matrix 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in adrenal adult (RPKM 122.5), ovary adult (RPKM 102.7) and 28 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**
Try the new Transcript table

Genomic context

Location: 17; 17 A3.3 — See Srrm2 in Genome Data Viewer

Exon count: 20

Source: https://www.ncbi.nlm.nih.gov/gene/75956

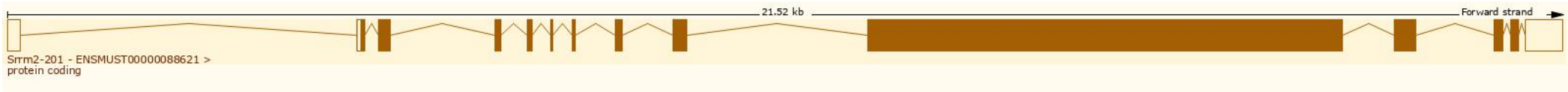
Transcript Information

The gene has 12 transcripts, all transcripts are shown below:

Show/hide columns (1 hidden) Filter

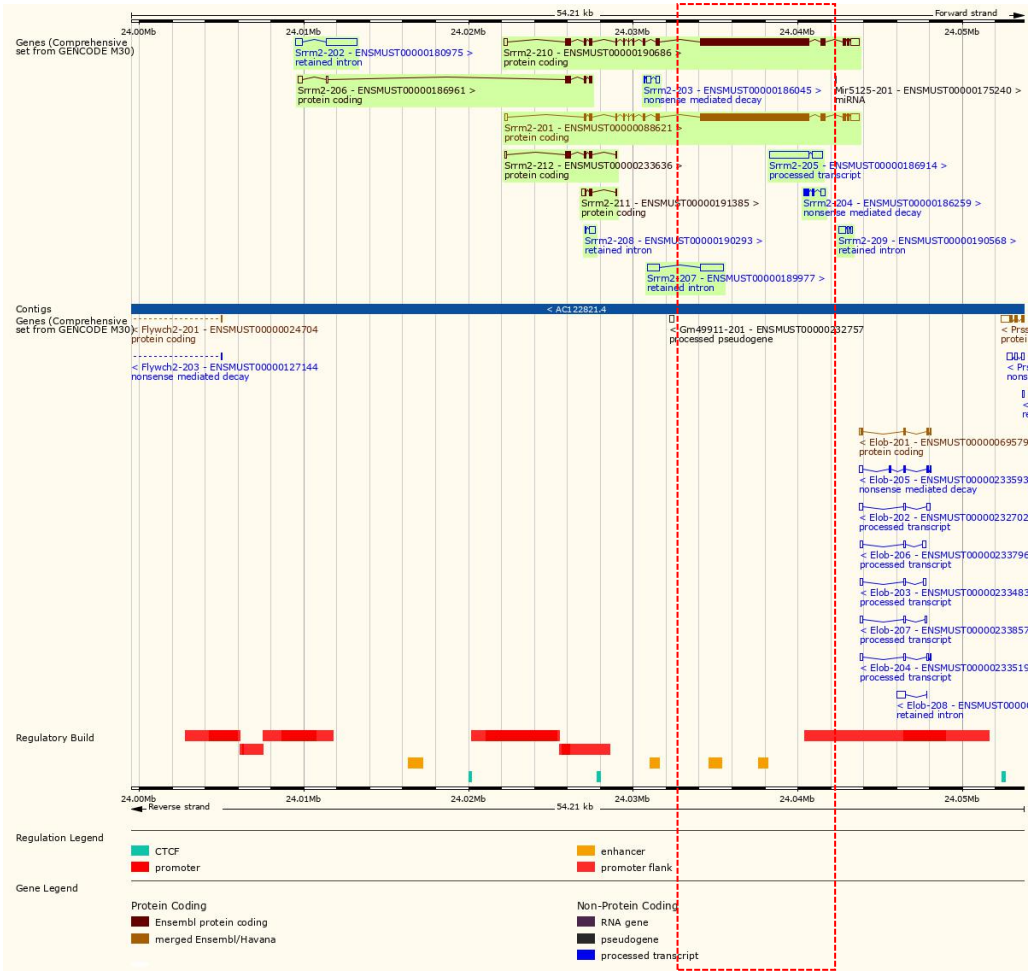
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000233636.2	Srrm2-212	678	191aa	Protein coding		A0A3B2W3Z4	CDS 3' incomplete
ENSMUST00000191385.3	Srrm2-211	459	88aa	Protein coding		A0A087WPS9	TSL:2 CDS 3' incomplete
ENSMUST00000190686.7	Srrm2-210	8864	2703aa	Protein coding		Q8BTI8-1	Ensembl Canonical GENCODE basic APPRIS P1 TSL:5
ENSMUST00000190568.2	Srrm2-209	597	No protein	Retained intron		-	TSL:2
ENSMUST00000190293.2	Srrm2-208	431	No protein	Retained intron		-	TSL:3
ENSMUST00000189977.2	Srrm2-207	2092	No protein	Retained intron		-	TSL:1
ENSMUST00000186961.7	Srrm2-206	950	171aa	Protein coding		A0A087WRX8	TSL:5 CDS 3' incomplete
ENSMUST00000186914.2	Srrm2-205	2991	No protein	Processed transcript		-	TSL:1
ENSMUST00000186259.2	Srrm2-204	647	105aa	Nonsense mediated decay		A0A087WR98	TSL:3 CDS 5' incomplete
ENSMUST00000186045.2	Srrm2-203	494	34aa	Nonsense mediated decay		A0A087WPU0	TSL:3 CDS 5' incomplete
ENSMUST00000180975.3	Srrm2-202	2266	No protein	Retained intron		-	TSL:1
ENSMUST00000088621.11	Srrm2-201	8564	2607aa	Protein coding	CCDS37475	Q8BTI8-2	GENCODE basic TSL:1

The strategy is based on the design of *Srrm2*-201 transcript, the transcription is shown below:



http://asia.ensembl.org/Mus_musculus/Transcript/Summary?db=core;g=ENSMUSG00000039218;r=17:24009506-24043715;t=ENSMUST00000088621

Genomic Information



http://asia.ensembl.org/Mus_musculus/Gene/Summary?db=core;g=ENSMUSG00000039218;r=17:24009506-24043715;t=ENSMUST00000088621

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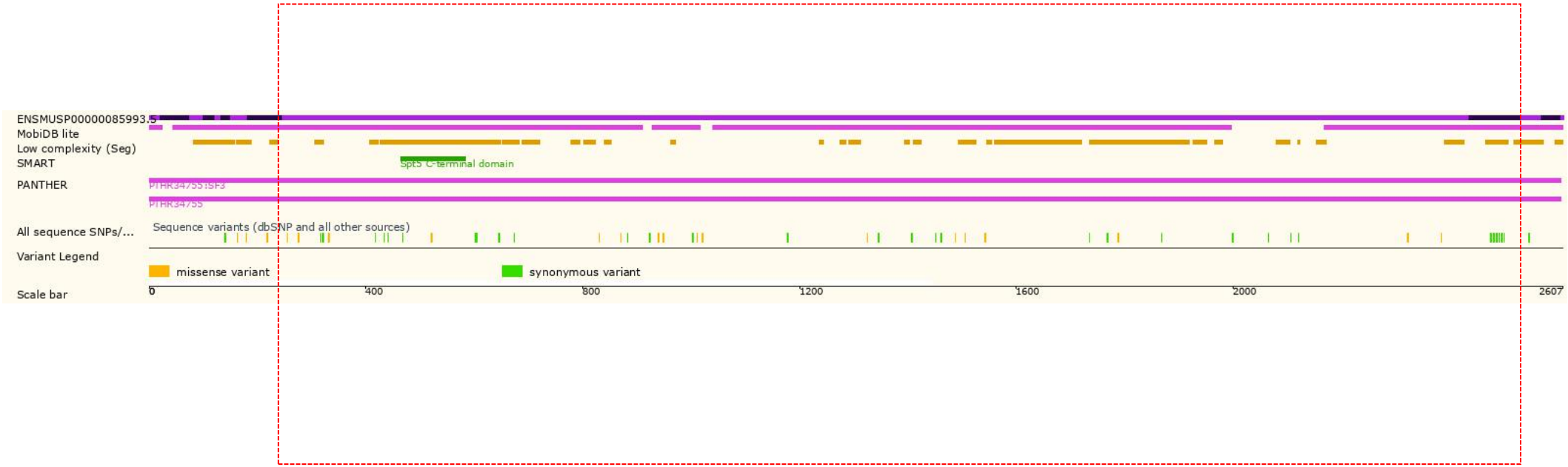
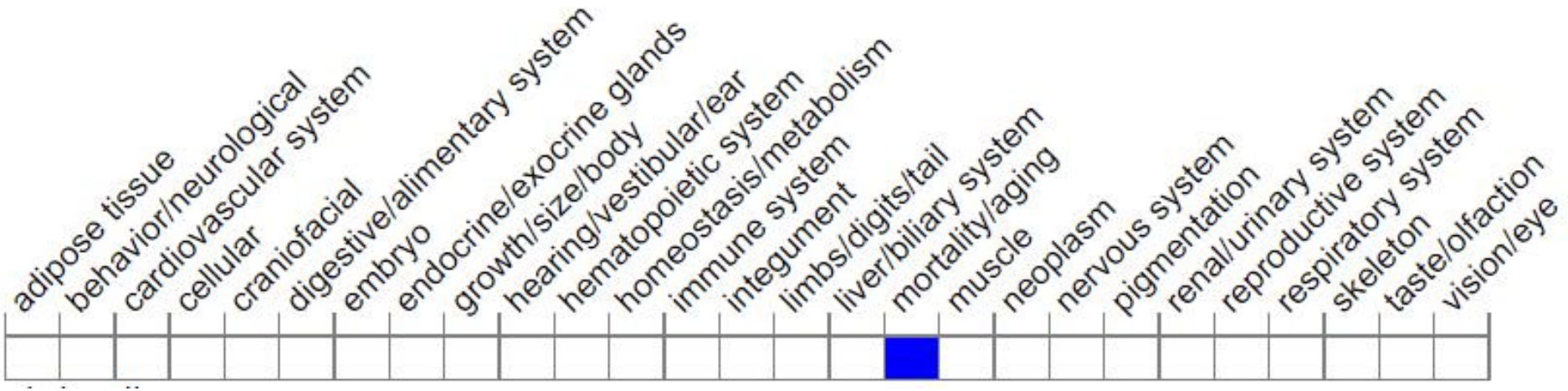
Protein Information



http://asia.ensembl.org/Mus_musculus/Transcript/ProteinSummary?db=core;g=ENSMUSG00000039218;r=17:24009506-24043715;t=ENSMUST00000088621

Mouse Phenotype Information (MGI)



Source: http://www.informatics.jax.org/marker/MGI:1923206

Important Information

- According to the available information (MGI), there is a certain lethality rate before weaning in mice homozygous for knock-out alleles.
  http://www.informatics.jax.org/diseasePortal/genoCluster/view/33639
- The sequences encoding transcripts *Srrm2*-203, *Srrm2*-204, *Srrm2*-206, *Srrm2*-211, and *Srrm2*-212 are incomplete and the effect of knocking out the target region on them is unknown.
- The knockdown region designed in this strategy is about 1.6 kp away from the 3' end of the *Elob* gene, and knockdown of the target gene may affect the regulation of the 3' end of the *Elob* gene.
- The effect of this strategy on the uncoded transcript *Gm49911*-201、*Mir5125*-201 is unknown.
- *Srrm2* is located on Chr 17. 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.