

Sarm1 Cas9-CKO Strategy

Designer: Xiangli Bian

Reviewer: Yao Yu

Design Date: 2023-3-28

Overview

Target Gene Name

- *Sarm1*

Project Type

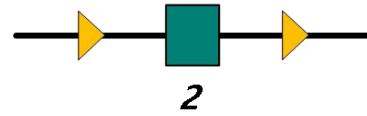
- Cas9-CKO

Genetic Background

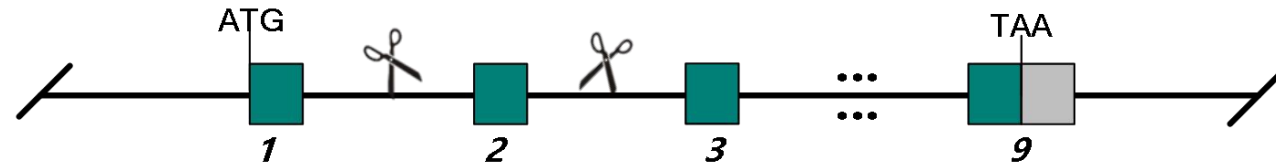
- C57BL/6JGpt

Strain Strategy

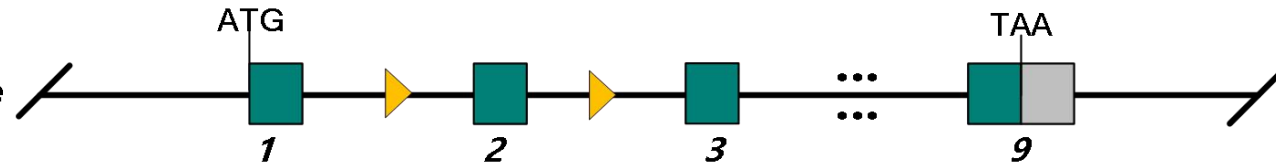
Donor and CRISPR-Cas9 System



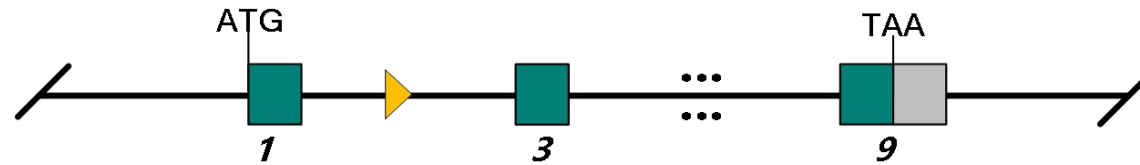
Wild-type allele



Conditional KO allele



KO allele



Schematic representation of CRISPR-Cas9 engineering used to edit the *Sarm1* gene.

Technical Information

- The *Sarm1* gene has 5 transcripts. According to the structure of *Sarm1* gene, exon 2 of *Sarm1-202* (ENSMUST00000108287.10) is recommended as the knockout region. The region contains 619 bp of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Sarm1* 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

Sarm1 sterile alpha and HEAT/Armadillo motif containing 1 [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 237868, updated on 5-Mar-2023

Summary

Official Symbol	Sarm1 provided by MGI
Official Full Name	sterile alpha and HEAT/Armadillo motif containing 1 provided by MGI
Primary source	MGI:MGI:2136419
See related	Ensembl:ENSMUSG00000050132 AllianceGenome:MGI:2136419
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	Sarm; MyD885; A830091115Rik
Summary	Enables NAD ⁺ nucleosidase activity. Involved in NAD catabolic process; positive regulation of neuron death; and regulation of dendrite morphogenesis. Acts upstream of or within regulation of apoptotic process and response to glucose. Located in several cellular components, including dendrite; microtubule; and mitochondrion. Is extrinsic component of mitochondrial outer membrane. Is expressed in immune system; nervous system; neural retina; and tongue. Orthologous to human SARM1 (sterile alpha and TIR motif containing 1). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in whole brain E14.5 (RPKM 11.0), CNS E18 (RPKM 9.7) and 9 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

Genomic context

Location: 11 B5; 11 46.74 cM

[See Sarm1 in Genome Data Viewer](#)

Exon count: 9

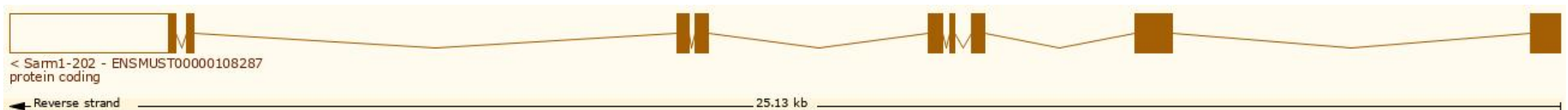
<https://www.ncbi.nlm.nih.gov/gene/237868>

Transcript Information

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

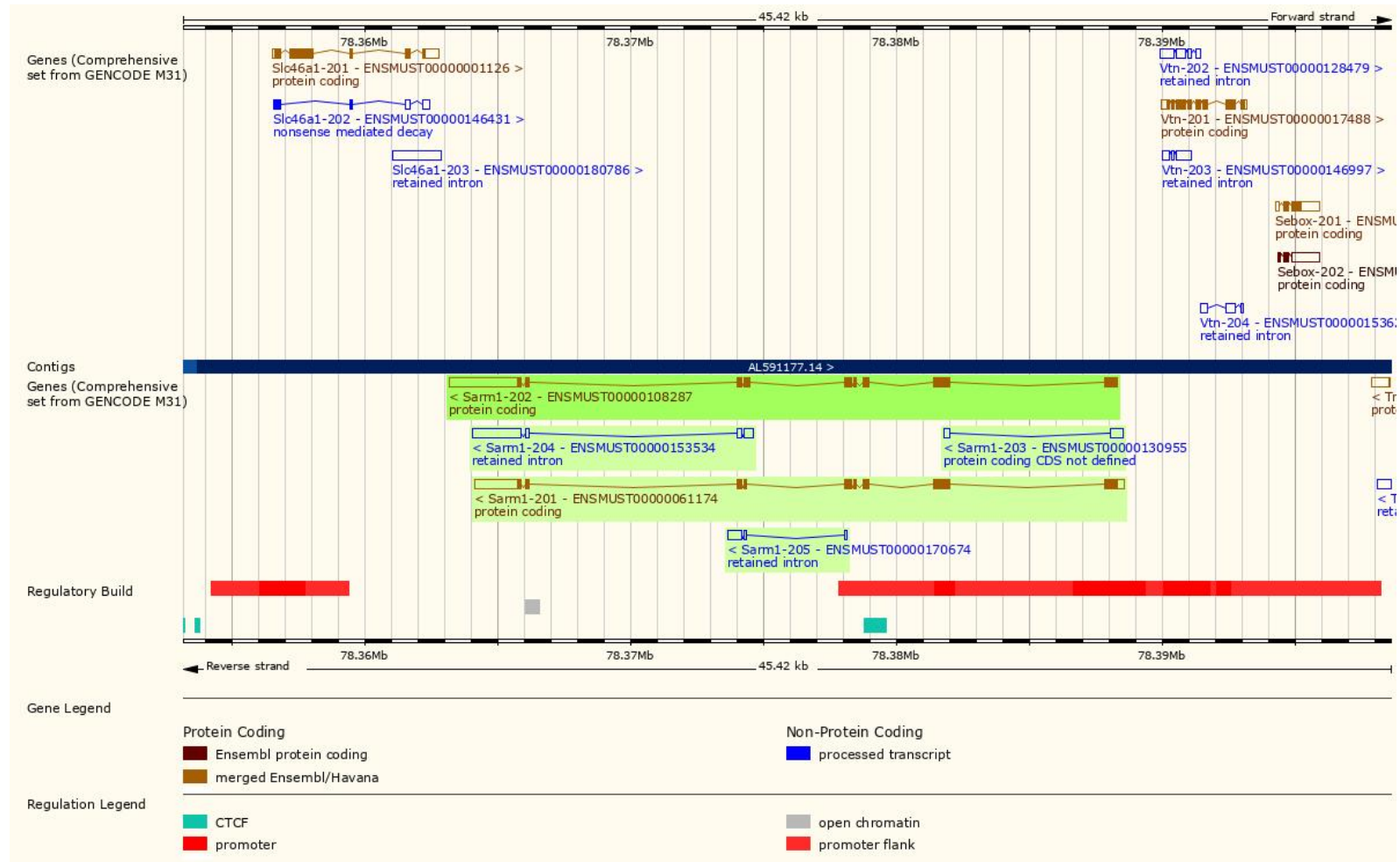
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000130955.2	Sarm1-203	702	No protein	Protein coding CDS not defined		-	TSL:2
ENSMUST00000153534.2	Sarm1-204	2497	No protein	Retained intron		-	TSL:1
ENSMUST00000170674.2	Sarm1-205	689	No protein	Retained intron		-	TSL:2
ENSMUST00000061174.7	Sarm1-201	4083	724aa	Protein coding	CCDS25105	Q6PDS3-1	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000108287.10	Sarm1-202	4868	764aa	Protein coding	CCDS48857	Q6PDS3-3	Ensembl Canonical GENCODE basic TSL:1

The strategy is based on the design of *Sarm1-202* transcript, the transcription is shown below:



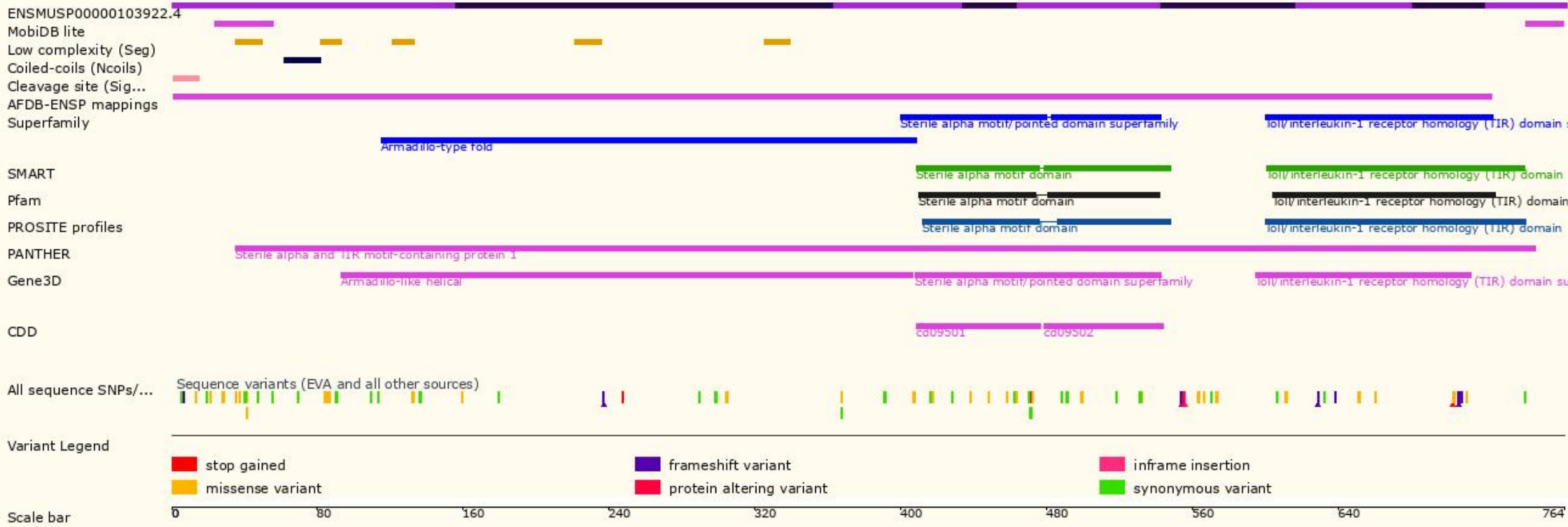
Source: <http://asia.ensembl.org/>

Genomic Information

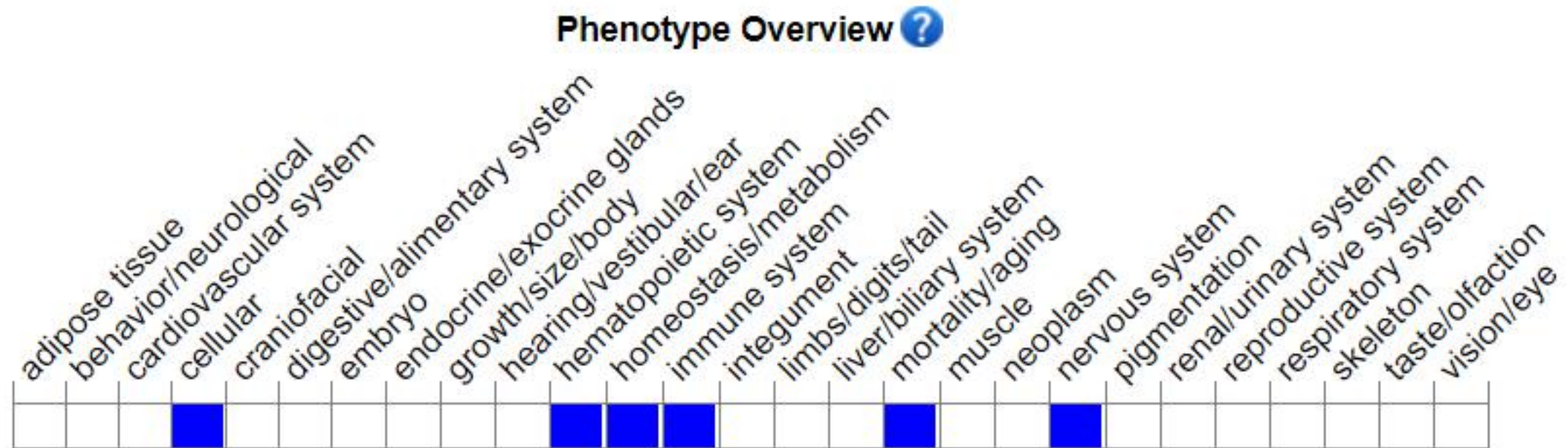


Source: <http://asia.ensembl.org/>

Protein Information



Mouse Phenotype Information (MGI)



- Mice homozygous for a null allele exhibit reduced apoptosis induced by oxygen and glucose deprivation in hippocampal slices.

Important Information

- According to the data of MGI, mice homozygous for a null allele exhibit reduced apoptosis induced by oxygen and glucose deprivation in hippocampal slices.
- This strategy may have no effect on *Sarm1-204* and *Sarm1-205* transcript.
- The knockout region is about 6.8 kb away from the 5' of the *Vtn* gene, which may affect the regulation of this gene.
- *Sarm1* is located on Chr 11. 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.