Sarm1 Cas9-KO Strategy

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Design Date: 2019-9-11
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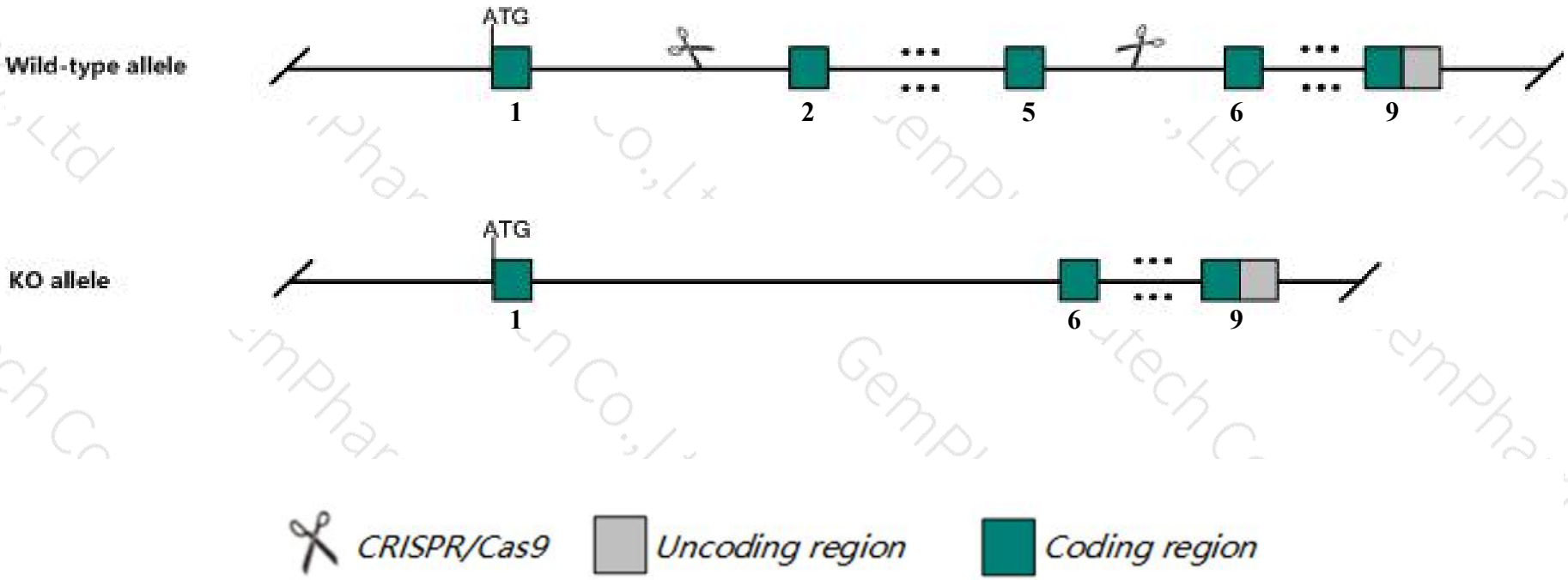
Project Overview

Project Name	***Sarm1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sarm1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Sarm1* gene has 5 transcripts. According to the structure of *Sarm1* gene, exon2-exon5 of *Sarm1-202* (ENSMUST00000108287.9) transcript is recommended as the knockout region.The region contains 1160bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Sarm1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a null allele exhibit reduced apoptosis induced by oxygen and glucose deprivation in hippocampal slices.

- The *Sarm1* gene is located on the Chr11. 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.

Gene information（NCBI）

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

Gene ID: 237868, updated on 9-Apr-2019

Summary

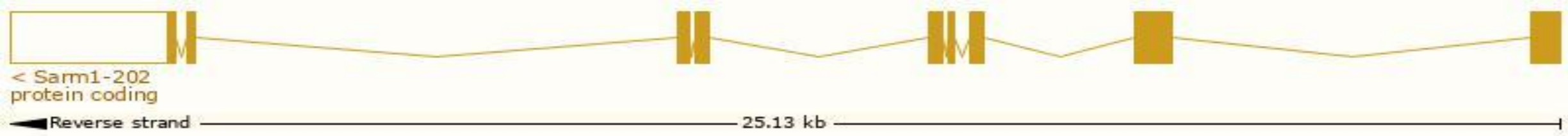
Official Symbol	Sarm1 provided by MGI
Official Full Name	sterile alpha and HEAT/Armadillo motif containing 1 provided by MGI
Primary source	MGI:MGI:2136419
See related	Ensembl:ENSMUSG00000050132
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A830091I15Rik, C78606, MyD885, Sarm
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

Transcript information（Ensembl）

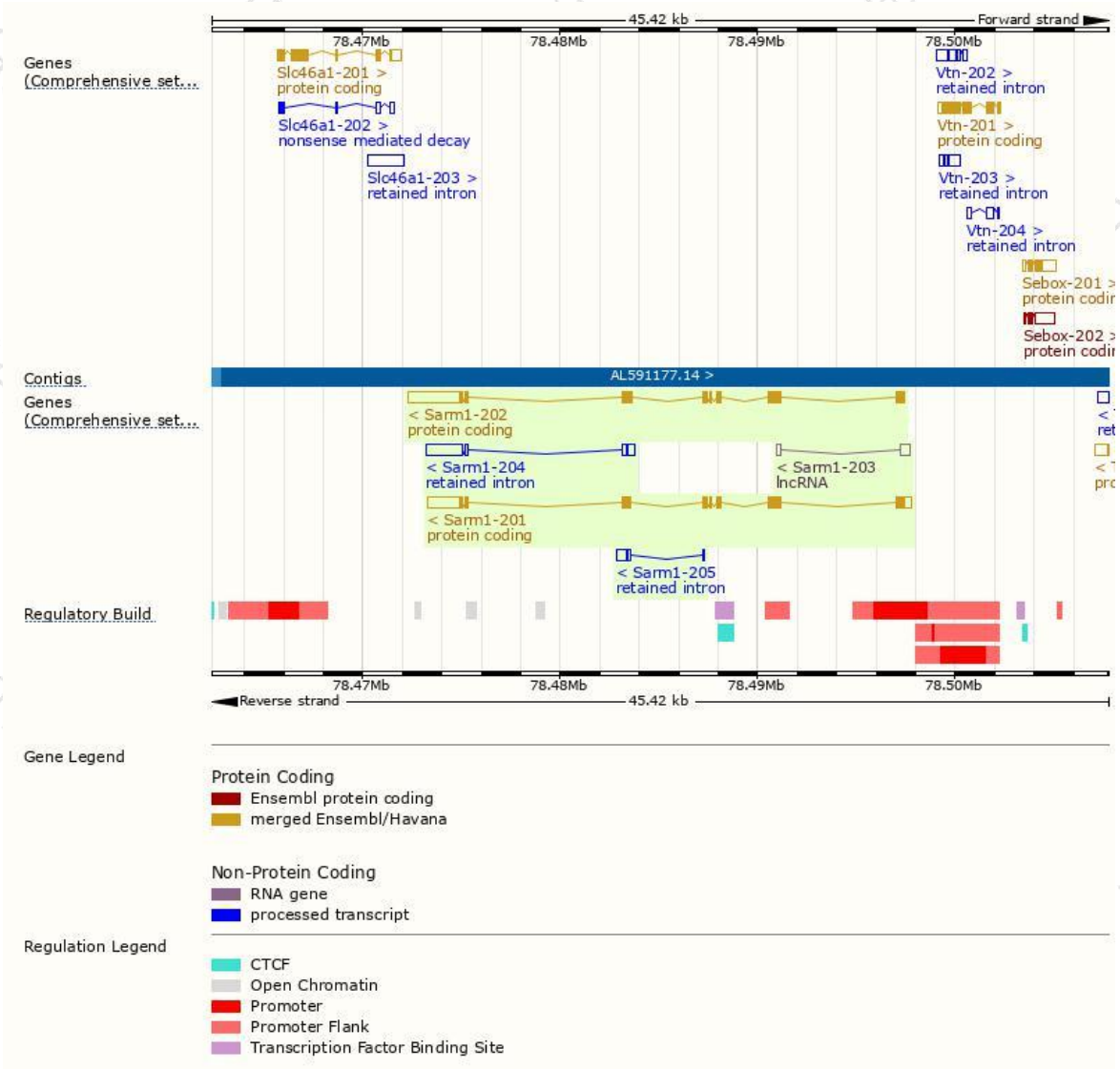
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sarm1-202	ENSMUST00000108287.9	4868	764aa	Protein coding	CCDS48857	Q6PDS3	TSL:1 GENCODE basic
Sarm1-201	ENSMUST00000061174.6	4083	724aa	Protein coding	CCDS25105	Q6PDS3	TSL:1 GENCODE basic APPRIS P1
Sarm1-204	ENSMUST00000153534.1	2497	No protein	Retained intron	-	-	TSL:1
Sarm1-205	ENSMUST00000170674.1	689	No protein	Retained intron	-	-	TSL:2
Sarm1-203	ENSMUST00000130955.1	702	No protein	lncRNA	-	-	TSL:2

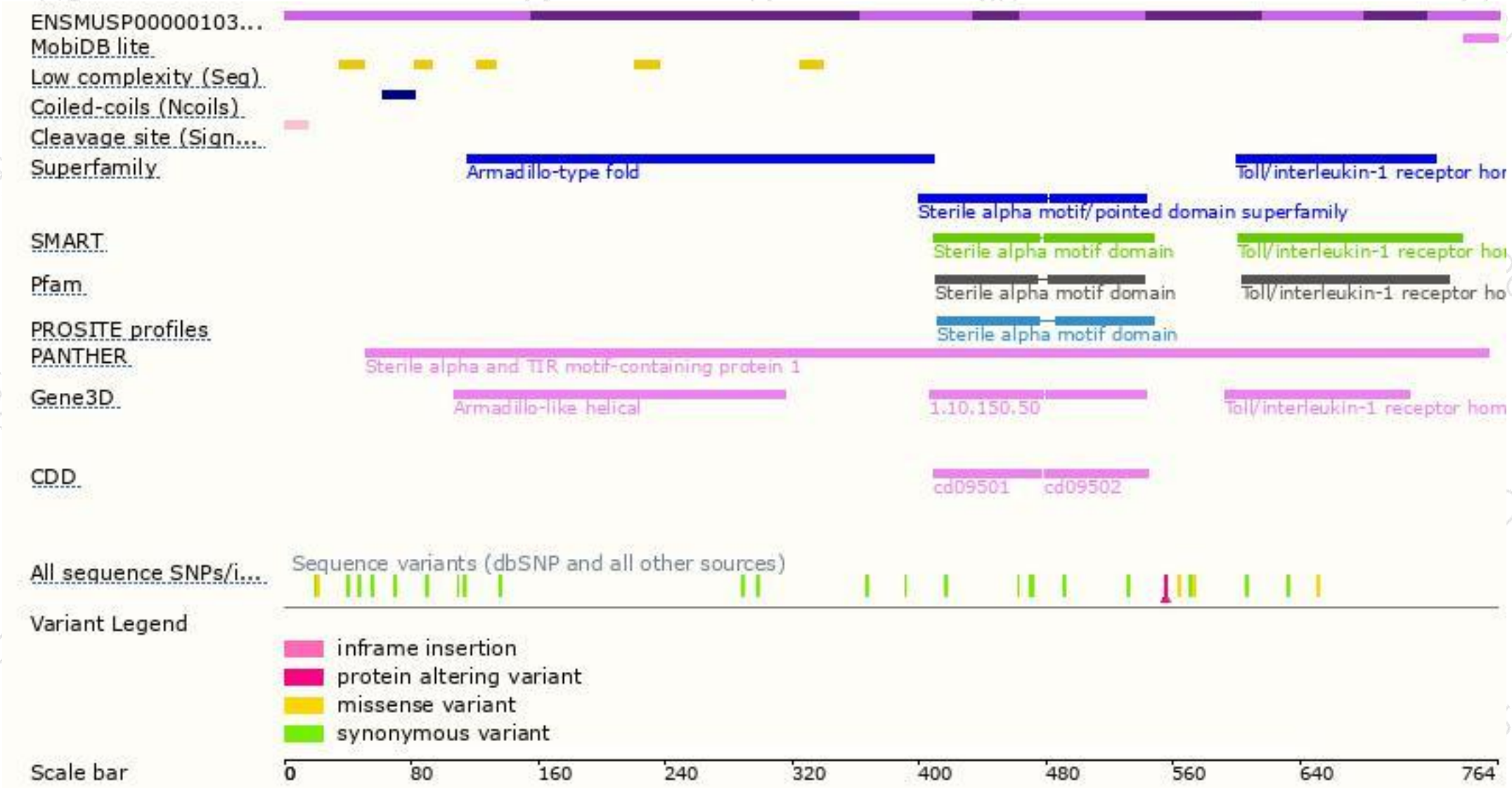
The strategy is based on the design of *Sarm1-202* transcript,The transcription is shown below



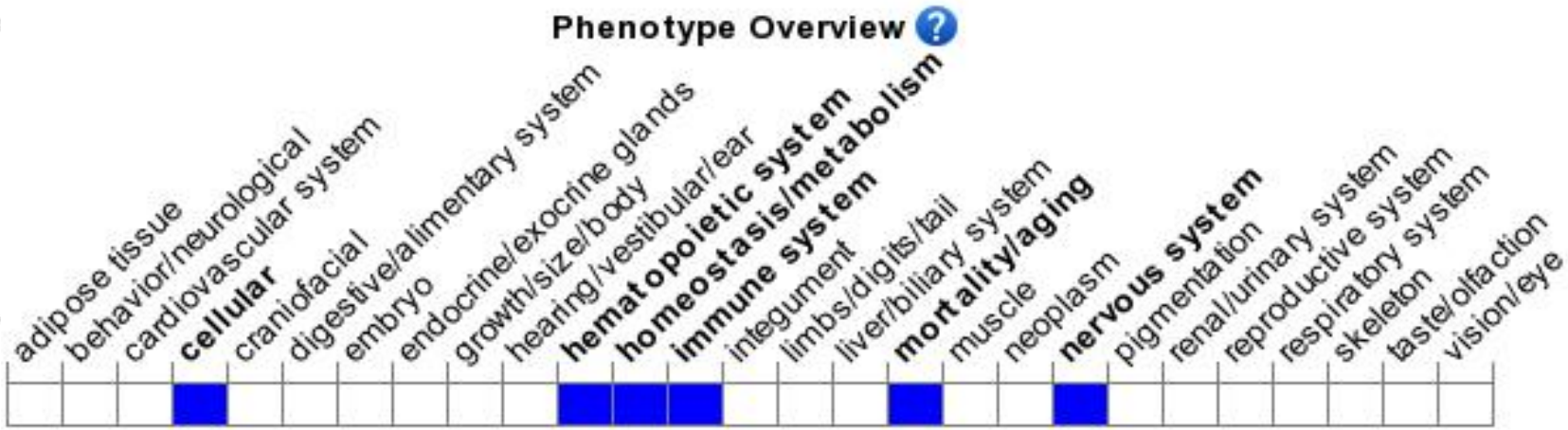
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data,Mice homozygous for a null allele exhibit reduced apoptosis induced by oxygen and glucose deprivation in hippocampal slices.

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

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