

Srgap1 Cas9-KO Strategy

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Project Overview

Project Name

Srgap1

Project type

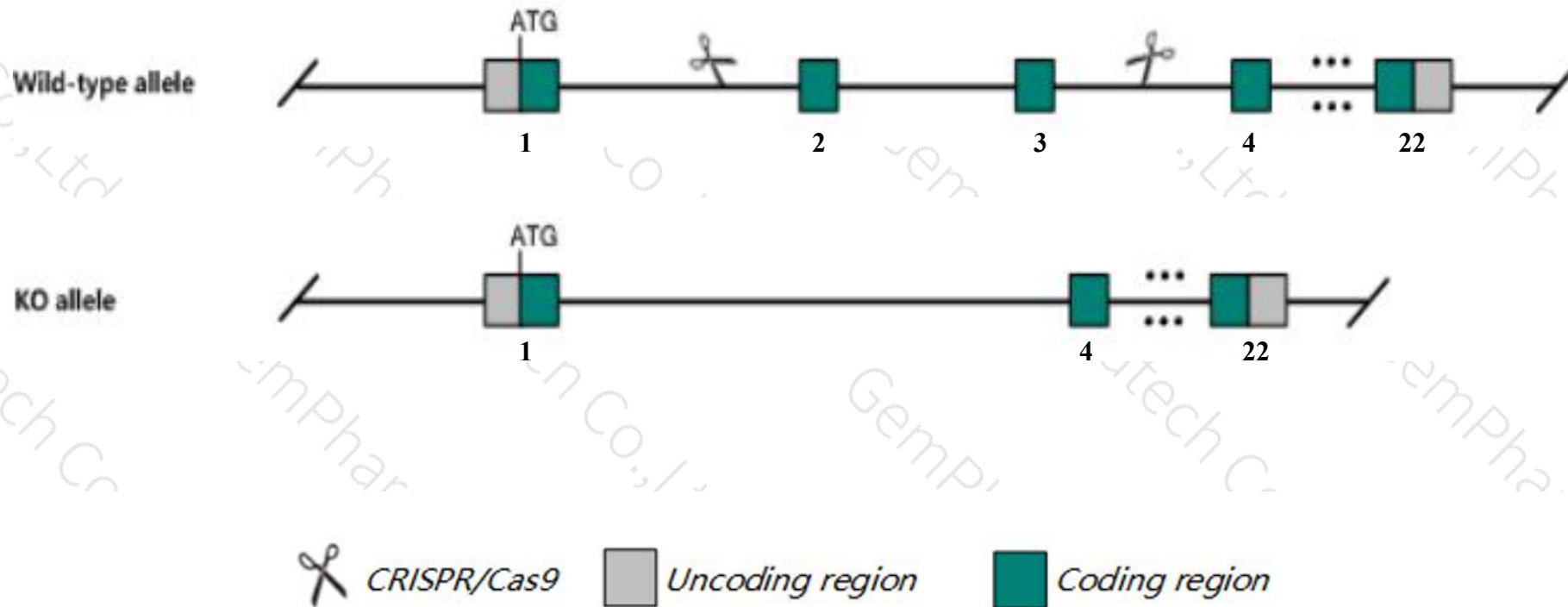
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Srgap1* gene. The schematic diagram is as follows:



- The *Srgap1* gene has 5 transcripts. According to the structure of *Srgap1* gene, exon2-exon3 of *Srgap1*-202 (ENSMUST00000081688.12) transcript is recommended as the knockout region. The region contains 359bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Srgap1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Srgap1* gene is located on the Chr10. 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)

Srgap1 SLIT-ROBO Rho GTPase activating protein 1 [Mus musculus (house mouse)]

Gene ID: 117600, updated on 13-Mar-2020

Summary



Official Symbol	Srgap1 provided by MGI
Official Full Name	SLIT-ROBO Rho GTPase activating protein 1 provided by MGI
Primary source	MGI:MGI:2152936
See related	Ensembl:ENSMUSG000000020121
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	4930572H05Rik, Arhgap13
Expression	Broad expression in whole brain E14.5 (RPKM 16.0), CNS E18 (RPKM 14.0) and 17 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

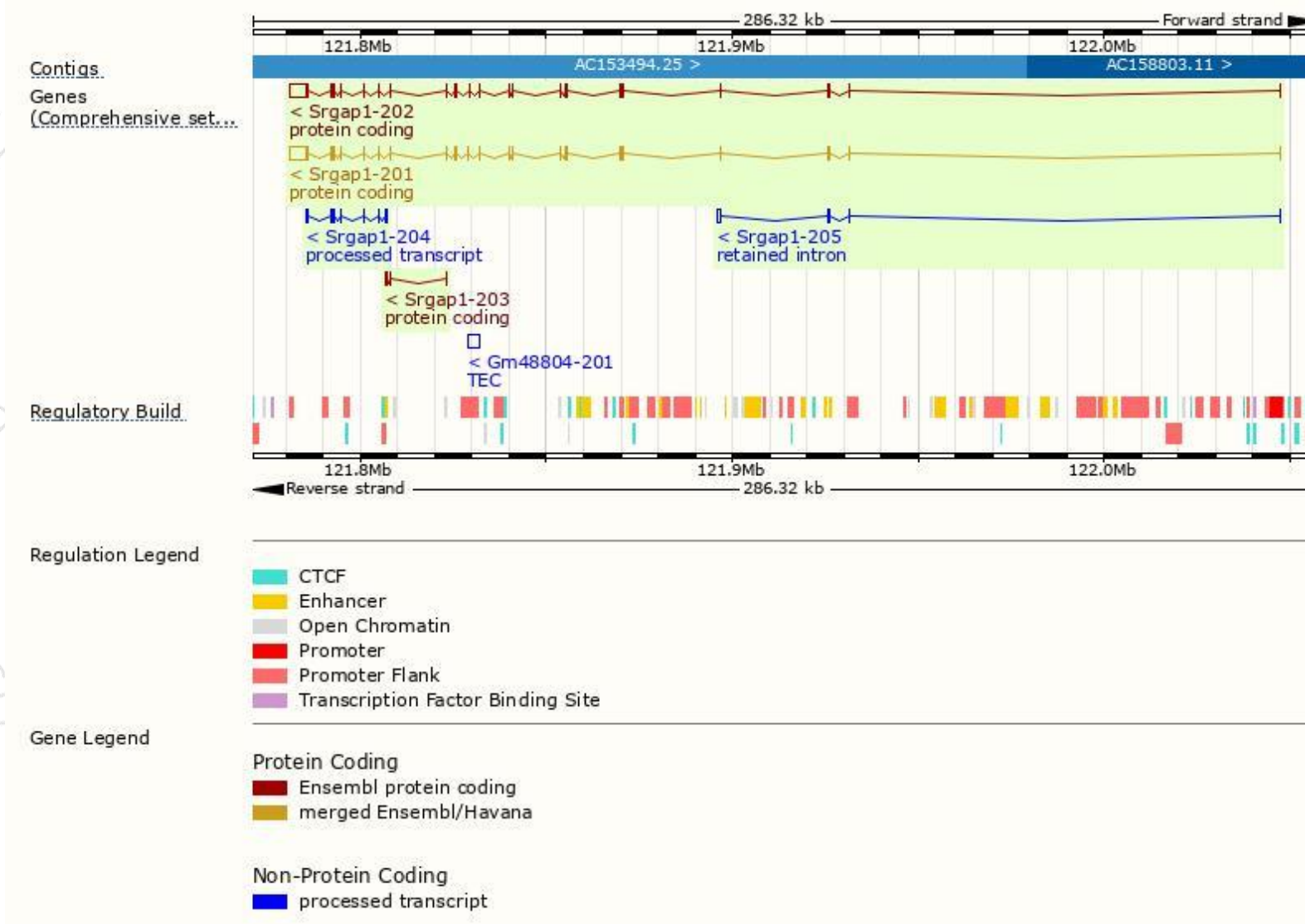
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srgap1-202	ENSMUST00000081688.12	7787	1085aa	Protein coding	CCDS36075	D3YZW1	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Srgap1-201	ENSMUST00000020322.11	7711	1062aa	Protein coding	CCDS56751	Q91Z69	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Srgap1-203	ENSMUST00000161156.1	595	68aa	Protein coding	-	F7D9F7	CDS 5' incomplete TSL:3
Srgap1-204	ENSMUST00000161996.1	1714	No protein	Processed transcript	-	-	TSL:1
Srgap1-205	ENSMUST00000162710.1	1457	No protein	Retained intron	-	-	TSL:1

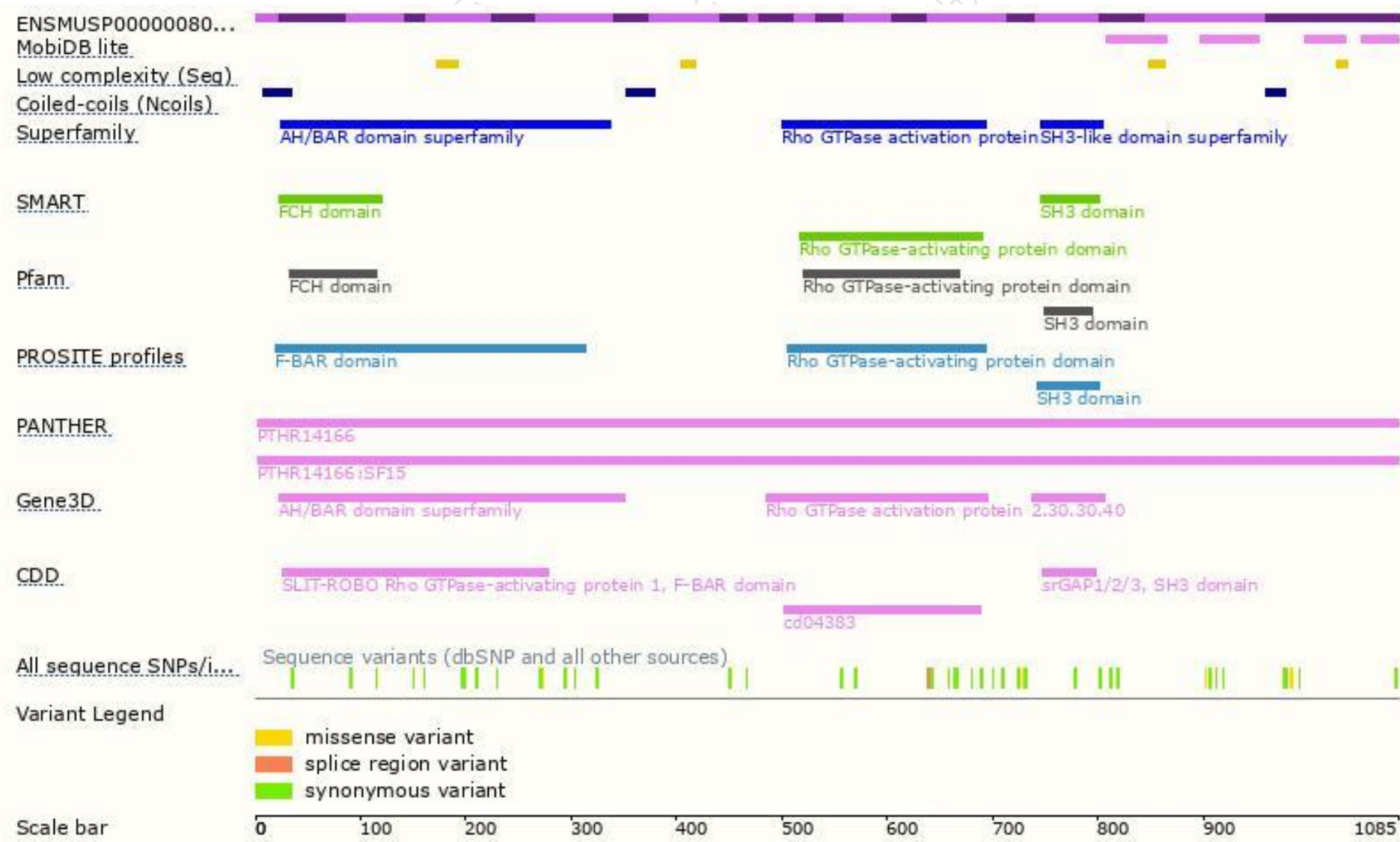
The strategy is based on the design of *Srgap1-202* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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