Srms Cas9-KO Strategy

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Project Overview

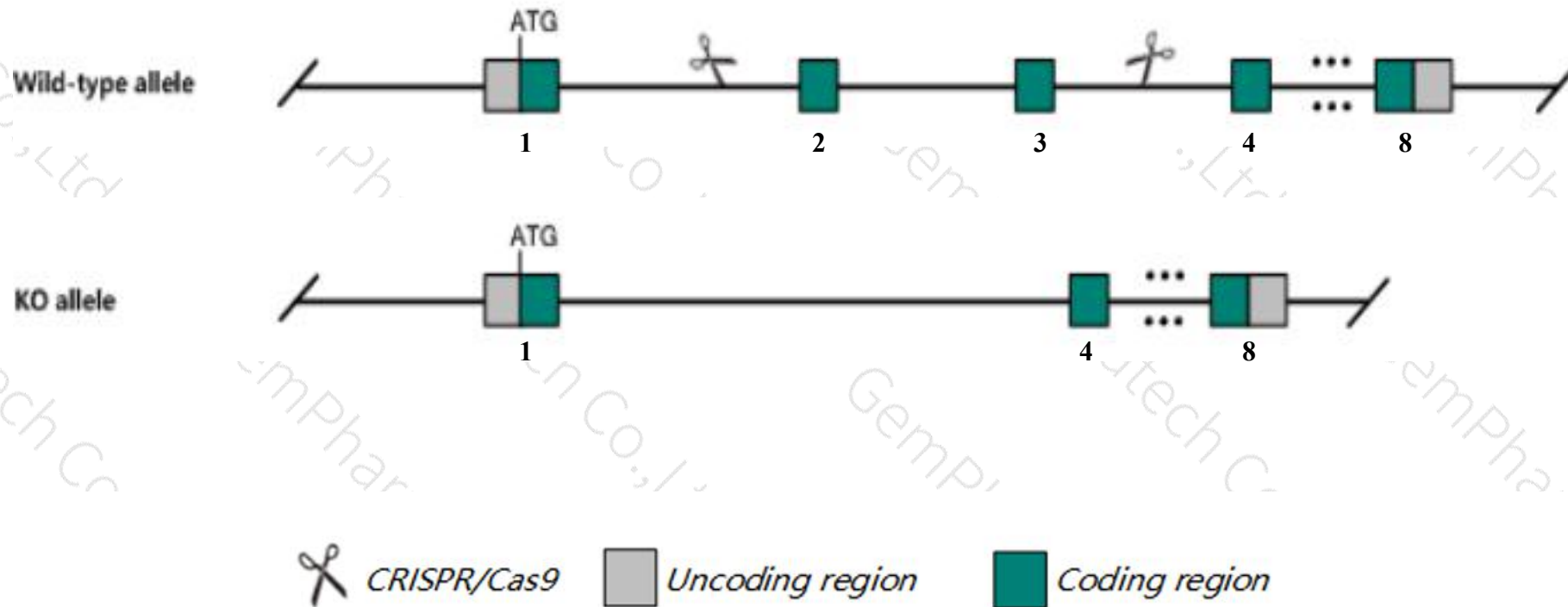|	
Project Name	*Srms*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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

Technical routes

➢ The *Srms* gene has 1 transcript. According to the structure of *Srms* gene, exon2-exon3 of *Srms-201* (ENSMUST00000016498.4) transcript is recommended as the knockout region. The region contains 289bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

➢ According to the existing MGI data,Homozygous mice exhibit no detectable abnormalities.

➢ The *Srms* gene is located on the Chr2. 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）

Srms src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites [Mus musculus (house mouse)]

Gene ID: 20811, updated on 13-Mar-2020

Summary

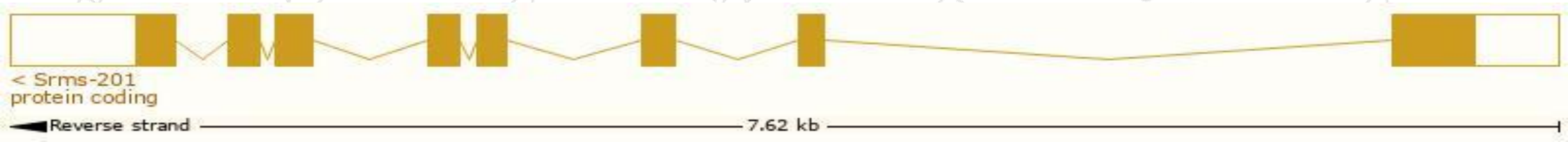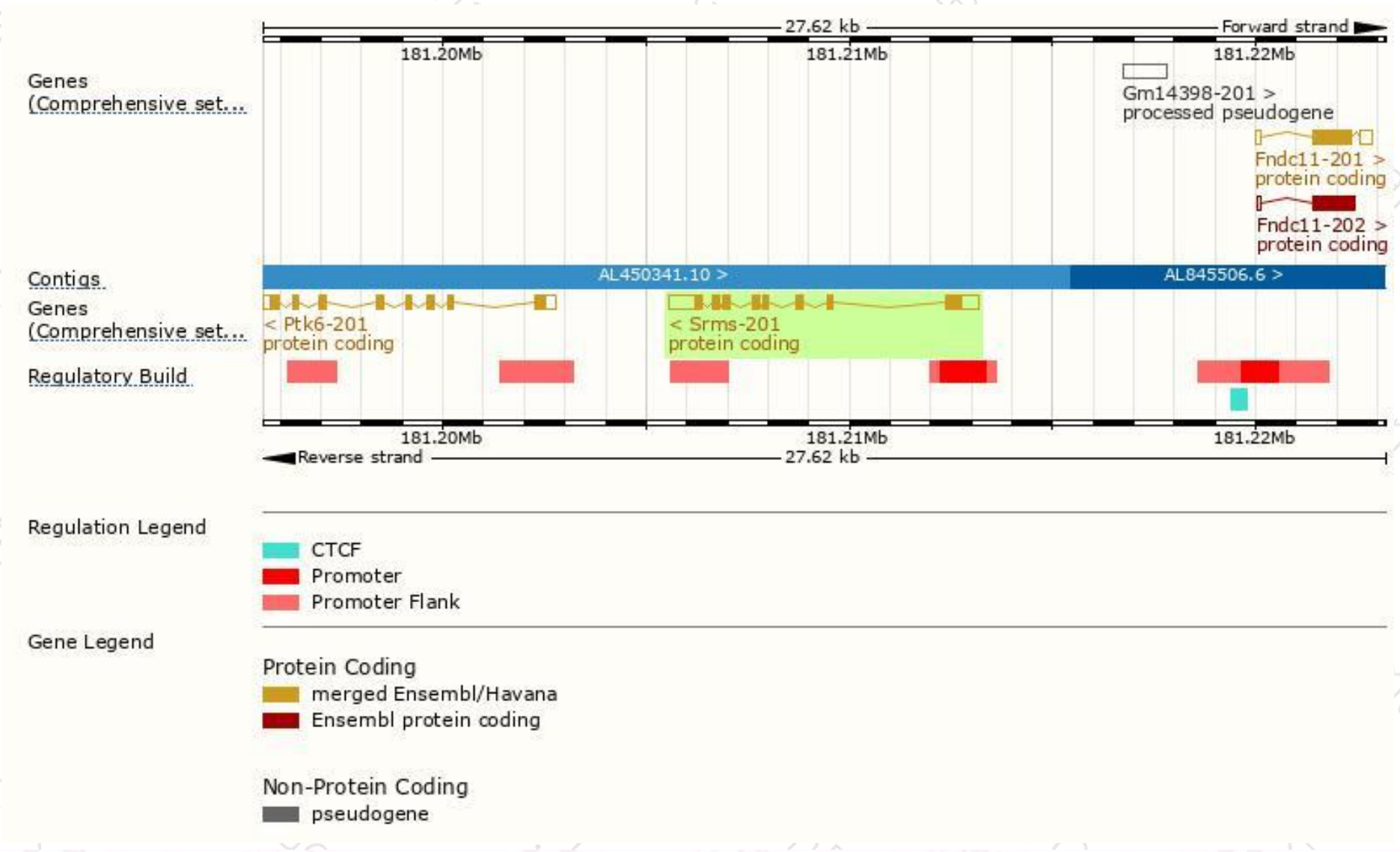|	
Official Symbol	Srms provided by MGI
Official Full Name	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites provided byMGI
Primary source	MGI:MGI:101865
See related	Ensembl:ENSMUSG00000027579
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A230069J08Rik, srm
Expression	Broad expression in lung adult (RPKM 3.6), testis adult (RPKM 3.1) and 18 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srms-201	ENSMUST00000016498.4	2562	507aa	Protein coding	CCDS17204	Q0VBH4	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 P1

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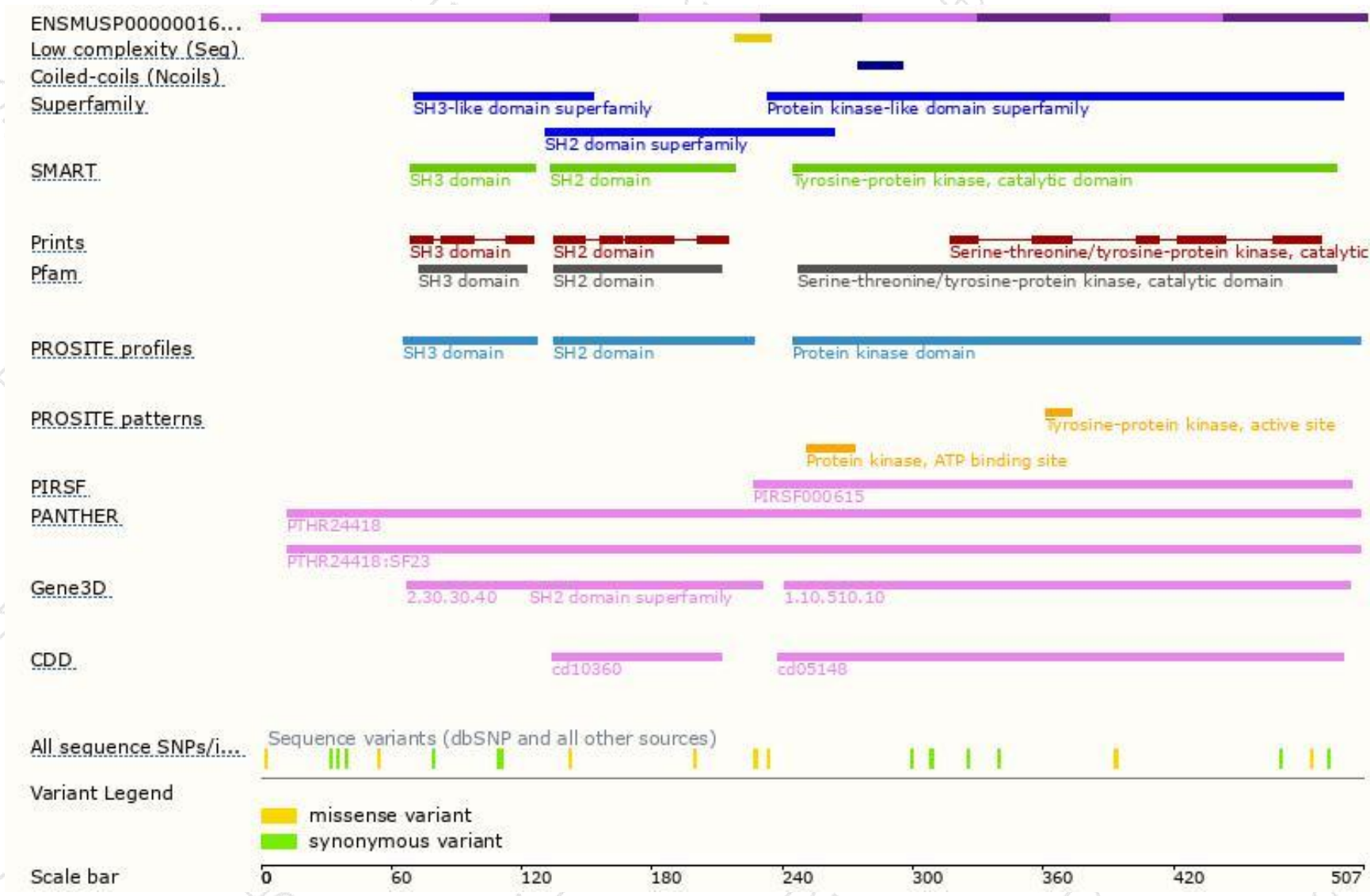

< Srms-201
protein coding

◀━ Reverse strand

7.62 kb

Genomic location distribution

Protein domain

ENSMUSP00000016...	
Low complexity (Seg)	
Coiled-coils (Ncoils)	
Superfamily	SH3-like domain superfamily, Protein kinase-like domain superfamily, SH2 domain superfamily
SMART	SH3 domain, SH2 domain, Tyrosine-protein kinase, catalytic domain
Prints	SH3 domain, SH2 domain, Serine-threonine/tyrosine-protein kinase, catalytic
Pfam	SH3 domain, SH2 domain, Serine-threonine/tyrosine-protein kinase, catalytic domain
PROSITE profiles	SH3 domain, SH2 domain, Protein kinase domain
PROSITE patterns	Tyrosine-protein kinase, active site, Protein kinase, ATP binding site
PIRSF	PIRSF000615
PANTHER	PTHR24418, PTHR24418:SF23
Gene3D	2.30.30.40, SH2 domain superfamily, 1.10.510.10
CDD	cd10360, cd05148
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)
Variant Legend	missense variant, synonymous variant
Scale bar	0 60 120 180 240 300 360 420 507

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