Rnf135 Cas9-KO Strategy

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Project Overview

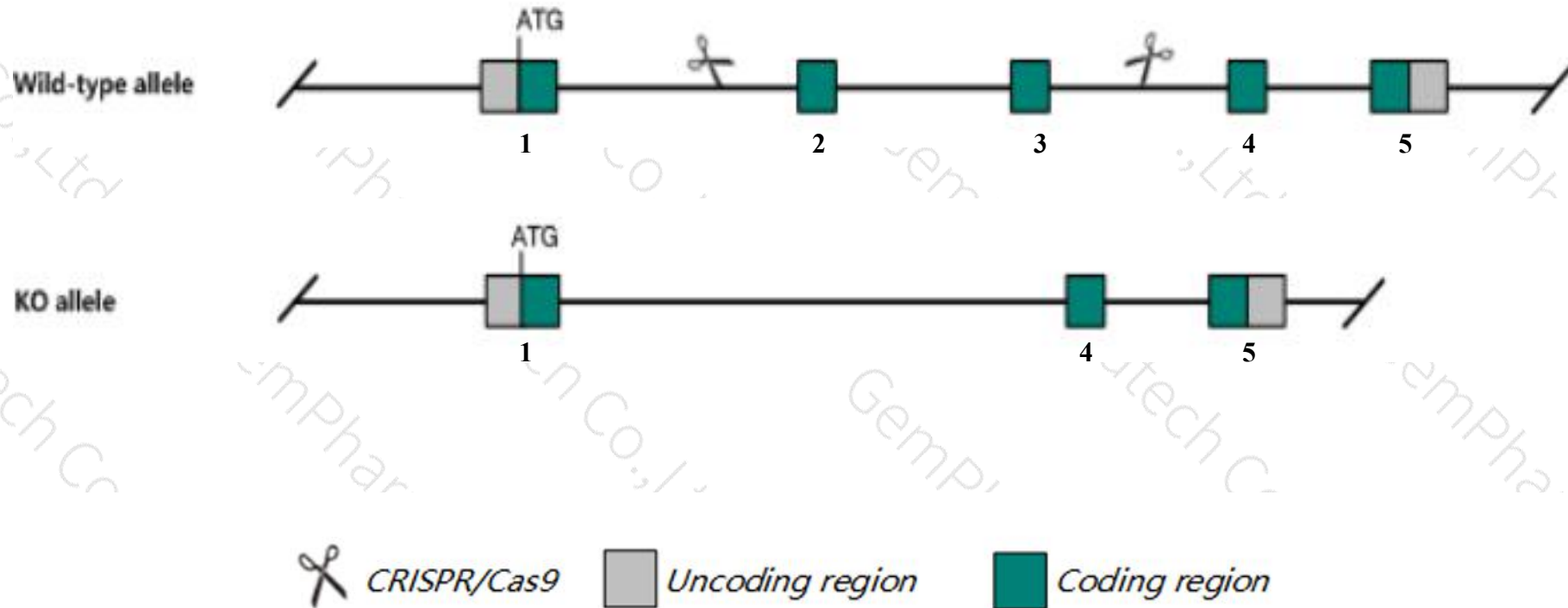|	
Project Name	***Rnf135***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf135* gene. The schematic diagram is as follows:

Technical routes

➢ The *Rnf135* gene has 2 transcripts. According to the structure of *Rnf135* gene, exon2-exon3 of *Rnf135-201* (ENSMUST00000017839.2) transcript is recommended as the knockout region.The region contains 307bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rnf135* gene. The brief process is as follows: CRISPR/Cas9 system

➢ The *Rnf135* 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）

Rnf135 ring finger protein 135 [Mus musculus (house mouse)]
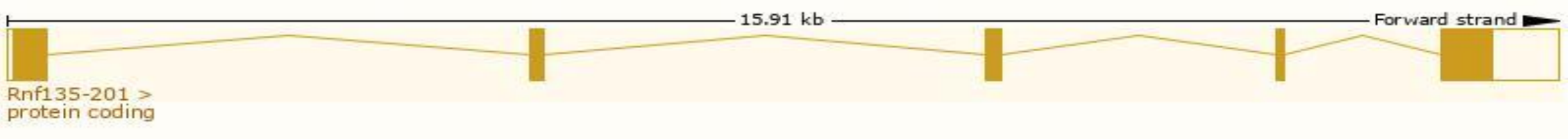
Gene ID: 71956, updated on 13-Mar-2020

▲Summary

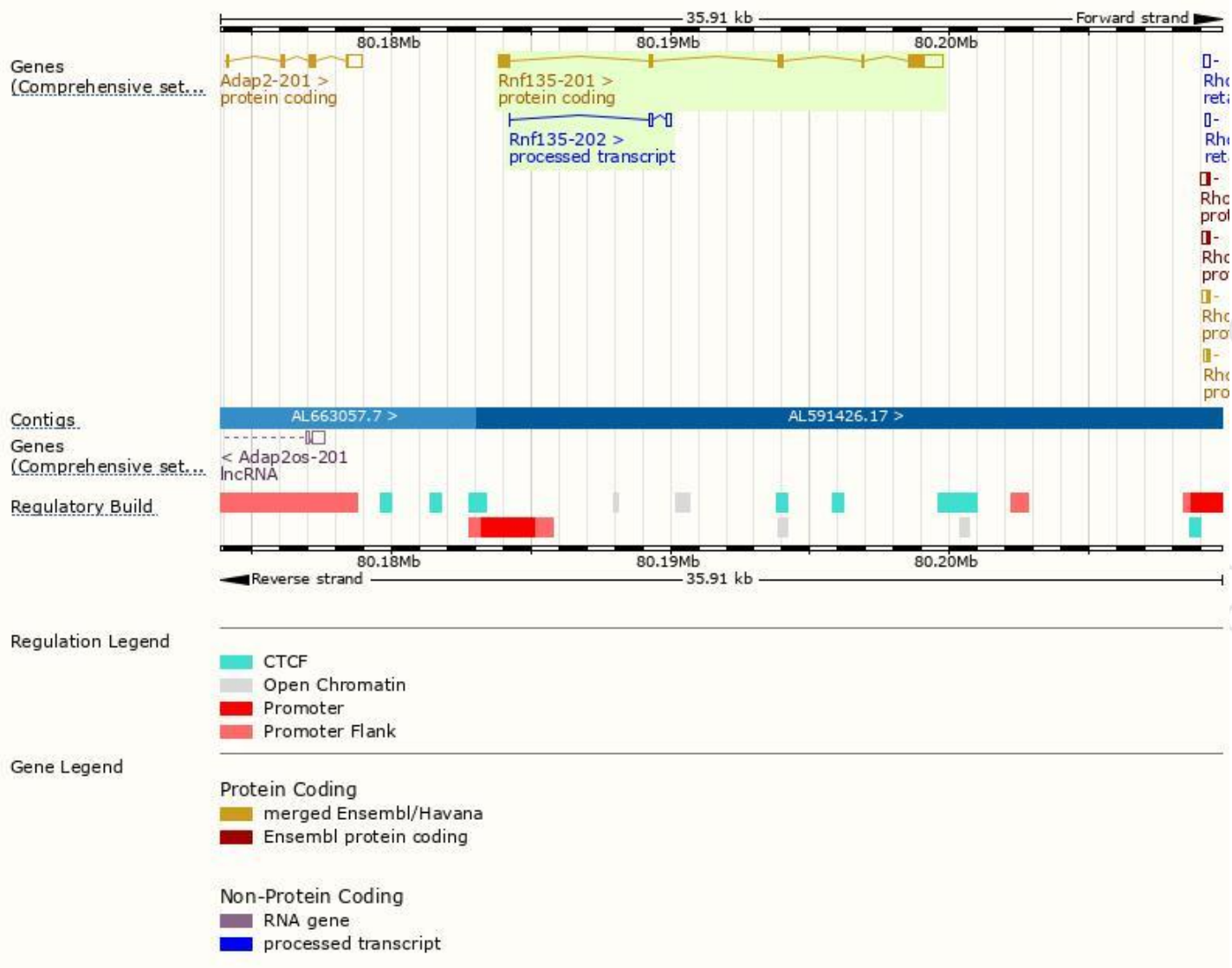|	
Official Symbol	Rnf135 provided by MGI
Official Full Name	ring finger protein 135 provided by MGI
Primary source	MGI:MGI:1919206
See related	Ensembl:ENSMUSG00000020707
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	0610037N03Rik, 2410006N06Rik, Riplet, U 2-3-0
Expression	Ubiquitous expression in ovary adult (RPKM 5.9), adrenal adult (RPKM 5.2) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf135-201	ENSMUST00000017839.2	1984	417aa	Protein coding	CCDS25129	B2RRA5 Q9CWS1	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
Rnf135-202	ENSMUST00000134909.1	333	No protein	Processed transcript	-	-	TSL:5

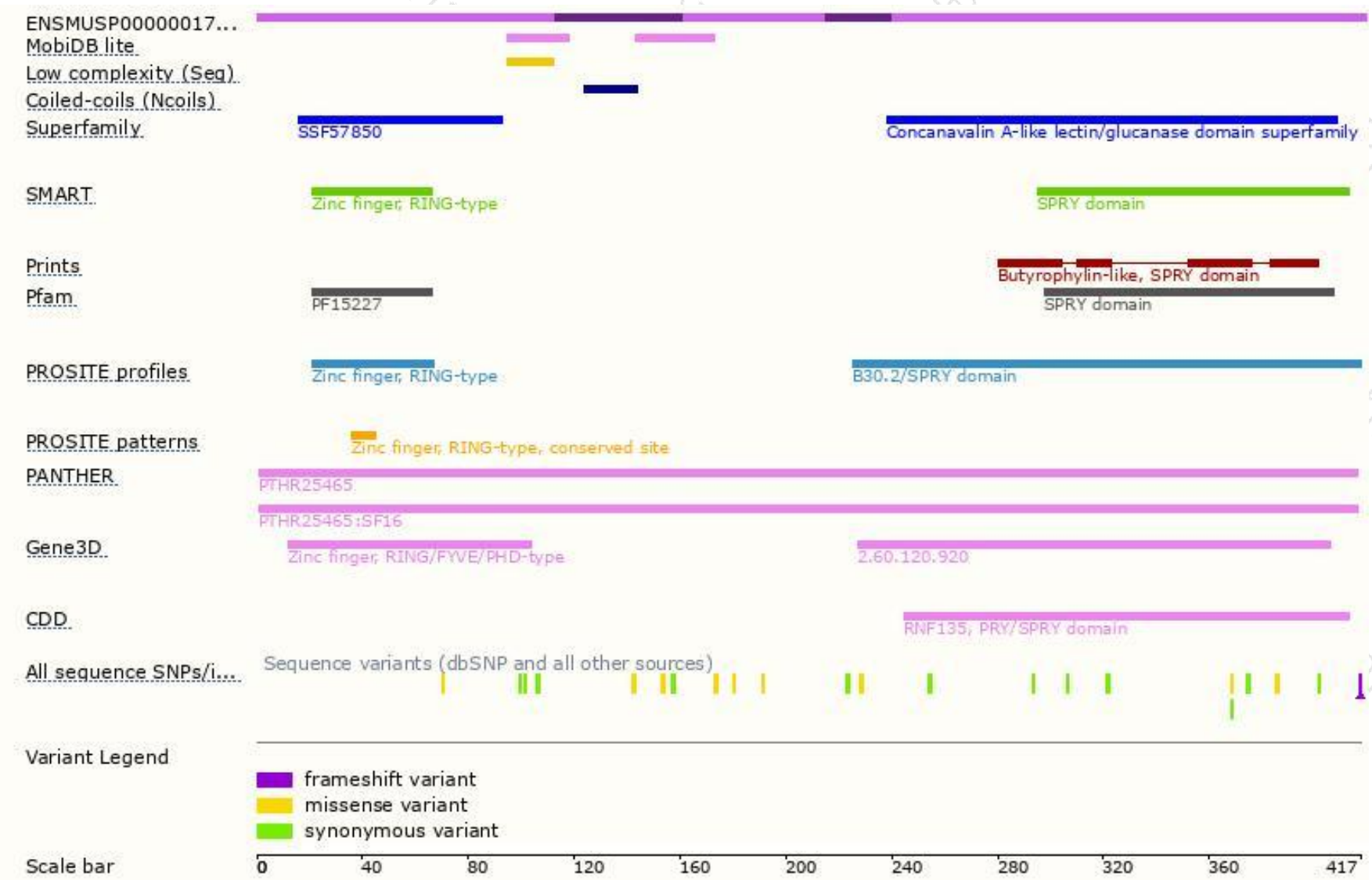The strategy is based on the design of *Rnf135-201* transcript,The transcription is shown below
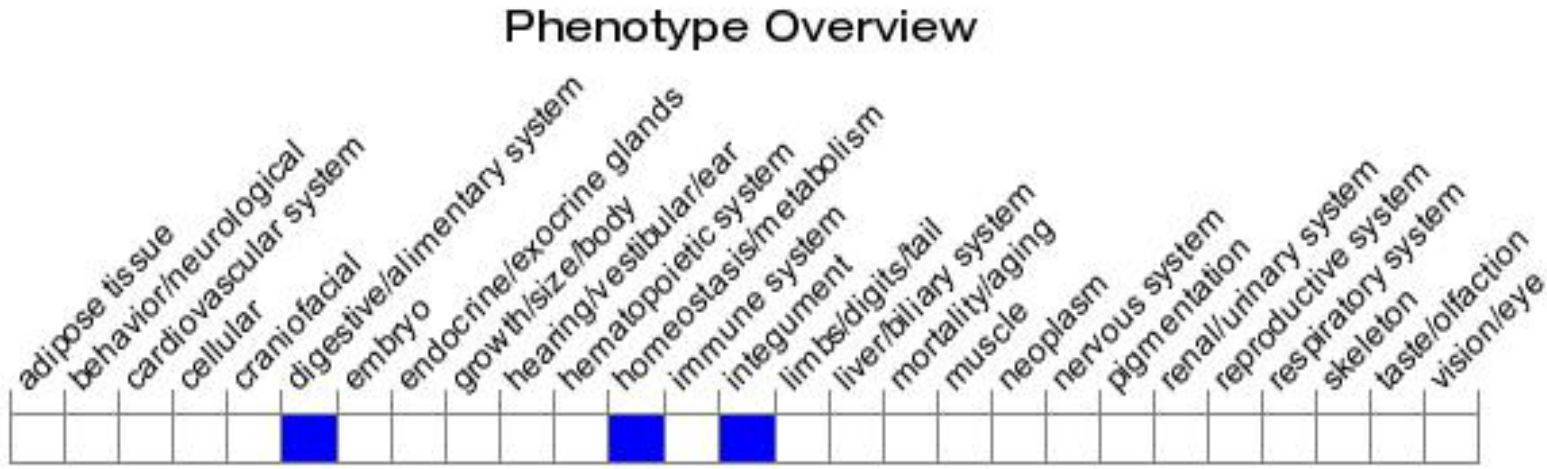
Genomic location distribution

Protein domain

		Scale bar
ENSMUSP00000017...		
MobiDB lite		
Low complexity (Seg)		
Coiled-coils (Ncoils)		
Superfamily	SSF57850	Concanavalin A-like lectin/glucanase domain superfamily
SMART	Zinc finger, RING-type	SPRY domain
Prints		Butyrophylin-like, SPRY domain
Pfam	PF15227	SPRY domain
PROSITE profiles	Zinc finger, RING-type	B30.2/SPRY domain
PROSITE patterns	Zinc finger, RING-type, conserved site	
PANTHER	PTHR25465	
	PTHR25465:SF16	
Gene3D	Zinc finger, RING/FYVE/PHD-type	2.60.120.920
CDD		RNF135, PRY/SPRY domain
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)	

Variant Legend
- frameshift variant
- missense variant
- synonymous variant

Scale bar: 0 40 80 120 160 200 240 280 320 360 417

Mouse phenotype description(MGI)

Phenotype Overview

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

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