Rnf32 Cas9-KO Strategy

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Project Overview

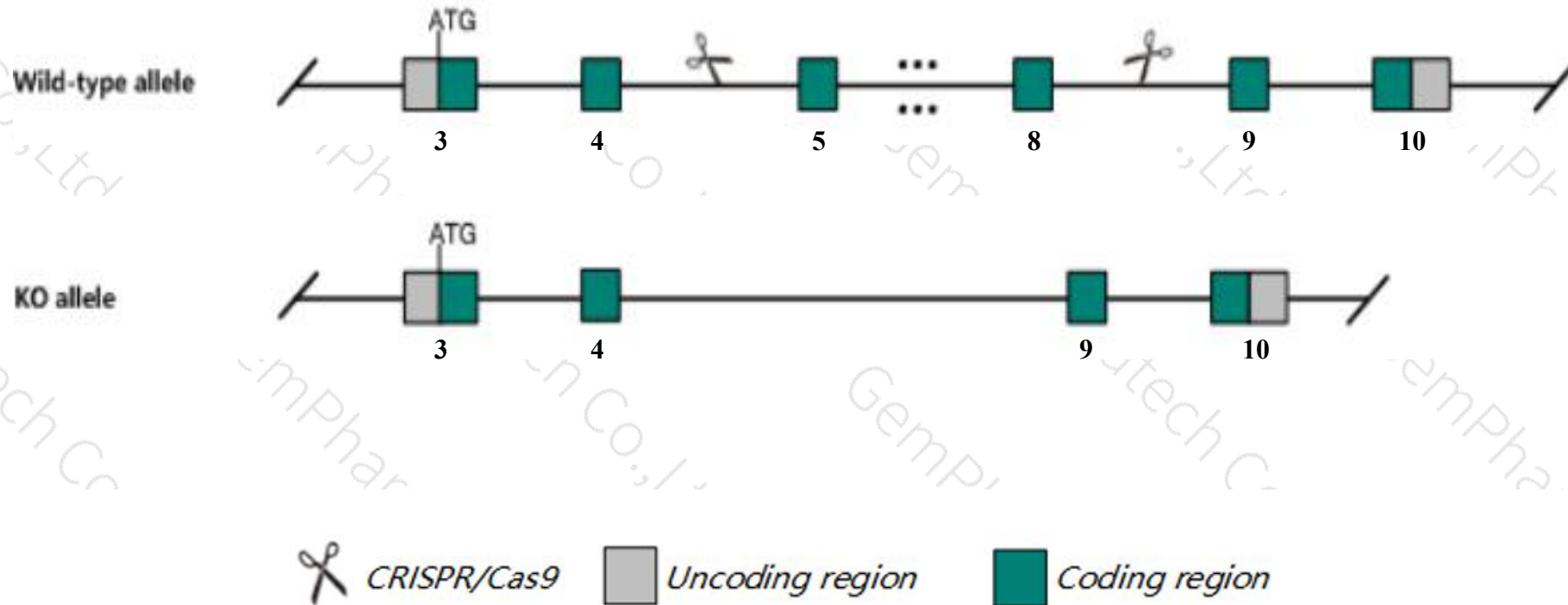|	
Project Name	***Rnf32***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf32* gene. The schematic diagram is as follows:

➤ The *Rnf32* gene has 12 transcripts. According to the structure of *Rnf32* gene, exon5-exon8 of *Rnf32-201*(ENSMUST00000001247.11) transcript is recommended as the knockout region.The region contains 410bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Rnf32* gene. The brief process is as follows: CRISPR/Cas9 system 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

Notice

➢ The *Rnf32* gene is located on the Chr5. 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）

Rnf32 ring finger protein 32 [Mus musculus (house mouse)]

Gene ID: 56874, updated on 13-Mar-2020

Summary

|	
Official Symbol	Rnf32 provided by MGI
Official Full Name	ring finger protein 32 provided by MGI
Primary source	MGI:MGI:1861747
See related	Ensembl:ENSMUSG00000029130
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	1700009J01Rik, 2700025B22Rik, 4930542N22Rik, Lmbr2
Expression	Biased expression in testis adult (RPKM 24.5), CNS E18 (RPKM 2.6) and 4 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 12 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf32-201	ENSMUST00000001247.11	1600	368aa	Protein coding	CCDS39041	Q9JIT1	TSL:1 GENCODE basic APPRIS P1
Rnf32-204	ENSMUST00000160246.7	1565	368aa	Protein coding	CCDS39041	Q9JIT1	TSL:1 GENCODE basic APPRIS P1
Rnf32-211	ENSMUST00000168460.7	1107	368aa	Protein coding	CCDS39041	Q9JIT1	TSL:1 GENCODE basic APPRIS P1
Rnf32-209	ENSMUST00000162975.1	837	275aa	Protein coding	-	F6URG7	CDS 5' incomplete TSL:3
Rnf32-208	ENSMUST00000161398.7	626	123aa	Protein coding	-	E0CZ33	CDS 3' incomplete TSL:3
Rnf32-207	ENSMUST00000160888.7	562	120aa	Protein coding	-	E0CY41	CDS 3' incomplete TSL:3
Rnf32-202	ENSMUST00000159272.7	374	46aa	Protein coding	-	E0CY22	CDS 3' incomplete TSL:2
Rnf32-212	ENSMUST00000198669.1	355	29aa	Protein coding	-	A0A0J9YUY1	CDS 3' incomplete TSL:5
Rnf32-205	ENSMUST00000160383.7	1295	103aa	Nonsense mediated decay	-	E0CZC4	TSL:1
Rnf32-203	ENSMUST00000160051.1	403	No protein	Processed transcript	-	-	TSL:3
Rnf32-210	ENSMUST00000163050.4	4672	No protein	Retained intron	-	-	TSL:NA
Rnf32-206	ENSMUST00000160887.5	1738	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Rnf32-201* transcript,the transcription is shown below:
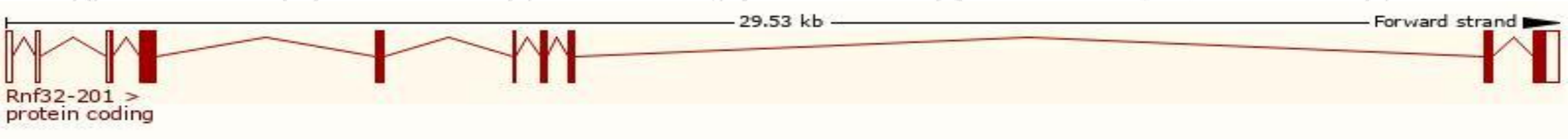
Genomic location distribution

Protein domain

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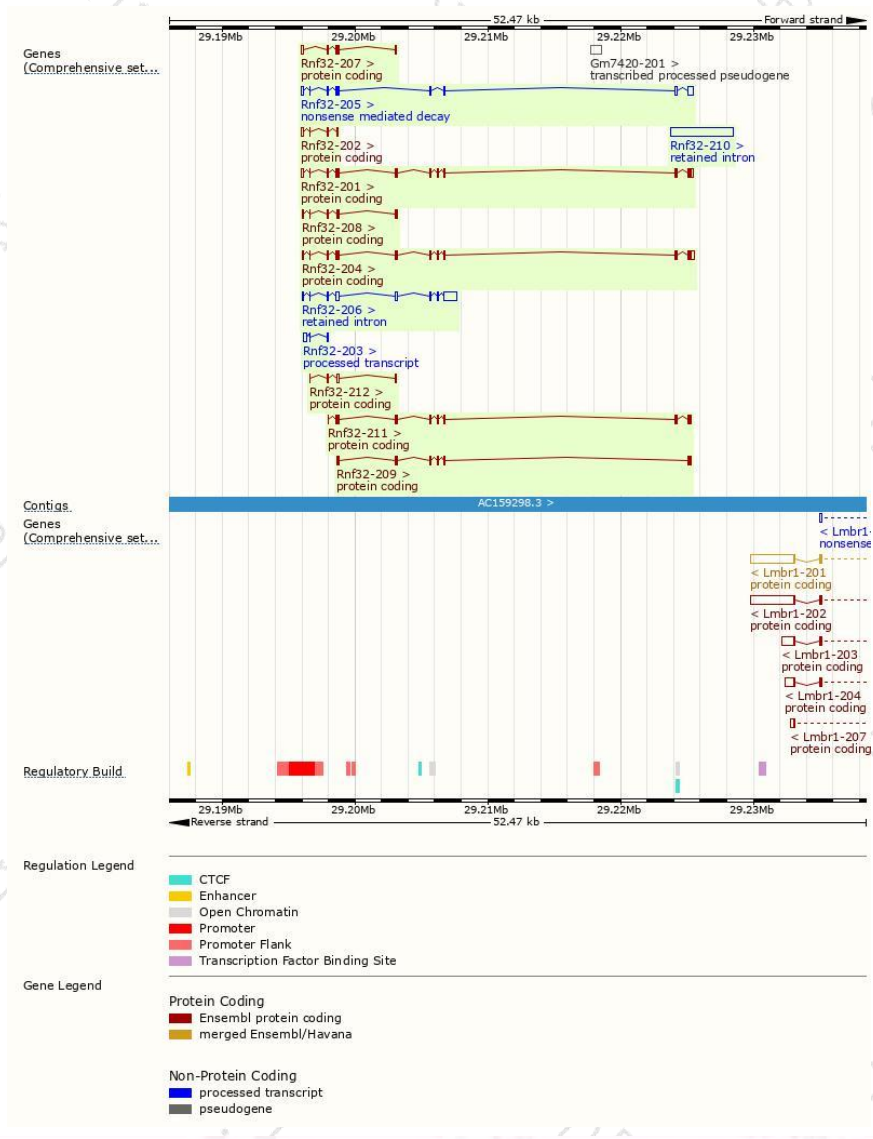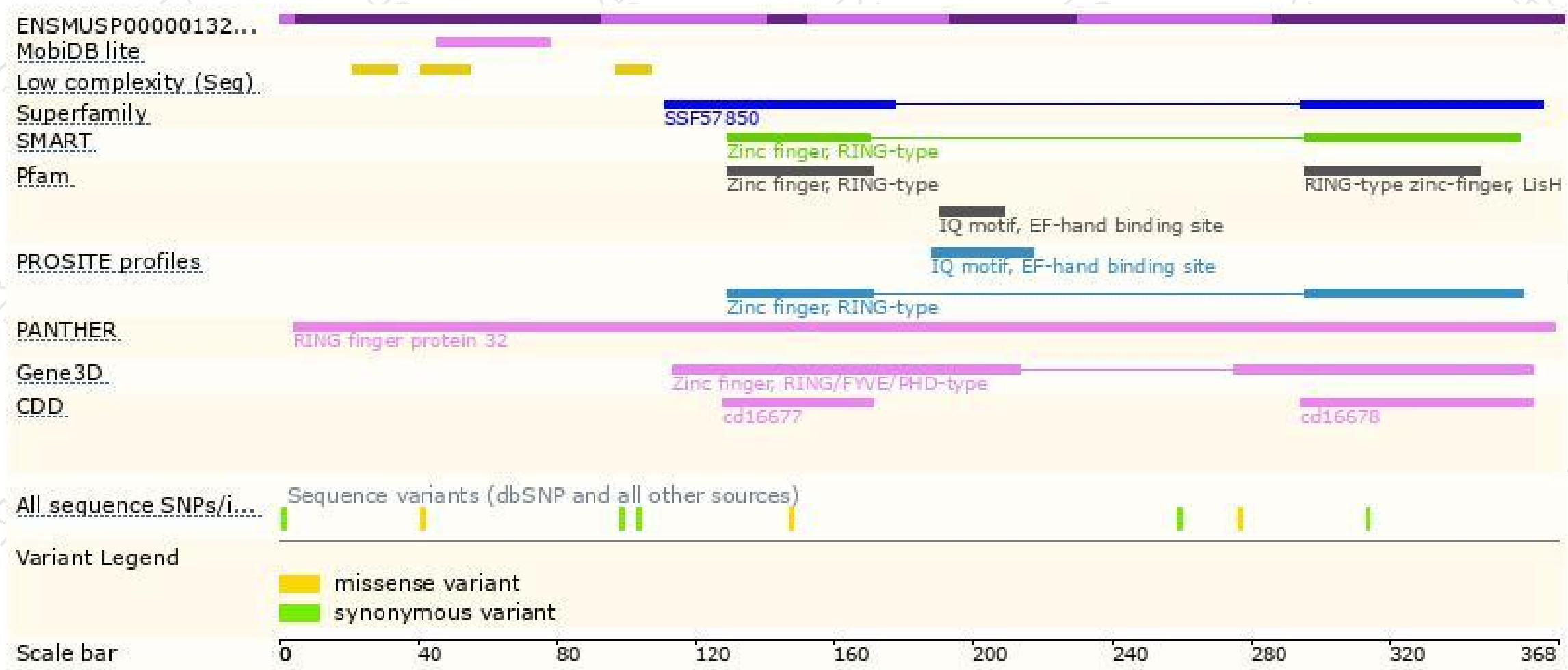
If you have any questions, you are welcome to inquire.
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