GemPharmatech™

Rmnd5a Cas9-CKO Strategy

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Design Date: 2023-11-07

Overview

Target Gene Name

- *Rmnd5a*

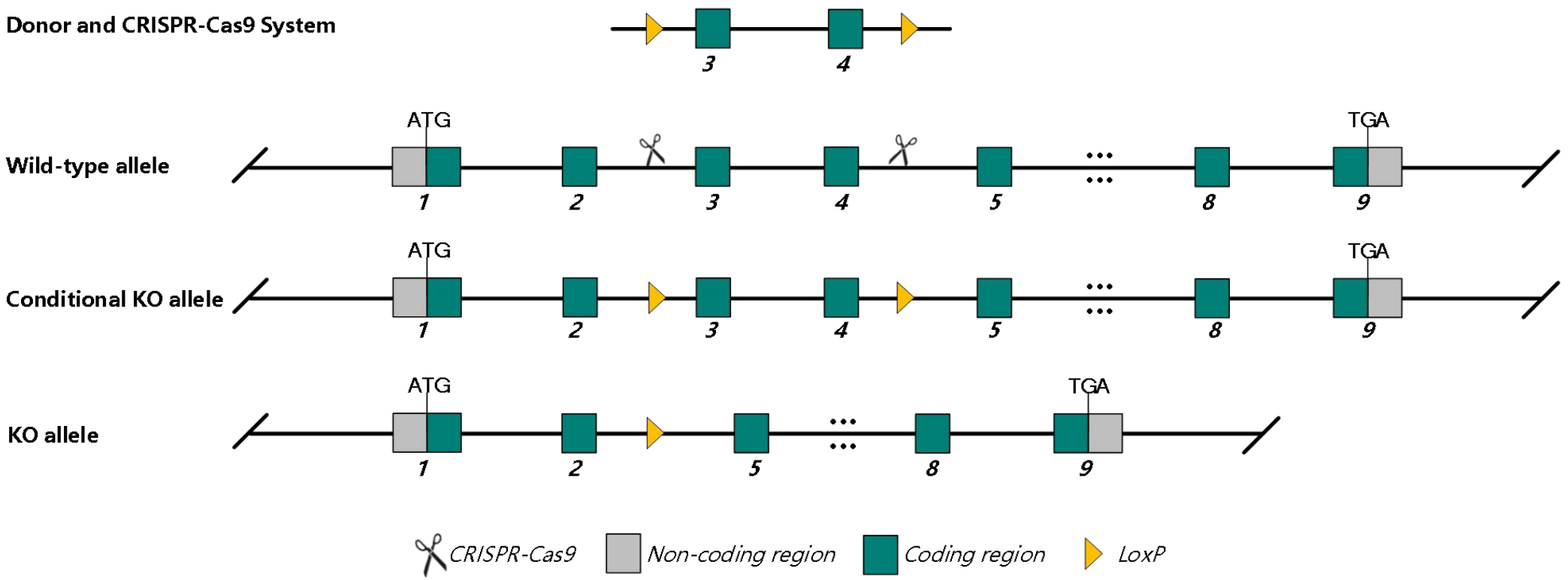
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Rmnd5a* gene.

Technical Information

- The *Rmnd5a* gene has 5 transcripts. According to the structure of *Rmnd5a* gene, exon 3-4 of *Rmnd5a*-201 (ENSMUST00000002292.15) is recommended as the knockout region. The region contains 236 bp of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Rmnd5a* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Gene Information

Rmnd5a required for meiotic nuclear division 5 homolog A [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 68477, updated on 7-Sep-2023

Summary

Official Symbol	Rmnd5a provided by MGI
Official Full Name	required for meiotic nuclear division 5 homolog A provided by MGI
Primary source	MGI:MGI:1915727
See related	Ensembl:ENSMUSG00000002222 AllianceGenome:MGI:1915727
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	Gid2; MTA.D02.090; 1110007A06Rik
Summary	Predicted to enable metal ion binding activity and ubiquitin protein ligase activity. Predicted to contribute to ubiquitin-protein transferase activity. Predicted to be involved in proteasome-mediated ubiquitin-dependent protein catabolic process. Predicted to be located in nucleoplasm. Predicted to be part of GID complex and ubiquitin ligase complex. Predicted to be active in cytoplasm and nucleus. Orthologous to human RMND5A (required for meiotic nuclear division 5 homolog A). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in thymus adult (RPKM 62.2), cerebellum adult (RPKM 22.9) and 28 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**

Try the new Transcript table

Genomic context

Location: 6 C1; 6 32.14 cM

See Rmnd5a in Genome Data Viewer

Exon count: 9

https://www.ncbi.nlm.nih.gov/gene/68477

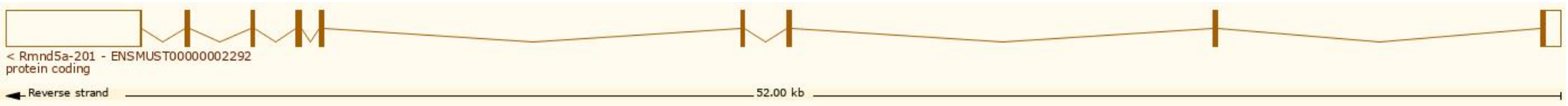
Transcript Information

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

Show/hide columns (1 hidden) Filter

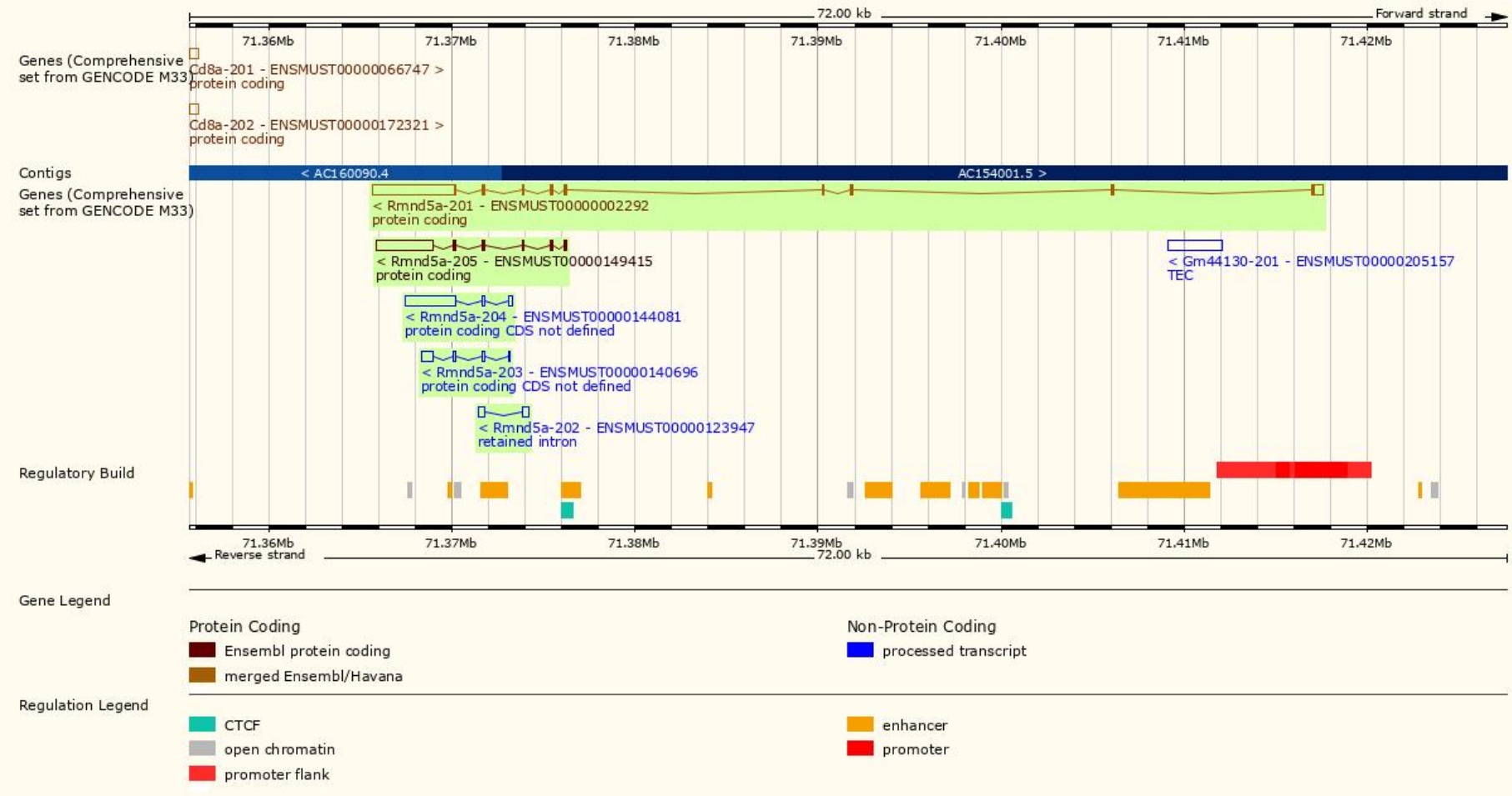
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000002292.15	Rmnd5a-201	6165	391aa	Protein coding	CCDS20231	Q80YQ8	Ensembl Canonical, GENCODE basic, APPRIS P1, TSL:1
ENSMUST00000149415.2	Rmnd5a-205	3768	218aa	Protein coding		F6V8A7	TSL:1, CDS 5' incomplete
ENSMUST00000144081.8	Rmnd5a-204	3086	No protein	Protein coding CDS not defined		-	TSL:1
ENSMUST00000140696.2	Rmnd5a-203	999	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000123947.2	Rmnd5a-202	667	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Rmnd5a*-201 transcript, the transcription is shown below:



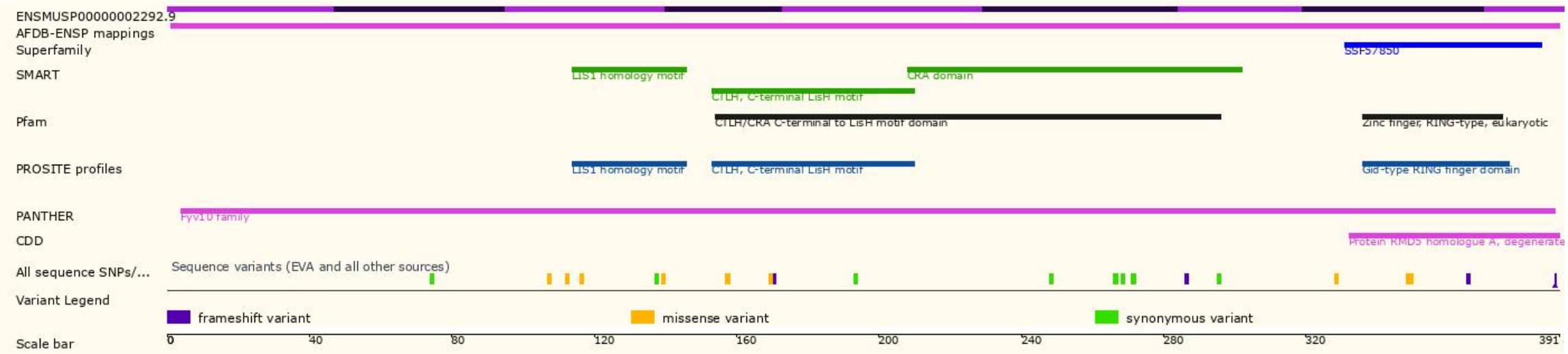
Source: http://asia.ensembl.org/

Genomic Information



Source: http://asia.ensembl.org/

Protein Information



Source: https://www.ensembl.org

Important Information

- Since the *Rmnd5a*-205 transcript 5’ is incomplete, the effect of this stratergy on *Rmnd5a*-205 transcript is unknown.
- This stratergy may not affect *Rmnd5a*-202, *Rmnd5a*-203 and *Rmnd5a*-204 transcript.
- *Rmnd5a* is located on Chr 6. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.