

Rbm28 Cas9-CKO Strategy

Designer: Xiangli Bian

Reviewer: Yao Yu

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Overview

Target Gene Name

- *Rbm28*

Project Type

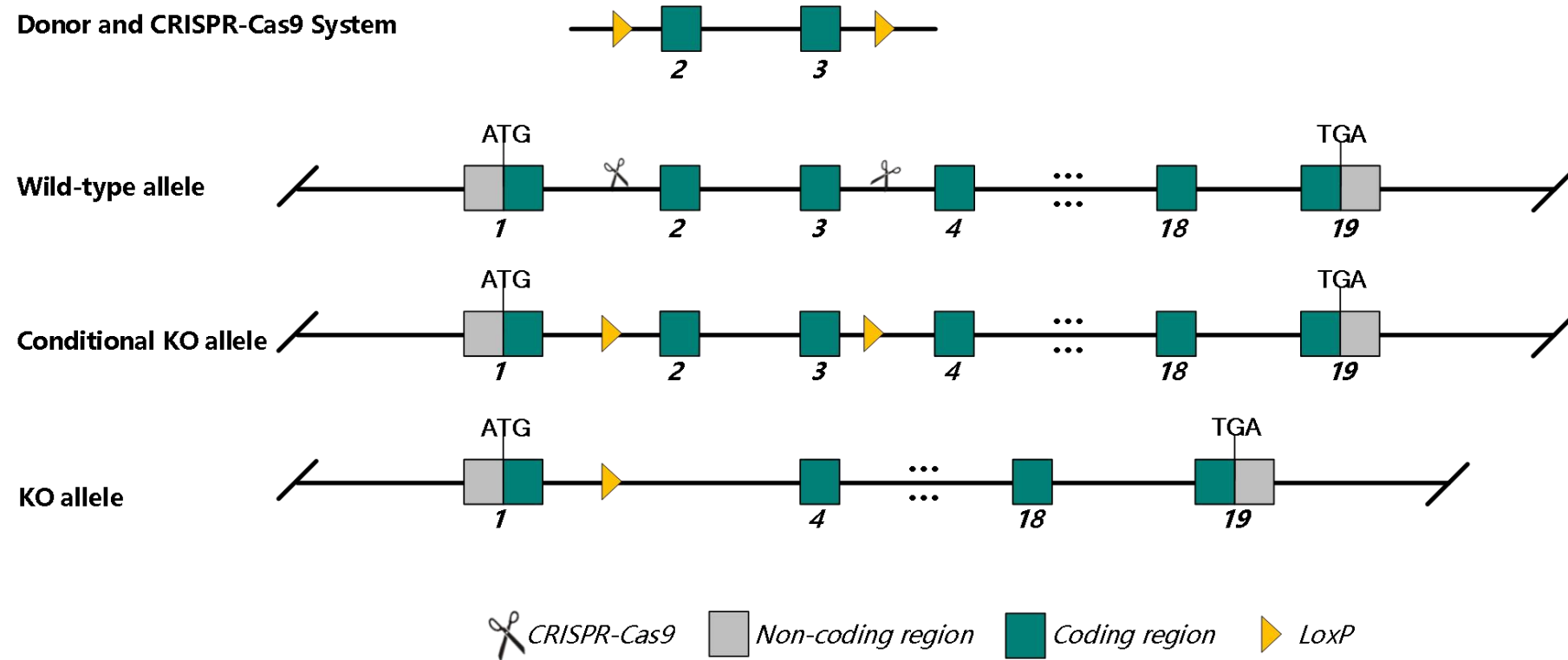
- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy

Donor and CRISPR-Cas9 System



Schematic representation of CRISPR-Cas9 engineering used to edit the *Rbm28* gene.

Technical Information

- The *Rbm28* gene has 6 transcripts. According to the structure of *Rbm28* gene, exon 2-3 of *Rbm28*-201 (ENSMUST00000007993.16) is recommended as the knockout region. The region contains 254 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 *Rbm28* 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

Rbm28 RNA binding motif protein 28 [*Mus musculus* (house mouse)]

Gene ID: 68272, updated on 5-Aug-2023

[Download Datasets](#)

Summary

Official Symbol	Rbm28 provided by MGI
Official Full Name	RNA binding motif protein 28 provided by MGI
Primary source	MGI:MGI:2655711
See related	Ensembl:ENSMUSG00000029701 AllianceGenome:MGI:2655711
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	2810480G15Rik
Summary	Predicted to enable RNA binding activity. Predicted to act upstream of or within RNA splicing and mRNA processing. Predicted to be located in nucleolus. Predicted to be part of spliceosomal complex. Is expressed in central nervous system and sensory organ. Human ortholog(s) of this gene implicated in alopecia, neurologic defects, and endocrinopathy syndrome. Orthologous to human RBM28 (RNA binding motif protein 28). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in CNS E11.5 (RPKM 20.2), CNS E18 (RPKM 15.5) and 24 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

Genomic context

Location: 6 A3.3; 6 12.33 cM

Exon count: 19

See Rbm28 in [Genome Data Viewer](#)

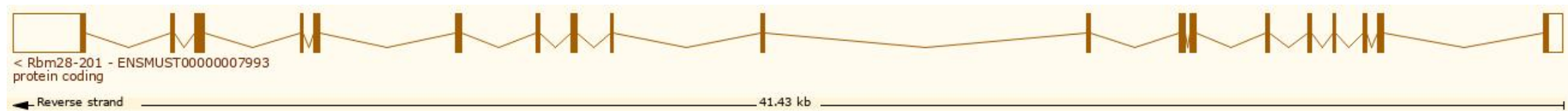
<https://www.ncbi.nlm.nih.gov/gene/68272>

Transcript Information

The gene has 6 transcripts, all transcripts are shown below:

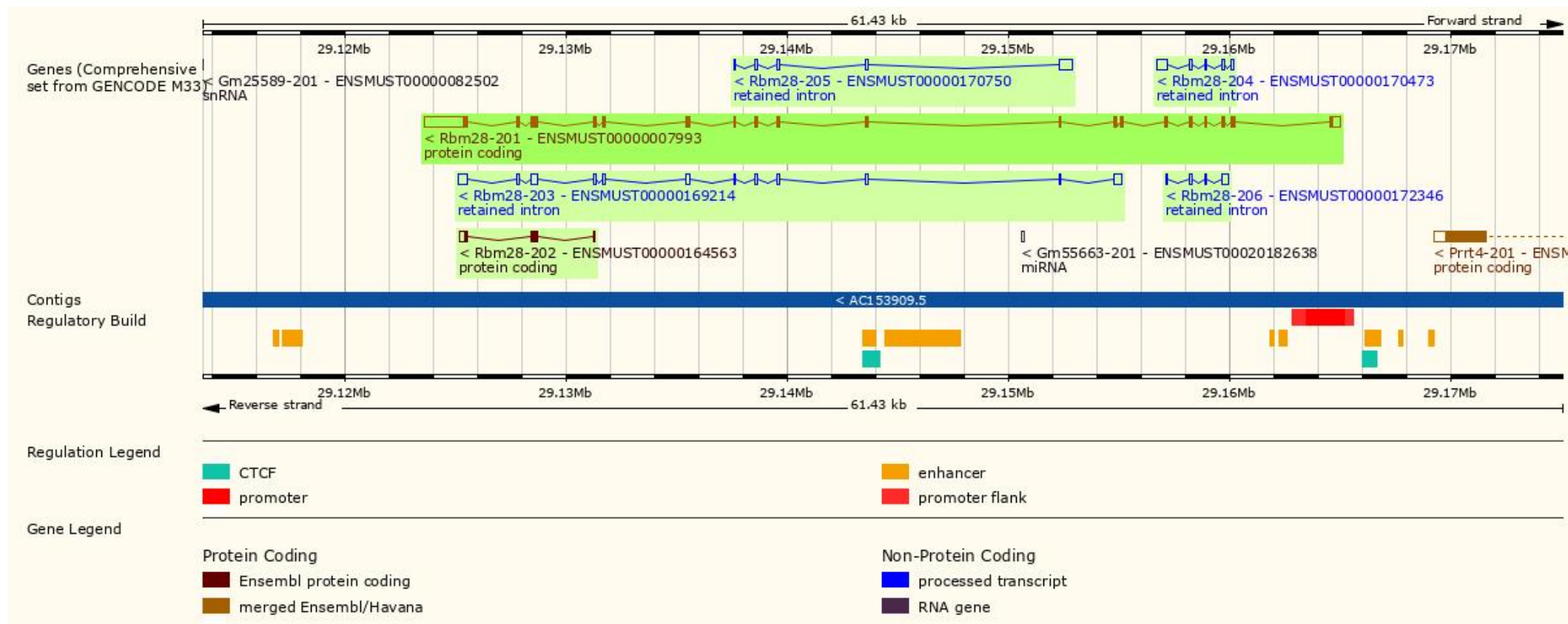
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST0000007993.16	Rbm28-201	4465	750aa	Protein coding	CCDS51733	Q8CGC6	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000164563.2	Rbm28-202	637	133aa	Protein coding		F6SB18	TSL:5 CDS 5' incomplete
ENSMUST00000169214.8	Rbm28-203	1923	No protein	Retained intron		-	TSL:1
ENSMUST00000170750.2	Rbm28-205	954	No protein	Retained intron		-	TSL:5
ENSMUST00000170473.8	Rbm28-204	844	No protein	Retained intron		-	TSL:5
ENSMUST00000172346.2	Rbm28-206	495	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Rbm28-201* transcript, the transcription is shown below:

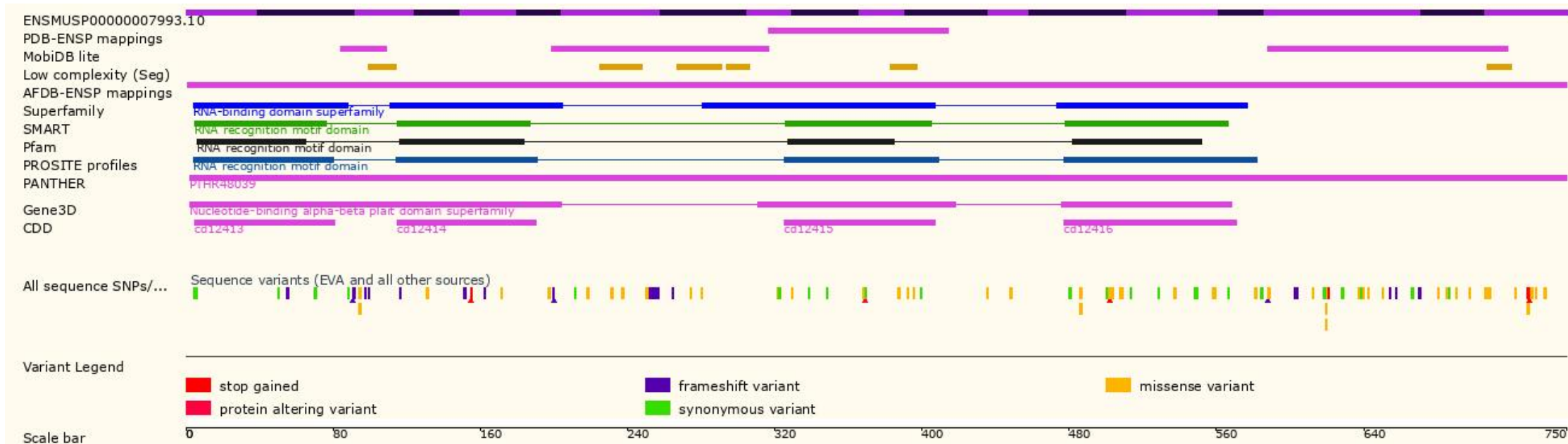


Source: <http://asia.ensembl.org/>

Genomic Information



Protein Information



Important Information

- The intron 3-4 of *Rbm28*-201 is 733 bp, the loxp insertion may affect the regulation of this gene.
- This strategy may not affect *Rbm28*-202, *Rbm28*-203 and *Aldoa*-205 transcript.
- The knockout region is about 8.5 kb away from the 5' of the *Gm55663* gene, which may affect the regulation of this gene.
- *Rbm28* 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.