

Rnf41 Cas9-KO Strategy

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Overview

Target Gene Name

- Rnf41

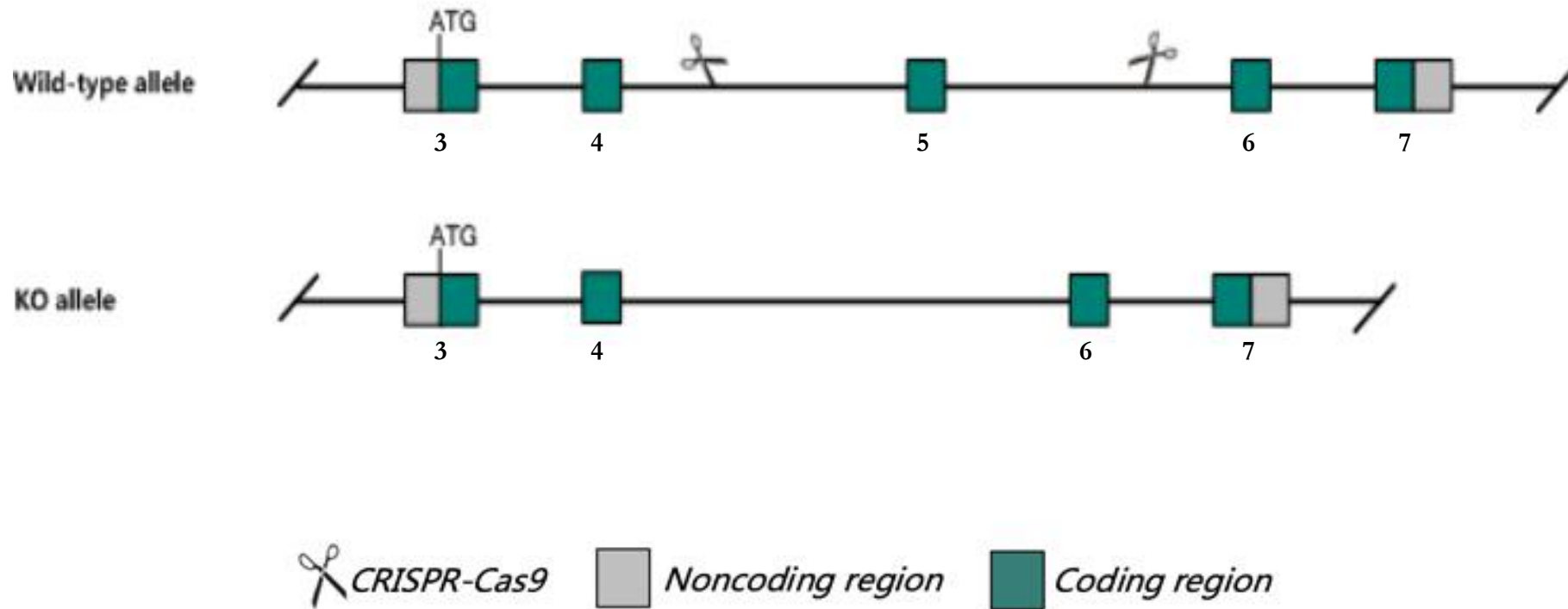
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Technical Information

- The *Rnf41* gene has 4 transcripts. According to the structure of *Rnf41* gene, exon5 of *Rnf41*-202 (ENSMUST00000171342.3) transcript is recommended as the knockout region. The region contains 136bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Rnf41* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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.

Gene Information

Rnf41 ring finger protein 41 [Mus musculus (house mouse)]

Gene ID: 67588, updated on 31-May-2023

Summary

Official Symbol	Rnf41 provided by MGI
Official Full Name	ring finger protein 41 provided by MGI
Primary source	MGI:MGI:1914838
See related	Ensembl:ENSMUSG00000025373
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	2210404G21Rik, 4930511A05Rik, 4933415P08Rik, D10Ert722e, FLRF, Nrpd1
Summary	Enables erythropoietin receptor binding activity and interleukin-3 receptor binding activity. Acts upstream of or within several processes, including negative regulation of mitophagy; positive regulation of DNA-binding transcription factor activity; and regulation of hemopoiesis. Predicted to be located in perinuclear region of cytoplasm. Predicted to be active in endoplasmic reticulum tubular network. Is expressed in several structures, including central nervous system; dorsal root ganglion; male reproductive system; and urinary system. Orthologous to human RNF41 (ring finger protein 41). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in testis adult (RPKM 22.7), CNS E18 (RPKM 16.8) and 28 other tissues See more
Orthologs	human all

Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 4 transcripts, all transcripts are shown below:

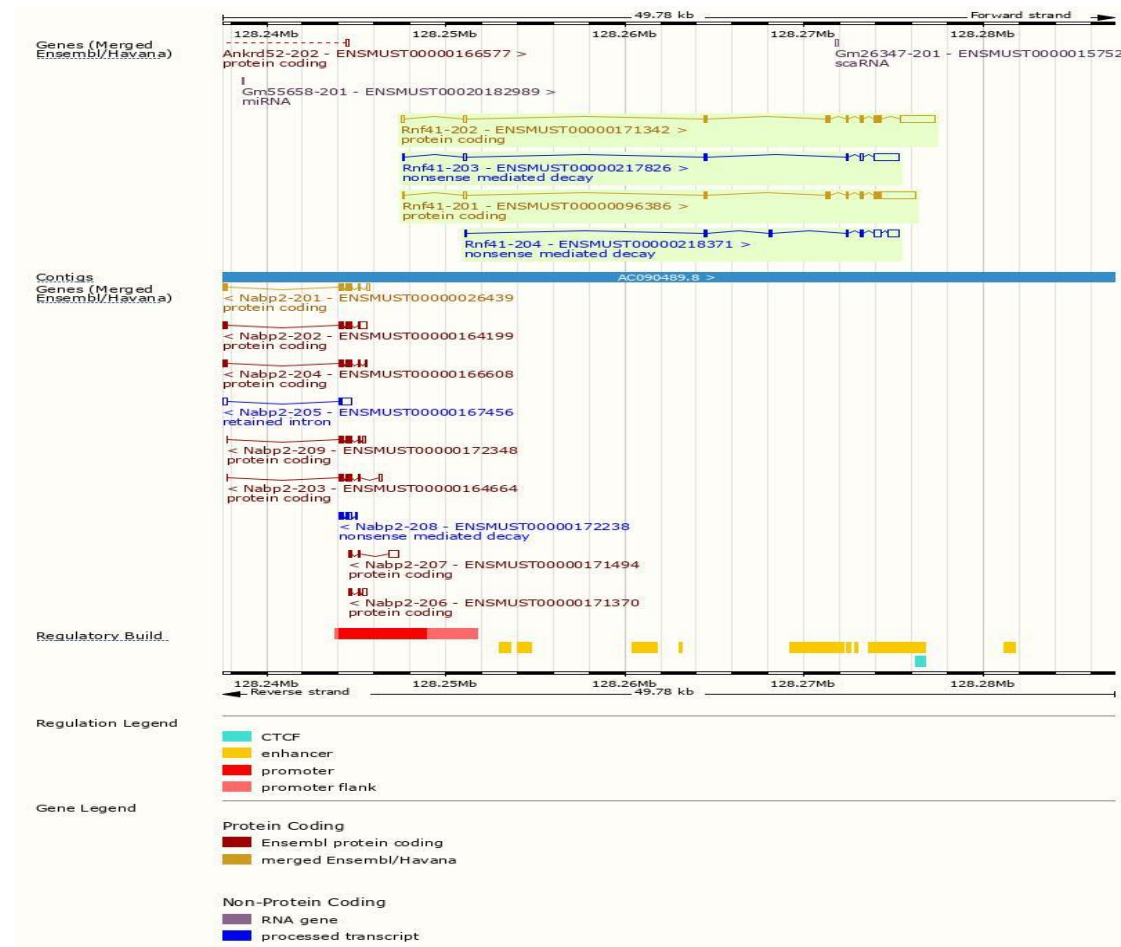
Show/hide columns (1 hidden) Filter										
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags			
ENSMUST00000171342.3	Rnf41-202	3283	317aa	Protein coding	CCDS24277	Q8BH75-1	Ensembl Canonical	GENCODE basic	APPRIS P1	TSL:1
ENSMUST00000096386.13	Rnf41-201	3144	317aa	Protein coding	CCDS24277	Q8BH75-1		GENCODE basic	APPRIS P1	TSL:1
ENSMUST00000217826.2	Rnf41-203	1984	36aa	Nonsense mediated decay		Q8BH75-2			TSL:1	
ENSMUST00000218371.2	Rnf41-204	1594	122aa	Nonsense mediated decay		A0A1W2P811			TSL:1	

The strategy is based on the design of *Rnf41-202* transcript, the transcription is shown below:

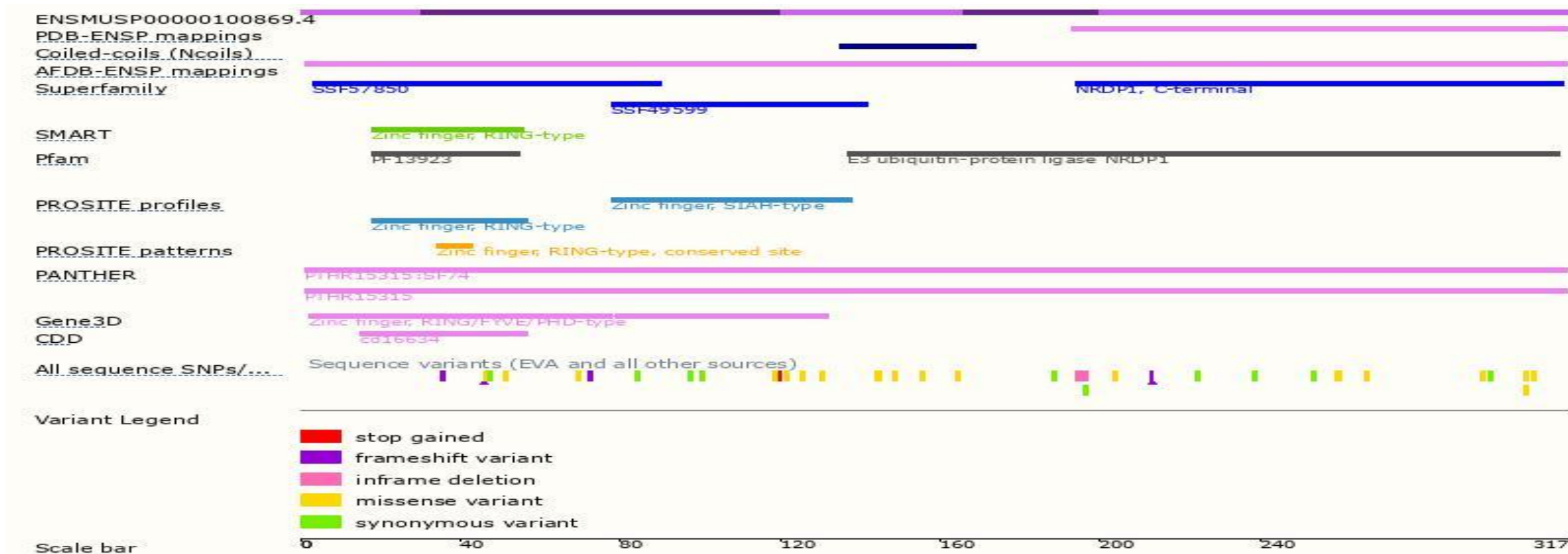


Source: <https://www.ensembl.org>

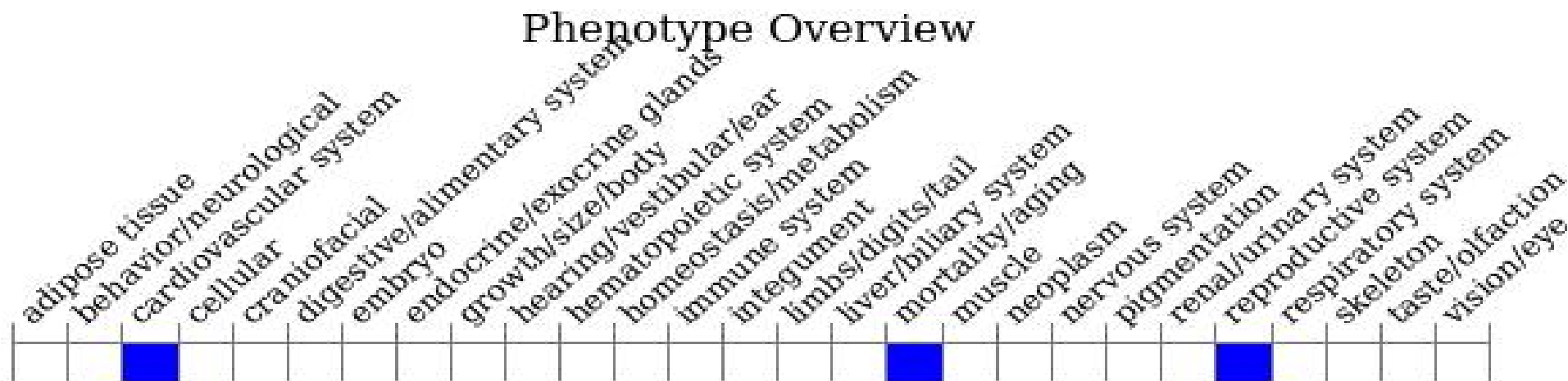
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Mice homozygous for a transgenic gene disruption exhibit male infertility. In contrast, mice homozygous for a gene trapped allele showed no overt phenotypes but show an increase in activation of naive CD8⁺ T cells before TCR engagement.

Important Information

- According to the existing MGI data, mice homozygous for a transgenic gene disruption exhibit male infertility. In contrast, mice homozygous for a gene trapped allele showed no overt phenotypes but show an increase in activation of naive CD8⁺ T cells before TCR engagement.
- There are amino acids of N-terminal will be residued.
- *Gm26347* gene will be destroyed.
- *Rnf41* is located on Chr10. 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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.