

Rnf43 Cas9-KO Strategy

Designer: Yao Yu

Reviewer: Mingzhu Xu

Design Date: 2023-3-16

Overview

Target Gene Name

- Rnf43

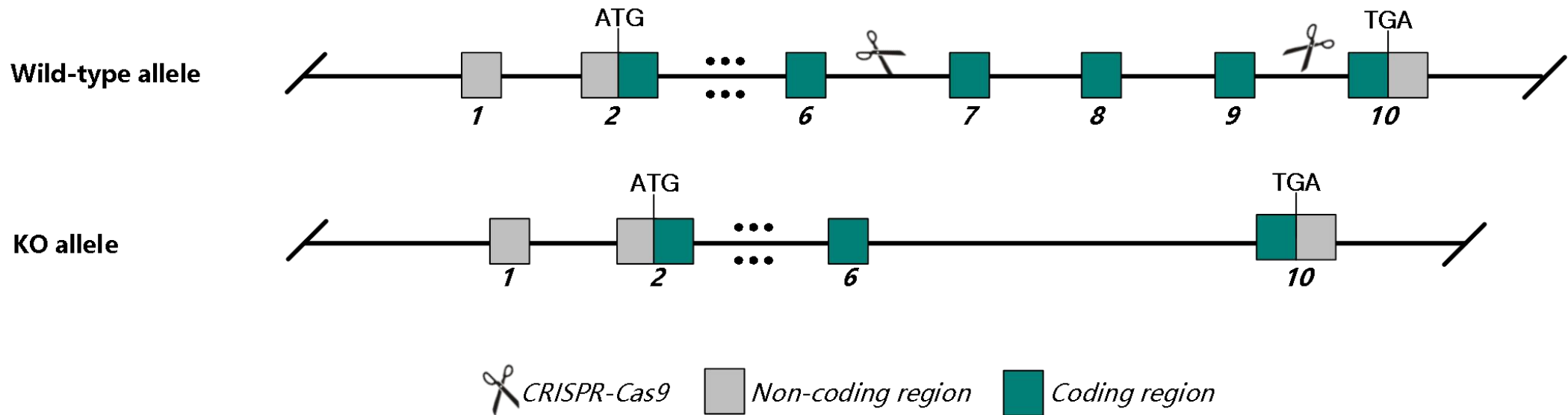
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Rnf43* gene.

Technical Information

- The *Rnf43* gene has 9 transcripts. According to the structure of *Rnf43* gene, exon 7-9 of *Rnf43*-201 (ENSMUST00000165679.8) transcript is recommended as the knockout region. The region contains 1624 bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Rnf43* 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

Rnf43 ring finger protein 43 [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 207742, updated on 3-Jan-2023

Summary

Official Symbol Rnf43 provided by [MGI](#)
Official Full Name ring finger protein 43 provided by [MGI](#)
Primary source [MGI:MGI:2442609](#)
See related [Ensembl:ENSMUSG00000034177](#) [AllianceGenome:MGI:2442609](#)
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 4732452J19Rik
Summary Predicted to enable frizzled binding activity and ubiquitin protein ligase activity. Involved in negative regulation of Wnt signaling pathway and stem cell proliferation. Predicted to be located in endoplasmic reticulum; nucleus; and plasma membrane. Predicted to be integral component of membrane. Predicted to be integral component of plasma membrane. Is expressed in alimentary system; genitourinary system; and lung. Orthologous to human RNF43 (ring finger protein 43). [provided by Alliance of Genome Resources, Apr 2022]
Expression Broad expression in duodenum adult (RPKM 7.3), colon adult (RPKM 5.7) and 19 other tissues [See more](#)
Orthologs [human](#) [all](#)
NEW Try the new [Gene table](#)
Try the new [Transcript table](#)

Genomic context

Location: 11; 11 C

Exon count: 11

See Rnf43 in [Genome Data Viewer](#)

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

Transcript Information

The gene has 9 transcripts, all transcripts are shown below:

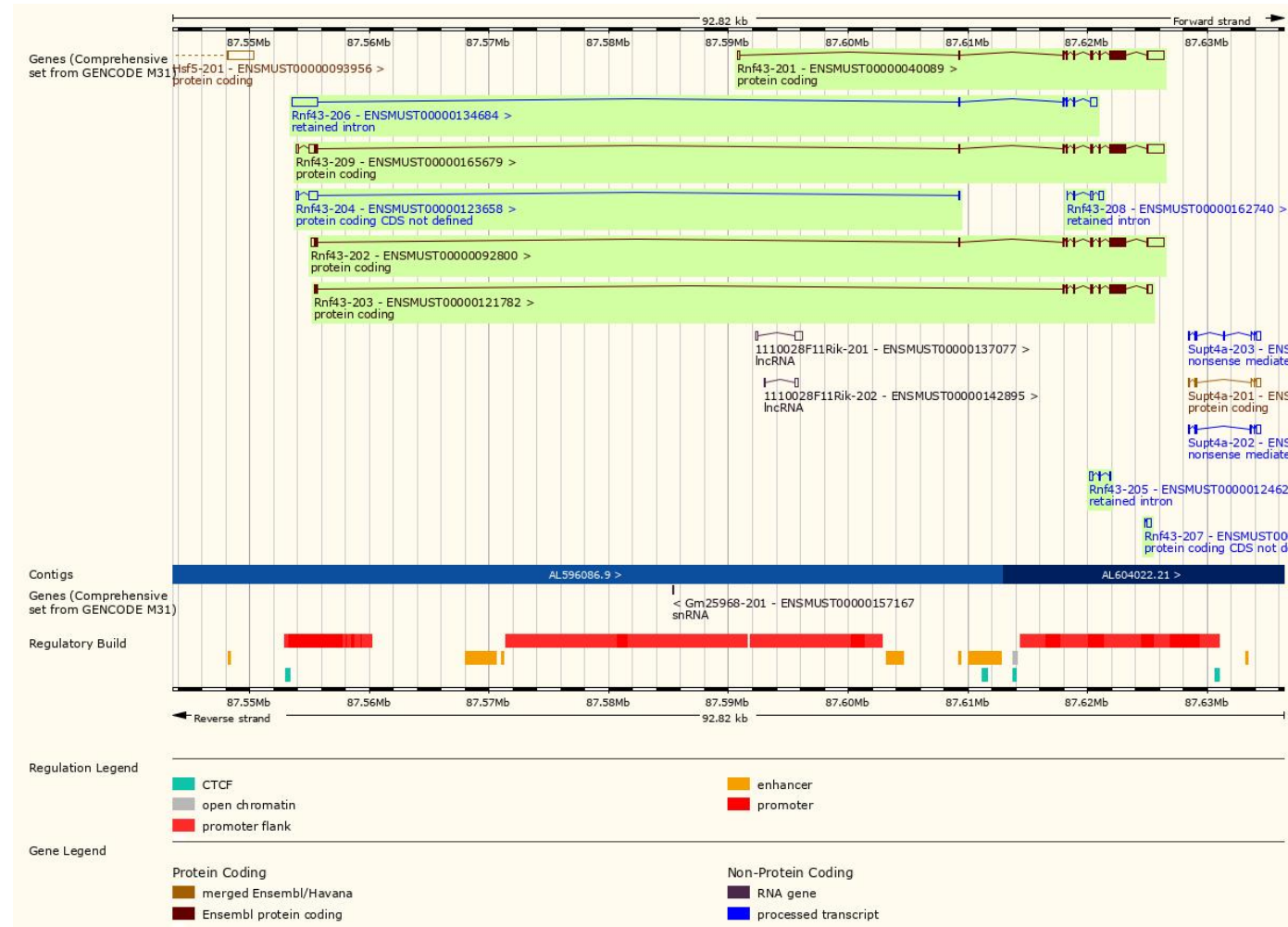
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000165679.8	Rnf43-209	4310	784aa	Protein coding	CCDS25215	Q5NCP0-1	Ensembl Canonical Gencode basic APPRIS P1 TSL:5
ENSMUST00000162740.2	Rnf43-208	704	No protein	Retained intron		-	TSL:5
ENSMUST00000150866.2	Rnf43-207	364	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000134684.8	Rnf43-206	3116	No protein	Retained intron		-	TSL:1
ENSMUST00000124625.2	Rnf43-205	378	No protein	Retained intron		-	TSL:3
ENSMUST00000123658.9	Rnf43-204	950	No protein	Protein coding CDS not defined		-	TSL:5
ENSMUST00000121782.9	Rnf43-203	2640	743aa	Protein coding		E9PWJ5	Gencode basic TSL:5
ENSMUST00000092800.12	Rnf43-202	4037	784aa	Protein coding	CCDS25215	Q5NCP0-1	Gencode basic APPRIS P1 TSL:5
ENSMUST00000040089.5	Rnf43-201	3670	657aa	Protein coding		Q5NCP0-2	Gencode basic TSL:1

The strategy is based on the design of *Rnf43-209* transcript, the transcription is shown below:

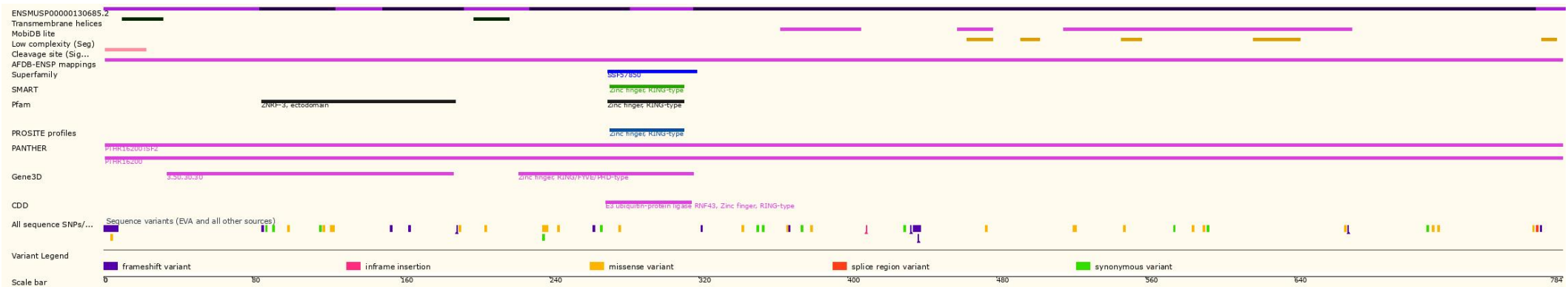


Source: <https://www.ensembl.org>

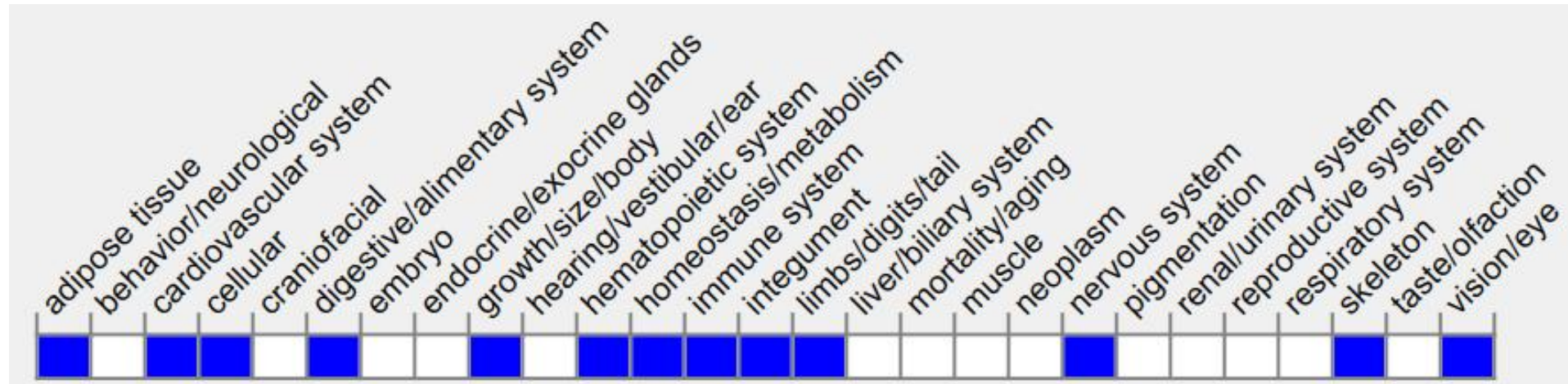
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



Homozygous knockout leads to hyperproliferation of stomach epithelium and increases the severity of chronic *H. pylori* infection pathology.

Important Information

- Homozygous knockout leads to hyperproliferation of stomach epithelium and increases the severity of chronic *H. pylori* infection pathology.
- The effect of this strategy on the uncoded transcript *Rnf43-204*, *Rnf43-207* is unknown.
- A part of amino acid sequence will still remain at the N-terminal of the *Rnf43* gene.
- The knockout region is about 4.5 kb away from the 5' of the *Supt4a* gene, which may affect the regulation of this gene.
- *Rnf43* is located on Chr 11. 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.