

# *Rnf43* Cas9-CKO Strategy

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# Overview

## Target Gene Name

- Rnf43

## Project Type

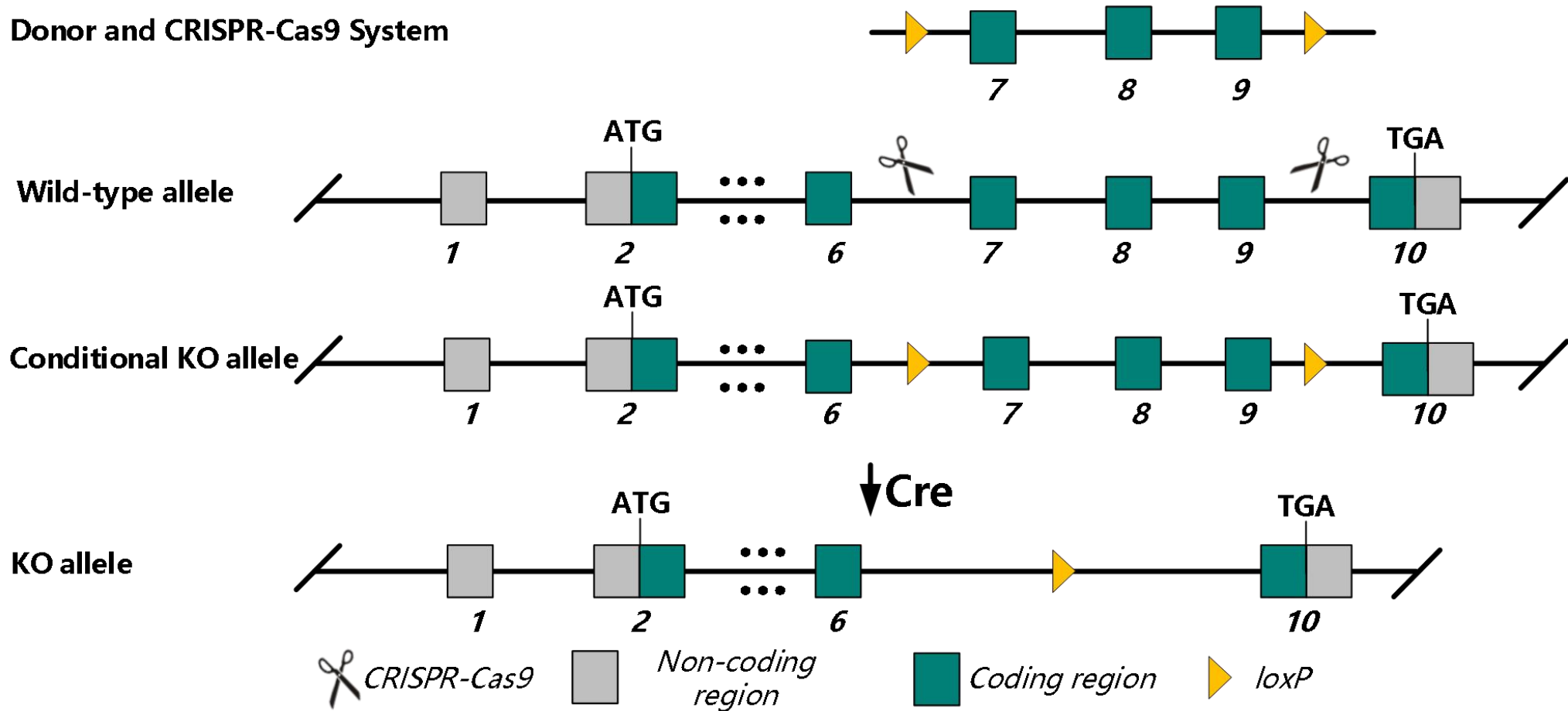
- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy

## Donor and CRISPR-Cas9 System



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

# Technical Information

- The *Rnf43* gene has 9 transcripts. According to the structure of *Rnf43* gene, exon 7-9 of *Rnf43-209* (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: 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

## 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

See Rnf43 in [Genome Data Viewer](#)

Exon count: 11

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

# Transcript Information

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

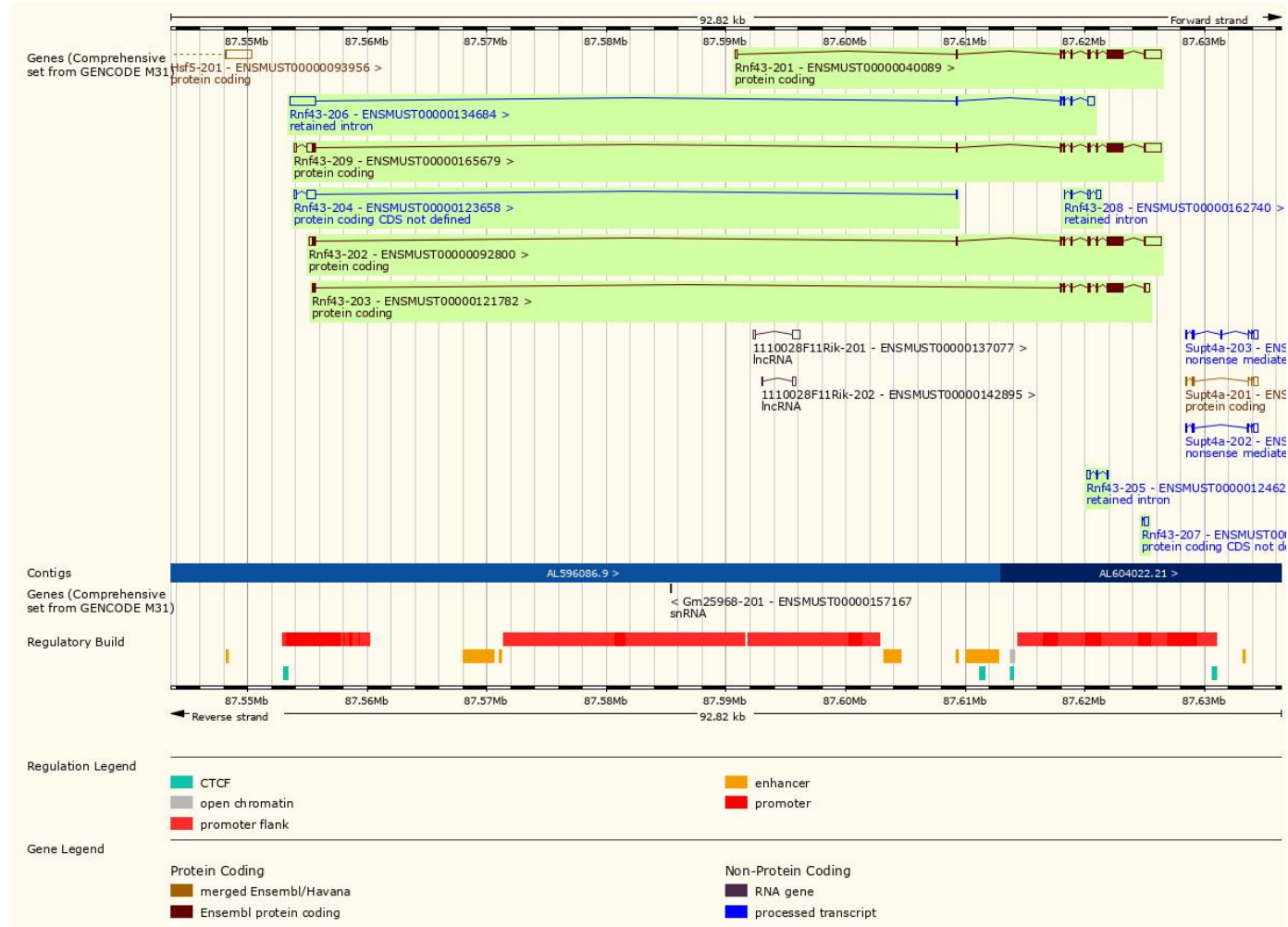
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000165679.8</a>	Rnf43-209	4310	<a href="#">784aa</a>	Protein coding	<a href="#">CCDS25215</a>	<a href="#">Q5NCP0-1</a>	Ensembl Canonical Gencode basic APPRIS P1 TSL:5
<a href="#">ENSMUST00000162740.2</a>	Rnf43-208	704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

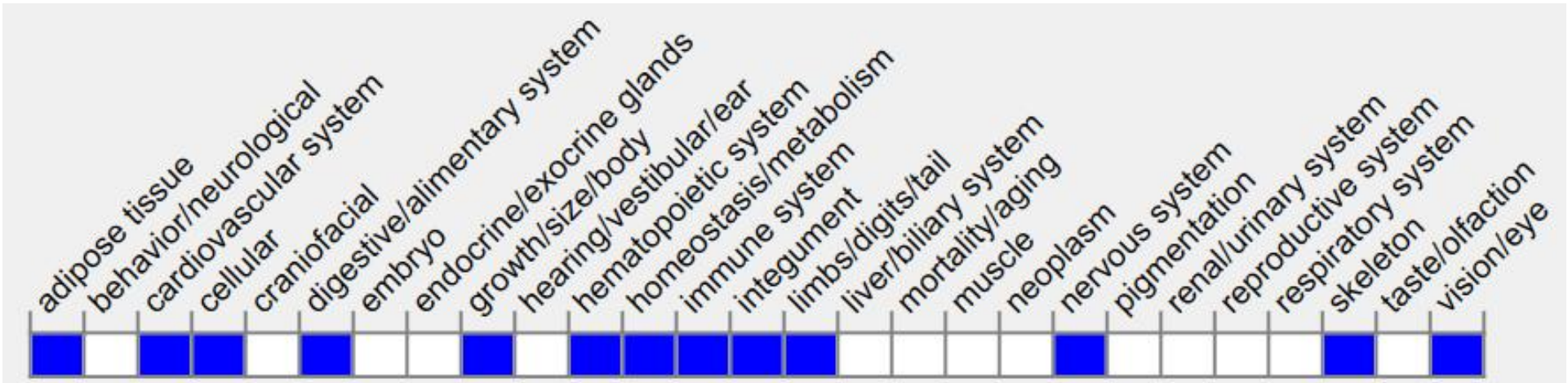
# Genomic Information







# 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 risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.