

# Rnf103 Cas9-CKO Strategy

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# **Project Overview**



**Project Name** 

Rnf103

**Project type** 

Cas9-CKO

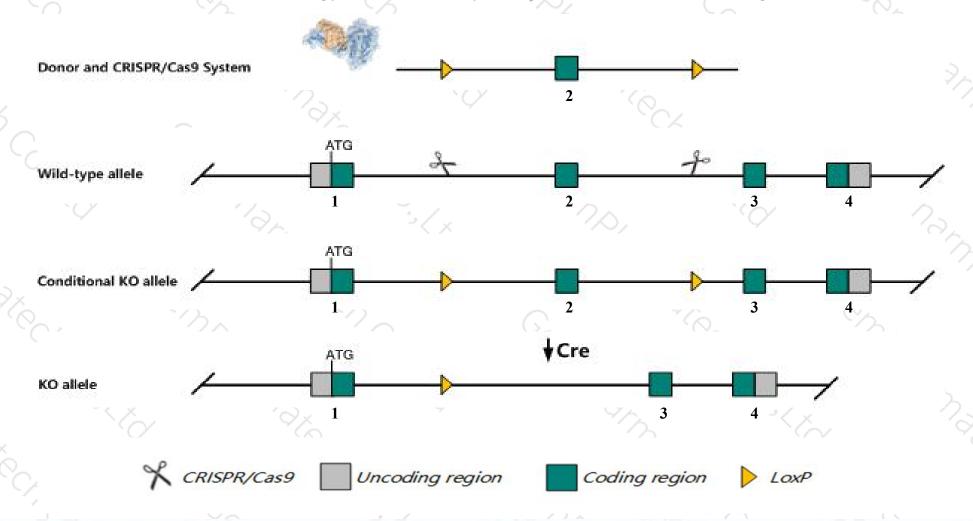
Strain background

C57BL/6JGpt

# Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Rnf103 gene. The schematic diagram is as follows:



### Technical routes



- The *Rnf103* gene has 4 transcripts. According to the structure of *Rnf103* gene, exon2 of *Rnf103-201* (ENSMUST00000064637.10) transcript is recommended as the knockout region. The region contains 140bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Rnf103* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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.

### **Notice**



- ➤ According to the existing MGI data, Mice homozygous for a knock-out allele display significantly increased anxiety-like behavior under stressful conditions as well as increased prepulse inhibition and a reduced startle amplitude with no detectable changes in exploratory locomotion or behavioral despair.
- > The *Rnf103* gene is located on the Chr6. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes 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 existing technological level.

### Gene information (NCBI)



#### Rnf103 ring finger protein 103 [Mus musculus (house mouse)]

Gene ID: 22644, updated on 31-Jan-2019

#### Summary

↑ ?

Official Symbol Rnf103 provided by MGI

Official Full Name ring finger protein 103 provided by MGI

Primary source MGI:MGI:109483

See related Ensembl:ENSMUSG00000052656

Gene type protein coding
RefSeq status REVIEWED
Organism Mus musculus

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as AW146237, AW212918, Zfp103, kf-1

Summary This gene encodes a member of the RING finger family of E3 ubiquitin-protein ligases. These proteins catalyze the transfer of the ubiquitin

protein from a ubiquitin E2 enzyme to a protein substrate. Homozygous knockout mice for this gene exhibit enhanced anxiety-like behavior.

Alternative splicing results in multiple transcript variants. [provided by RefSeq, May 2015]

Expression Ubiquitous expression in colon adult (RPKM 26.1), duodenum adult (RPKM 20.1) and 28 other tissuesSee more

Orthologs <u>human all</u>

# Transcript information (Ensembl)



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

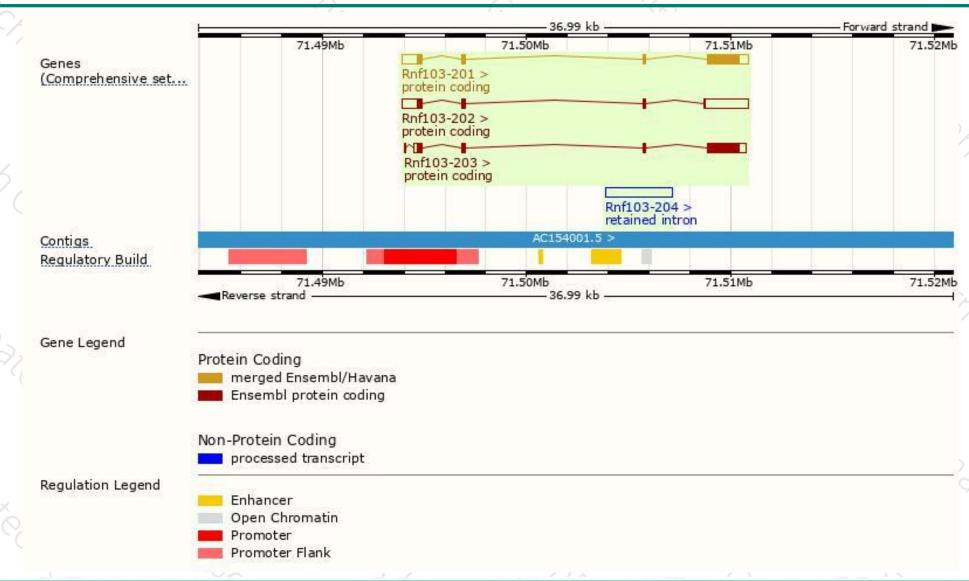
| Name       | Transcript ID         | bp   | Protein      | Biotype         | CCDS      | UniProt | Flags                         |
|------------|-----------------------|------|--------------|-----------------|-----------|---------|-------------------------------|
| Rnf103-201 | ENSMUST00000064637.10 | 3264 | 683aa        | Protein coding  | CCDS39508 | Q9R1W3  | TSL:1 GENCODE basic APPRIS P1 |
| Rnf103-203 | ENSMUST00000114179.2  | 2671 | <u>683aa</u> | Protein coding  | CCDS39508 | Q9R1W3  | TSL:5 GENCODE basic APPRIS P1 |
| Rnf103-202 | ENSMUST00000114178.7  | 3431 | <u>185aa</u> | Protein coding  | 820       | D3Z0Y5  | TSL:1 GENCODE basic           |
| Rnf103-204 | ENSMUST00000150069.2  | 3271 | No protein   | Retained intron | 75        | 2       | TSL:NA                        |

The strategy is based on the design of Rnf103-201 transcript, The transcription is shown below



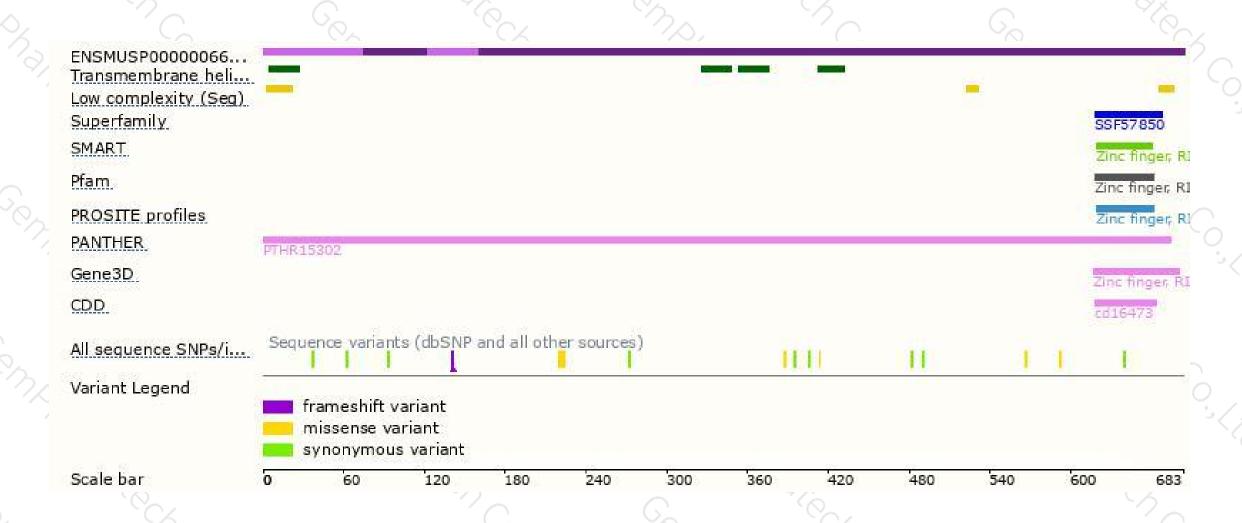
### Genomic location distribution





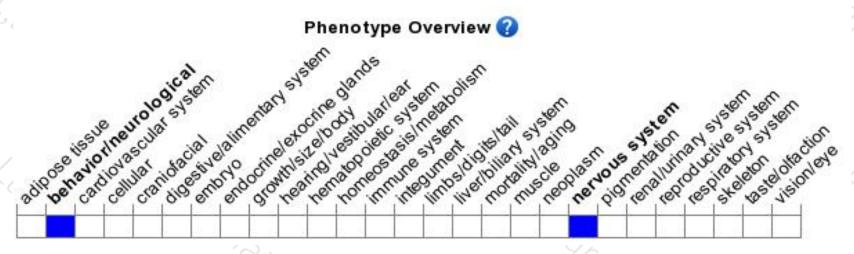
### Protein domain





# Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data, Mice homozygous for a knock-out allele display significantly increased anxiety-like behavior under stressful conditions as well as increased prepulse inhibition and a reduced startle amplitude with a detectable changes in exploratory locomotion or behavioral despair.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





