# *Rnf13* Cas9-KO Strategy

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**Reviewer:** Huan Fan

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# Project Overview

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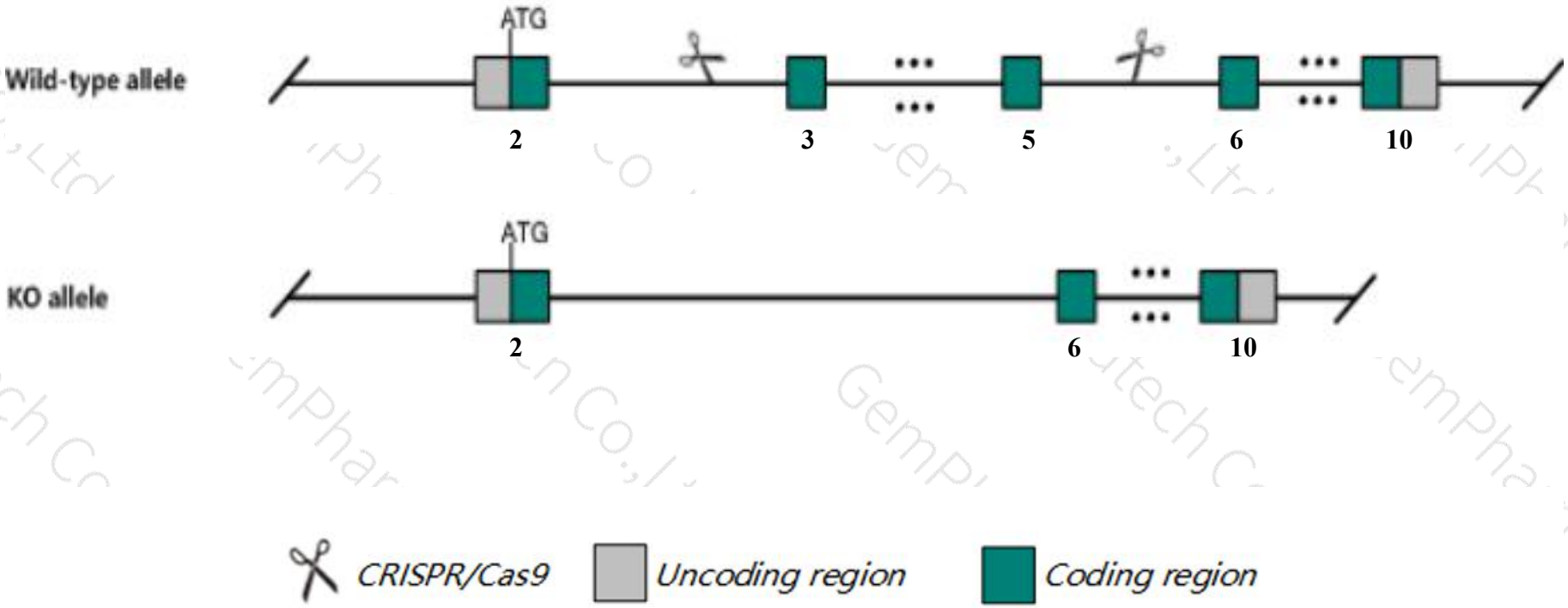
|---|---|
| **Project Name** | ***Rnf13*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf13* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Rnf13* gene has 11 transcripts. According to the structure of *Rnf13* gene, exon3-exon5 of *Rnf13-201* (ENSMUST00000041826.13) transcript is recommended as the knockout region.The region contains 295bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rnf13* gene. The brief process is as follows: CRISPR/Cas9 system

# Notice

- The *Rnf13* gene is located on the Chr3. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information（NCBI）

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## Rnf13 ring finger protein 13 [Mus musculus (house mouse)]

Gene ID: 24017, updated on 13-Mar-2020

### Summary

| | |
|---|---|
| **Official Symbol** | Rnf13 provided by MGI |
| **Official Full Name** | ring finger protein 13 provided by MGI |
| **Primary source** | MGI:MGI:1346341 |
| **See related** | Ensembl:ENSMUSG00000036503 |
| **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** | 2010001H16Rik, Rzf |
| **Summary** | This gene encodes a member of the PA-TM-RING family of proteins that contain a protease associated (PA) domain and a RING finger domain separated by a transmembrane (TM) domain. The encoded protein is an E3 ubiquitin ligase localized to the endosomal-lysosomal vesicles and inner nuclear membrane. Mice lacking the encoded protein have impaired learning abilities associated with a decreased synaptic vesicle density and dysregulated SNARE complex assembly. Alternative splicing of this gene results in multiple transcript variants. A pseudogene for this gene has been identified on the X chromosome. [provided by RefSeq, Jan 2015] |
| **Expression** | Ubiquitous expression in cerebellum adult (RPKM 16.4), bladder adult (RPKM 14.8) and 28 other tissues See more |
| **Orthologs** | human all |

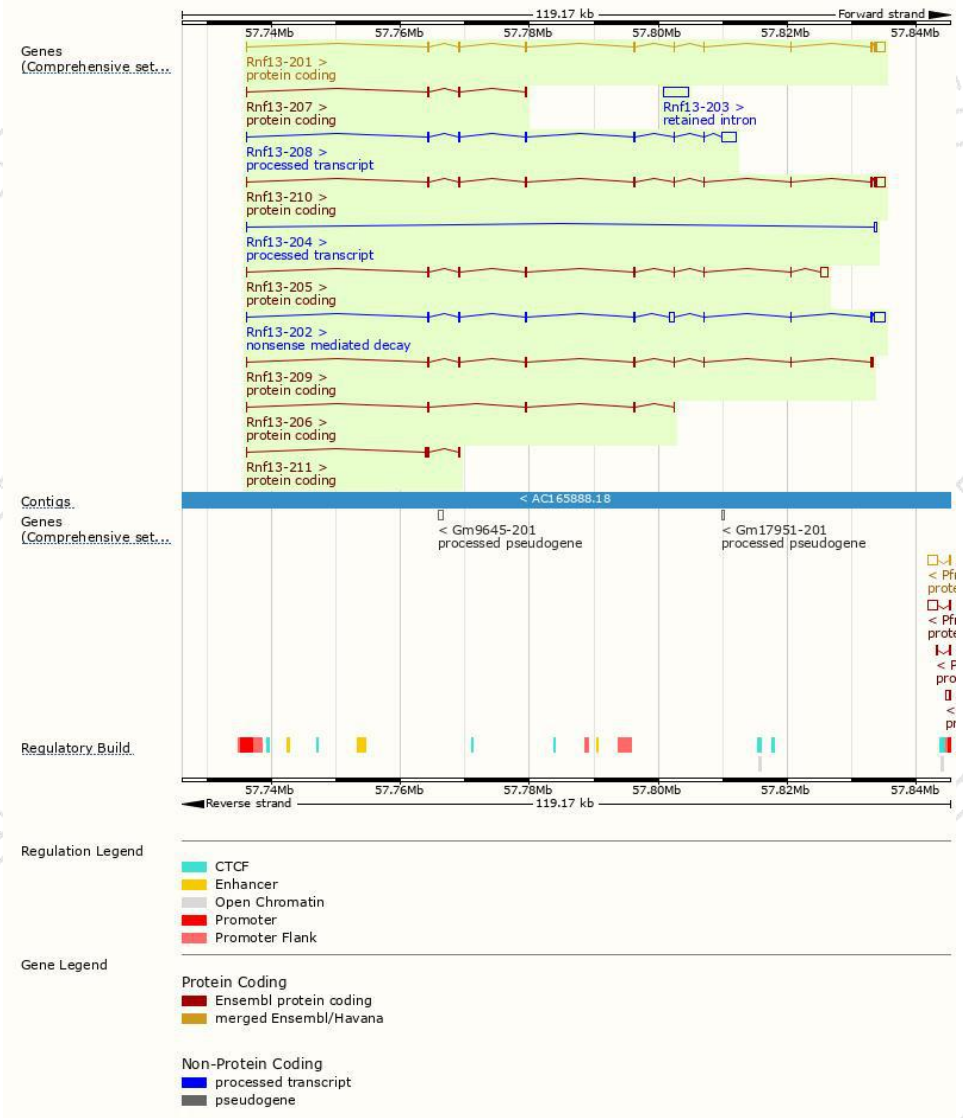
# Transcript information（Ensembl）

The gene has 11 transcripts,all transcripts are shown below:

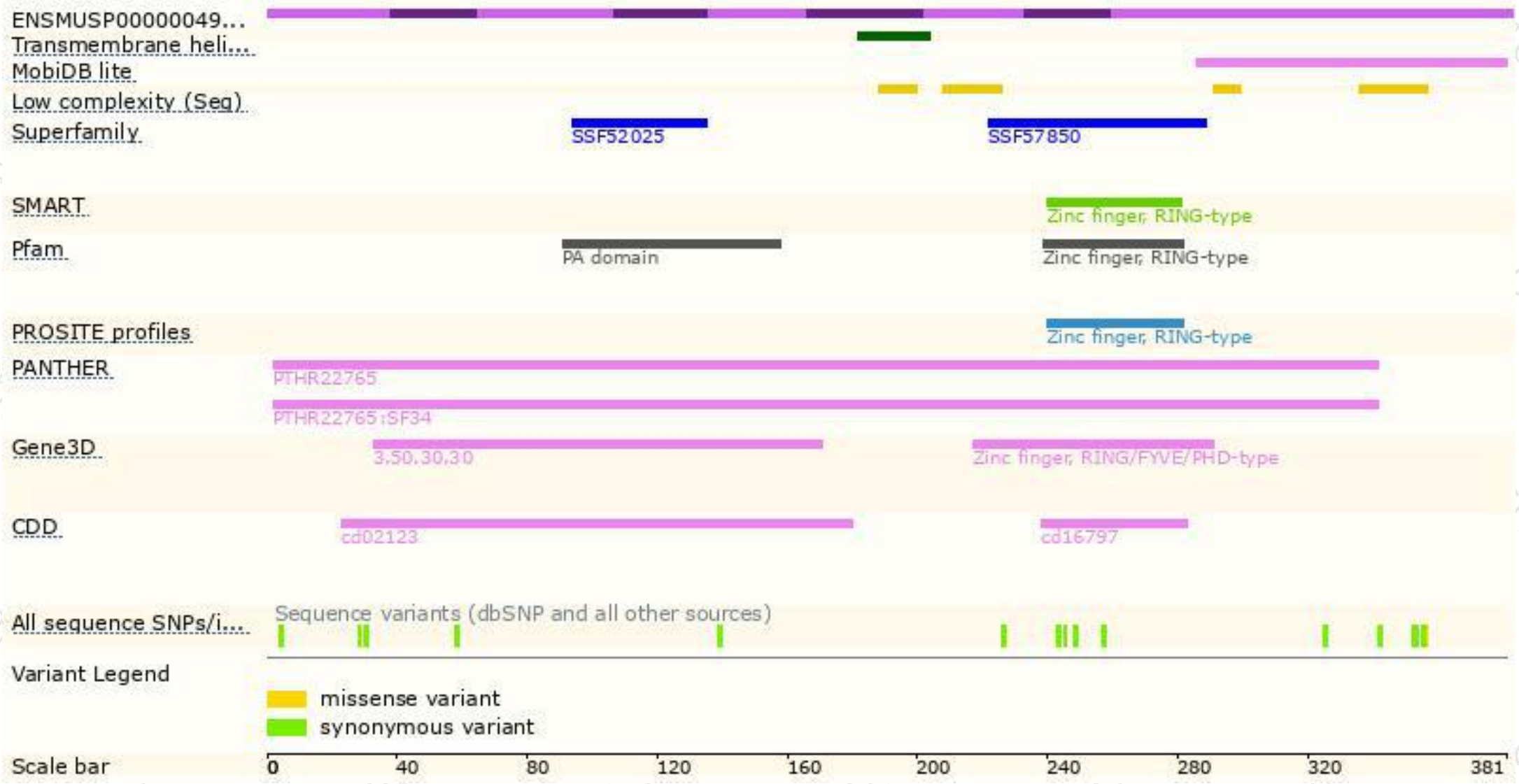
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Rnf13-201 | ENSMUST00000041826.13 | 2678 | 381aa | Protein coding | CCDS50913 | O54965 | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| Rnf13-210 | ENSMUST00000200497.4 | 2573 | 352aa | Protein coding | CCDS84623 | Q8CB78 | TSL:1 GENCODE basic |
| Rnf13-205 | ENSMUST00000198214.4 | 2027 | 244aa | Protein coding | CCDS84622 | Q8C4F9 | TSL:1 GENCODE basic |
| Rnf13-209 | ENSMUST00000199041.1 | 1062 | 268aa | Protein coding | CCDS79910 | O54965 Q3UTG4 | TSL:1 GENCODE basic |
| Rnf13-206 | ENSMUST00000198249.4 | 486 | 131aa | Protein coding | - | A0A0G2JEM4 | CDS 3' incomplete TSL:3 |
| Rnf13-211 | ENSMUST00000200600.4 | 352 | 64aa | Protein coding | - | A0A0G2JE17 | CDS 3' incomplete TSL:3 |
| Rnf13-207 | ENSMUST00000198510.4 | 347 | 96aa | Protein coding | - | A0A0G2JDP6 | CDS 3' incomplete TSL:2 |
| Rnf13-202 | ENSMUST00000197205.4 | 3244 | 166aa | Nonsense mediated decay | - | A0A0G2JGT7 | TSL:1 |
| Rnf13-208 | ENSMUST00000198996.4 | 2848 | No protein | Processed transcript | - | - | TSL:1 |
| Rnf13-204 | ENSMUST00000197920.4 | 435 | No protein | Processed transcript | - | - | TSL:3 |
| Rnf13-203 | ENSMUST00000197783.1 | 3873 | No protein | Retained intron | - | - | TSL:NA |

The strategy is based on the design of *Rnf13-201* transcript,the transcription is shown below:

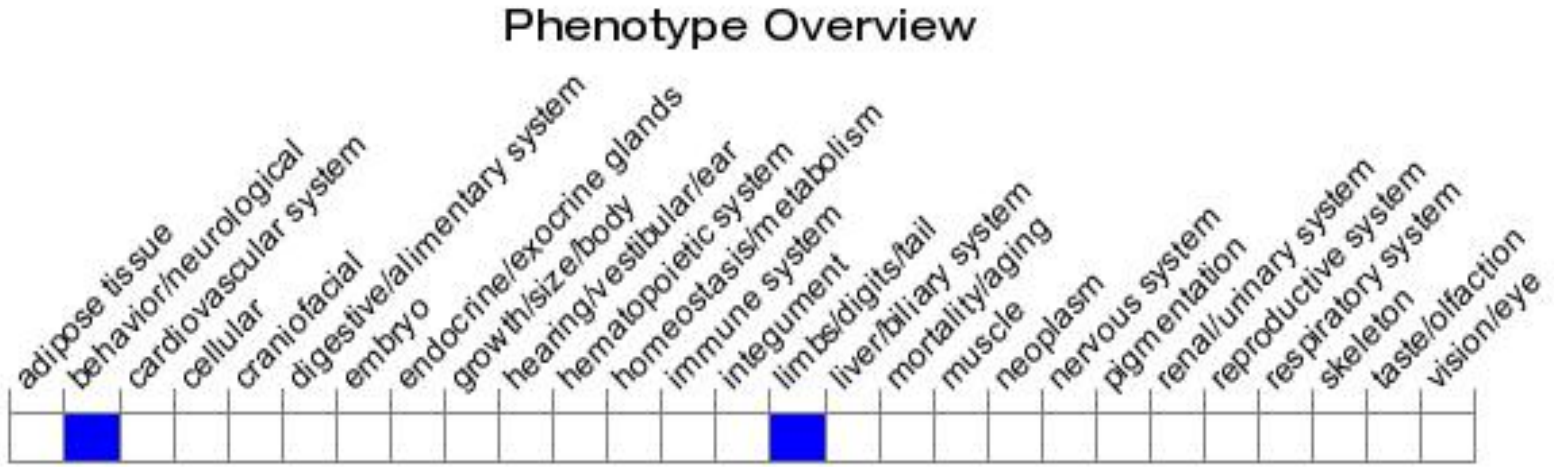
# Genomic location distribution



# 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/).*

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If you have any questions, you are welcome to inquire.

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