

# Rab37 Cas9-CKO Strategy

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# Overview

## Target Gene Name

- Rab37

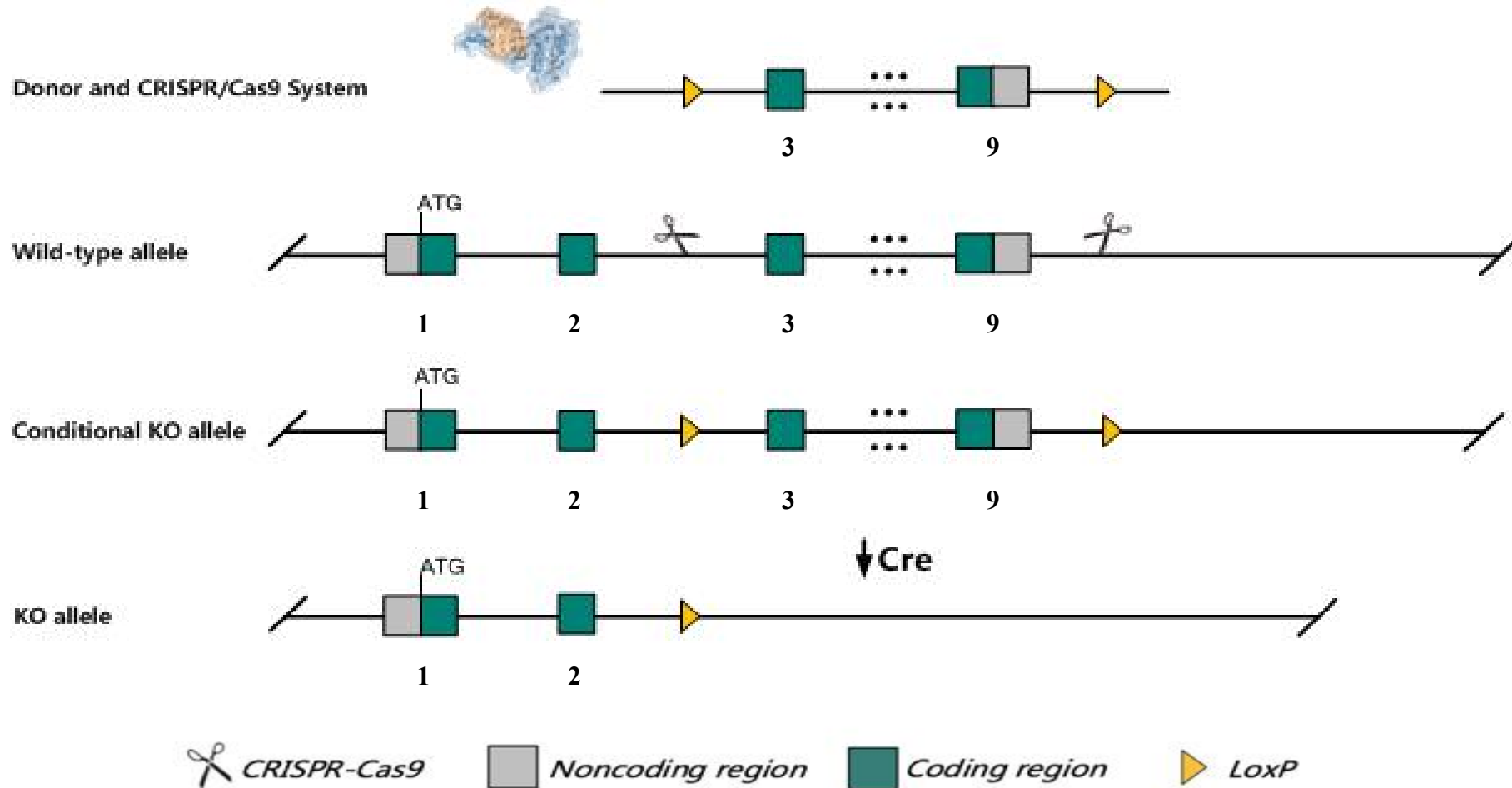
## Project Type

- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Rab37* gene.

# Technical Information

- The *Rab37* gene has 4 transcripts. According to the structure of *Rab37* gene, exon3-exon9 of *Rab37*-201 (ENSMUST00000021076.6) transcript is recommended as the knockout region. The region contains 469bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Rab37* 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

## Rab37 RAB37, member RAS oncogene family [Mus musculus (house mouse)]

Gene ID: 58222, updated on 31-May-2023

### Summary

<b>Official Symbol</b>	Rab37 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	RAB37, member RAS oncogene family provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1929945</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000020732</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	B230331O03Rik, B230354I04Rik
<b>Summary</b>	Predicted to enable GTPase activity. Predicted to act upstream of or within protein transport. Located in secretory granule. Is expressed in brain and retina. Orthologous to human RAB37 (RAB37, member RAS oncogene family). [provided by Alliance of Genome Resources, Apr 2022]
<b>Expression</b>	Broad expression in cerebellum adult (RPKM 5.8), frontal lobe adult (RPKM 3.4) and 16 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

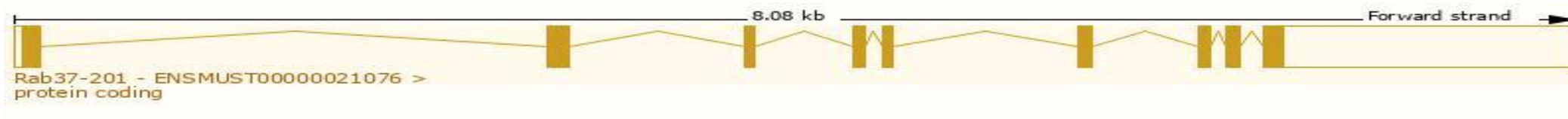
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

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

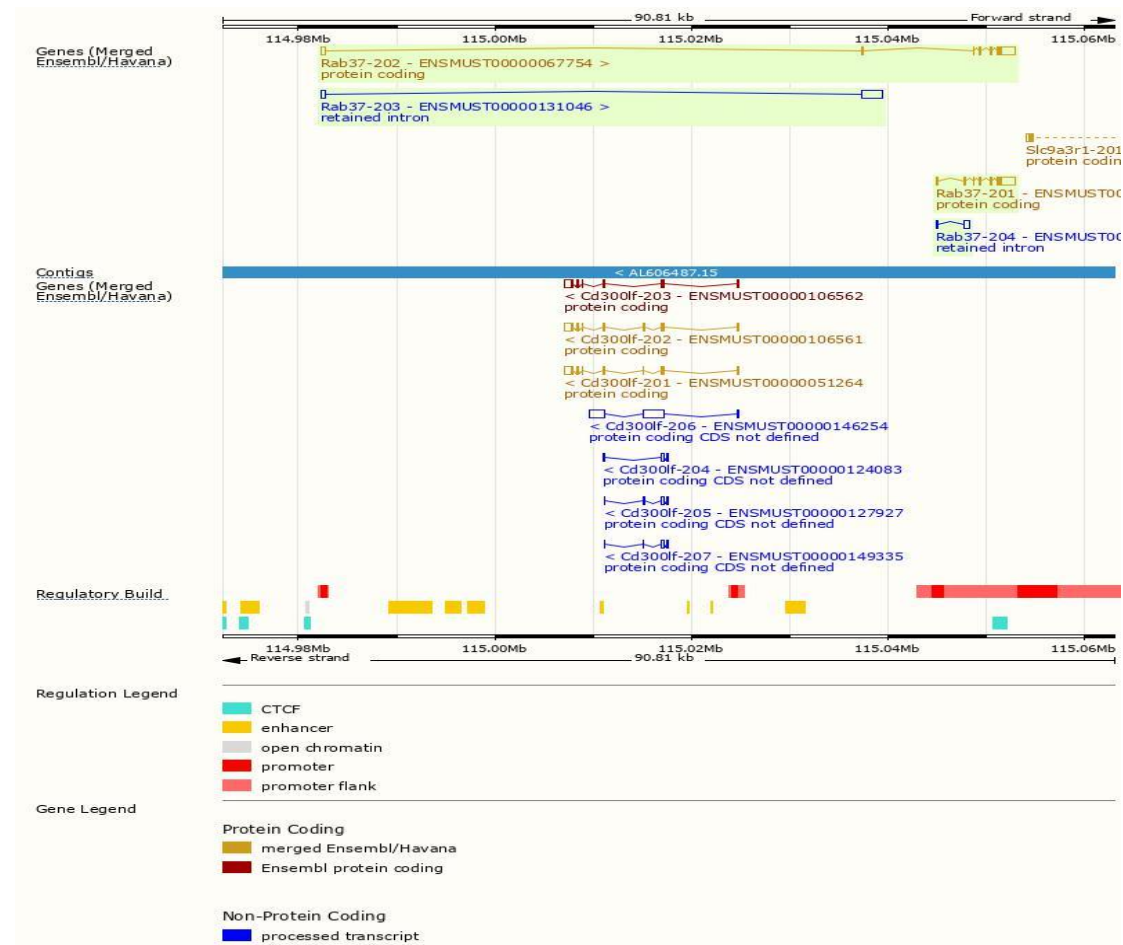
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000021076.6</a>	Rab37-201	2210	<a href="#">223aa</a>	Protein coding	<a href="#">CCDS25620</a>	<a href="#">Q544E8</a>	Ensembl Canonical Gencode basic APPRIS ALT1 TSL:1
<a href="#">ENSMUST00000067754.11</a>	Rab37-202	2577	<a href="#">216aa</a>	Protein coding	<a href="#">CCDS48979</a>	<a href="#">Q8BQX0</a>	Gencode basic APPRIS P4 TSL:1
<a href="#">ENSMUST00000131046.2</a>	Rab37-203	2608	No protein	Retained intron		-	TSL:1
<a href="#">ENSMUST00000156383.2</a>	Rab37-204	712	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Rab37-201* transcript, the transcription is shown below:



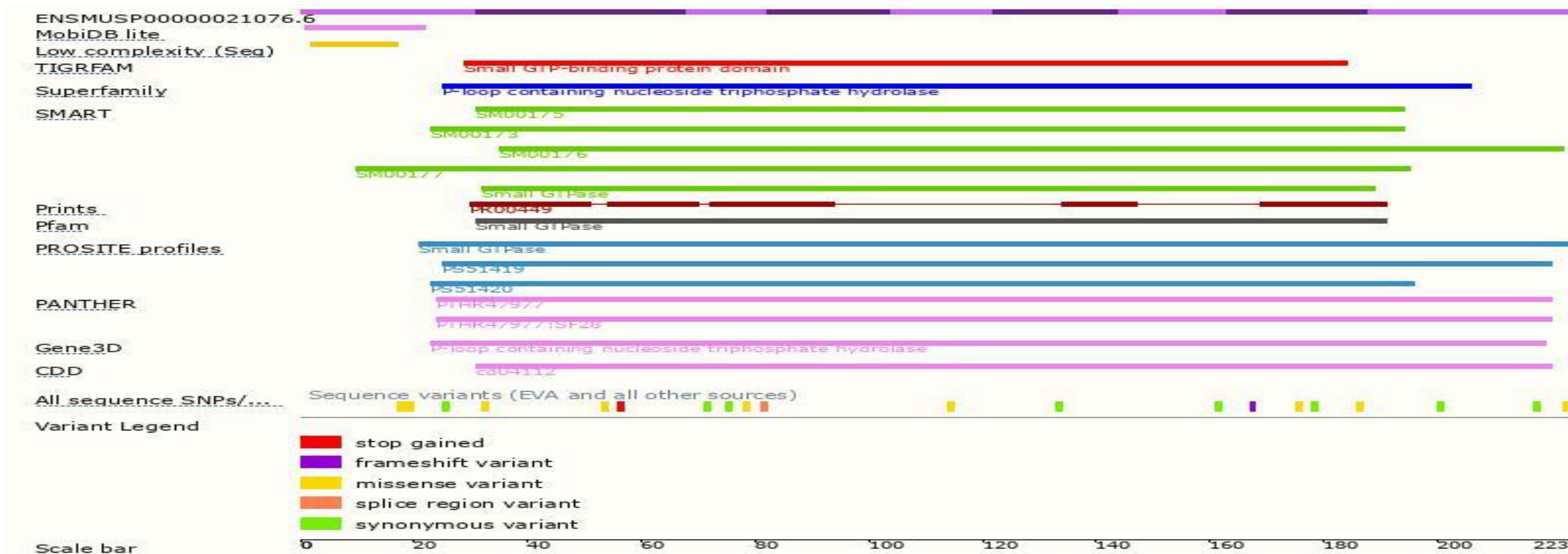
Source: <https://www.ensembl.org>

# Genomic Information



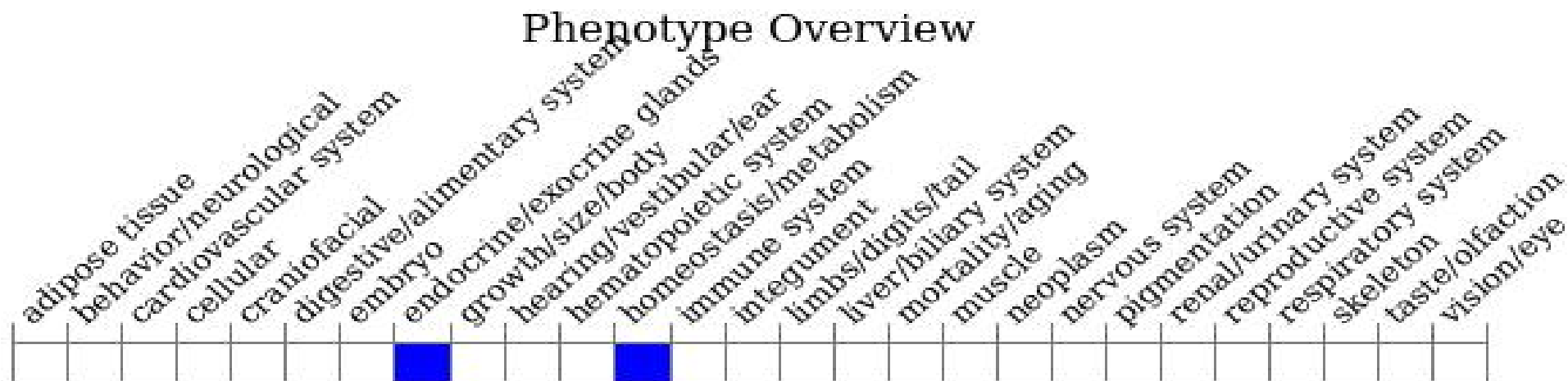


# Protein Information





# Mouse Phenotype Information (MGI)



- Mice homozygous for a null allele exhibit reduced insulin secretion even under high glucose conditions and hyperglycemia.

# Important Information

- The flox region is about 1.1 kb away from the N-terminus of the *Nherf1-201* gene, this strategy may influence the regulatory function of the N-terminal of *Nherf1-201* gene.
- *Rab37* is located on Chr11. 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.