

Rab28 Cas9-CKO Strategy

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Overview

Target Gene Name

- Rab28

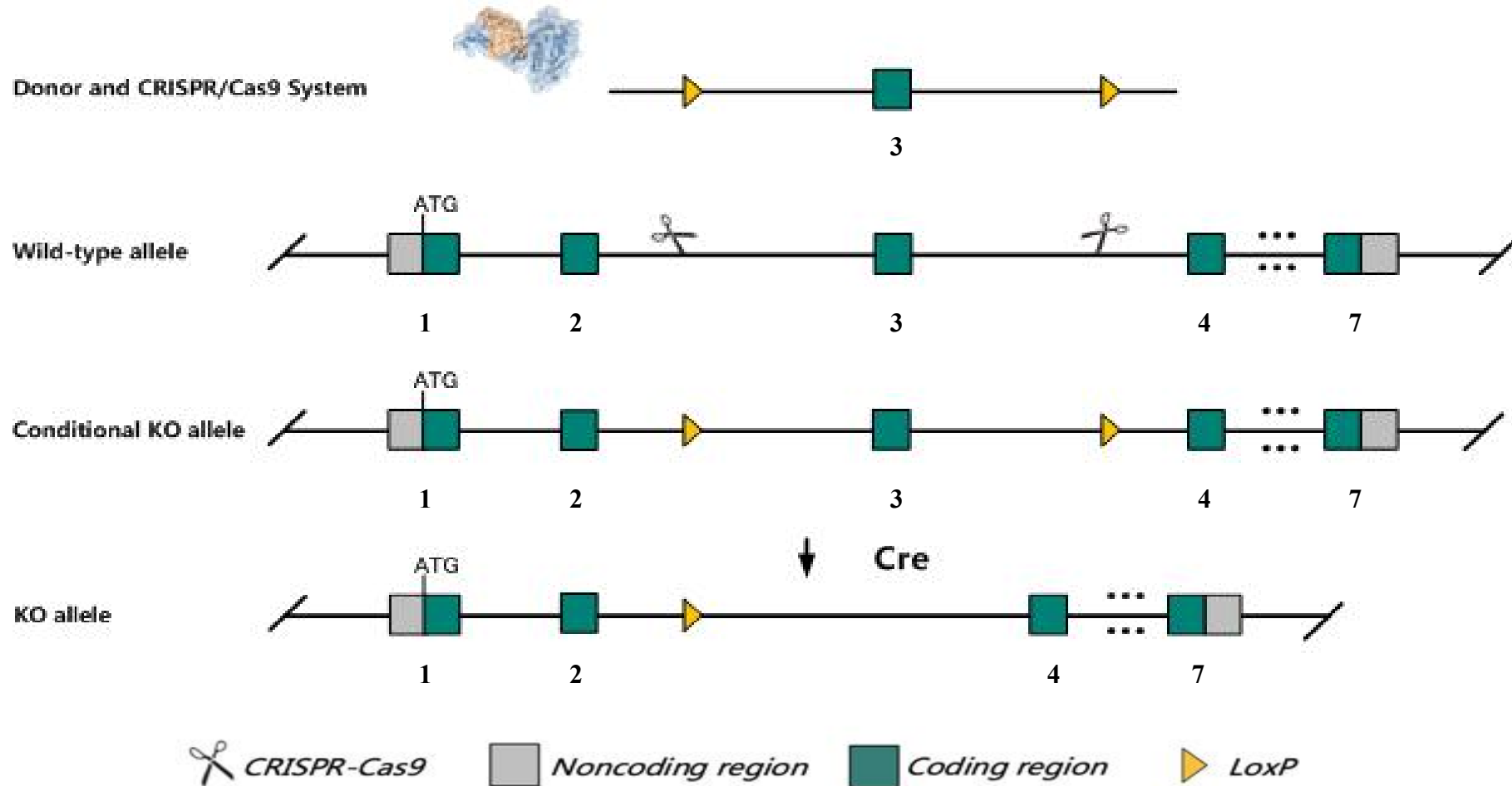
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Rab28* gene.

Technical Information

- The *Rab28* gene has 5 transcripts. According to the structure of *Rab28* gene, exon3 of *Rab28*-201 (ENSMUST00000031011.12) transcript is recommended as the knockout region. The region contains 89bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Rab28* 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

Rab28 RAB28, member RAS oncogene family [*Mus musculus* (house mouse)]

Gene ID: 100972, updated on 15-Apr-2023

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Summary

Official Symbol	Rab28 provided by MGI
Official Full Name	RAB28, member RAS oncogene family provided by MGI
Primary source	MGI:MGI:1917285
See related	Ensembl:ENSMUSG00000029128 AllianceGenome:MGI:1917285
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	2700023P08Rik
Summary	Predicted to enable GDP binding activity; GTP binding activity; and GTPase activity. Acts upstream of or within toxin transport. Predicted to be located in ciliary basal body and ciliary rootlet. Predicted to be active in endomembrane system. Is expressed in bone; digit mesenchyme; and naris. Used to study cone-rod dystrophy 18. Human ortholog(s) of this gene implicated in cone-rod dystrophy 18. Orthologous to human RAB28 (RAB28, member RAS oncogene family). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in adrenal adult (RPKM 18.3), testis adult (RPKM 14.6) and 28 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

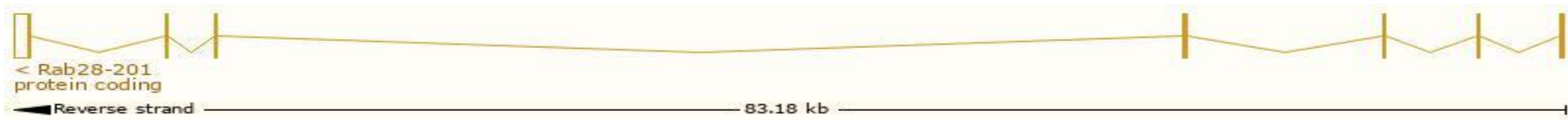
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rab28-203	ENSMUST00000201422.4	1697	220aa	Protein coding	CCDS80272		TSL:5 , GENCODE basic , APPRIS ALT1 ,
Rab28-201	ENSMUST0000031011.12	1635	221aa	Protein coding	CCDS19258		TSL:1 , GENCODE basic , APPRIS P3 ,
Rab28-205	ENSMUST00000202913.2	863	193aa	Protein coding	CCDS80271		TSL:1 , GENCODE basic ,
Rab28-204	ENSMUST00000201473.2	2891	No protein	Retained intron	-		TSL:NA ,
Rab28-202	ENSMUST00000200702.2	646	No protein	Retained intron	-		TSL:2 ,

The strategy is based on the design of *Rab28-201* transcript, the transcription is shown below:

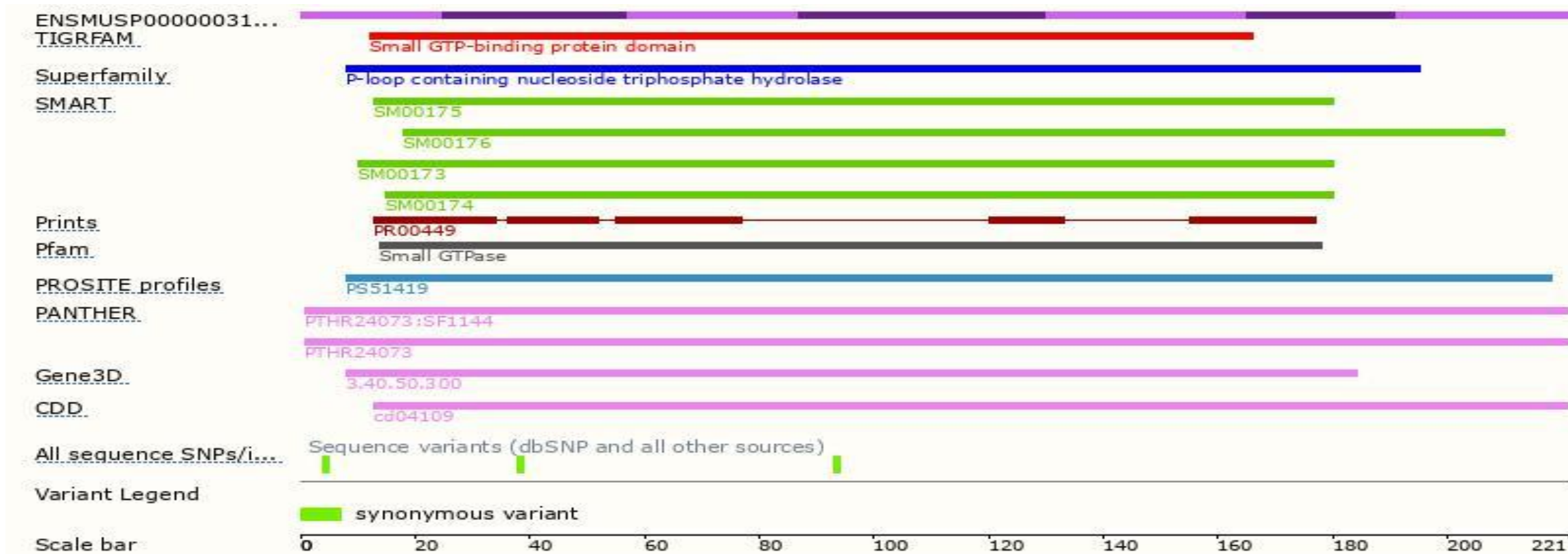


Source: <https://www.ensembl.org>

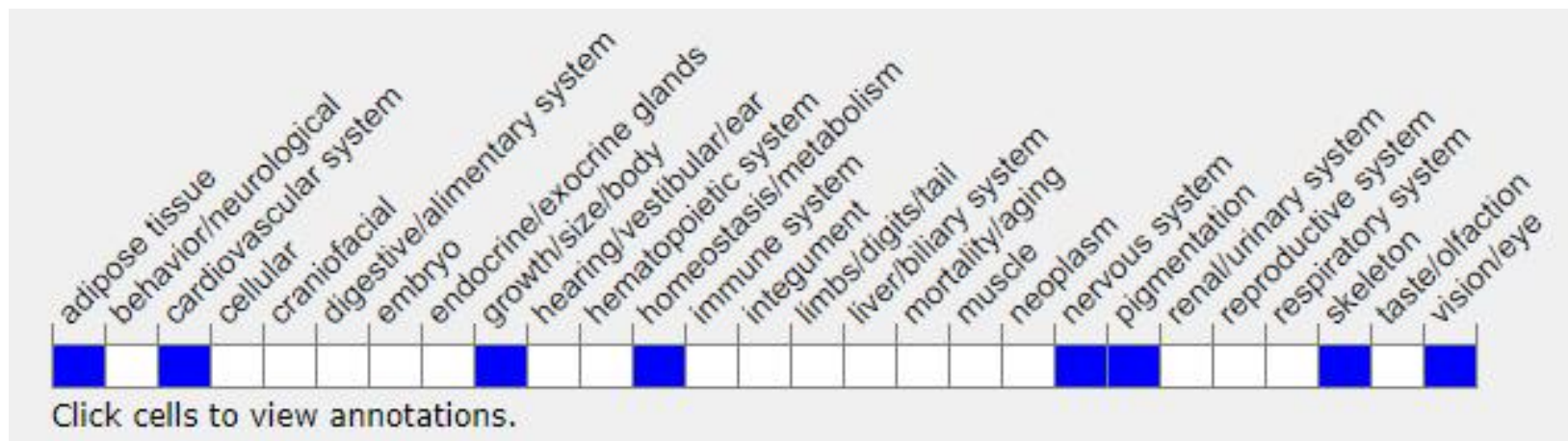
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Homozygous inactivation of this gene leads to reduced cone and rod ERG responses, defects in cone-specific disc shedding and phagocytosis, and progressive retina degeneration.

Important Information

- *Rab28* is located on Chr5. 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.