

# Rab18 Cas9-KO Strategy

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**Reviewer:** Huan Fan

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## **Project Overview**



**Project Name** 

Rab18

**Project type** 

Cas9-KO

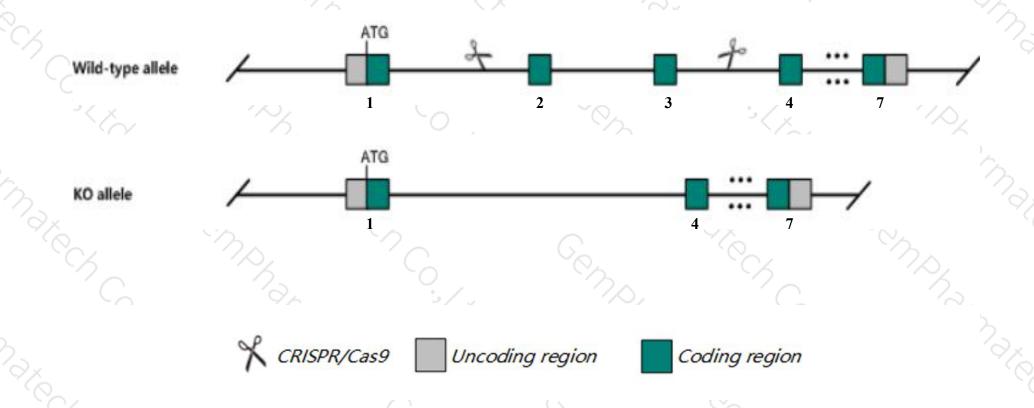
Strain background

C57BL/6JGpt

## **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Rab18* gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *Rab18* gene has 5 transcripts. According to the structure of *Rab18* gene, exon2-exon3 of *Rab18-205*(ENSMUST00000234810.1) transcript is recommended as the knockout region. The region contains 118bp coding sequence.

  Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Rab18* gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



- ➤ According to the existing MGI data, homozygous null mice show partial perinatal lethality and abnormal eye development, and develop nuclear cataracts, atonic pupils, progressive limb weakness, disruption of neuronal cytoskeleton, and accumulation of neurofilament and microtubule proteins in synaptic terminals.
- The *Rab18* gene is located on the Chr18. 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)



#### Rab18 RAB18, member RAS oncogene family [Mus musculus (house mouse)]

Gene ID: 19330, updated on 13-Mar-2020

#### Summary

☆ ?

Official Symbol Rab18 provided by MGI

Official Full Name RAB18, member RAS oncogene family provided by MGI

Primary source MGI:MGI:102790

See related Ensembl: ENSMUSG00000073639

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 AA959686

Summary This gene encodes a member of the Ras-related small GTPases, which regulate membrane trafficking in organelles and transport vesicles. This

protein is expressed predominantly in lipid droplets, organelles that store neutral lipids, and is proposed to play a role in lipolysis and

lipogenesis. In humans mutations in this gene are associated with Warburg micro syndrome type 3. A pseudogene of this gene is located on

chromosome X. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Jun 2013]

Expression Ubiquitous expression in bladder adult (RPKM 20.0), CNS E18 (RPKM 19.1) and 25 other tissuesSee more

Orthologs human all

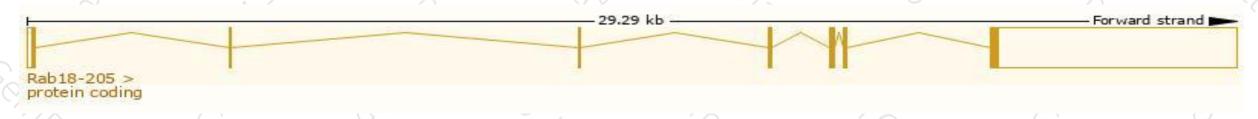
## Transcript information (Ensembl)



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

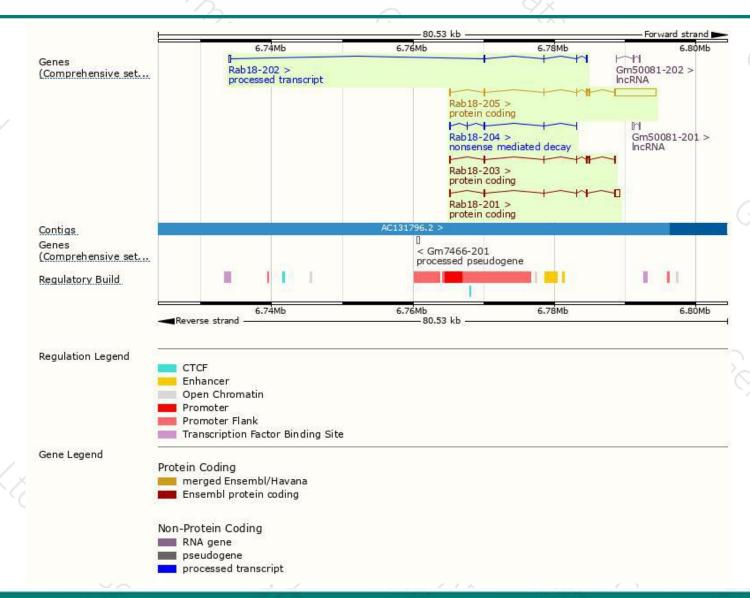
| Name      | Transcript ID        | bp   | Protein      | Biotype                 | CCDS      | UniProt       | Flags   |
|-----------|----------------------|------|--------------|-------------------------|-----------|---------------|---|
| Rab18-205 | ENSMUST00000234810.1 | 6515 | 206aa        | Protein coding          | CCDS29044 | P35293 Q0PD38 | 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 |
| Rab18-201 | ENSMUST00000097680.6 | 1184 | <u>194aa</u> | Protein coding          | -         | A0A452J8C1    | TSL:1 GENCODE basic   |
| Rab18-203 | ENSMUST00000234626.1 | 729  | 212aa        | Protein coding          | -         | A0A3Q4EI12    | GENCODE basic   |
| Rab18-204 | ENSMUST00000234720.1 | 354  | 41aa         | Nonsense mediated decay | -         | A0A3Q4EIF7    |   |
| Rab18-202 | ENSMUST00000234356.1 | 535  | No protein   | Processed transcript    | -         | -             |   |

The strategy is based on the design of *Rab18-205* transcript, the transcription is shown below:



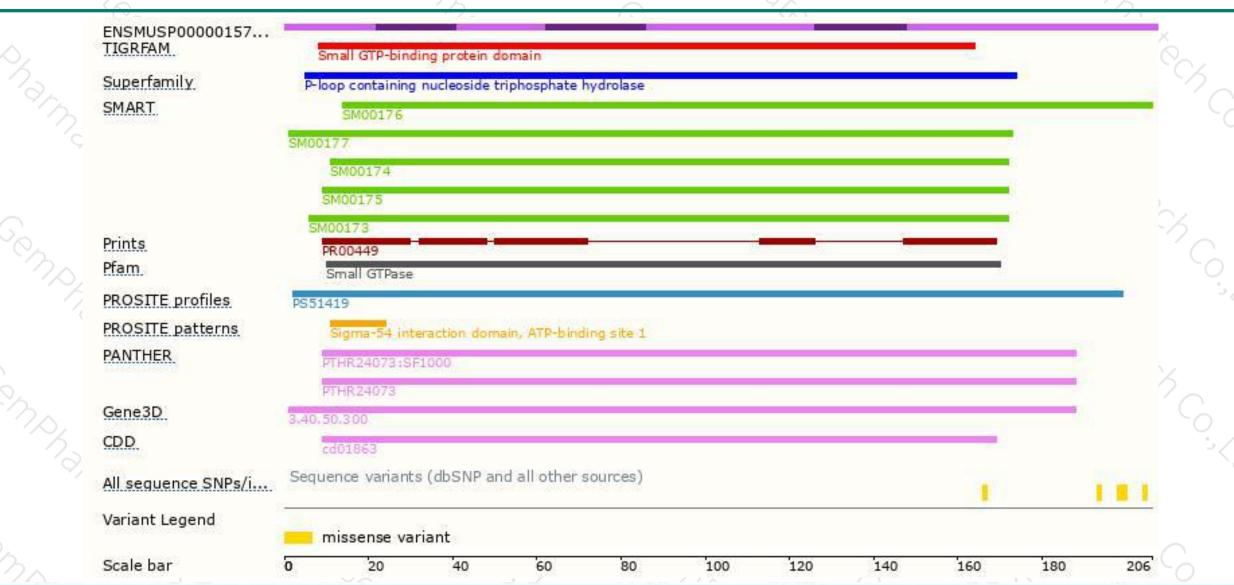
### Genomic location distribution





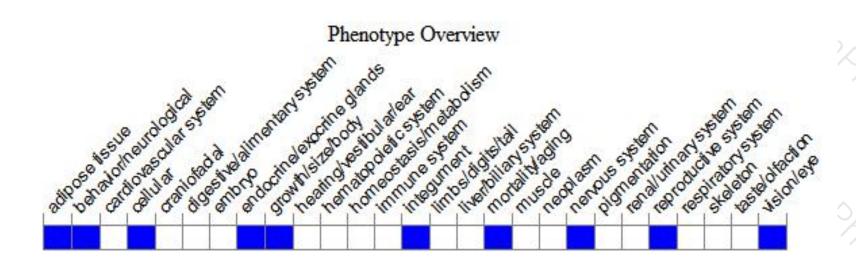
### Protein domain





## 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, homozygous null mice show partial perinatal lethality and abnormal eye development, and develop nuclear cataracts, atonic pupils, progressive limb weakness, disruption of neuronal cytoskeleton, are accumulation of neurofilament and microtubule proteins in synaptic terminals.



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





