

***Rab32* Cas9-CKO Strategy**

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Project Overview

Project Name

Rab32

Project type

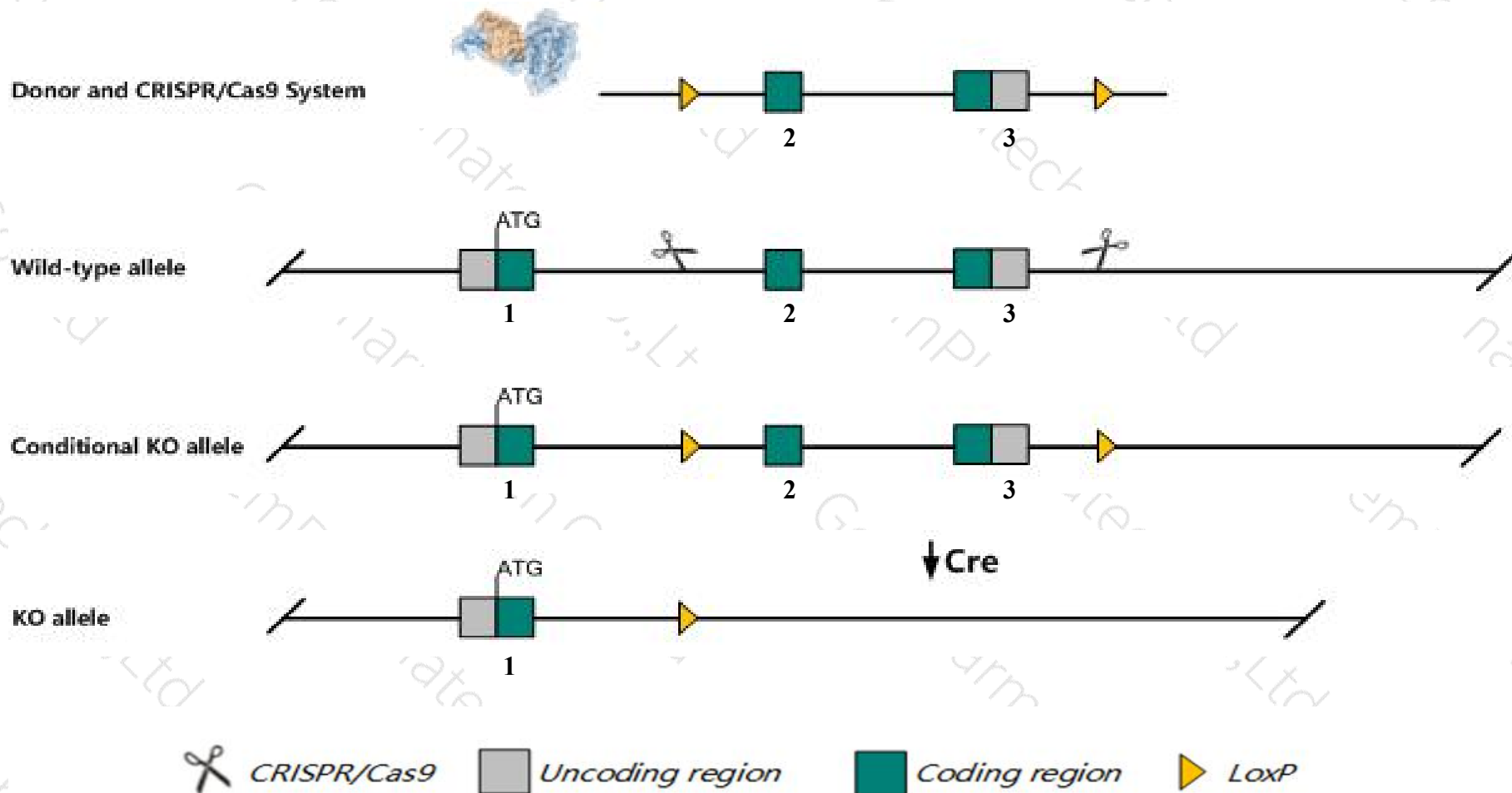
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rab32* gene. The schematic diagram is as follows:



- The *Rab32* gene has 2 transcripts. According to the structure of *Rab32* gene, exon2-exon3 of *Rab32-201* (ENSMUST00000019974.4) transcript is recommended as the knockout region. The region contains 428bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rab32* 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

- The N-terminal of *Rab32* gene will remain 81aa, it may remain the partial function of *Rab32* gene.
- The *Rab32* gene is located on the Chr10. 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)

Rab32 RAB32, member RAS oncogene family [Mus musculus (house mouse)]

Gene ID: 67844, updated on 31-Jan-2019

Summary



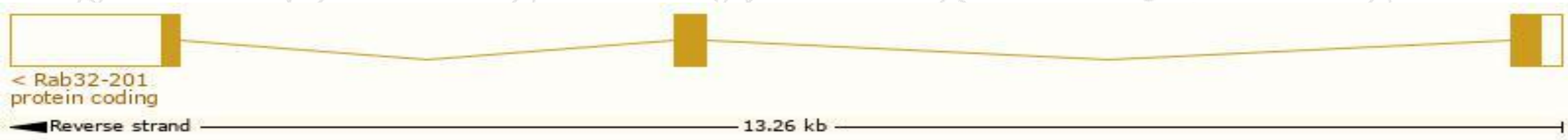
Official Symbol	Rab32 provided by MGI
Official Full Name	RAB32, member RAS oncogene family provided by MGI
Primary source	MGI:MGI:1915094
See related	Ensembl:ENSMUSG00000019832
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810011A17Rik, AU022057
Expression	Ubiquitous expression in subcutaneous fat pad adult (RPKM 13.2), liver adult (RPKM 10.4) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

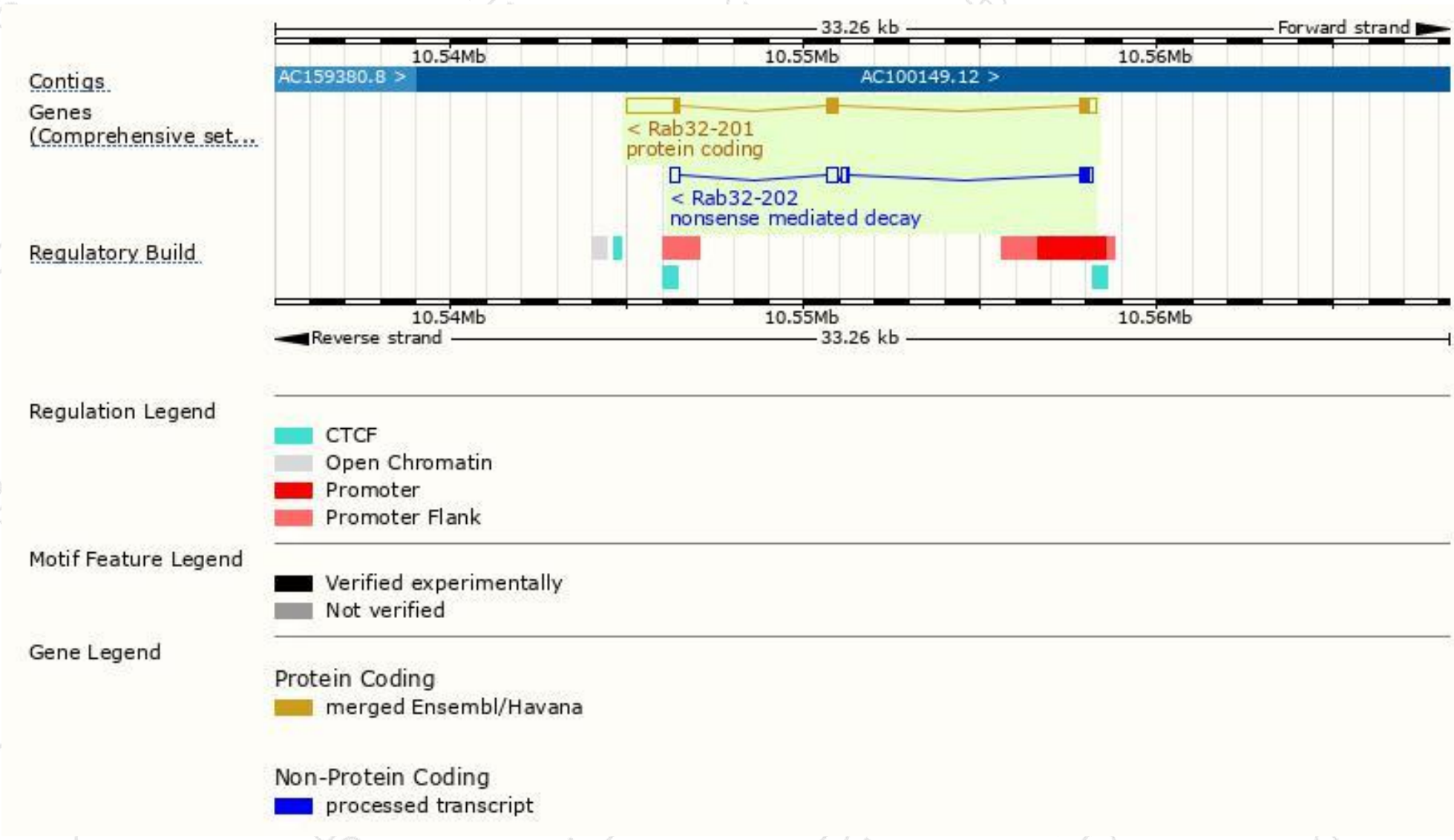
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rab32-201	ENSMUST00000019974.4	2149	223aa	Protein coding	CCDS23695	Q0PD23 Q9CZE3	TSL:1 GENCODE basic APPRIS P1
Rab32-202	ENSMUST00000220018.2	1062	100aa	Nonsense mediated decay	-	A0A1Y7VIZ0	TSL:5

The strategy is based on the design of *Rab32-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000019...

Conserved Domains

hmmpantther

PTHR24073:SF862

PTHR24073

TIGRFAM domain

Small GTP-binding protein domain

Superfamily domains

P-loop containing nucleoside triphosphate hydrolase

SMART domains

SM00173

SM00175

SM00176

SM00174

Prints domain

PR00449

Pfam domain

Small GTPase superfamily

PROSITE profiles

PS51419

Gene3D

3.40.50.300

All sequence SNPs/i...

Sequence variants (dbSNP and all other sources)

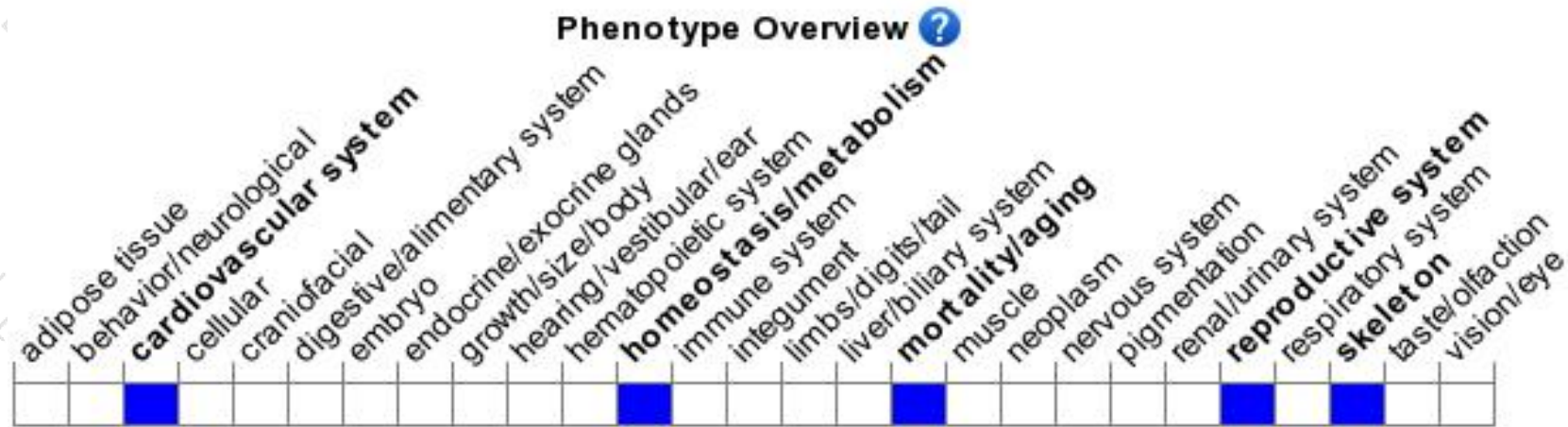
Variant Legend

-  missense variant
-  synonymous variant

Scale bar

0 20 40 60 80 100 120 140 160 180 200 223

Mouse phenotype description(MGI)



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

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

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