

Rab30 Cas9-CKO Strategy

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Design Date: 2023-10-09

Overview

Target Gene Name

• Rab30

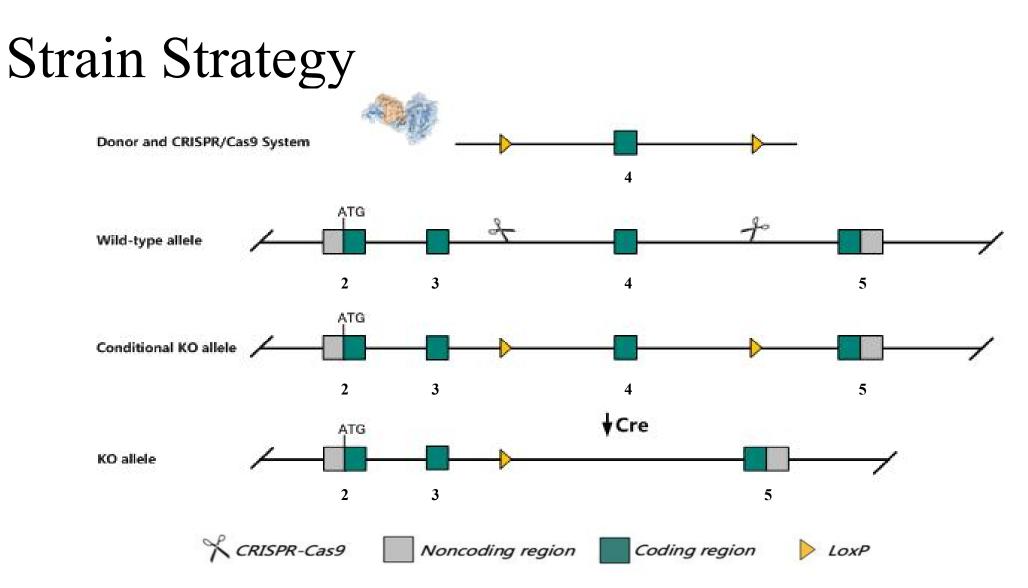
Project Type

• Cas9-CKO

Genetic Background

• C57BL/6JGpt





Schematic representation of CRISPR-Cas9 engineering used to edit the Rab30 gene.

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Technical Information

- The *Rab30* gene has 5 transcripts. According to the structure of *Rab30* gene, exon4 of *Rab30*-201 (ENSMUST0000032879.15) transcript is recommended as the knockout region. The region contains 184bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Rab30* 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.

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Gene Information

Rab30 RAB30, member RAS oncogene family [Mus musculus (house mouse)]

Gene ID: 75985, updated on 25-Sep-2020

Summary

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Official Symbol	Rab30 provided by MGI
Official Full Name	RAB30, member RAS oncogene family provided by MGI
Primary source	MGI:MGI:1923235
See related	Ensembl:ENSMUSG0000030643
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	5033421K01Rik, AI323892, Rsb30
Expression	Broad expression in cerebellum adult (RPKM 3.5), CNS E18 (RPKM 2.7) and 20 other tissuesSee more
Orthologs	human all

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		
Rab30-201	ENSMUST0000032879.15	9456	<u>203aa</u>	Protein coding	CCDS21450		TSL:1, GENCODE basic, APPRIS P1,		
Rab30-203	ENSMUST00000107180.8	1406	<u>203aa</u>	Protein coding	CCDS21450		TSL:1, GENCODE basic, APPRIS P1,		
Rab30-202	ENSMUST00000107179.2	1304	<u>175aa</u>	Protein coding	-		TSL:5 , GENCODE basic ,		
Rab30-205	ENSMUST00000208945.2	437	<u>107aa</u>	Protein coding	-		CDS 3' incomplete , TSL:3 ,		
Rab30-204	ENSMUST00000208470.2	436	No protein	Processed transcript	-		TSL:3 ,		

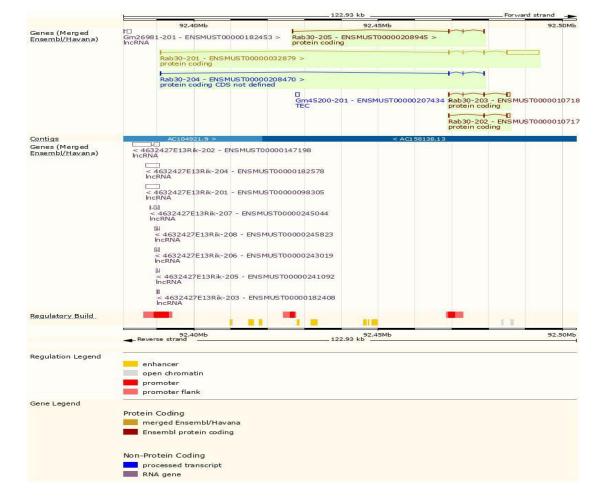
The strategy is based on the design of *Rab30*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



Genomic Information



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

Protein Information

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ENSMUSP0000032879	9.8		1911								
AFDB-ENSP mappings	17 <u>1</u>										
TIGREAM	Small GIP-bit	nding protein	domain								
Superfamily	P-loop containing	nucleoside tri	phosphate h	ydrolase							
SMART	SIGIDIDE 7 5										
	SIMIPIDE 7 S										
	SM0D175										
	Small GIPas	e									
Prints	PR00449										
Pfam	Small GIPase	2 000									
PROSITE profiles	Small G1Pase										
	PS51419										
	PS51420										
PANTHER	PTHR47977										
	PIRR42977:SF4										
Gene3D	P-loop containing n	ucleoside tripi	nosphate hyd	Irolase							
CDD	Rab30										
All sequence SNPs/	Sequence variant	s (EVA and a	all other sou	rces)							
Variant Legend											
	splice accep	tor variant									
	stop gained										
	frameshift v	ariant									
	start lost										
	missense va	riant									
	splice polyp	yrimidine tra	act variant								
	synonymous	s variant									
Scale bar	b 20	40	<i>,</i> eo	80	100	120	140	160	180	203	

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

Important Information

- *Rab30* is located on Chr7. 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.

