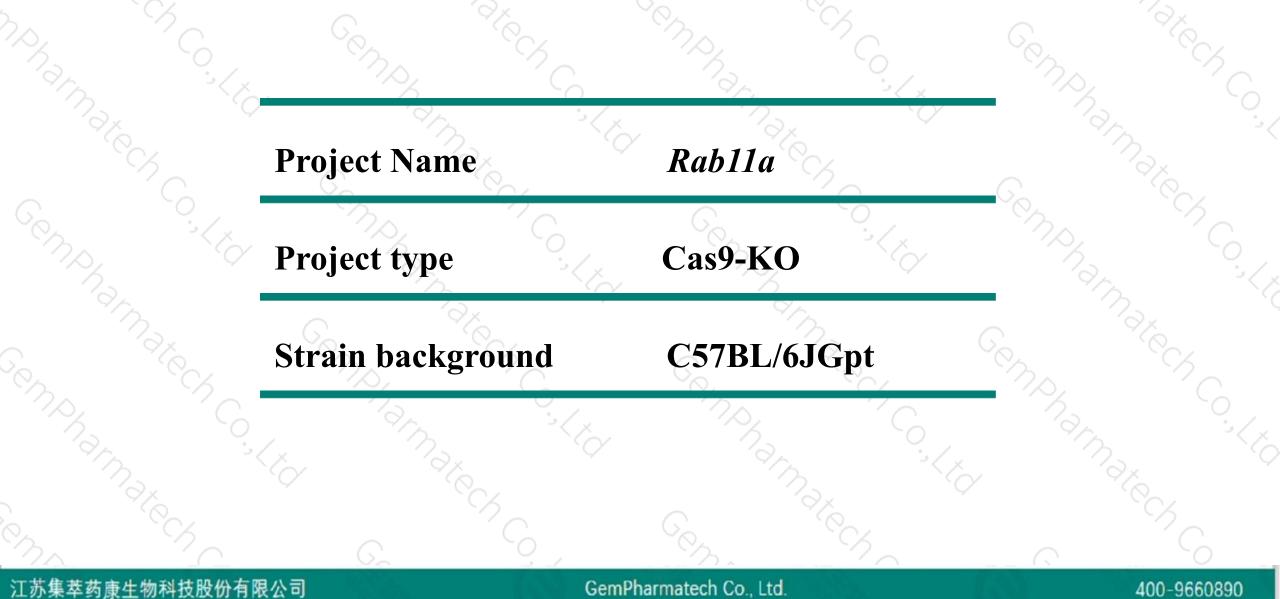


# Rab11a Cas9-KO Strategy

Designer: Reviewer: Design Date: Ruirui Zhang Huimin Su 2020-2-25

## **Project Overview**

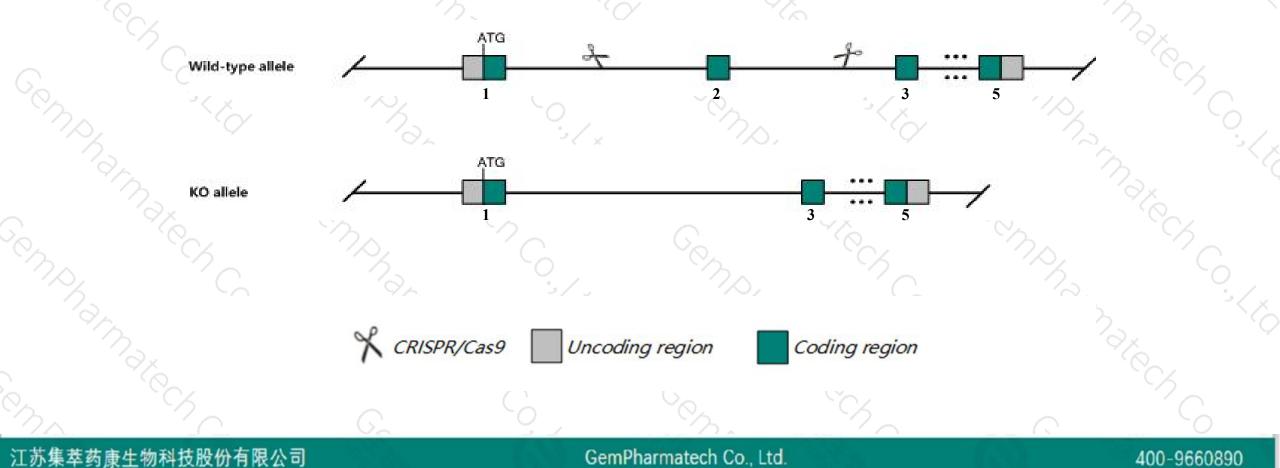




# **Knockout** strategy



This model will use CRISPR/Cas9 technology to edit the *Rab11a* gene. The schematic diagram is as follows:





- The Rab11a gene has 9 transcripts. According to the structure of Rab11a gene, exon2 of Rab11a-208 (ENSMUST00000172298.7) transcript is recommended as the knockout region. The region contains 196bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Rab11a gene. The brief process is as follows: CRISPR/Cas9 system



- According to the existing MGI data, mice homozygous for a knock-out allele exhibit decreased embryo size, a rudimentary egg cylinder, failure of primitive streak formation, absent primitive node and head folds, failure to gastrulate, and complete lethality prior to organogenesis.
- Transcript Rab11a-204,205,207 may not be affected.
- The Rab11a gene is located on the Chr9. 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.

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# **Gene information (NCBI)**



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#### Rab11a RAB11A, member RAS oncogene family [ Mus musculus (house mouse) ]

Gene ID: 53869, updated on 10-Dec-2019

#### Summary

**Official Symbol** Rab11a provided by MGI **Official Full Name** RAB11A, member RAS oncogene family provided by MGI Primary source MGI:MGI:1858202 Ensembl:ENSMUSG0000004771 See related 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

Expression Ubiquitous expression in CNS E18 (RPKM 50.9), bladder adult (RPKM 49.3) and 28 other tissues See more

Orthologs human all

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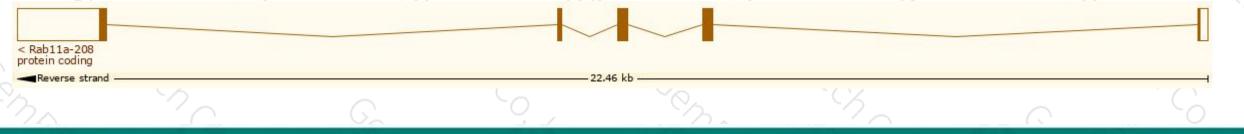
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# **Transcript information (Ensembl)**



Name 🍦	Transcript ID 👙	bp 🖕	Protein 🖕	Biotype 🔺	CCDS 🍦	UniProt 🖕	Flags	
Rab11a-209	ENSMUST00000172444.1	603	No protein	Retained intron	8.7	-	TSL:1	
Rab11a-208	ENSMUST00000172298.7	2336	<u>216aa</u>	Protein coding	<u>CCDS23282</u>	P62492 & Q0PD45 &	TSL:1 GENCODE basic APPRIS P1	
Rab11a-204	ENSMUST00000167569.7	726	<u>86aa</u>	Protein coding	877	<u>E9Q6B3</u>	TSL:3 GENCODE basic	
Rab11a-201	ENSMUST0000004892.6	595	<u>155aa</u>	Protein coding	-	F8WGS1	CDS 3' incomplete TSL:5	
Rab11a-207	ENSMUST00000171100.1	508	<u>80aa</u>	Protein coding	87	<u>E9PZB2</u>	CDS 3' incomplete TSL:2	
Rab11a-205	ENSMUST00000168366.1	500	<u>87aa</u>	Protein coding	-	F6R2Z5 🗗	CDS 5' incomplete TSL:3	
Rab11a-206	ENSMUST00000169058.7	462	<u>153aa</u>	Protein coding	877	<u>E9Q3P9</u> &	TSL:5 GENCODE basic	
Rab11a-202	ENSMUST00000165083.1	695	No protein	Processed transcript	t -	-	TSL:5	
Rab11a-203	ENSMUST00000166857.1	397	No protein	Processed transcript	t -		TSL:3	

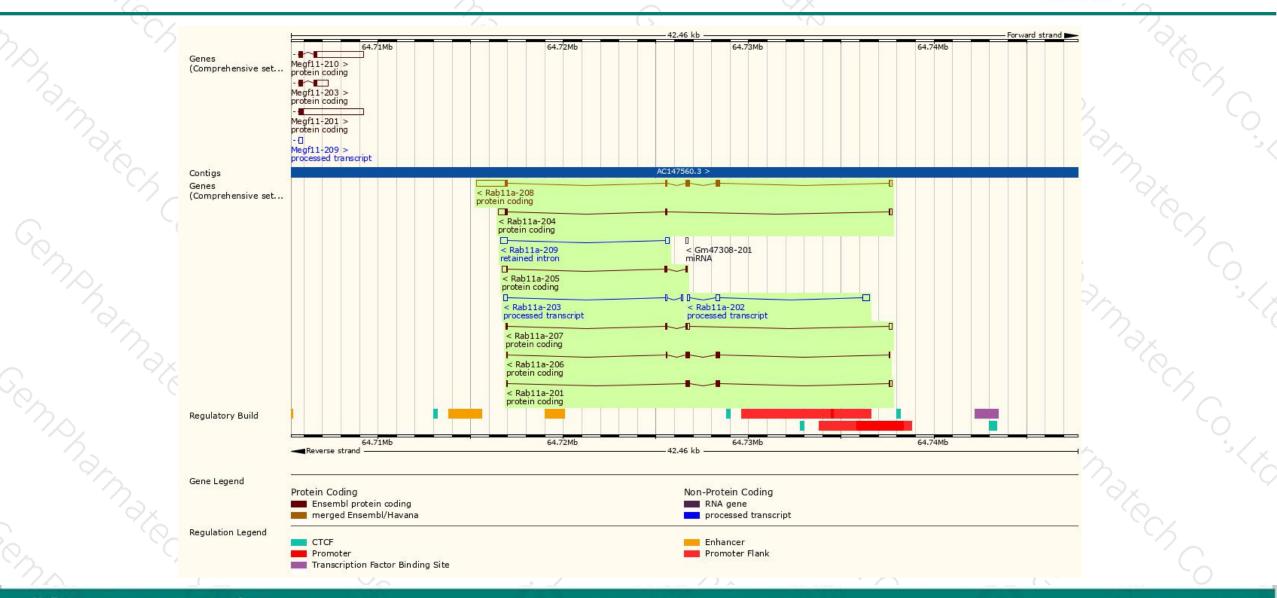
The strategy is based on the design of *Rab11a-208* transcript, the transcription is shown below:



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### **Genomic location distribution**



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400-9660890

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## **Protein domain**



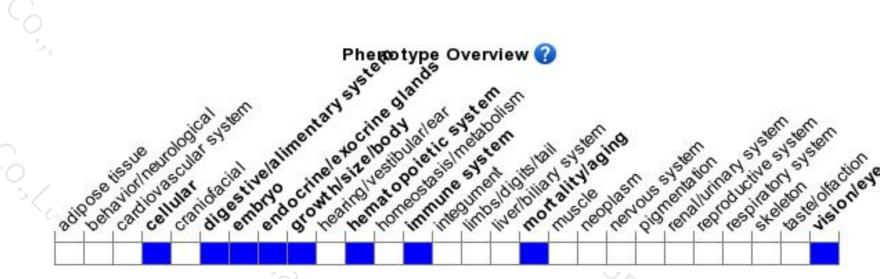
ENSMUSP00000129		N. Such	n. der de					1
TIGRFAM	Small GTP-binding	ı protein domain					- 1	
Superfamily	P-loop containing nuc	leoside triphosphate hydro	lase					
SMART	SM00173							
	SM00174							
	SM00175							
	SM00176				<u>a a</u>			
Prints Pfam	PR00449				20 x0	1997 - 1997 - 1997 - 1997 - 1997 - 1997 - 1997 - 1997 - 1997 - 1997 - 1997 - 1997 - 1997 - 1997 - 1997 - 1997 -		
	Small GTPase							
PROSITE profiles	PS51419							
PANTHER	PTHR24073;SF625							
	PTHR24073							
Gene3D	3.40.50.300							
CDD	cd01868						-	
All sequence SNPs/i	Sequence variants (dbSI	NP and all other sources)						
Variant Legend	missense variant							
Scale bar	0 20	40	60 80	100	synonymous vari 120	140 160	180	216
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### 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, mice homozygous for a knock-out allele exhibit decreased embryo size, a rudimentary egg cylinder, failure of primitive streak formation, absent primitive node and head folds, failure to gastrulate, and complete lethality prior to organogenesis.

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



