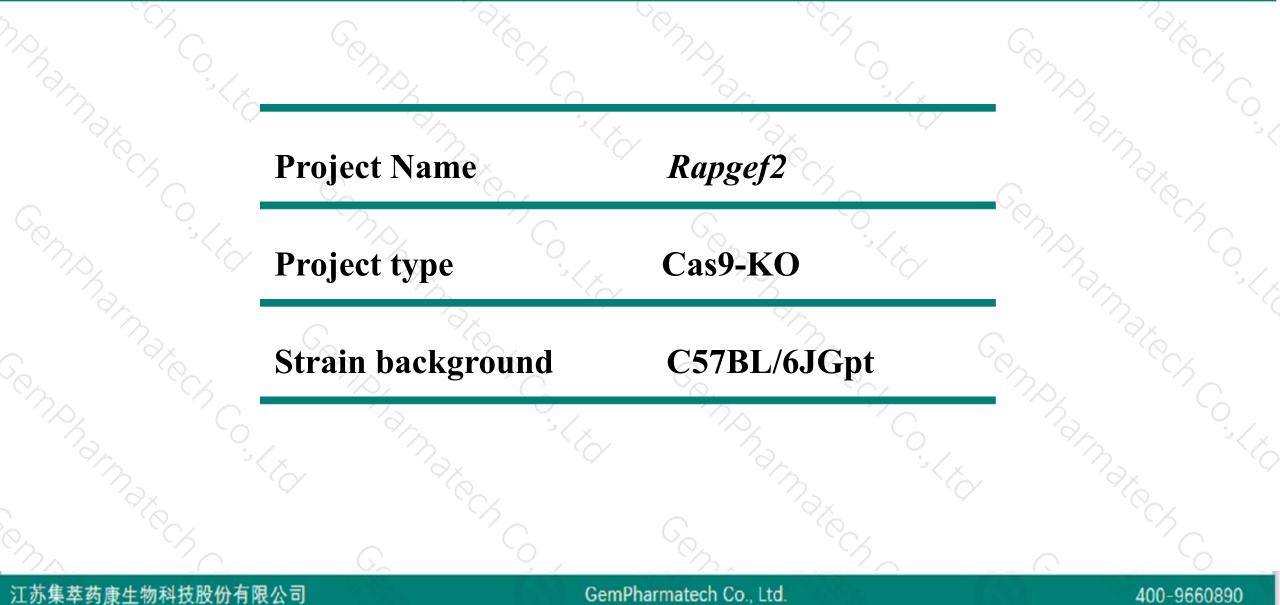


Rapgef2 Cas9-KO Strategy

Designer: Reviewer: Design Date: Yang Zeng Jia Yu 2019-12-16

Project Overview

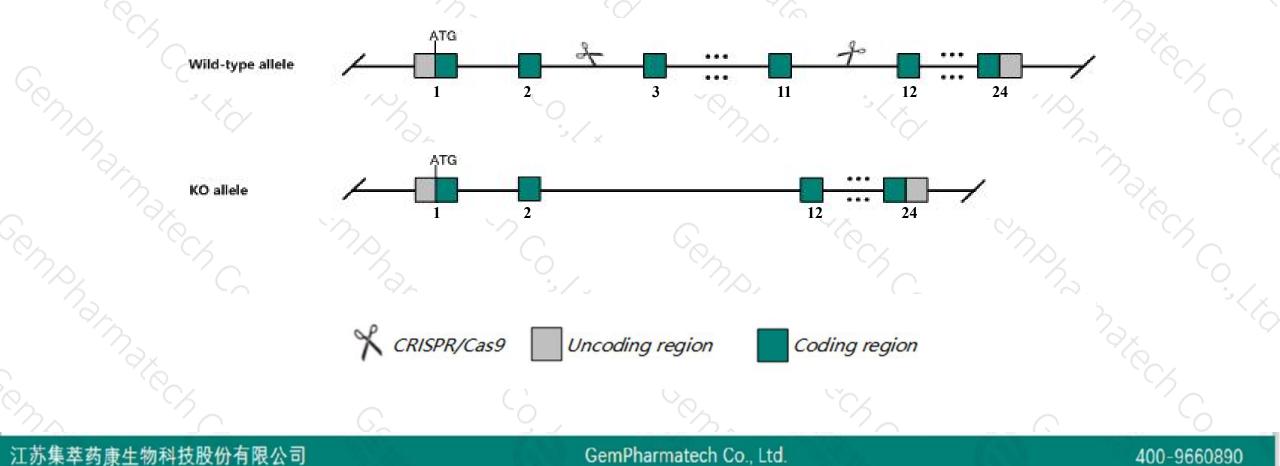




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Rapgef2 gene. The schematic diagram is as follows:





- The Rapgef2 gene has 6 transcripts. According to the structure of Rapgef2 gene, exon3-exon11 of Rapgef2-202 (ENSMUST00000118340.6) transcript is recommended as the knockout region. The region contains 1460bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Rapgef2 gene. The brief process is as follows: CRISPR/Cas9 syste

Notice



- According to the existing MGI data, Homozygotes for a null allele die at mid-gestation exhibiting growth arrest and defects in vascular development, neural tube closure and embryo turning. Homozygotes for another null allele show yolk sac vascular defects, impaired cell physiology and heart, primitive gut, liver and brain formation.
- > Transcript *Rapgef2-203* lncRNA may not be affected.
- The Rapgef2 gene is located on the Chr3. 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)



\$?

Rapgef2 Rap guanine nucleotide exchange factor (GEF) 2 [Mus musculus (house mouse)]

Gene ID: 76089, updated on 24-Oct-2019

Summary

 Official Symbol
 Rapgef2 provided by MGI

 Official Full Name
 Rap guanine nucleotide exchange factor (GEF) 2 provided by MGI

 Primary source
 MGI:MGI:2659071

 See related
 Ensembl:ENSMUSG0000062232

 Gene type
 protein coding

RefSeq status VALIDATED

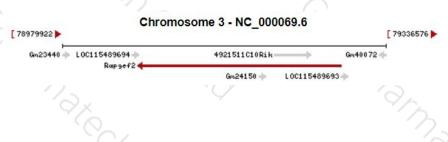
Organism Mus musculus

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Muridae; Mus; Mus

Also known as Pdzgef1; nRapGEP; CNRasGEF; RA-GEF-1; mKIAA0313; 5830453M24Rik

Expression Ubiquitous expression in frontal lobe adult (RPKM 10.4), cortex adult (RPKM 8.4) and 27 other tissues See more

Orthologs human all



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Transcript information (Ensembl)



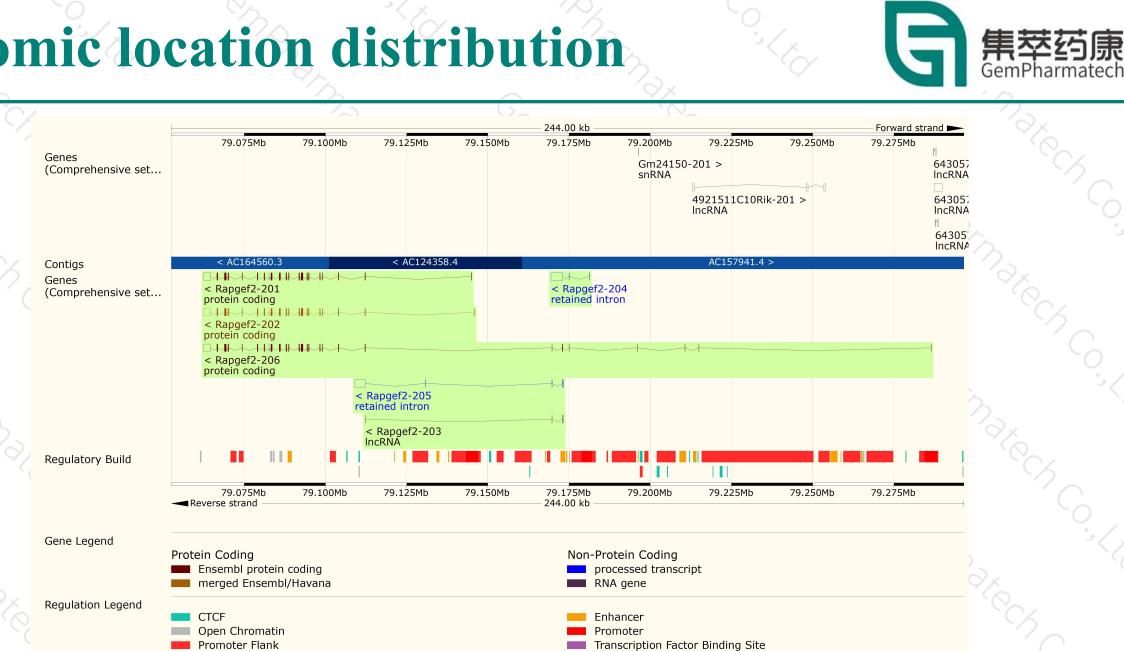
The gene has 6 transcripts, all transcripts are shown below:

Name 🖕	Name 🖕 Transcript ID 🖕 bp 🖕 Protein 🧅		Translation ID	Biotype 💧	CCDS 🖕	UniProt 🖕	Flags		
Rapgef2-202	ENSMUST00000118340.6	6544	<u>1494aa</u>	ENSMUSP00000113778.1	Protein coding	<u>CCDS50932</u> &	E9QNQ4	TSL:1 GENCODE basic	
Rapgef2-206	ENSMUST00000195708.1	6964	<u>1644aa</u>	ENSMUSP00000141542.1	Protein coding	-	A0A0A6YWG7	TSL:5 GENCODE basic APPRIS P1	
Rapgef2-201	ENSMUST00000118100.7	6573	<u>1496aa</u>	ENSMUSP00000114119.1	Protein coding	2	Q8CHG7 ₽	TSL:1 GENCODE basic	
Rapgef2-204	ENSMUST00000136126.1	3837	No protein	-	Retained intron	-		TSL:1	
Rapgef2-205	ENSMUST00000152275.7	<mark>3486</mark>	No protein	-	Retained intron	5	12	TSL:3	
Rapgef2-203	ENSMUST00000124647.1	454	No protein		IncRNA	-	0.50	TSL:2	

The strategy is based on the design of *Rapgef2-202* transcript, The transcription is shown below



Genomic location distribution



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Protein domain

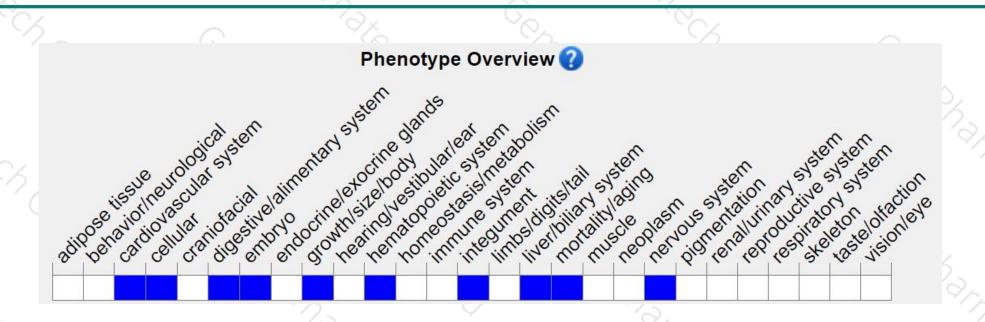


	ENSMUSP00000113 MobiDB lite Low complexity (Seg) Coiled-coils (Ncoils)					-			[°] [°]			
	Superfamily	Cyclic nucleotide-binding-like	PDZ superfamily	Ubiquitin-like	e domain superfamily							
		Ras guanine nucleotide exchange factor domain superfamily										
	SMART	Ras-like	guanine nucleotide exchange fa	actor, N-terminal	Ras guanine-nucleotide	exchange factors catalytic do	omain					
		Cyclic nucleotide-binding do	omain PDZ domain	Ras-associati	ng (RA) domain							
	Pfam		PDZ domain	Ras-associati	ng (RA) domain							
		Ras-like	guanine nucleotide exchange f	actor, N-terminal	Ras guanine-nucleotide	e exchange factors catalytic d	lomain					
	PROSITE profiles	Cyclic nucleotide-binding do	omain PDZ domain		Ras guanine-nucleotide	exchange factors catalytic de	omain					
				Ras-associati	ng (RA) domain							
		Ras-like	guanine nucleotide exchange fa	actor, N-terminal								
	PANTHER	Ras-like guanine nucleotide exchange factor		,,								
		Rap guanine nucleotide exchange factor 2							3/			
	Gene3D	1.20.870.	10 2.30.42.10									
Υ.		RmIC-like jelly roll fold										
	CDD	Cyclic nucleotide-binding do	omain cd00992	cd01785	Ras quanine-nucleotide	exchange factors catalytic do	omain					
Ras-like guanine nucleotide exchange factor, N-terminal												
		Sequence variants (dbSNP and all other sources)										
	All sequence SNPs/i											
	Variant Legend											
		frameshift variantsplice region variant										
	Scale bar	0 200	400	600	800	1000	1200	1494	·			
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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, Homozygotes for a null allele die at mid-gestation exhibiting growth arrest and defects in vascular development, neural tube closure and embryo turning. Homozygotes for another null allele show yolk sac vascular defects, impaired cell physiology and heart, primitive gut, liver and brain formation.

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



