

Rasgrf1 Cas9-CKO Strategy

Designer:Xueting Zhang

Reviewer: Yanhua Shen

Date:2019-10-27

Project Overview



Project Name

Rasgrf1

Project type

Cas9-CKO

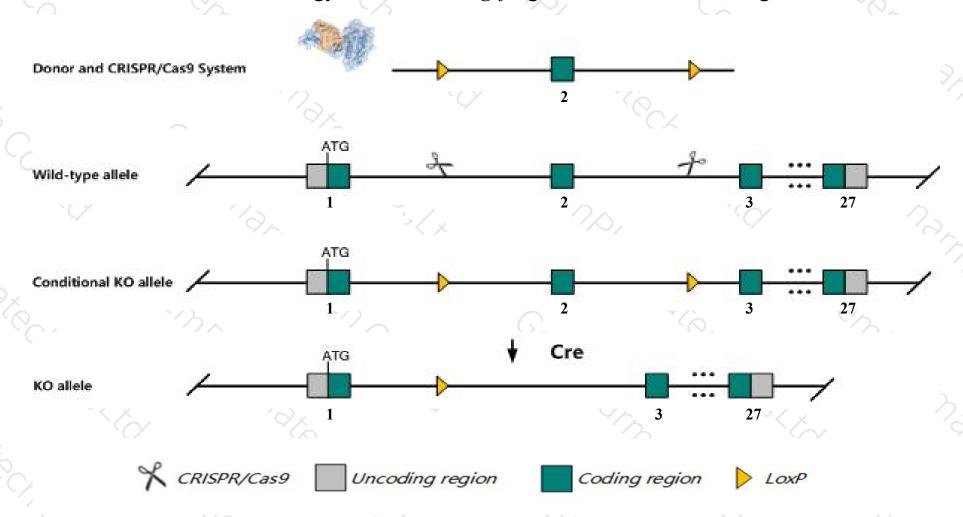
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Rasgrf1* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Rasgrf1* gene has 4 transcripts. According to the structure of *Rasgrf1* gene, exon2 of *Rasgrf1-202*(ENSMUST00000034912.5) transcript is recommended as the knockout region. The region contains 110bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Rasgrf1* 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



- > According to the existing MGI data, Homozygotes for null mutations (and heterozygotes with a paternally inherited mutant allele) exhibit reduced postnatal growth, low insulin and IGF I levels, glucose intolerance, beta-cell hypoplasia, impaired long-term synaptic plasticity, and impaired hippocampal-dependent learning.
- ➤ Transcript *Rasgrf1*-201&203 may not be affected.
- The *Rasgrf1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



Rasgrf1 RAS protein-specific guanine nucleotide-releasing factor 1 [Mus musculus (house mouse)]

Gene ID: 19417, updated on 13-Aug-2019

Summary

☆ ?

Official Symbol Rasgrf1 provided by MGI

Official Full Name RAS protein-specific guanine nucleotide-releasing factor 1 provided by MGI

Primary source MGI:MGI:99694

See related Ensembl:ENSMUSG00000032356

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

Also known as Gnrp; Grf1; p190; CDC25; P190-A; CDC25Mm; Grfbeta; Al844718; Ras-GRF1; p190RhoGEF

Expression Biased expression in cerebellum adult (RPKM 26.4), frontal lobe adult (RPKM 25.1) and 6 other tissues See more

Orthologs human all

Genomic context



Location: 9 E3.1; 9 47.31 cM

See Rasgrf1 in Genome Data Viewer

Exon count: 29

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	9	NC_000075.6 (8990950890026979)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	9	NC_000075.5 (8980461389921817)

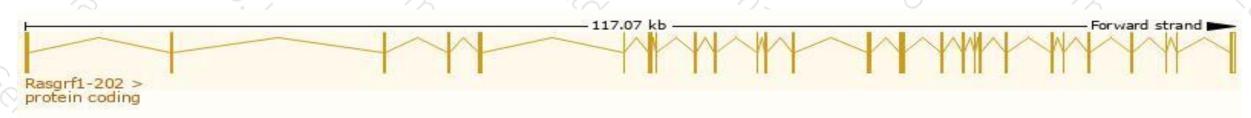
Transcript information (Ensembl)



The gene has 4 transcripts, all transcripts are shown below:

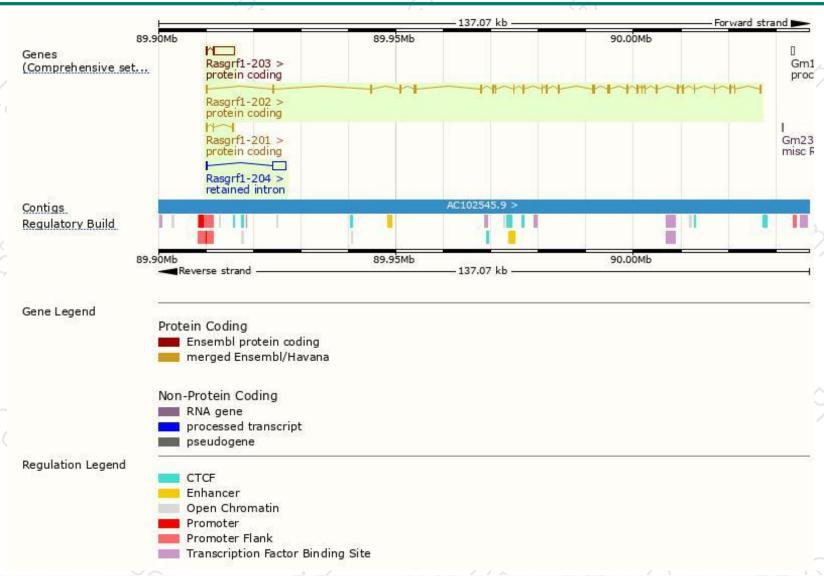
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rasgrf1-202	ENSMUST00000034912.5	4092	1262aa	Protein coding	CCDS40722	B2RS27 P27671	TSL:1 GENCODE basic APPRIS P1
Rasgrf1-201	ENSMUST00000034909.10	853	<u>178aa</u>	Protein coding	CCDS40723	Q9QZR7	TSL:1 GENCODE basic
Rasgrf1-203	ENSMUST00000189545.1	4766	<u>153aa</u>	Protein coding	-	A0A087WS68	TSL:1 GENCODE basic
Rasgrf1-204	ENSMUST00000190073.1	3042	No protein	Retained intron	2	14	TSL:1

The strategy is based on the design of Rasgrf1-202 transcript, The transcription is shown below



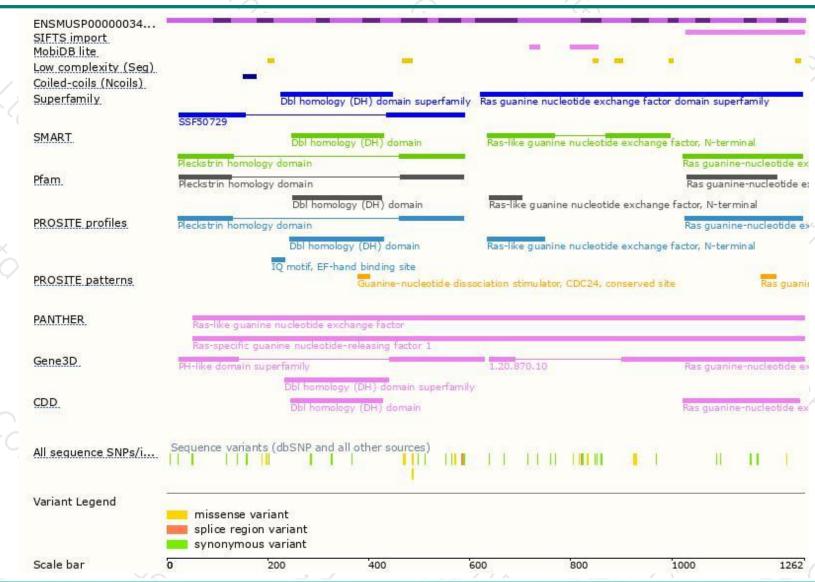
Genomic location distribution





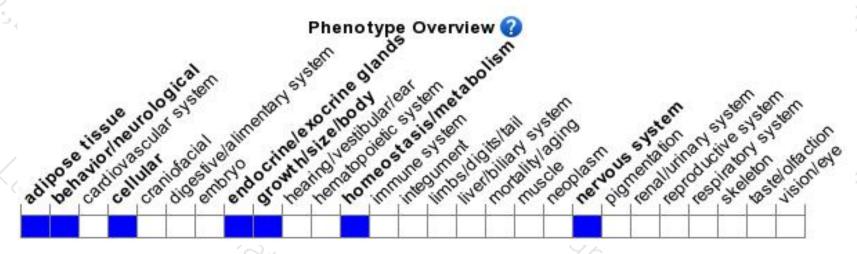
Protein domain





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, Homozygotes for null mutations (and heterozygotes with a paternally inherited mutant allele) exhibit reduced postnatal growth, low insulin and IGF I levels, glucose intolerance, beta-cell hypoplasia, impaired long-term synaptic plasticity, and impaired hippocampal-dependent learning.



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





