

Rapgef4 Cas9-KO Strategy

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Project Overview



Project Name

Rapgef4

Project type

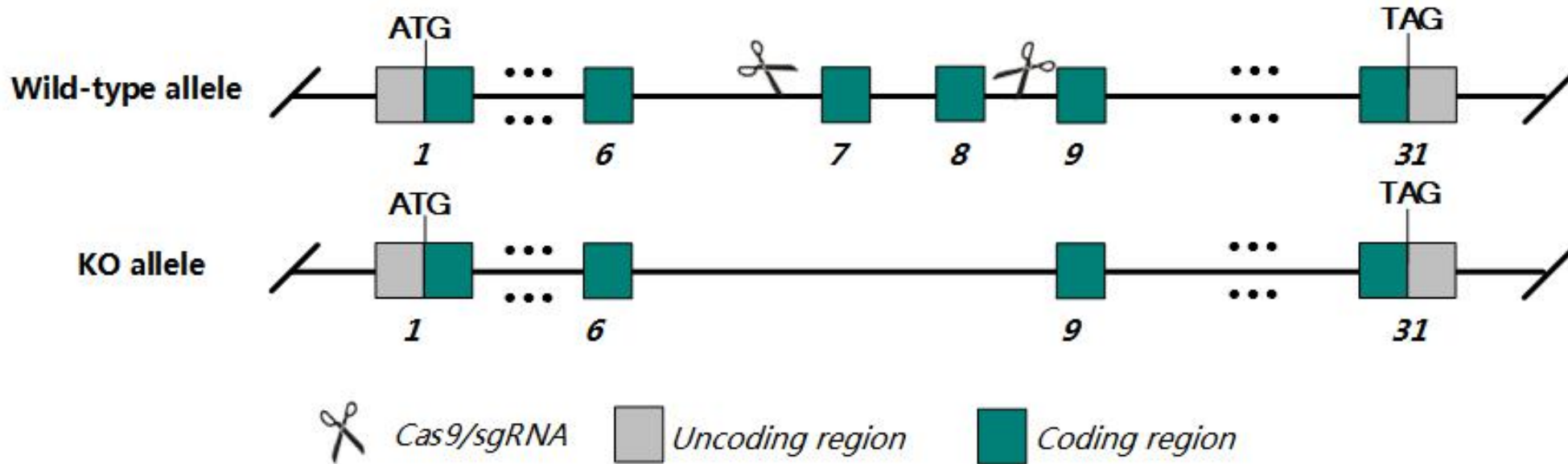
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rapgef4* gene. The schematic diagram is as follows:



- The *Rapgef4* gene has 11 transcripts. According to the structure of *Rapgef4* gene, exon7-exon8 of *Rapgef4-202* (ENSMUST00000090826.11) transcript is recommended as the knockout region. The region contains 161bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rapgef4* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Mice homozygous for a null allele exhibit decreased insulin granule fusion in pancreatic islet cells during the first phase of cAMP-dependent insulin granule exocytosis. Mice homozygous for a knock-out allele exhibit impaired isoproterenol-induced SR calcium leak and arrhythmia.
- Transcript *Rapgef4*-205&206&207&208&209&210&211 may not be affected.
- The *Rapgef4* gene is located on the Chr2. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Rapgef4 Rap guanine nucleotide exchange factor (GEF) 4 [Mus musculus (house mouse)]

Gene ID: 56508, updated on 31-Jan-2019

Summary



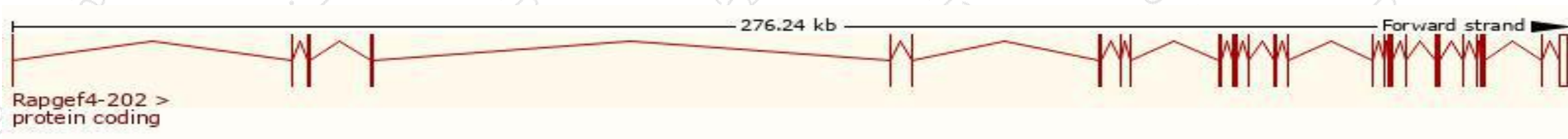
Official Symbol	Rapgef4 provided by MGI
Official Full Name	Rap guanine nucleotide exchange factor (GEF) 4 provided by MGI
Primary source	MGI:MGI:1917723
See related	Ensembl:ENSMUSG00000049044
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1300003D15Rik, 5730402K07Rik, 6330581N18Rik, EPAC 2, Epac-2, Epac2, mKIAA4040
Expression	Biased expression in cortex adult (RPKM 46.5), frontal lobe adult (RPKM 40.1) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

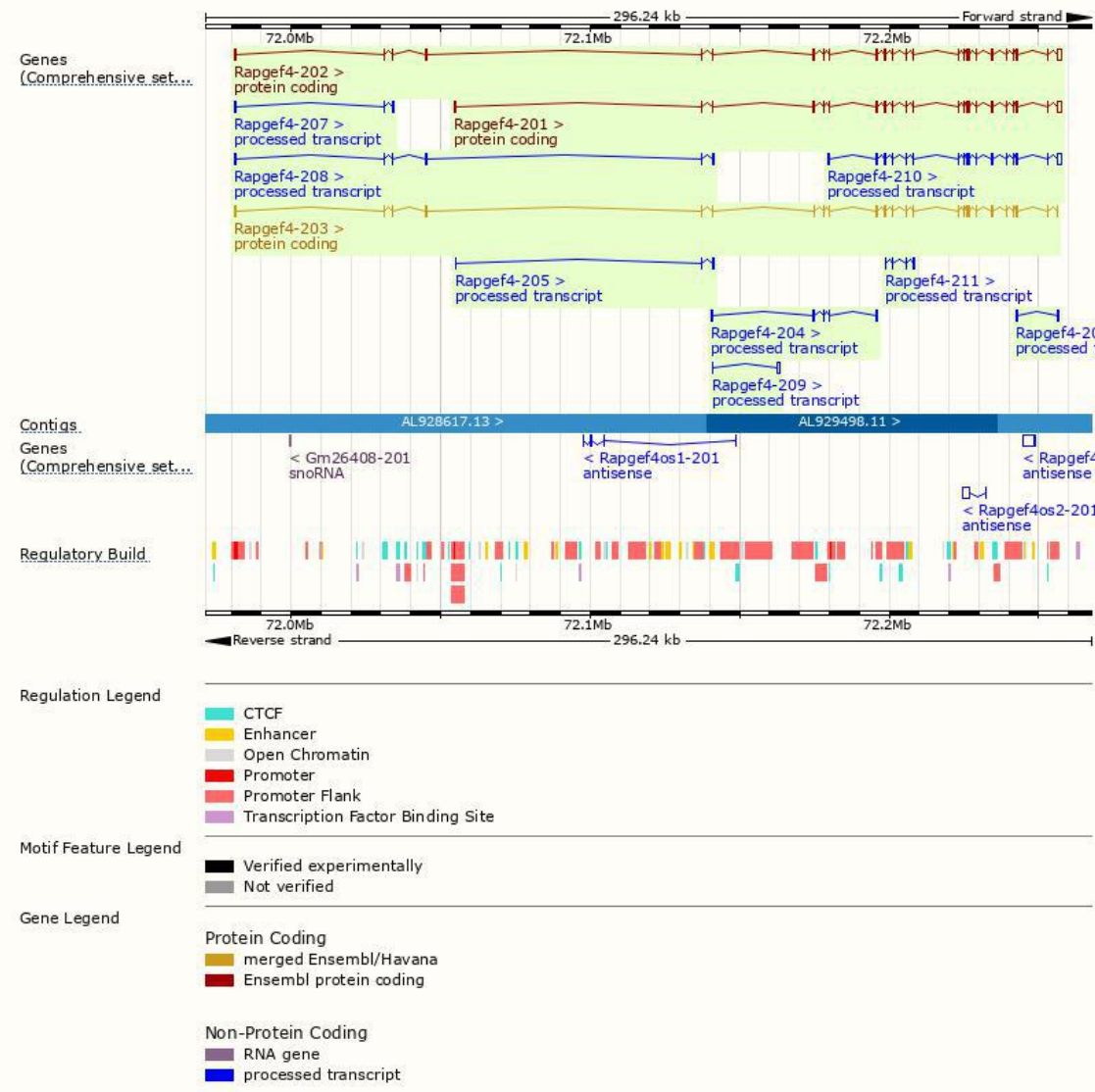
The gene has 11 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rapgef4-202	ENSMUST00000090826.11	4181	1011aa	Protein coding	CCDS57176	A2ASW4 Q9EQZ6	TSL:1 GENCODE basic APPRIS ALT 1
Rapgef4-201	ENSMUST00000028525.5	4109	867aa	Protein coding	CCDS57177	A2ASW8	TSL:1 GENCODE basic
Rapgef4-203	ENSMUST00000102698.9	2982	993aa	Protein coding	CCDS16120	Q9EQZ6	TSL:1 GENCODE basic APPRIS P3
Rapgef4-210	ENSMUST00000153887.7	3539	No protein	Processed transcript	-	-	TSL:1
Rapgef4-209	ENSMUST00000151236.1	987	No protein	Processed transcript	-	-	TSL:1
Rapgef4-208	ENSMUST00000150234.7	694	No protein	Processed transcript	-	-	TSL:1
Rapgef4-204	ENSMUST00000122975.7	666	No protein	Processed transcript	-	-	TSL:3
Rapgef4-211	ENSMUST00000156031.1	664	No protein	Processed transcript	-	-	TSL:3
Rapgef4-207	ENSMUST00000149421.7	623	No protein	Processed transcript	-	-	TSL:1
Rapgef4-206	ENSMUST00000146970.1	500	No protein	Processed transcript	-	-	TSL:3
Rapgef4-205	ENSMUST00000124004.1	438	No protein	Processed transcript	-	-	TSL:3

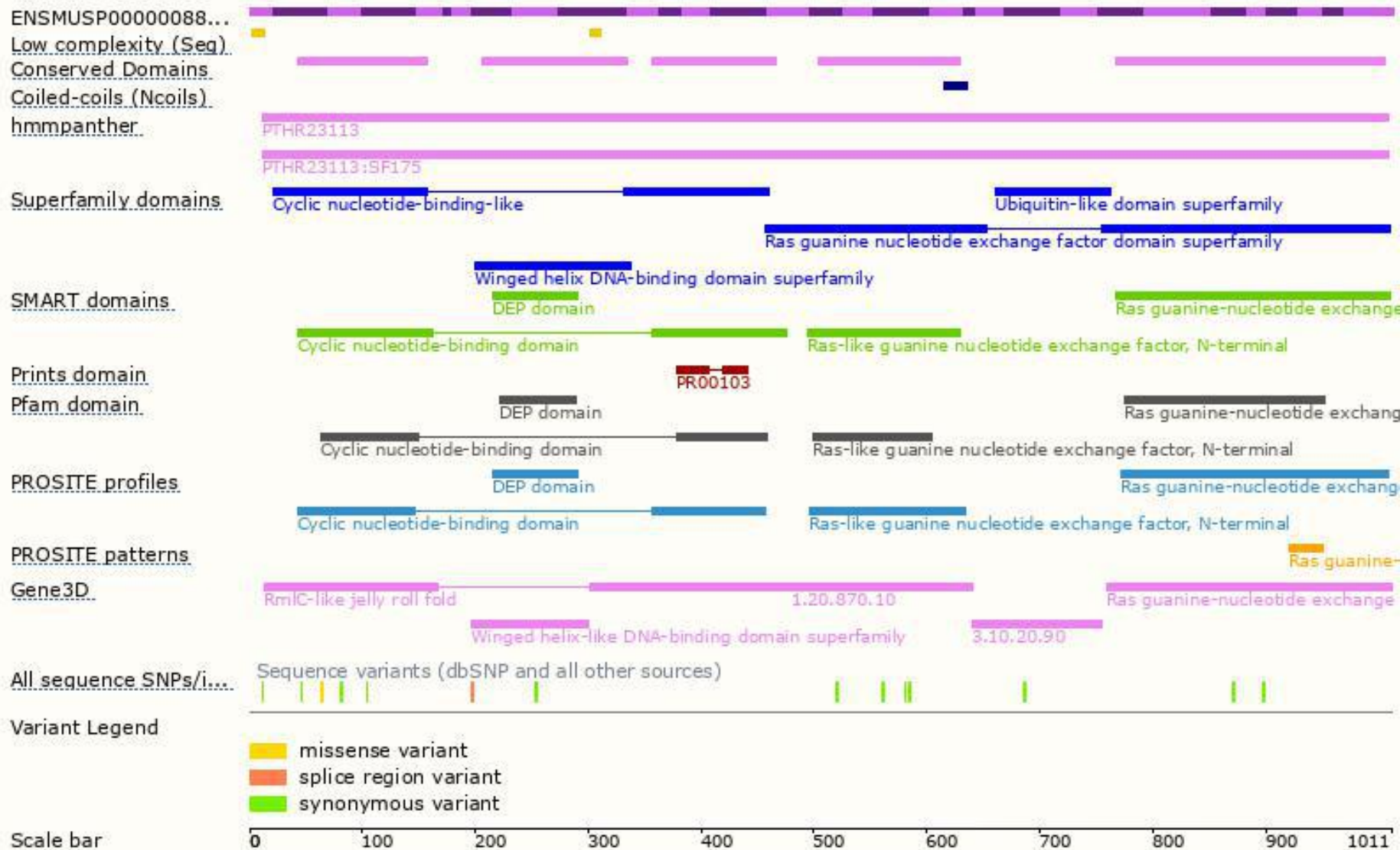
The strategy is based on the design of *Rapgef4-202* transcript, The transcription is shown below



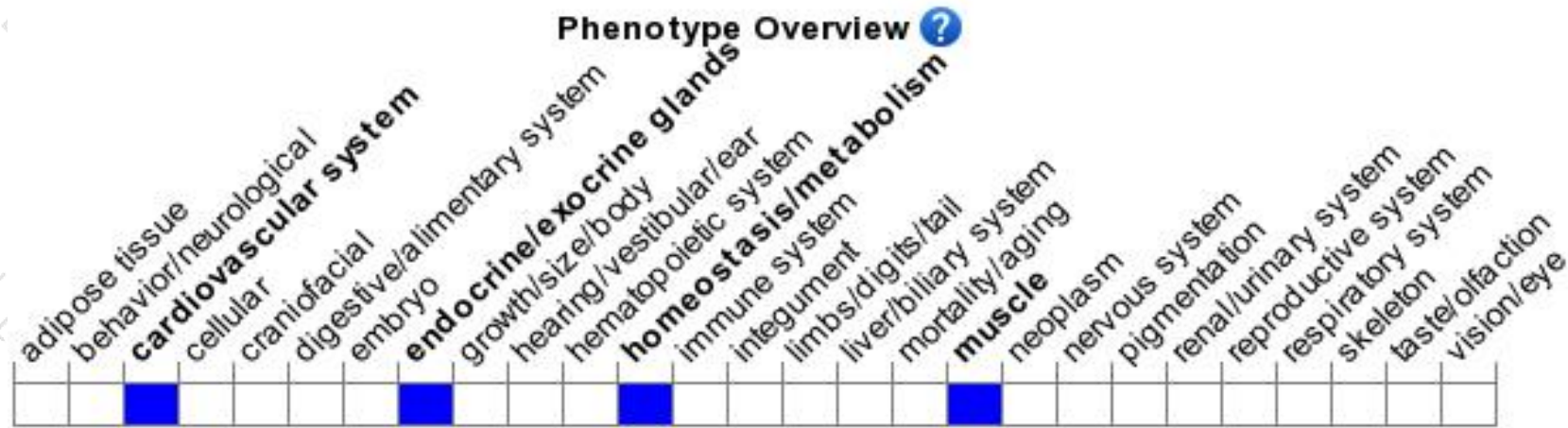
Genomic location distribution



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, Mice homozygous for a null allele exhibit decreased insulin granule fusion in pancreatic islet cells during the first phase of cAMP-dependent insulin granule exocytosis. Mice homozygous for a knock-out allele exhibit impaired isoproterenol-induced SR calcium leak and arrhythmia.

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

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