

Ralgapa2 Cas9-KO Strategy

Designer: JiaYu

Reviewer: Xiaojing Li

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Project Overview

Project Name

Ralgapa2

Project type

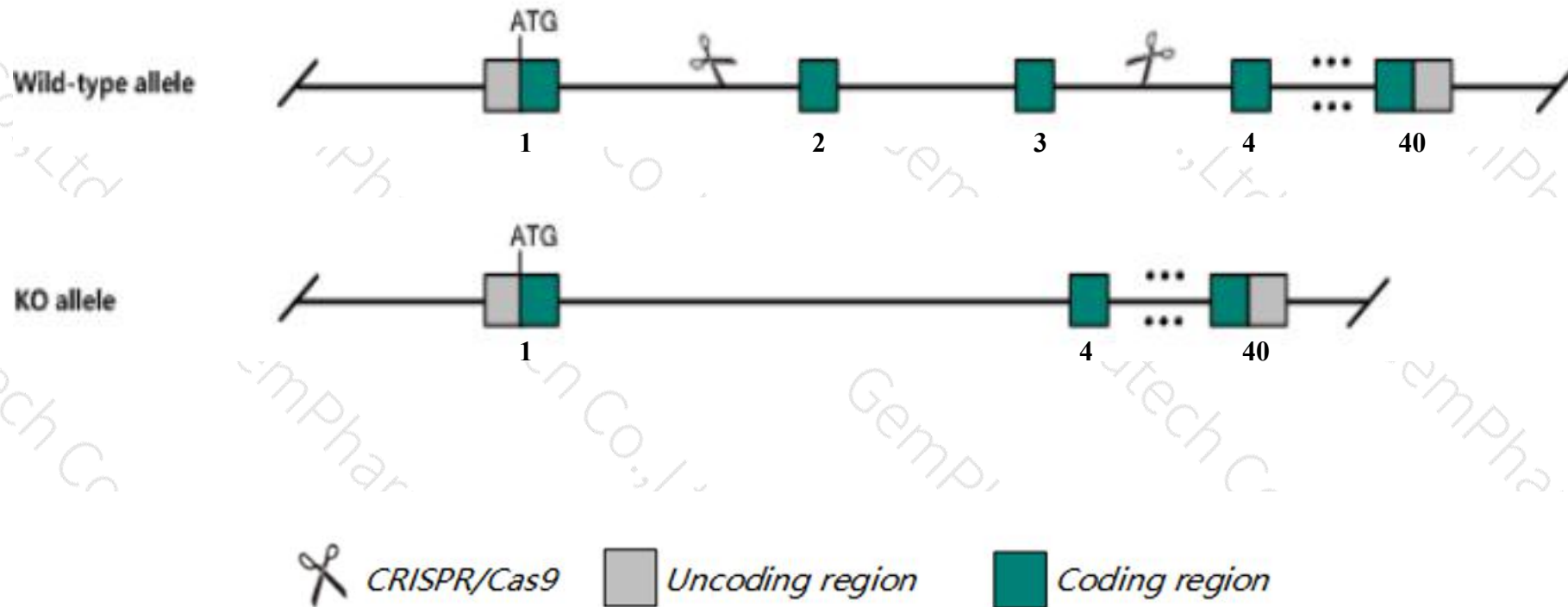
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ralgapa2* gene. The schematic diagram is as follows:



- The *Ralgapa2* gene has 11 transcripts. According to the structure of *Ralgapa2* gene, exon2-exon3 of *Ralgapa2*-202(ENSMUST00000109986.8) transcript is recommended as the knockout region. The region contains 164bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ralgapa2* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit increased incidence and severity of induced urothelial bladder tumors.
- The *Ralgapa2* 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 biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Ralgapa2 Ral GTPase activating protein, alpha subunit 2 (catalytic) [Mus musculus (house mouse)]

Gene ID: 241694, updated on 13-Mar-2020

Summary



Official Symbol	Ralgapa2 provided by MGI
Official Full Name	Ral GTPase activating protein, alpha subunit 2 (catalytic) provided by MGI
Primary source	MGI:MGI:3036245
See related	Ensembl:ENSMUSG00000037110
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	A230067G21Rik, AS250, BC053994, RGC2, pp250
Expression	Ubiquitous expression in heart adult (RPKM 4.9), subcutaneous fat pad adult (RPKM 4.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

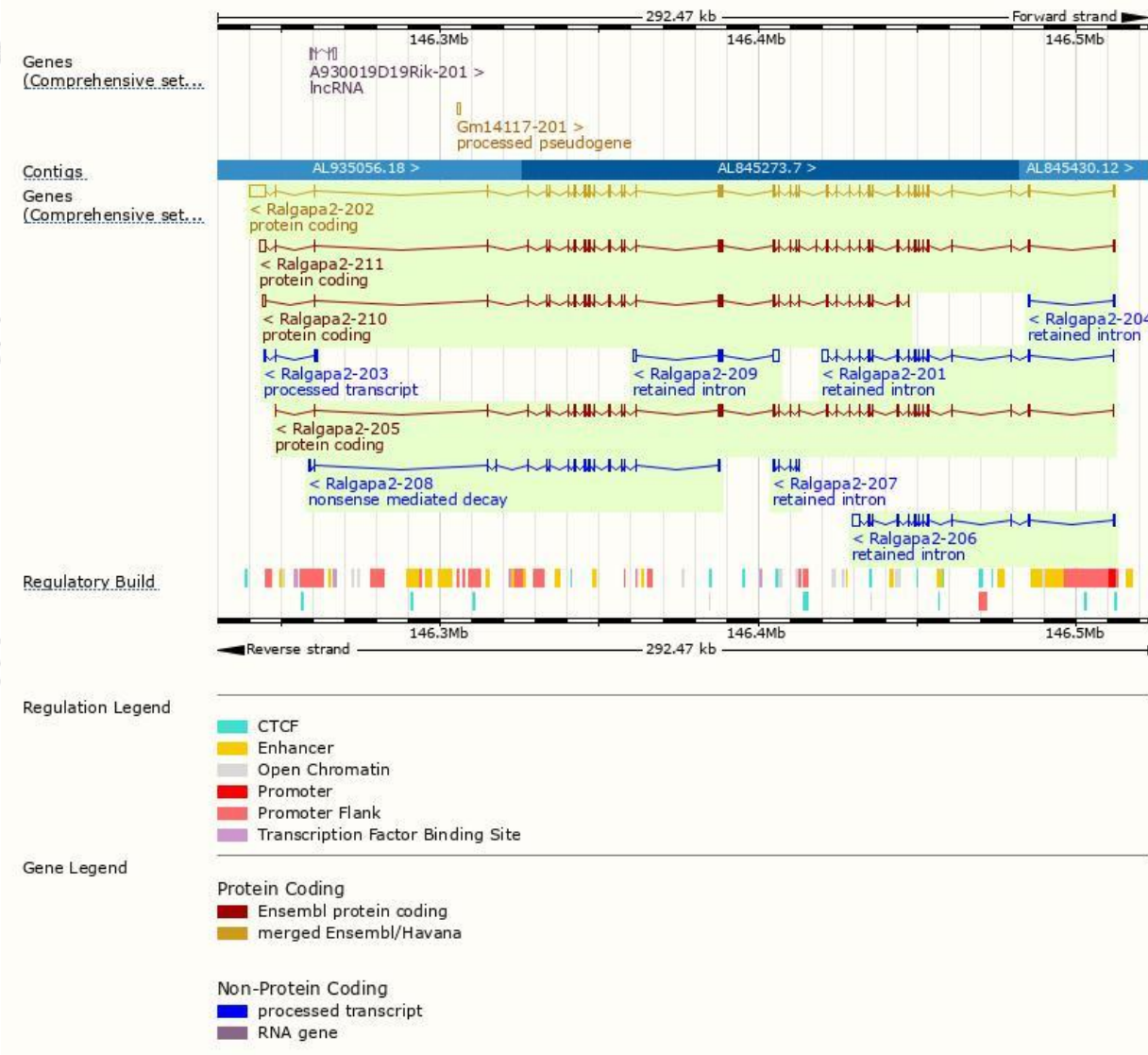
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ralgapa2-202	ENSMUST00000109986.8	11030	1910aa	Protein coding	CCDS16831	A0A0A0MQD7	TSL:5 GENCODE basic APPRIS P2
Ralgapa2-211	ENSMUST00000228797.1	8245	1957aa	Protein coding	-	A0A2I3BPN8	GENCODE basic APPRIS ALT2
Ralgapa2-210	ENSMUST00000149499.8	5686	1567aa	Protein coding	-	F7CGP0	CDS 5' incomplete TSL:5
Ralgapa2-205	ENSMUST00000131824.7	5624	1872aa	Protein coding	-	A3KGS3	TSL:5 GENCODE basic APPRIS ALT2
Ralgapa2-208	ENSMUST00000146307.1	3095	834aa	Nonsense mediated decay	-	F7AI67	CDS 5' incomplete TSL:2
Ralgapa2-203	ENSMUST00000124583.1	1194	No protein	Processed transcript	-	-	TSL:1
Ralgapa2-206	ENSMUST00000135974.1	4159	No protein	Retained intron	-	-	TSL:1
Ralgapa2-201	ENSMUST00000109982.8	3730	No protein	Retained intron	-	-	TSL:1
Ralgapa2-209	ENSMUST00000148784.1	2704	No protein	Retained intron	-	-	TSL:2
Ralgapa2-207	ENSMUST00000146024.1	651	No protein	Retained intron	-	-	TSL:2
Ralgapa2-204	ENSMUST00000124709.1	597	No protein	Retained intron	-	-	TSL:3

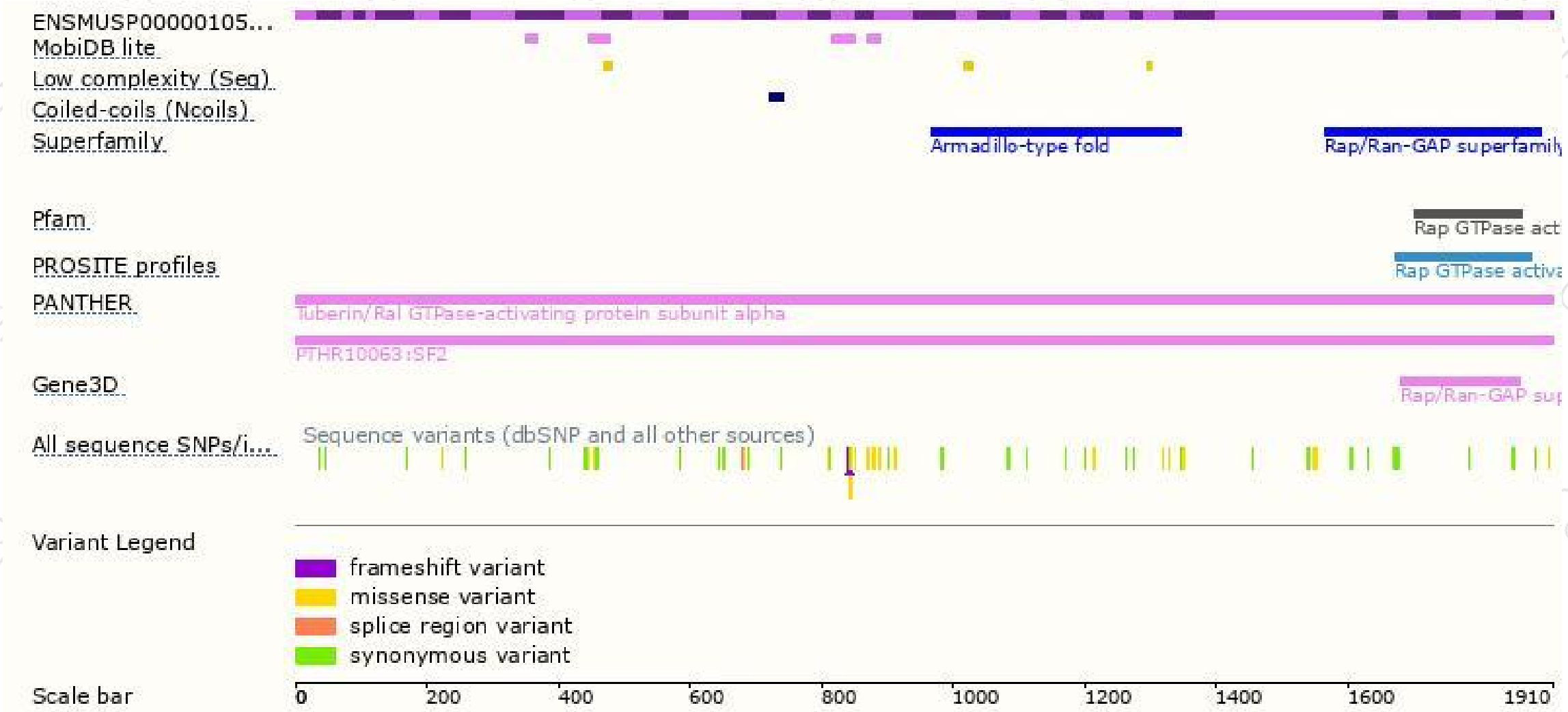
The strategy is based on the design of *Ralgapa2-202* transcript,the transcription is shown below:



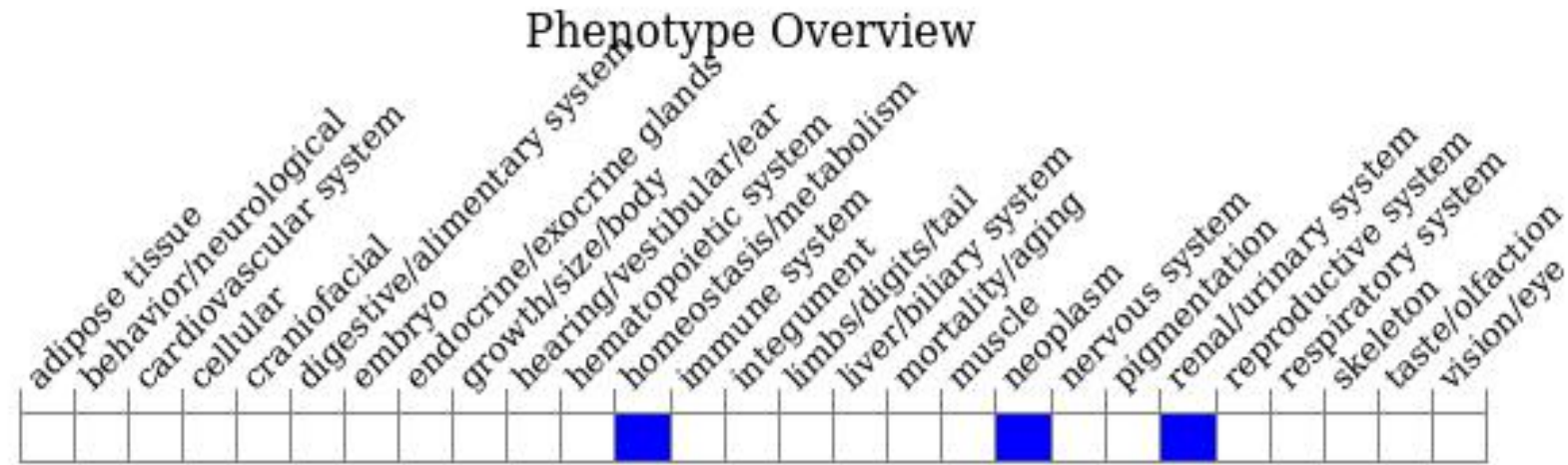
Genomic location distribution



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 knock-out allele exhibit increased incidence and severity of induced urothelial bladder tumors.

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

Tel: 400-9660890

