Rab3gap2 Cas9-KO Strategy

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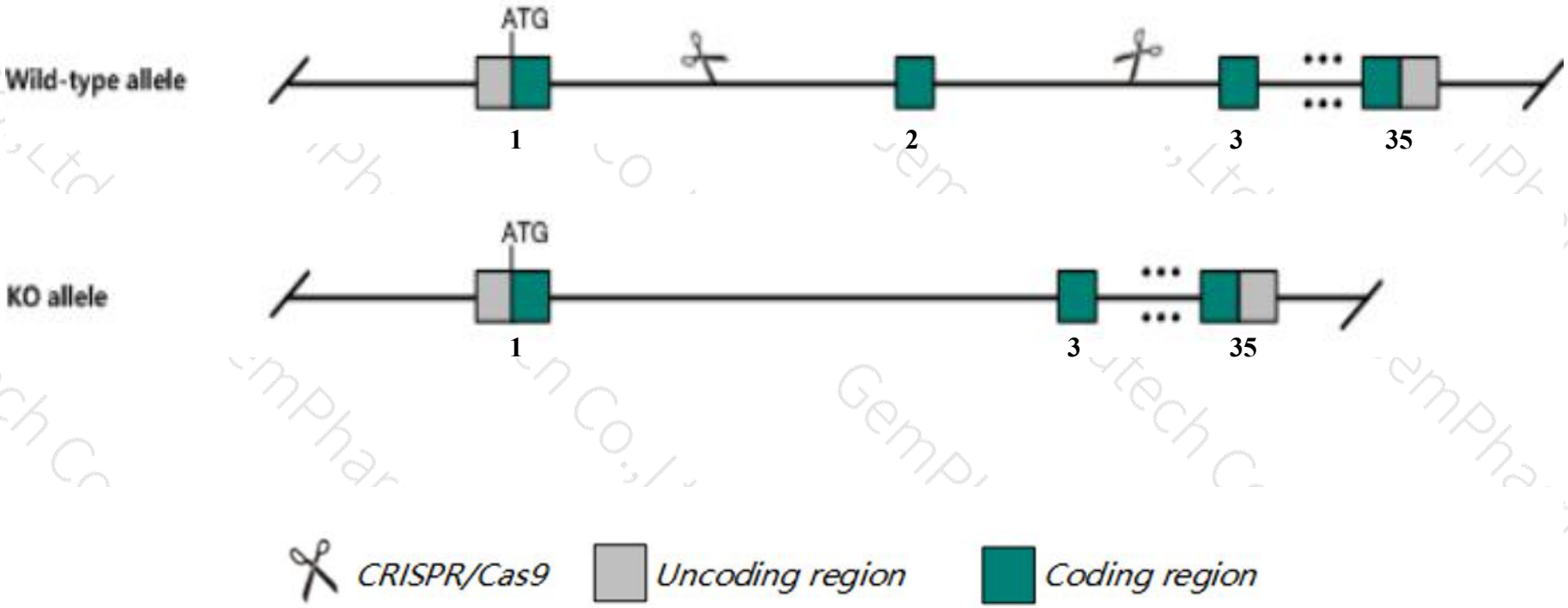
Project Overview

Project Name	***Rab3gap2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rab3gap2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Rab3gap2* gene has 6 transcripts. According to the structure of *Rab3gap2* gene, exon2 of *Rab3gap2-201* (ENSMUST00000069652.7) transcript is recommended as the knockout region.The region contains 65bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rab3gap2* gene. The brief process is as follows: CRISPR/Cas9 sys

Notice

- The *Rab3gap2* gene is located on the Chr1. 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）

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Rab3gap2 RAB3 GTPase activating protein subunit 2 [Mus musculus (house mouse)]

Gene ID: 98732, updated on 13-Mar-2020

Summary

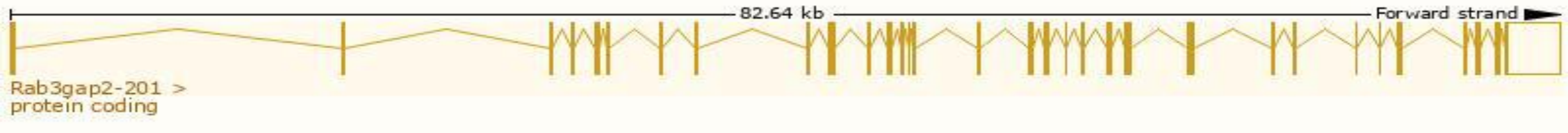
Official Symbol	Rab3gap2 provided by MGI
Official Full Name	RAB3 GTPase activating protein subunit 2 provided byMGI
Primary source	MGI:MGI:1916043
See related	Ensembl:ENSMUSG00000039318
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110059F07Rik, 2010002H18Rik, 5830469C09, AI851069, AW743433, RAB3-GAP150, mKIAA0839
Expression	Ubiquitous expression in frontal lobe adult (RPKM 9.3), cortex adult (RPKM 8.7) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

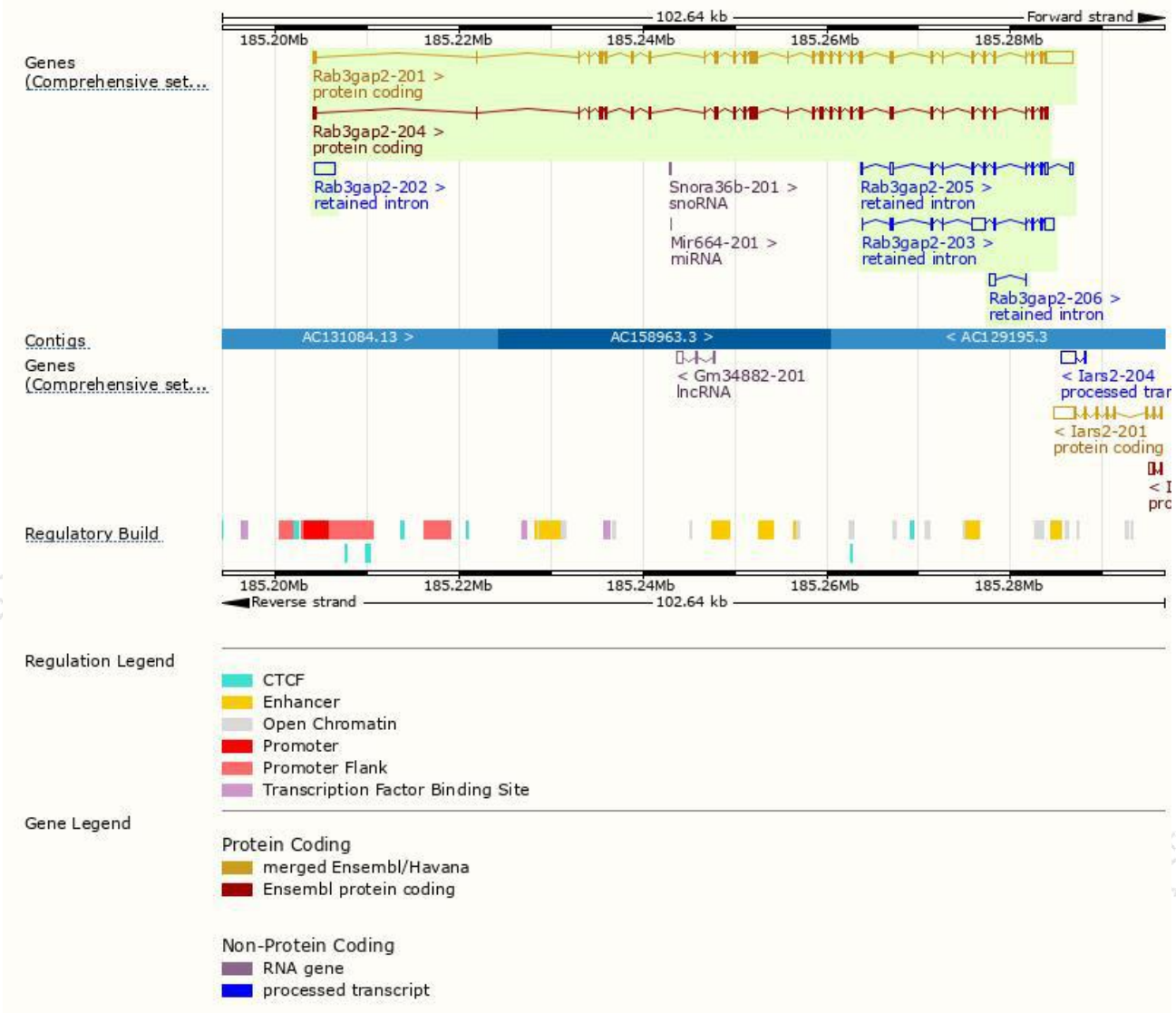
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rab3gap2-201	ENSMUST00000069652.7	7052	1387aa	Protein coding	CCDS48478	E9QKE4	TSL:5 GENCODE basic APPRIS P2
Rab3gap2-204	ENSMUST00000194740.5	4418	1367aa	Protein coding	-	A0A0A6YWM5	TSL:5 GENCODE basic APPRIS ALT2
Rab3gap2-203	ENSMUST00000193482.1	3245	No protein	Retained intron	-	-	TSL:5
Rab3gap2-202	ENSMUST00000191966.1	2277	No protein	Retained intron	-	-	TSL:NA
Rab3gap2-205	ENSMUST00000195042.5	1981	No protein	Retained intron	-	-	TSL:5
Rab3gap2-206	ENSMUST00000195534.1	614	No protein	Retained intron	-	-	TSL:3

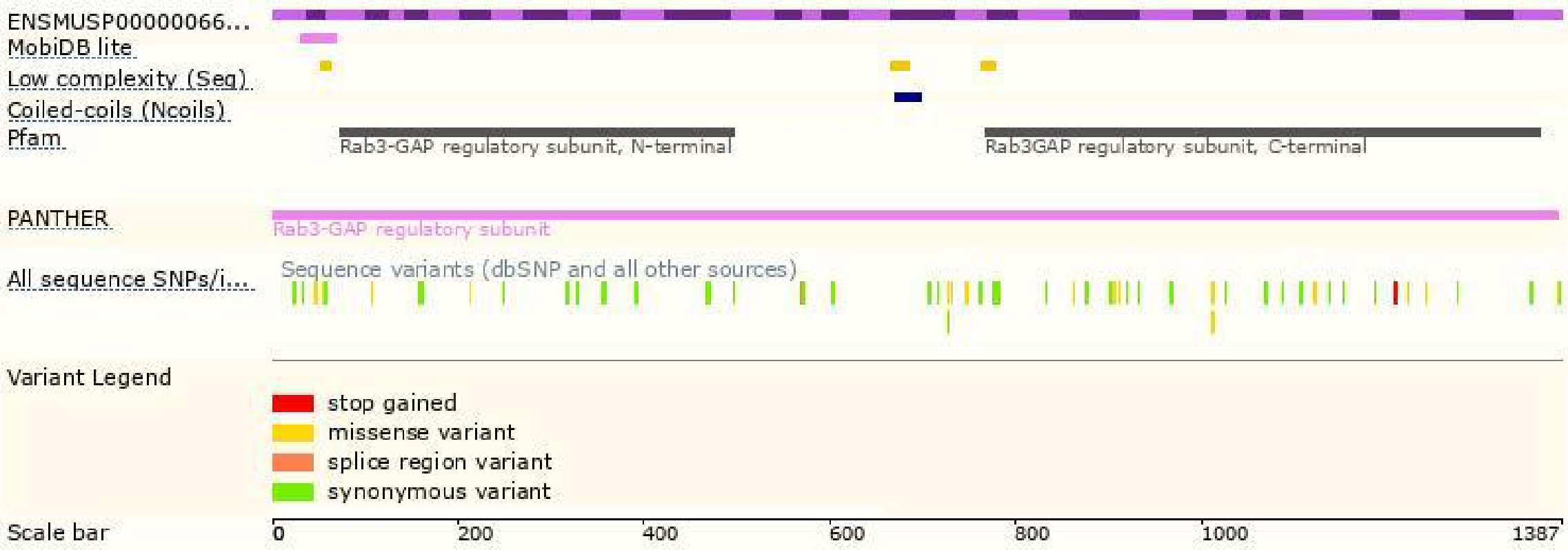
The strategy is based on the design of *Rab3gap2-201* transcript,the transcription is shown below:



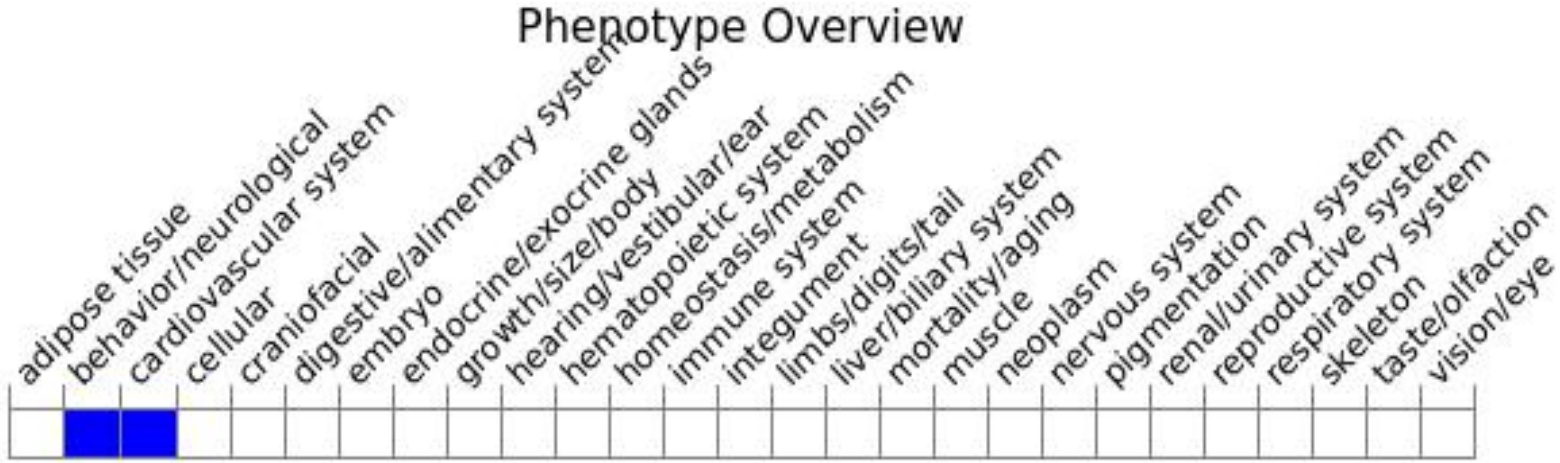
Genomic location distribution



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/).

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

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