Rab27a Cas9-KO Strategy

Designer: Daohua Xu
Reviewer: Huimin Su

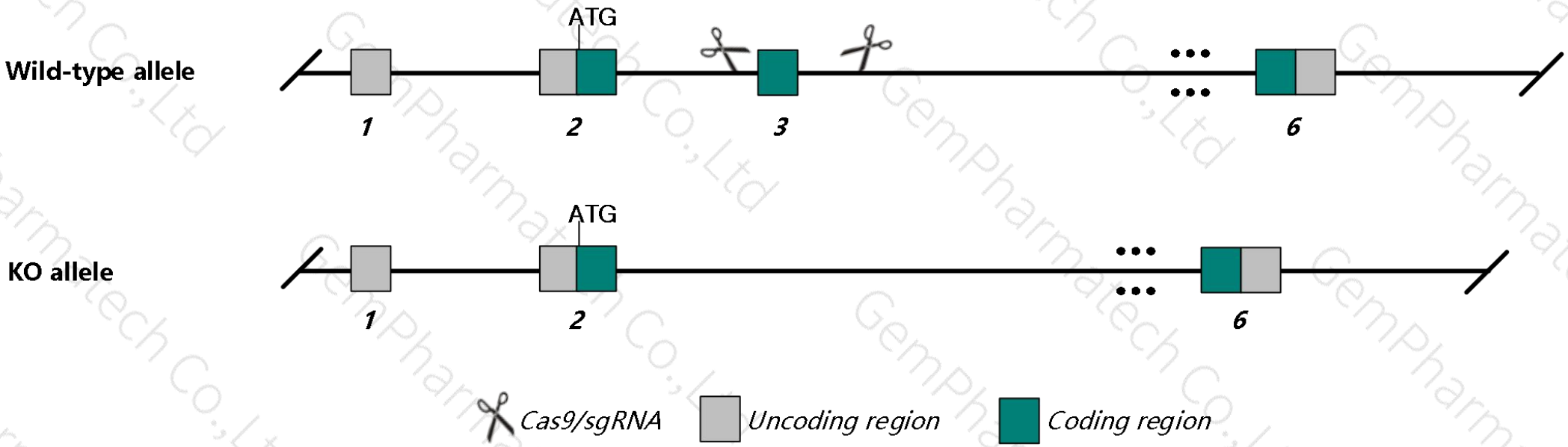
Design Date: 2019-11-22

Project Overview

Project Name	***Rab27a***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rab27a* gene. The schematic diagram is as follows:



Technical routes

➢ The *Rab27a* gene has 4 transcripts. According to the structure of *Rab27a* gene, exon3 of *Rab27a-201* (ENSMUST00000034722.4) transcript is recommended as the knockout region.The region contains 86bp codon seqence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rab27a* gene. The brief process is as follows:CRISPR/Cas9 system t 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.

Notice

- According to the existing MGI data,Homozygotes have abnormal melanocyte development producing abnormal pigmentation and a gray coat color.

- The *Rab27a* 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 gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

集萃药康 GemPharmatech

Rab27a RAB27A, member RAS oncogene family [Mus musculus (house mouse)]

Gene ID: 11891, updated on 7-Apr-2019

Summary

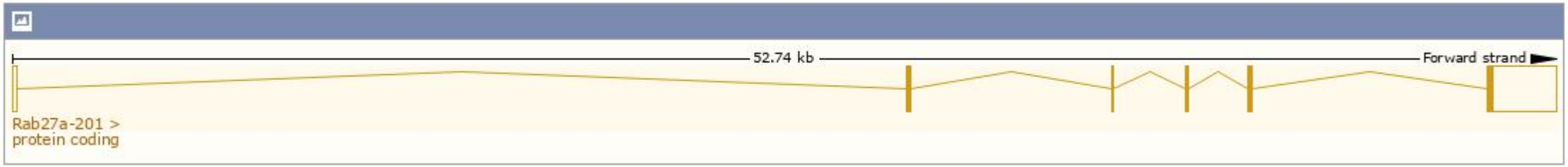
Official Symbol	Rab27a provided by MGI
Official Full Name	RAB27A, member RAS oncogene family provided by MGI
Primary source	MGI:MGI:1861441
See related	Ensembl:ENSMUSG00000032202
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2210402C08Rik, 2410003M20Rik, 4933437C11Rik, ash
Summary	The protein encoded by this gene is a member of the Rab family of proteins, which is the largest family within the Ras superfamily of GTPases. This gene product is thought to regulate vesicular transport, together with its specific effectors. Mutations in this gene cause several defects, including actin-based melanosome transport defects and immunodeficiency. Mutations in the human ortholog of this gene are associated with Griscelli syndrome type 2. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jul 2014]
Expression	Ubiquitous expression in lung adult (RPKM 6.4), stomach adult (RPKM 4.8) and 26 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

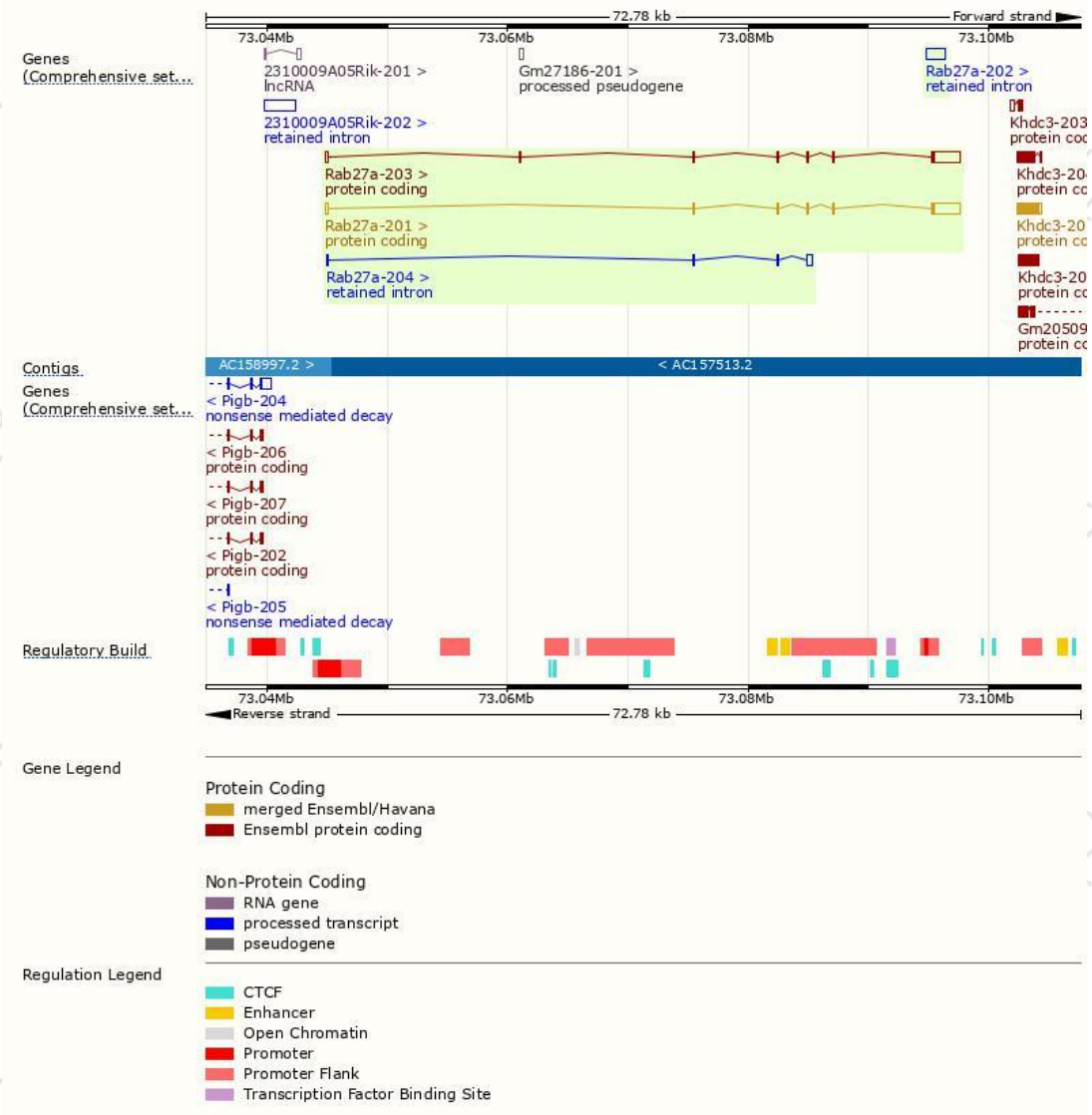
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rab27a-203	ENSMUST00000184146.7	3168	221aa	Protein coding	CCDS23335	Q544U7 Q9ERI2	TSL:1 GENCODE basic APPRIS P1
Rab27a-201	ENSMUST00000034722.4	2979	221aa	Protein coding	CCDS23335	Q544U7 Q9ERI2	TSL:1 GENCODE basic APPRIS P1
Rab27a-202	ENSMUST00000184032.1	1583	No protein	Retained intron	-	-	TSL:NA
Rab27a-204	ENSMUST00000184575.1	679	No protein	Retained intron	-	-	TSL:2

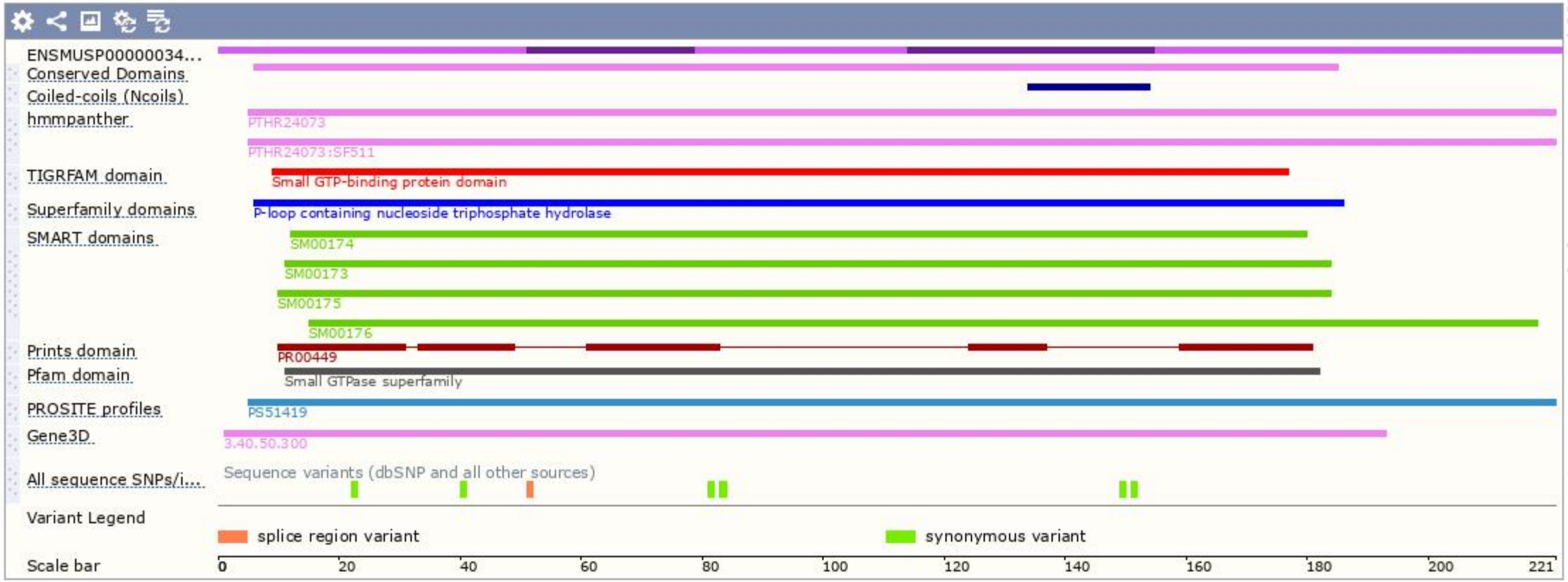
The strategy is based on the design of *Rab27a-201* transcript,The transcription is shown below



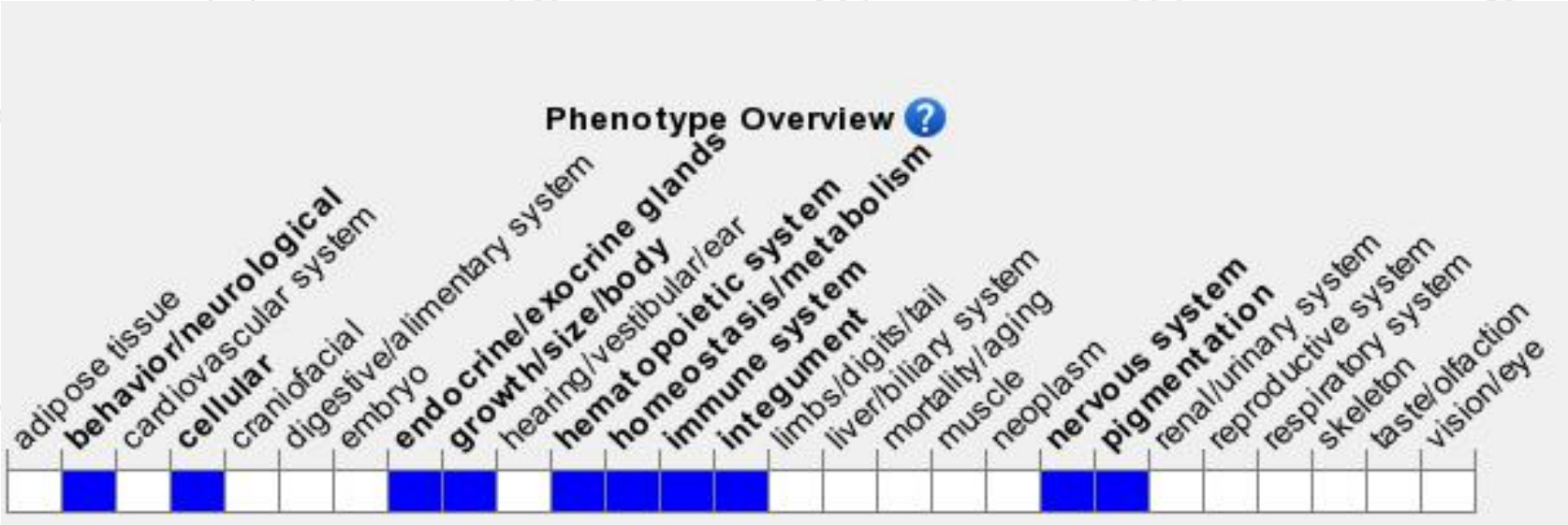
Genomic location distribution



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/).

According to the existing MGI data,Homozygotes have abnormal melanocyte development producing abnormal pigmentation a gray coat color.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd