

Rasa4 Cas9-KO Strategy

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Project Overview

Project Name

Rasa4

Project type

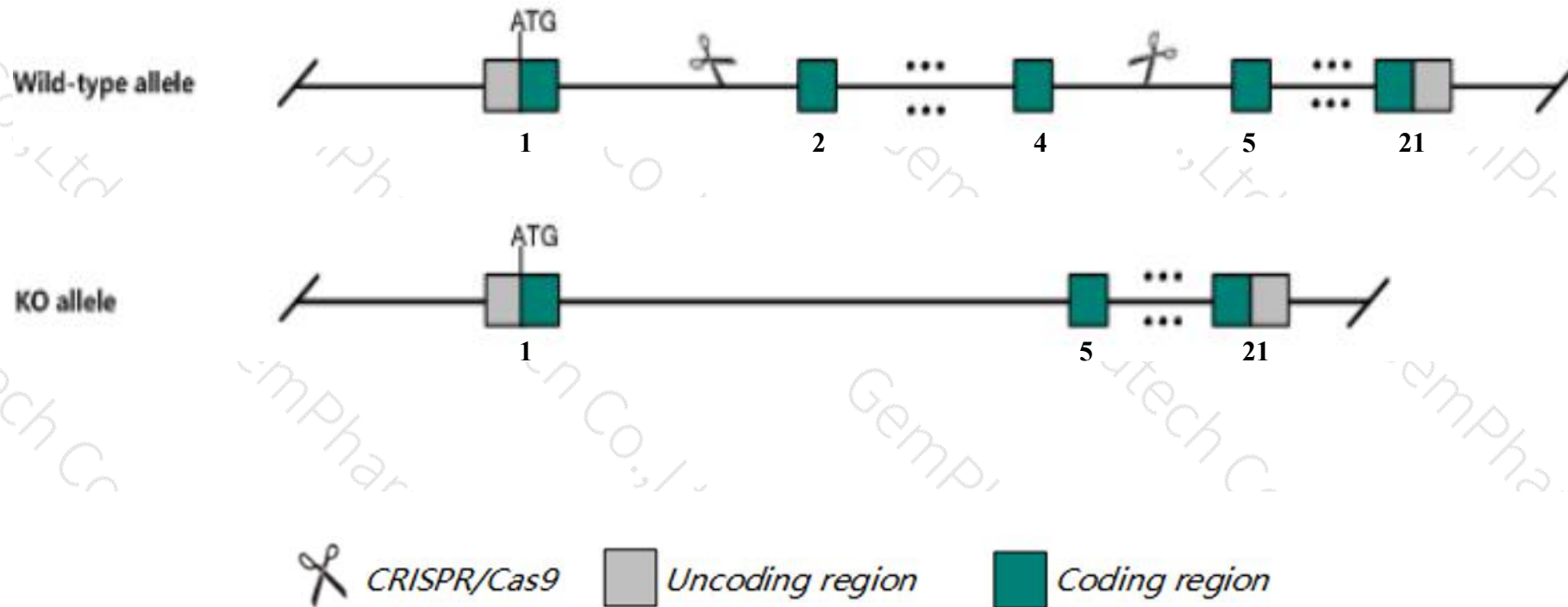
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rasa4* gene. The schematic diagram is as follows:



- The *Rasa4* gene has 13 transcripts. According to the structure of *Rasa4* gene, exon2-exon4 of *Rasa4-201* (ENSMUST00000042135.13) transcript is recommended as the knockout region. The region contains 233bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rasa4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for disruptions in this gene display an increased sensitivity to bacterial infections which involves reduced phagocyte function.
- Transcript *Rasa4-203* may not be affected.
- The *Rasa4* gene is located on the Chr5. 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)

Rasa4 RAS p21 protein activator 4 [Mus musculus (house mouse)]

Gene ID: 54153, updated on 20-Mar-2020

Summary



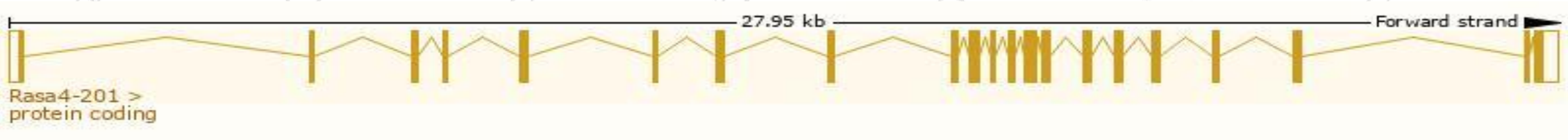
Official Symbol	Rasa4 provided by MGI
Official Full Name	RAS p21 protein activator 4 provided by MGI
Primary source	MGI:MGI:1858600
See related	Ensembl:ENSMUSG000000004952
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA793972, AW112107, BB079060, CAPRI, GAPL
Expression	Ubiquitous expression in colon adult (RPKM 17.6), spleen adult (RPKM 15.3) and 23 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

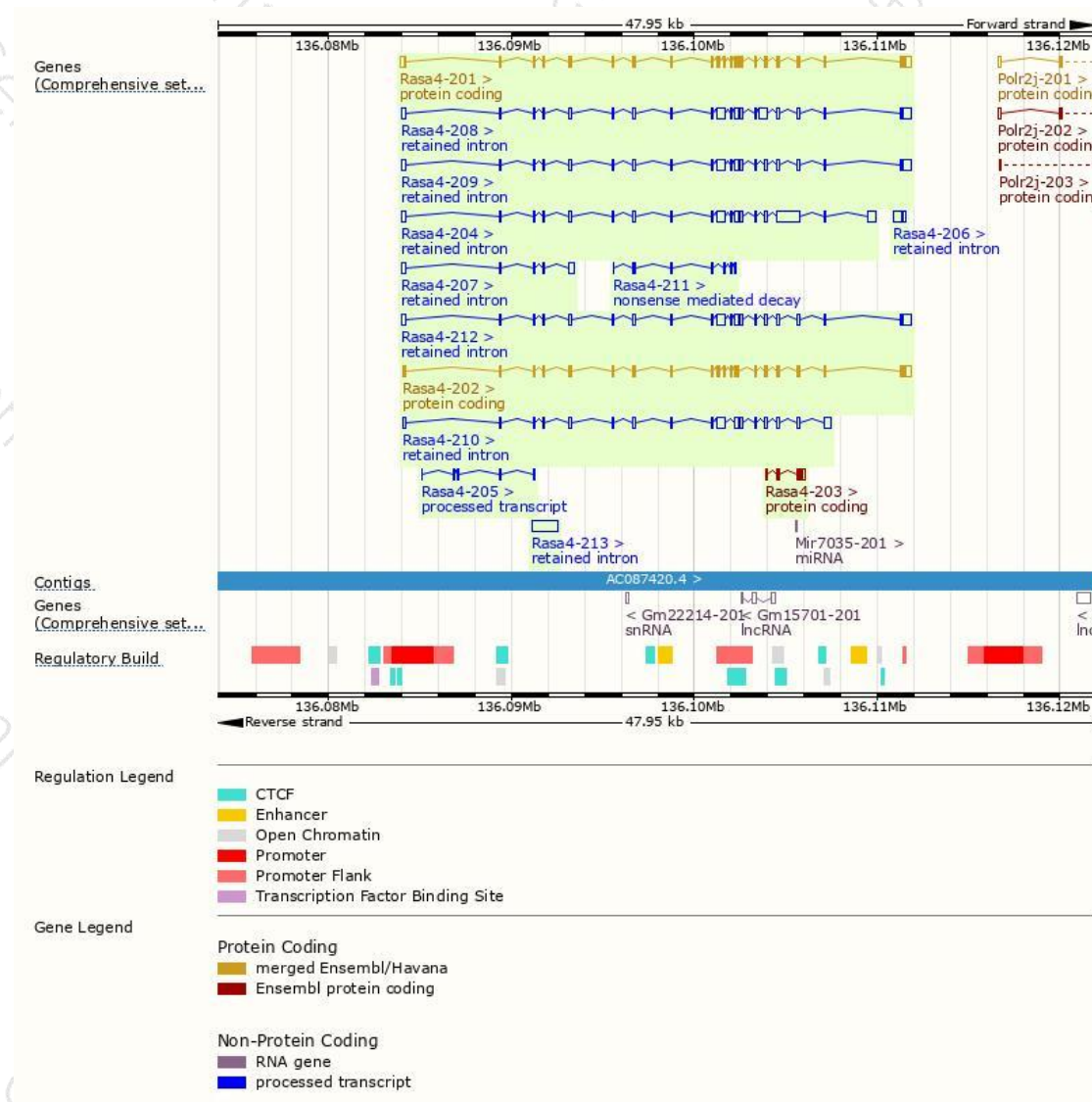
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rasa4-201	ENSMUST00000042135.13	2914	802aa	Protein coding	CCDS39324	Q6PFQ7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Rasa4-202	ENSMUST00000100570.9	2660	756aa	Protein coding	CCDS39325	Q6PFQ7	TSL:1 GENCODE basic
Rasa4-203	ENSMUST00000122887.1	681	178aa	Protein coding	-	F6W8M5	CDS 5' incomplete TSL:2
Rasa4-211	ENSMUST00000145294.1	600	141aa	Nonsense mediated decay	-	F6WTE9	CDS 5' incomplete TSL:5
Rasa4-205	ENSMUST00000125247.1	371	No protein	Processed transcript	-	-	TSL:2
Rasa4-204	ENSMUST00000125048.7	3967	No protein	Retained intron	-	-	TSL:2
Rasa4-208	ENSMUST00000134509.7	3396	No protein	Retained intron	-	-	TSL:2
Rasa4-209	ENSMUST00000135344.7	3057	No protein	Retained intron	-	-	TSL:2
Rasa4-212	ENSMUST00000152723.7	3030	No protein	Retained intron	-	-	TSL:2
Rasa4-210	ENSMUST00000140972.7	2683	No protein	Retained intron	-	-	TSL:2
Rasa4-213	ENSMUST00000199502.1	1470	No protein	Retained intron	-	-	TSL:NA
Rasa4-207	ENSMUST00000131353.7	722	No protein	Retained intron	-	-	TSL:2
Rasa4-206	ENSMUST00000130598.1	485	No protein	Retained intron	-	-	TSL:2

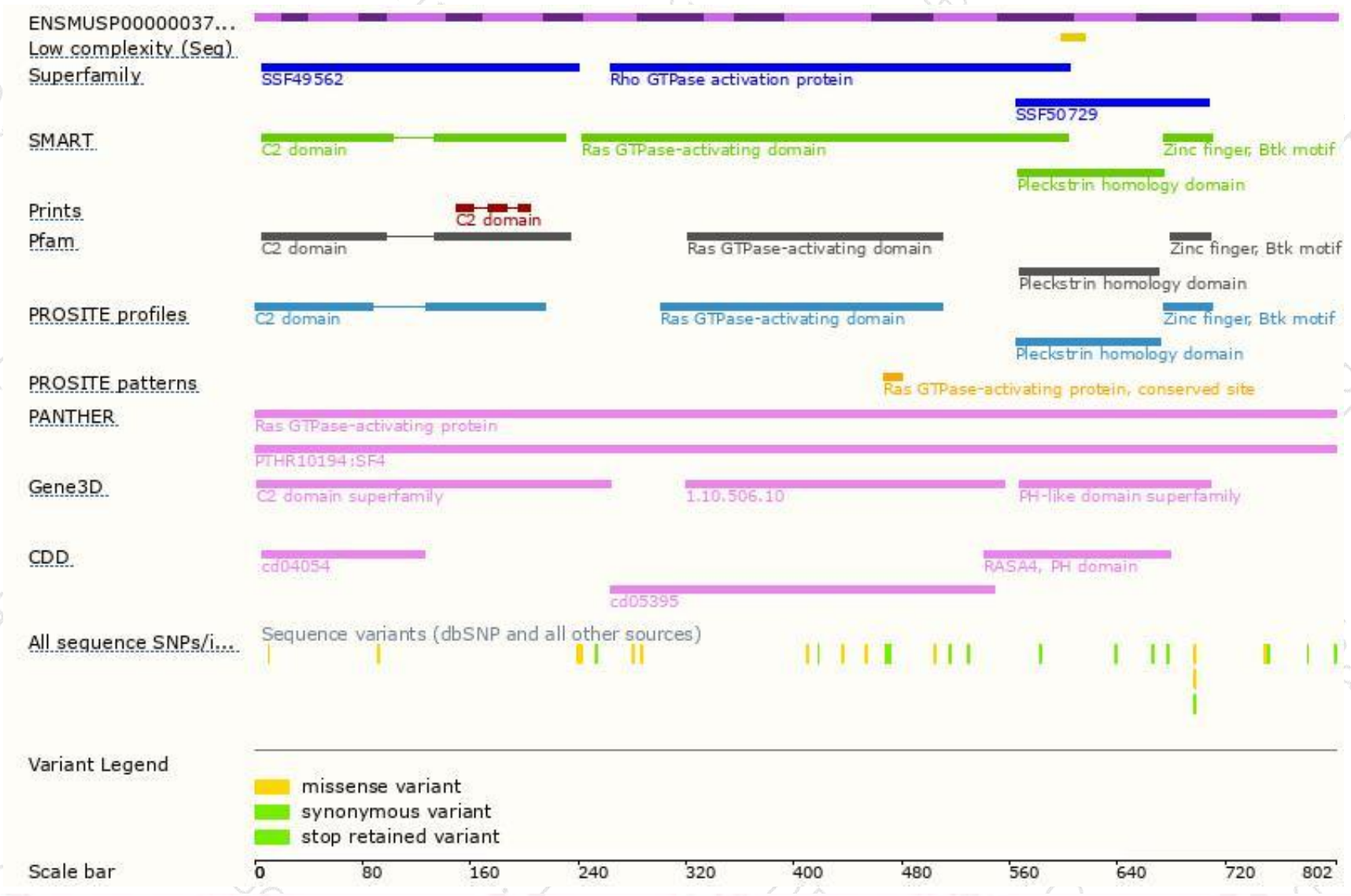
The strategy is based on the design of *Rasa4-201* transcript,the transcription is shown below:



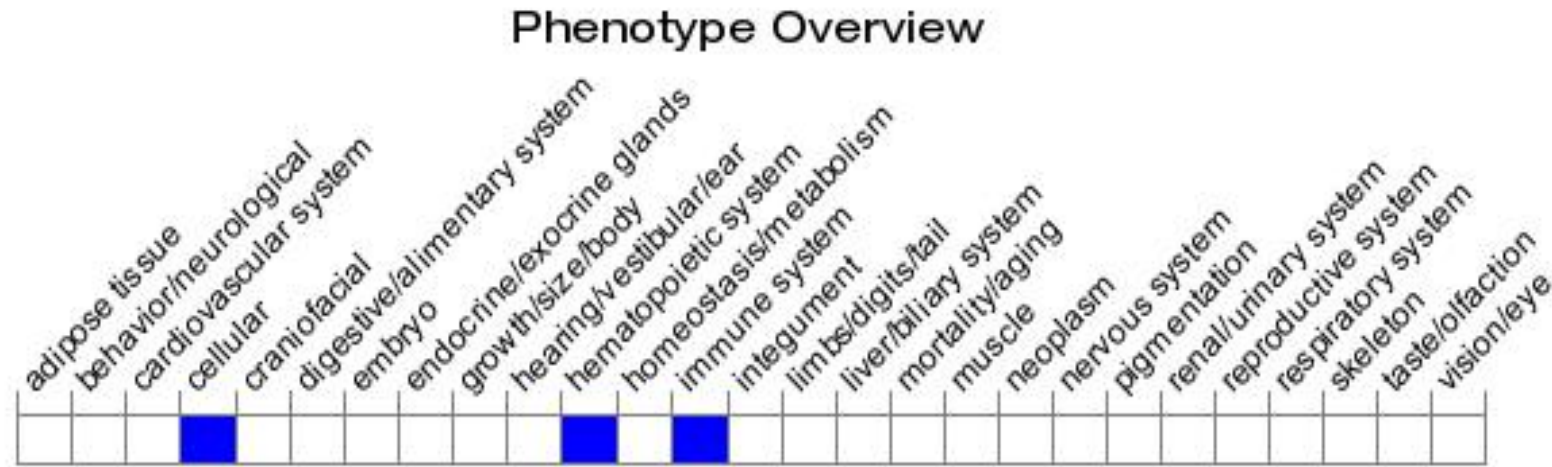
Genomic location distribution



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, mice homozygous for disruptions in this gene display an increased sensitivity to bacterial infections which involves reduced phagocyte function.

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

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