

# *Rit2* Cas9-KO Strategy

**Designer:**

**Daohua Xu**

**Reviewer:**

**Huimin Su**

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# Project Overview

**Project Name**

***Rit2***

**Project type**

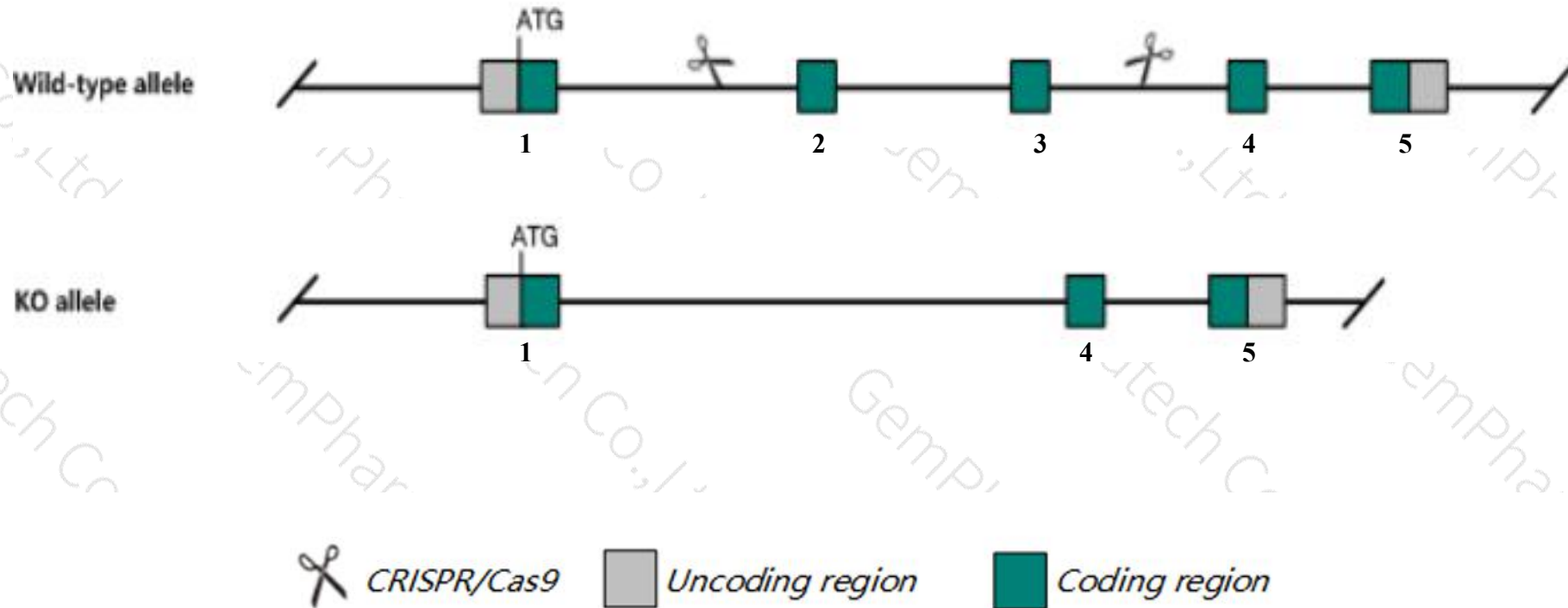
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rit2* gene. The schematic diagram is as follows:



- The *Rit2* gene has 4 transcripts. According to the structure of *Rit2* gene, exon2-exon3 of *Rit2-203* (ENSMUST00000153060.7) transcript is recommended as the knockout region. The region contains 131bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rit2* gene. The brief process is as follows: CRISPR/Cas9 system w

- The *Rit2* gene is located on the Chr18. 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)

## Rit2 Ras-like without CAAX 2 [Mus musculus (house mouse)]

Gene ID: 19762, updated on 13-Mar-2020

### Summary



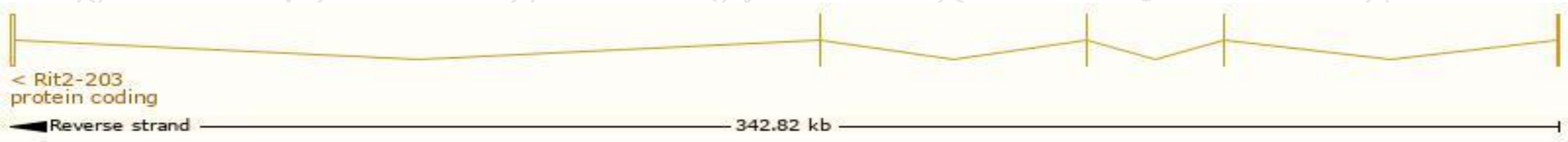
<b>Official Symbol</b>	Rit2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	Ras-like without CAAX 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:108054</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000057455</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	PROVISIONAL
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	RIBA, Rin, Roc2
<b>Expression</b>	Biased expression in cerebellum adult (RPKM 36.4), CNS E18 (RPKM 18.8) and 4 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

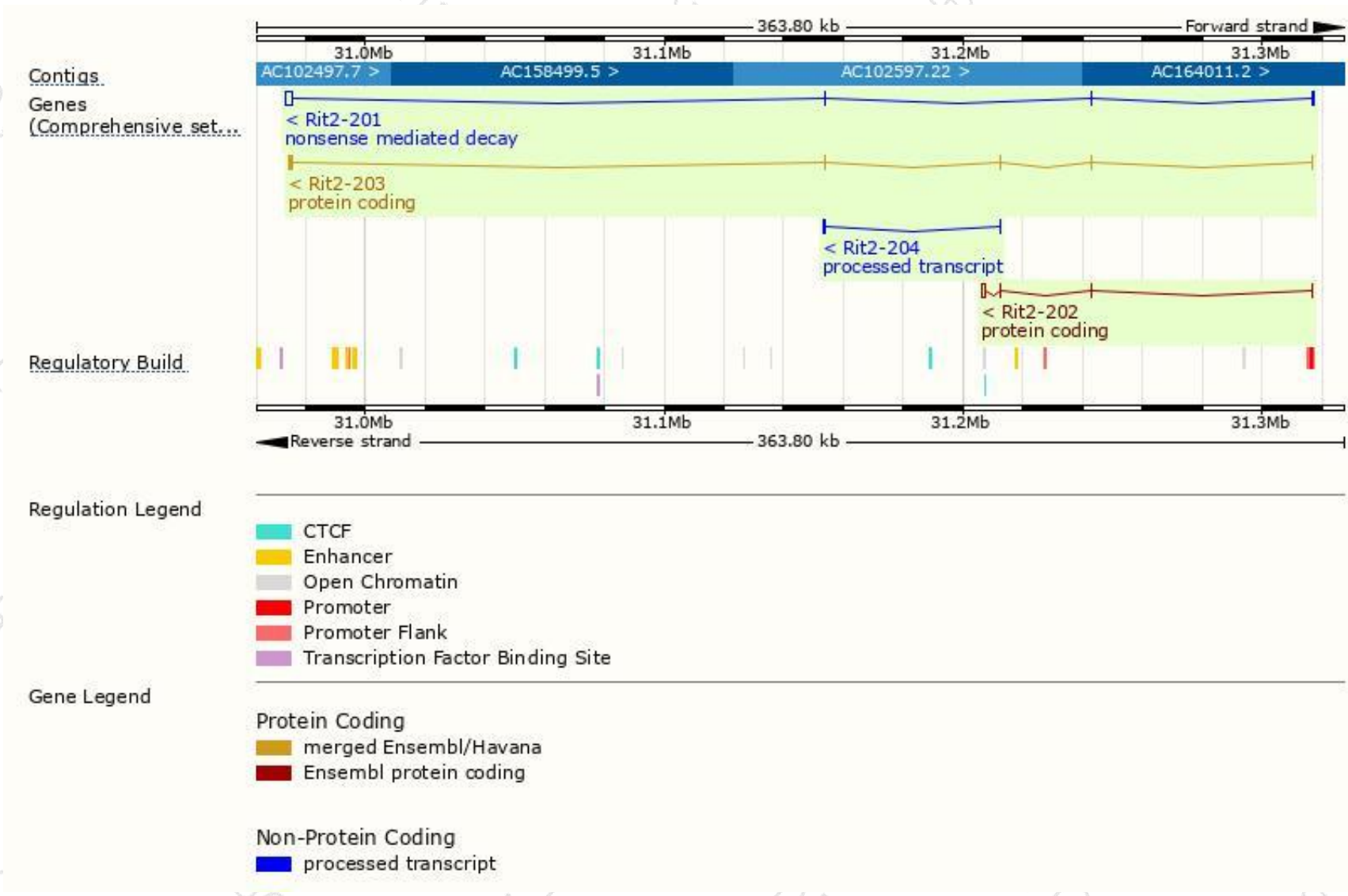
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rit2-203	<a href="#">ENSMUST00000153060.7</a>	1806	<a href="#">217aa</a>	Protein coding	<a href="#">CCDS29108</a>	<a href="#">P70425</a>	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
Rit2-202	<a href="#">ENSMUST00000139924.1</a>	1674	<a href="#">97aa</a>	Protein coding	-	<a href="#">F2Z432</a>	TSL:1 GENCODE basic
Rit2-201	<a href="#">ENSMUST00000082070.12</a>	2715	<a href="#">77aa</a>	Nonsense mediated decay	-	<a href="#">F8WGU6</a>	TSL:1
Rit2-204	<a href="#">ENSMUST00000153196.1</a>	701	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Rit2-203* transcript,The transcription is shown below



# Genomic location distribution





# Protein domain



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

Tel: 400-9660890

