

# ***Rnf122 Cas9-KO Strategy***

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**Reviewer:**

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# Project Overview

**Project Name**

***Rnf122***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnfl22* gene. The schematic diagram is as follows:



- The *Rnfl22* gene has 5 transcripts. According to the structure of *Rnfl22* gene, exon2-exon4 of *Rnfl22-201* (ENSMUST00000046941.7) transcript is recommended as the knockout region. The region contains 245bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rnfl22* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Rnfl22* gene is located on the Chr8. 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)

## Rnf122 ring finger protein 122 [ *Mus musculus* (house mouse) ]

Gene ID: 68867, updated on 15-Aug-2019

### Summary

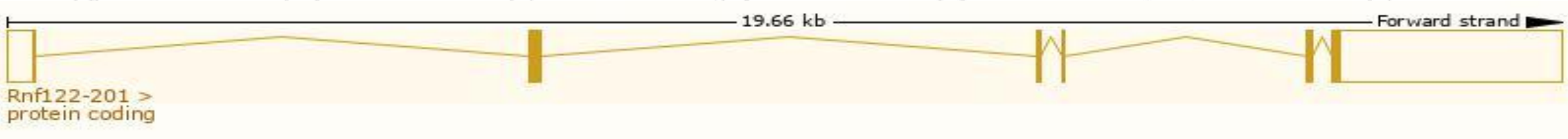
Official Symbol	Rnf122 provided by <a href="#">MGI</a>
Official Full Name	ring finger protein 122 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1916117</a>
See related	<a href="#">Ensembl:ENSMUSG00000039328</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110063C11Rik
Expression	Broad expression in limb E14.5 (RPKM 11.2), CNS E11.5 (RPKM 10.1) and 23 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

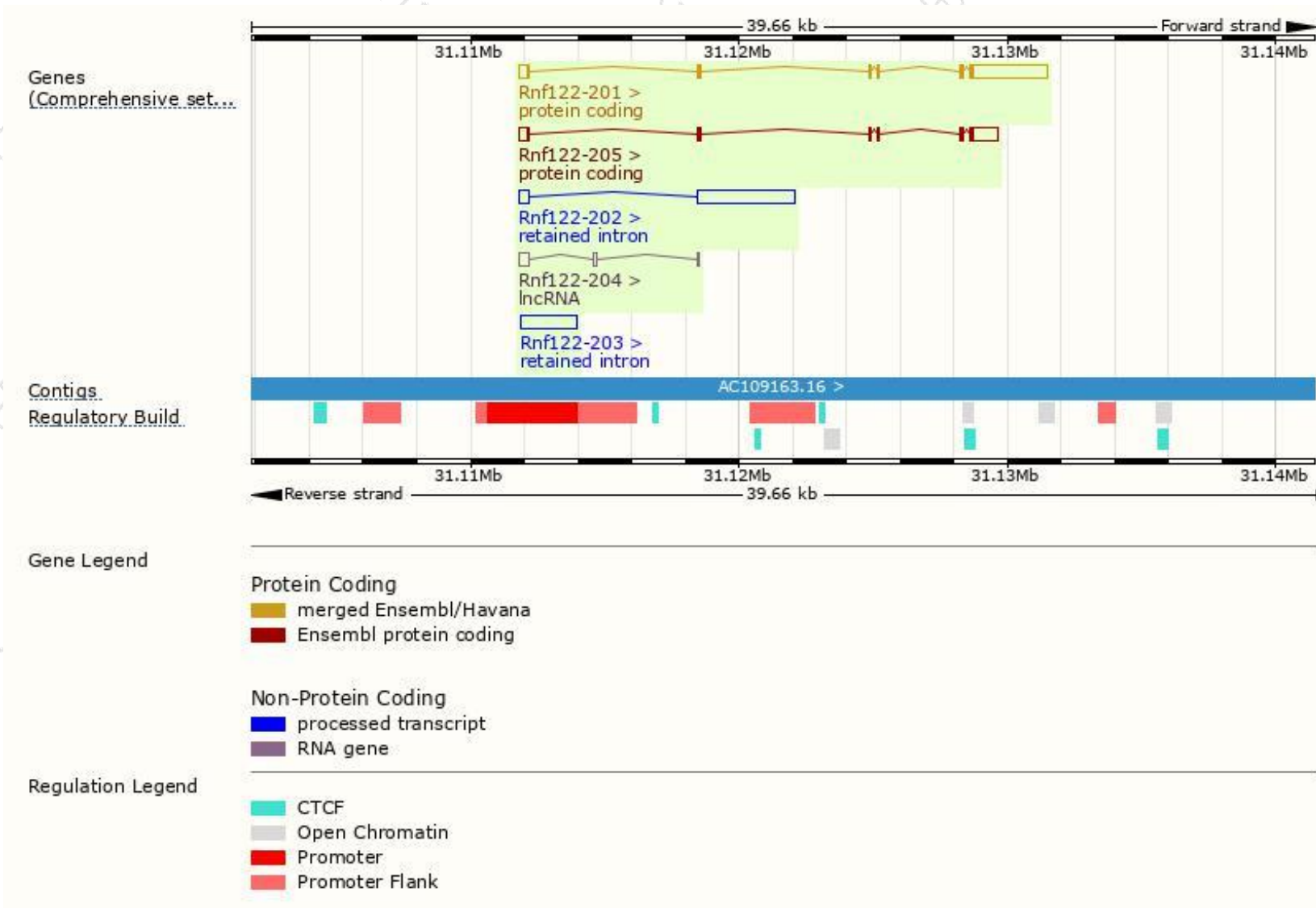
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf122-201	<a href="#">ENSMUST00000046941.7</a>	3582	<a href="#">154aa</a>	Protein coding	<a href="#">CCDS22220</a>	<a href="#">A0A0R4J0G8</a>	TSL:1 GENCODE basic APPRIS P2
Rnf122-205	<a href="#">ENSMUST00000217278.1</a>	1726	<a href="#">155aa</a>	Protein coding	-	<a href="#">Q8BP31</a>	TSL:1 GENCODE basic APPRIS ALT 1
Rnf122-202	<a href="#">ENSMUST00000162640.1</a>	3998	No protein	Retained intron	-	-	TSL:1
Rnf122-203	<a href="#">ENSMUST00000209547.1</a>	2114	No protein	Retained intron	-	-	TSL:NA
Rnf122-204	<a href="#">ENSMUST00000216520.1</a>	567	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Rnf122-201* transcript,The transcription is shown below



# Genomic location distribution





# Protein domain



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

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