

***Lym2* Cas9-KO Strategy**

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Project Overview

Project Name

Lyrm2

Project type

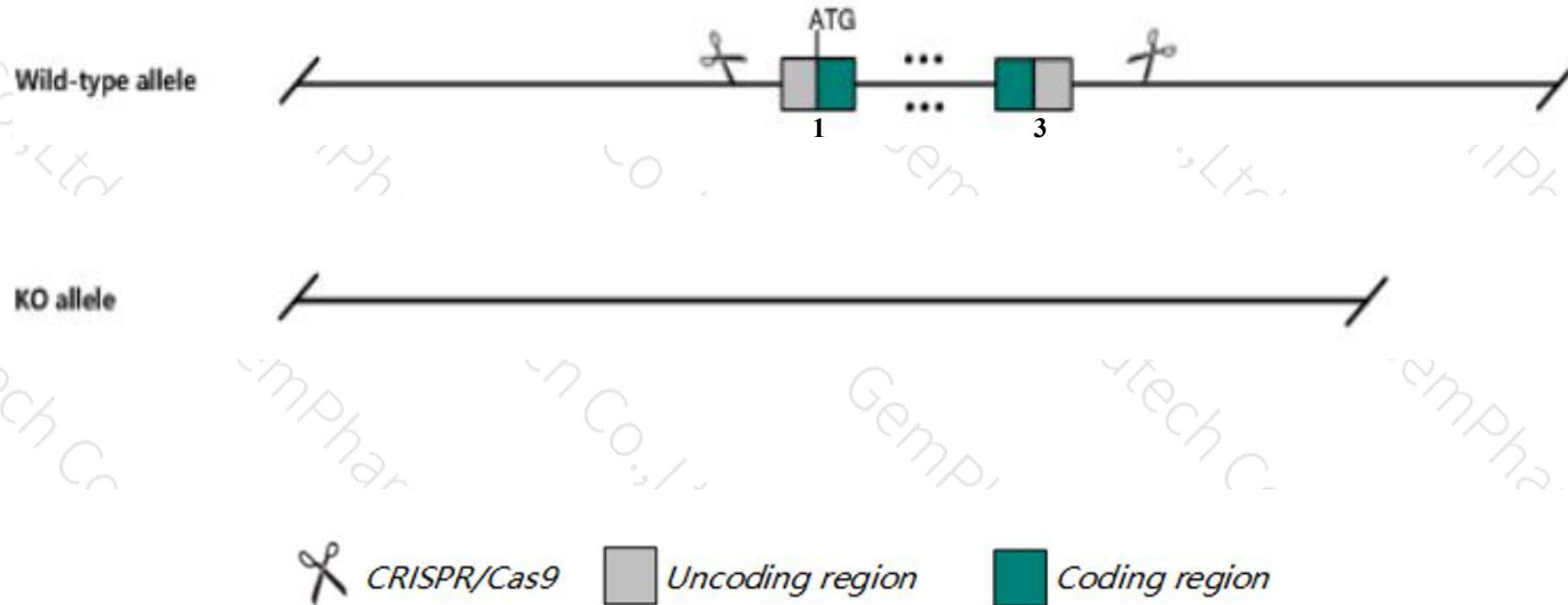
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lymr2* gene. The schematic diagram is as follows:



- The *Lymr2* gene has 3 transcripts. According to the structure of *Lymr2* gene, exon1-exon3 of *Lymr2-201* (ENSMUST00000062802.4) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lymr2* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Lym2* gene is located on the Chr4. 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)

Lyrm2 LYR motif containing 2 [Mus musculus (house mouse)]

Gene ID: 108755, updated on 13-Mar-2020

Summary



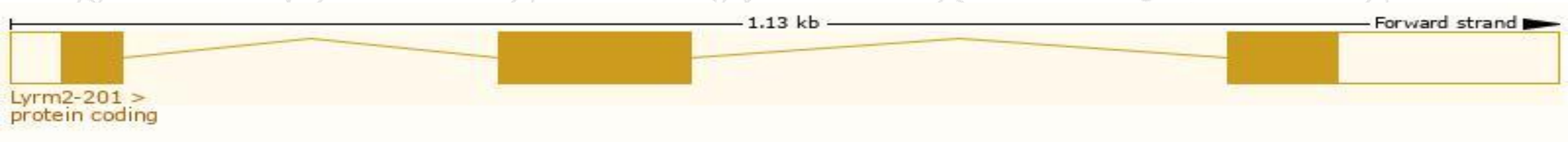
Official Symbol	Lyrm2 provided by MGI
Official Full Name	LYR motif containing 2 provided by MGI
Primary source	MGI:MGI:1917573
See related	Ensembl:ENSMUSG00000045854
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610208E05Rik
Expression	Broad expression in CNS E11.5 (RPKM 19.1), CNS E14 (RPKM 15.5) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

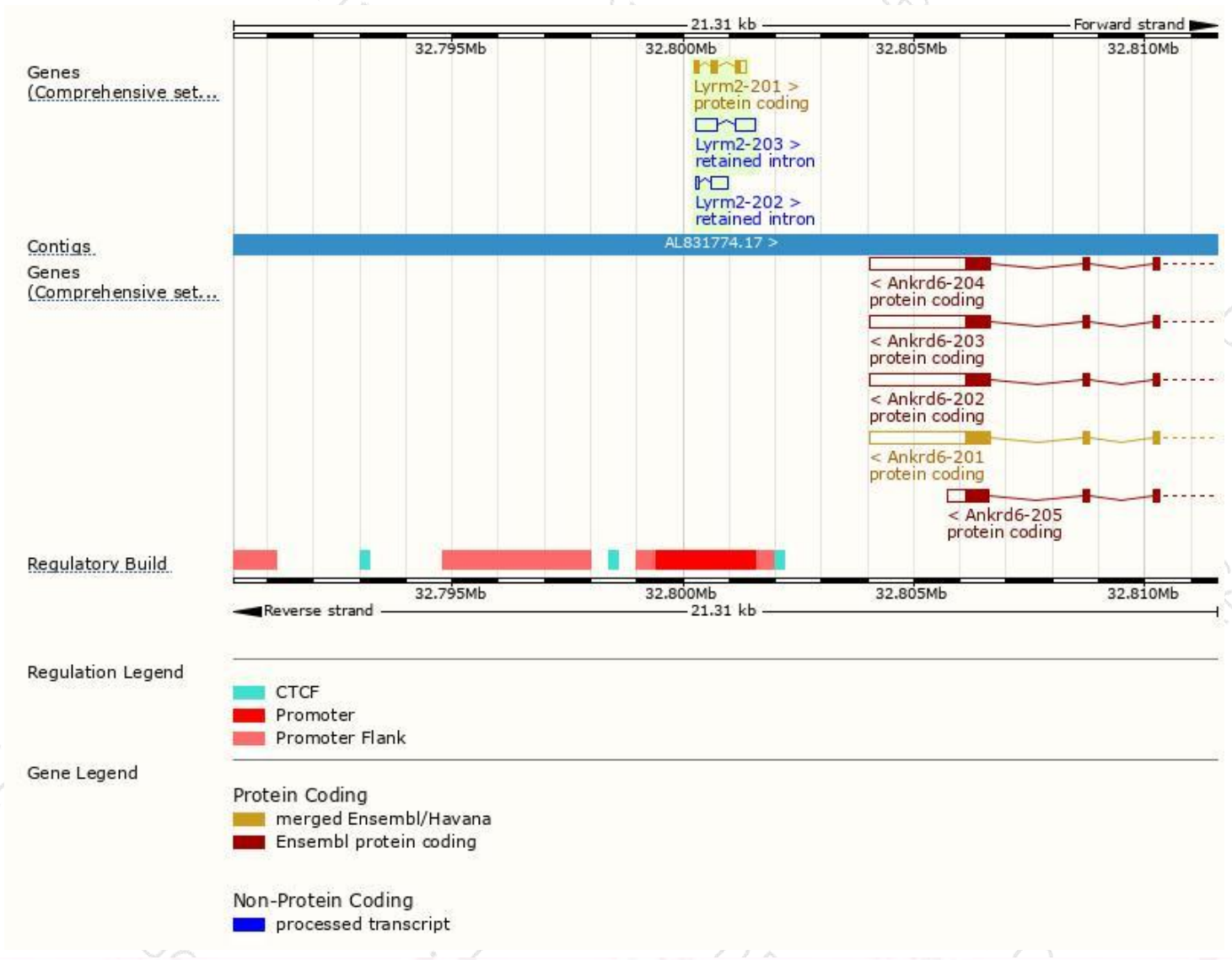
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lyrm2-201	ENSMUST00000062802.4	465	88aa	Protein coding	CCDS38703	Q8R033	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
Lyrm2-203	ENSMUST00000135833.1	889	No protein	Retained intron	-	-	TSL:2
Lyrm2-202	ENSMUST00000130321.1	420	No protein	Retained intron	-	-	TSL:3

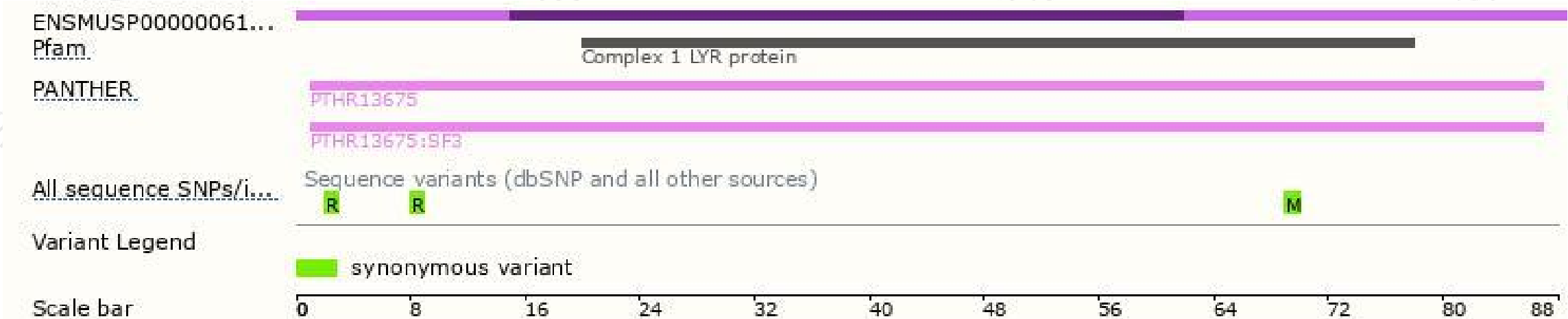
The strategy is based on the design of *Lyrm2-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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