

Clrn3 Cas9-KO Strategy

Designer:

Yanhua Shen

Reviewer:

Xueting Zhang

Design Date:

2020-5-7

Project Overview

Project Name

Cln3

Project type

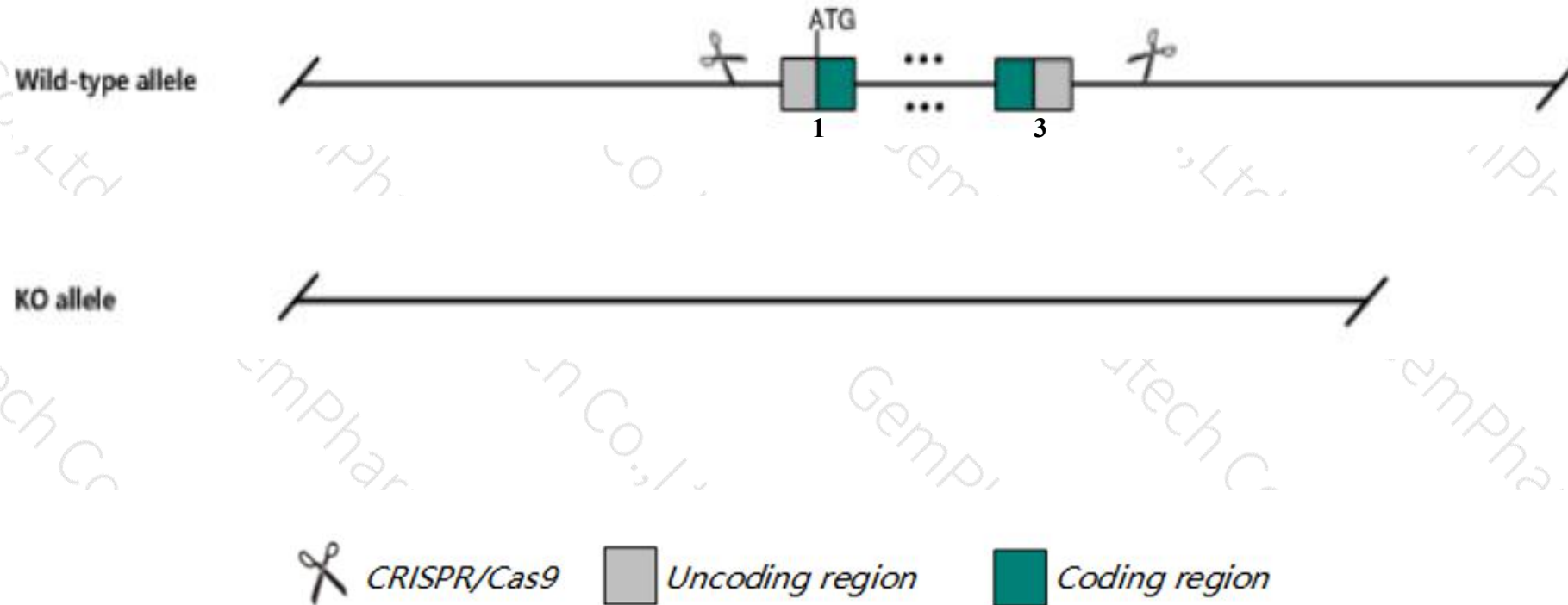
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cln3* gene. The schematic diagram is as follows:



- The *Clrn3* gene has 1 transcript. According to the structure of *Clrn3* gene, exon1-exon3 of *Clrn3-201* (ENSMUST00000053716.7) 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 *Clrn3* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Clrn3* gene is located on the Chr7. 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)

Clrn3 clarin 3 [Mus musculus (house mouse)]

Gene ID: 212070, updated on 13-Mar-2020

Summary



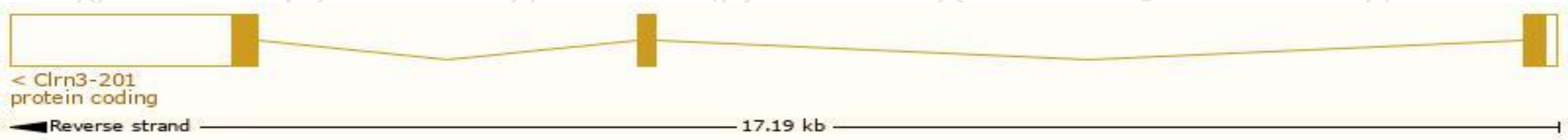
Official Symbol	Clrn3 provided by MGI
Official Full Name	clarin 3 provided by MGI
Primary source	MGI:MGI:2142022
See related	Ensembl:ENSMUSG00000050866
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Al649392, Tmem12
Expression	Biased expression in large intestine adult (RPKM 28.2), small intestine adult (RPKM 11.9) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

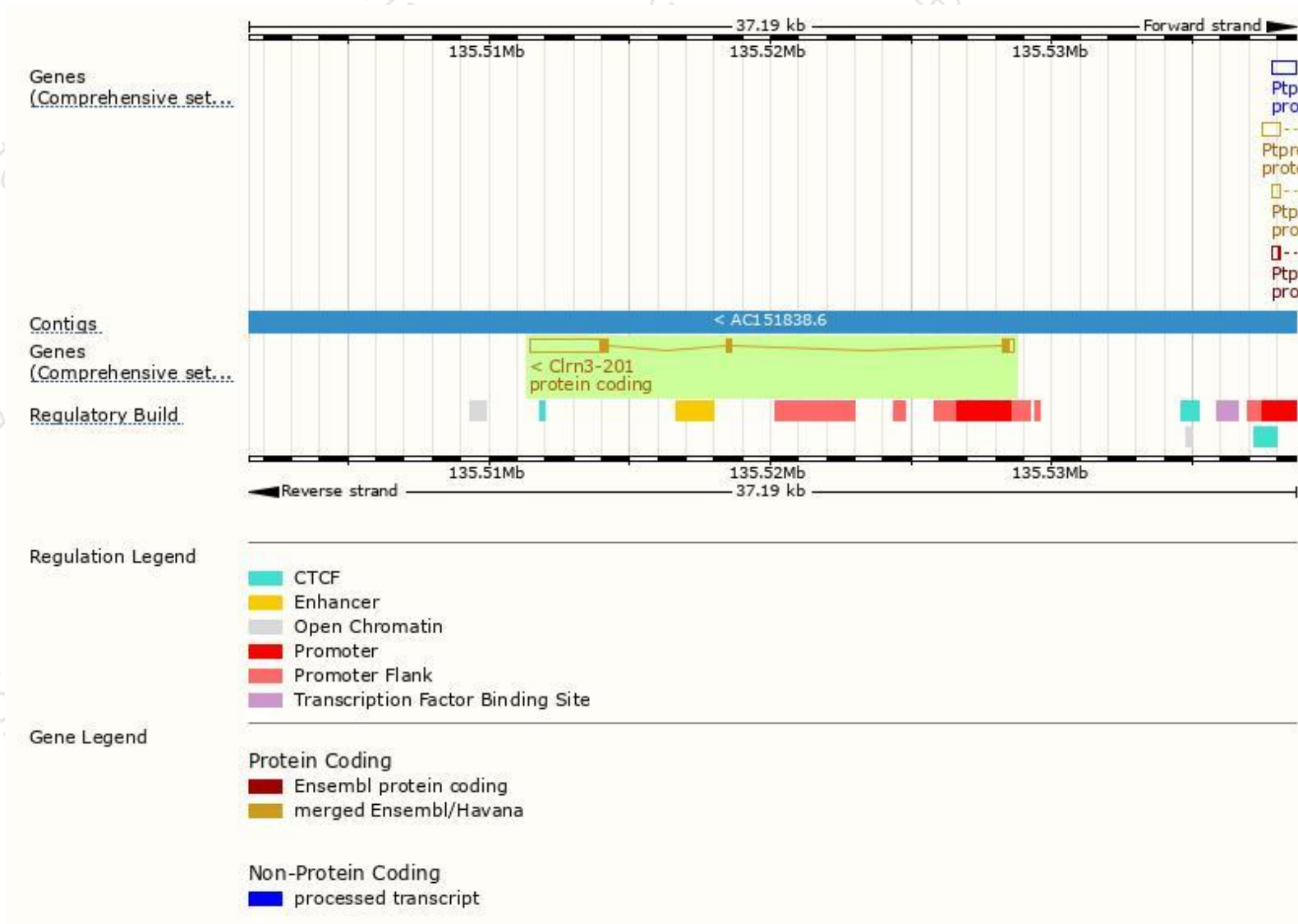
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Clrn3-201	ENSMUST00000053716.7	3305	226aa	Protein coding	CCDS21943	Q8BHH8	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

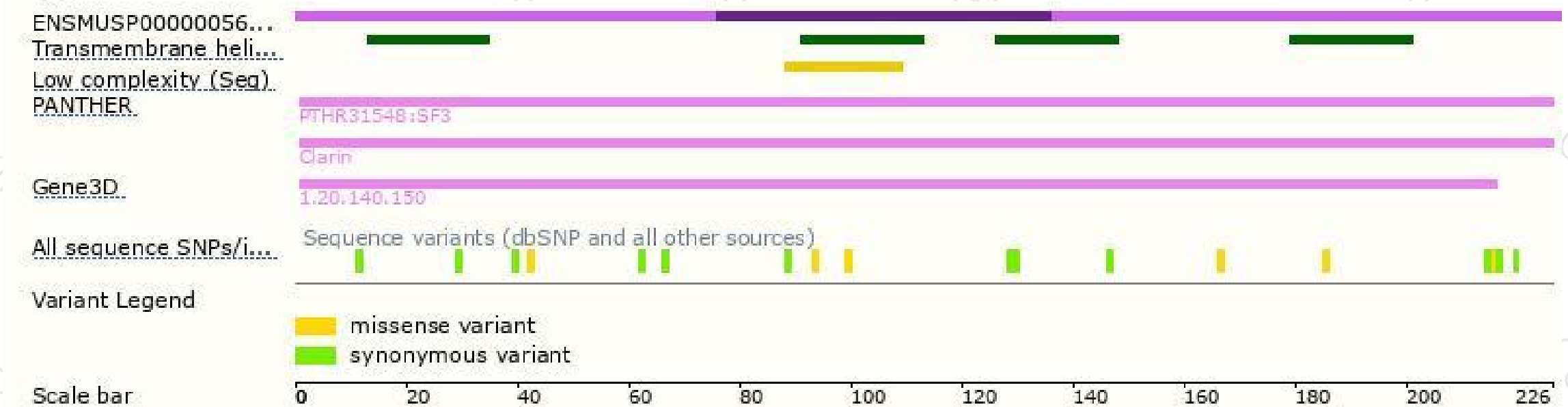
The strategy is based on the design of *Clrn3-201* transcript, the transcription is shown below:



Genomic location distribution



Protein domain



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

Tel: 400-9660890

