Cldn17 Cas9-KO Strategy

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Project Overview

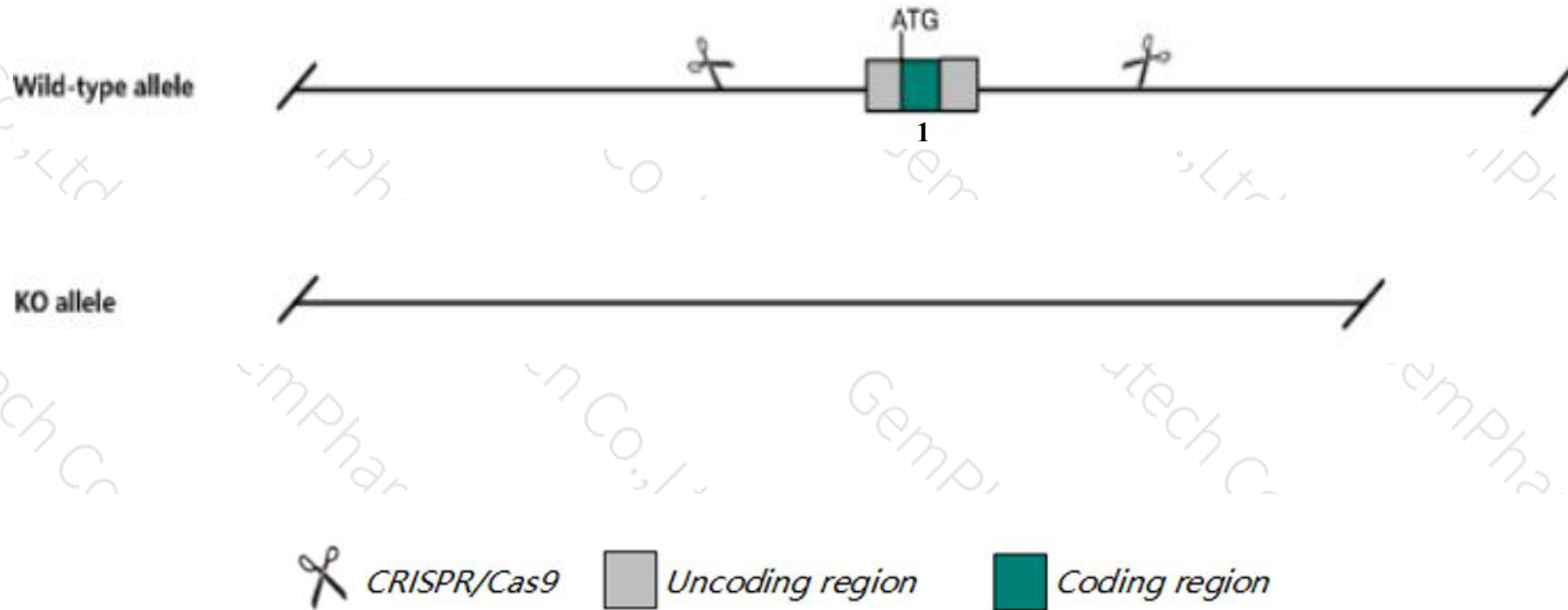|	
Project Name	*Cldn17*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cldn17* gene. The schematic diagram is as follows:

Technical routes

➢ The *Cldn17* gene has 1 transcript. According to the structure of *Cldn17* gene, exon1 of *Cldn17-201* (ENSMUST00000069549.2) 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 *Cldn17* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ The *Cldn17* gene is located on the Chr16. 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）

Cldn17 claudin 17 [Mus musculus (house mouse)]

Gene ID: 239931, updated on 13-Mar-2020

▲ Summary

|	
Official Symbol	Cldn17 provided by MGI
Official Full Name	claudin 17 provided by MGI
Primary source	MGI:MGI:2652030
See related	Ensembl:ENSMUSG00000055811
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	This gene encodes a member of the claudin family. Claudins are integral membrane proteins and components of tight junction strands. Tight junction strands serve as a physical barrier to prevent solutes and water from passing freely through the paracellular space between epithelial or endothelial cell sheets, and also play critical roles in maintaining cell polarity and signal transductions. This gene is intronless and is clustered with the Cldn8 gene on chromosome 16. [provided by RefSeq, Aug 2010]
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
Cldn17-201	ENSMUST00000069549.2	1172	224aa	Protein coding	CCDS28295	Q8BXA6	TSL:NA 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 *Cldn17-201* transcript,the transcription is shown below:

< Cldn17-201
protein coding

◀─ Reverse strand ───────────────── 1.17 kb ─────────
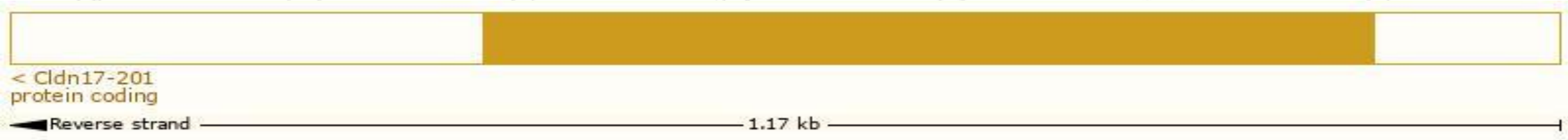
Genomic location distribution
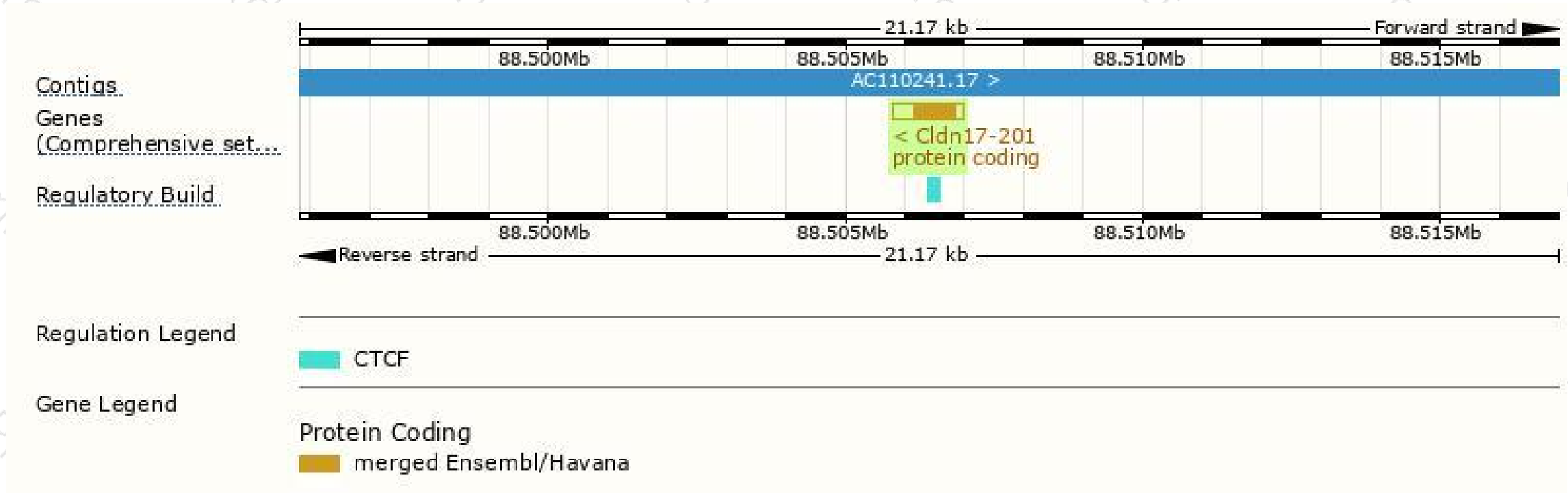
Protein domain
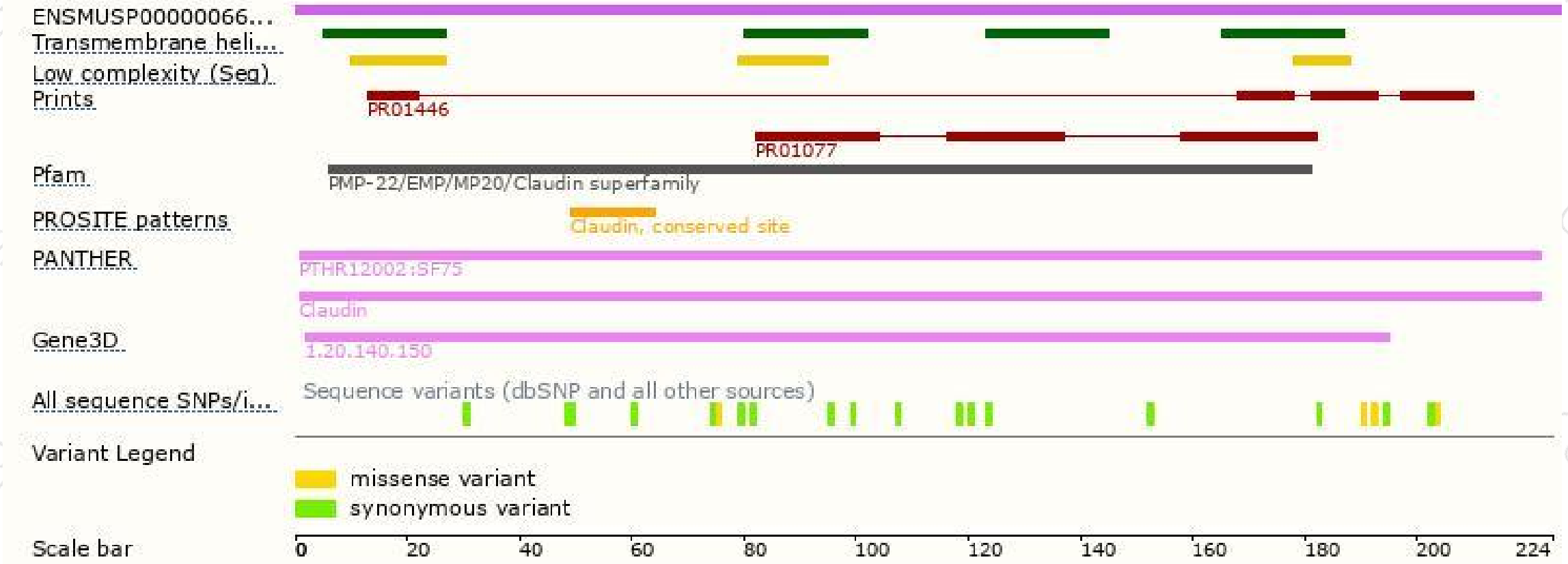
If you have any questions, you are welcome to inquire.
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