

# *Cldn18* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Cldn18***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cldn18* gene. The schematic diagram is as follows:



- The *Cldn18* gene has 4 transcripts. According to the structure of *Cldn18* gene, exon2-exon3 of *Cldn18-201* (ENSMUST00000035048.11) transcript is recommended as the knockout region. The region contains 292bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cldn18* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit increased bone resorption and osteoclast differentiation. Homozygotes for another knock-out allele have impaired alveolarization and alveolar epithelial barrier function.
- The *Cldn18* gene is located on the Chr9. 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)

## Cldn18 claudin 18 [Mus musculus (house mouse)]

Gene ID: 56492, updated on 31-Jan-2019

### Summary



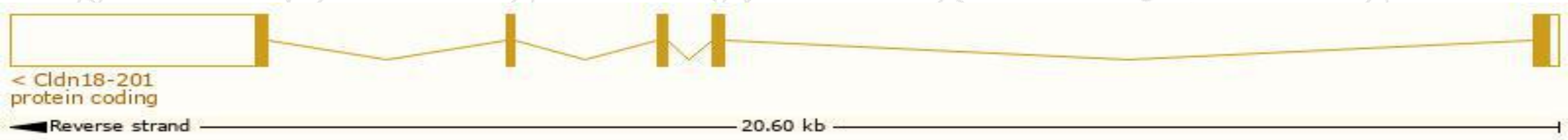
<b>Official Symbol</b>	Cldn18 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	claudin 18 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1929209</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000032473</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<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>Summary</b>	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 a downstream target gene regulated by the T/EBP/NKX2.1 homeodomain transcription factor. Four alternatively spliced transcript variants resulted from alternative promoters and alternative splicing have been identified, which encode two lung-specific isoforms and two stomach-specific isoforms respectively. This gene is also expressed in colons, inner ear and skin, and its expression is increased in both experimental colitis and ulcerative colitis. [provided by RefSeq, Aug 2010]
<b>Expression</b>	Biased expression in lung adult (RPKM 177.1), stomach adult (RPKM 118.5) and 1 other tissue <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

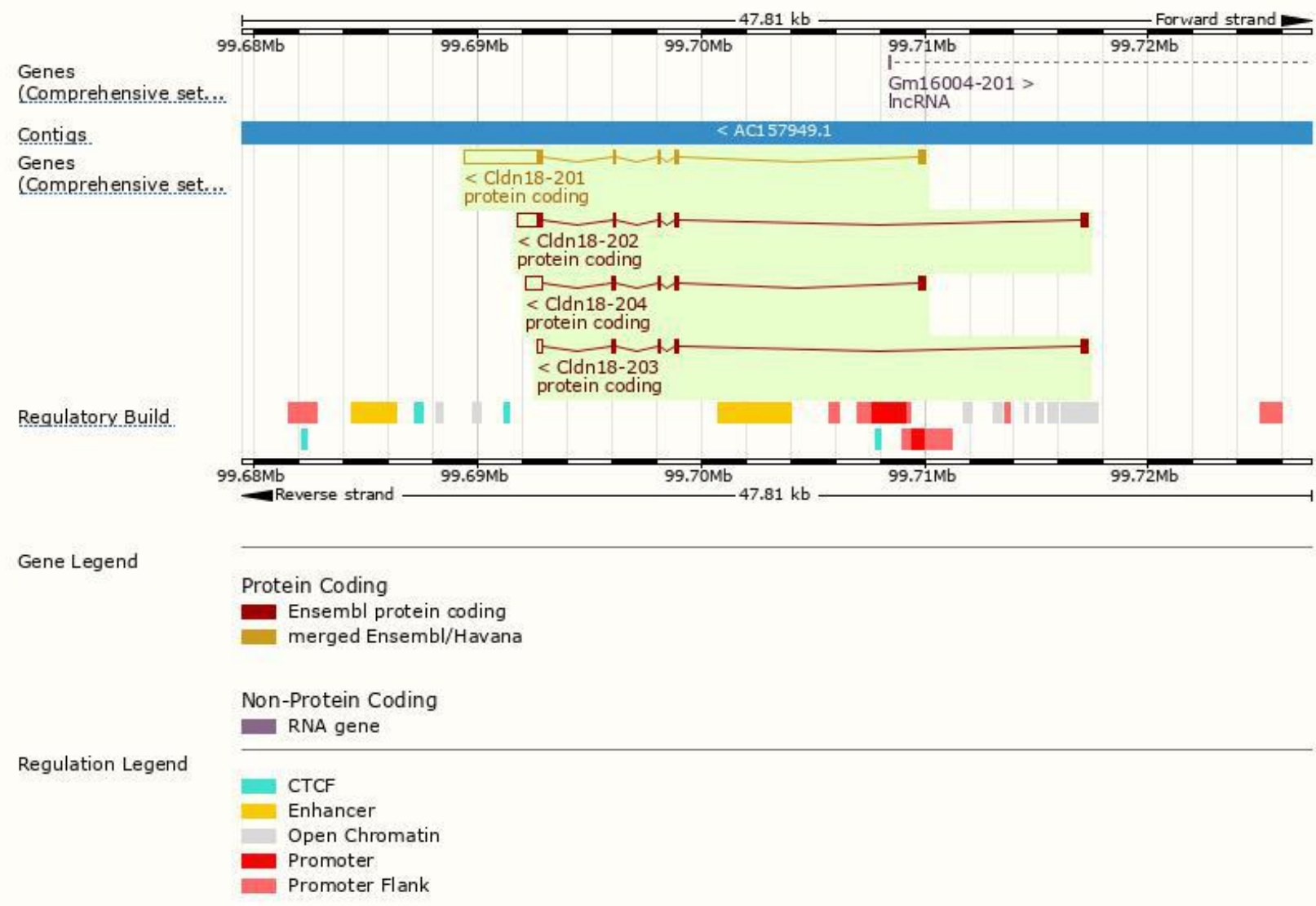
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cldn18-201	<a href="#">ENSMUST00000035048.11</a>	4172	<a href="#">264aa</a>	Protein coding	<a href="#">CCDS23437</a>	<a href="#">P56857</a>	TSL:1 GENCODE basic APPRIS P3
Cldn18-202	<a href="#">ENSMUST00000112882.8</a>	1750	<a href="#">264aa</a>	Protein coding	<a href="#">CCDS57694</a>	<a href="#">P56857</a>	TSL:1 GENCODE basic APPRIS ALT 1
Cldn18-204	<a href="#">ENSMUST00000136429.7</a>	1409	<a href="#">208aa</a>	Protein coding	<a href="#">CCDS57692</a>	<a href="#">P56857</a>	TSL:1 GENCODE basic
Cldn18-203	<a href="#">ENSMUST00000131922.1</a>	860	<a href="#">208aa</a>	Protein coding	<a href="#">CCDS57693</a>	<a href="#">P56857</a>	TSL:1 GENCODE basic

The strategy is based on the design of *Cldn18-201* transcript,The transcription is shown below

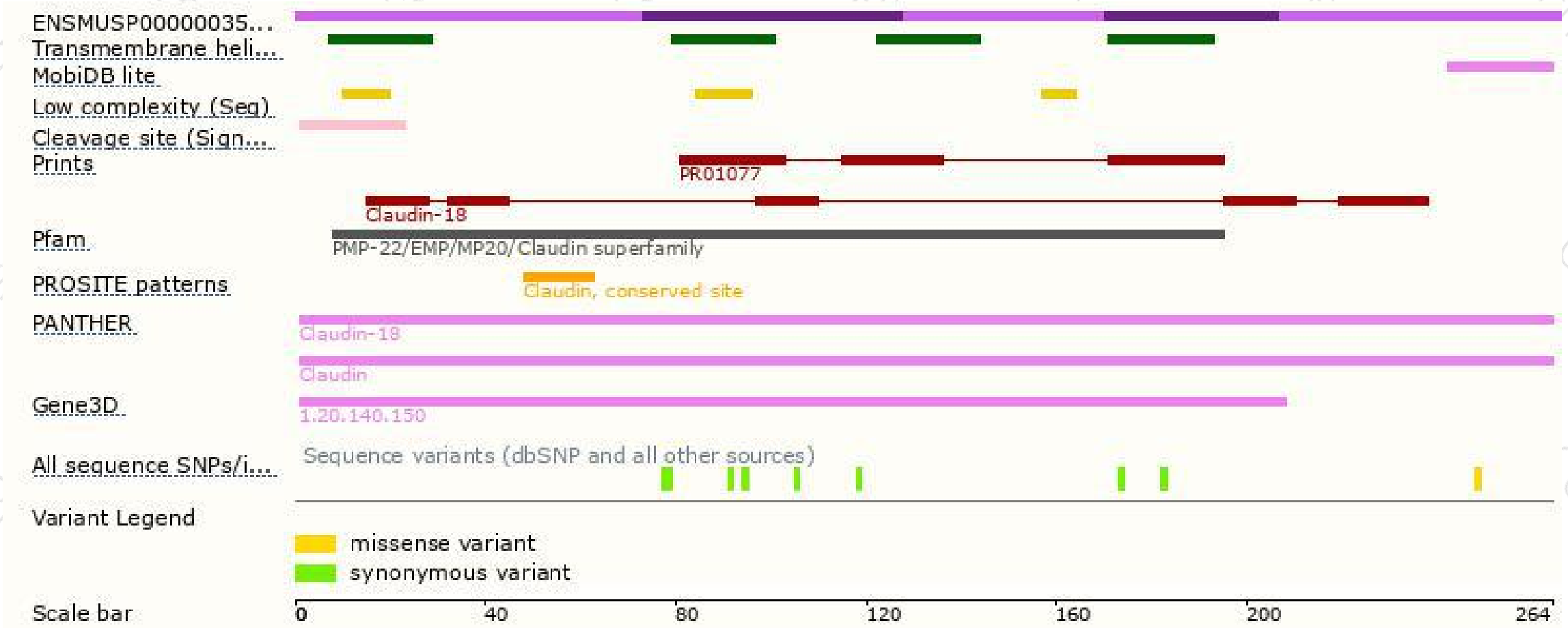


# Genomic location distribution

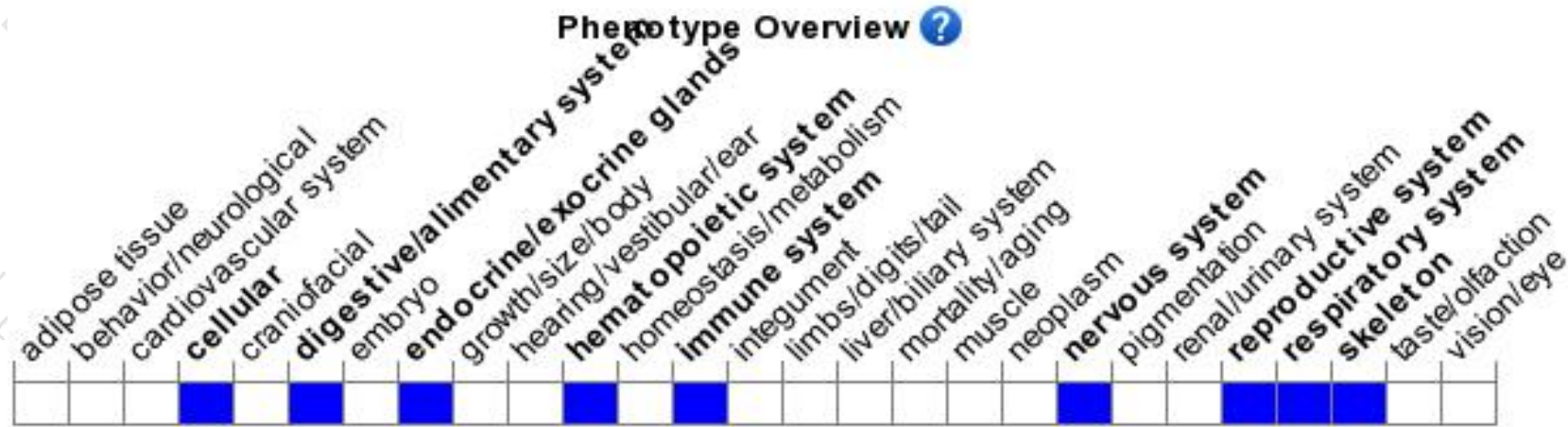




# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, Mice homozygous for a knock-out allele exhibit increased bone resorption and osteoclast differentiation. Homozygotes for another knock-out allele have impaired alveolarization and alveolar epithelial barrier function.

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

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