Cldn15 Cas9-KO Strategy

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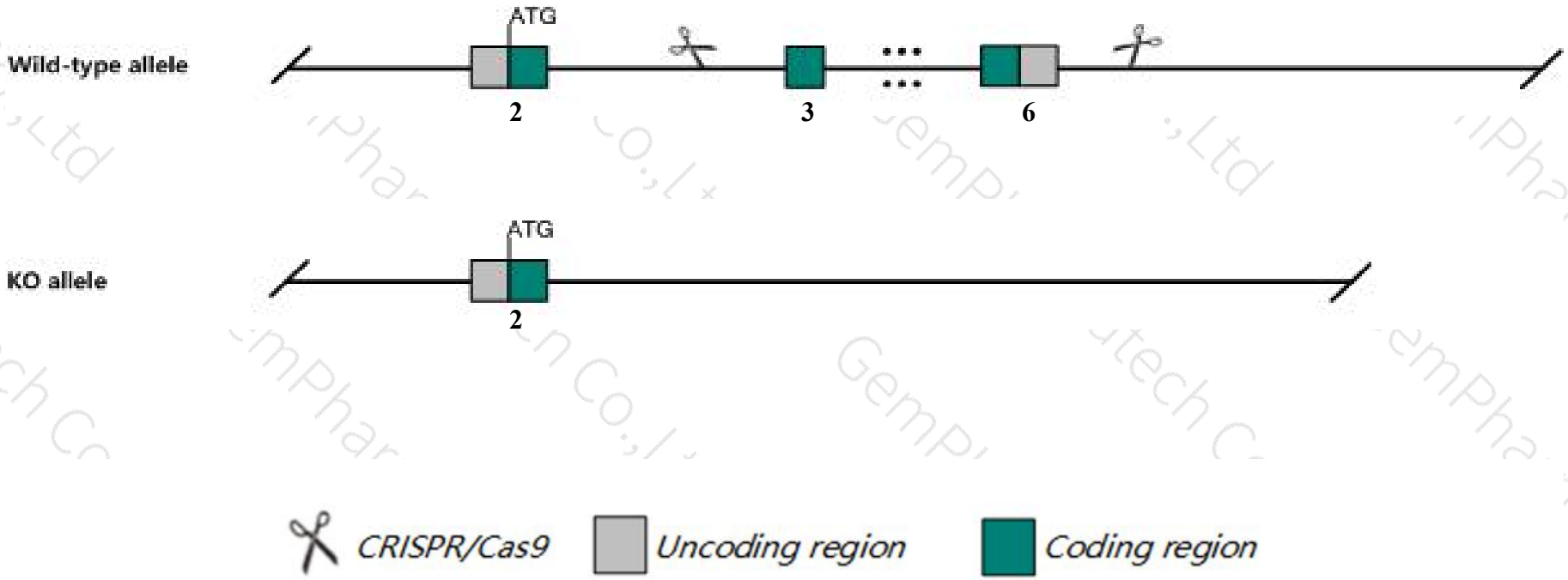
Project Overview

Project Name	***Cldn15***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cldn15* gene. The schematic diagram is as follows:



Technical routes

➢ The *Cldn15* gene has 3 transcripts. According to the structure of *Cldn15* gene, exon3-exon6 of *Cldn15-202* (ENSMUST00000111093.7) transcript is recommended as the knockout region.The region contains 467bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cldn15* gene. The brief process is as follows: CRISPR/Cas9 syster

Notice

➢ According to the existing MGI data,Mice homozygous for a knock-out allele are viable and grow normally with an enlarged upper small intestinal phenotype (megaintestine) resulting from enhanced proliferation of normal cryptic cells after weaning.

➢ The *Cldn15* gene is located on the Chr5. 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）

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Cldn15 claudin 15 [*Mus musculus* (house mouse)]

Gene ID: 60363, updated on 12-Aug-2019

Summary

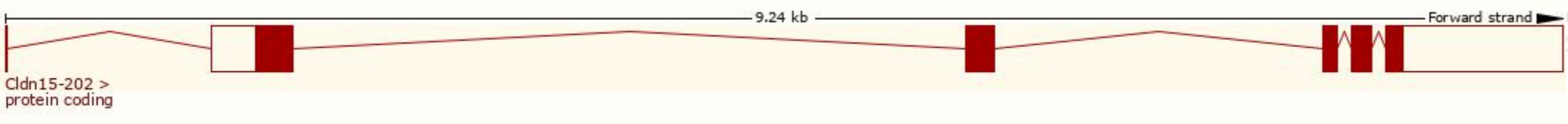
Official Symbol	Cldn15 provided by MGI
Official Full Name	claudin 15 provided by MGI
Primary source	MGI:MGI:1913103
See related	Ensembl:ENSMUSG00000001739
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BB107105; 2210009B08Rik
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 protein increases permeability for sodium ions in anion-selective epithelial cell sheets. The gene deficiency leads to megaintestine and decreases in intestinal epithelial paracellular ion permeability. This gene is a direct target for hepatocyte-nuclear-factor-4alpha, a mediator of ion epithelial transport, and is down-modulated in inflammatory bowel disease. [provided by RefSeq, Aug 2010]
Expression	Biased expression in duodenum adult (RPKM 299.4), large intestine adult (RPKM 256.9) and 3 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

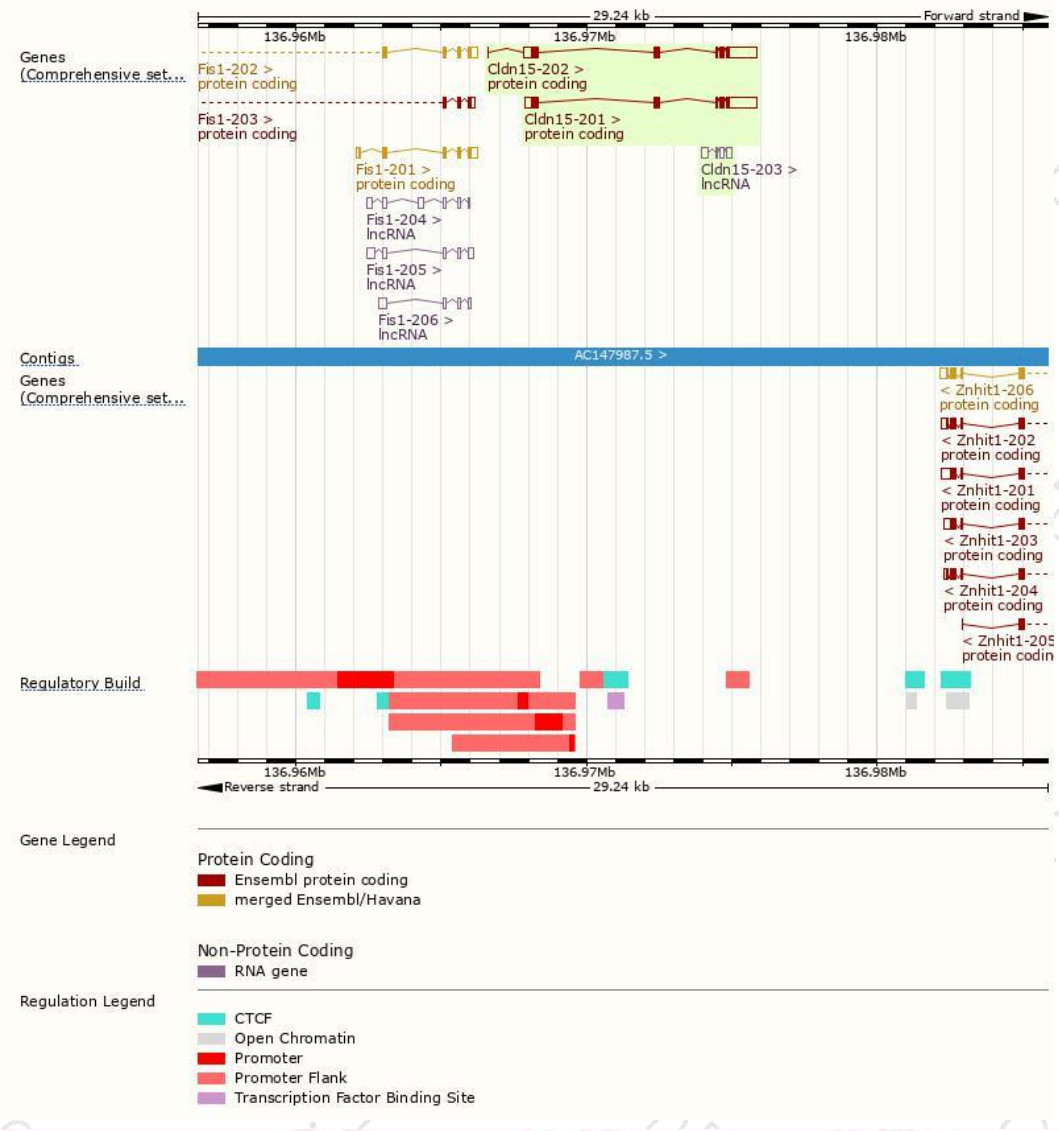
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt ▲	Flags
Cldn15-202	ENSMUST00000111093.7	1902	227aa	Protein coding	CCDS19758	Q9Z0S5	TSL:5 GENCODE basic APPRIS P1
Cldn15-201	ENSMUST00000001790.5	1850	227aa	Protein coding	CCDS19758	Q9Z0S5	TSL:1 GENCODE basic APPRIS P1
Cldn15-203	ENSMUST00000128391.1	621	No protein	Processed transcript	-	-	TSL:3

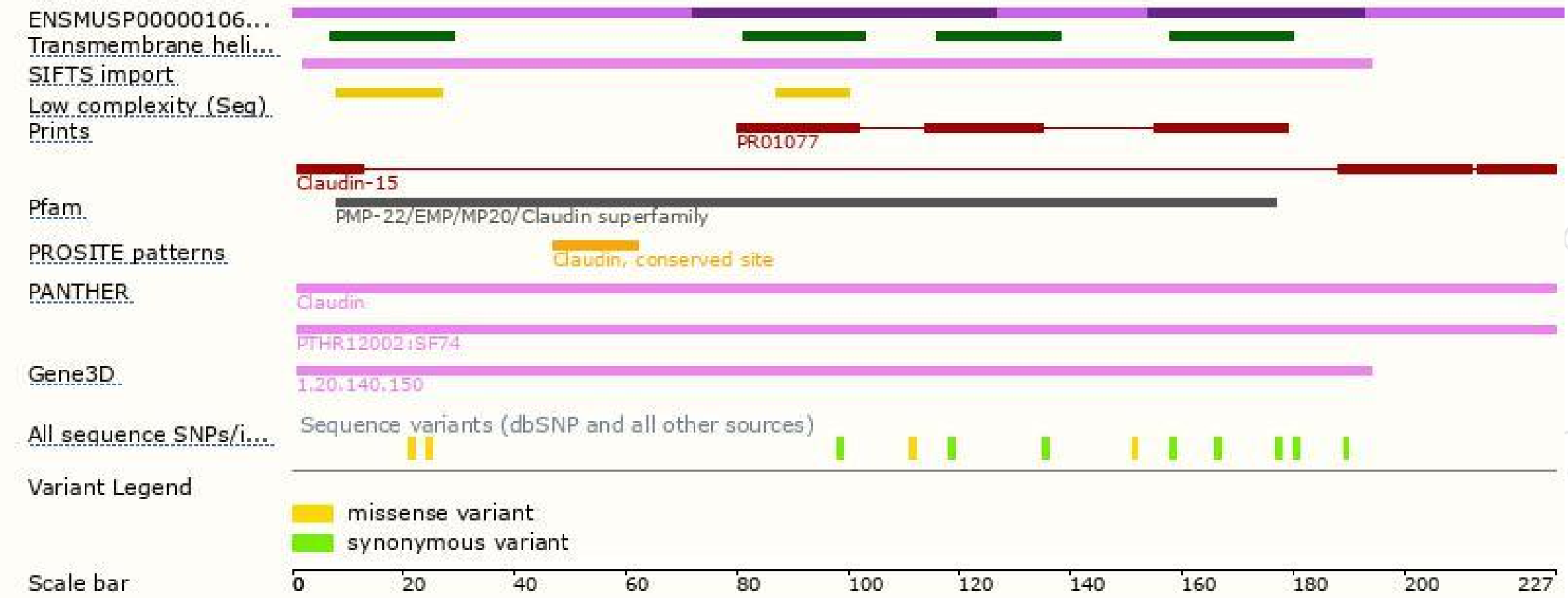
The strategy is based on the design of *Cldn15-202* transcript,The transcription is shown below



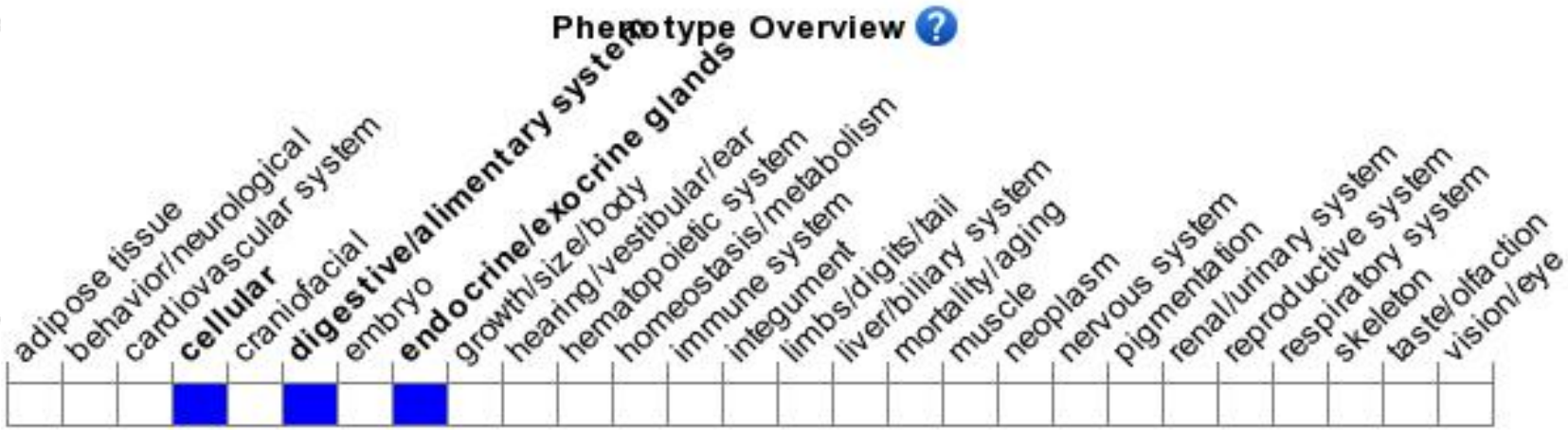
Genomic location distribution



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/).

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

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