Cldn11 Cas9-CKO Strategy

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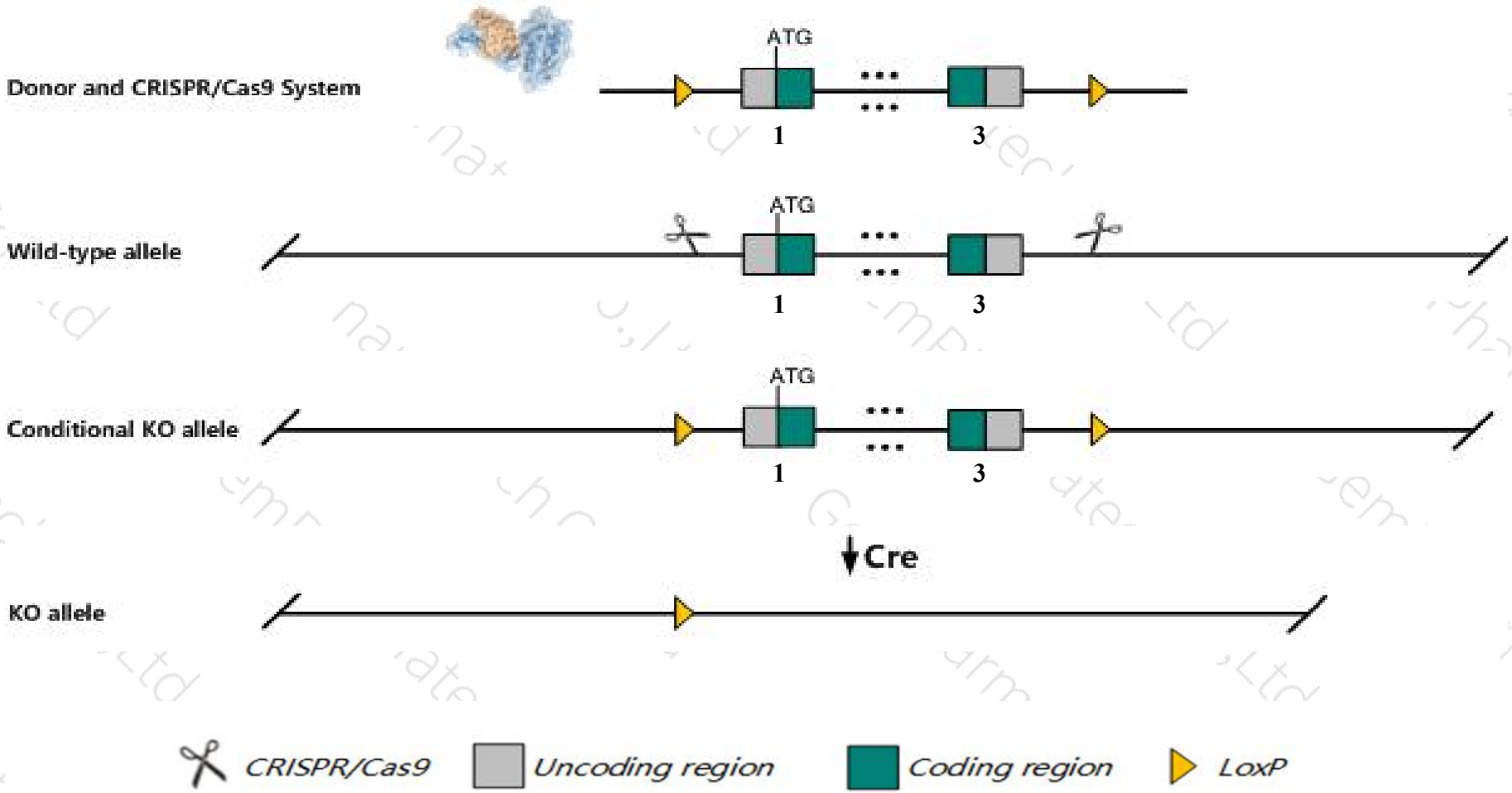
Project Overview

Project Name	***Cldn11***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cldn11* gene. The schematic diagram is as follows:



Technical routes

- The *Cldn11* gene has 1 transcript. According to the structure of *Cldn11* gene, exon1-exon3 of *Cldn11-201* (ENSMUST00000046174.7) 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 *Cldn11* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- According to the existing MGI data,homozygous null mice exhibit tremors, impaired coordination, hindlimb weakness, abnormal myelination of the cranial nerves, increased auditory thresholds, and abnormal stria vascularis. mutant males have small testes, abnormal seminiferous tubules, and sperm abnormalities resulting in infertility.
- The *Cldn11* gene is located on the Chr3. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Cldn11 claudin 11 [Mus musculus (house mouse)]

Gene ID: 18417, updated on 13-Mar-2020

Summary

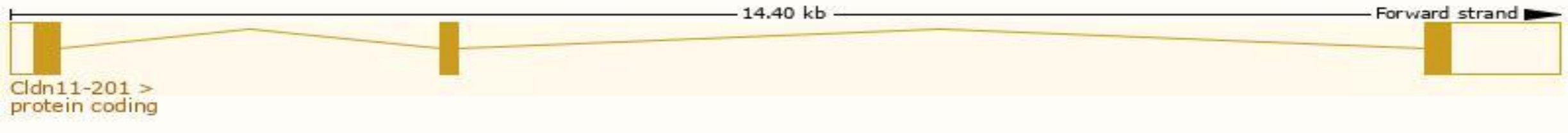
Official Symbol	Cldn11 provided by MGI
Official Full Name	claudin 11 provided by MGI
Primary source	MGI:MGI:106925
See related	Ensembl:ENSMUSG00000037625
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Claudin-11, Claudin11, Osp, Otm
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. The protein encoded by this gene is a major component of CNS (central nervous system) myelin and plays an important role in regulating proliferation and migration of oligodendrocytes. The basal cell tight junctions in stria vascularis are primarily composed of this protein, and the gene-null mice suffer severe deafness. This protein is also an obligatory protein for tight junction formation and barrier integrity in the testis and the gene deficiency results in loss of the Sertoli cell epithelial phenotype in the testis. [provided by RefSeq, Aug 2010]
Expression	Biased expression in cerebellum adult (RPKM 80.9), cortex adult (RPKM 73.0) and 8 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

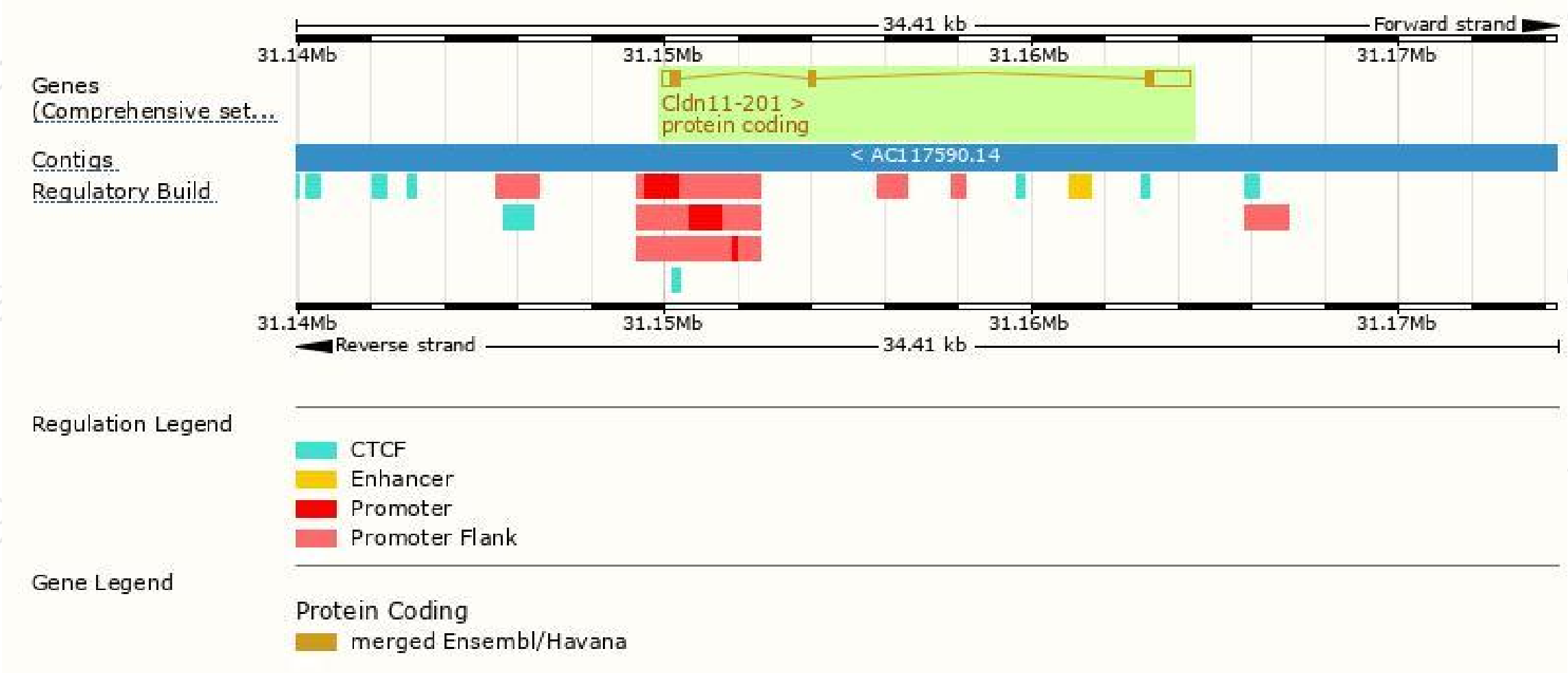
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cldn11-201	ENSMUST00000046174.7	1870	207aa	Protein coding	CCDS17290	Q60771	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 *Cldn11-201* transcript,the transcription is shown below:

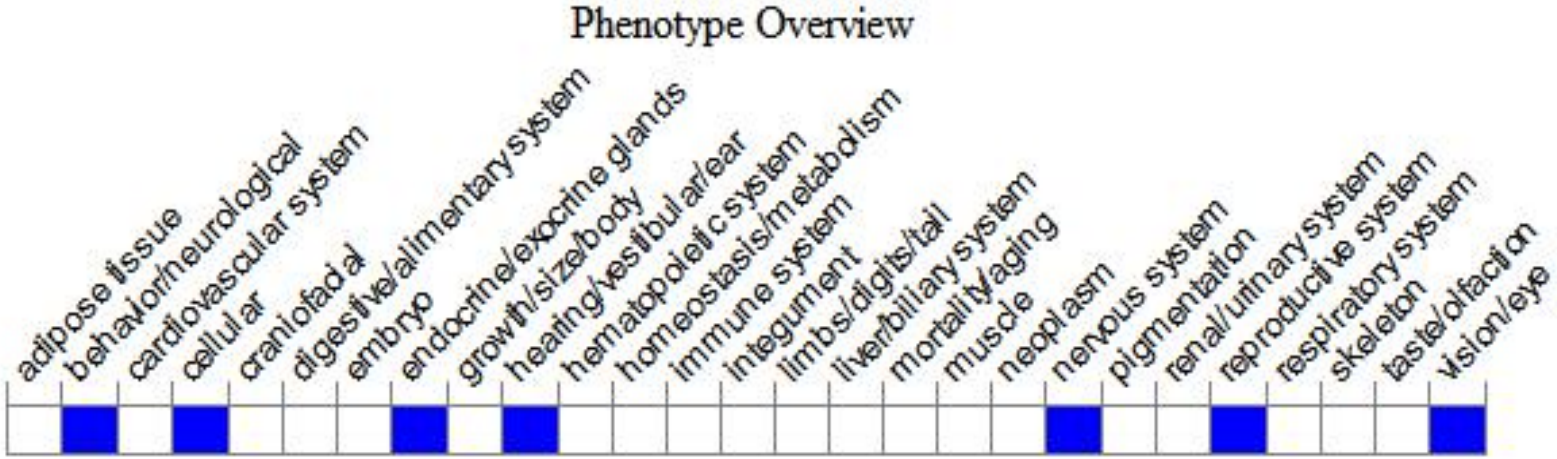


Genomic location distribution



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/).

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

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