# Cldn2 Cas9-CKO Strategy

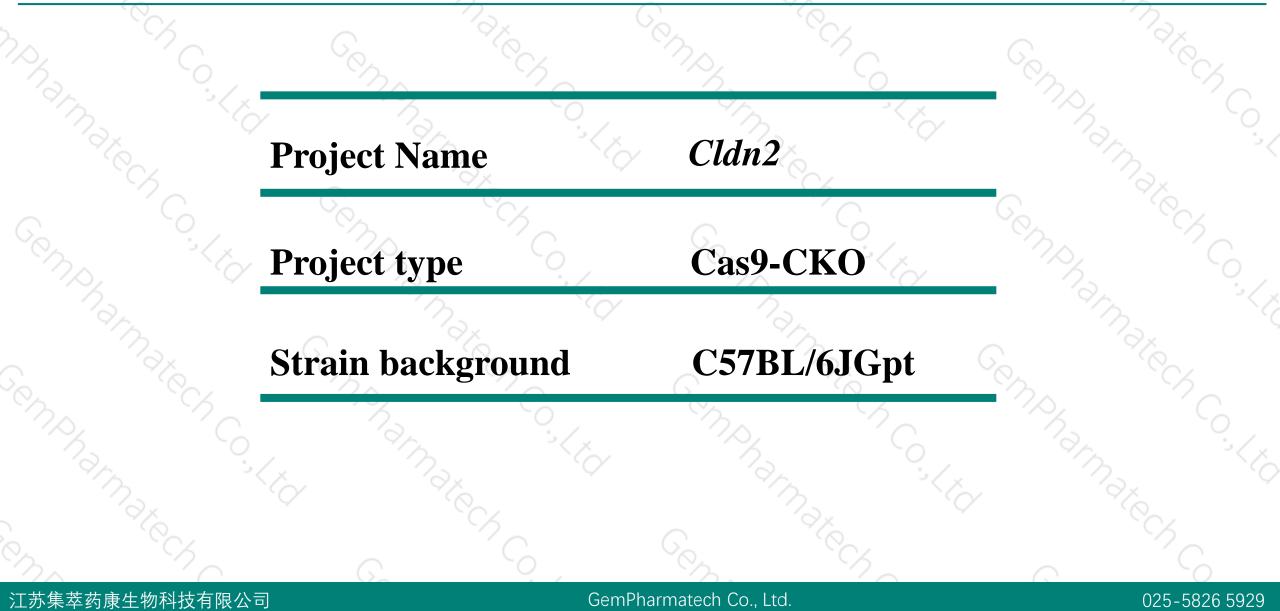
Designer: Reviewer: Design Date:

Yang Zeng Ruirui Zhang

2020-2-10

## **Project Overview**



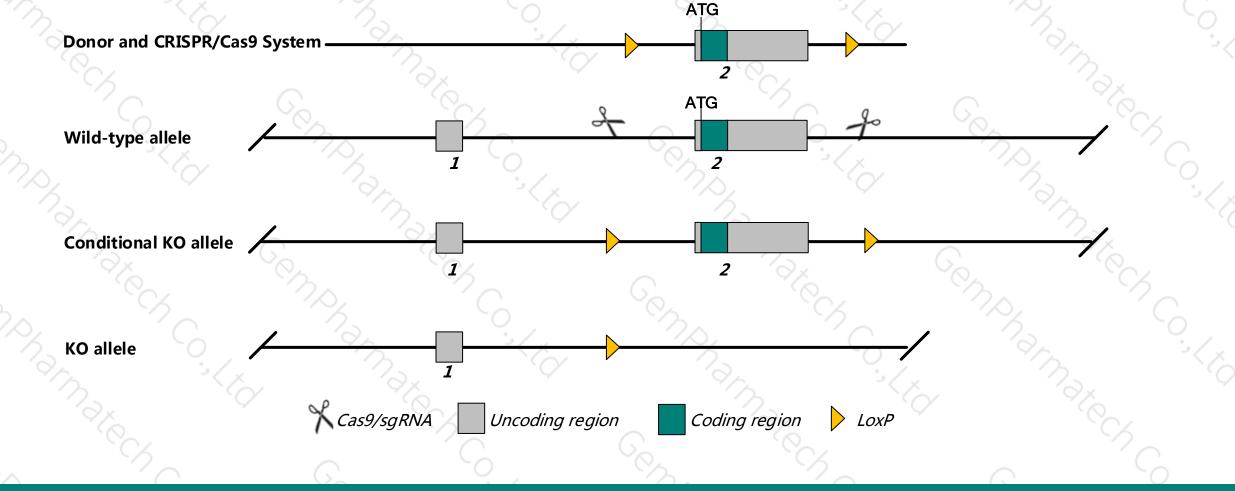


# **Conditional Knockout strategy**



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This model will use CRISPR/Cas9 technology to edit the *Cldn2* gene. The schematic diagram is as follows:



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- The Cldn2 gene has 3 transcripts.According to the structure of Cldn2 gene, exon2 of Cldn2-201 (ENSMUST00000054889.3)transcript is recommended as the knockout region.The region contains all the coding sequence.Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cldn2* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

### Notice



- According to the existing MGI data, nullizygous females show altered Na+ and water reabsorption in the kidney proximal tubules. Males hemizygous for a null allele show increased transcellular Na+ reabsorption in the thick ascending limb, higher renal oxygen consumption, medullary hypoxia, and susceptibility to ischemic renal injury.
- The *Cldn2* gene is located on the ChrX. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

### Gene information (NCBI)



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#### Cldn2 claudin 2 [ Mus musculus (house mouse) ]

Gene ID: 12738, updated on 12-Nov-2019

#### Summary

Official Symbol Cldn2 provided by MGI claudin 2 provided by MGI Official Full Name Primary source MGI:MGI:1276110 Ensembl:ENSMUSG00000047230 See related protein coding Gene type RefSeq status REVIEWED Mus musculus Organism Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Lineage Murinae; Mus; Mus AL022813 Also known as This gene encodes a member of the claudin family. Claudins are integral membrane proteins and components of tight junction strands. Tight junction strands Summary 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 knockout mice lacking this gene display normal appearance, activity, growth and behavior, but are defective in the leaky and cation-selective paracellular permeability properties of renal proximal tubules. The proteins encoded by this gene and another family member Cldn12 are also critical for vitamin D-dependent Ca2+ absorption between enterocytes. [provided by RefSeq, Aug 2010] Biased expression in kidney adult (RPKM 78.3), genital fat pad adult (RPKM 58.9) and 6 other tissues See more Expression Orthologs human all

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# **Transcript information (Ensembl)**



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

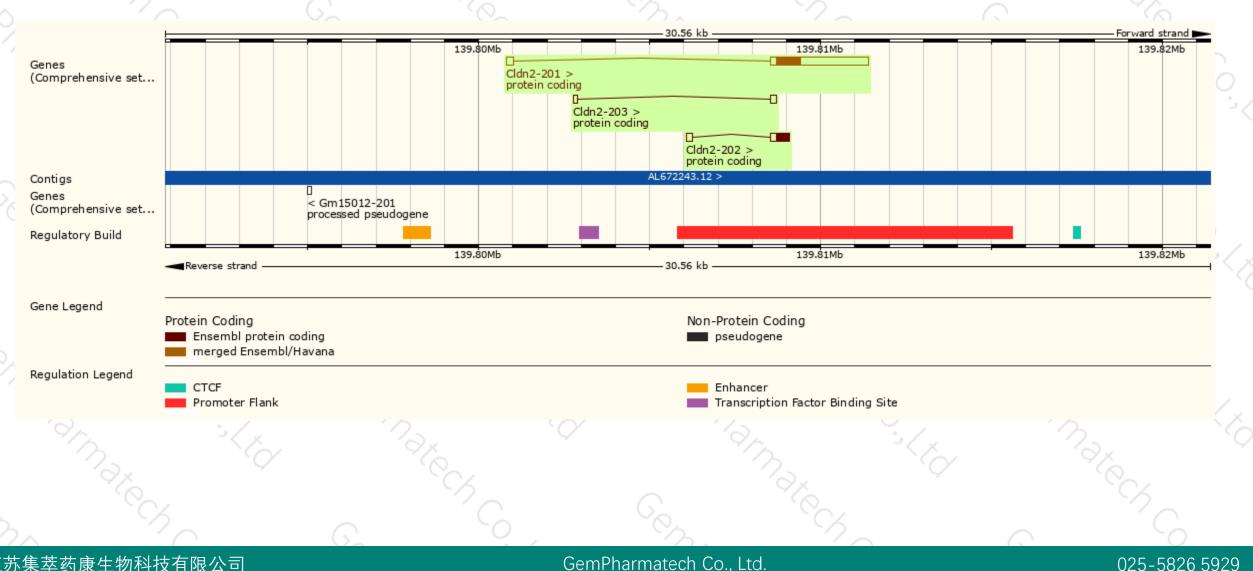
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Name 🍦	Transcript ID 💧	bp 🍦	Protein 🖕	Biotype 🔺	CCDS 🍦	UniProt 🖕	Flags 🔶			
Cldn2-201	ENSMUST0000054889.3	3044	<u>230aa</u>	Protein coding	<u>CCDS30437</u> &	<u>088552</u> &	TSL:1 GENCODE basic APPRIS P1			
Cldn2-202	ENSMUST00000135224.1	755	<u>131aa</u>	Protein coding	-	<u>A3KGB5</u> &	CDS 3' incomplete TSL:3			
Cldn2-203	ENSMUST00000172779.1	290	<u>2aa</u>	Protein coding	-	-	CDS 3' incomplete TSL:3			

The strategy is based on the design of *Cldn2*-201 transcript, the transcription is shown below:

	10.56 kb	Forward strand
Cldn2-201 > protein coding		
non Col	narm "Kty	
	G C	

### **Genomic location distribution**





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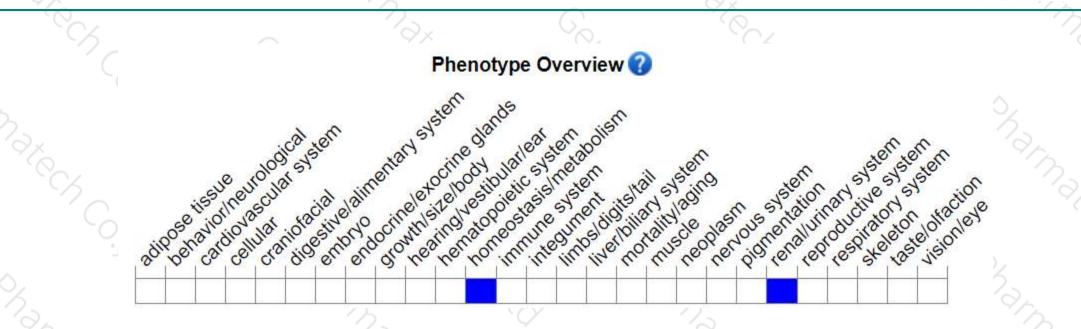
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# **Protein domain**



<u> </u>												
	ENSMUSP0000054 Transmembrane heli PDB-ENSP mappings	_	-	•								)
	Low complexity (Seg) Prints			Claud	in-2							
	56				PR01077							
	Pfam	PMP-22/EMP/MP20/Claudin superfamily										
	PROSITE patterns	Claudin, conserved site										
	PANTHER	Claudin										
		PTHR12002:SF110										
	Gene3D	1.20.140.150										
	All sequence SNPs/i	Sequence variants (dbSNP and all other sources)										
	Variant Legend	missense va	ariant			synonymous variant						
	Scale bar	0 20	40	60	30 100	120	140	160	180	200	230	
	ALW3K	3 < x								Nate Ch		
Z	3. °C/		G_	6	, G	2	°°°		0		6	
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### 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 , nullizygous females show altered Na+ and water reabsorption in the kidney proximal tubules. Males hemizygous for a null allele show increased transcellular Na+ reabsorption in the thick ascending limb, higher renal oxygen consumption, medullary hypoxia, and susceptibility to ischemic renal injury.

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If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



