

# Clic3 Cas9-CKO Strategy

Designer: Xingkai Xiao

Reviewer: Qin Xia

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### Overview

#### **Target Gene Name**

• Clic3

#### **Project Type**

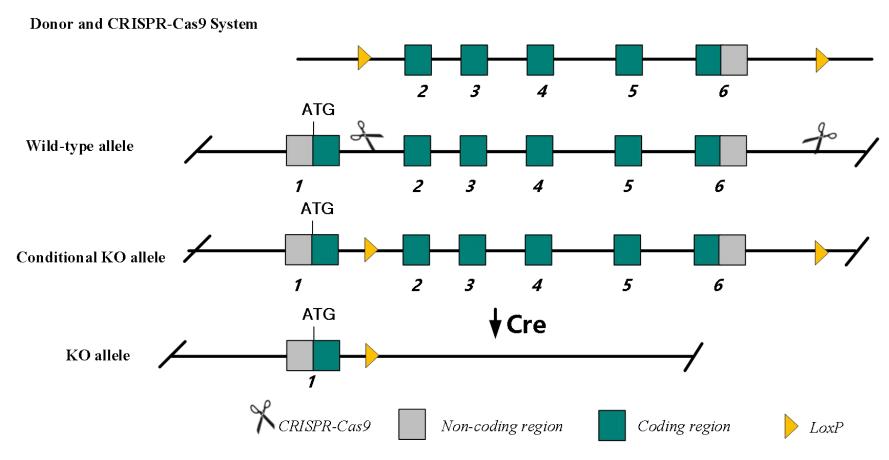
• Cas9-CKO

#### Genetic Background

• C57BL/6JGpt



## Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Clic3 gene.



#### **Technical Information**

- The *Clic3* gene has 6 transcripts. According to the structure of *Clic3* gene, exon2-6 of *Clic3*-202 (ENSMUST00000114265.9) transcript is recommended as the knockout region. The region contains most of coding sequences and all 3'UTR of *Clic3*. Knocking out the region will result in disruption of the function of *Clic3*.
- In this project we use CRISPR-Cas9 technology to modify *Clic3* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.



#### Gene Information

#### Clic3 chloride intracellular channel 3 [ Mus musculus (house mouse) ]

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Gene ID: 69454, updated on 12-Apr-2023



☆ ?

Official Symbol Clic3 provided by MGI

Official Full Name chloride intracellular channel 3 provided by MGI

Primary source MGI:MGI:1916704

See related Ensembl: ENSMUSG00000015093 AllianceGenome: MGI: 1916704

Gene type protein coding
RefSeq status PROVISIONAL
Organism Mus musculus

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 2300003G24Rik

Summary Predicted to enable chloride channel activity. Predicted to be involved in chloride transport. Predicted to act upstream of or

within ion transport and regulation of ion transmembrane transport. Predicted to be located in nuclear body. Predicted to be part of chloride channel complex. Predicted to be active in cytoplasm and membrane. Orthologous to human CLIC3 (chloride

intracellular channel 3). [provided by Alliance of Genome Resources, Apr 2022]

Expression Biased expression in lung adult (RPKM 601.4), stomach adult (RPKM 133.5) and 2 other tissues See more

Orthologs <u>human</u> all

Try the new Gene table

Try the new Transcript table

Source: https://www.ncbi.nlm.nih.gov/

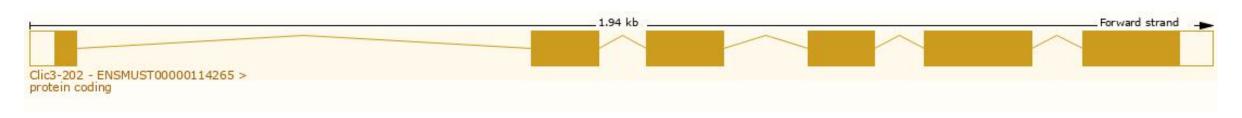


### Transcript Information

The gene has 6 transcripts, all transcripts are shown below:

Show/hide columns (1 hidden)							Filter	
Transcript ID ▼	Name 🌲	bp 🌲	Protein 🍦	Biotype	CCDS .	UniProt Match	Flags	
ENSMUST00000143862.2	Clic3-206	362	No protein	Protein coding CDS not defined		( <del>-</del>	TSL:3	
ENSMUST00000142006.8	Clic3-205	918	No protein	Protein coding CDS not defined		8.58	TSL:5	
ENSMUST00000140022.8	Clic3-204	724	No protein	Protein coding CDS not defined		150	TSL:5	
ENSMUST00000132311.2	Clic3-203	734	No protein	Protein coding CDS not defined		-	TSL:5	
ENSMUST00000114265.9	Clic3-202	808	<u>237aa</u>	Protein coding	CCDS15774₺	Q9D7P7₺	Ensembl Canonical GENCODE basic APPRIS P4 TSL:1	
ENSMUST00000102918.3	Clic3-201	791	235aa	Protein coding		A2AJ28₺	GENCODE basic APPRIS ALT1 TSL:3	

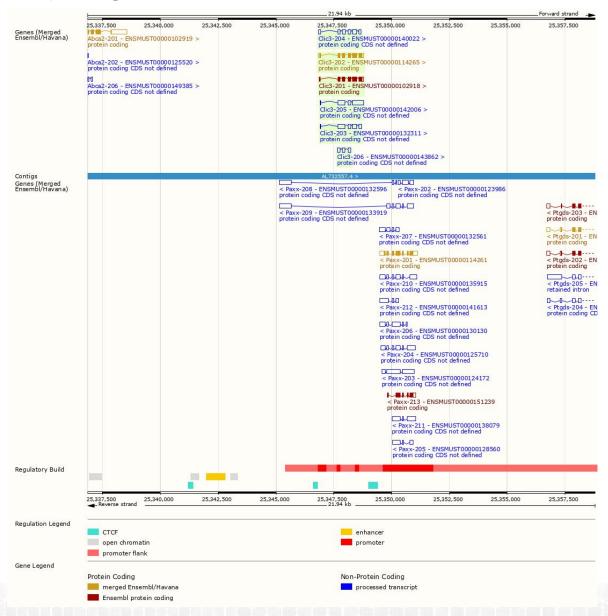
The strategy is based on the design of *Clic3*-202 transcript, the transcription is shown below:

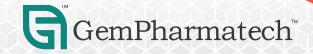


Source: https://www.ensembl.org

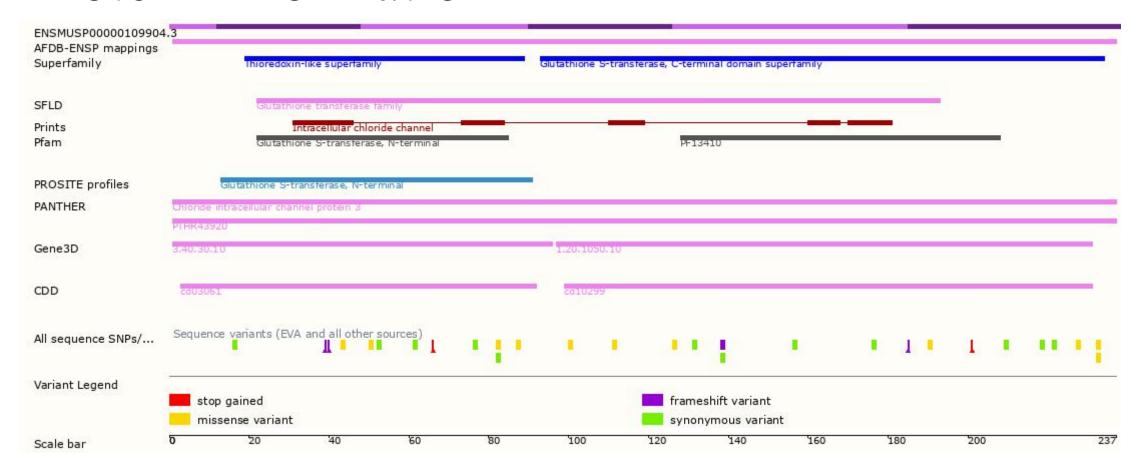


### Genomic Information





#### Protein Information





Source: : https://www.ensembl.org

### Important Information

- *This* strategy may affect the expression of *Paxx*.
- *Clic3* is located on Chr2. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.

