

# Plcb4 Cas9-KO Strategy

**Designer:** Yang Zeng

**Reviewer:** 

Ruirui Zhang

**Design Date:** 

2019-11-22

## **Project Overview**



**Project Name** 

Plcb4

**Project type** 

Cas9-KO

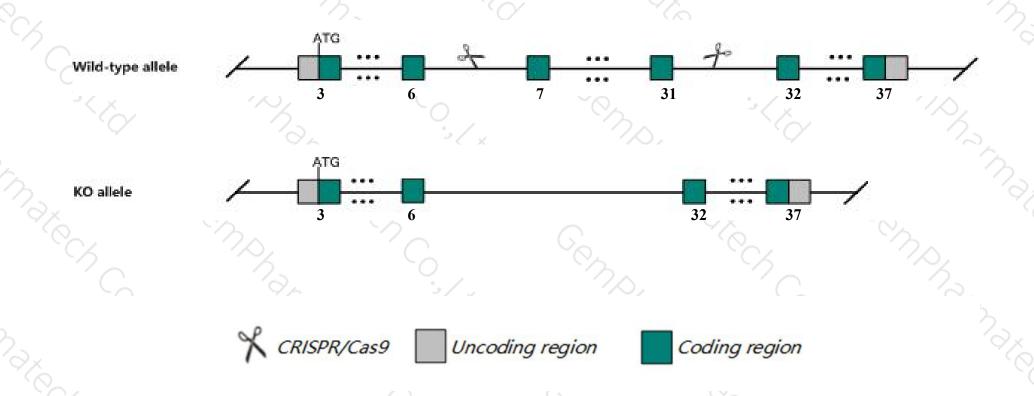
Strain background

C57BL/6JGpt

## **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Plcb4* gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *Plcb4* gene has 15 transcripts. According to the structure of *Plcb4* gene, exon7-exon31 of *Plcb4-202*(ENSMUST00000110109.7) transcript is recommended as the knockout region. The region contains 2591bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Plcb4* gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



According to the existing MGI data, Homozygotes for targeted mutations may exhibit ataxia, impaired elimination of excess climbing fiber synapses in the developing cerebellum, abnormal cerebellar foliation, reduced visual processing ability and loss of circadian rhythm in constant darkness, mice survived in the absence of normal littermates, indicating a reduced ability to compete with normal littermates.

- The *Plcb4* gene is located on the Chr2. 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)



#### Plcb4 phospholipase C, beta 4 [ Mus musculus (house mouse) ]

Gene ID: 18798, updated on 14-Jan-2020

#### Summary



Official Symbol Plcb4 provided by MGI

Official Full Name phospholipase C, beta 4 provided by MGI

Primary source MGI:MGI:107464

See related Ensembl: ENSMUSG00000039943

Gene type protein coding
RefSeq status VALIDATED
Organism Mus musculus

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

Murinae; Mus; Mus

Also known as Al854601; A930039J07Rik; C230058B11Rik

Expression Biased expression in bladder adult (RPKM 32.1), cerebellum adult (RPKM 16.4) and 11 other tissues See more

Orthologs human all

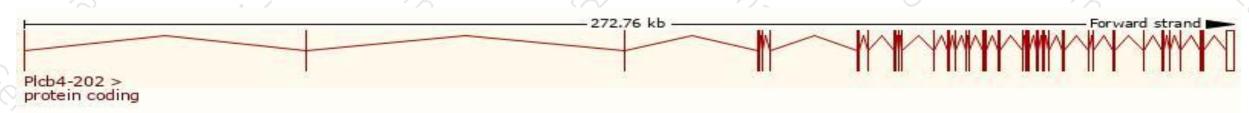
## Transcript information (Ensembl)



#### The gene has 15 transcripts, all transcripts are shown below:

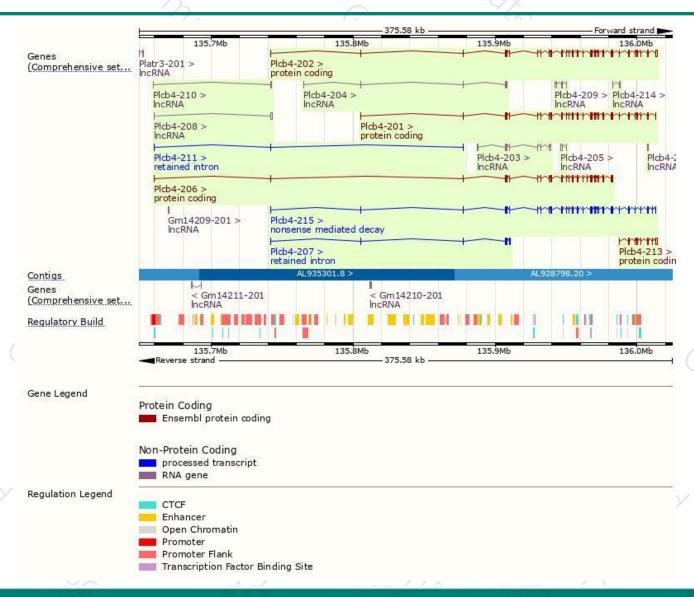
			′ / ) .				
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plcb4-202	ENSMUST00000110109.7	5217	<u>1175aa</u>	Protein coding	CCDS16788	Q91UZ1	TSL:1 GENCODE basic APPRIS P1
Plcb4-201	ENSMUST00000035646.10	3635	<u>1175aa</u>	Protein coding	CCDS16788	Q91UZ1	TSL:5 GENCODE basic APPRIS P1
Plcb4-206	ENSMUST00000134310.7	2744	883aa	Protein coding	-	A2AT91	CDS 3' incomplete TSL:1
Plcb4-213	ENSMUST00000147744.1	2307	<u>255aa</u>	Protein coding	10	A2AT93	CDS 5' incomplete TSL:1
Plcb4-215	ENSMUST00000184371.7	3754	<u>1022aa</u>	Nonsense mediated decay	-	V9GXQ9	TSL:5
Plcb4-207	ENSMUST00000137969.7	739	No protein	Retained intron			TSL:5
Plcb4-211	ENSMUST00000146018.7	613	No protein	Retained intron	-	-	TSL:5
Plcb4-210	ENSMUST00000144931.1	1366	No protein	IncRNA	90	-	TSL:1
Plcb4-208	ENSMUST00000139480.1	1186	No protein	IncRNA	-		TSL:1
Plcb4-205	ENSMUST00000132686.1	779	No protein	IncRNA		-	TSL:2
Plcb4-203	ENSMUST00000127044.1	669	No protein	IncRNA	-	-	TSL:3
Plcb4-214	ENSMUST00000150072.1	508	No protein	IncRNA	12	-	TSL:2
Plcb4-209	ENSMUST00000141025.1	449	No protein	IncRNA	-		TSL:5
Plcb4-204	ENSMUST00000127729.7	441	No protein	IncRNA			TSL:5
Plcb4-212	ENSMUST00000147122.1	389	No protein	IncRNA		2	TSL:3

The strategy is based on the design of *Plcb4-202* transcript, The transcription is shown below



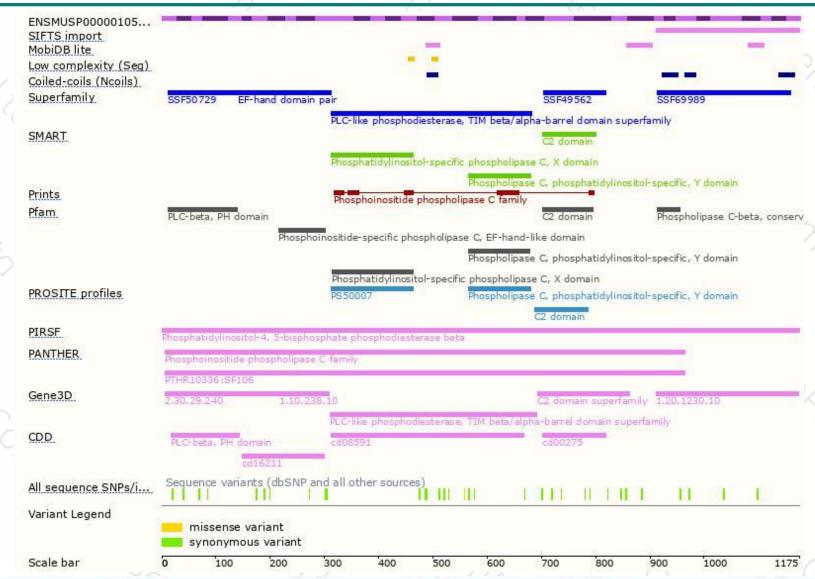
### Genomic location distribution





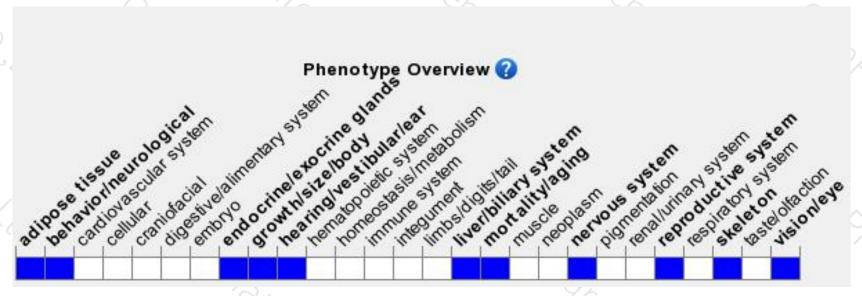
### Protein domain





## Mouse phenotype description(MGI)





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

According to the existing MGI data, Homozygotes for targeted mutations may exhibit ataxia, impaired elimination of excess climbing fiber synapses in the developing cerebellum, abnormal cerebellar foliation, reduced visual processing ability and loss of circadian rhythm in constant darkness, mice survived in the absence of normal littermates, indicating a reduced ability to compete with normal littermates.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





