

***Plcb3* Cas9-CKO Strategy**

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Project Overview

Project Name

Plcb3

Project type

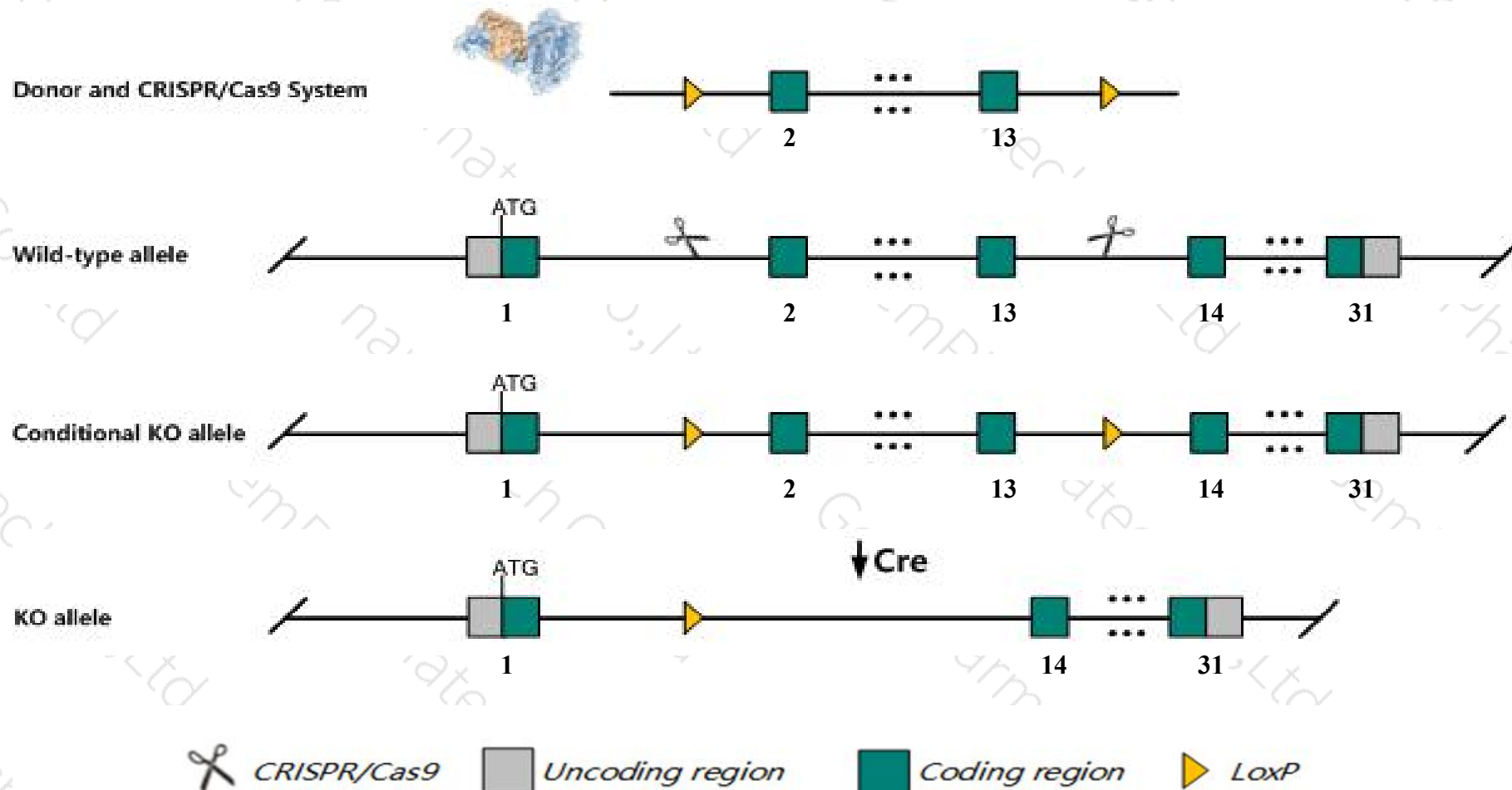
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Plcb3* gene. The schematic diagram is as follows:



Technical routes

- The *Plcb3* gene has 10 transcripts. According to the structure of *Plcb3* gene, exon2-exon13 of *Plcb3-201*(ENSMUST00000025912.9) transcript is recommended as the knockout region. The region contains 1426bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Plcb3* 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.

- According to the existing MGI data, mice homozygous for one targeted mutation die at E2.5 and exhibit poor embryonic organization and hypocellularity. Mice homozygous for a second targeted mutation survive to adulthood and exhibit an increased antinociceptive response to opioids.
- The effect on transcript *Plcb3*-207&210 is unknown.
- Transcript *Plcb3*-203&205 may not be affected.
- The *Plcb3* gene is located on the Chr19. 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)

Plcb3 phospholipase C, beta 3 [Mus musculus (house mouse)]

Gene ID: 18797, updated on 13-Mar-2020

Summary



Official Symbol Plcb3 provided by [MGI](#)

Official Full Name phospholipase C, beta 3 provided by [MGI](#)

Primary source [MGI:MGI:104778](#)

See related [Ensembl:ENSMUSG00000024960](#)

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 mKIAA4098

Expression Broad expression in large intestine adult (RPKM 158.9), duodenum adult (RPKM 122.8) and 16 other tissues [See more](#)

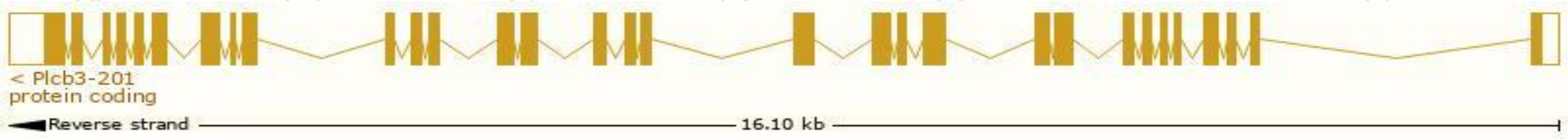
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

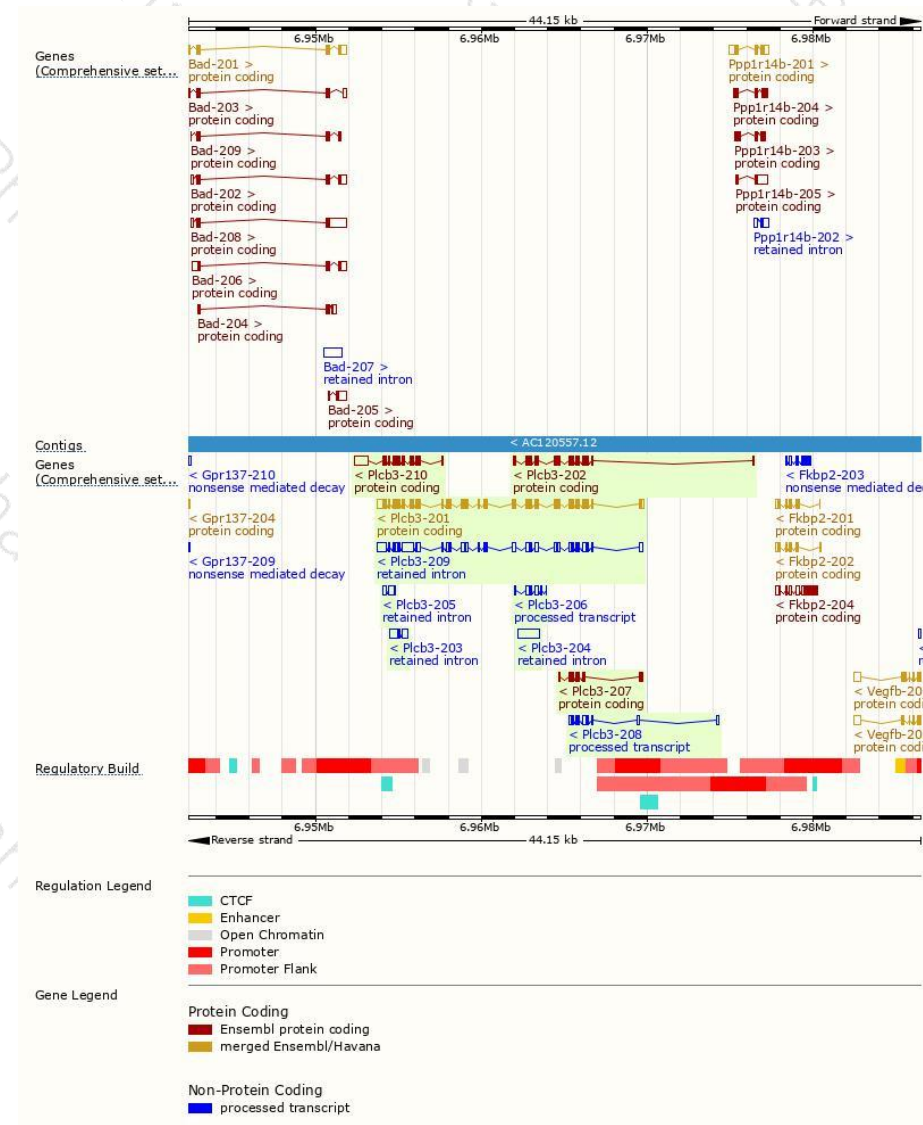
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plcb3-201	ENSMUST0000025912.9	4257	1234aa	Protein coding	CCDS70925	P51432	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
Plcb3-210	ENSMUST00000237808.1	1986	378aa	Protein coding	-	Q8C8I0	CDS 5' incomplete
Plcb3-202	ENSMUST00000235352.1	1665	508aa	Protein coding	-	A0A494B9C1	CDS 3' incomplete
Plcb3-207	ENSMUST00000237074.1	636	191aa	Protein coding	-	A0A494BAY4	CDS 3' incomplete
Plcb3-208	ENSMUST00000237446.1	887	No protein	Processed transcript	-	-	
Plcb3-206	ENSMUST00000236961.1	660	No protein	Processed transcript	-	-	
Plcb3-209	ENSMUST00000237726.1	4558	No protein	Retained intron	-	-	
Plcb3-204	ENSMUST00000235832.1	1268	No protein	Retained intron	-	-	
Plcb3-203	ENSMUST00000235560.1	921	No protein	Retained intron	-	-	
Plcb3-205	ENSMUST00000236597.1	604	No protein	Retained intron	-	-	

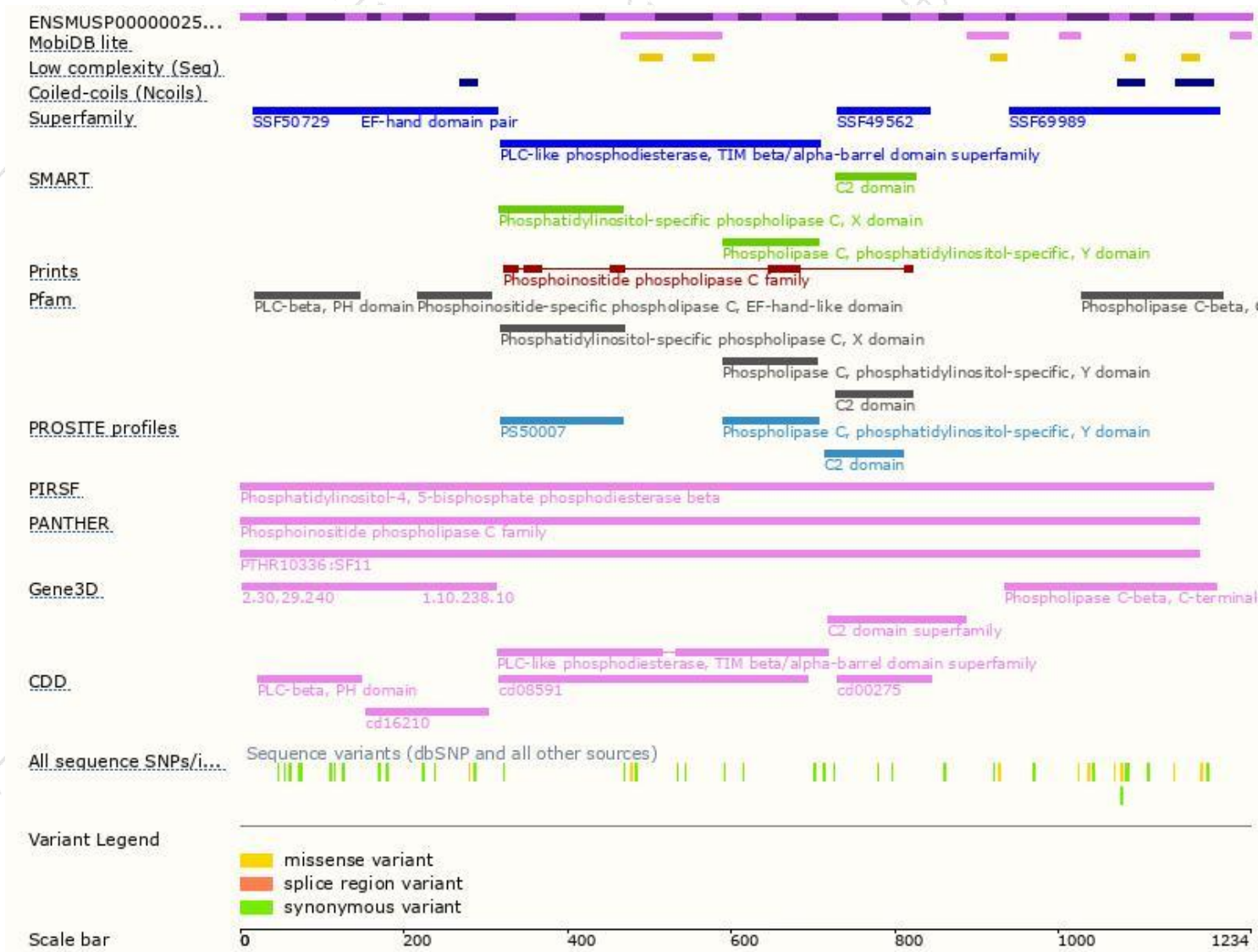
The strategy is based on the design of *Plcb3-201* transcript,the transcription is shown below:



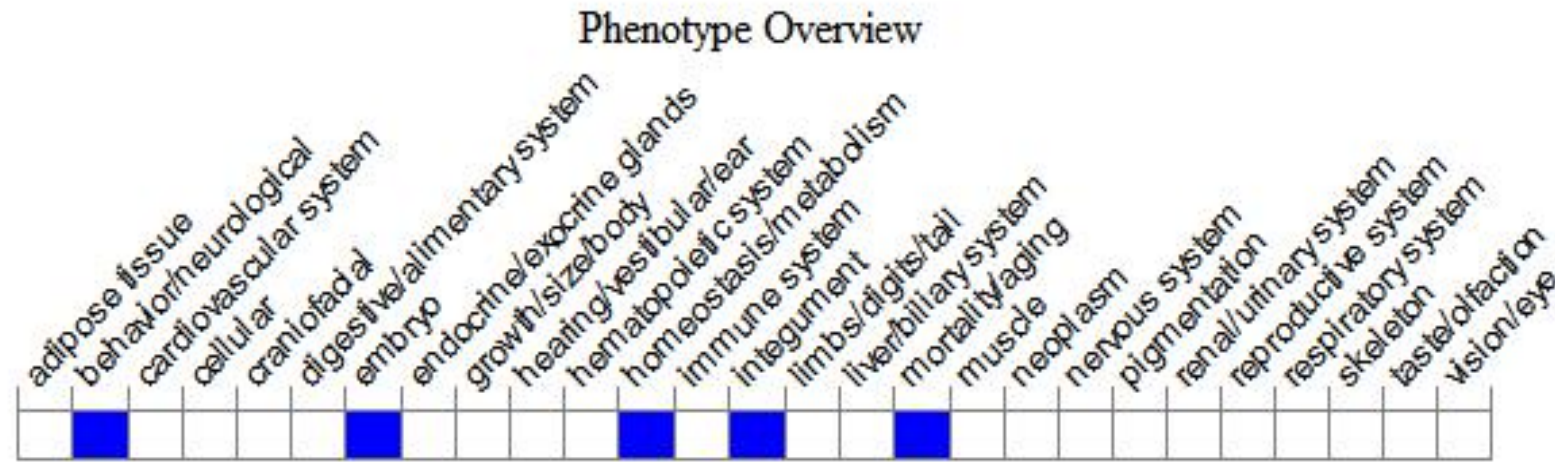
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for one targeted mutation die at E2.5 and exhibit poor embryonic organization and hypocellularity. Mice homozygous for a second targeted mutation survive to adulthood and exhibit an increased antinociceptive response to opioids.

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

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