

Ppp3ca Cas9-KO Strategy

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Project Overview

Project Name

Ppp3ca

Project type

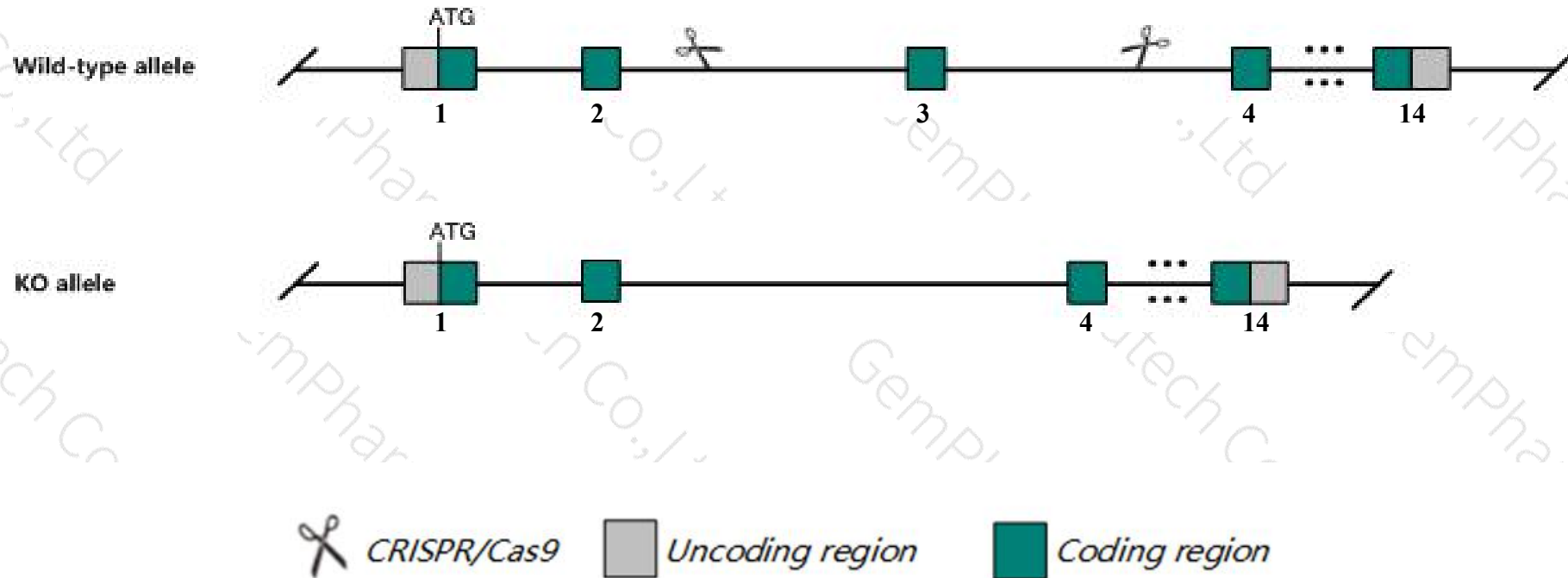
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ppp3ca* gene. The schematic diagram is as follows:



- The *Ppp3ca* gene has 8 transcripts. According to the structure of *Ppp3ca* gene, exon3 of *Ppp3ca-201* (ENSMUST00000056758.8) transcript is recommended as the knockout region. The region contains 125bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ppp3ca* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit decreased T cell proliferation and abnormal mossy fibers.
- The *Ppp3ca* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Ppp3ca protein phosphatase 3, catalytic subunit, alpha isoform [*Mus musculus* (house mouse)]

Gene ID: 19055, updated on 8-Oct-2019

Summary

Official Symbol	Ppp3ca provided by MGI
Official Full Name	protein phosphatase 3, catalytic subunit, alpha isoform provided by MGI
Primary source	MGI:MGI:107164
See related	Ensembl:ENSMUSG00000028161
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	CN; CnA; Caln; Calna; 2900074D19Rik
Expression	Broad expression in cortex adult (RPKM 101.0), frontal lobe adult (RPKM 75.5) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppp3ca-202	ENSMUST00000070198.13	4758	511aa	Protein coding	CCDS80027	P63328	TSL:1 Gencode basic APPRIS ALT1
Ppp3ca-201	ENSMUST00000056758.8	2194	521aa	Protein coding	CCDS17860	B2RRX2 P63328	TSL:1 Gencode basic APPRIS P3
Ppp3ca-207	ENSMUST00000196170.1	2647	No protein	Retained intron	-	-	TSL:NA
Ppp3ca-208	ENSMUST00000196603.1	2038	No protein	Retained intron	-	-	TSL:NA
Ppp3ca-205	ENSMUST00000130114.1	441	No protein	Retained intron	-	-	TSL:2
Ppp3ca-203	ENSMUST00000124206.1	990	No protein	lncRNA	-	-	TSL:3
Ppp3ca-204	ENSMUST00000124777.1	713	No protein	lncRNA	-	-	TSL:3
Ppp3ca-206	ENSMUST00000130768.1	412	No protein	lncRNA	-	-	TSL:5

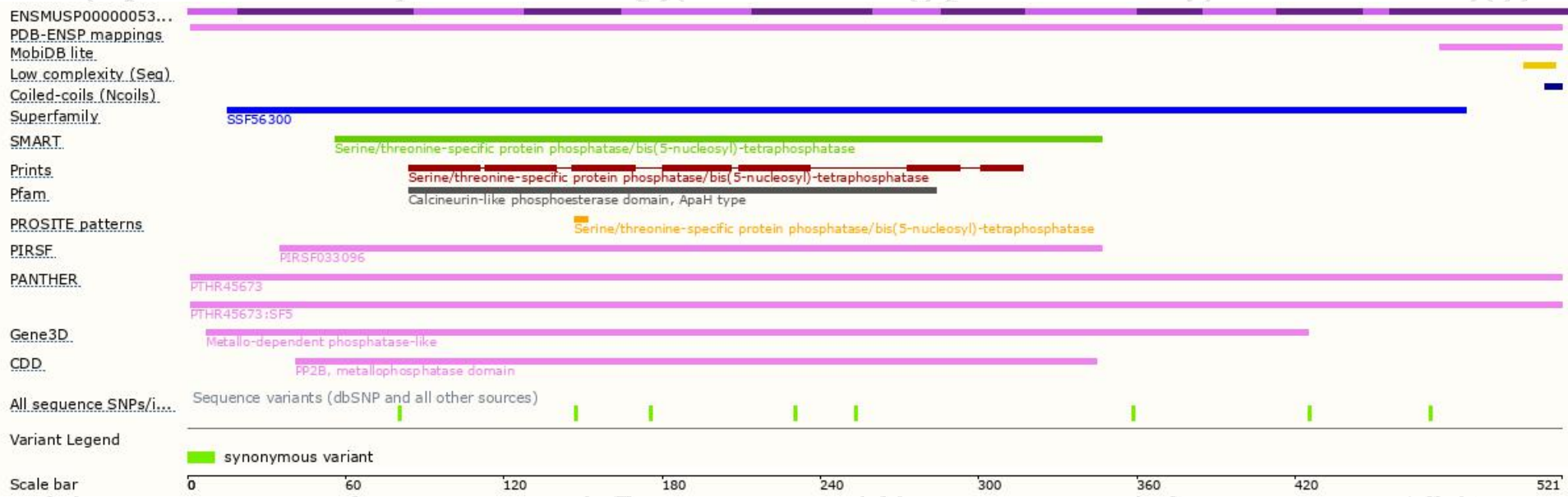
The strategy is based on the design of *Ppp3ca-201* transcript,The transcription is shown below



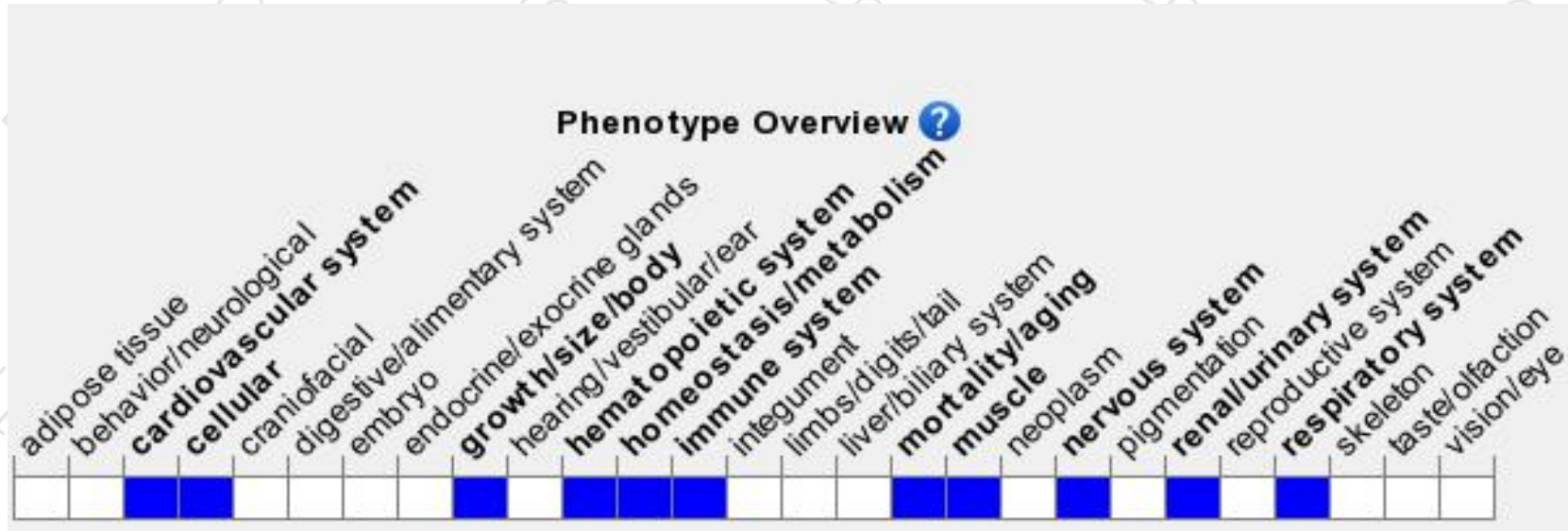
Genomic location distribution



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 a null allele exhibit decreased T cell proliferation and abnormal mossy fibers.

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

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