

Pitpna Cas9-KO Strategy

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Project Overview

Project Name

Pitpna

Project type

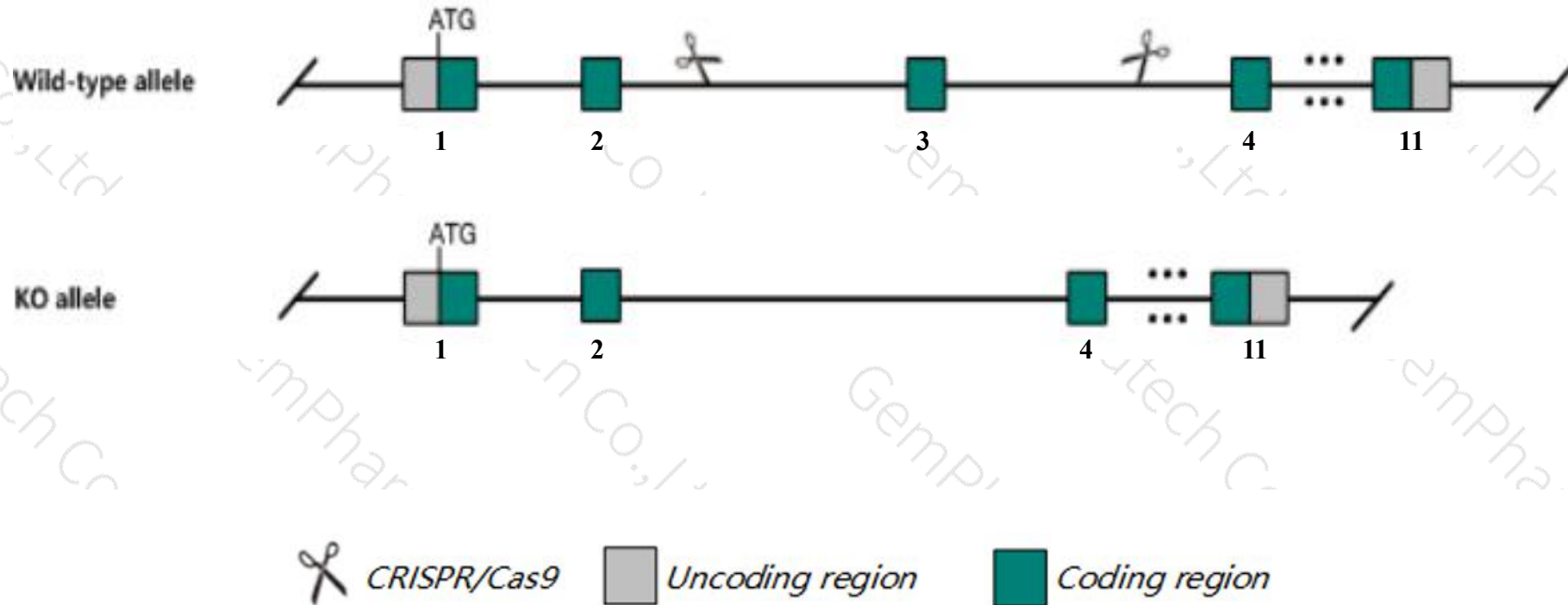
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Pitpna* gene has 6 transcripts. According to the structure of *Pitpna* gene, exon3 of *Pitpna-203* (ENSMUST00000143219.7) transcript is recommended as the knockout region. The region contains 149bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pitpna* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mutations of this gene result in motor coordination abnormalities and early death.
- The floxed region is near to the N-terminal of *4931413K12Rik* gene, this strategy may influence the regulatory function of the N-terminal of *4931413K12Rik* gene.
- The *Pitpna* gene is located on the Chr11. 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)

Pitpna phosphatidylinositol transfer protein, alpha [Mus musculus (house mouse)]

Gene ID: 18738, updated on 13-Mar-2020

Summary

Official Symbol Pitpna provided by [MGI](#)

Official Full Name phosphatidylinositol transfer protein, alpha provided by [MGI](#)

Primary source [MGI:MGI:99887](#)

See related [Ensembl:ENSMUSG00000017781](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

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

Also known as Pitpn, vb, vibrator

Summary This gene encodes a member of a family of lipid-binding proteins that transfer molecules of phosphatidylinositol or phosphatidylcholine between membrane surfaces. The protein is implicated in phospholipase C signaling and in the production of phosphatidylinositol 3,4,5-trisphosphate by phosphoinositide-3-kinase. [provided by RefSeq, Sep 2015]

Expression Ubiquitous expression in cerebellum adult (RPKM 61.1), cortex adult (RPKM 50.1) and 28 other tissues [See more](#)

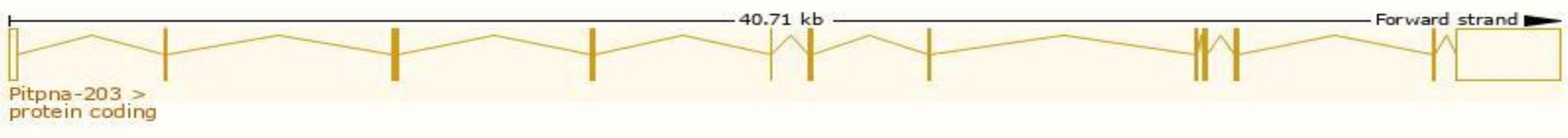
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

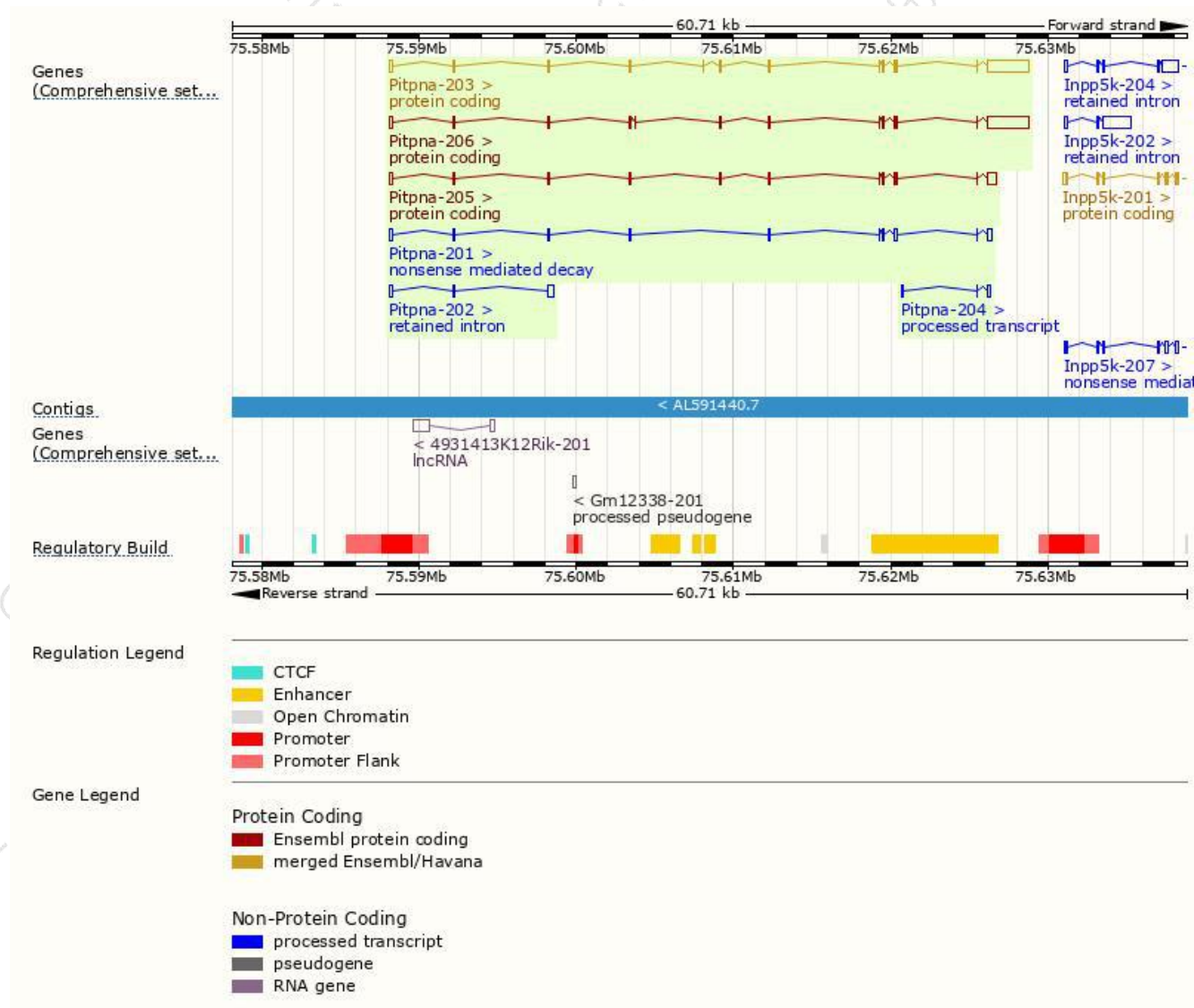
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pitpna-203	ENSMUST00000143219.7	3761	271aa	Protein coding	CCDS25052	P53810 Q5ND42	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 P2
Pitpna-206	ENSMUST00000179521.7	3727	272aa	Protein coding	-	J3QPW1	TSL:5 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 ALT1
Pitpna-205	ENSMUST00000179445.7	1665	271aa	Protein coding	-	J3QQ30	TSL:5 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 ALT1
Pitpna-201	ENSMUST00000102509.10	1245	99aa	Nonsense mediated decay	-	F8WGG5	TSL:5
Pitpna-204	ENSMUST00000153768.1	384	No protein	Processed transcript	-	-	TSL:2
Pitpna-202	ENSMUST00000140841.1	594	No protein	Retained intron	-	-	TSL:1

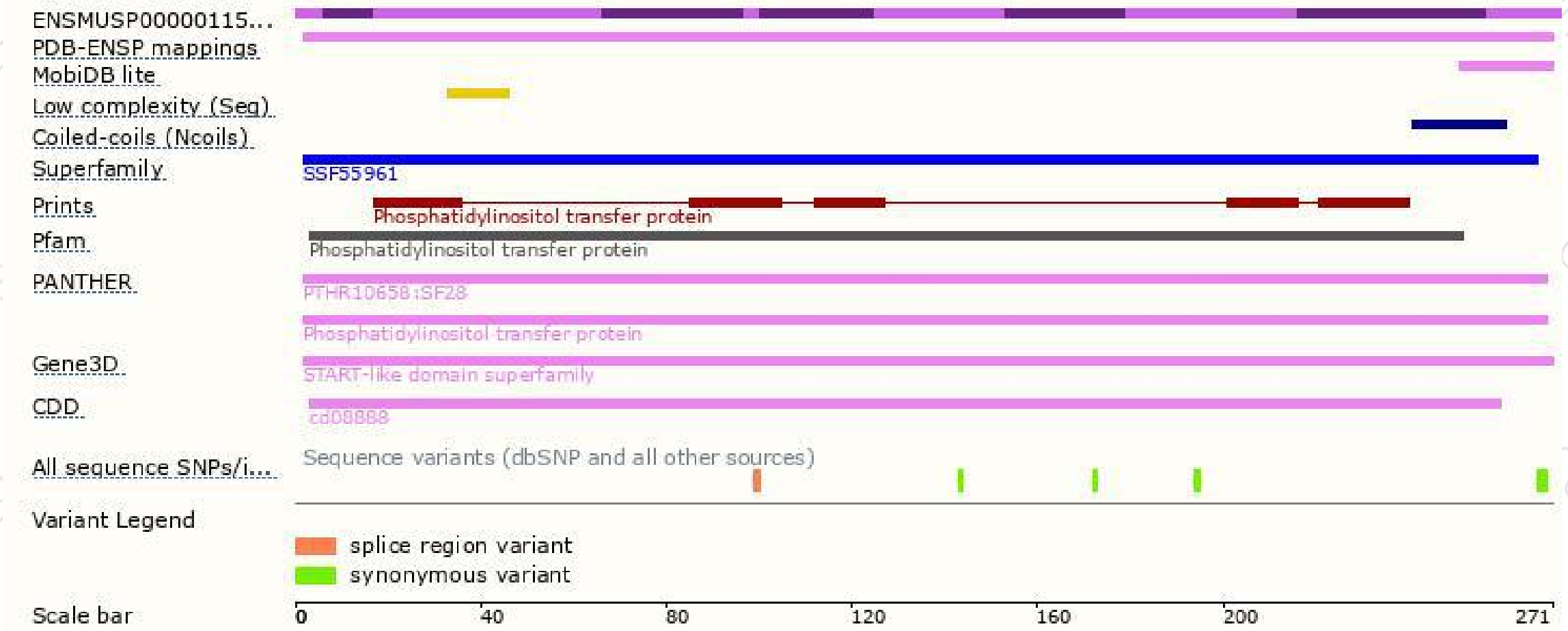
The strategy is based on the design of *Pitpna-203* transcript,the transcription is shown below:



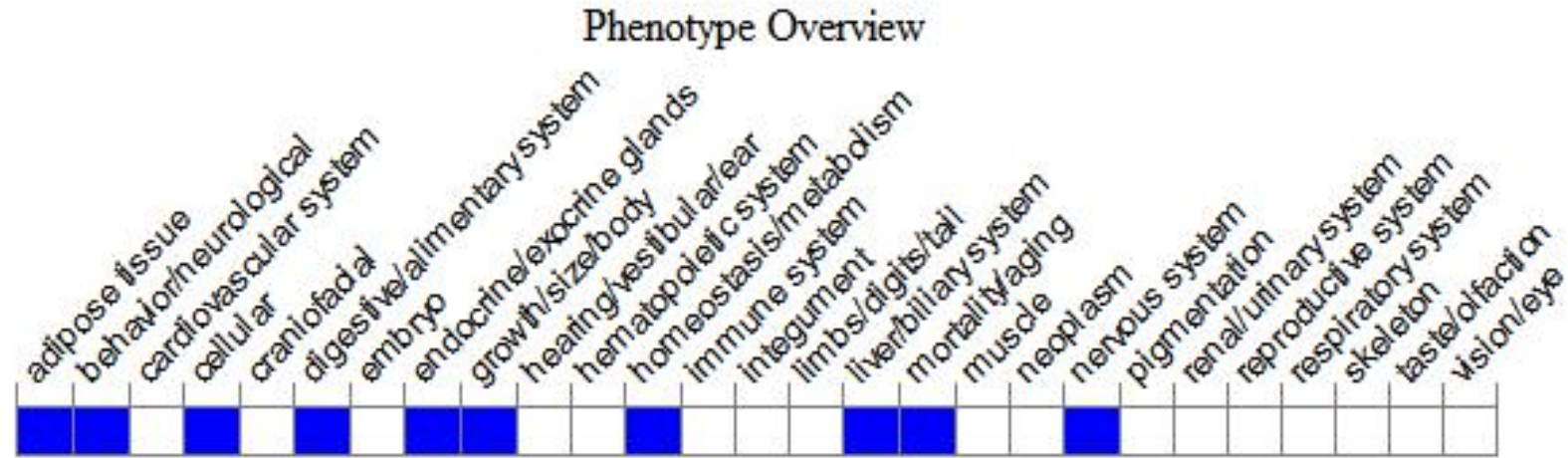
Genomic location distribution



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, mutations of this gene result in motor coordination abnormalities and early death.

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

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