

Pitpnb Cas9-CKO Strategy

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Project Overview

Project Name

Pitpnb

Project type

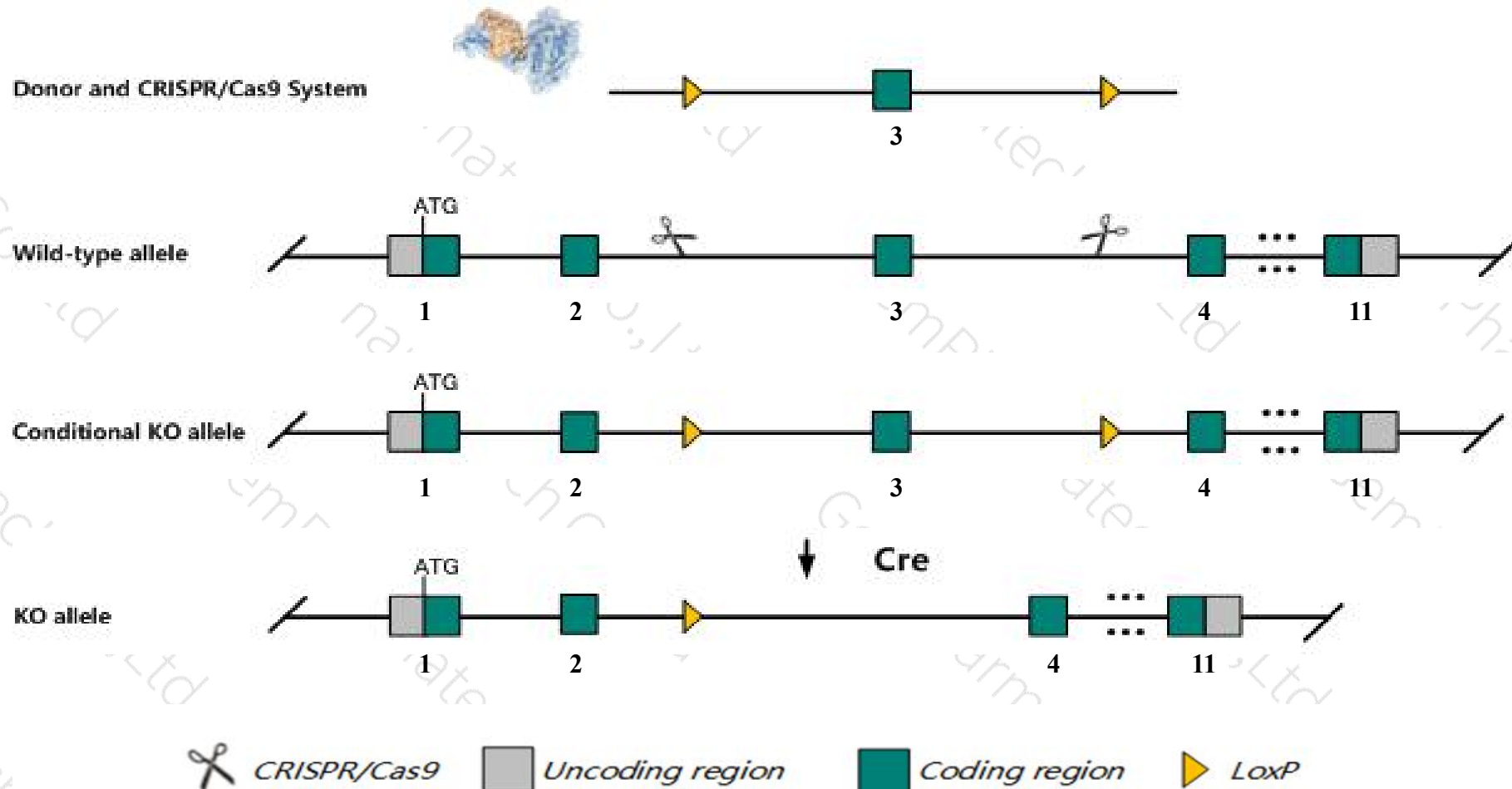
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Pitpnb* gene has 4 transcripts. According to the structure of *Pitpnb* gene, exon3 of *Pitpnb*-204 (ENSMUST00000200298.1) transcript is recommended as the knockout region. The region contains 146bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pitpnb* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J 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.

Notice

- According to the existing MGI data, homozygous null mice die before e7.5.
- Transcript *Pitpnb-202&203* may not be affected.
- The *Pitpnb* gene is located on the Chr5. 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)

Pitpnb phosphatidylinositol transfer protein, beta [Mus musculus (house mouse)]

Gene ID: 56305, updated on 13-Mar-2020

Summary



Official Symbol Pitpnb provided by [MGI](#)

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

Primary source [MGI:MGI:1927542](#)

See related [Ensembl:ENSMUSG00000050017](#)

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 PI-TP-beta

Summary This gene encodes a member of the phosphatidylinositol transfer protein family. The encoded protein catalyzes the transfer of phospholipids (phosphatidylinositol and phosphatidylcholine) between membranes. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Aug 2014]

Expression Ubiquitous expression in limb E14.5 (RPKM 26.4), bladder adult (RPKM 24.5) and 28 other tissues [See more](#)

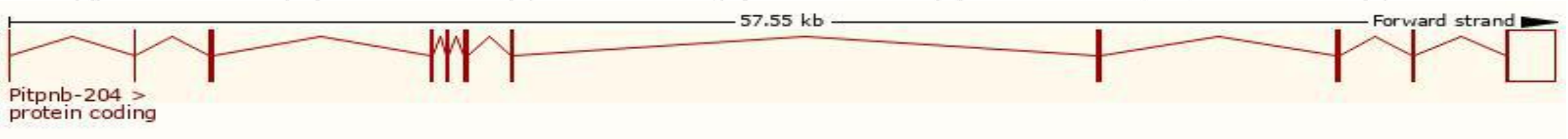
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

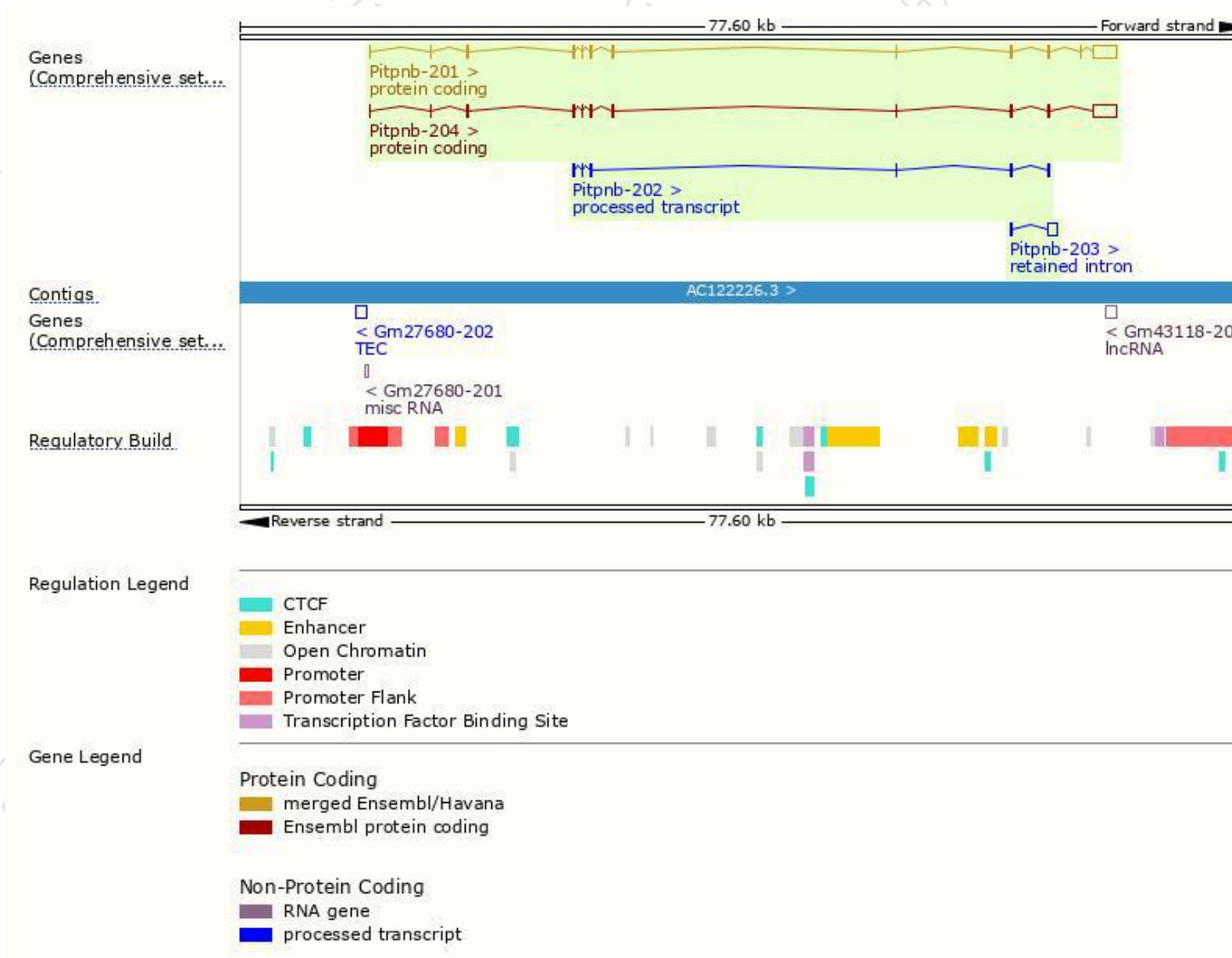
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pitpnb-201	ENSMUST00000086635.8	2761	271aa	Protein coding	CCDS39213	P53811	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 P3
Pitpnb-204	ENSMUST00000200298.1	2632	272aa	Protein coding	CCDS80368	Q8JZZ5	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 ALT1
Pitpnb-202	ENSMUST00000196192.1	485	No protein	Processed transcript	-	-	TSL:5
Pitpnb-203	ENSMUST00000198137.1	850	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Pitpnb-204* transcript,the transcription is shown below:



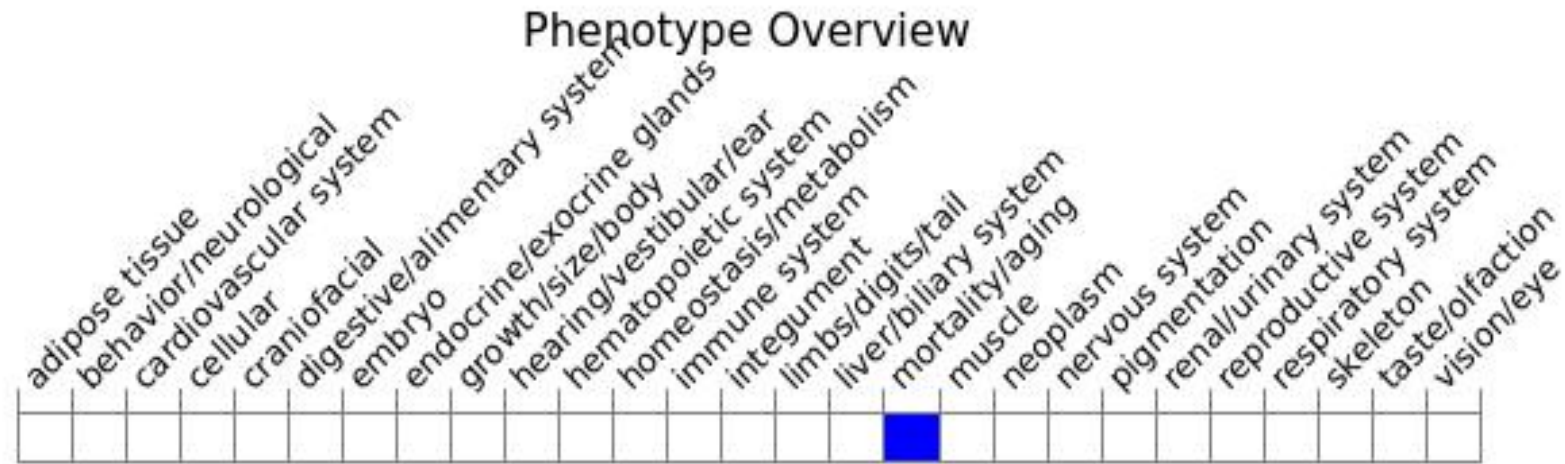
Genomic location distribution



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, homozygous null mice die before E7.5.

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

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