

Pitpnm3 Cas9-CKO Strategy

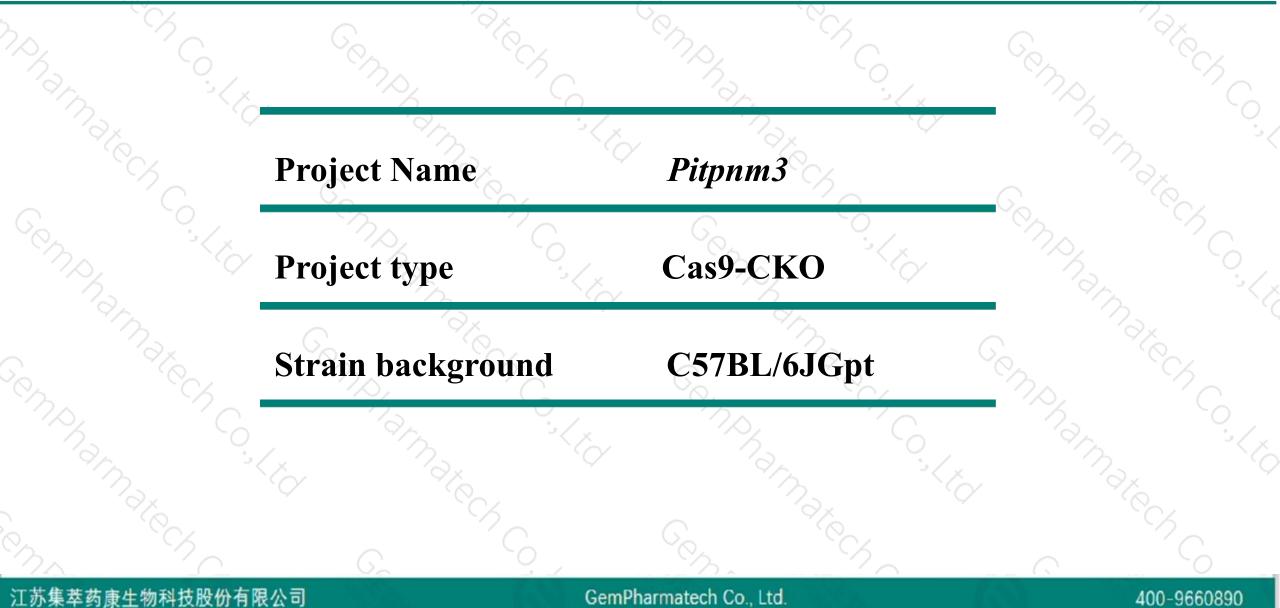
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Reviewer: Rui Xiong

Design Date: 2020-8-14

Project Overview



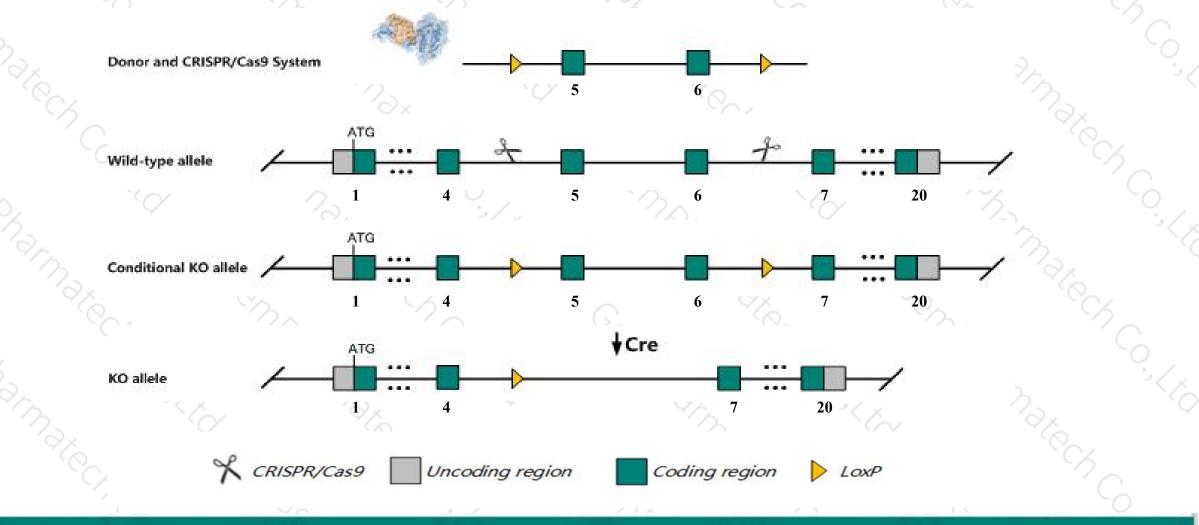


Conditional Knockout strategy



400-9660890

This model will use CRISPR/Cas9 technology to edit the *Pitpnm3* gene. The schematic diagram is as follows:



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The *Pitpnm3* gene has 5 transcripts. According to the structure of *Pitpnm3* gene, exon5-exon6 of *Pitpnm3*-201(ENSMUST00000075258.12) transcript is recommended as the knockout region. The region contains 313bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Pitpnm3* 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.



- > The *Pitpnm3* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



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Pitpnm3 PITPNM family member 3 [Mus musculus (house mouse)]

Gene ID: 327958, updated on 13-Mar-2020

Summary

Official Symbol	Pitpnm3 provided by MGI
Official Full Name	PITPNM family member 3 provided byMGI
Primary source	MGI:MGI:2685726
See related	Ensembl:ENSMUSG00000040543
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	A330068P14Rik, Al848332, Ackr6, Gm880
Expression	Broad expression in frontal lobe adult (RPKM 23.6), cortex adult (RPKM 15.6) and 17 other tissuesSee more
Orthologs	human all

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Transcript information (Ensembl)



The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Pitpnm3-201	ENSMUST0000075258.12	6555	<u>974aa</u>	Protein coding	CCD524978	Q3UHE1	TSL:1 GENCODE basic APPRIS P3	
Pitpnm3-202	ENSMUST00000108508.2	6450	<u>958aa</u>	Protein coding	CCDS36213	Q3UHE1	TSL:1 GENCODE basic APPRIS AL	
Pitpnm3-204	ENSMUST00000134210.1	461	No protein	Processed transcript	100 - 100 -	2	TSL:2	
Pitpnm3-205	ENSMUST00000142471.1	3993	No protein	Retained intron	10		TSL:2	
Pitpnm3-203	ENSMUST00000132781.1	879	No protein	Retained intron	12	-	TSL:2	
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The strategy is based on the design of *Pitpnm3-201* transcript, the transcription is shown below:

< Pitpnm3-201 protein coding

Reverse strand

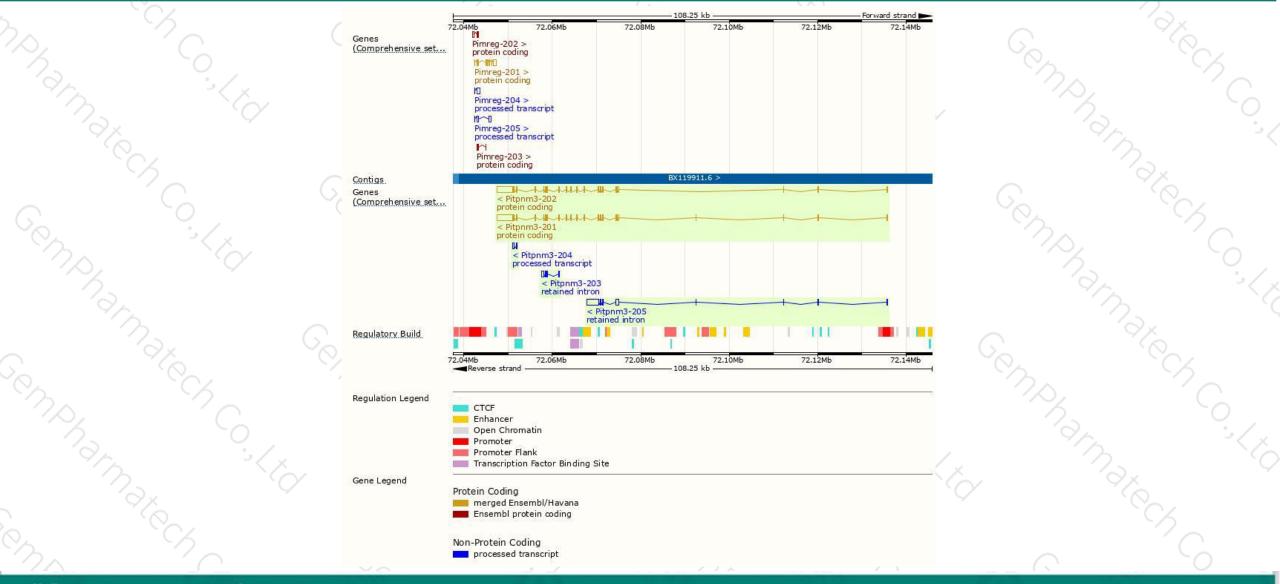
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Genomic location distribution





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Protein domain



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9	ENSMUSP00000074 MobiDB lite Low complexity (Seq) Superfamily						HAD-I	ike superfamily		
	SMART	DDHD domain LNS2/PITP								
6	<u>Pfam</u>			DDHD d	omain					
	PROSITE profiles			DDHD d	omain					
	PANTHER	PTHR23509 PTHR23509 (SF22								
	All sequence SNPs/i	Sequence variants (dbSNP and all of	her sources)		n n n	1.1.11	1.1.11		
	Variant Legend	stop lost missense varia synonymous va	- Si Si						0.< ~< X0	
	Scale bar	0 100	200	300 400	500	600	700	800	974	
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



