

Frmpd4 Cas9-KO Strategy

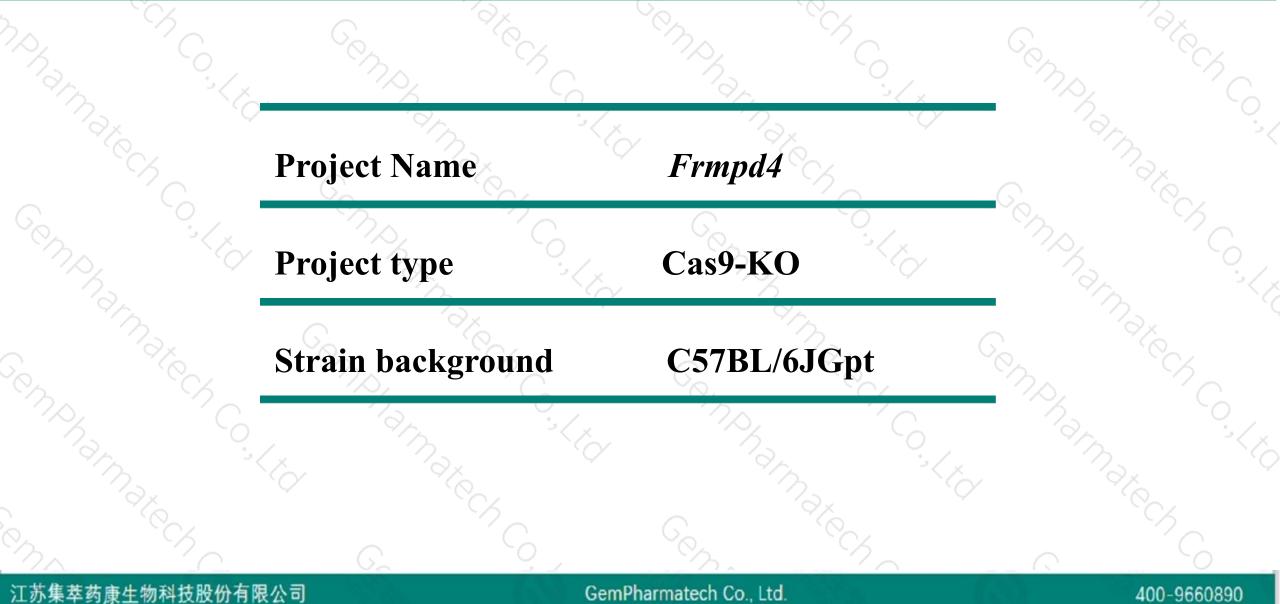
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Design Date: 2020-8-24

Project Overview

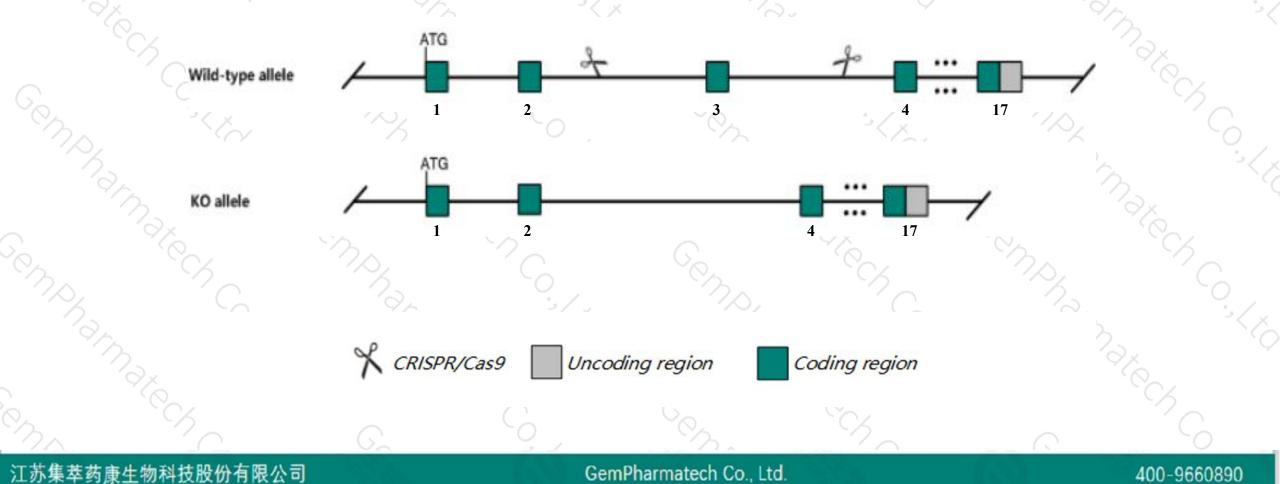




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Frmpd4* gene. The schematic diagram is as follows:





> The *Frmpd4* gene has 7 transcripts. According to the structure of *Frmpd4* gene, exon3 of *Frmpd4*-201(ENSMUST00000112145.2) transcript is recommended as the knockout region. The region contains 161bp coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify *Frmpd4* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- > According to the existing MGI data, mice homozygous for a knock-out allele exhibit increased inflammation-induced pain and thermal pain in a chronic pain model.
- The *Frmpd4* gene is located on the ChrX. 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.

Notice

Gene information (NCBI)



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Frmpd4 FERM and PDZ domain containing 4 [Mus musculus (house mouse)]

Gene ID: 333605, updated on 13-Mar-2020

Summary

Official Symbol	Frmpd4 provided by MGI
Official Full Name	FERM and PDZ domain containing 4 provided by MGI
Primary source	MGI:MGI:3042378
See related	Ensembl:ENSMUSG0000049176
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	Gm196, PKAP1, Pdzd10, Pdzk10, Preso1, preso
Expression	Biased expression in cortex adult (RPKM 3.1), frontal lobe adult (RPKM 2.7) and 6 other tissues See more
Orthologs	human all

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Transcript information (Ensembl)



The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Frmpd4-205	ENSMUST00000238211.1	8153	<u>1280aa</u>	Protein coding	CCDS72470	-	GENCODE basic
Frmpd4-201	ENSMUST00000112145.2	7924	<u>1312aa</u>	Protein coding	CCDS41210	A2AFR3	TSL:1 GENCODE basic
Frmpd4-207	ENSMUST00000239138.1	4305	<u>1312aa</u>	Protein coding	CCDS41210	12	GENCODE basic
Frmpd4-204	ENSMUST00000112149.8	6330	<u>1320aa</u>	Protein coding		A2AFR3	TSL:5 GENCODE basic APPRIS ALT2
Frmpd4-206	ENSMUST00000238709.1	5337	<u>1778aa</u>	Protein coding	-		GENCODE basic APPRIS P5
Frmpd4-202	ENSMUST00000112146.8	5283	<u>1760aa</u>	Protein coding	1170	A2AFR3	TSL:1 GENCODE basic
Frmpd4-203	ENSMUST00000112147.8	8607	<u>37aa</u>	Nonsense mediated decay	5 - 0	A2AFR3	TSL:1

The strategy is based on the design of *Frmpd4-201* transcript, the transcription is shown below:

< Frmpd4-201 protein coding

Reverse strand

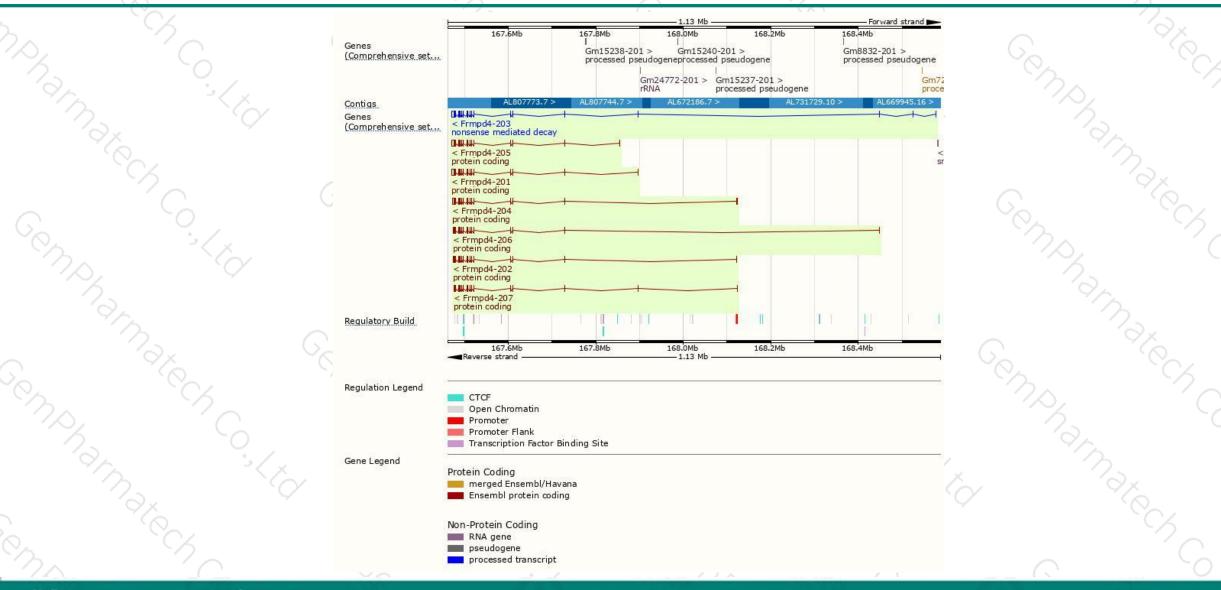
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426.25 kb

Genomic location distribution





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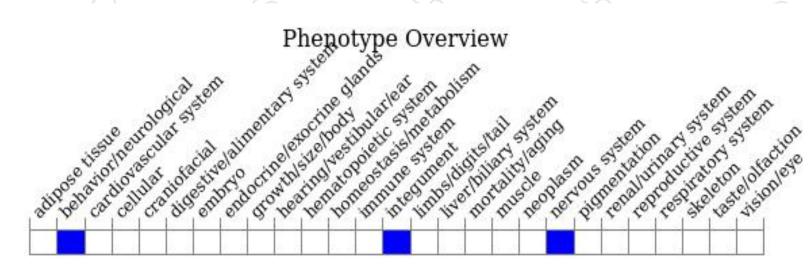
Protein domain



ENSMUSP00000107		25
MobiDB lite		
Low complexity (Seg) Superfamily	WW domain superfamily SSF50729	
	Ubiquitin-like domain superfamily	
	PDZ superfamily FERM superfamily, second domain	
SMART.	PDZ domain	
Pfam.	Band 4.1 domain	
rialli	PDZ domain FERM central domain	
PROSITE profiles	PDZ domain FERM domain	
	WW domain	
PANTHER	PTHR46221:SF4	
3	PTHR46221	XC-
Gene3D	2.30.42.10 FERM/acyl-CoA-binding protein superfamily	
CDD	2.20.70.10 3.10.20.90 PH-like domain superfamily	
<u></u>	cd00992 cd17170 FERM central domain WW domain FERM and PDZ domain-containing protein 1/3/4, FERM dom	and the latter
All assuence CNDe/i	Sequence variants (dbSNP and all other sources)	hain chobe
All sequence SNPs/i		<u> </u>
Variant Legend	missense variant	
	synonymous variant	

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 knock-out allele exhibit increased inflammation-induced pain and thermal pain in a chronic pain model.

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If you have any questions, you are welcome to inquire. Tel: 400-9660890



