

Ptgfrn Cas9-KO Strategy

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Project Overview



Project Name

Ptgfrn

Project type

Cas9-KO

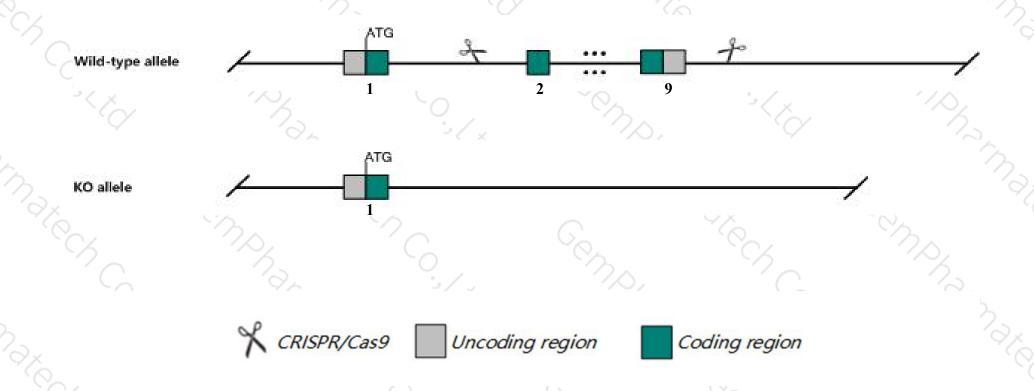
Strain background

C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Ptgfrn* gene has 3 transcripts. According to the structure of *Ptgfrn* gene, exon2-exon9 of *Ptgfrn-201*(ENSMUST00000102694.3) transcript is recommended as the knockout region. The region contains 2591bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Ptgfrn* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- ➤ According to the existing MGI data, Homozygous mice for a null gene trap mutation exhibit a decreased depressive-like response during tail suspension testing when compared with their wild-type littermates,
- > The *Ptgfrn* 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)



Ptgfrn prostaglandin F2 receptor negative regulator [Mus musculus (house mouse)]

Gene ID: 19221, updated on 7-Apr-2019

Summary

☆ ?

Official Symbol Ptgfrn provided by MGI

Official Full Name prostaglandin F2 receptor negative regulator provided by MGI

Primary source MGI:MGI:1277114

See related Ensembl: ENSMUSG00000027864

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 4833445A08Rik, AU042434, CD9P-1, EWI-F, FPRP, Trim45

Expression Broad expression in lung adult (RPKM 30.6), bladder adult (RPKM 17.8) and 21 other tissuesSee more

Orthologs <u>human</u> all

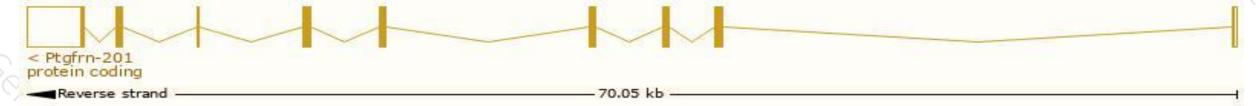
Transcript information (Ensembl)



The gene has 3 transcripts, all transcripts are shown below:

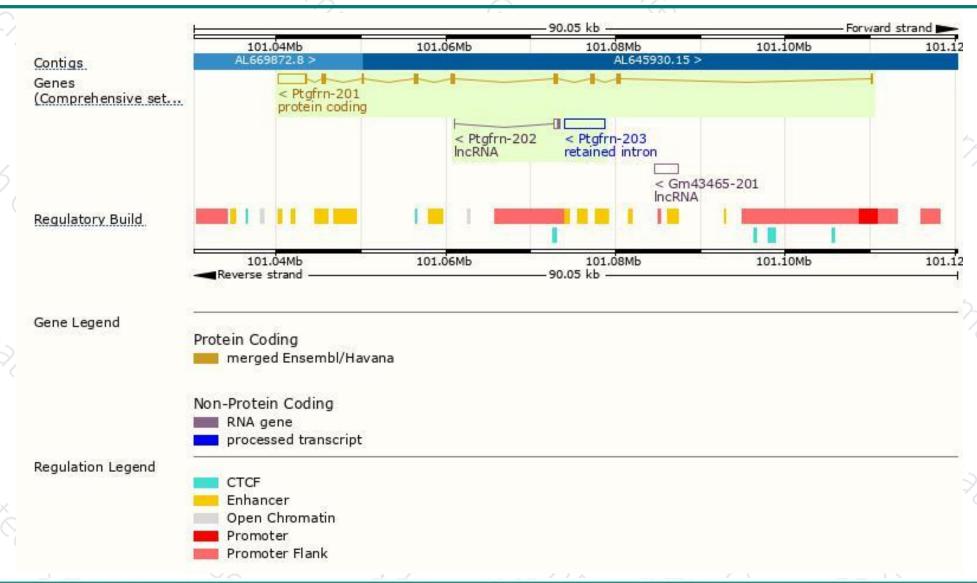
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptgfrn-201	ENSMUST00000102694.3	5902	879aa	Protein coding	CCDS17680	Q9WV91	TSL:1 GENCODE basic APPRIS P1
Ptgfrn-203	ENSMUST00000200065.1	4786	No protein	Retained intron	-	-8	TSL:NA
Ptgfrn-202	ENSMUST00000198037.1	660	No protein	IncRNA	ų.	28	TSL:3

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



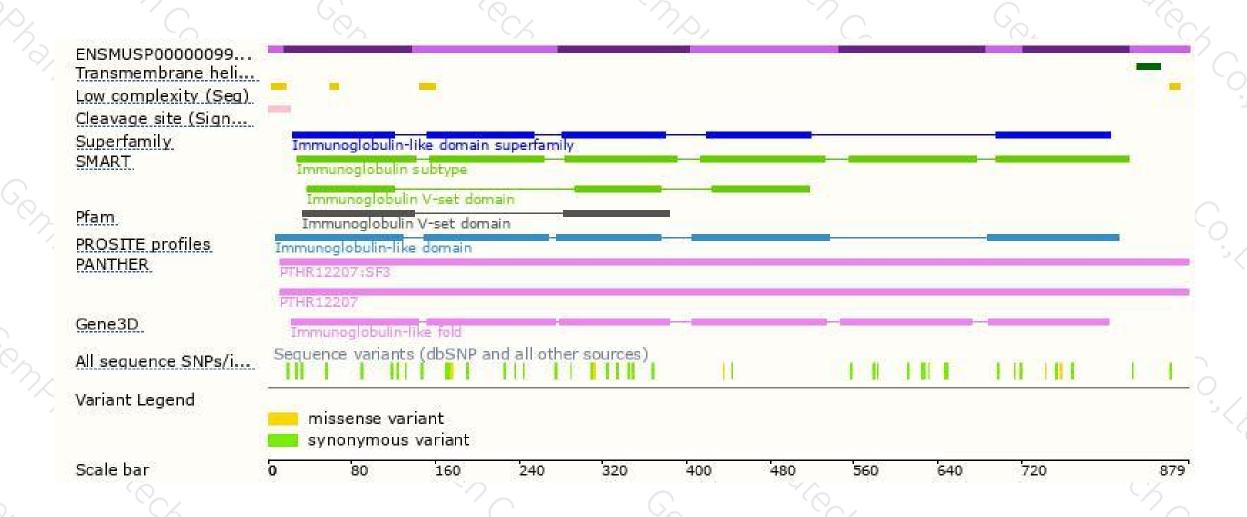
Genomic location distribution





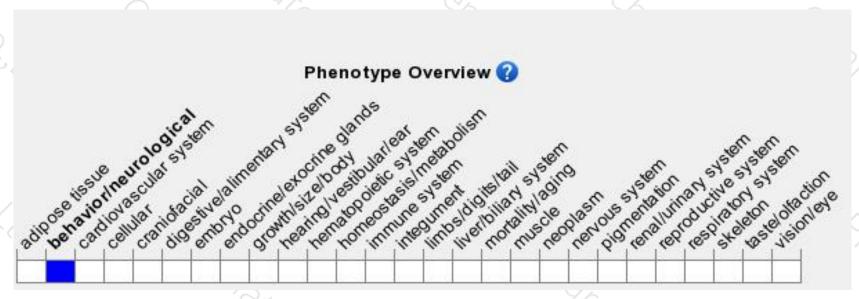
Protein domain





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, Homozygous mice for a null gene trap mutation exhibit a decreased depressive-like response during tail suspension testing when compared with their wild-type littermates,



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





