

# Ptprg Cas9-KO Strategy

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## **Project Overview**



Project Name Ptprg

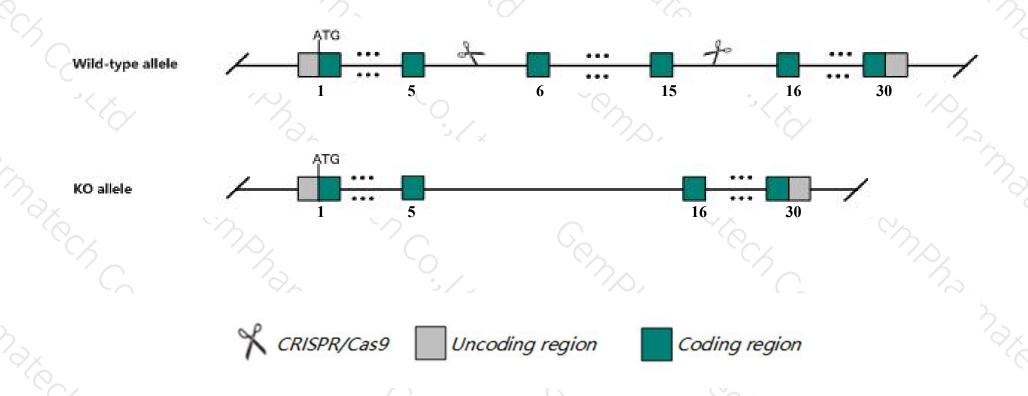
Project type Cas9-KO

Strain background C57BL/6JGpt

## **Knockout strategy**



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



### **Technical routes**



- > The *Ptprg* gene has 8 transcripts. According to the structure of *Ptprg* gene, exon6-exon15 of *Ptprg-201*(ENSMUST00000022264.12) transcript is recommended as the knockout region. The region contains 1843bp coding sequence Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Ptprg* gene. The brief process is as follows: CRISPR/Cas9 system

### **Notice**



- > According to the existing MGI data, Mice homozygous for a knock-out allele are overtly normal but exhibit minor behavioral changes including specific motor deficits, reduced latency to react in the tail flick test, enhanced sensory processing for acoustic stimuli, and reduced performance with cued fear conditioning.
- $\succ$  The KO region contains functional region of the Gm48603 gene. Knockout the region may affect the function of Gm48603 gene.
- > The *Ptprg* gene is located on the Chr14. 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)



#### Ptprg protein tyrosine phosphatase, receptor type, G [Mus musculus (house mouse)]

Gene ID: 19270, updated on 31-Jan-2019

#### Summary

☆ ?

Official Symbol Ptprg provided by MGI

Official Full Name protein tyrosine phosphatase, receptor type, G provided by MGI

Primary source MGI:MGI:97814

See related Ensembl: ENSMUSG00000021745

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 5430405N12Rik, AW046354, AW549872, RPTPgamma

Expression Ubiquitous expression in adrenal adult (RPKM 13.7), ovary adult (RPKM 13.0) and 26 other tissuesSee more

Orthologs <u>human</u> all

## Transcript information (Ensembl)



The gene has 8 transcripts, all transcripts are shown below:

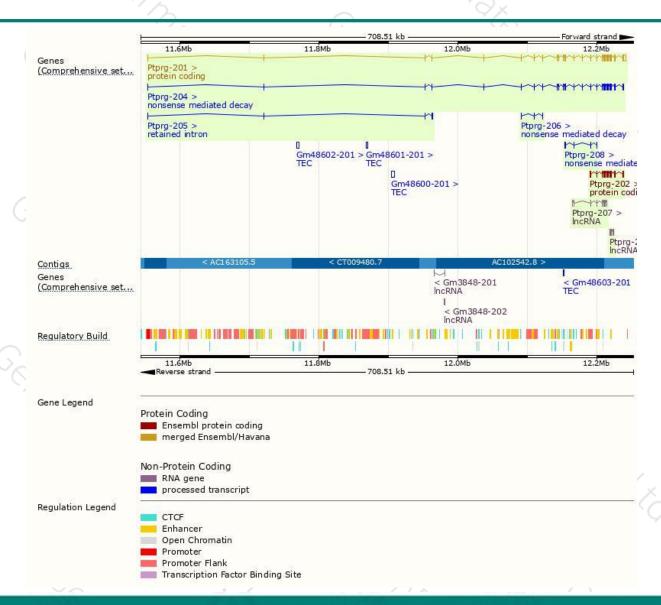
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST000000022264.12	9213	1442aa	Protein coding	CCDS26816	F8VQD7	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000119888.1	2787	<u>667aa</u>	Protein coding	CCDS84092	E9Q6E7	TSL:1 GENCODE basic
ENSMUST00000142917.7	5591	260aa	Nonsense mediated decay	84	D6RD11	TSL:1
ENSMUST00000226099.1	739	<u>156aa</u>	Nonsense mediated decay	ė.	A0A286YCH6	CDS 5' incomplete
ENSMUST00000155727.2	408	<u>65aa</u>	Nonsense mediated decay		D3Z2S6	CDS 5' incomplete TSL:3
ENSMUST00000148113.1	2595	No protein	Retained intron	19 <del>-</del>	-8	TSL:2
ENSMUST00000223890.1	905	No protein	IncRNA	<u> </u>	9	
ENSMUST00000134290.1	426	No protein	IncRNA	12	20	TSL:3
	ENSMUST00000022264.12 ENSMUST00000119888.1 ENSMUST00000142917.7 ENSMUST00000226099.1 ENSMUST00000155727.2 ENSMUST00000148113.1 ENSMUST00000223890.1	ENSMUST00000022264.12 9213 ENSMUST00000119888.1 2787 ENSMUST00000142917.7 5591 ENSMUST00000226099.1 739 ENSMUST00000155727.2 408 ENSMUST00000148113.1 2595 ENSMUST00000223890.1 905	ENSMUST00000022264.12 9213 1442aa  ENSMUST00000119888.1 2787 667aa  ENSMUST00000142917.7 5591 260aa  ENSMUST00000226099.1 739 156aa  ENSMUST00000155727.2 408 65aa  ENSMUST00000148113.1 2595 No protein  ENSMUST00000223890.1 905 No protein	ENSMUST00000022264.12         9213         1442aa         Protein coding           ENSMUST00000119888.1         2787         667aa         Protein coding           ENSMUST00000142917.7         5591         260aa         Nonsense mediated decay           ENSMUST00000226099.1         739         156aa         Nonsense mediated decay           ENSMUST00000155727.2         408         65aa         Nonsense mediated decay           ENSMUST00000148113.1         2595         No protein         Retained intron           ENSMUST00000223890.1         905         No protein         IncRNA	ENSMUST00000022264.12         9213         1442aa         Protein coding         CCDS26816           ENSMUST00000119888.1         2787         667aa         Protein coding         CCDS84092           ENSMUST00000142917.7         5591         260aa         Nonsense mediated decay         -           ENSMUST00000226099.1         739         156aa         Nonsense mediated decay         -           ENSMUST00000155727.2         408         65aa         Nonsense mediated decay         -           ENSMUST00000148113.1         2595         No protein         Retained intron         -           ENSMUST00000223890.1         905         No protein         IncRNA         -	ENSMUST00000022264.12         9213         1442aa         Protein coding         CCDS26816         F8VQD7           ENSMUST00000119888.1         2787         667aa         Protein coding         CCDS84092         E9Q6E7           ENSMUST00000142917.7         5591         260aa         Nonsense mediated decay         -         D6RD11           ENSMUST00000226099.1         739         156aa         Nonsense mediated decay         -         A0A286YCH6           ENSMUST00000155727.2         408         65aa         Nonsense mediated decay         -         D3Z2S6           ENSMUST00000148113.1         2595         No protein         Retained intron         -         -           ENSMUST00000223890.1         905         No protein         IncRNA         -         -

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



### Genomic location distribution





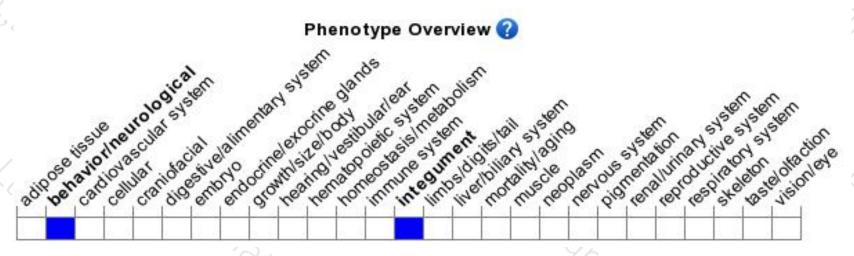
### Protein domain





### 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, Mice homozygous for a knock-out allele are overtly normal but exhibit minor behavioral changes including specific motor deficits, reduced latency to react in the tail flick test, enhanced sensory processing for acoustic stimuli, and reduced performance with cued fear conditioning.



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





