

# Ppfia1 Cas9-CKO Strategy

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# **Project Overview**



**Project Name** 

Ppfia1

**Project type** 

Cas9-CKO

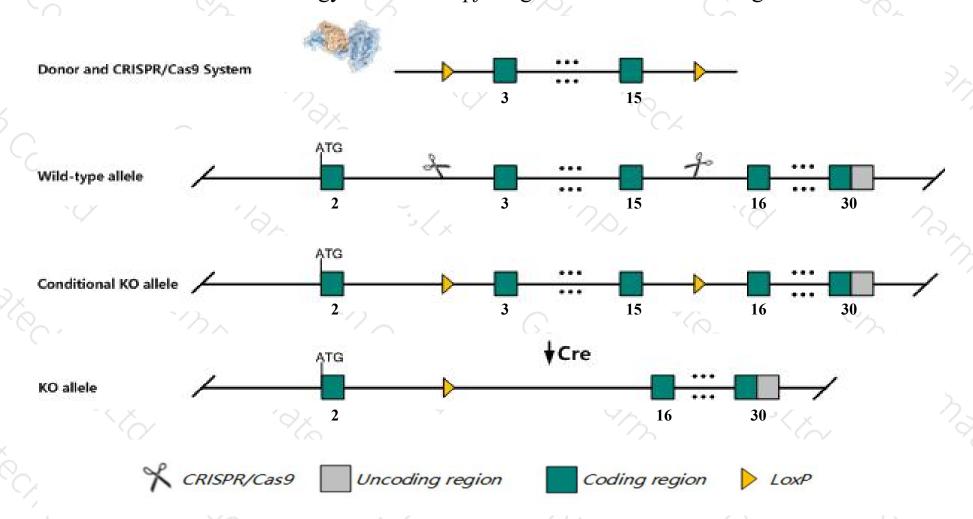
Strain background

C57BL/6JGpt

## Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Ppfia1* gene. The schematic diagram is as follows:



### Technical routes



- The *Ppfia1* gene has 11 transcripts. According to the structure of *Ppfia1* gene, exon3-exon15 of *Ppfia1-201* (ENSMUST00000168134.9) transcript is recommended as the knockout region. The region contains 1664bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ppfia1* 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.

### **Notice**



- > Transcript *Ppfia1*-205&206&209&210&211 may not be affected.
- > The *Ppfia1* gene is located on the Chr7. 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)



Ppfia1 protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 [ Mus musculus (house mouse) ]

Gene ID: 233977, updated on 12-Nov-2019

#### Summary

△ ?

Official Symbol Ppfia1 provided by MGI

Official Full Name protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 provided by MGI

Primary source MGI:MGI:1924750

See related Ensembl:ENSMUSG00000037519

Gene type protein coding
RefSeq status VALIDATED
Organism <u>Mus musculus</u>

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;

Muroidea; Muridae; Murinae; Mus; Mus

Also known as LIP1; LIP.1; C87158; C030014K08Rik

Expression Ubiquitous expression in cerebellum adult (RPKM 13.1), CNS E11.5 (RPKM 12.8) and 28 other tissues See more

Orthologs <u>human</u> all

#### Genomic context



Location: 7; 7 F5

See Ppfia1 in Genome Data Viewer

Exon count: 32

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (144476755144553762, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (151662883151739591, complement)

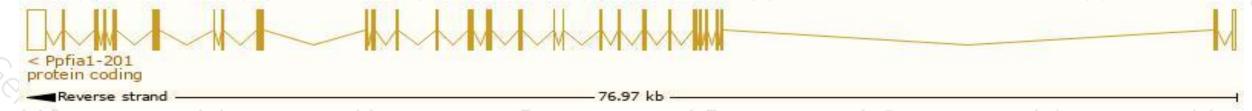
# Transcript information (Ensembl)



The gene has 11 transcripts, all transcripts are shown below:

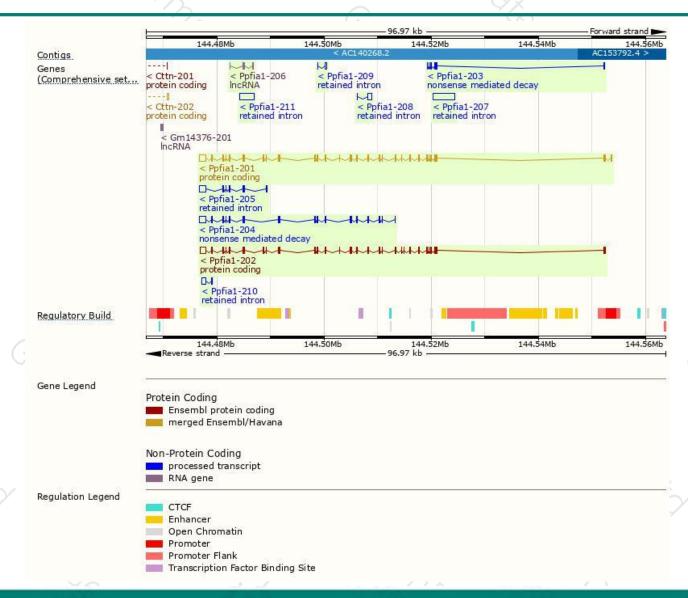
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000168134.9	5181	<u>1241aa</u>	Protein coding	CCDS52464	B2RXW8	TSL:1 GENCODE basic APPRIS P3
ENSMUST00000182226.7	4829	<u>1266aa</u>	Protein coding	CCDS59738	B2RXQ2	TSL:1 GENCODE basic APPRIS ALT1
ENSMUST00000182958,7	3444	<u>562aa</u>	Nonsense mediated decay	827	S4R1D4	CDS 5' incomplete TSL:5
ENSMUST00000182731.1	696	94aa	Nonsense mediated decay	1028	S4R117	CDS 5' incomplete TSL:3
ENSMUST00000183106.1	4088	No protein	Retained intron	187	-	TSL:NA
ENSMUST00000207471.1	2782	No protein	Retained intron	3.5	* .	TSL:NA
ENSMUST00000182982.7	2055	No protein	Retained intron	127	-	TSL:5
ENSMUST00000183183.1	928	No protein	Retained intron	3523	20	TSL:3
ENSMUST00000207298.1	804	No protein	Retained intron	187	-	TSL:2
ENSMUST00000183197.1	405	No protein	Retained intron	-	*	TSL:3
ENSMUST00000183063.1	357	No protein	IncRNA	12	-	TSL:5
	ENSMUST00000168134.9 ENSMUST00000182226.7 ENSMUST00000182958.7 ENSMUST00000182731.1 ENSMUST00000183106.1 ENSMUST00000182982.7 ENSMUST00000182982.7 ENSMUST00000183183.1 ENSMUST00000183183.1 ENSMUST00000183197.1	ENSMUST00000168134.9 5181 ENSMUST00000182226.7 4829 ENSMUST00000182958.7 3444 ENSMUST00000182731.1 696 ENSMUST00000183106.1 4088 ENSMUST00000207471.1 2782 ENSMUST00000182982.7 2055 ENSMUST00000183183.1 928 ENSMUST00000183183.1 928 ENSMUST00000183197.1 405	ENSMUST00000168134.9 5181 1241aa  ENSMUST00000182226.7 4829 1266aa  ENSMUST00000182958.7 3444 562aa  ENSMUST00000182731.1 696 94aa  ENSMUST00000183106.1 4088 No protein  ENSMUST00000207471.1 2782 No protein  ENSMUST00000182982.7 2055 No protein  ENSMUST00000183183.1 928 No protein  ENSMUST00000207298.1 804 No protein  ENSMUST00000183197.1 405 No protein	ENSMUST00000168134.9         5181         1241aa         Protein coding           ENSMUST00000182226.7         4829         1266aa         Protein coding           ENSMUST00000182958.7         3444         562aa         Nonsense mediated decay           ENSMUST00000182731.1         696         94aa         Nonsense mediated decay           ENSMUST00000183106.1         4088         No protein         Retained intron           ENSMUST00000207471.1         2782         No protein         Retained intron           ENSMUST00000182982.7         2055         No protein         Retained intron           ENSMUST00000183183.1         928         No protein         Retained intron           ENSMUST000000207298.1         804         No protein         Retained intron           ENSMUST00000183197.1         405         No protein         Retained intron	ENSMUST00000168134.9         5181         1241aa         Protein coding         CCDS52464           ENSMUST00000182226.7         4829         1266aa         Protein coding         CCDS59738           ENSMUST00000182958.7         3444         562aa         Nonsense mediated decay         -           ENSMUST00000182731.1         696         94aa         Nonsense mediated decay         -           ENSMUST00000183106.1         4088         No protein         Retained intron         -           ENSMUST00000207471.1         2782         No protein         Retained intron         -           ENSMUST00000183183.1         928         No protein         Retained intron         -           ENSMUST00000207298.1         804         No protein         Retained intron         -           ENSMUST00000183197.1         405         No protein         Retained intron         -	ENSMUST00000168134.9         5181         1241aa         Protein coding         CCDS52464         B2RXW8           ENSMUST00000182226.7         4829         1266aa         Protein coding         CCDS59738         B2RXQ2           ENSMUST00000182958.7         3444         562aa         Nonsense mediated decay         -         S4R1D4           ENSMUST00000182731.1         696         94aa         Nonsense mediated decay         -         S4R1I7           ENSMUST00000183106.1         4088         No protein         Retained intron         -         -           ENSMUST00000183183.10         2782         No protein         Retained intron         -         -           ENSMUST00000183183.1         928         No protein         Retained intron         -         -           ENSMUST00000183183.1         928         No protein         Retained intron         -         -           ENSMUST00000183197.1         804         No protein         Retained intron         -         -           ENSMUST00000183197.1         405         No protein         Retained intron         -         -

The strategy is based on the design of *Ppfia1-201* transcript, The transcription is shown below



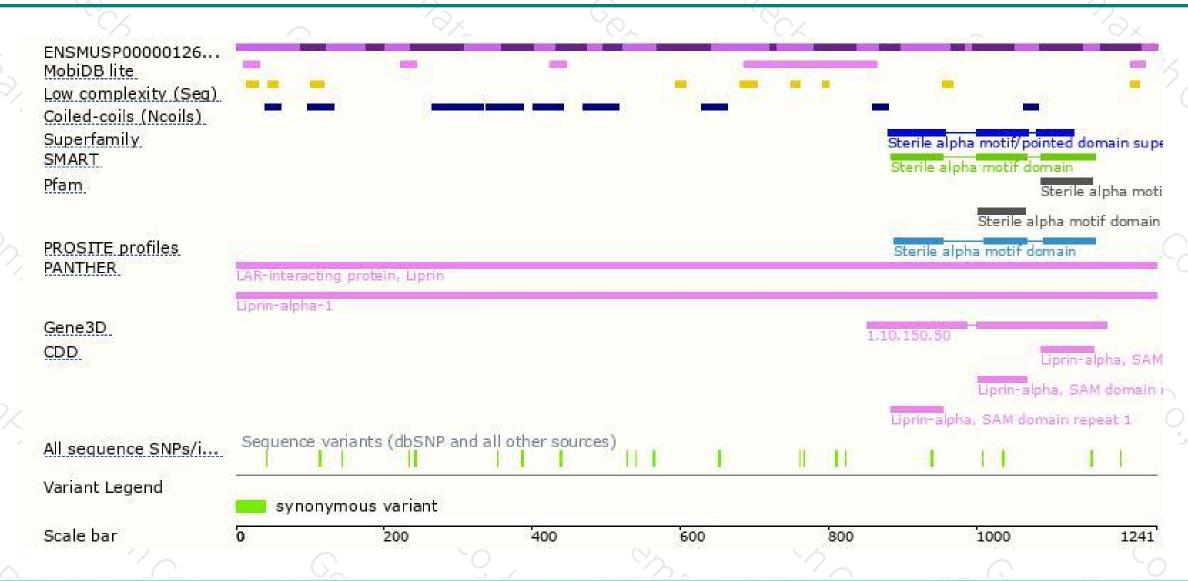
### Genomic location distribution





### Protein domain







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





