

Ppfi1 Cas9-KO Strategy

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Project Overview

Project Name

Ppfia1

Project type

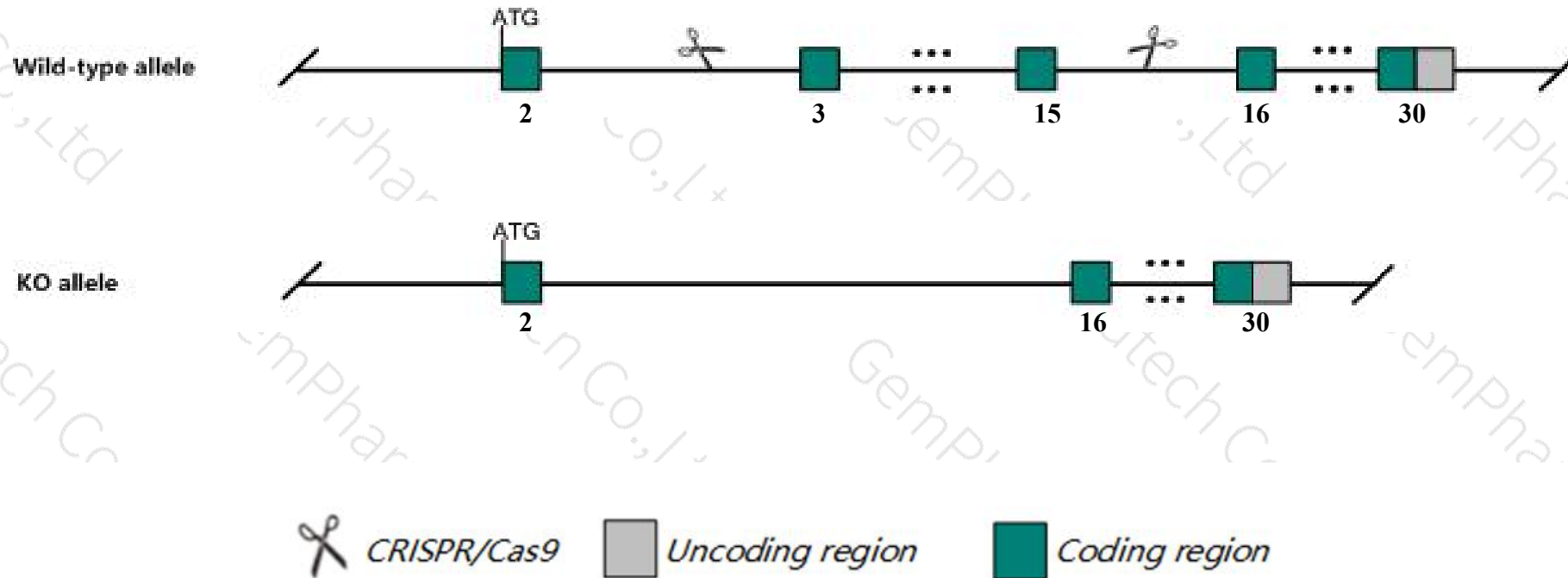
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Ppfial* gene has 11 transcripts. According to the structure of *Ppfial* gene, exon3-exon15 of *Ppfial*-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 *Ppfial* gene. The brief process is as follows: CRISPR/Cas9 system

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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	Mus musculus
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	human all

Genomic context

Location: 7; 7 F5

See Ppfia1 in [Genome Data Viewer](#)

Exon count: 32

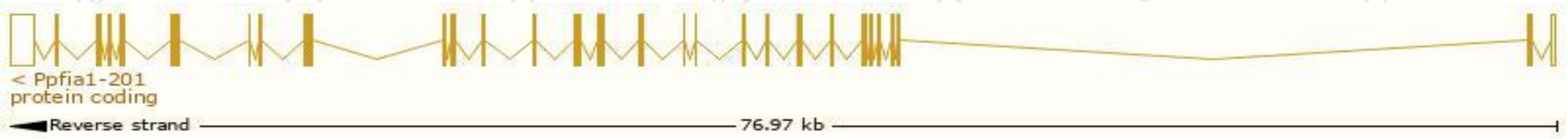
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (144476755..144553762, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (151662883..151739591, complement)

Transcript information (Ensembl)

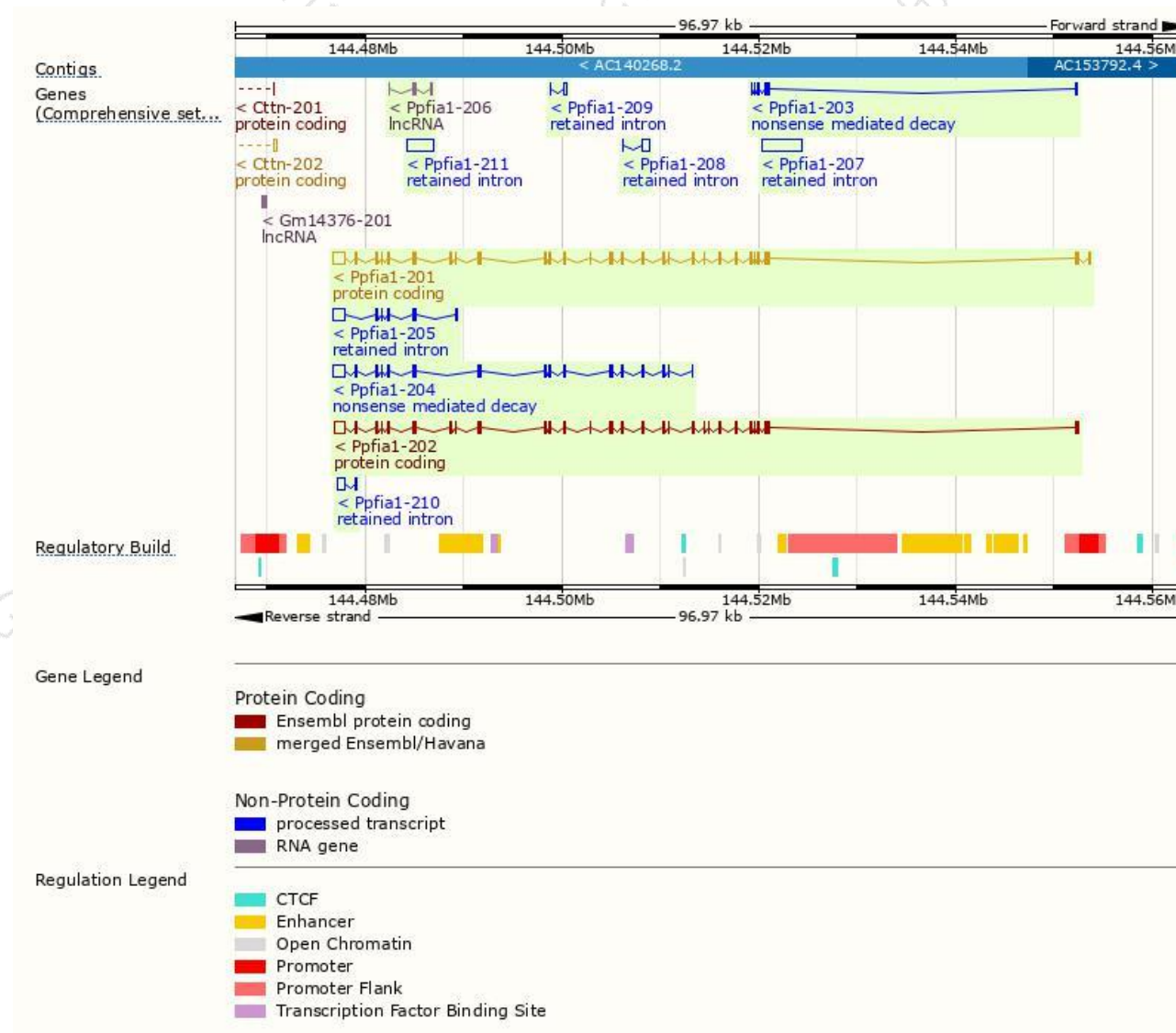
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppfia1-201	ENSMUST00000168134.9	5181	1241aa	Protein coding	CCDS52464	B2RXW8	TSL:1 GENCODE basic APPRIS P3
Ppfia1-202	ENSMUST00000182226.7	4829	1266aa	Protein coding	CCDS59738	B2RXQ2	TSL:1 GENCODE basic APPRIS ALT1
Ppfia1-204	ENSMUST00000182958.7	3444	562aa	Nonsense mediated decay	-	S4R1D4	CDS 5' incomplete TSL:5
Ppfia1-203	ENSMUST00000182731.1	696	94aa	Nonsense mediated decay	-	S4R1I7	CDS 5' incomplete TSL:3
Ppfia1-207	ENSMUST00000183106.1	4088	No protein	Retained intron	-	-	TSL:NA
Ppfia1-211	ENSMUST00000207471.1	2782	No protein	Retained intron	-	-	TSL:NA
Ppfia1-205	ENSMUST00000182982.7	2055	No protein	Retained intron	-	-	TSL:5
Ppfia1-208	ENSMUST00000183183.1	928	No protein	Retained intron	-	-	TSL:3
Ppfia1-210	ENSMUST00000207298.1	804	No protein	Retained intron	-	-	TSL:2
Ppfia1-209	ENSMUST00000183197.1	405	No protein	Retained intron	-	-	TSL:3
Ppfia1-206	ENSMUST00000183063.1	357	No protein	lncRNA	-	-	TSL:5

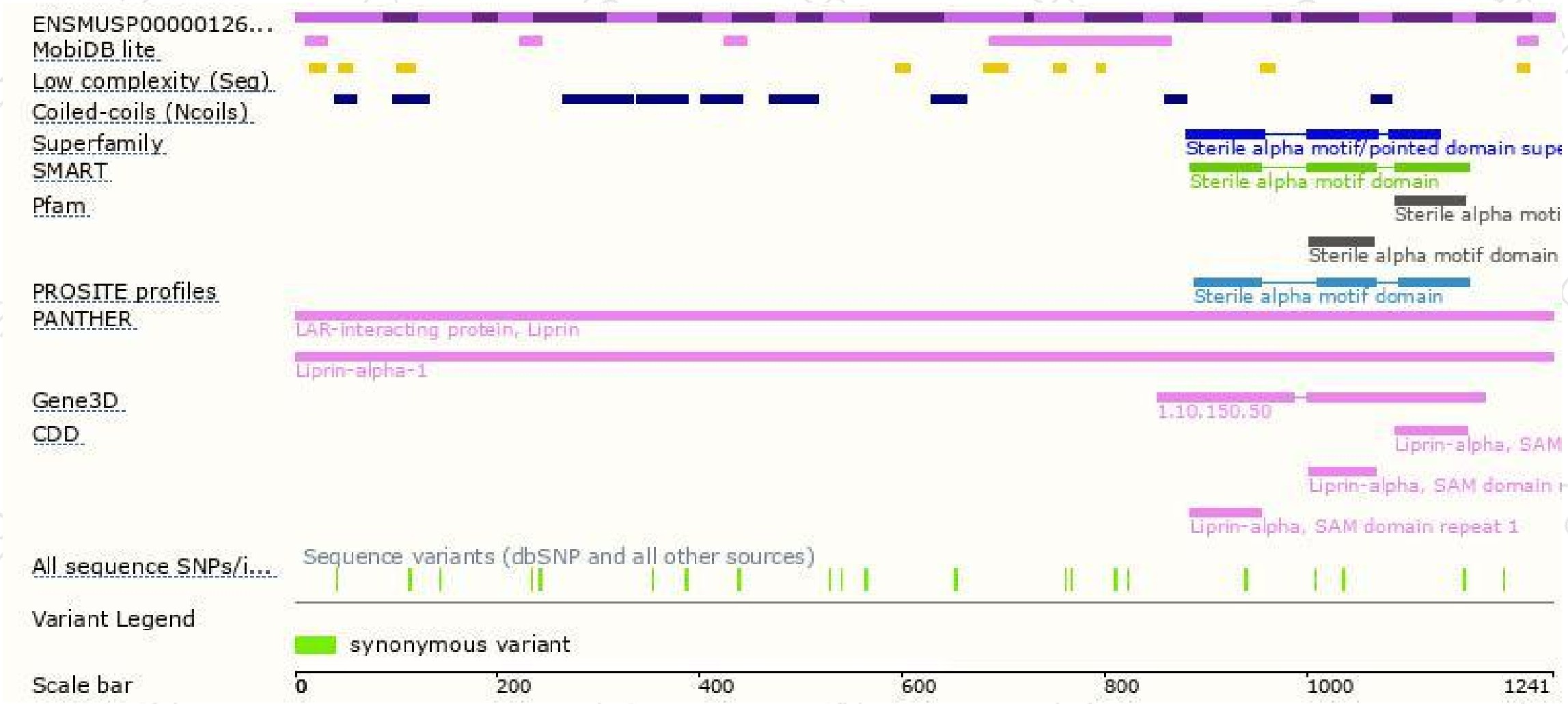
The strategy is based on the design of *Ppfia1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



If you have any questions, you are welcome to inquire.

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