

Ptprj Cas9-KO Strategy

Designer: Lingyan Wu

Reviewer: Rui Xiong

Design Date: 2020-5-13

Project Overview

Project Name

Ptprj

Project type

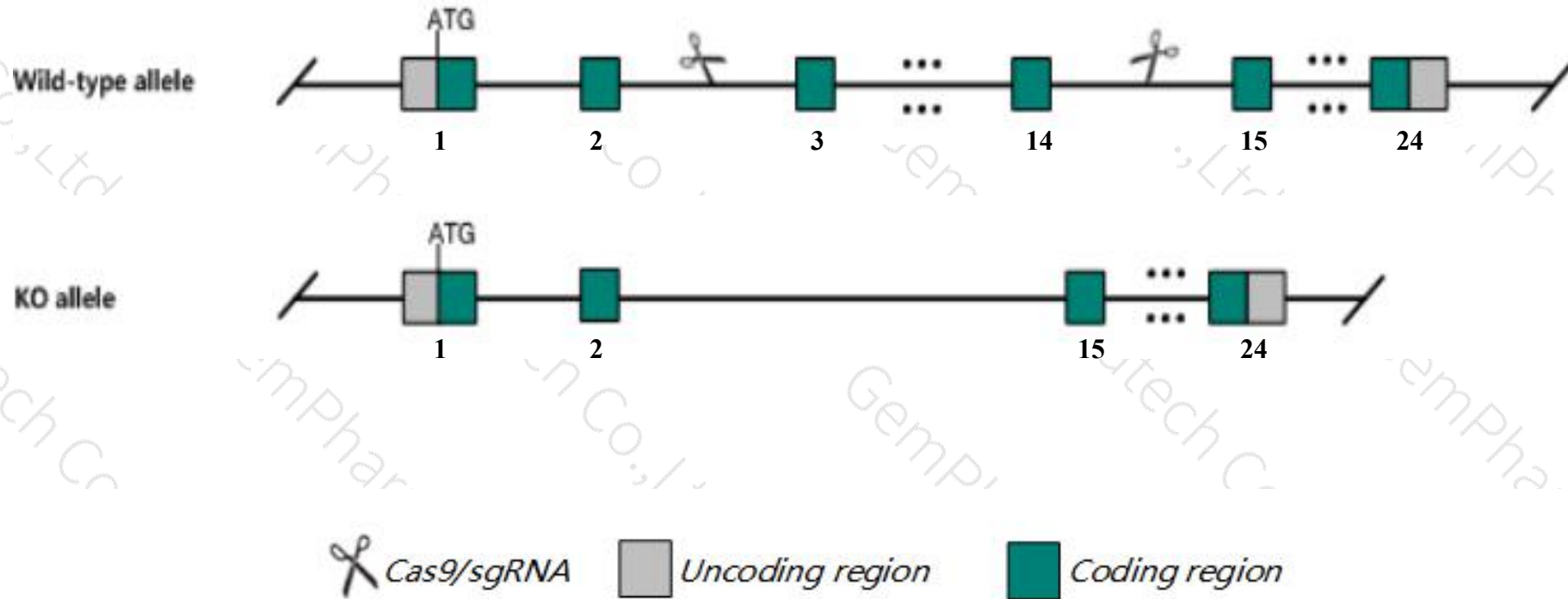
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

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



- The *Ptprj* gene has 4 transcripts. According to the structure of *Ptprj* gene, exon3-exon14 of *Ptprj-204* (ENSMUST00000168621.2) transcript is recommended as the knockout region. The region contains 2587bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ptprj* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, mice homozygous for a null allele die in utero displaying severe growth retardation and cardiovascular defects. homozygotes for a second null allele are viable, fertile and healthy with no spontaneous tumor formation. homozygotes for a third null allele show sterility and a block b cell development.
- The *Ptprj* gene is located on the Chr2. 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)

Ptprj protein tyrosine phosphatase, receptor type, J [Mus musculus (house mouse)]

Gene ID: 19271, updated on 13-Mar-2020

Summary

Official Symbol Ptprj provided by [MGI](#)

Official Full Name protein tyrosine phosphatase, receptor type, J provided by [MGI](#)

Primary source [MGI:MGI:104574](#)

See related [Ensembl:ENSMUSG00000025314](#)

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 AI450271, BET, Byp, CD148, DEP-1, PTPbeta2, Ptpb2, R-PTP-J, R-PTP-eta, RPTPJ, Scc-1, Scc1

Expression Ubiquitous expression in spleen adult (RPKM 9.5), cortex adult (RPKM 8.5) and 28 other tissues [See more](#)

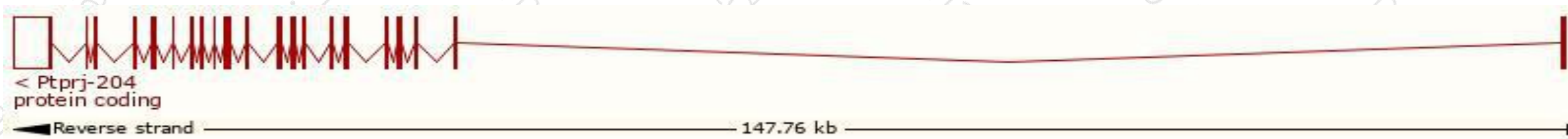
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

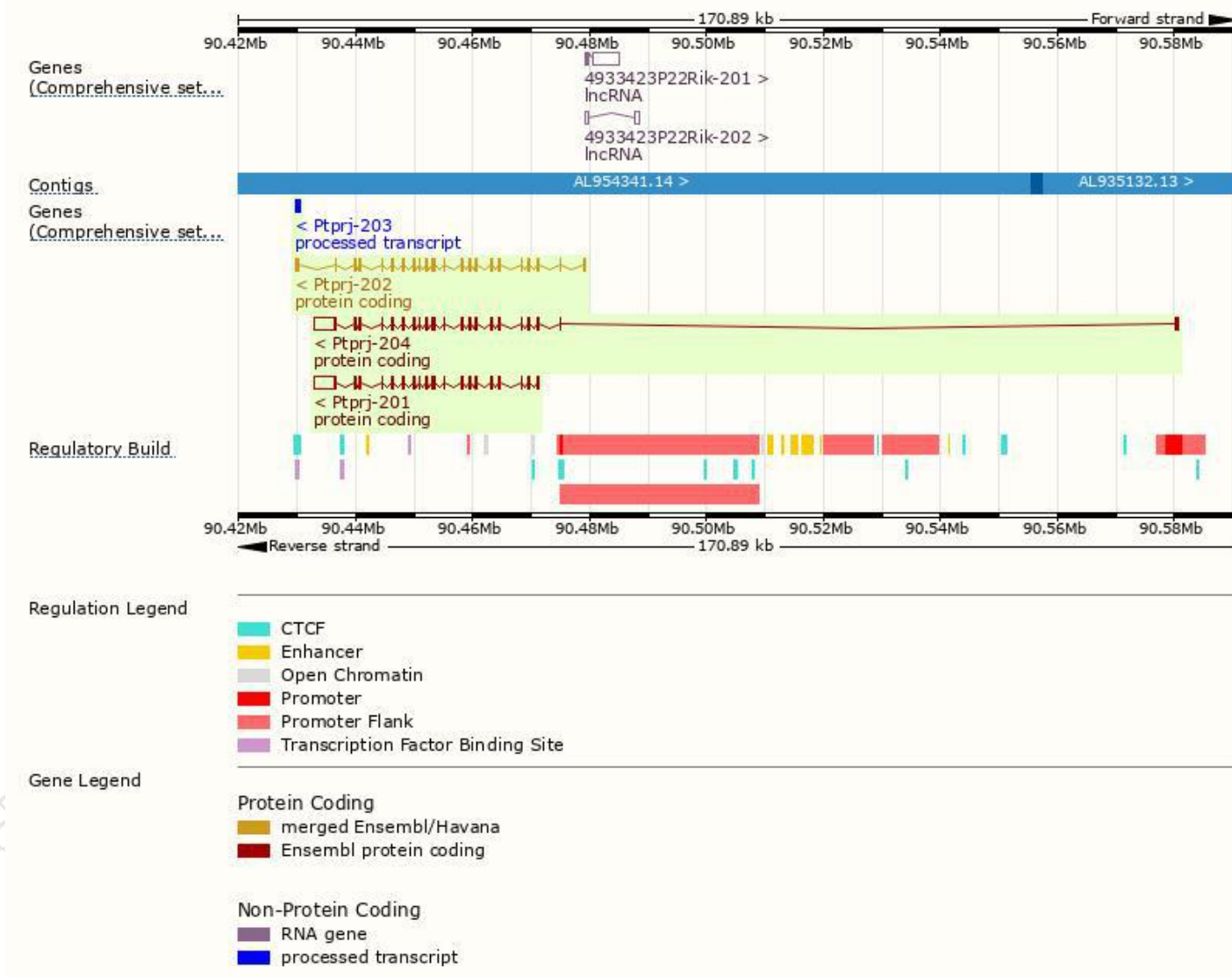
The gene has 4 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ptprj-204	ENSMUST00000168621.2	7634	1350aa	Protein coding	CCDS50630	E9Q4S7	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P4
Ptprj-202	ENSMUST00000111495.8	4197	1299aa	Protein coding	CCDS50629	A2AWF9	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Ptprj-201	ENSMUST00000111493.7	7124	1164aa	Protein coding	-	A2AWF8	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Ptprj-203	ENSMUST00000129323.1	513	No protein	Processed transcript	-	-	TSL:2

The strategy is based on the design of *Ptprj-204* transcript, the transcription is shown below:



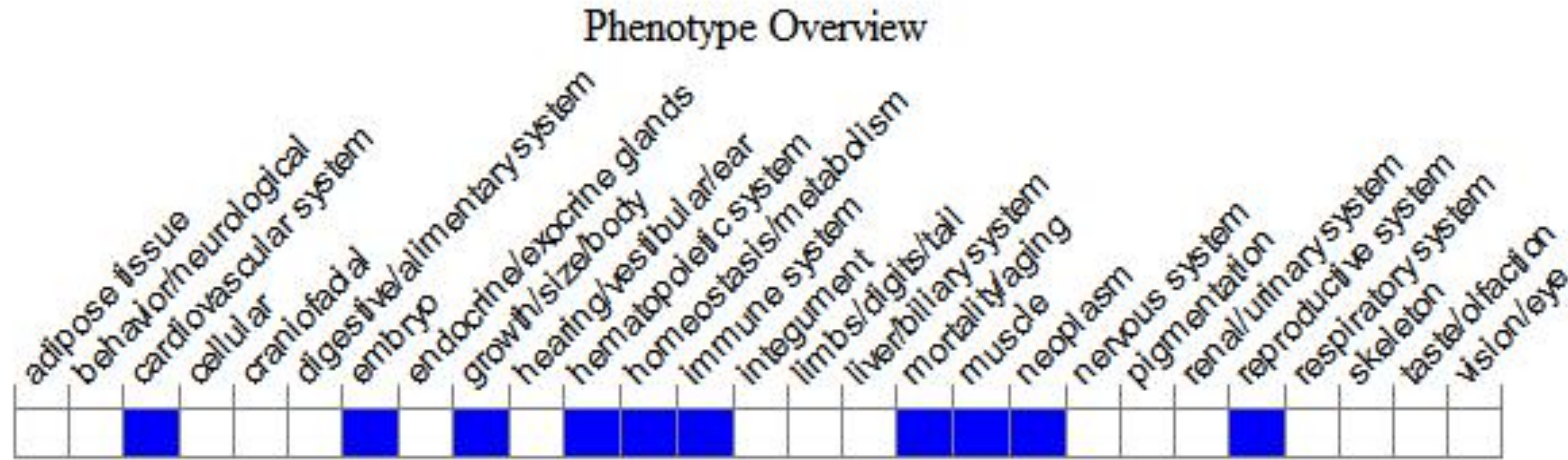
Genomic location distribution



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 null allele die in utero displaying severe growth retardation and cardiovascular defects. Homozygotes for a second null allele are viable, fertile and healthy with no spontaneous tumor formation. Homozygotes for a third null allele show sterility and a block B cell development.

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

Tel: 025-5864 1534

