

Ppp1r1c Cas9-KO Strategy

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Project Overview

Project Name

Ppp1r1c

Project type

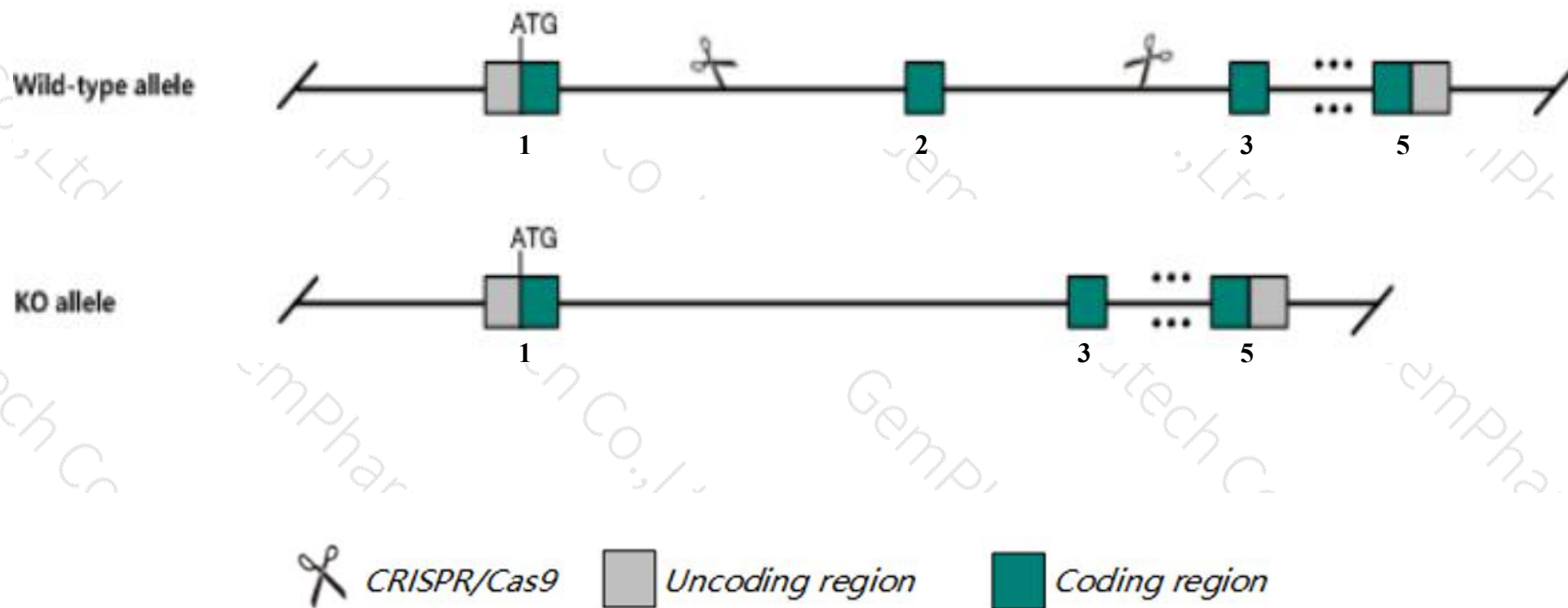
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ppp1r1c* gene. The schematic diagram is as follows:



- The *Ppp1r1c* gene has 5 transcripts. According to the structure of *Ppp1r1c* gene, exon2 of *Ppp1r1c*-203 (ENSMUST00000111780.2) transcript is recommended as the knockout region. The region contains 61bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ppp1r1c* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Ppp1r1c* 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)

Ppp1r1c protein phosphatase 1, regulatory inhibitor subunit 1C [Mus musculus (house mouse)]

Gene ID: 75276, updated on 13-Mar-2020

Summary



Official Symbol	Ppp1r1c provided by MGI
Official Full Name	protein phosphatase 1, regulatory inhibitor subunit 1C provided by MGI
Primary source	MGI:MGI:1923185
See related	Ensembl:ENSMUSG000000034683
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	4930565M23Rik, 4930579P15Rik
Expression	Low expression observed in reference dataset See more
Orthologs	human all

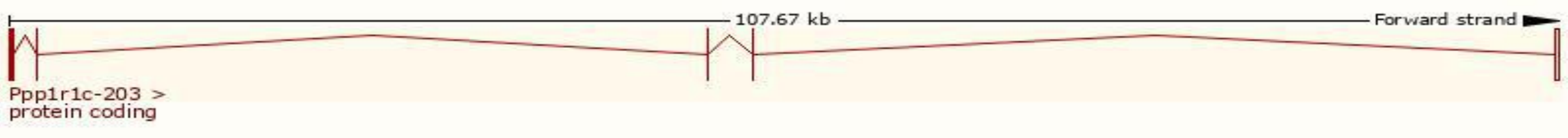
Transcript information（Ensembl）



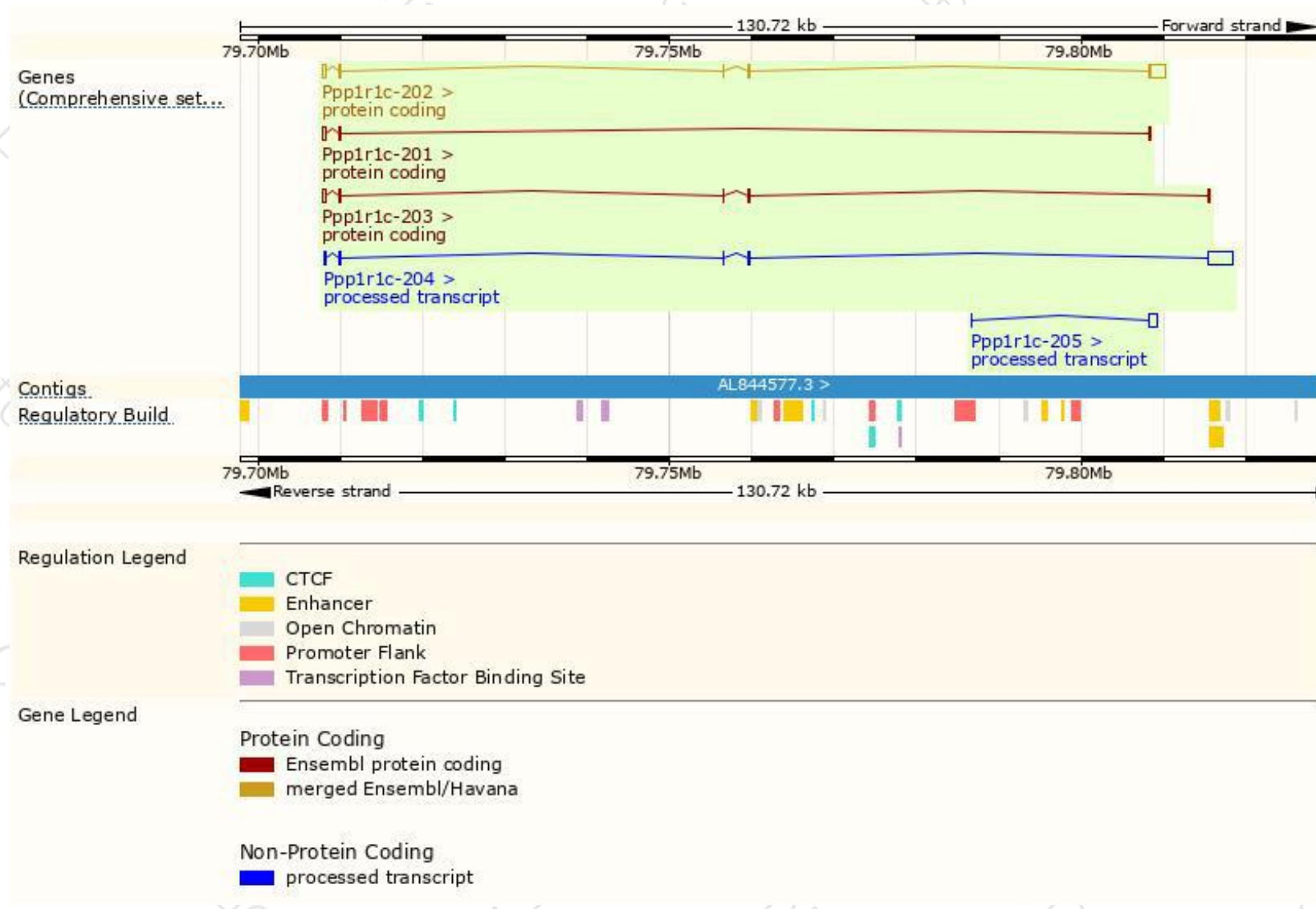
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppp1r1c-202	ENSMUST00000090760.8	2644	108aa	Protein coding	CCDS16171	Q8BKK4	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 P1
Ppp1r1c-203	ENSMUST00000111780.2	708	91aa	Protein coding	CCDS71081	Q8BKK4	TSL:1 GENCODE basic
Ppp1r1c-201	ENSMUST00000040863.10	629	76aa	Protein coding	CCDS79810	Q8BKK4	TSL:1 GENCODE basic
Ppp1r1c-204	ENSMUST00000141978.1	3467	No protein	Processed transcript	-	-	TSL:1
Ppp1r1c-205	ENSMUST00000144432.1	1051	No protein	Processed transcript	-	-	TSL:1

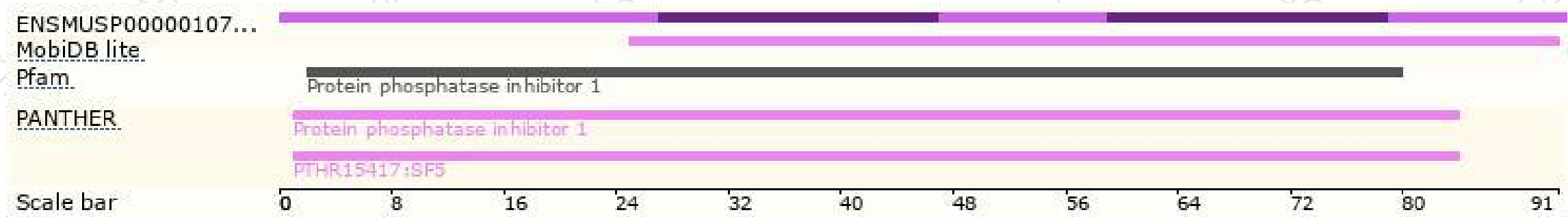
The strategy is based on the design of *Ppp1r1c-203* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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