

Ppih Cas9-KO Strategy

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Project Overview

Project Name

Ppih

Project type

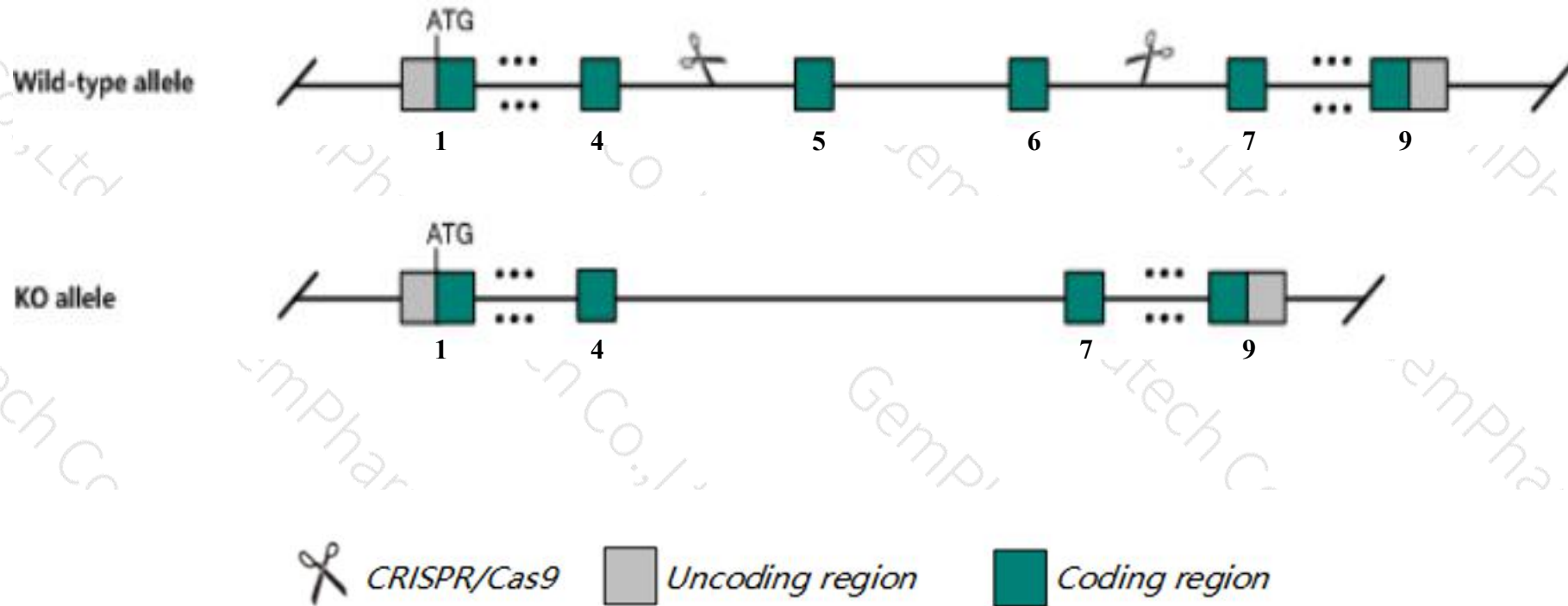
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Ppih* gene has 6 transcripts. According to the structure of *Ppih* gene, exon5-exon6 of *Ppih*-202 (ENSMUST00000106317.1) transcript is recommended as the knockout region. The region contains 136bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ppih* gene. The brief process is as follows: CRISPR/Cas9 system v

- The N-terminal of *Ppih* gene will remain several amino acids ,it may remain the partial function of *Ppih* gene.
- The *Ppih* gene is located on the Chr4. 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)

Ppih peptidyl prolyl isomerase H [Mus musculus (house mouse)]

Gene ID: 66101, updated on 13-Mar-2020

Summary



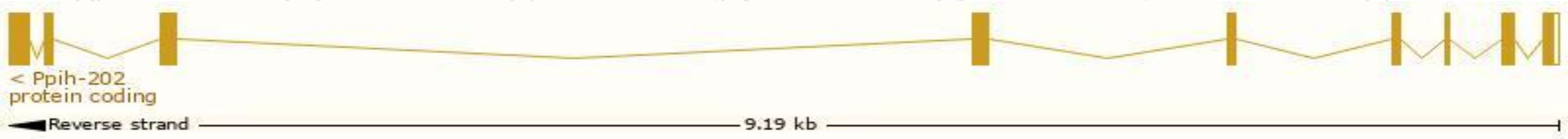
Official Symbol	Ppih provided by MGI
Official Full Name	peptidyl prolyl isomerase H provided by MGI
Primary source	MGI:MGI:106499
See related	Ensembl:ENSMUSG00000060288
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1100001J08Rik, 2010111B15Rik, 4833408F11Rik, AI464484, CYP-20, CYPH, D4Wsu43e
Expression	Broad expression in CNS E11.5 (RPKM 13.0), liver E14 (RPKM 10.6) and 22 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

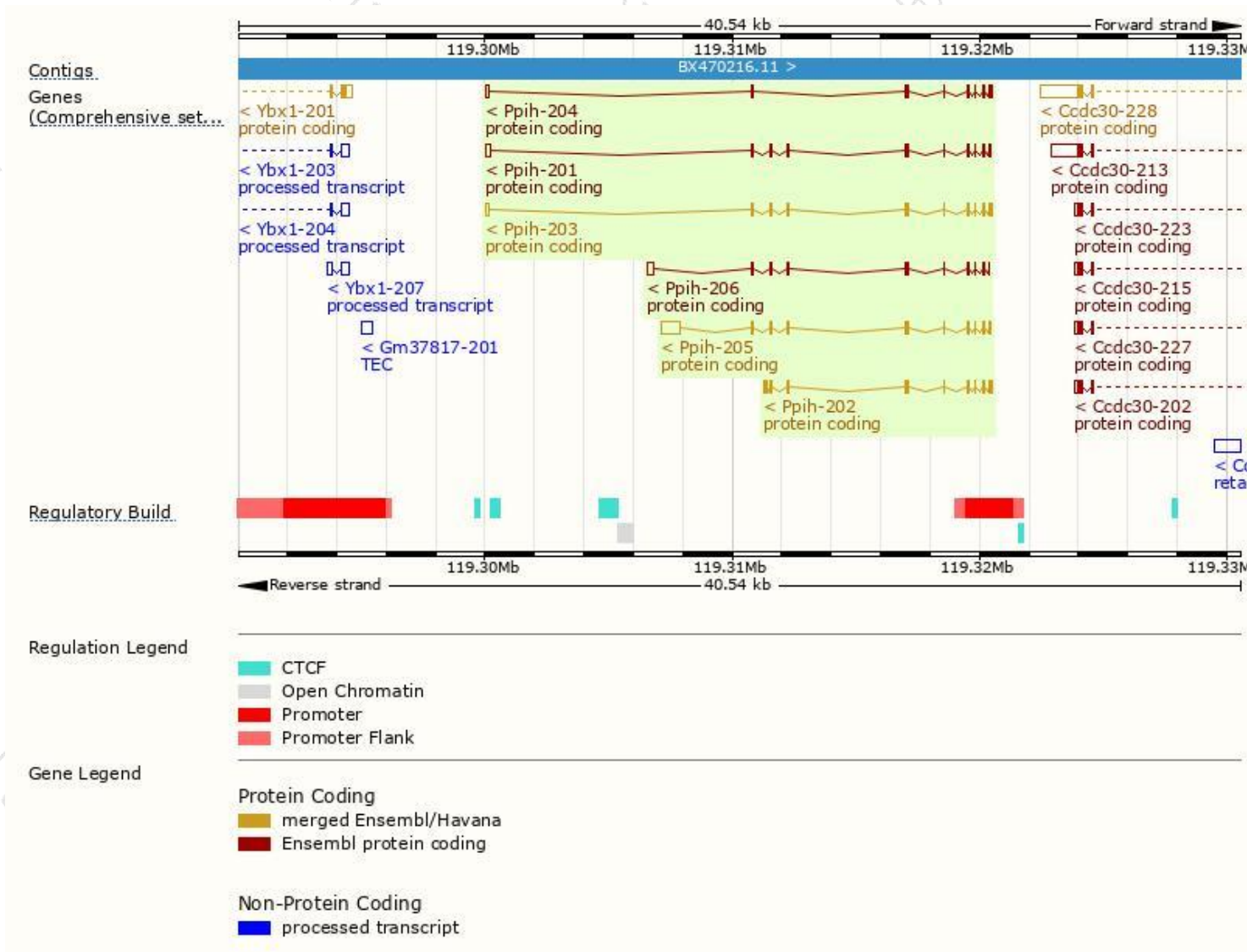
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppih-205	ENSMUST00000106321.8	1288	177aa	Protein coding	CCDS18580	Q4G0C5 Q9D868	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
Ppih-203	ENSMUST00000106318.7	800	177aa	Protein coding	CCDS18580	Q4G0C5 Q9D868	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
Ppih-201	ENSMUST00000056458.13	757	177aa	Protein coding	CCDS18580	Q4G0C5 Q9D868	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
Ppih-202	ENSMUST00000106317.1	613	188aa	Protein coding	CCDS51288	Q9D868	TSL:1 GENCODE basic
Ppih-206	ENSMUST00000147077.7	725	158aa	Protein coding	-	A2BGI8	CDS 5' incomplete TSL:5
Ppih-204	ENSMUST00000106319.7	622	134aa	Protein coding	-	A2BGI9	TSL:3 GENCODE basic

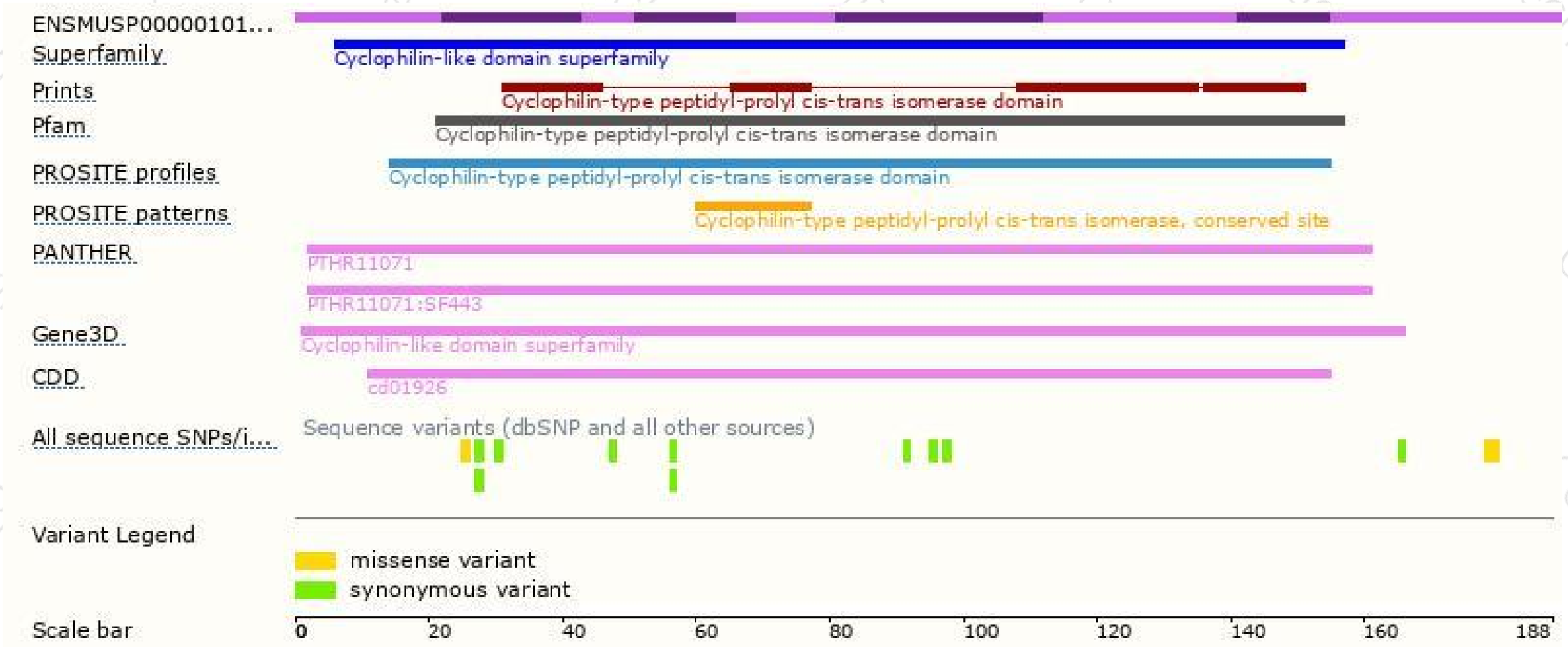
The strategy is based on the design of *Ppih-202* transcript,the transcription is shown below



Genomic location distribution



Protein domain



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

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