

Ppil1 Cas9-KO Strategy

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Project Overview

Project Name

Ppil1

Project type

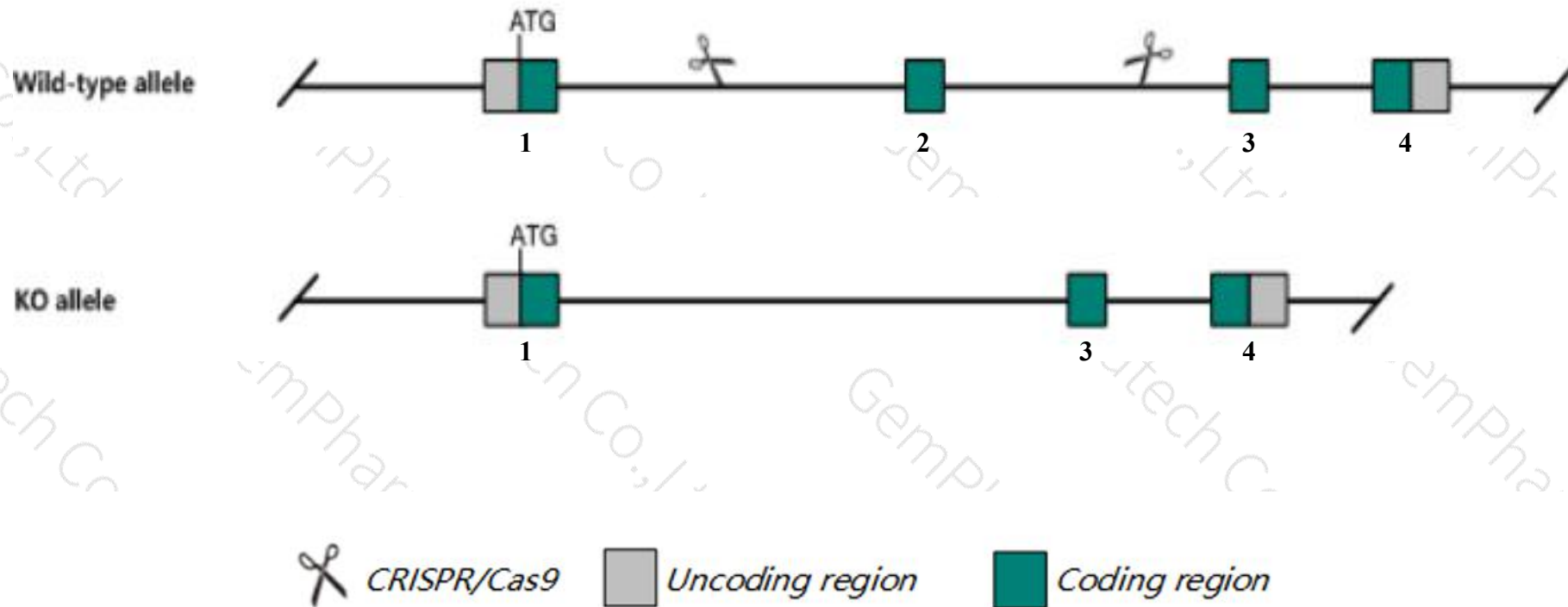
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Ppill* gene has 7 transcripts. According to the structure of *Ppill* gene, exon2 of *Ppill*-201 (ENSMUST00000024802.9) transcript is recommended as the knockout region. The region contains 155bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ppill* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Ppill*-204&205&206&207 may not be affected.
- The knockout region is near to the N-terminal of *BC004004* gene and *Gm50068* gene, this strategy may influence the regulatory function of the N-terminal of these genes.
- The *Ppill* gene is located on the Chr17. 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)

Ppil1 peptidylprolyl isomerase (cyclophilin)-like 1 [Mus musculus (house mouse)]

Gene ID: 68816, updated on 13-Mar-2020

Summary



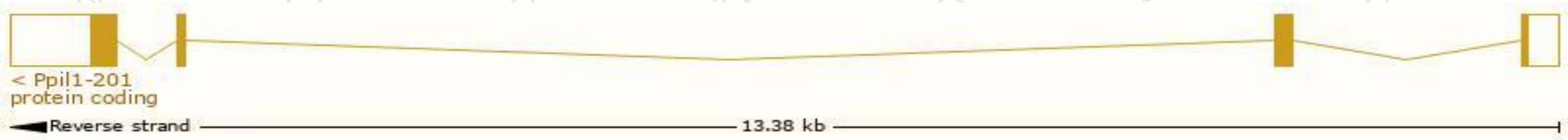
Official Symbol	Ppil1 provided by MGI
Official Full Name	peptidylprolyl isomerase (cyclophilin)-like 1 provided by MGI
Primary source	MGI:MGI:1916066
See related	Ensembl:ENSMUSG00000024007
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110060O10Rik, A1327391, Cyp11
Expression	Ubiquitous expression in liver E14.5 (RPKM 35.3), CNS E11.5 (RPKM 34.7) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

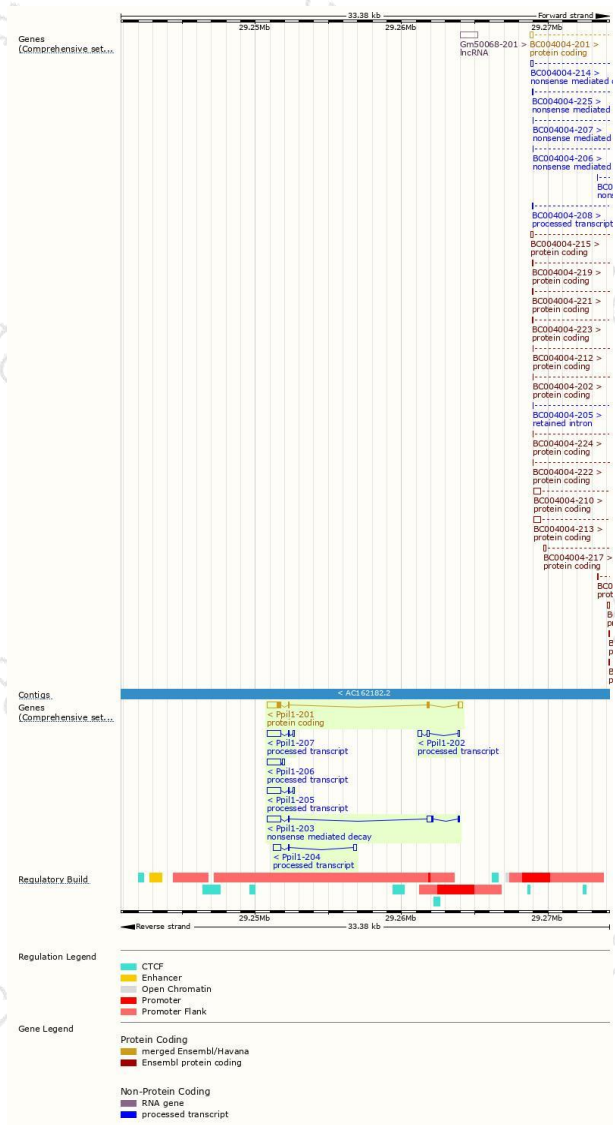
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppil1-201	ENSMUST00000024802.9	1462	166aa	Protein coding	CCDS28593	B9EJX8 Q9D0W5	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
Ppil1-203	ENSMUST00000135123.2	1476	64aa	Nonsense mediated decay	-	F6SSV9	TSL:5
Ppil1-207	ENSMUST00000234880.1	1117	No protein	Processed transcript	-	-	
Ppil1-205	ENSMUST00000234139.1	1101	No protein	Processed transcript	-	-	
Ppil1-206	ENSMUST00000234315.1	1050	No protein	Processed transcript	-	-	
Ppil1-204	ENSMUST00000136811.7	734	No protein	Processed transcript	-	-	TSL:3
Ppil1-202	ENSMUST00000129157.2	508	No protein	Processed transcript	-	-	TSL:3

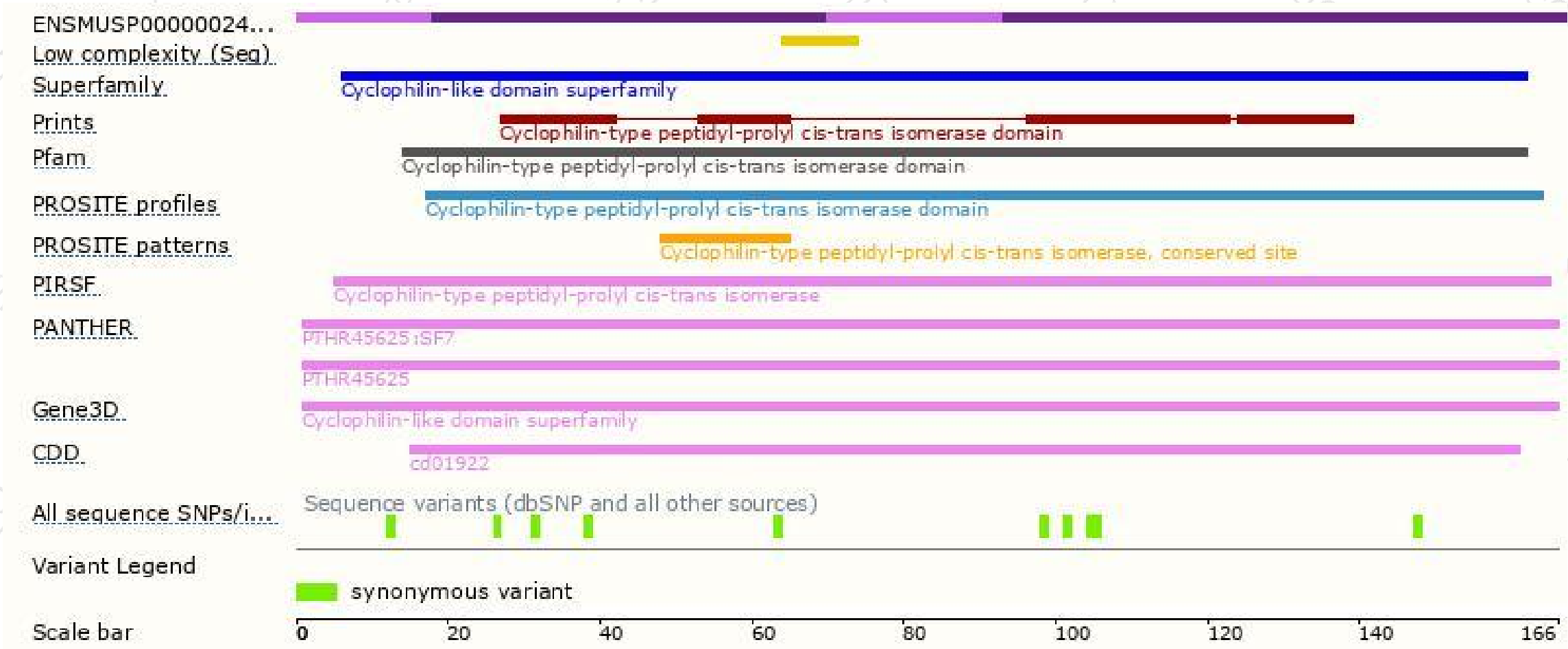
The strategy is based on the design of *Ppil1-201* transcript,the transcription is shown below



Genomic location distribution



Protein domain



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

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