

Ppil3 Cas9-KO Strategy

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Project Overview

Project Name

Ppil3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ppil3* gene. The schematic diagram is as follows:



- The *Ppil3* gene has 9 transcripts. According to the structure of *Ppil3* gene, exon3-exon4 of *Ppil3-201* (ENSMUST00000081677.11) transcript is recommended as the knockout region. The region contains 169bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ppil3* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- The *Ppil3* gene is located on the Chr1. 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.
- *Nif3l1* gene may be affected.

Gene information (NCBI)

Ppil3 peptidylprolyl isomerase (cyclophilin)-like 3 [Mus musculus (house mouse)]

Gene ID: 70225, updated on 13-Mar-2020

Summary



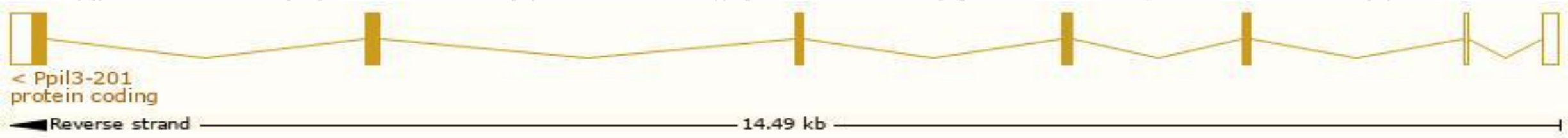
Official Symbol	Ppil3 provided by MGI
Official Full Name	peptidylprolyl isomerase (cyclophilin)-like 3 provided by MGI
Primary source	MGI:MGI:1917475
See related	Ensembl:ENSMUSG00000026035
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310076N22Rik, 2510026K04Rik, Cyp10l
Expression	Ubiquitous expression in CNS E11.5 (RPKM 6.4), CNS E14 (RPKM 5.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

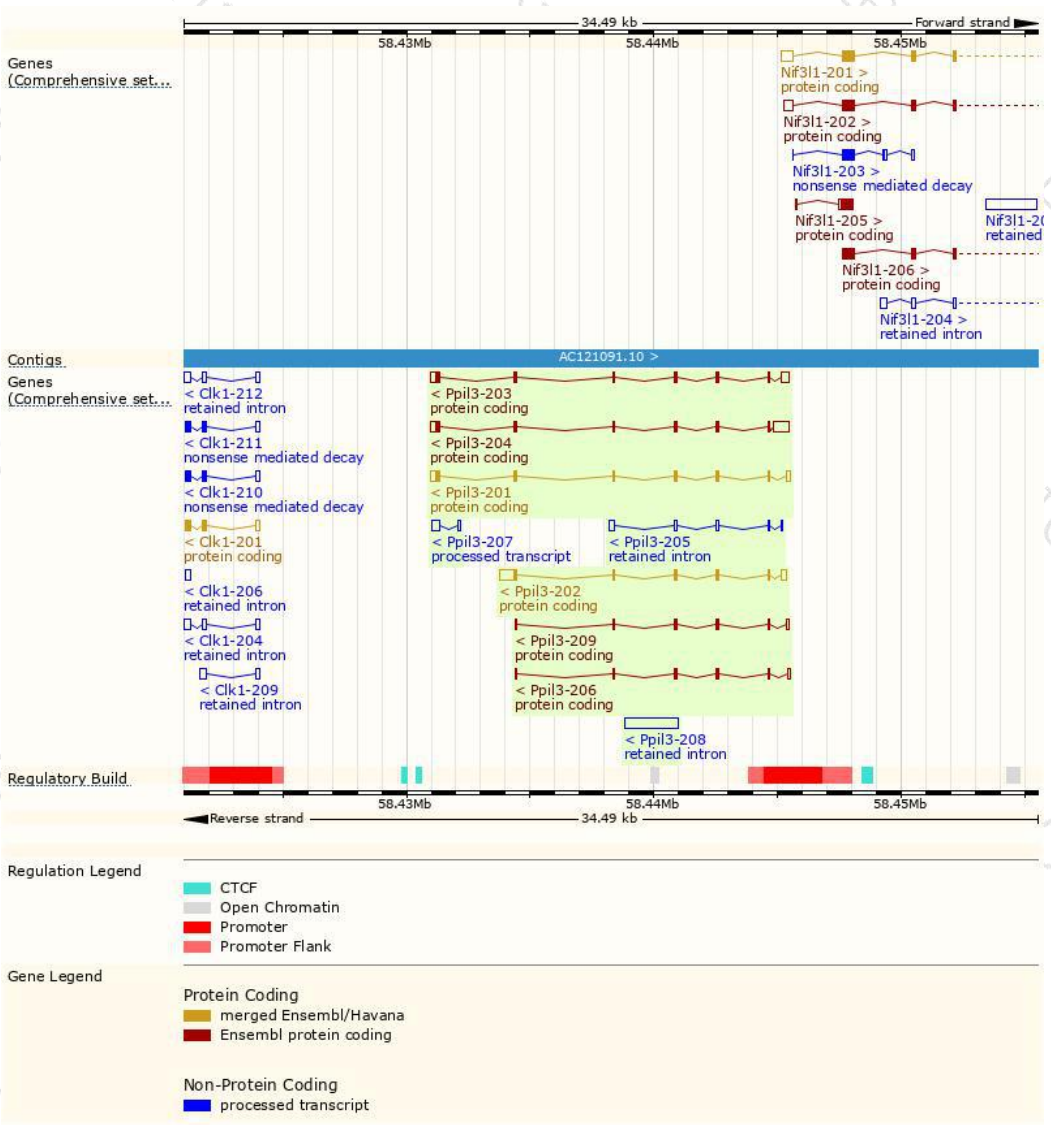
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ppil3-204	ENSMUST00000117069.7	1363	161aa	Protein coding	CCDS35579	Q9D6L8	TSL:1 GENCODE basic APPRIS P1
Ppil3-202	ENSMUST00000114345.8	1175	120aa	Protein coding	CCDS35580	Q9D6L8	TSL:1 GENCODE basic
Ppil3-203	ENSMUST00000114348.7	1033	161aa	Protein coding	CCDS35579	Q9D6L8	TSL:1 GENCODE basic APPRIS P1
Ppil3-201	ENSMUST00000081677.11	896	161aa	Protein coding	CCDS35579	Q9D6L8	TSL:1 GENCODE basic APPRIS P1
Ppil3-206	ENSMUST00000185990.1	392	90aa	Protein coding	-	A0A087WPZ6	CDS 3' incomplete TSL:3
Ppil3-209	ENSMUST00000190048.6	391	91aa	Protein coding	-	A0A087WP41	CDS 3' incomplete TSL:3
Ppil3-207	ENSMUST00000186242.1	425	No protein	Processed transcript	-	-	TSL:3
Ppil3-208	ENSMUST00000188896.1	2139	No protein	Retained intron	-	-	TSL:NA
Ppil3-205	ENSMUST00000124550.1	487	No protein	Retained intron	-	-	TSL:2

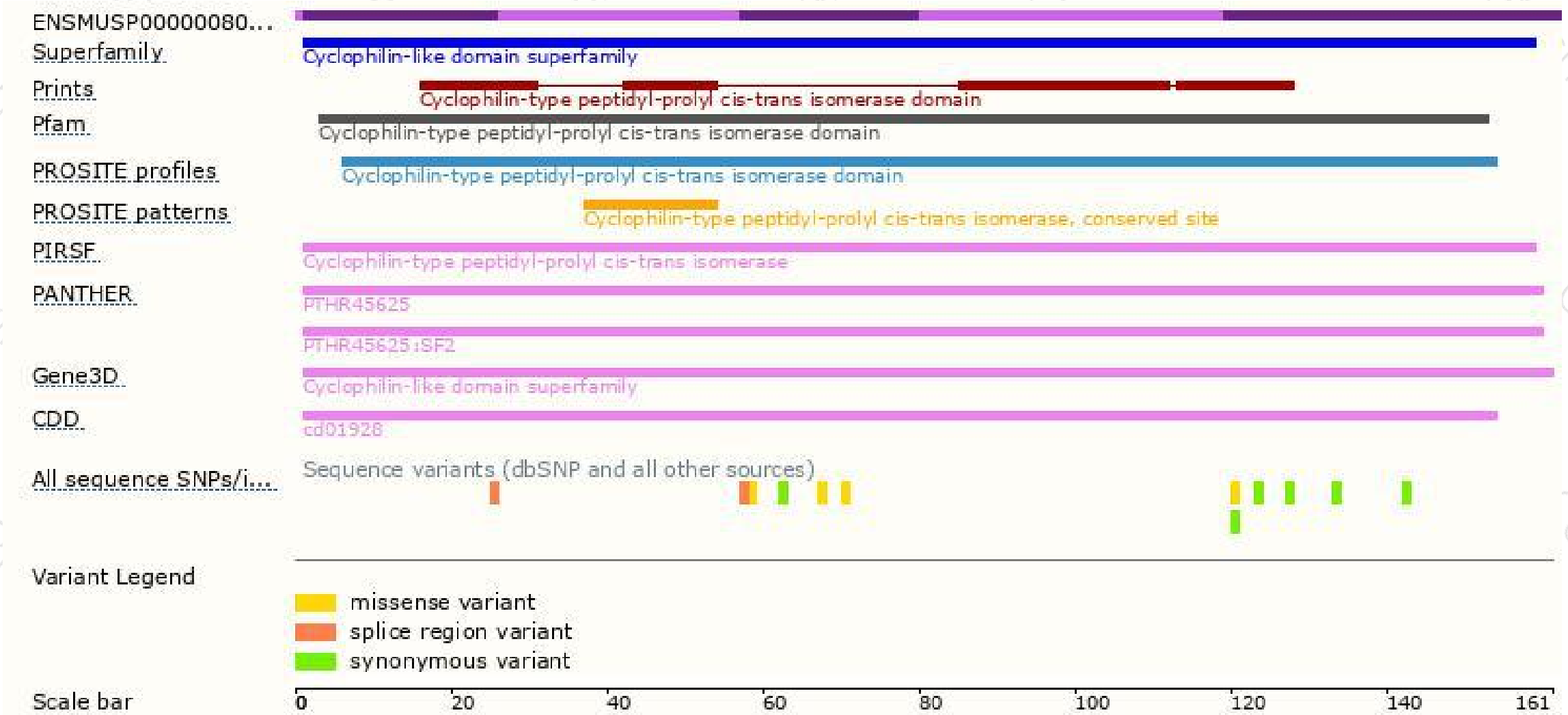
The strategy is based on the design of *Ppil3-201* transcript,the transcription is shown below:



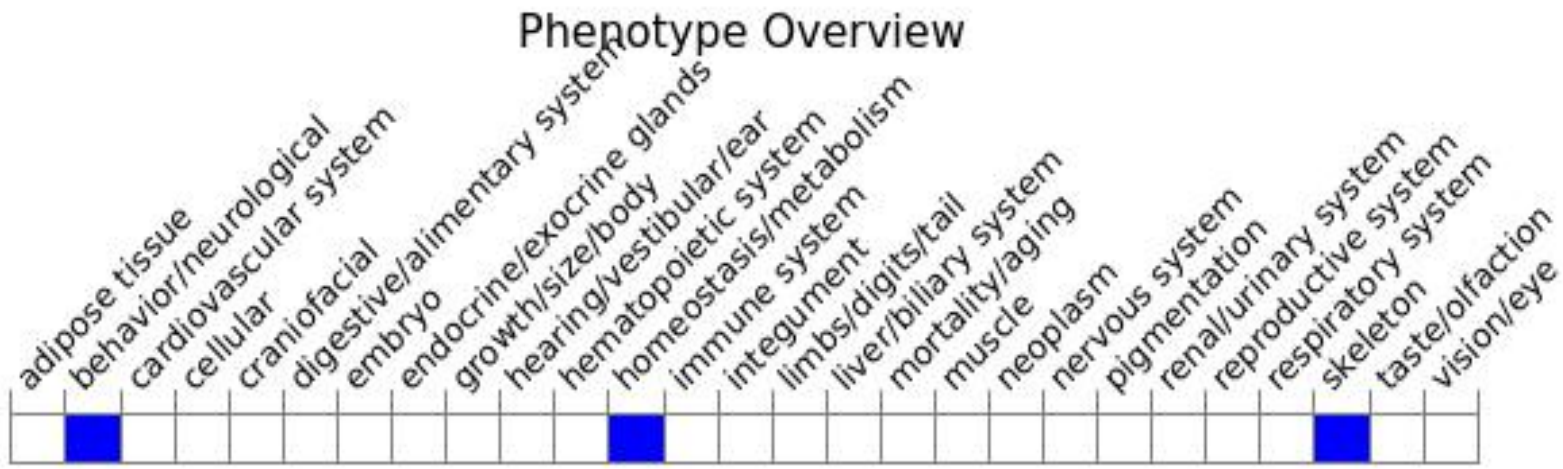
Genomic location distribution



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/>).

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

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