

Phyhipl Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Phyhipl

Project type

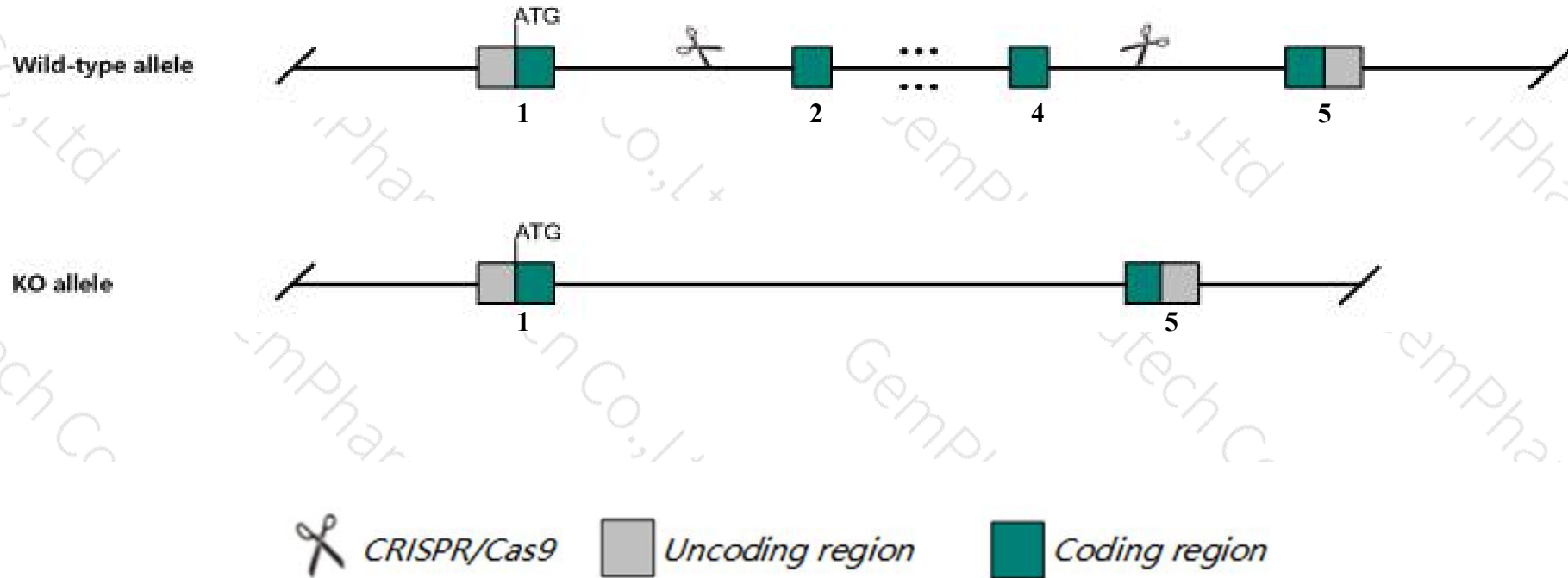
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Phyhipl* gene has 10 transcripts. According to the structure of *Phyhipl* gene, exon2-exon4 of *Phyhipl*-201 (ENSMUST00000046513.9) transcript is recommended as the knockout region. The region contains 490bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Phyhipl* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Phyhipl* gene is located on the Chr10. 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)

Phyhipl phytanoyl-CoA hydroxylase interacting protein-like [Mus musculus (house mouse)]

Gene ID: 70911, updated on 7-Apr-2019

Summary



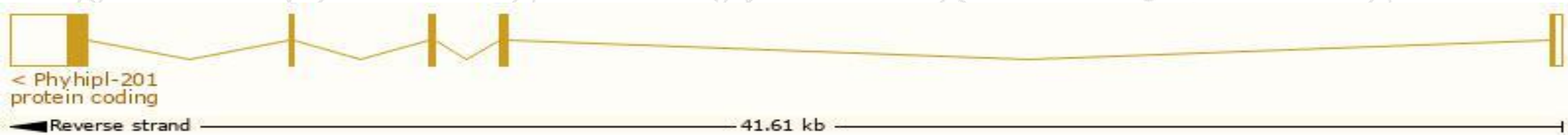
Official Symbol	Phyhipl provided by MGI
Official Full Name	phytanoyl-CoA hydroxylase interacting protein-like provided by MGI
Primary source	MGI:MGI:1918161
See related	Ensembl:ENSMUSG00000037747
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4921522K17Rik, AI267048
Expression	Biased expression in testis adult (RPKM 75.5), cerebellum adult (RPKM 31.7) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

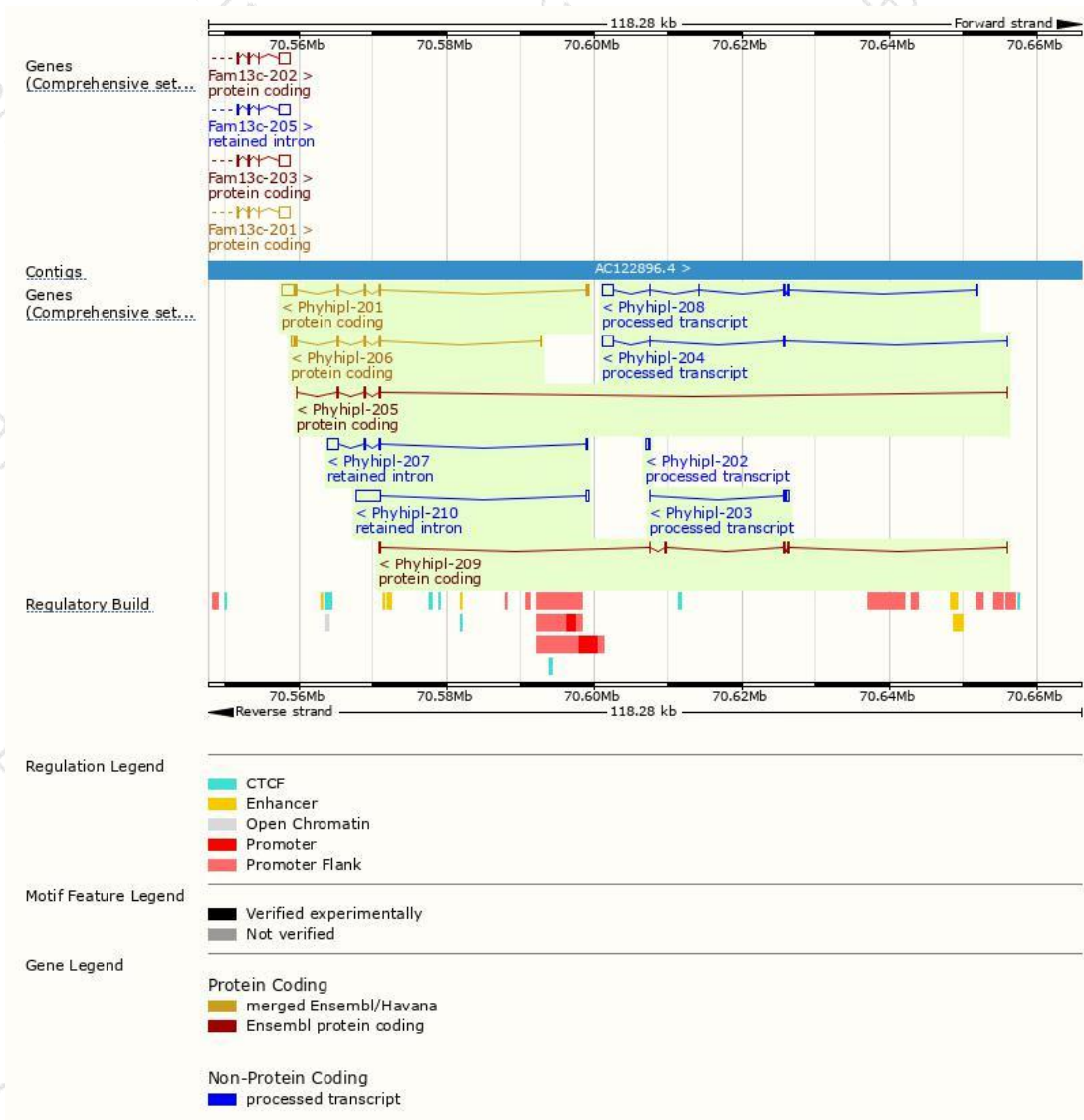
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Phyhipl-201	ENSMUST00000046513.9	2877	375aa	Protein coding	CCDS23914	Q8BGT8	TSL:1 GENCODE basic APPRIS P3
Phyhipl-206	ENSMUST00000162251.7	1540	330aa	Protein coding	CCDS48593	F7D3N3	TSL:3 GENCODE basic APPRIS ALT1
Phyhipl-205	ENSMUST00000162144.1	635	212aa	Protein coding	-	F6U6Z2	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Phyhipl-209	ENSMUST00000162793.7	598	41aa	Protein coding	-	E0CXW9	CDS 3' incomplete TSL:3
Phyhipl-208	ENSMUST00000162571.7	2011	No protein	Processed transcript	-	-	TSL:1
Phyhipl-204	ENSMUST00000161687.7	1665	No protein	Processed transcript	-	-	TSL:1
Phyhipl-203	ENSMUST00000160127.1	359	No protein	Processed transcript	-	-	TSL:5
Phyhipl-202	ENSMUST00000159025.1	326	No protein	Processed transcript	-	-	TSL:3
Phyhipl-210	ENSMUST00000163054.1	3485	No protein	Retained intron	-	-	TSL:1
Phyhipl-207	ENSMUST00000162470.1	1877	No protein	Retained intron	-	-	TSL:1

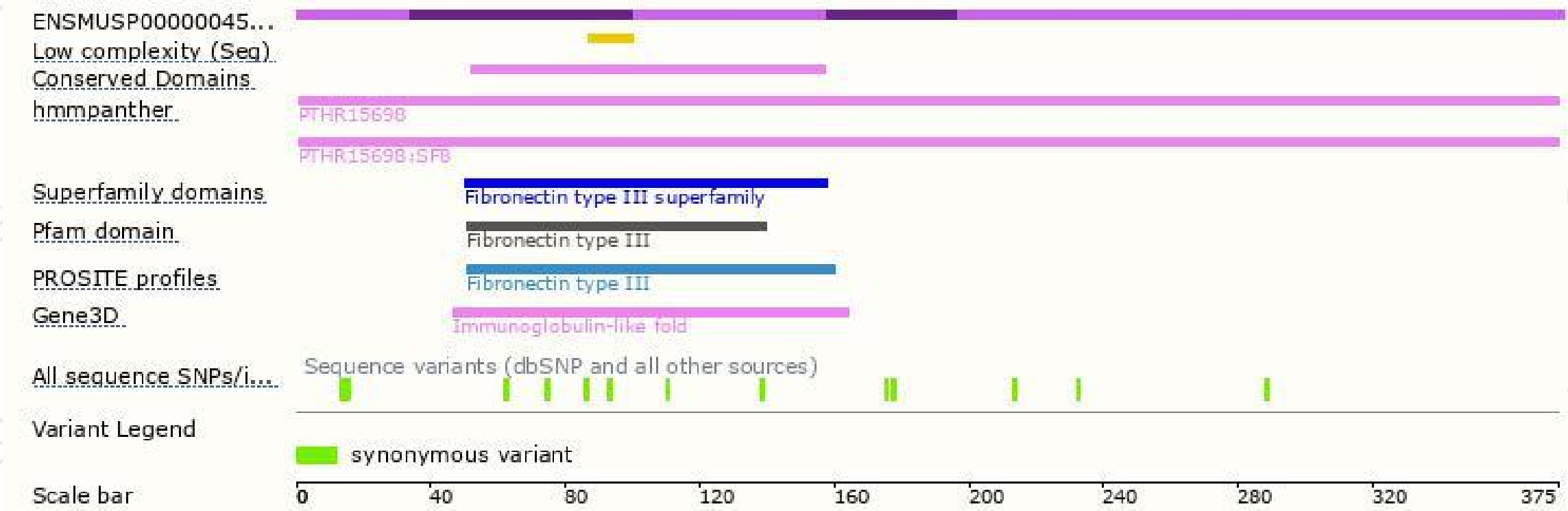
The strategy is based on the design of *Phyhipl-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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