

Ypel1 Cas9-CKO Strategy

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Project Overview

Project Name

Ypell

Project type

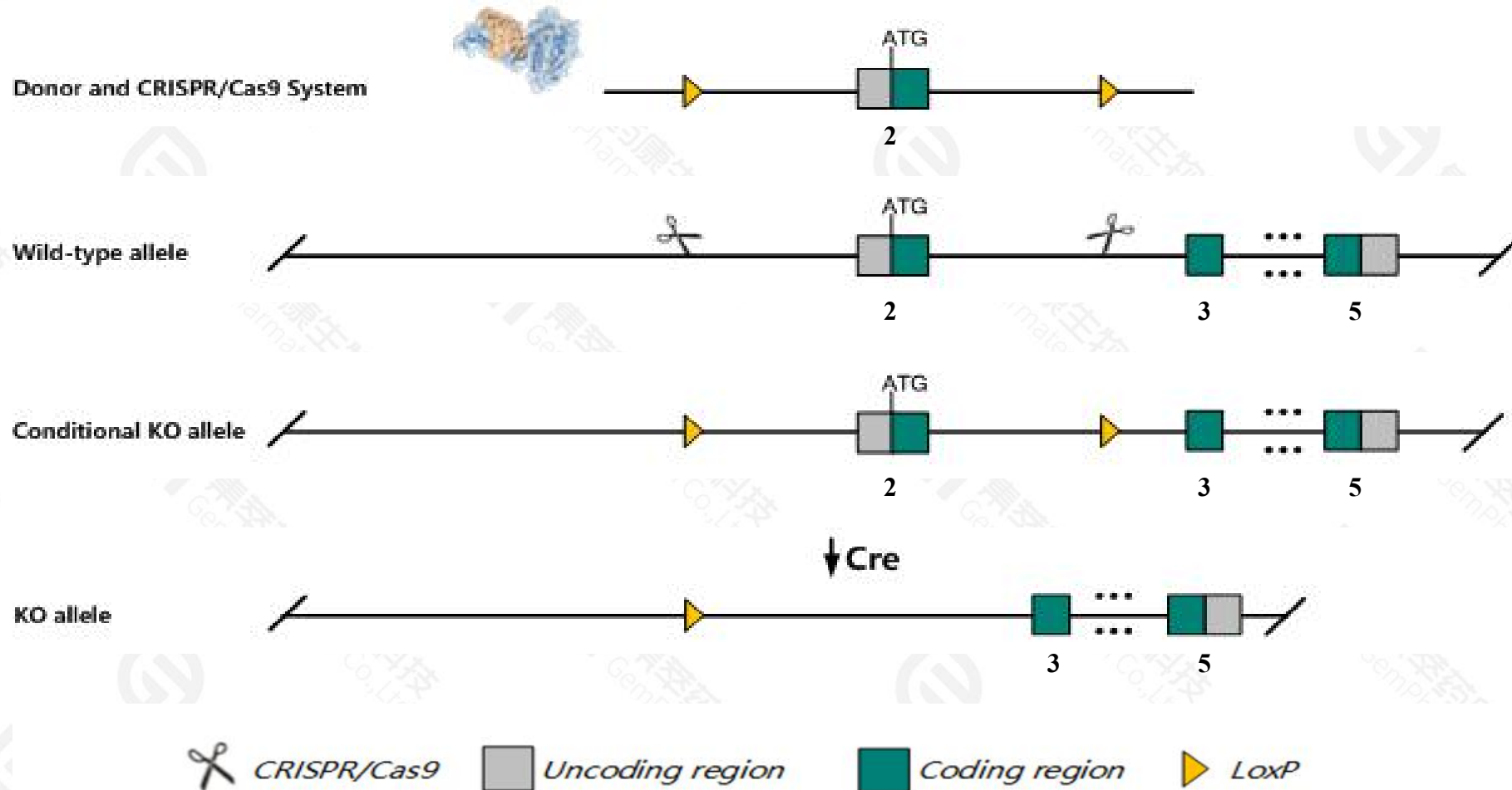
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Ypell* gene has 8 transcripts. According to the structure of *Ypell* gene, exon2 of *Ypell-201*(ENSMUST00000035682.16) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ypell* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- The *Ypell* gene is located on the Chr16. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Ypel1 yippee like 1 [Mus musculus (house mouse)]

Gene ID: 106369, updated on 12-Feb-2021

Summary



Official Symbol Ypel1 provided by [MGI](#)

Official Full Name yippee like 1 provided by [MGI](#)

Primary source [MGI:MGI:1913303](#)

See related [Ensembl:ENSMUSG00000022773](#)

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 0610009L05Rik, 1700016N17Rik, 1700019O22Rik, 4921520K19Rik, 4930511F14Rik, AV118478, DGL-1, Dgl, Dgl1, P, Ppil2, mdgl-, mdgl-1

Expression Biased expression in testis adult (RPKM 54.8), CNS E18 (RPKM 18.8) and 7 other tissues [See more](#)

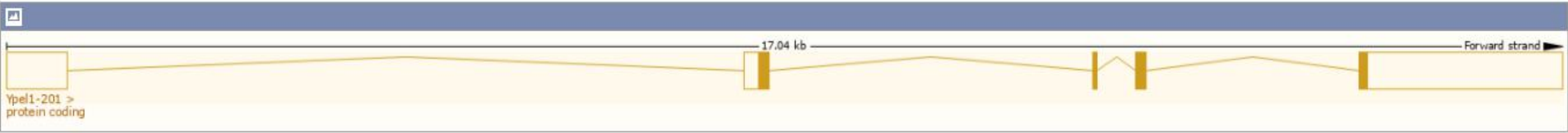
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

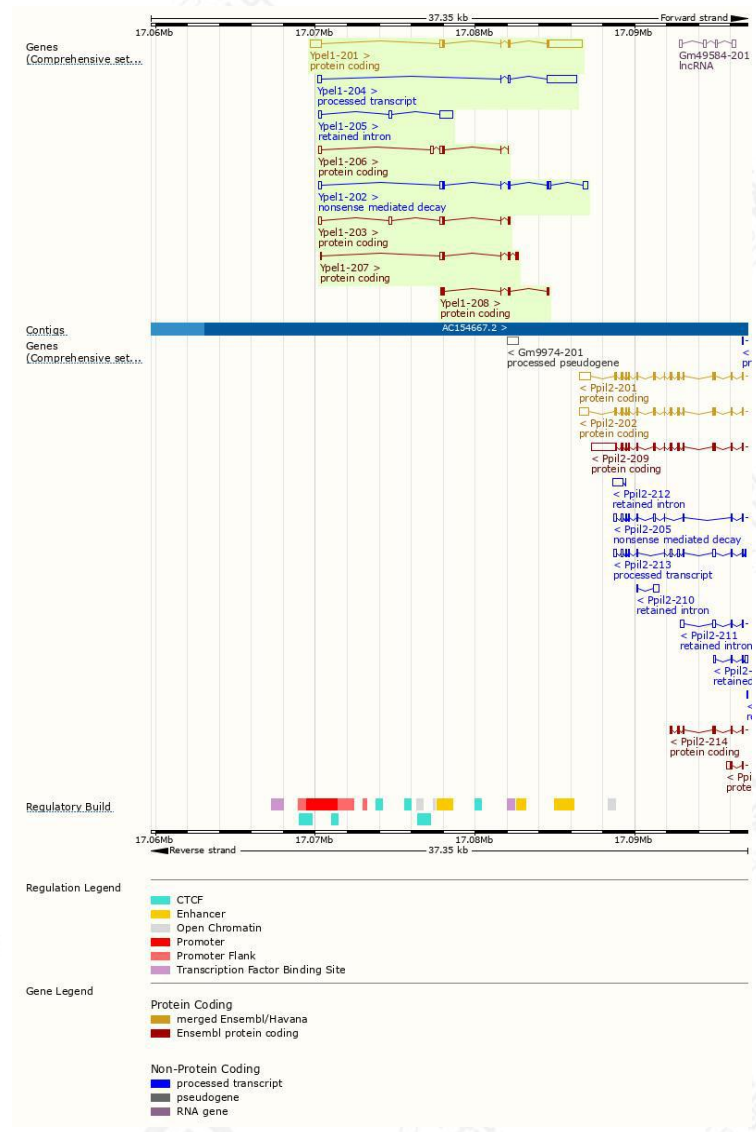
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ypel1-201	ENSMUST00000035682.16	3322	118aa	Protein coding	CCDS37268		TSL:1 , GENCODE basic , APPRIS P1 ,
Ypel1-206	ENSMUST00000232258.2	726	62aa	Protein coding	-		CDS 3' incomplete ,
Ypel1-203	ENSMUST00000231514.2	694	90aa	Protein coding	-		CDS 3' incomplete ,
Ypel1-207	ENSMUST00000232574.2	631	130aa	Protein coding	-		GENCODE basic ,
Ypel1-208	ENSMUST00000239090.2	459	152aa	Protein coding	-		GENCODE basic ,
Ypel1-202	ENSMUST00000231394.2	1082	118aa	Nonsense mediated decay	CCDS37268		
Ypel1-204	ENSMUST00000231518.2	2185	No protein	Processed transcript	-		
Ypel1-205	ENSMUST00000232168.2	1137	No protein	Retained intron	-		

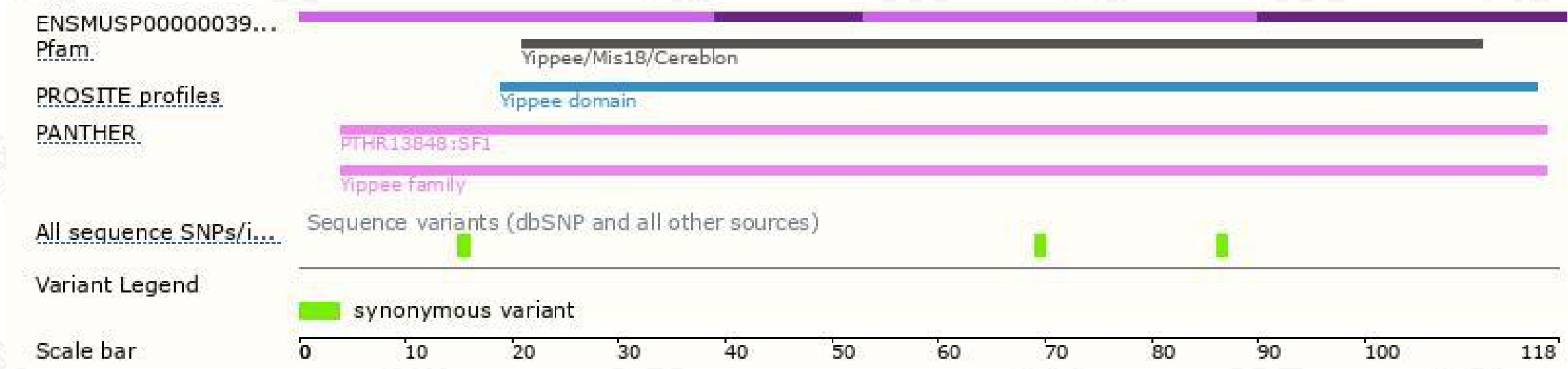
The strategy is based on the design of *Ypel1-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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