

Yipf1 Cas9-CKO Strategy

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Project Overview

Project Name

Yipf1

Project type

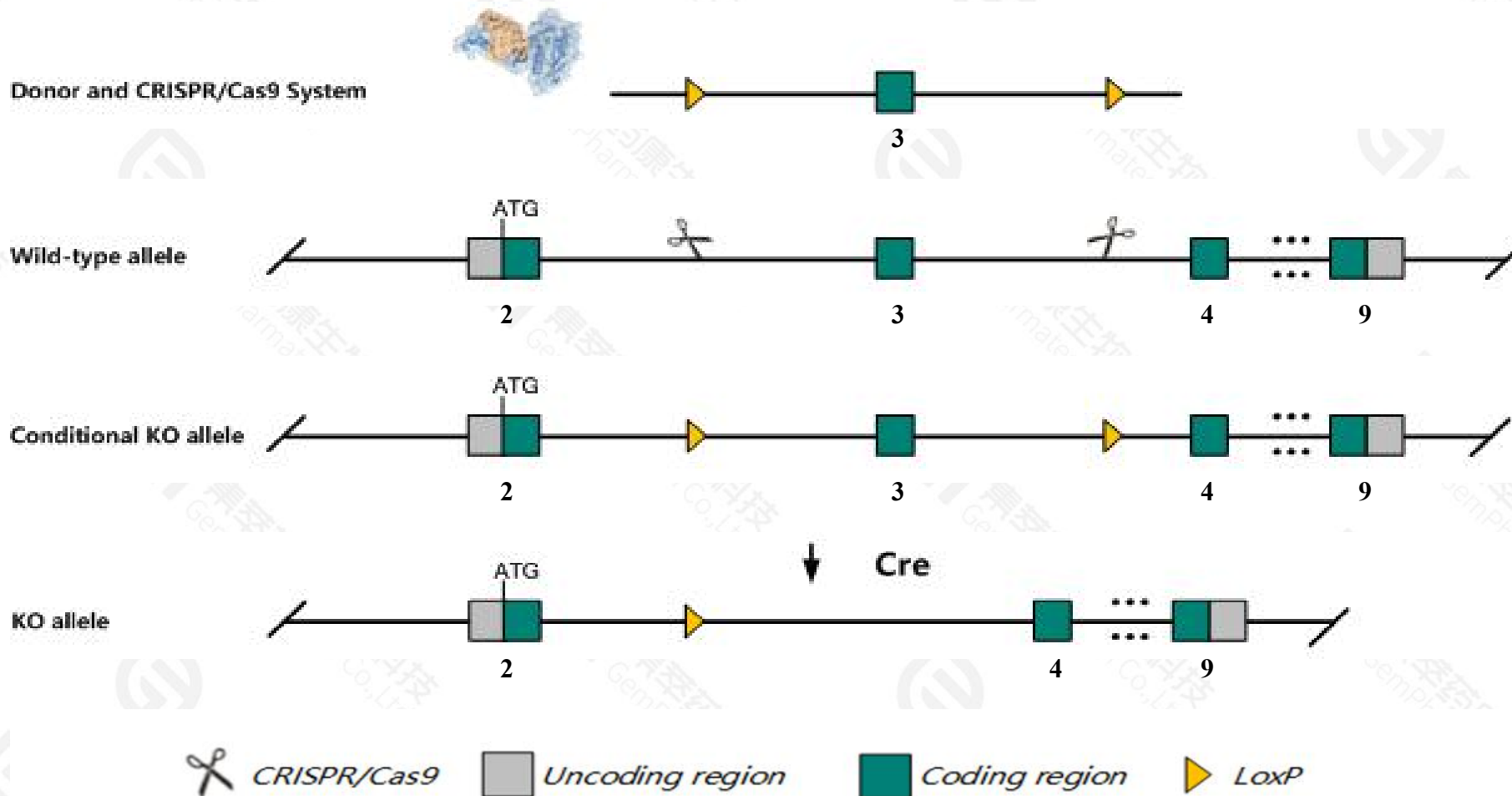
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Yipf1* gene. The schematic diagram is as follows:



- The *Yipfl* gene has 11 transcripts. According to the structure of *Yipfl* gene, exon3 of *Yipfl*-201(ENSMUST00000075693.12) transcript is recommended as the knockout region. The region contains 164bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Yipfl* 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit no detectable phenotypic abnormalities.
- The *Yipf1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Yipf1 Yip1 domain family, member 1 [Mus musculus (house mouse)]

Gene ID: 230584, updated on 17-Dec-2020

Summary



Official Symbol Yipf1 provided by [MGI](#)

Official Full Name Yip1 domain family, member 1 provided by [MGI](#)

Primary source [MGI:MGI:1915532](#)

See related [Ensembl:ENSMUSG00000057375](#)

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 C030002N13Rik

Expression Ubiquitous expression in large intestine adult (RPKM 32.5), colon adult (RPKM 31.0) and 28 other tissues [See more](#)

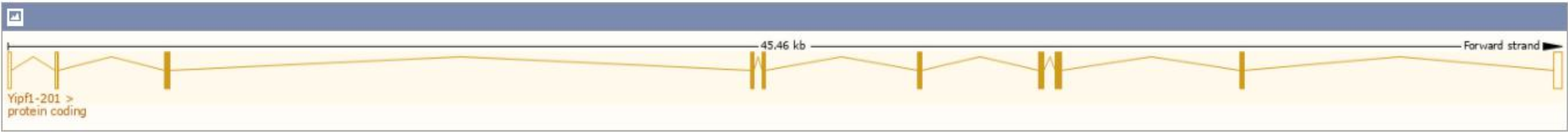
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

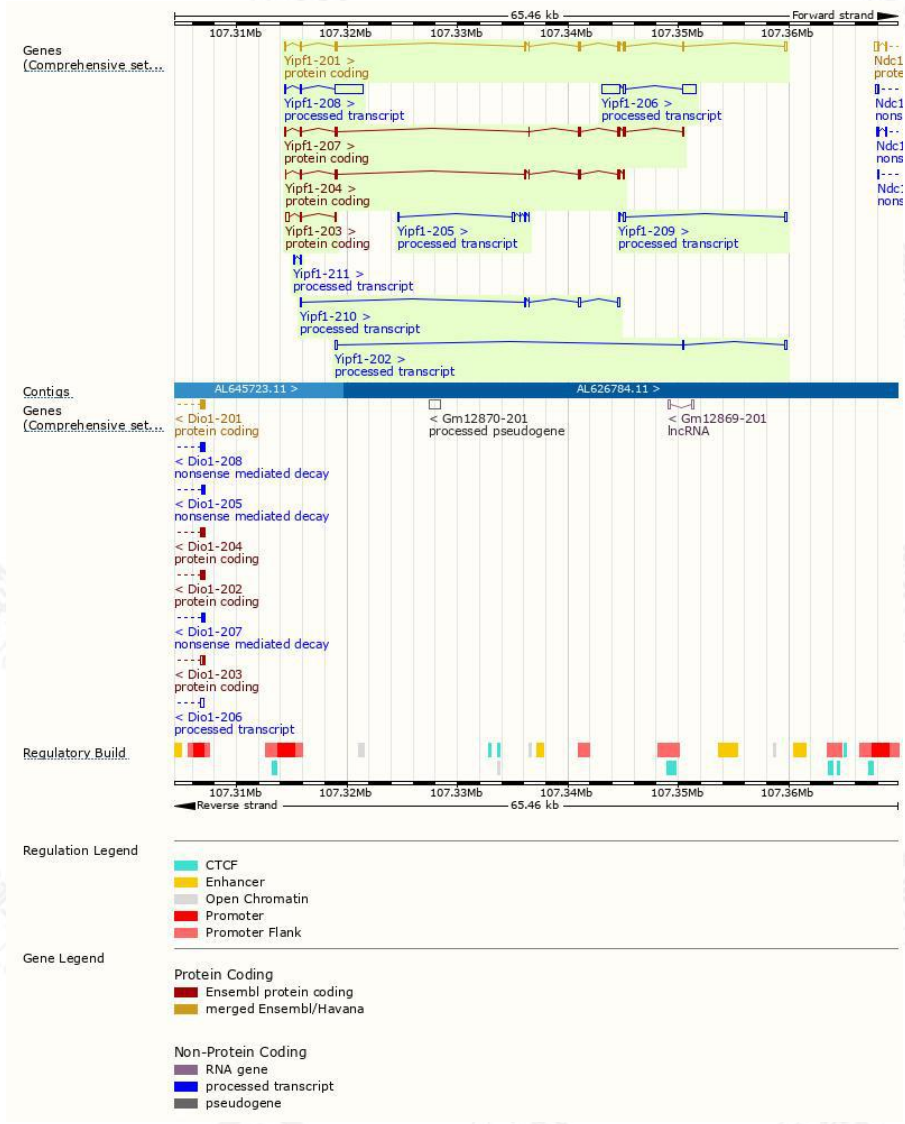
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Yipf1-201	ENSMUST00000075693.12	1321	306aa	Protein coding	CCDS18437		TSL:1 , GENCODE basic , APPRIS P1 ,
Yipf1-207	ENSMUST00000139527.8	937	269aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Yipf1-204	ENSMUST00000128284.8	831	243aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Yipf1-203	ENSMUST00000124650.2	470	35aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Yipf1-206	ENSMUST00000137391.8	2927	No protein	Processed transcript	-		TSL:2 ,
Yipf1-208	ENSMUST00000140162.8	2672	No protein	Processed transcript	-		TSL:2 ,
Yipf1-210	ENSMUST00000146829.8	533	No protein	Processed transcript	-		TSL:5 ,
Yipf1-209	ENSMUST00000143106.2	524	No protein	Processed transcript	-		TSL:3 ,
Yipf1-202	ENSMUST00000124254.2	477	No protein	Processed transcript	-		TSL:2 ,
Yipf1-205	ENSMUST00000128507.2	384	No protein	Processed transcript	-		TSL:5 ,
Yipf1-211	ENSMUST00000155975.2	224	No protein	Processed transcript	-		TSL:3 ,

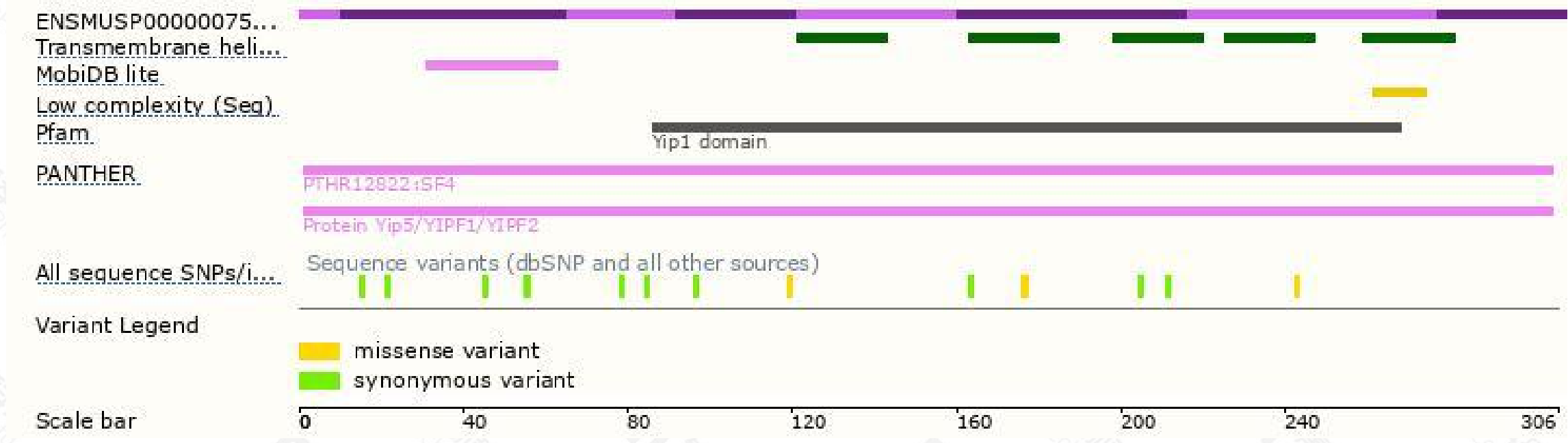
The strategy is based on the design of *Yipf1-201* transcript,the transcription is shown below:



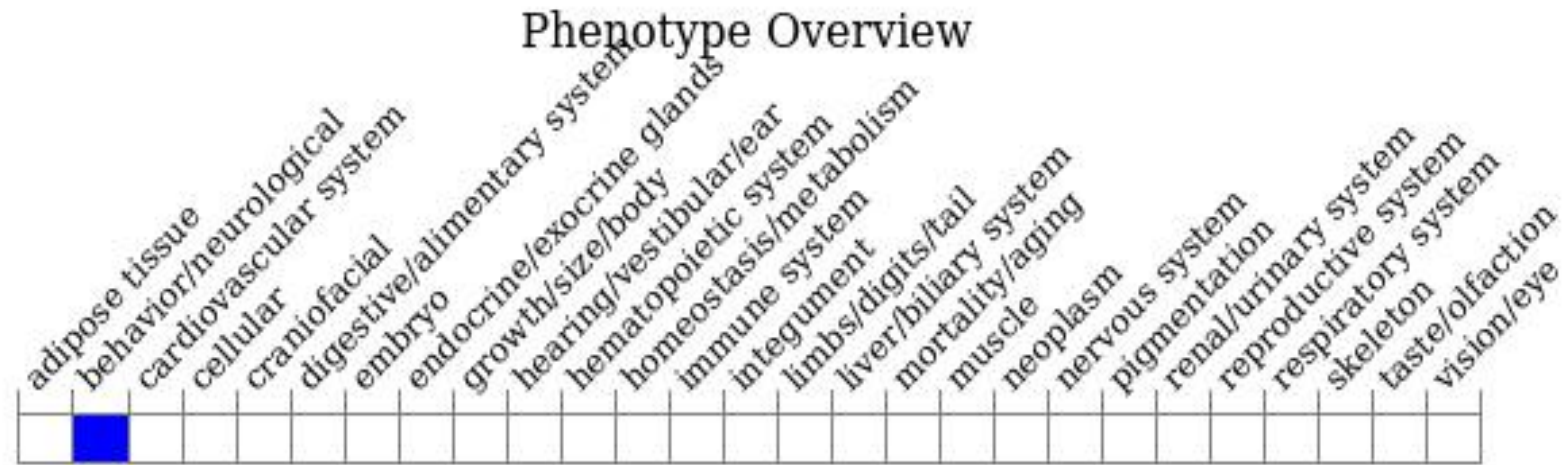
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a knock-out allele exhibit no detectable phenotypic abnormalities.

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