

# *Yipf1* Cas9-KO Strategy

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# Project Overview

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**Project Name**

*Yipf1*

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**Project type**

**Cas9-KO**

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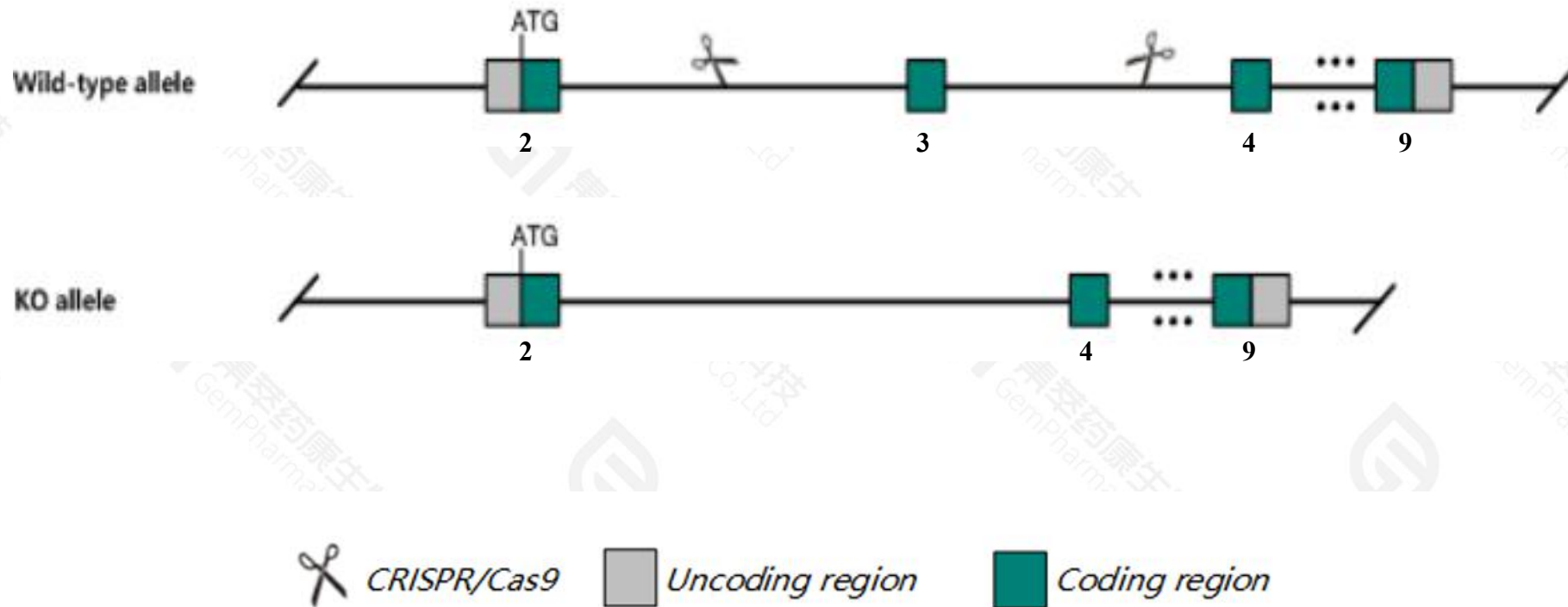
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

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



- The *Yipf1* gene has 11 transcripts. According to the structure of *Yipf1* gene, exon3 of *Yipf1*-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 *Yipf1* gene. The brief process is as follows: CRISPR/Cas9 system 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.



- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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](#)

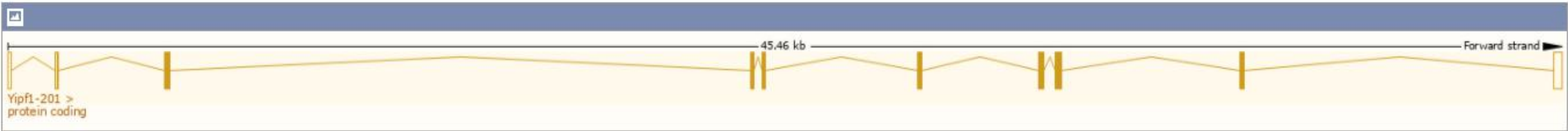
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

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

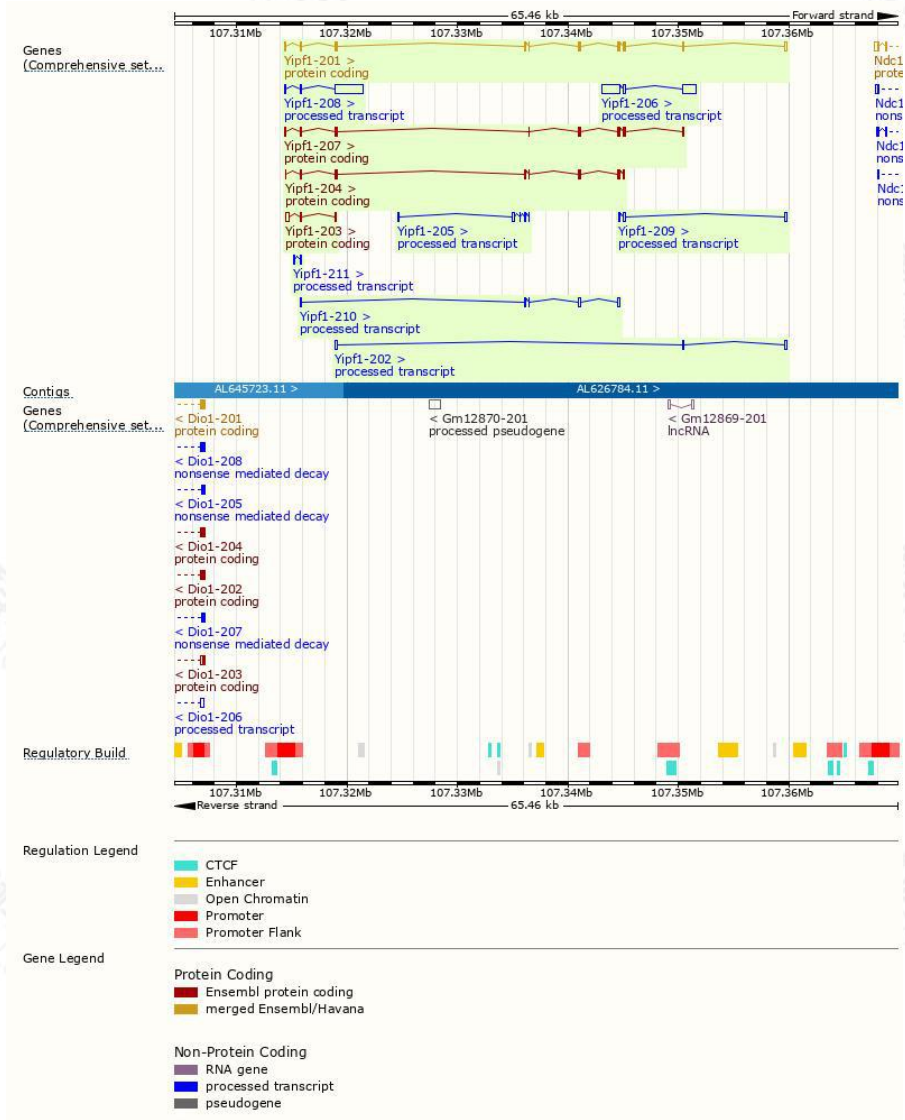
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Yipf1-201	<a href="#">ENSMUST00000075693.12</a>	1321	<a href="#">306aa</a>	Protein coding	<a href="#">CCDS18437</a>		TSL:1 , GENCODE basic , APPRIS P1 ,
Yipf1-207	<a href="#">ENSMUST00000139527.8</a>	937	<a href="#">269aa</a>	Protein coding	-	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

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



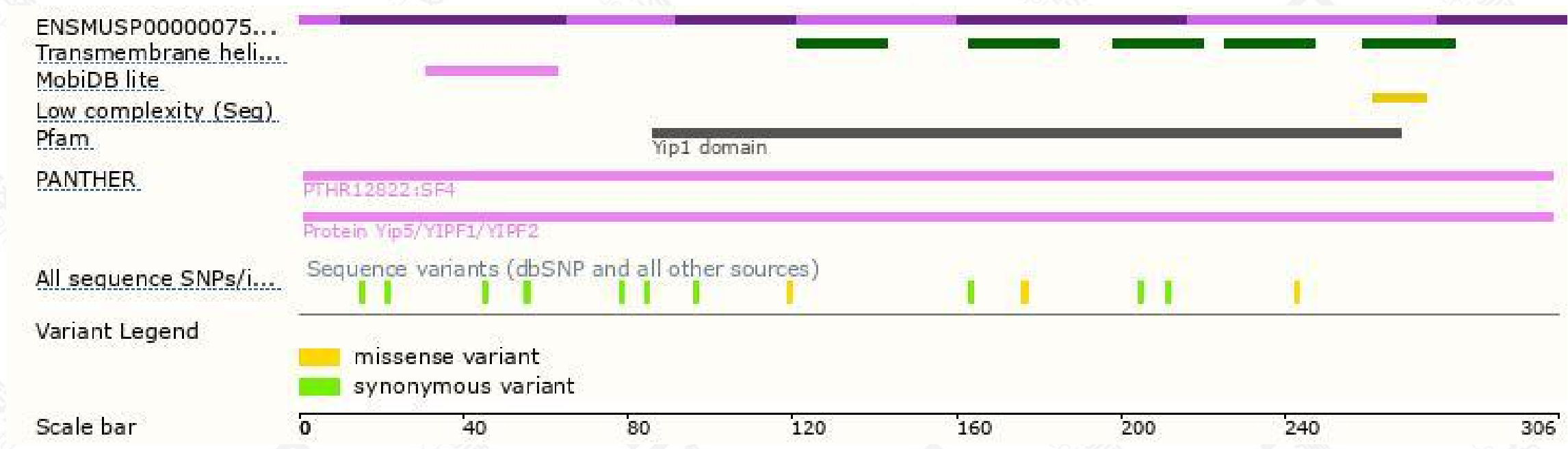


# Genomic location distribution

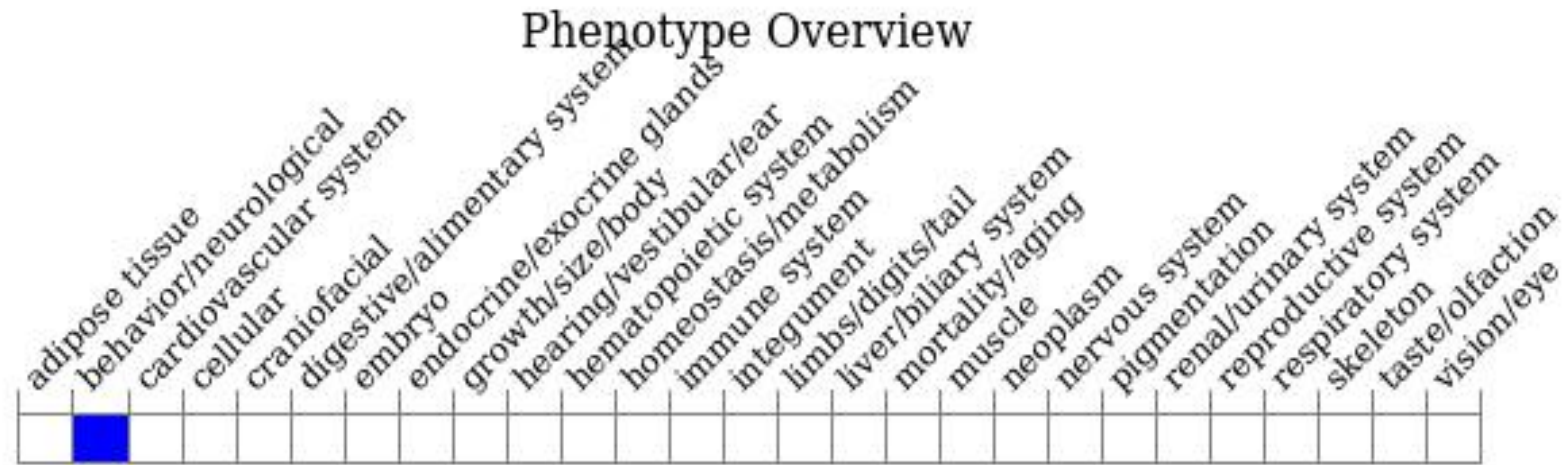




# Protein domain



# 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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