

Pilra Cas9-KO Strategy

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Project Overview

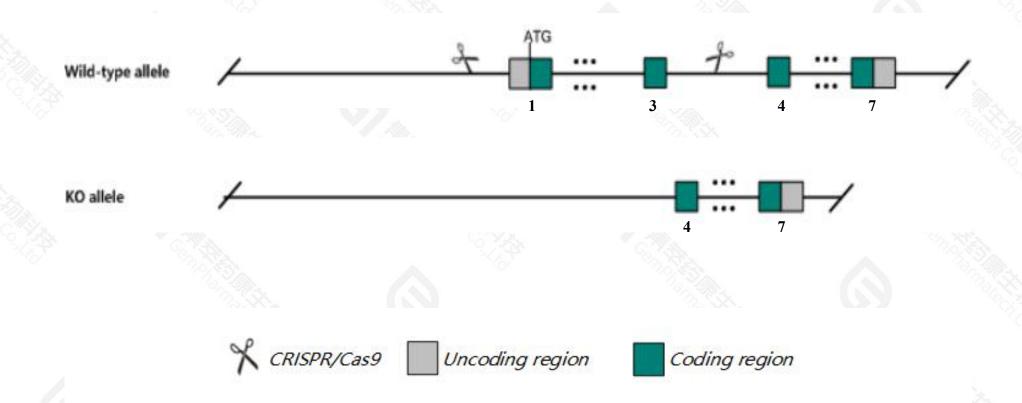


Project Name	Pilra
Project type	Cas9-KO
Strain background	C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Pilra* gene has 5 transcripts. According to the structure of *Pilra* gene, exon1-exon3 of *Pilra-*201(ENSMUST0000058897.11) 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 *Pilra* 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.

Notice



- > According to the existing MGI data,mice homozygous for a knock-out allele exhibit increased increased alanine transferase, blood urea nitrogen, lactate dehydrogenase, neutrophils and mortality and altered liver morphology (massive hemorrhage, disorganized hepatic cords and karyolysis of hepatocytes) following treatment with LPS.
- > The *Pilra* gene is located on the Chr5. 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)



Pilra paired immunoglobin-like type 2 receptor alpha [Mus musculus (house mouse)]

Gene ID: 231805, updated on 25-Sep-2020

Summary

☆ ?

Official Symbol Pilra provided by MGI

Official Full Name paired immunoglobin-like type 2 receptor alpha provided by MGI

Primary source MGI:MGI:2450529

See related Ensembl: ENSMUSG00000046245

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 AV021745, FDF03

Expression Broad expression in spleen adult (RPKM 6.1), bladder adult (RPKM 3.6) and 25 other tissuesSee more

Orthologs <u>human all</u>

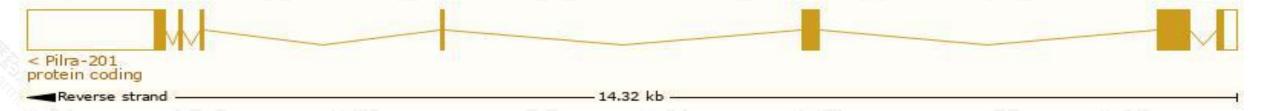
Transcript information (Ensembl)



The gene has 5 transcripts, all transcripts are shown below:

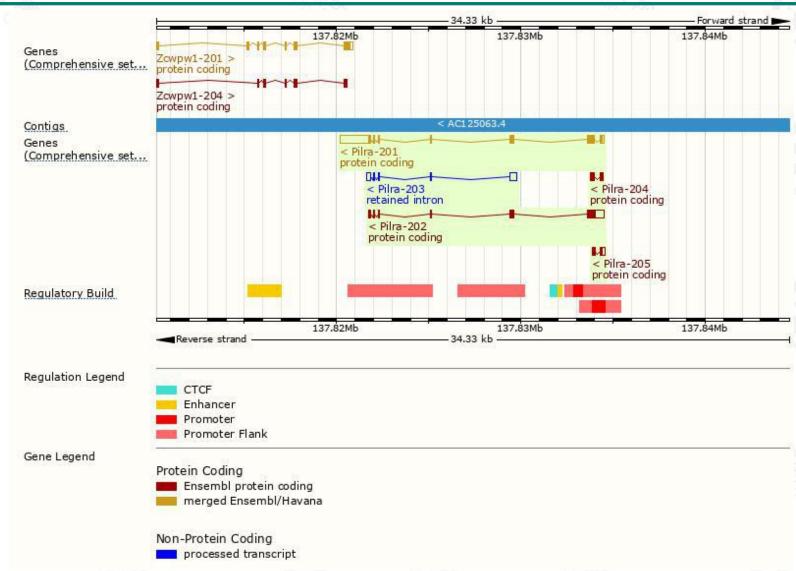
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pilra-201	ENSMUST00000058897.11	2578	<u>302aa</u>	Protein coding	CCDS19780		TSL:1 , GENCODE basic , APPRIS P2 ,
Pilra-202	ENSMUST00000110980.2	1371	299aa	Protein coding	-		TSL:2 , GENCODE basic , APPRIS ALT2 ,
Pilra-205	ENSMUST00000199028.2	369	<u>69aa</u>	Protein coding	10		CDS 3' incomplete , TSL:5 ,
Pilra-204	ENSMUST00000197586.2	351	94aa	Protein coding			CDS 3' incomplete , TSL:2 ,
Pilra-203	ENSMUST00000130460.2	708	No protein	Retained intron	-		TSL:2,

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



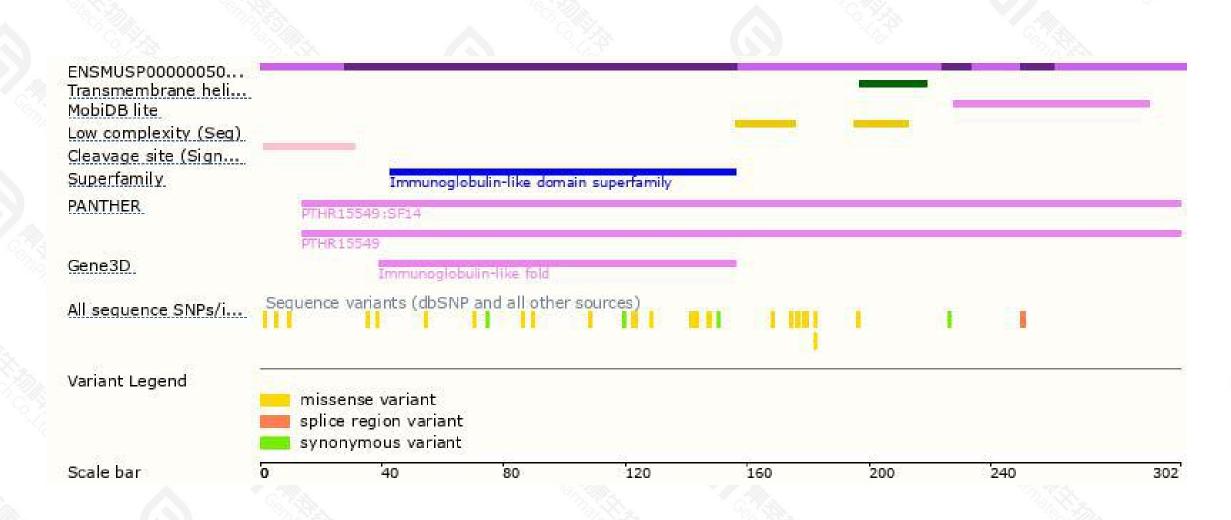
Genomic location distribution





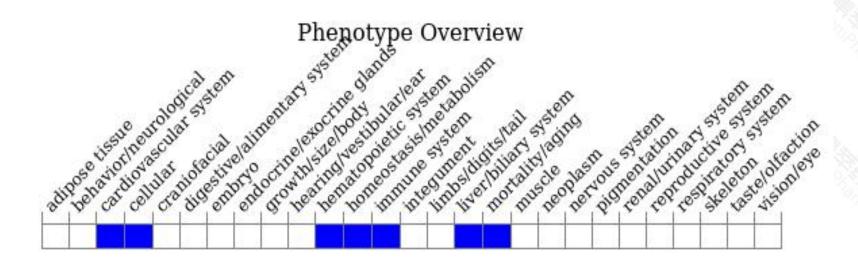
Protein domain





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 increased increased alanine transferase, blood urea nitrogen, lactate dehydrogenase, neutrophils and mortality and altered liver morphology (massive hemorrhage, disorganized hepatic cords and karyolysis of hepatocytes) following treatment with LPS.



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

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