

Plagl2 Cas9-KO Strategy

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Project Overview

Project Name

Plagl2

Project type

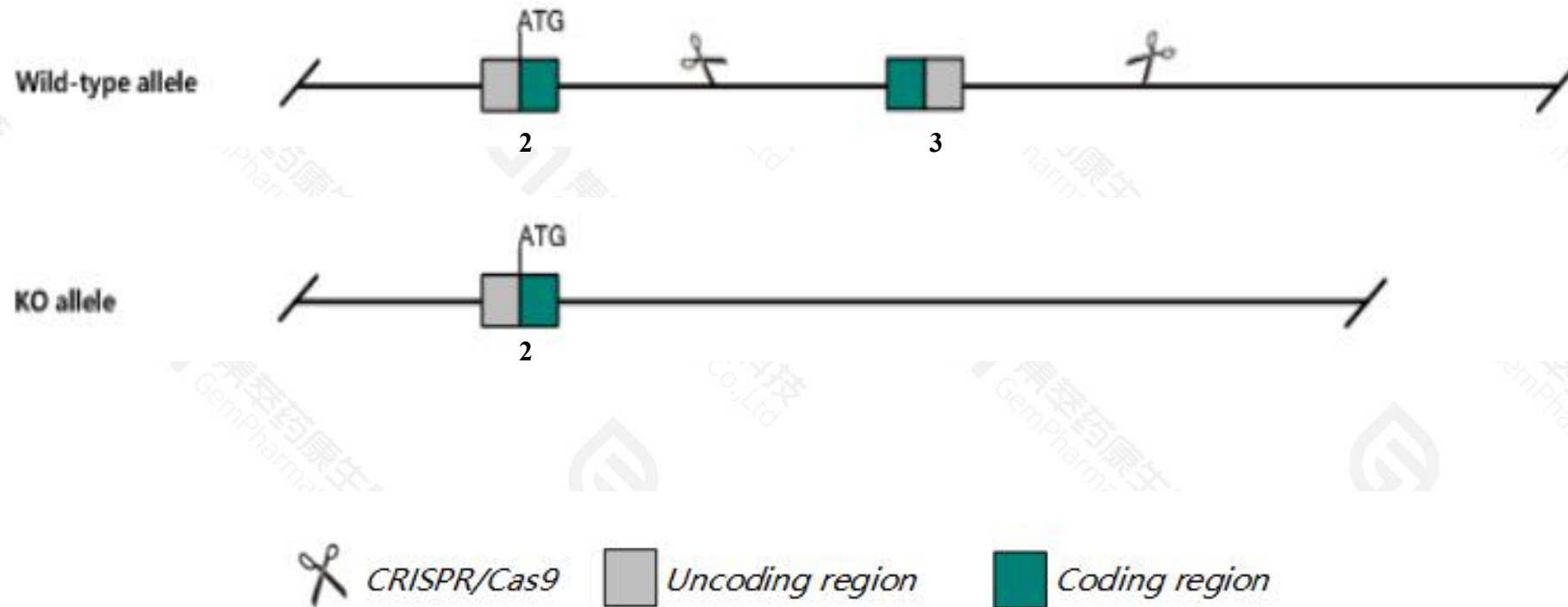
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Plagl2* gene. The schematic diagram is as follows:



- The *Plagl2* gene has 2 transcripts. According to the structure of *Plagl2* gene, exon3 of *Plagl2*-201(ENSMUST00000056924.14) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Plagl2* 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 null allele exhibit postnatal death due to a failure to absorb lipids in the intestine and other organs.
- The KO region is close to *Tspyl3* gene. Knockout the region may affect the function of *Tspyl3* gene.
- The *Plagl2* gene is located on the Chr2. 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.

Plagl2 pleiomorphic adenoma gene-like 2 [Mus musculus (house mouse)]

Gene ID: 54711, updated on 3-Oct-2020

Summary



Official Symbol Plagl2 provided by [MGI](#)

Official Full Name pleiomorphic adenoma gene-like 2 provided by [MGI](#)

Primary source [MGI:MGI:1933165](#)

See related [Ensembl:ENSMUSG00000051413](#)

Gene type protein coding

RefSeq status PROVISIONAL

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as AU018672, AW552839, mKIAA0198

Expression Ubiquitous expression in liver E14.5 (RPKM 11.2), thymus adult (RPKM 10.9) and 28 other tissues [See more](#)

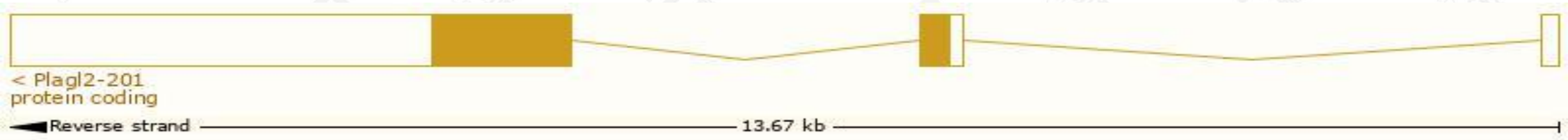
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

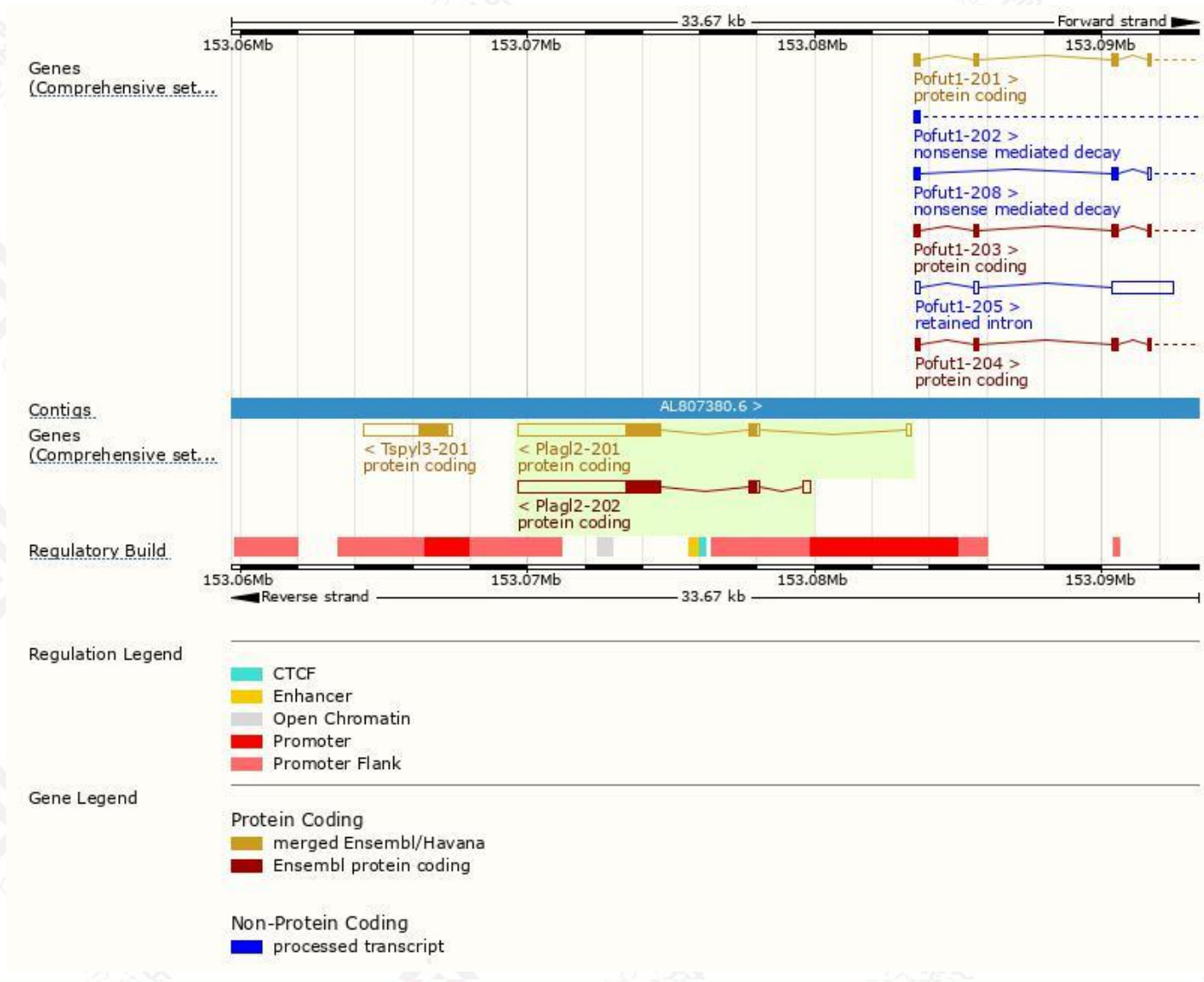
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plagl2-202	ENSMUST00000109795.2	5571	496aa	Protein coding	CCDS16908		TSL:1 , GENCODE basic , APPRIS P1 ,
Plagl2-201	ENSMUST00000056924.14	5485	496aa	Protein coding	CCDS16908		TSL:1 , GENCODE basic , APPRIS P1 ,

The strategy is based on the design of *Plagl2-201* transcript,the transcription is shown below:



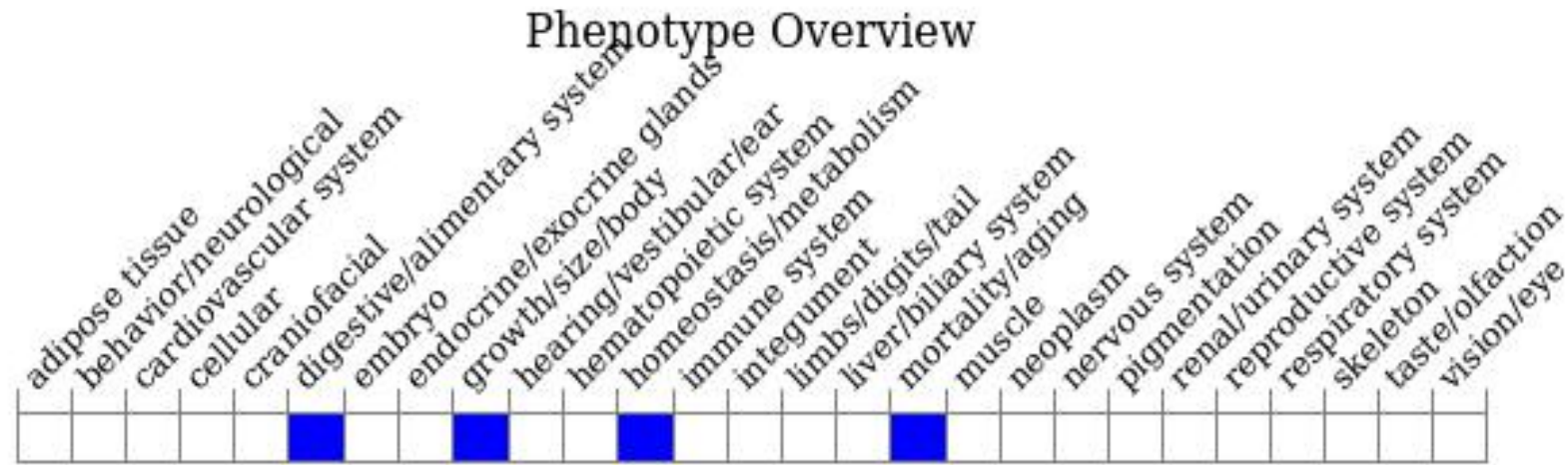
Genomic location distribution



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 null allele exhibit postnatal death due to a failure to absorb lipids in the intestine and other organs.

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