Lpar6 Cas9-KO Strategy

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Design Date: 2019-12-18

Project Overview



Project Name

Lpar6

Project type

Cas9-KO

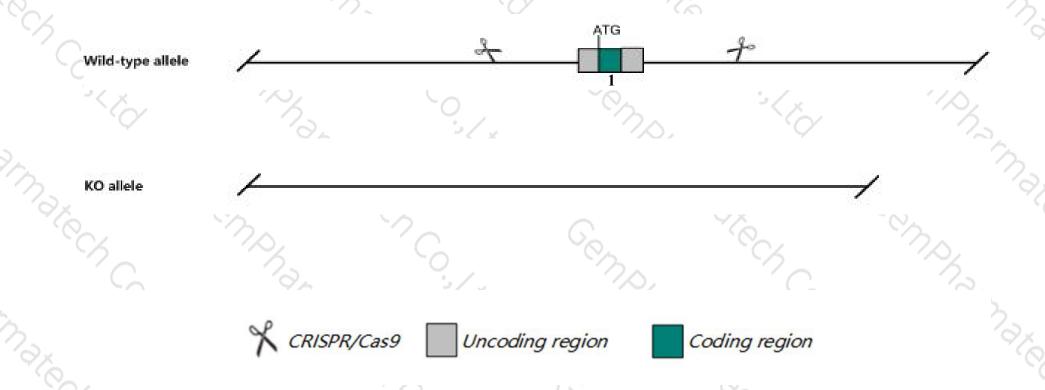
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Lpar6* gene. The schematic diagram is as follows:



Technical routes



- The *Lpar6* gene has 1 transcript. According to the structure of *Lpar6* gene, exon 1 of *Lpar6*-201 (ENSMUST00000044405.7) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Lpar6* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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



- The KO region contains functional region of the *Rb1* gene. Knockout the region may affect the function of *Rb1* gene.
- ➤ The *Lpar6* gene is located on the Chr 14. 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.
- > The KO region contains functional region of the Rb1 gene. Knockout the region affect the function of Rb1 gene.
- ➤ 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)



Lpar6 lysophosphatidic acid receptor 6 [Mus musculus (house mouse)]

Gene ID: 67168, updated on 19-Mar-2019

Summary

↑ ?

Official Symbol Lpar6 provided by MGI

Official Full Name lysophosphatidic acid receptor 6 provided by MGI

Primary source MGI:MGI:1914418

See related Ensembl: ENSMUSG00000033446

Gene type protein coding
RefSeq status VALIDATED
Organism <u>Mus musculus</u>

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

Murinae; Mus; Mus

Also known as P2y5; P2ry5; 2610302l02Rik

Orthologs human all

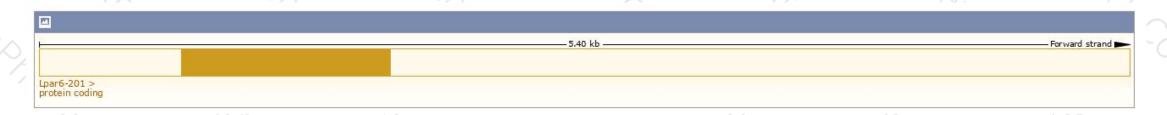
Transcript information (Ensembl)



The gene has 1 transcript, and the transcript is shown below:

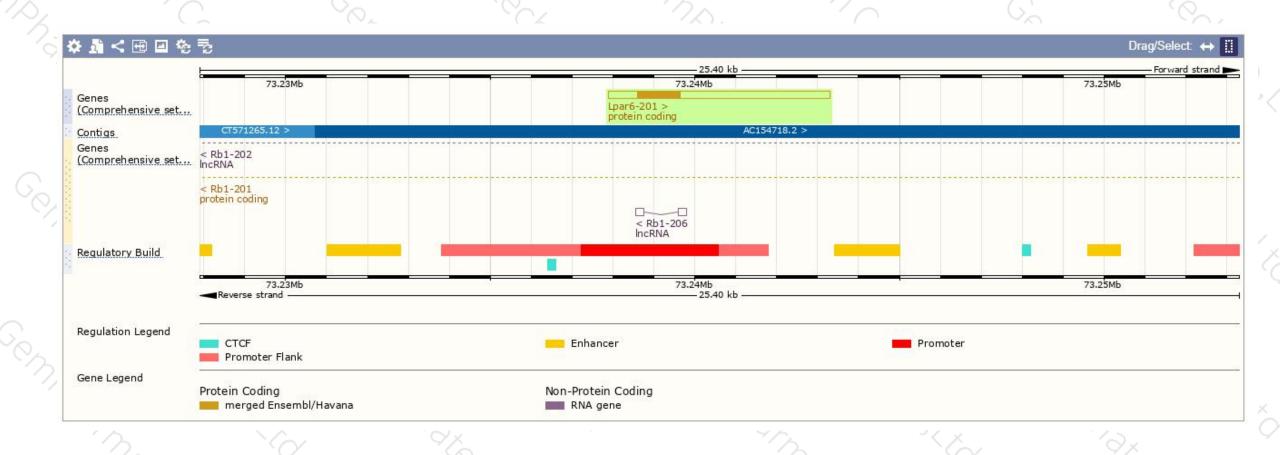
Show/hide columns (1 hidden)							Filter		
Name 🍦	Transcript ID 👙	bp 🛊	Protein 🍦	Biotype	CCDS 🍦	UniProt 🍦	Flags		
Lpar6-201	ENSMUST00000044405.7	5400	<u>344aa</u>	Protein coding	CCDS27268 ₽	Q8BMC0₽	TSL:NA	GENCODE basic	APPRIS P1

The strategy is based on the design of *Lpar6-201* transcript, The transcription is shown below



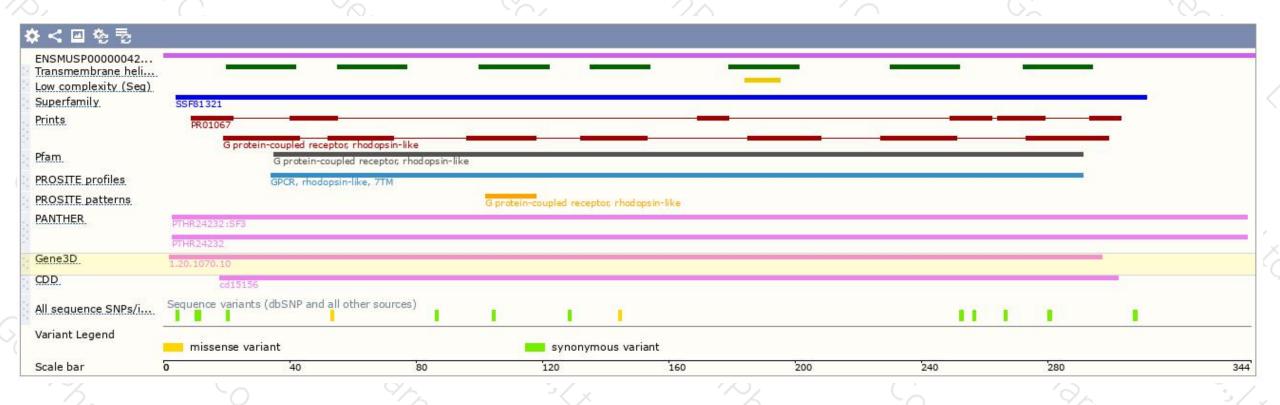
Genomic location (Ensembl)





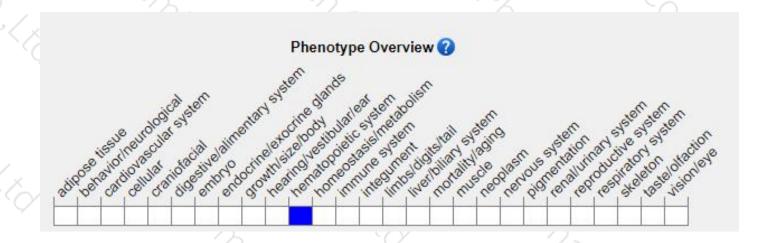
Protein domain (Ensembl)





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, Mutations in this locus affect cell-cycle regulation and apoptos is. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

If you have any questions, you are welcome to inquire. Tel: 400-9660890





