

Lpar2 Cas9-KO Strategy

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Project Overview

Project Name

Lpar2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lpar2* gene. The schematic diagram is as follows:



- The *Lpar2* gene has 3 transcripts. According to the structure of *Lpar2* gene, exon2 of *Lpar2-201* (ENSMUST00000034325.5) 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 *Lpar2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Animals homozygous for a targeted mutation appear phenotypically normal.
- The knockout region is near to the N-terminal of *Pbx4* gene and C-terminal of *Gmip* gene, this strategy may influence the regulatory function of the N-terminal of *Pbx4* gene and C-terminal of *Gmip* gene.
- The *Lpar2* gene is located on the Chr8. 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)

Lpar2 lysophosphatidic acid receptor 2 [*Mus musculus* (house mouse)]

Gene ID: 53978, updated on 10-Oct-2019

Summary

- Official Symbol** Lpar2 provided by [MGI](#)
- Official Full Name** lysophosphatidic acid receptor 2 provided by [MGI](#)
- Primary source** [MGI:1858422](#)
- See related** [Ensembl:ENSMUSG00000031861](#)
- 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** Edg4; IPA2; LPA2
- Expression** Ubiquitous expression in testis adult (RPKM 4.0), spleen adult (RPKM 3.8) and 25 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 8 B3.3; 8 33.91 cM [See Lpar2 in Genome Data Viewer](#)

Exon count: 3

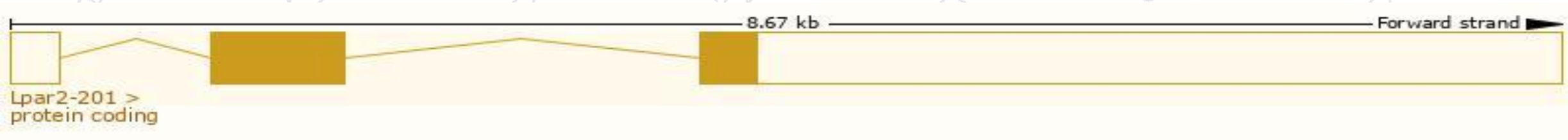
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	8	NC_000074.6 (69822565..69831102)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	8	NC_000074.5 (72346464..72355001)

Transcript information (Ensembl)

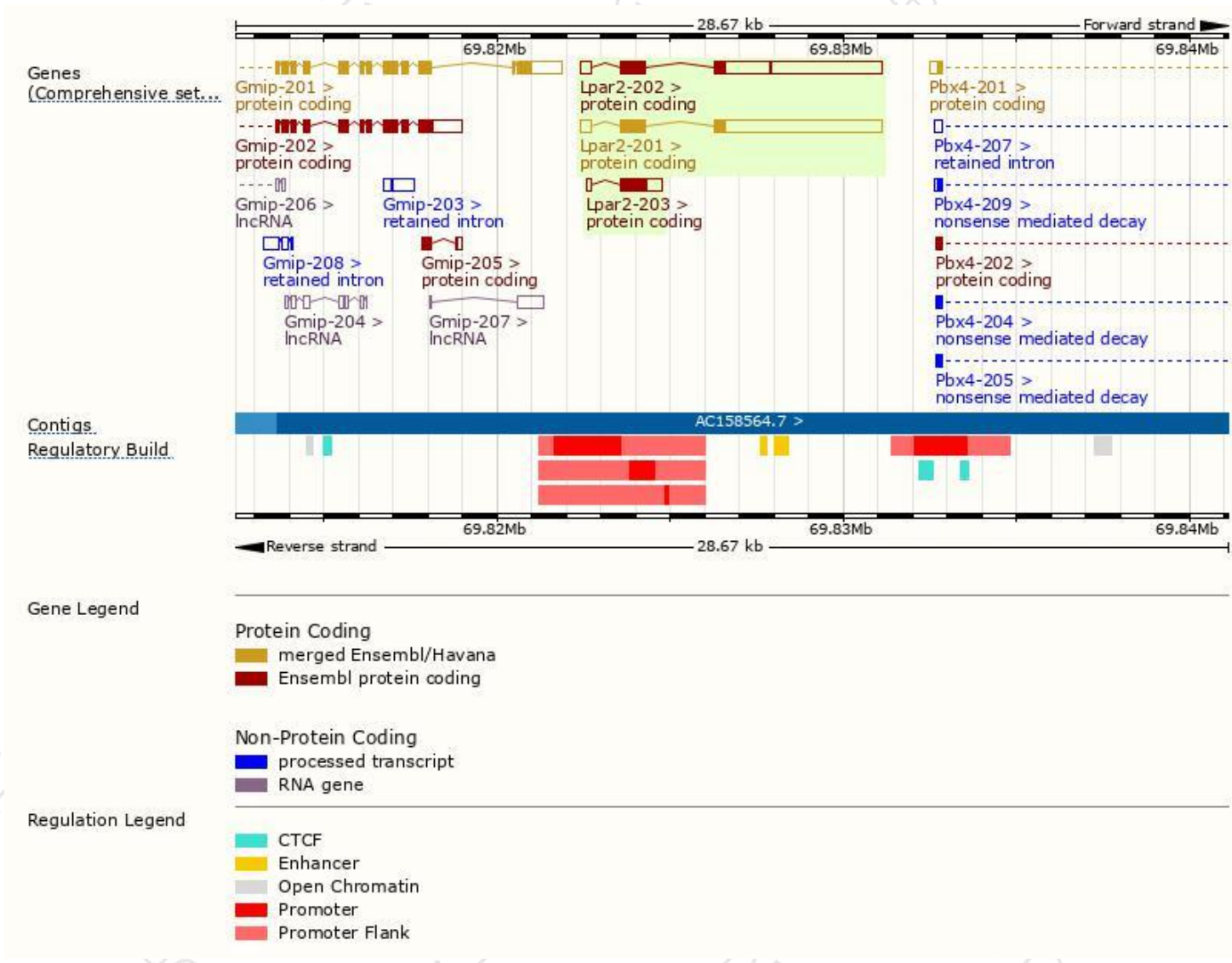
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lpar2-201	ENSMUST00000034325.5	5837	348aa	Protein coding	CCDS40362	Q6P290	TSL:1 GENCODE basic APPRIS P1
Lpar2-202	ENSMUST00000164890.7	5800	348aa	Protein coding	CCDS40362	Q6P290	TSL:1 GENCODE basic APPRIS P1
Lpar2-203	ENSMUST00000238452.1	1350	249aa	Protein coding	-	-	GENCODE basic

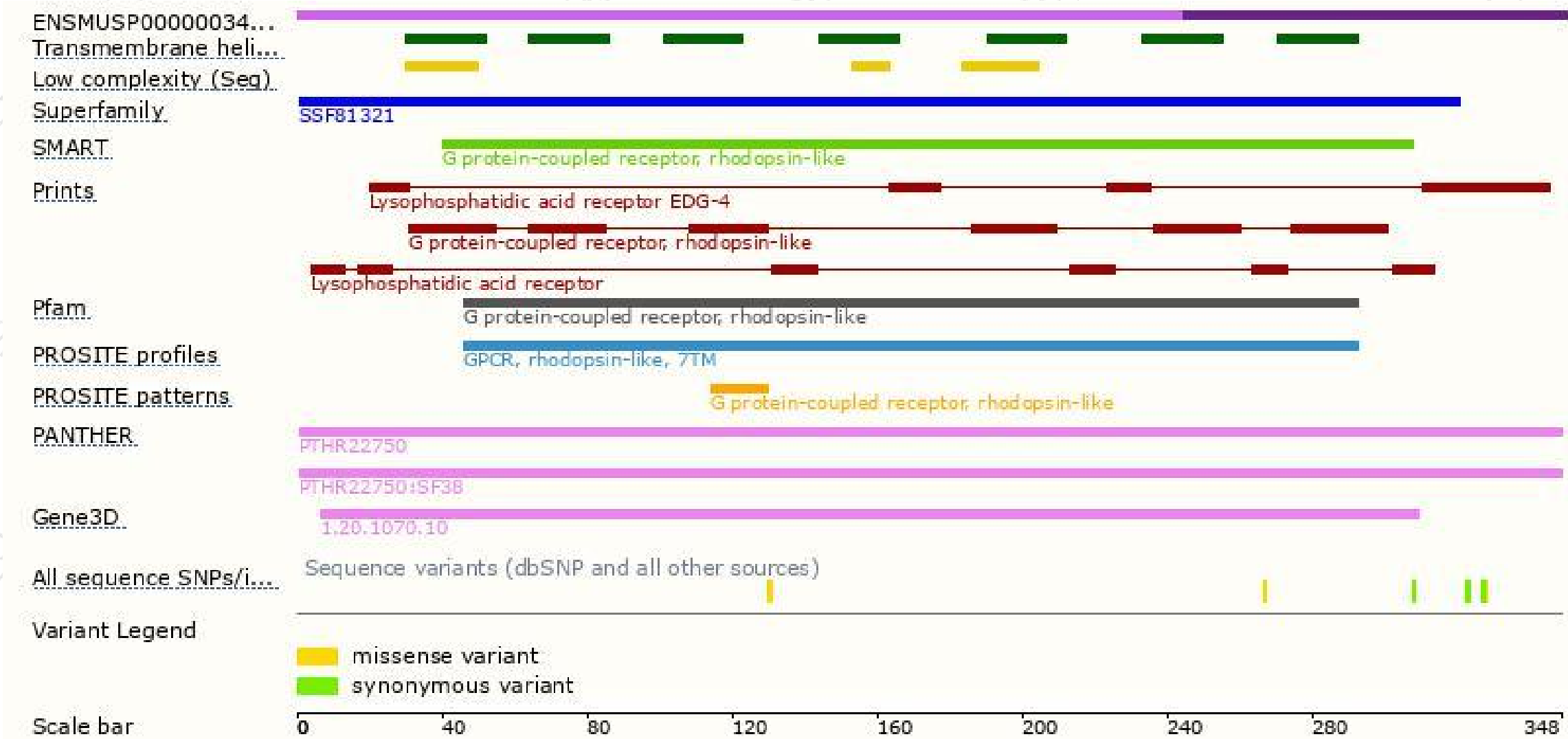
The strategy is based on the design of *Lpar2-201* transcript,The transcription is shown below



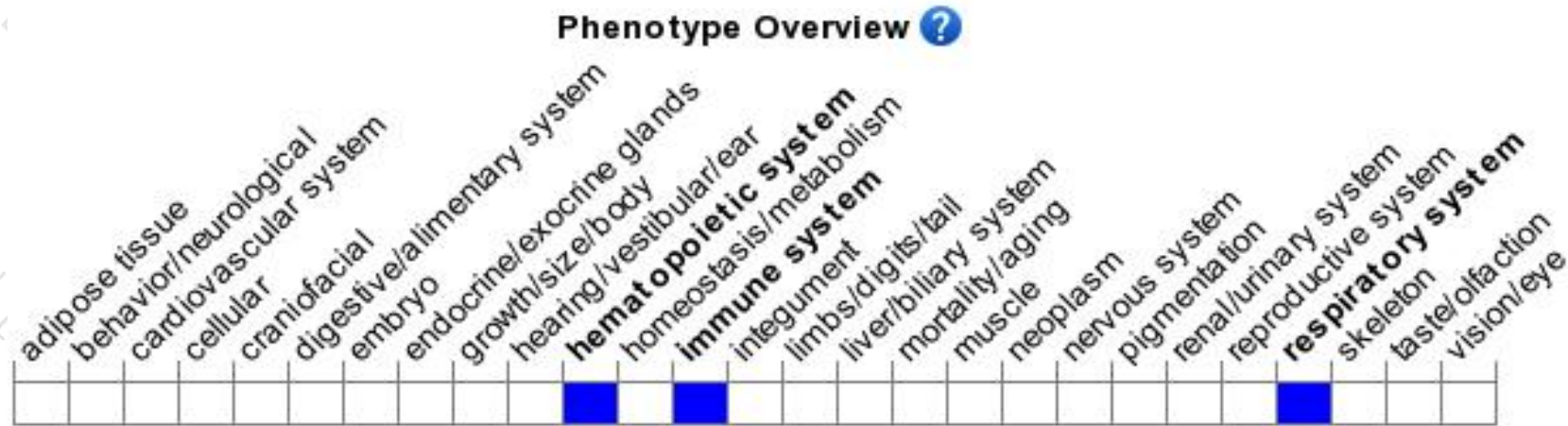
Genomic location distribution



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, Animals homozygous for a targeted mutation appear phenotypically normal.

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

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