

# *Lypd8* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Lypd8*

**Project type**

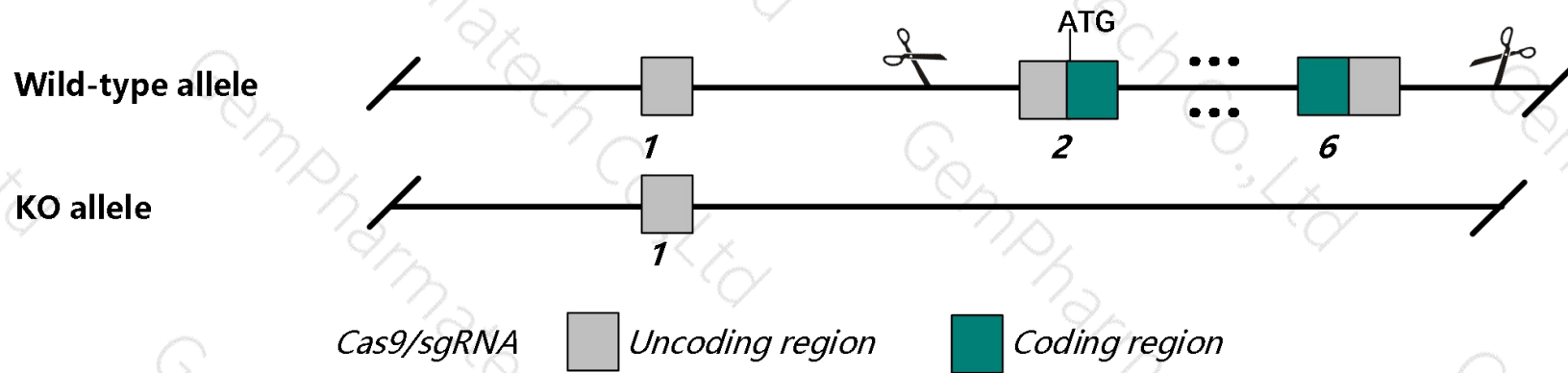
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lypd8* gene. The schematic diagram is as follows:



- The *Lypd8* gene has 2 transcripts. According to the structure of *Lypd8* gene, exon2-exon6 of *Lypd8-202* (ENSMUST00000108826.2) 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 *Lypd8* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, no notable phenotype was detected in a high throughput screen of homozygous mice.
- The *Lypd8* gene is located on the Chr11. 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)

## Lypd8 LY6/PLAUR domain containing 8 [Mus musculus (house mouse)]

Gene ID: 70163, updated on 13-Mar-2020

### Summary



**Official Symbol** Lypd8 provided by [MGI](#)

**Official Full Name** LY6/PLAUR domain containing 8 provided by [MGI](#)

**Primary source** [MGI:MGI:1917413](#)

**See related** [Ensembl:ENSMUSG00000013643](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Mus musculus](#)

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

**Also known as** 2210415F13Rik

**Summary** This gene encodes a member of the Ly6/PLAUR family of cysteine-rich proteins that plays an important role in the protection of colonic epithelium from flagellated microbiota. The encoded protein undergoes proteolytic processing to generate a mature, glycosylphosphatidylinositol-anchored protein that is localized to the apical surface of the colonic epithelial cells. Mice lacking the encoded protein are sensitive to chemically induced intestinal inflammation. [provided by RefSeq, Aug 2016]

**Expression** Biased expression in colon adult (RPKM 5322.9), large intestine adult (RPKM 2859.0) and 4 other tissues [See more](#)

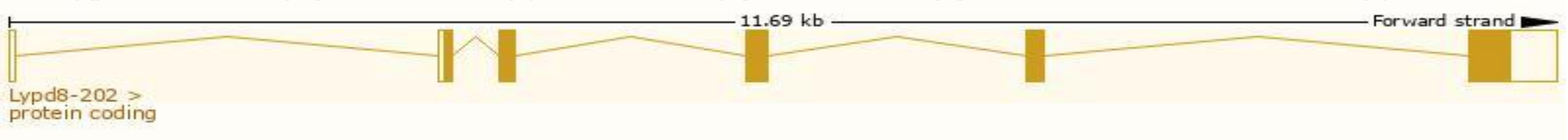
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

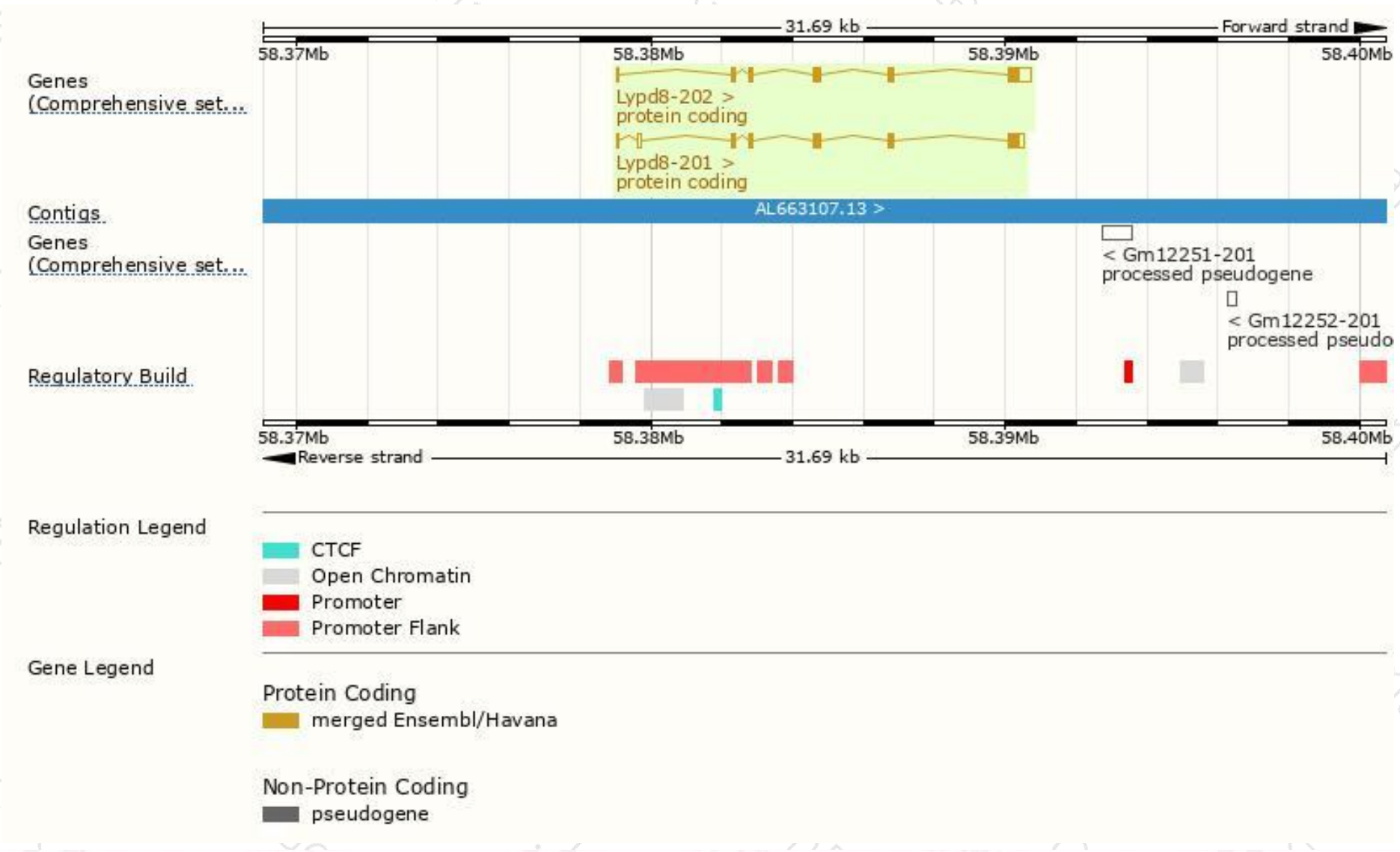
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lypd8-202	<a href="#">ENSMUST00000108826.2</a>	1219	<a href="#">255aa</a>	Protein coding	<a href="#">CCDS36163</a>	<a href="#">Q9D7S0</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Lypd8-201	<a href="#">ENSMUST00000013787.10</a>	1093	<a href="#">255aa</a>	Protein coding	<a href="#">CCDS36163</a>	<a href="#">Q9D7S0</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

The strategy is based on the design of *Lypd8-202* transcript,the transcription is shown below:

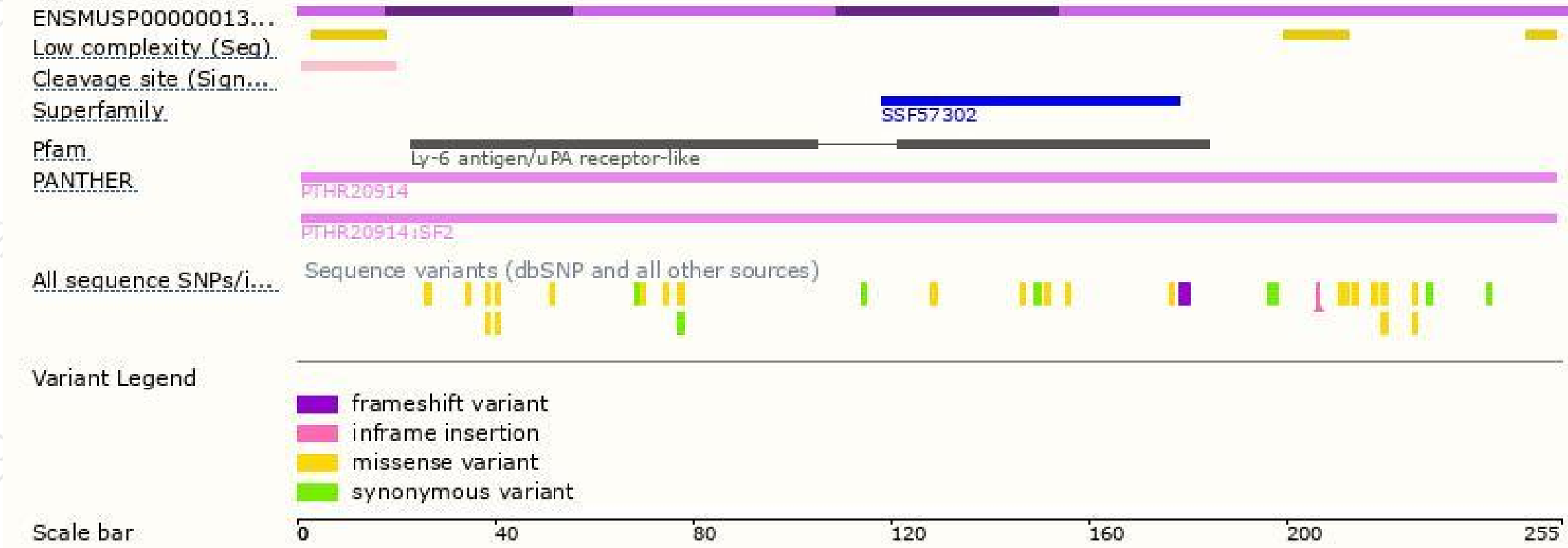


# Genomic location distribution





# Protein domain



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

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