

# *Lypd3* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Lypd3*

**Project type**

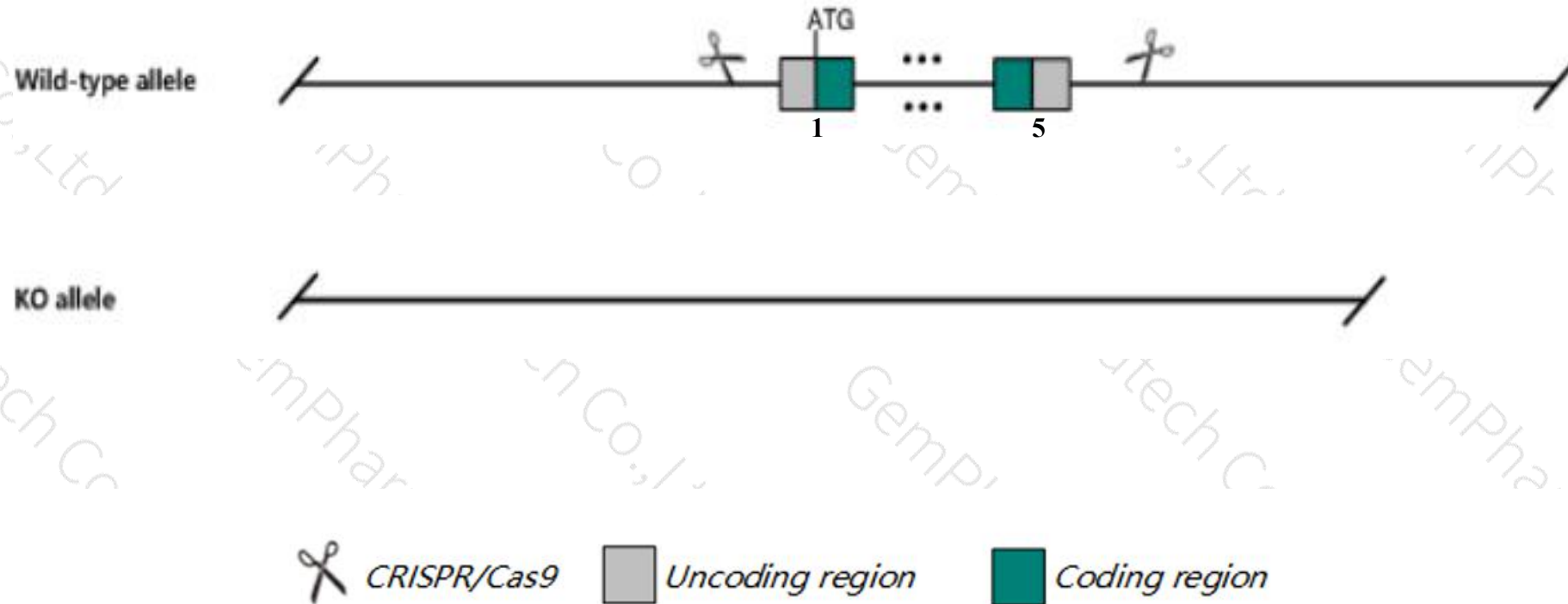
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lypd3* gene. The schematic diagram is as follows:



- The *Lypd3* gene has 1 transcript. According to the structure of *Lypd3* gene, exon1-exon5 of *Lypd3-201* (ENSMUST00000080718.5) 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 *Lypd3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygous null mice show no overt epidermal phenotype and have normal squamous epithelia morphology but are lighter and leaner than controls. males display delayed wound healing whereas females show reduced food intake and a lower incidence of invasive lesions in a bbn-induced bladder cancer model.
- The KO region contains functional region of the *Gm26550* gene. Knockout the region may affect the function of *Gm26550* gene.
- The *Lypd3* gene is located on the Chr7. 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)

## Lypd3 Ly6/Plaur domain containing 3 [Mus musculus (house mouse)]

Gene ID: 72434, updated on 13-Mar-2020

### Summary



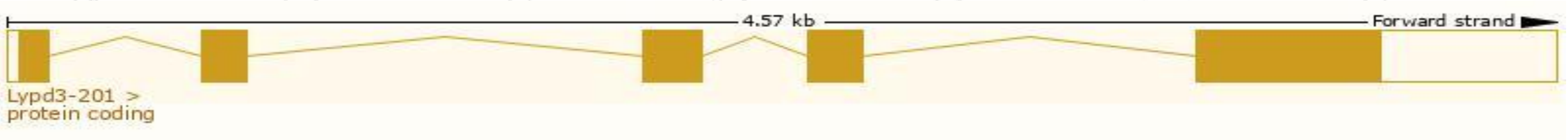
<b>Official Symbol</b>	Lypd3 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	Ly6/Plaur domain containing 3 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1919684</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000057454</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	PROVISIONAL
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	2310061G07Rik, C4.4a
<b>Expression</b>	Biased expression in stomach adult (RPKM 103.6), bladder adult (RPKM 19.2) and 2 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

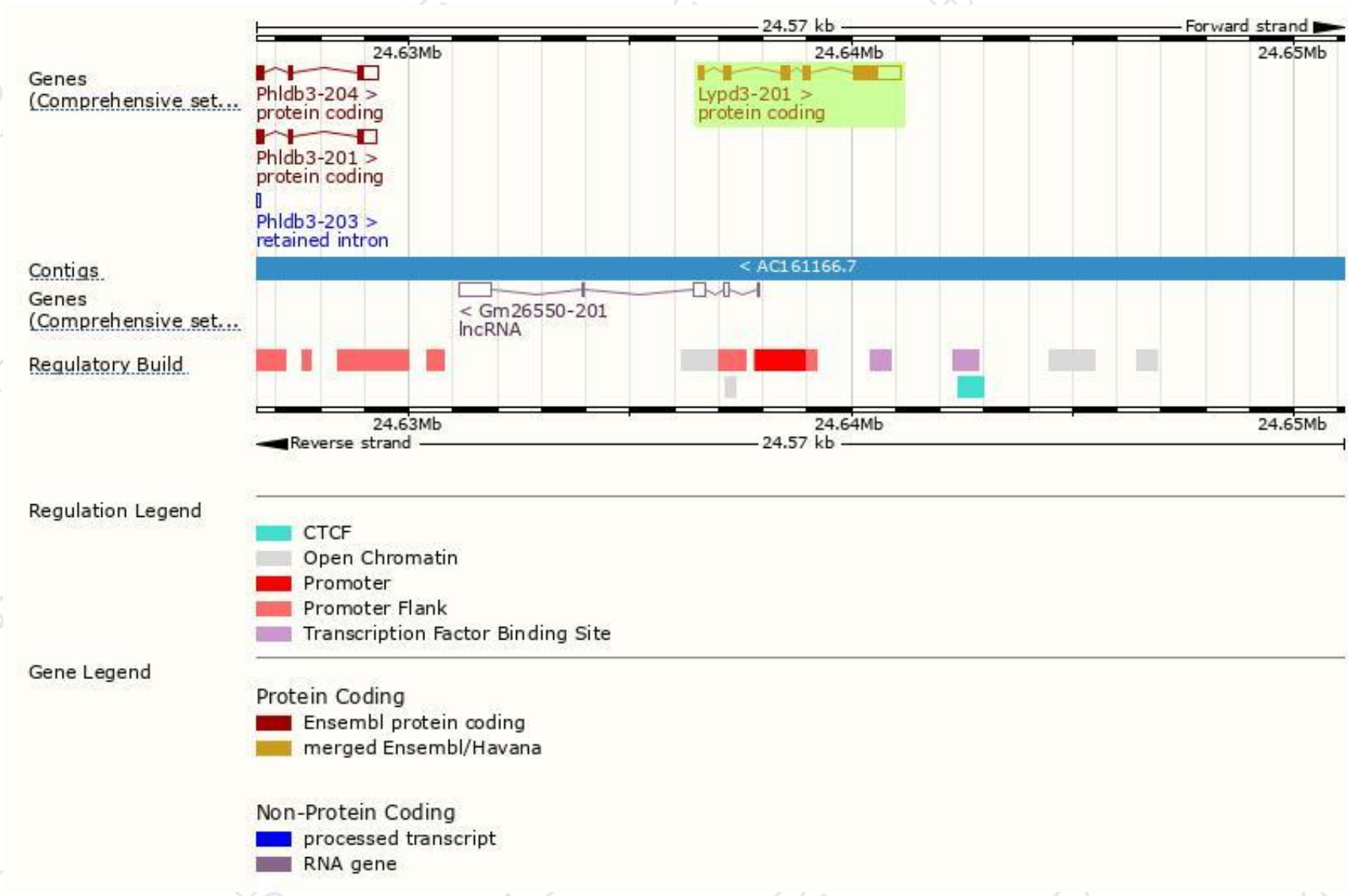
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lypd3-201	<a href="#">ENSMUST00000080718.5</a>	1649	<a href="#">363aa</a>	Protein coding	<a href="#">CCDS20958</a>	<a href="#">Q91YK8</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 *Lypd3-201* transcript, the transcription is shown below:

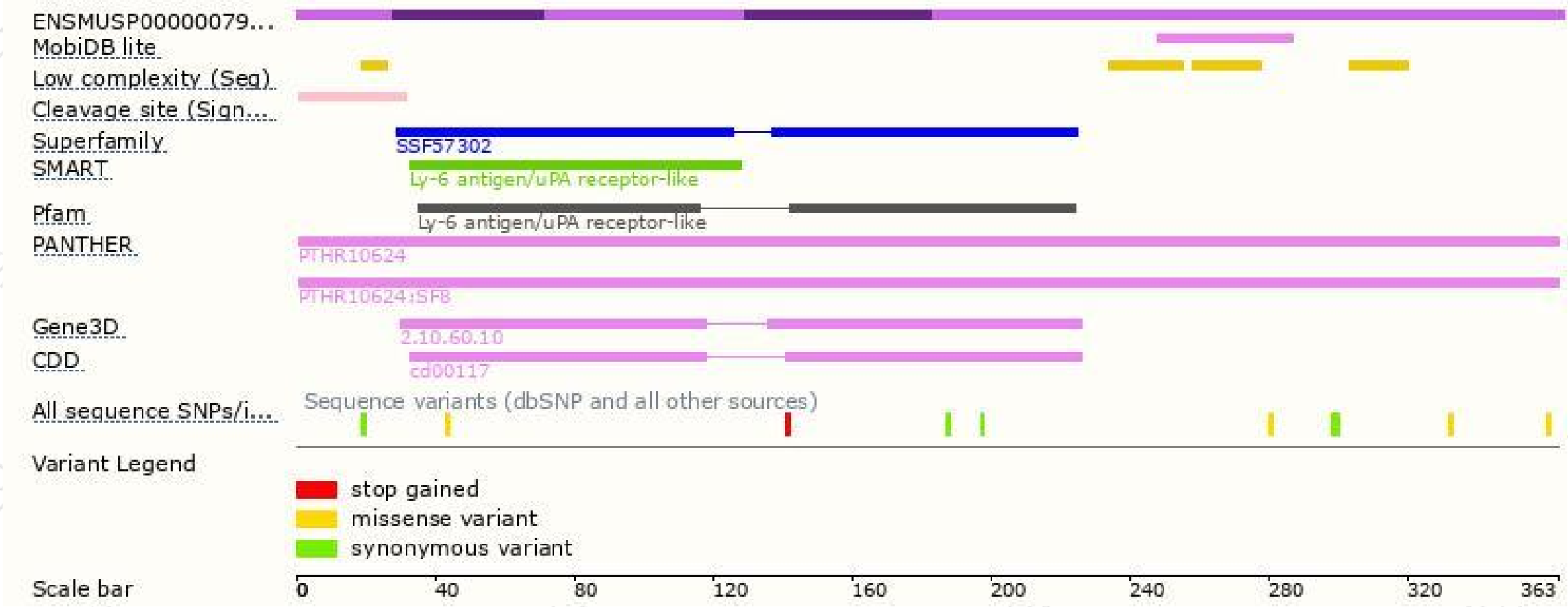


# Genomic location distribution

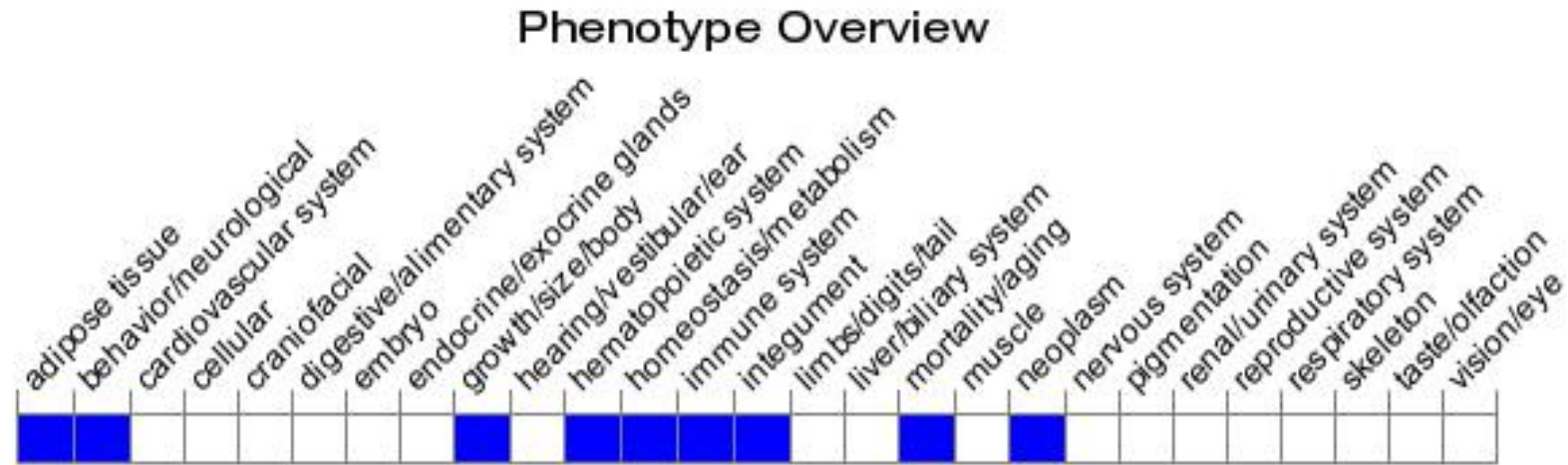




# Protein domain



# 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, homozygous null mice show no overt epidermal phenotype and have normal squamous epithelia morphology but are lighter and leaner than controls. Males display delayed wound healing whereas females show reduced food intake and a lower incidence of invasive lesions in a BBN-induced bladder cancer model.

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

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