

# *Lrp6* Cas9-KO Strategy

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# Project Overview

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**Project Name**

*Lrp6*

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**Project type**

**Cas9-KO**

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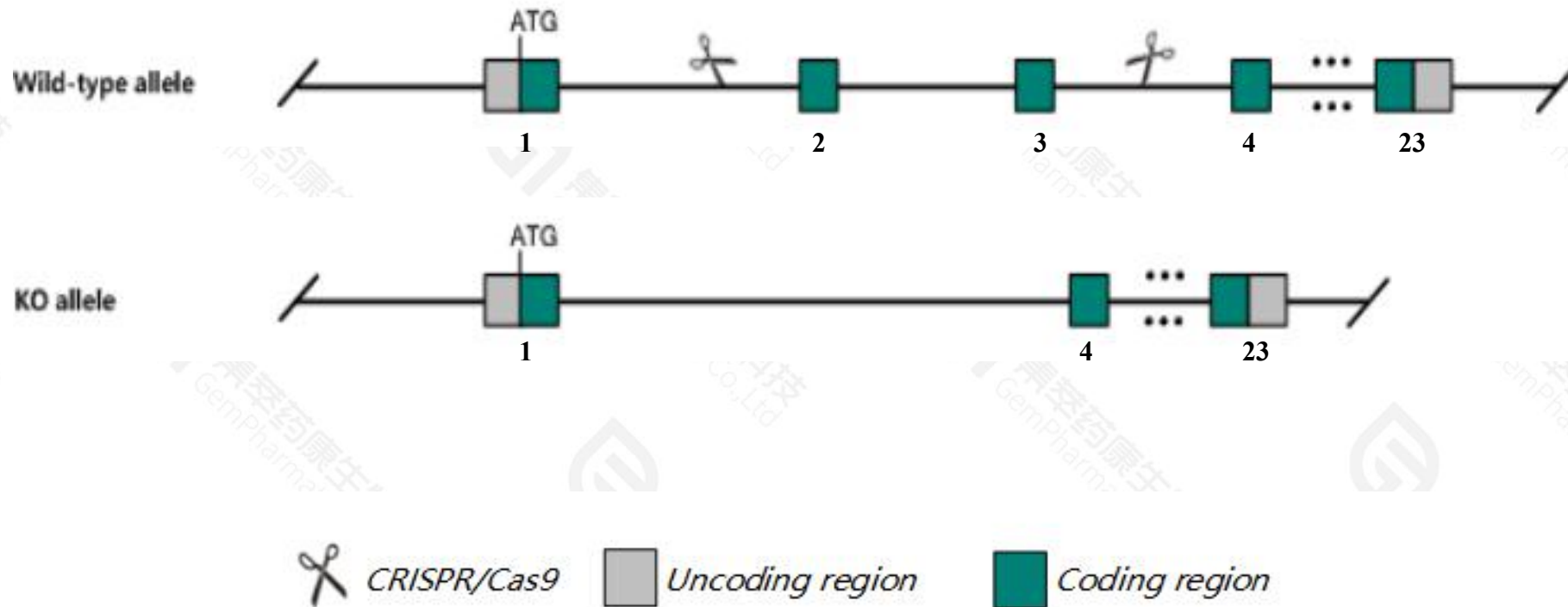
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lrp6* gene. The schematic diagram is as follows:



- The *Lrp6* gene has 6 transcripts. According to the structure of *Lrp6* gene, exon2-exon3 of *Lrp6*-201(ENSMUST00000032322.15) transcript is recommended as the knockout region. The region contains 592bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lrp6* 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, animals homozygous for this mutation exhibit partial embryonic lethality, growth retardation, crooked tail, abnormal vertebrae, small skull with occasional bent nose, absence of the third molars and small and/or unerupted lower incisors. Heterozygotes exhibit a crooked tail and abnormal vertebrae.
- The *Lrp6* gene is located on the Chr6. 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)

## Lrp6 low density lipoprotein receptor-related protein 6 [Mus musculus (house mouse)]

Gene ID: 16974, updated on 22-Mar-2020

### Summary

**Official Symbol** Lrp6 provided by [MGI](#)

**Official Full Name** low density lipoprotein receptor-related protein 6 provided by [MGI](#)

**Primary source** [MGI:MGI:1298218](#)

**See related** [Ensembl:ENSMUSG00000030201](#)

**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** C030016K15Rik, Cd, Gw, ska26, ska, skax26

**Expression** Ubiquitous expression in bladder adult (RPKM 13.4), kidney adult (RPKM 13.4) and 28 other tissues [See more](#)

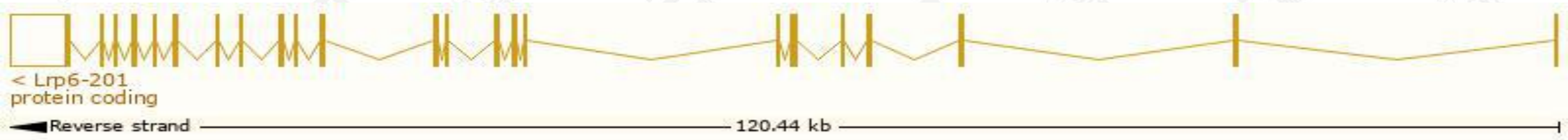
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

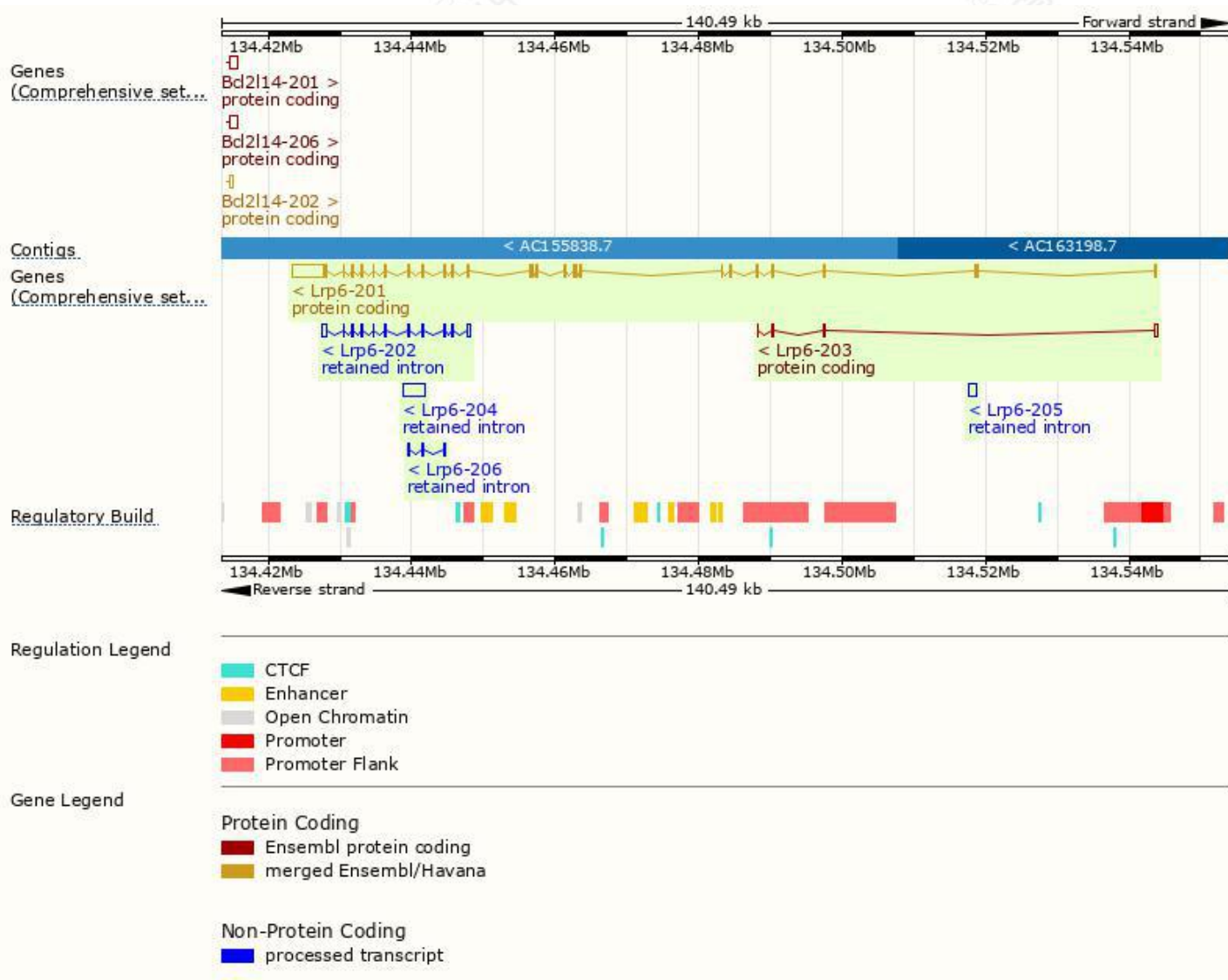
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lrp6-201	<a href="#">ENSMUST00000032322.14</a>	9368	<a href="#">1613aa</a>	Protein coding	<a href="#">CCDS39678</a>	<a href="#">A0A0R4J0A9</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
Lrp6-203	<a href="#">ENSMUST00000126836.3</a>	722	<a href="#">131aa</a>	Protein coding	-	<a href="#">A0A0N4SUL9</a>	CDS 3' incomplete TSL:5
Lrp6-204	<a href="#">ENSMUST00000203016.1</a>	3246	No protein	Retained intron	-	-	TSL:NA
Lrp6-202	<a href="#">ENSMUST00000111950.3</a>	2756	No protein	Retained intron	-	-	TSL:1
Lrp6-205	<a href="#">ENSMUST00000203235.1</a>	941	No protein	Retained intron	-	-	TSL:NA
Lrp6-206	<a href="#">ENSMUST00000203773.1</a>	727	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Lrp6-201* transcript,the transcription is shown below:

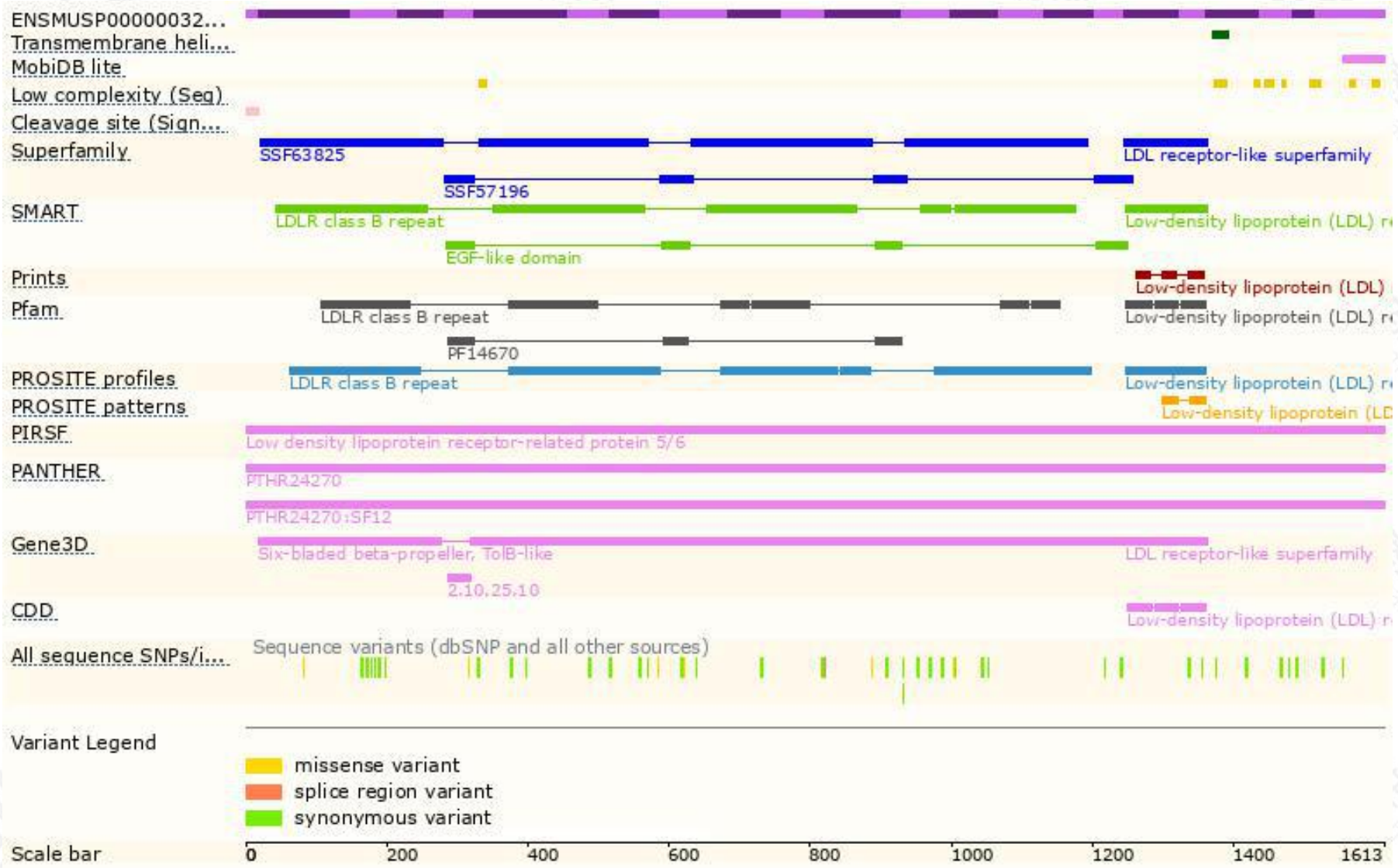


# Genomic location distribution

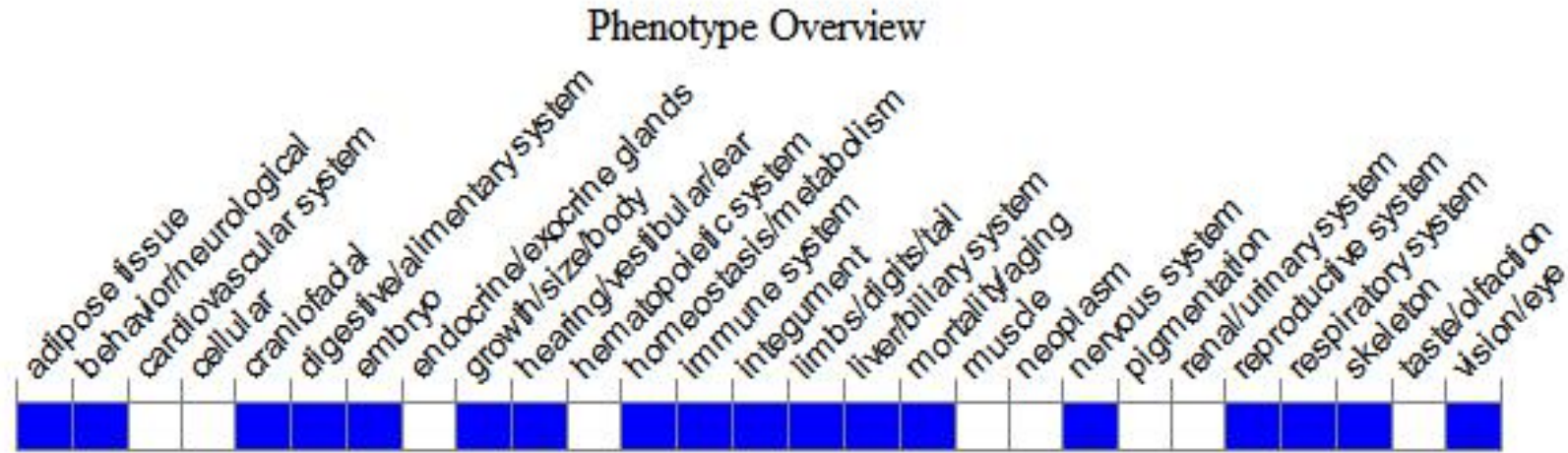




# Protein domain



# 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 this mutation exhibit partial embryonic lethality, growth retardation, crooked tail, abnormal vertebrae, small skull with occasional bent nose, absence of the third molars and small and/or unerupted lower incisors. Heterozygotes exhibit a crooked tail and abnormal vertebrae.

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