

Lpp Cas9-KO Strategy

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Design Date:

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Project Overview



Project Name

Lpp

Project type

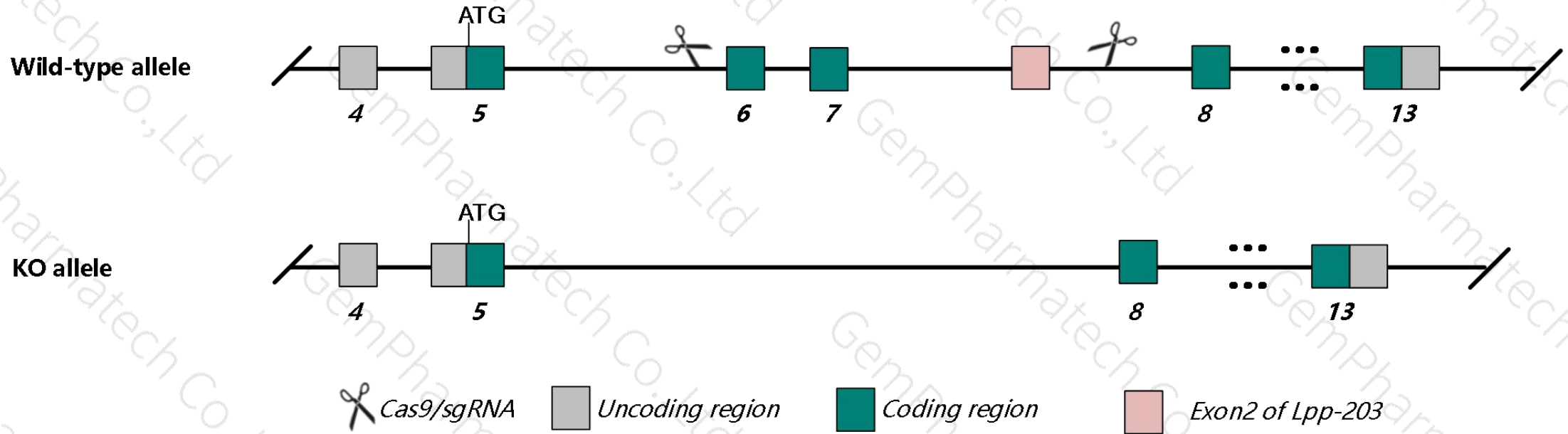
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Lpp* gene has 6 transcripts. According to the structure of *Lpp* gene, exon6-exon7 of *Lpp-201* (ENSMUST0000038053.13) transcript is recommended as the knockout region. The region contains 239bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lpp* gene. The brief process is as follows: CRISPR/Cas9 system were

- According to the existing MGI data, Gene disruption results in fertility problems involving females but not males. Migration and survival of MEFs are also abnormal.
- The *Lpp* gene is located on the Chr16. 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.

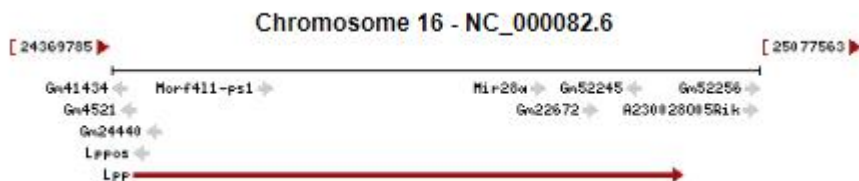
Gene information (NCBI)

Lpp LIM domain containing preferred translocation partner in lipoma [*Mus musculus* (house mouse)]

Gene ID: 210126, updated on 12-Aug-2019

Summary

Official Symbol	Lpp provided by MGI
Official Full Name	LIM domain containing preferred translocation partner in lipoma provided by MGI
Primary source	MGI:MGI:2441849
See related	Ensembl:ENSMUSG00000033306
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	C79715; AA959454; AU024130; D630048H16; 9430020K16Rik; B130055L10Rik
Expression	Biased expression in bladder adult (RPKM 60.6), subcutaneous fat pad adult (RPKM 8.5) and 10 other tissues See more
Orthologs	human all



Transcript information (Ensembl)

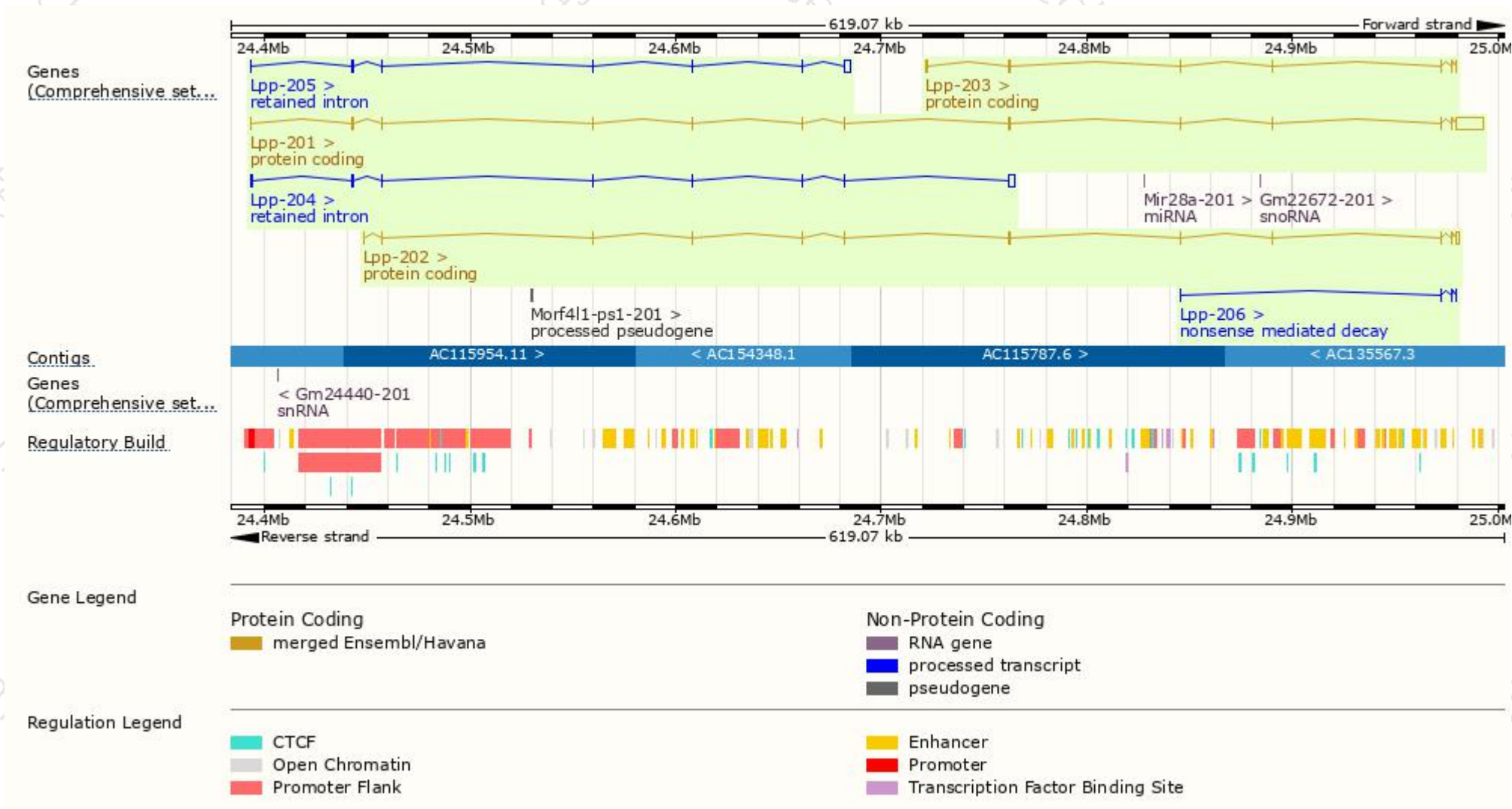
The gene has 6 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lpp-201	ENSMUST00000038053.13	15459	613aa	Protein coding	CCDS28083	Q8BFW7	TSL:1 GENCODE basic APPRIS P1
Lpp-202	ENSMUST00000078988.9	3894	613aa	Protein coding	CCDS28083	Q8BFW7	TSL:1 GENCODE basic APPRIS P1
Lpp-203	ENSMUST00000115314.3	1808	488aa	Protein coding	CCDS49807	Q8BFW7	TSL:1 GENCODE basic
Lpp-206	ENSMUST00000232546.1	601	51aa	Nonsense mediated decay	-	A0A338P705	-
Lpp-204	ENSMUST00000231279.1	4306	No protein	Retained intron	-	-	-
Lpp-205	ENSMUST00000231352.1	4137	No protein	Retained intron	-	-	-

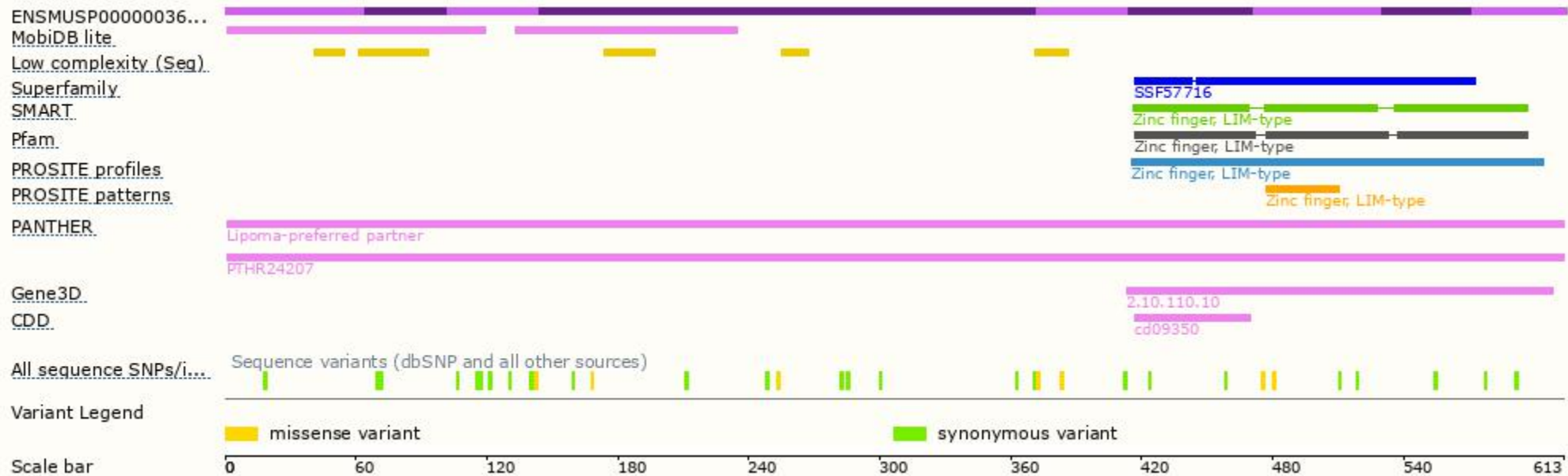
The strategy is based on the design of *Lpp-201* transcript, The transcription is shown below



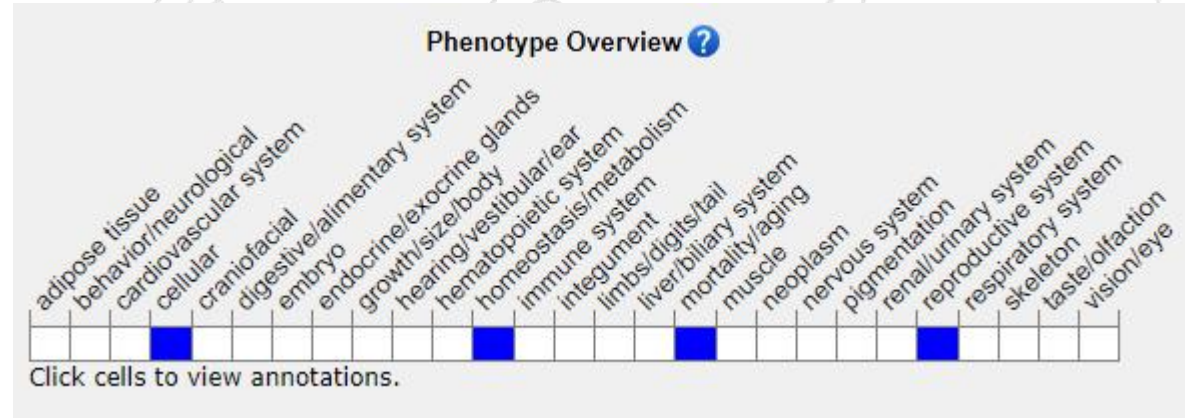
Genomic location distribution



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, Gene disruption results in fertility problems involving females but not males.

Migration and survival of MEFs are also abnormal.

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

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