

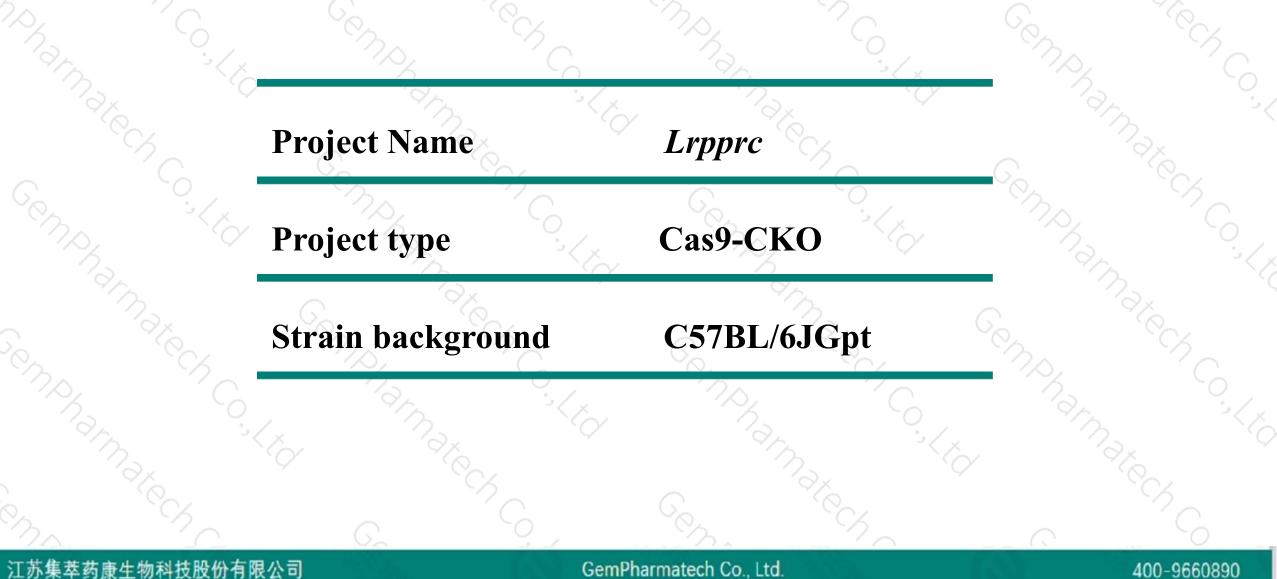
Lrpprc Cas9-CKO Strategy Andramater Control

Cemphamatech, Cenphamaten Designer:Xueting Zhang

CMPHarmarect

Project Overview



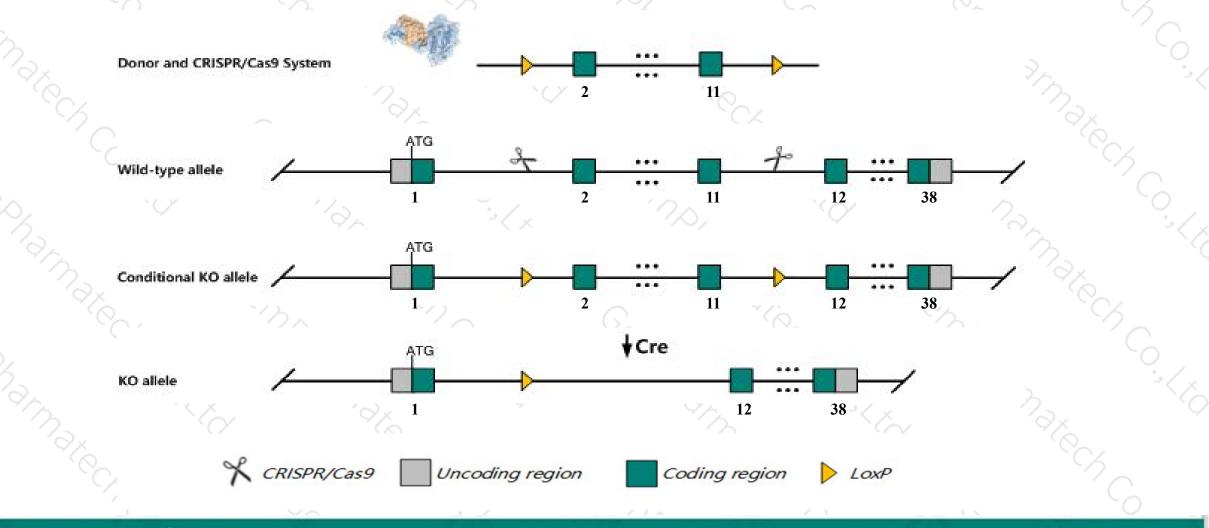


Conditional Knockout strategy



400-9660890

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



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The Lrpprc gene has 7 transcripts. According to the structure of Lrpprc gene, exon2-exon11 of Lrpprc-201 (ENSMUST00000112308.8) transcript is recommended as the knockout region. The region contains 1217bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Lrpprc* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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.

The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice



According to the existing MGI data, Mice homozygous for a gene trap allele exhibit embryonic lethality during organogenesis associated with growth retardation. Mice homozygous for a knock-out allele exhibit embryonic lethality between somite formation and embryo turning.

Transcript *Lrpprc*-203&204&207 may not be affected.

- The Lrpprc gene is located on the Chr17. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

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Gene information (NCBI)



\$?

Lrpprc leucine-rich PPR-motif containing [Mus musculus (house mouse)]

Gene ID: 72416, updated on 31-Jan-2019

Summary

Official Symbol	Lrpprc provided by MGI
Official Full Name	leucine-rich PPR-motif containing provided by MGI
Primary source	MGI:MGI:1919666
See related	Ensembl:ENSMUSG0000024120
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	3110001K13Rik, C76645, Gp130, Lrp130, Lsfc
Expression	Ubiquitous expression in placenta adult (RPKM 18.8), liver E18 (RPKM 15.7) and 28 other tissues See more
Orthologs	human all

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The gene has 7 transcripts, all transcripts are shown below:

Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000112308.8	4393	<u>1392aa</u>	Protein coding	CCDS29003	<u>Q6PB66</u>	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000160011.1	565	<u>142aa</u>	Nonsense mediated decay	÷.	<u>F6V2A3</u>	CDS 5' incomplete TSL:3
ENSMUST00000159222.1	967	No protein	Processed transcript	-	2	TSL:5
ENSMUST00000162799.1	809	No protein	Processed transcript	<u>1</u> 2	2	TSL:3
ENSMUST00000161299.7	4012	No protein	Retained intron	-		TSL:2
ENSMUST00000161928.7	2875	No protein	Retained intron	-	-	TSL:2
ENSMUST00000160414.1	513	No protein	Retained intron	2	2	TSL:2
	ENSMUST00000112308.8 ENSMUST00000160011.1 ENSMUST00000159222.1 ENSMUST00000162799.1 ENSMUST00000161299.7 ENSMUST00000161928.7	ENSMUST00000112308.8 4393 ENSMUST00000160011.1 565 ENSMUST00000159222.1 967 ENSMUST00000162799.1 809 ENSMUST00000161299.7 4012 ENSMUST00000161928.7 2875	ENSMUST00000112308.8 4393 1392aa ENSMUST00000160011.1 565 142aa ENSMUST00000159222.1 967 No protein ENSMUST00000162799.1 809 No protein ENSMUST00000161299.7 4012 No protein ENSMUST00000161928.7 2875 No protein	ENSMUST00000112308.843931392aaProtein codingENSMUST00000160011.1565142aaNonsense mediated decayENSMUST00000159222.1967No proteinProcessed transcriptENSMUST00000162799.1809No proteinProcessed transcriptENSMUST00000161299.74012No proteinRetained intronENSMUST00000161928.72875No proteinRetained intron	ENSMUST00000112308.843931392aaProtein codingCCDS29003ENSMUST00000160011.1565142aaNonsense mediated decay-ENSMUST00000159222.1967No proteinProcessed transcript-ENSMUST00000162799.1809No proteinProcessed transcript-ENSMUST00000161299.74012No proteinRetained intron-ENSMUST00000161928.72875No proteinRetained intron-	ENSMUST00000112308.843931392aaProtein codingCCDS29003Q6PB66ENSMUST0000160011.1565142aaNonsense mediated decay-F6V2A3ENSMUST0000159222.1967No proteinProcessed transcriptENSMUST00000162799.1809No proteinProcessed transcriptENSMUST0000161299.74012No proteinRetained intronENSMUST0000161299.72875No proteinRetained intron

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

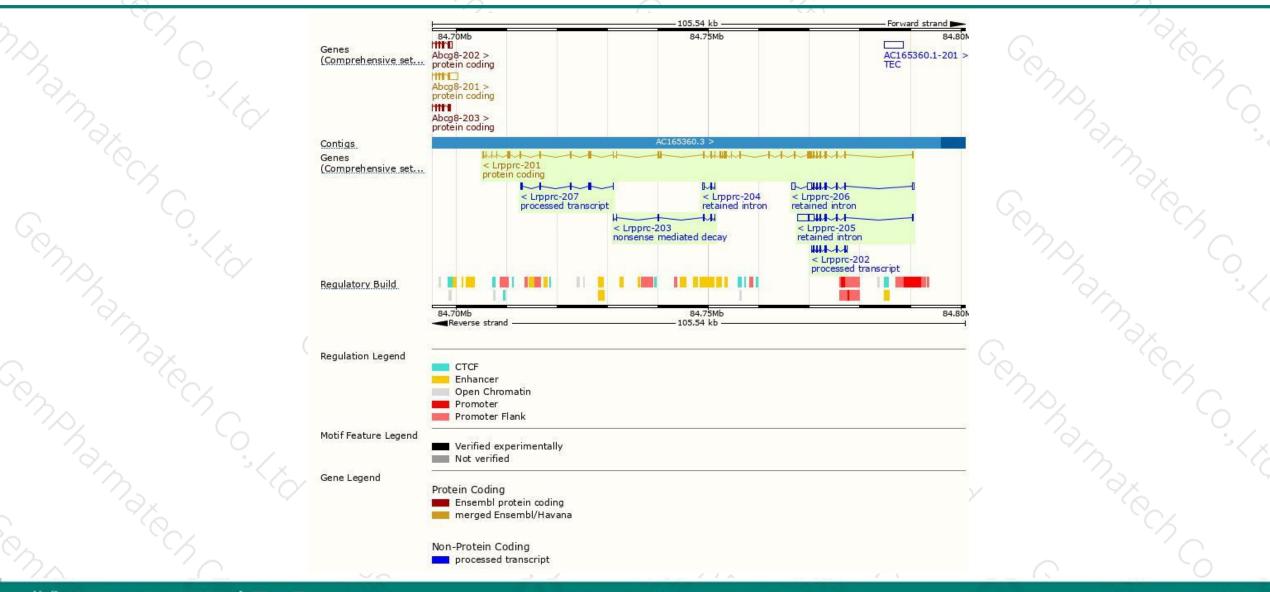
< Lrpprc-201 protein coding

Reverse strand -

- 85.31 kb -

Genomic location distribution



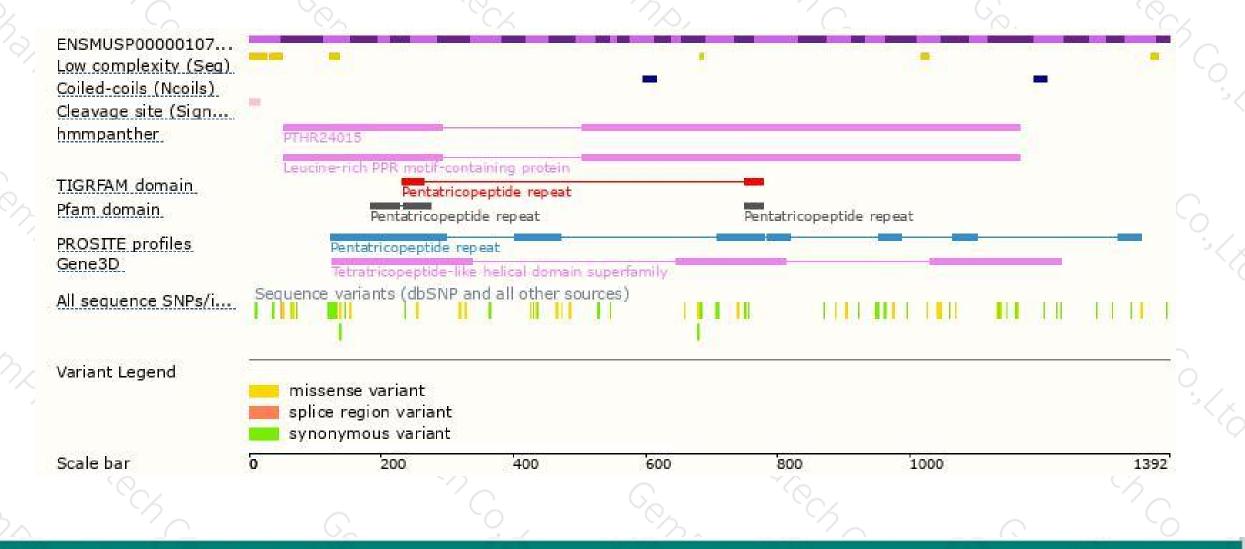


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Protein domain



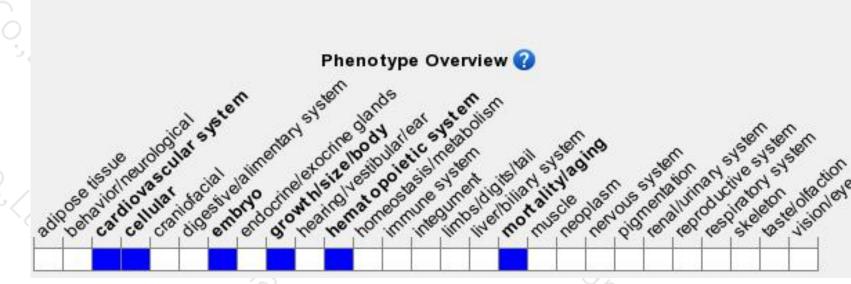


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Mouse phenotype description(MGI)





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, Mice homozygous for a gene trap allele exhibit embryonic lethality during organogenesis associated with growth retardation. Mice homozygous for a knock-out allele exhibit embryonic lethality betwe somite formation and embryo turning.

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If you have any questions, you are welcome to inquire. Tel: 400-9660890



