

Lhfpl2 Cas9-CKO Strategy

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Project Overview

Project Name

Lhfpl2

Project type

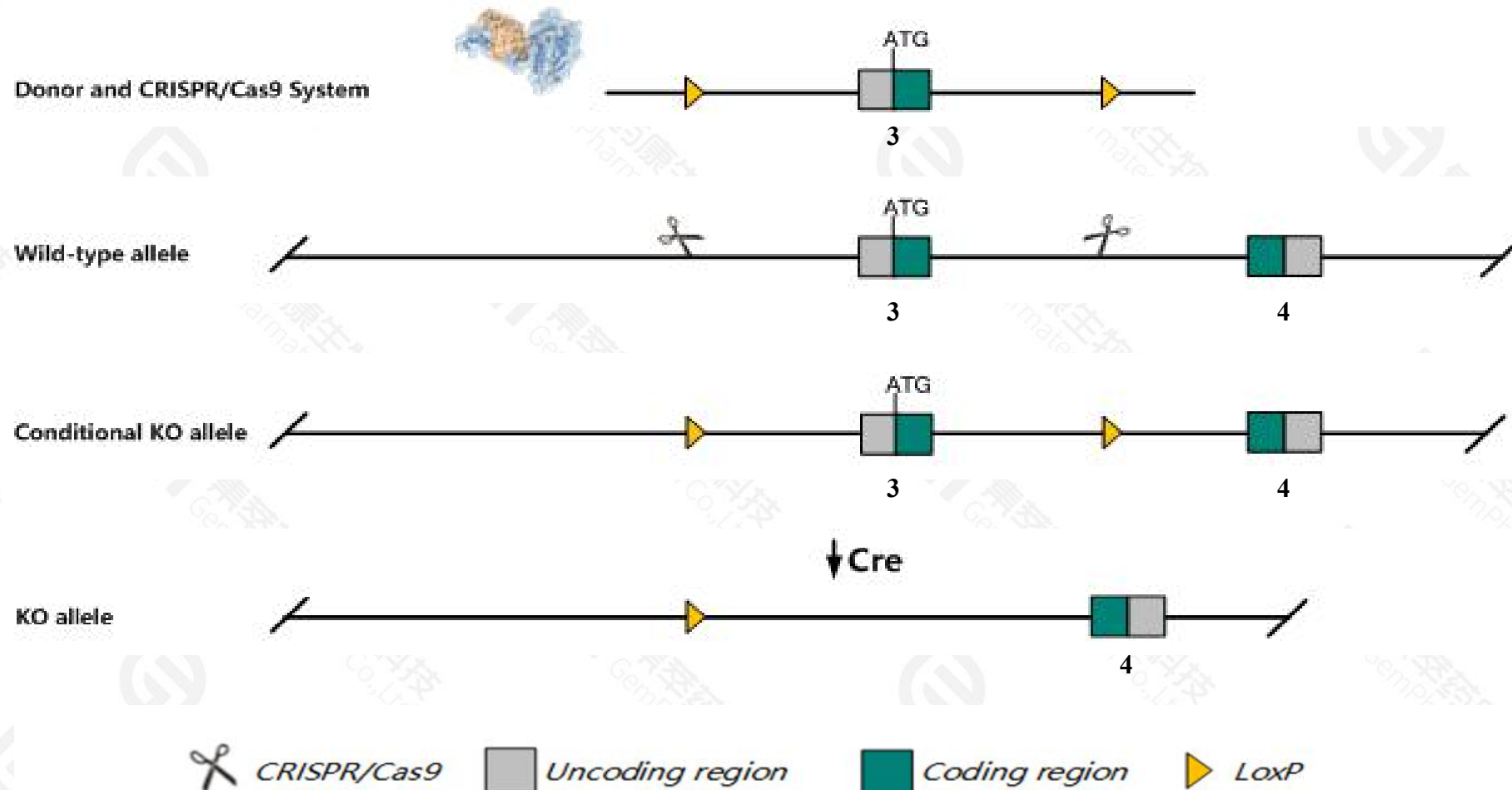
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lhfpl2* gene. The schematic diagram is as follows:



Technical routes

- The *Lhfpl2* gene has 9 transcripts. According to the structure of *Lhfpl2* gene, exon3 of *Lhfpl2*-201(ENSMUST00000054274.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lhfpl2* 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.

- According to the existing MGI data, females homozygous for a spontaneous point mutation have a completely closed vagina, soft swelling of the perineum and buildup of viscous fluid in the uteri.
- The *Lhfpl2* gene is located on the Chr13. 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.

Gene information (NCBI)

Lhfp12 lipoma HMGIC fusion partner-like 2 [Mus musculus (house mouse)]

Gene ID: 218454, updated on 13-Mar-2020

Summary



Official Symbol Lhfp12 provided by [MGI](#)

Official Full Name lipoma HMGIC fusion partner-like 2 provided by [MGI](#)

Primary source [MGI:MGI:2145236](#)

See related [Ensembl:ENSMUSG00000045312](#)

Gene type protein coding

RefSeq status PROVISIONAL

Organism [Mus musculus](#)

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

Also known as 6030465B15, AI447312, AW050335, mKIAA0206, vgim

Expression Broad expression in subcutaneous fat pad adult (RPKM 19.7), limb E14.5 (RPKM 15.8) and 23 other tissues [See more](#)

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

Transcript information (Ensembl)

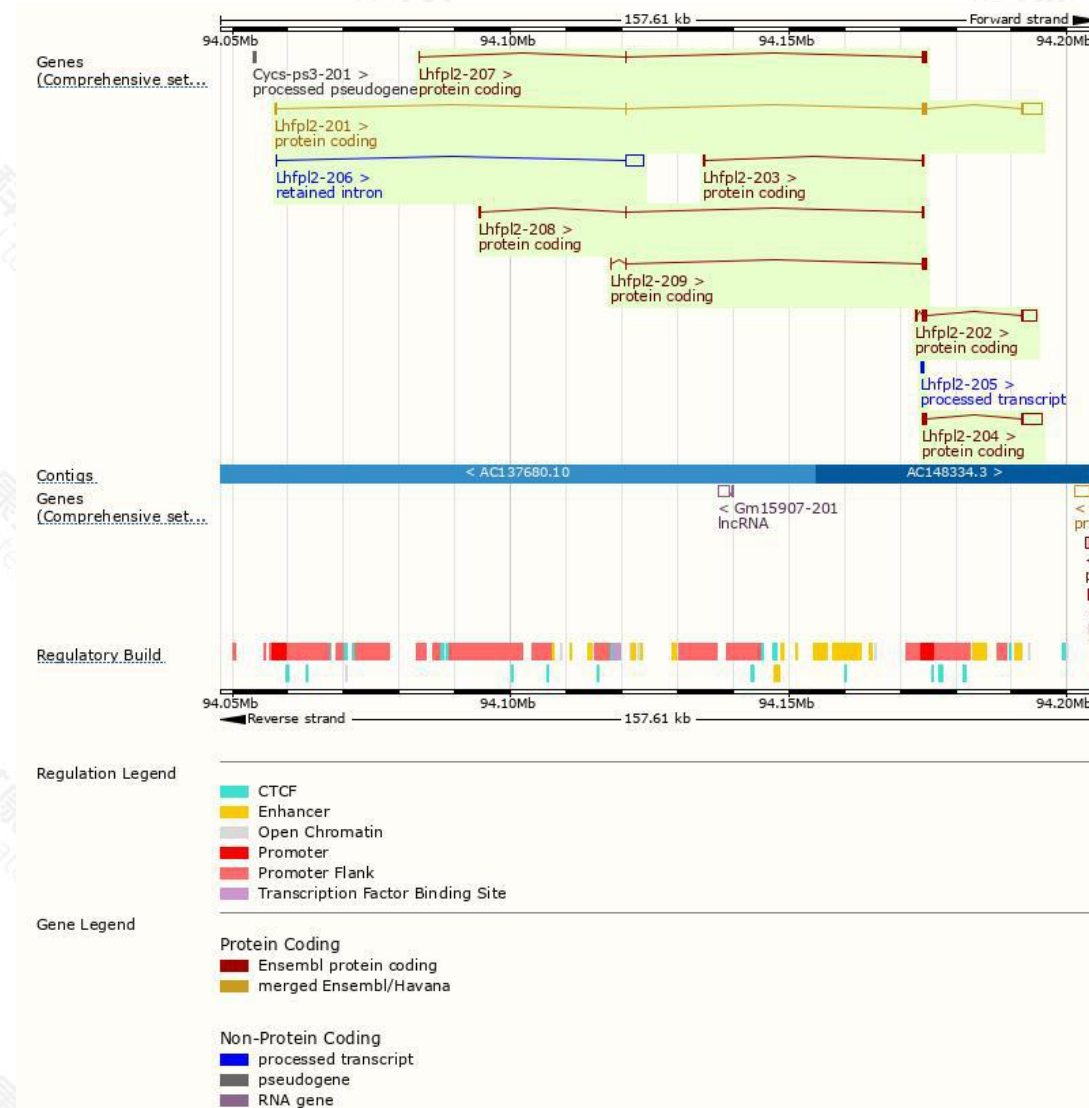
The gene has 9 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------------|--------------------------------------|------|-----------------------|----------------------|---------------------------|----------------------------|-------------------------------|
| Lhfpl2-201 | ENSMUST00000054274.7 | 4348 | 222aa | Protein coding | CCDS26692 | Q8BGA2 | TSL:1 GENCODE basic APPRIS P1 |
| Lhfpl2-204 | ENSMUST00000121618.1 | 4209 | 222aa | Protein coding | CCDS26692 | Q8BGA2 | TSL:1 GENCODE basic APPRIS P1 |
| Lhfpl2-202 | ENSMUST00000118195.1 | 3611 | 222aa | Protein coding | CCDS26692 | Q8BGA2 | TSL:1 GENCODE basic APPRIS P1 |
| Lhfpl2-209 | ENSMUST00000223423.1 | 771 | 141aa | Protein coding | - | A0A1Y7VJ20 | CDS 3' incomplete TSL:3 |
| Lhfpl2-207 | ENSMUST00000156071.1 | 768 | 139aa | Protein coding | - | D3Z698 | CDS 3' incomplete TSL:3 |
| Lhfpl2-203 | ENSMUST00000120051.1 | 488 | 34aa | Protein coding | - | D3Z4C4 | CDS 3' incomplete TSL:5 |
| Lhfpl2-208 | ENSMUST00000221096.1 | 362 | 19aa | Protein coding | - | A0A1Y7VNJ3 | CDS 3' incomplete TSL:3 |
| Lhfpl2-205 | ENSMUST00000131595.1 | 347 | No protein | Processed transcript | - | - | TSL:2 |
| Lhfpl2-206 | ENSMUST00000144838.1 | 3273 | No protein | Retained intron | - | - | TSL:1 |

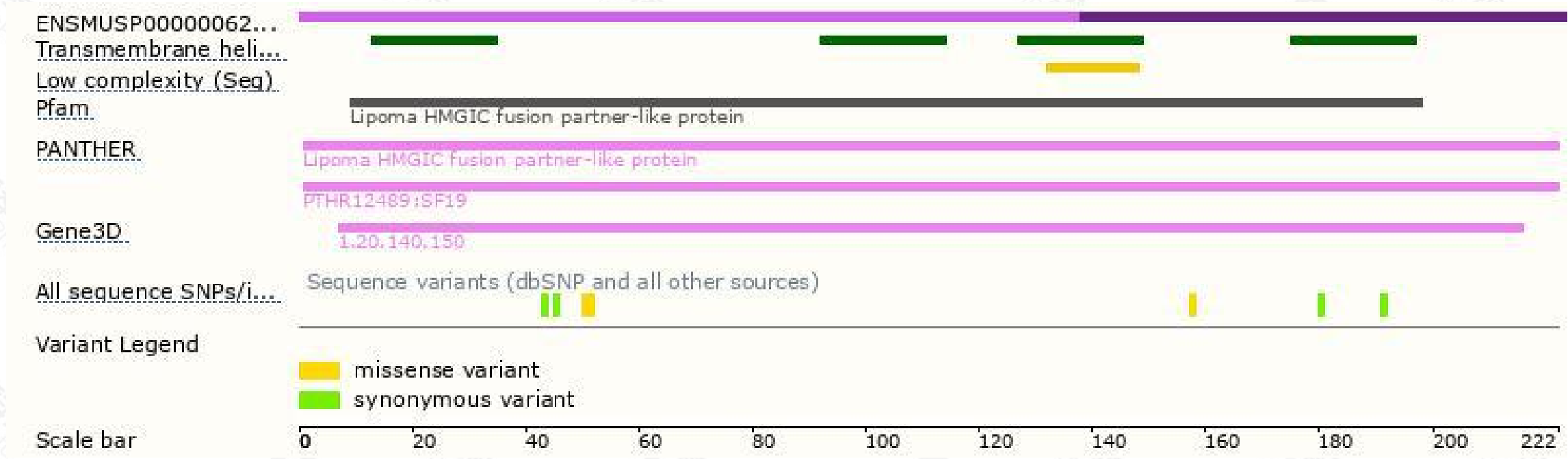
The strategy is based on the design of *Lhfpl2-201* transcript,the transcription is shown below:



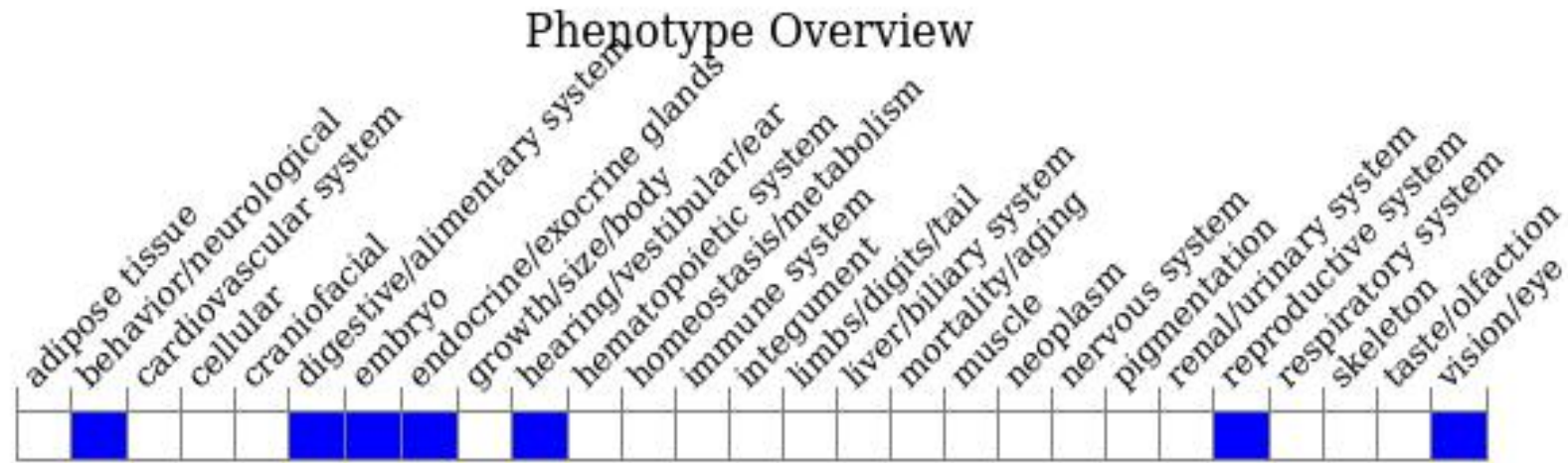
Genomic location distribution



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, females homozygous for a spontaneous point mutation have a completely closed vagina, soft swelling of the perineum and buildup of viscous fluid in the uteri.

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