# *Lfng* Cas9-CKO Strategy

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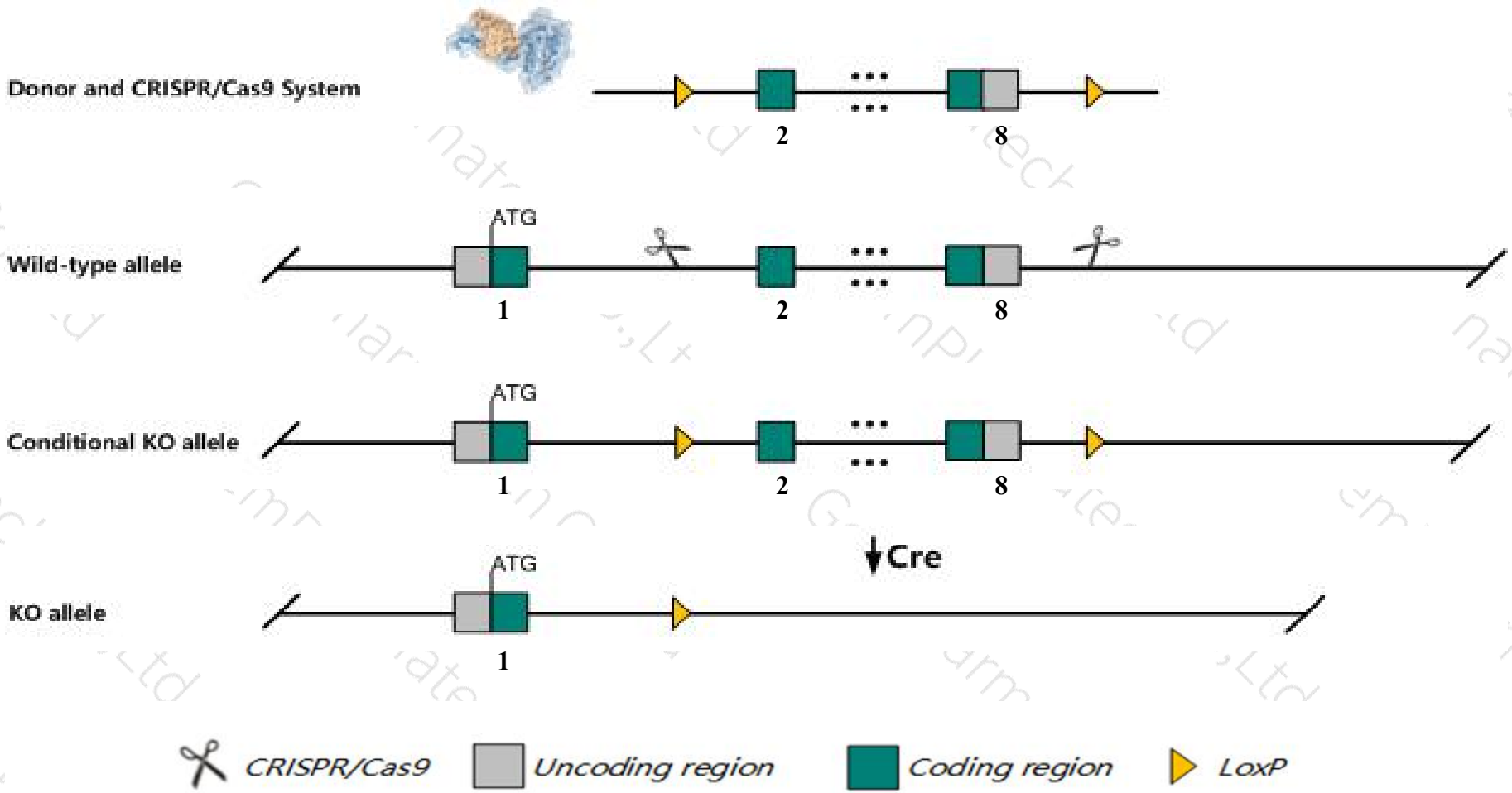
Date:2019-10-16

# Project Overview

| | |
|---|---|
| **Project Name** | ***Lfng*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

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



# Technical routes

➢ The *Lfng* gene has 3 transcripts. According to the structure of *Lfng* gene, exon2-exon8 of *Lfng-201* (ENSMUST00000031555.2) transcript is recommended as the knockout region.The region contains most of coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Lfng* gene. The brief process is as follows:gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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 knock-out allele exhibit a short tail and abnormal rib, somite, and lung development. Mice homozygous mice exhibit reduced female fertility, abnormal hair cells, and abnormal axial skeleton morphology.
- The floxed region is near to the N-terminal of *Gm43703* gene,this strategy may influence the regulatory function of the N-terminal of *Gm43703* gene.
- The *Lfng* gene is located on the Chr5. 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）

集萃药康 GemPharmatech

## Lfng LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase [ *Mus musculus* (house mouse) ]

Gene ID: 16848, updated on 10-Oct-2019

### Summary

| | |
|---|---|
| **Official Symbol** | Lfng provided by MGI |
| **Official Full Name** | LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase provided by MGI |
| **Primary source** | MGI:MGI:1095413 |
| **See related** | Ensembl:ENSMUSG00000029570 |
| **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** | AW061165 |
| **Expression** | Broad expression in spleen adult (RPKM 77.7), mammary gland adult (RPKM 72.5) and 25 other tissues See more |
| **Orthologs** | human all |

### Genomic context

**Location:** 5 G2; 5 79.15 cM

See Lfng in Genome Data Viewer

**Exon count:** 8

| Annotation release | Status | Assembly | Chr | Location |
|---|---|---|---|---|
| 108 | current | GRCm38.p6 (GCF_000001635.26) | 5 | NC_000071.6 (140607341..140615545) |
| Build 37.2 | previous assembly | MGSCv37 (GCF_000001635.18) | 5 | NC_000071.5 (141083295..141091499) |

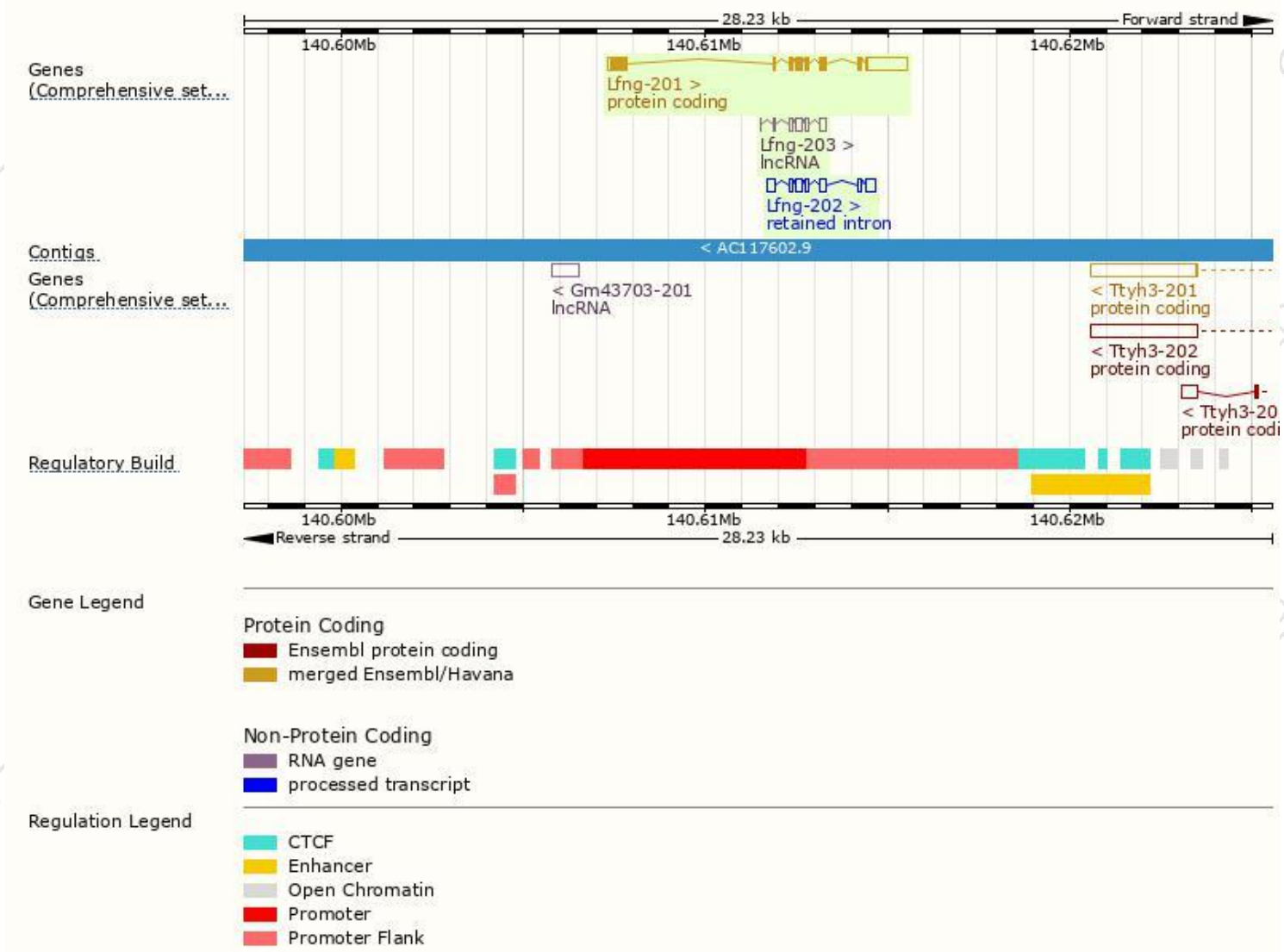
# Transcript information（Ensembl）

The gene has 3 transcripts,all transcripts are shown below:

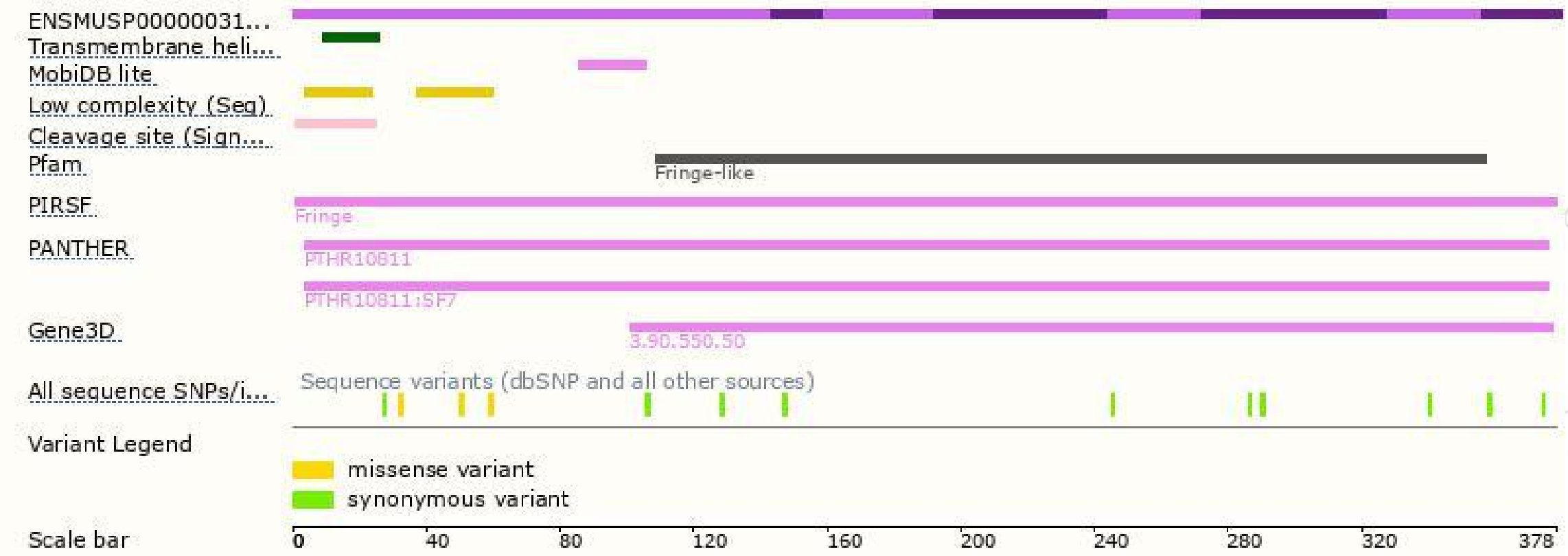
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Lfng-201 | ENSMUST00000031555.2 | 2305 | 378aa | Protein coding | CCDS19821 | B2RRW2 O09010 | TSL:1 GENCODE basic APPRIS P1 |
| Lfng-202 | ENSMUST00000199848.1 | 1074 | No protein | Retained intron | - | - | TSL:1 |
| Lfng-203 | ENSMUST00000200626.4 | 590 | No protein | lncRNA | - | - | TSL:3 |

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

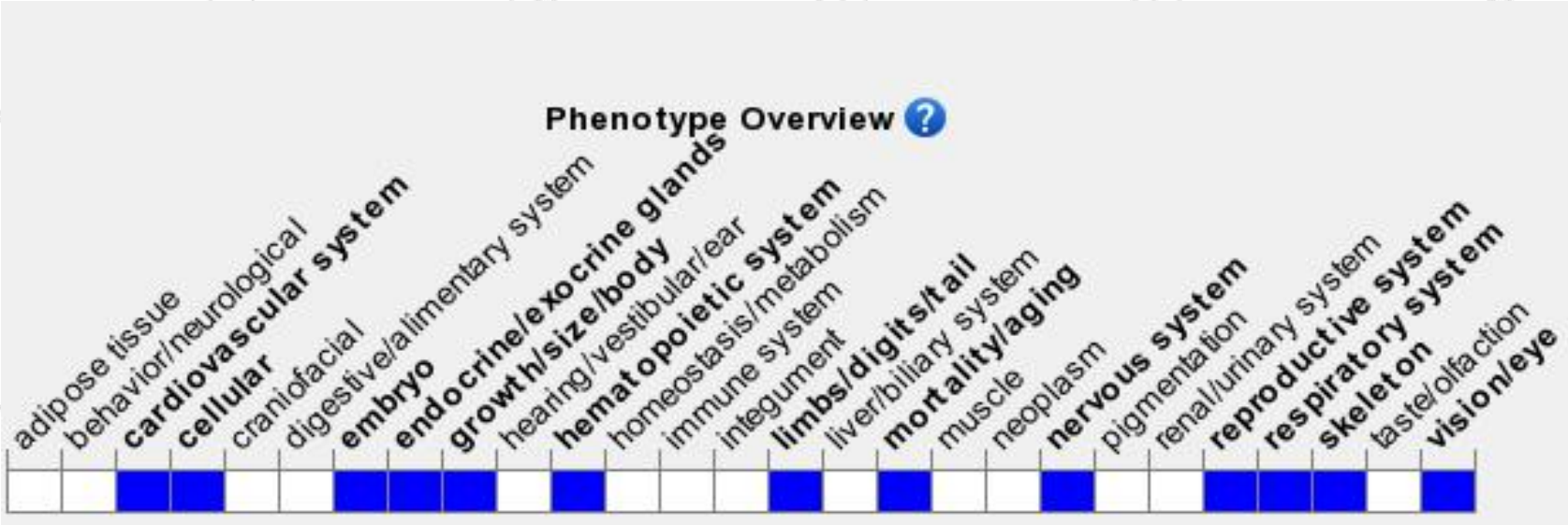
# Genomic location distribution



# 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/).*

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

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