# *Letm1* Cas9-CKO Strategy

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**Reviewer: Miaomiao Cui**

**Design Date: 2021-3-1**

# Project Overview

| | |
|---|---|
| **Project Name** | ***Letm1*** |
| **Project type** | **Cas9-CKO** |
| **Strain background** | **C57BL/6JGpt** |

# Conditional Knockout strategy

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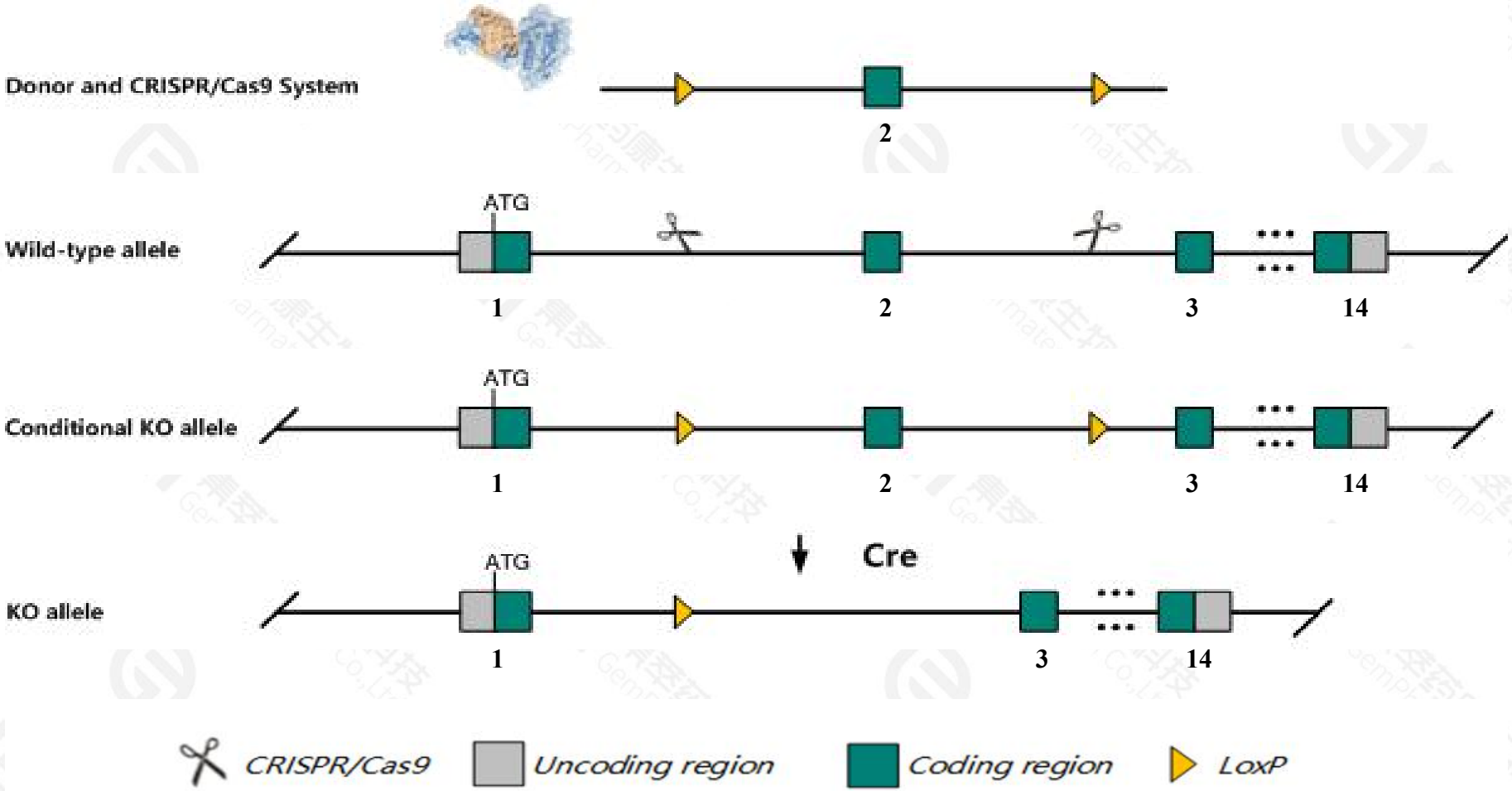
This model will use CRISPR/Cas9 technology to edit the *Letm1* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Letm1* gene has 6 transcripts. According to the structure of *Letm1* gene, exon2 of *Letm1-201*(ENSMUST00000005431.5) transcript is recommended as the knockout region.The region contains 61bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Letm1* 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,homozygous deletion of this gene causes embryonic lethality prior to E6.5 while ~50% of heterozygotes die before E13.5. Surviving heterozygous mice show altered glucose metabolism, impaired control of brain ATP levels, and increased susceptibility to kainic acid-induced seizures.

➢ The *Letm1* 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）

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## Letm1 leucine zipper-EF-hand containing transmembrane protein 1 [Mus musculus (house mouse)]

Gene ID: 56384, updated on 13-Mar-2020

### Summary

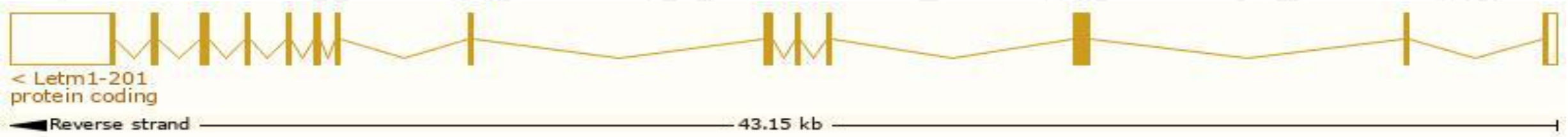
| | |
|---|---|
| **Official Symbol** | Letm1 provided by MGI |
| **Official Full Name** | leucine zipper-EF-hand containing transmembrane protein 1 provided byMGI |
| **Primary source** | MGI:MGI:1932557 |
| **See related** | Ensembl:ENSMUSG00000005299 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Expression** | Ubiquitous expression in duodenum adult (RPKM 18.7), colon adult (RPKM 16.5) and 28 other tissuesSee more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

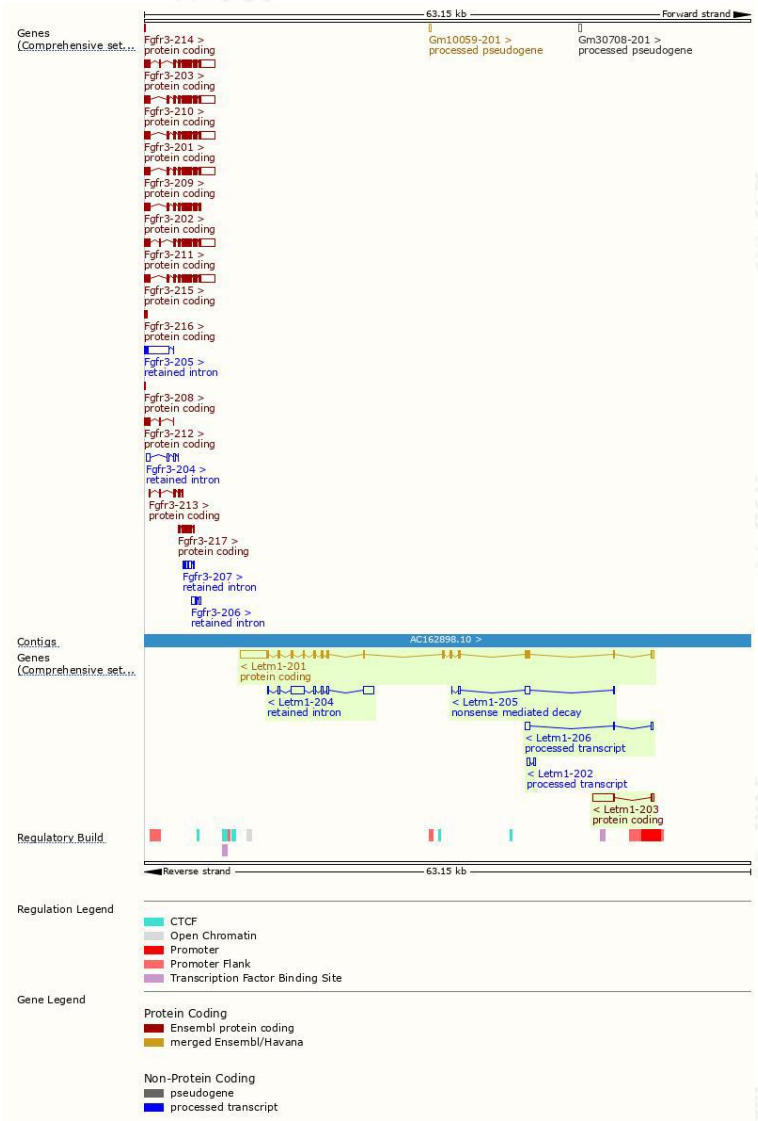
The gene has 6 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| **Letm1-201** | ENSMUST00000005431.5 | 5272 | 738aa | Protein coding | CCDS19207 | Q9Z2I0 | TSL:1 GENCODE basic APPRIS P1 |
| **Letm1-203** | ENSMUST00000148451.1 | 2478 | 47aa | Protein coding | - | A0A0J9YTQ9 | TSL:2 GENCODE basic |
| **Letm1-205** | ENSMUST00000200827.1 | 642 | 13aa | Nonsense mediated decay | - | A0A0J9YV52 | CDS 5' incomplete TSL:5 |
| **Letm1-206** | ENSMUST00000201981.1 | 747 | No protein | Processed transcript | - | - | TSL:3 |
| **Letm1-202** | ENSMUST00000144071.1 | 488 | No protein | Processed transcript | - | - | TSL:2 |
| **Letm1-204** | ENSMUST00000149886.1 | 3056 | No protein | Retained intron | - | - | TSL:1 |

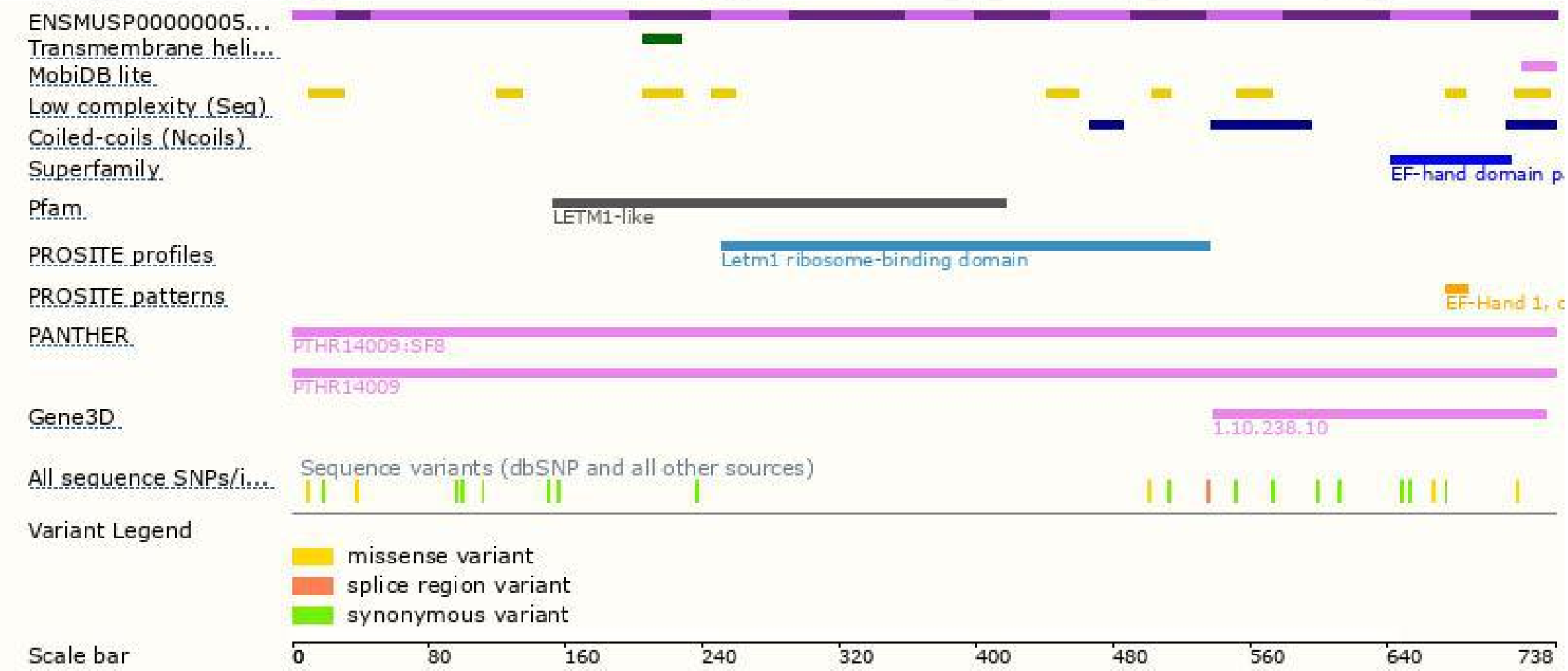
The strategy is based on the design of *Letm1-201* transcript,the transcription is shown below:



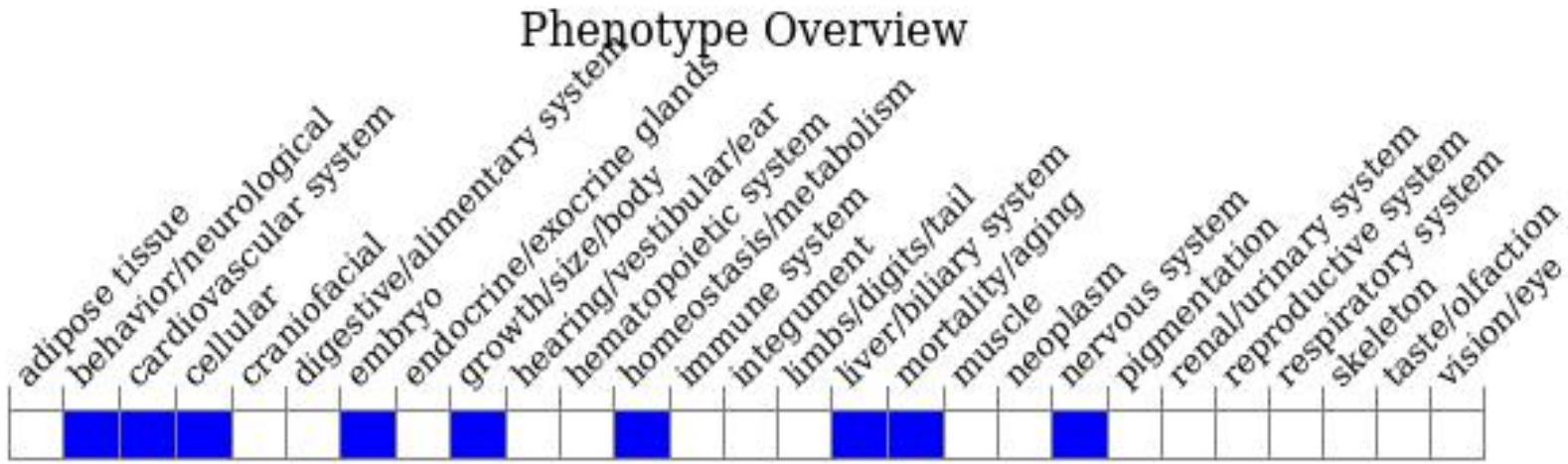
# Genomic location distribution



# 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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