GemPharmatech™

Lamtor1 Cas9-CKO Strategy

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Reviewer: Jia Yu

Design Date: 2023-10-9

Overview

Target Gene Name

- Lamtor1

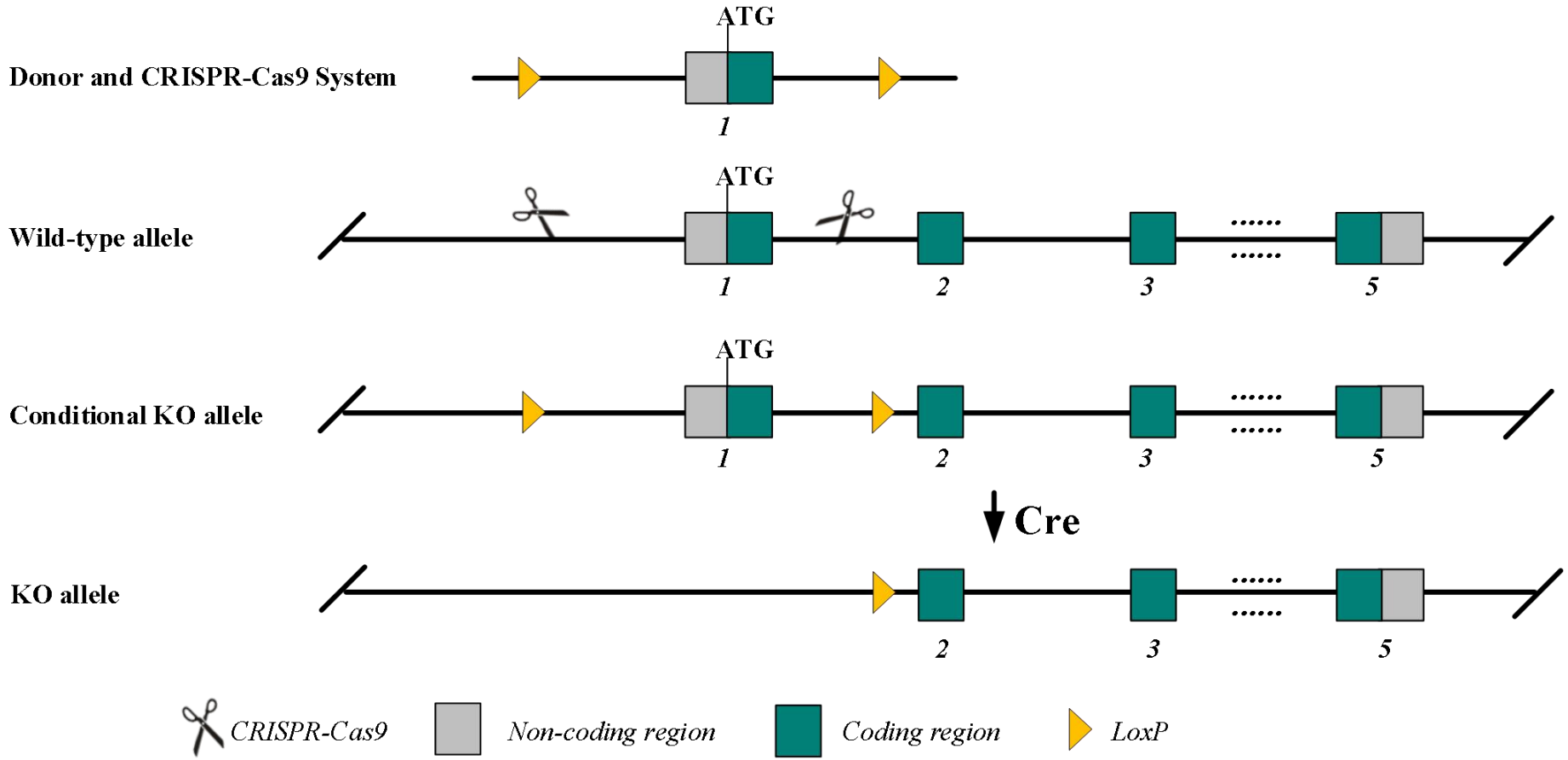
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Lamtor1* gene.

Technical Information

- The *Lamtor1* gene has 3 transcripts. According to the structure of *Lamtor1* gene, exon1 of *Lamtor1*-201 (ENSMUST00000033131.12) transcript is recommended as the knockout region. The region contains ATG of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Lamtor1* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Lamtor1 late endosomal/lysosomal adaptor, MAPK and MTOR activator 1 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 66508, updated on 7-Sep-2023

Summary

Official Symbol	Lamtor1 provided by MGI
Official Full Name	late endosomal/lysosomal adaptor, MAPK and MTOR activator 1 provided by MGI
Primary source	MGI:MGI:1913758
See related	Ensembl:ENSMUSG00000030842 AllianceGenome:MGI:1913758
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	p18; Pdro; 2400001E08Rik
Summary	Predicted to enable GTPase binding activity. Predicted to contribute to guanyl-nucleotide exchange factor activity and molecular adaptor activity. Involved in several processes, including lysosome localization; positive regulation of MAPK cascade; and regulation of receptor recycling. Predicted to be located in late endosome membrane and membrane raft. Predicted to be part of Ragulator complex. Predicted to be active in lysosome. Is expressed in several structures, including adipose tissue; alimentary system; early conceptus; nervous system; and reproductive system. Orthologous to human LAMTOR1 (late endosomal/lysosomal adaptor, MAPK and MTOR activator 1). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in adrenal adult (RPKM 108.3), genital fat pad adult (RPKM 107.5) and 28 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

Genomic context

Location: 7 E2; 7 54.68 cM — See Lamtor1 in Genome Data Viewer

Exon count: 5

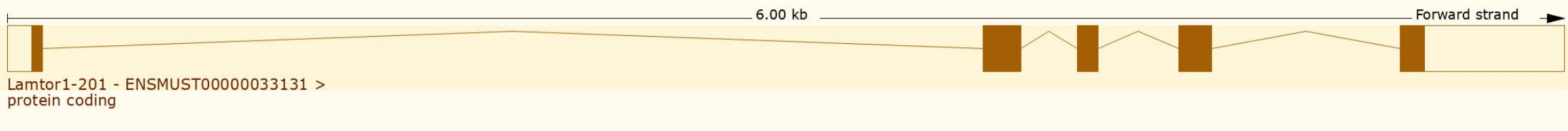
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

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

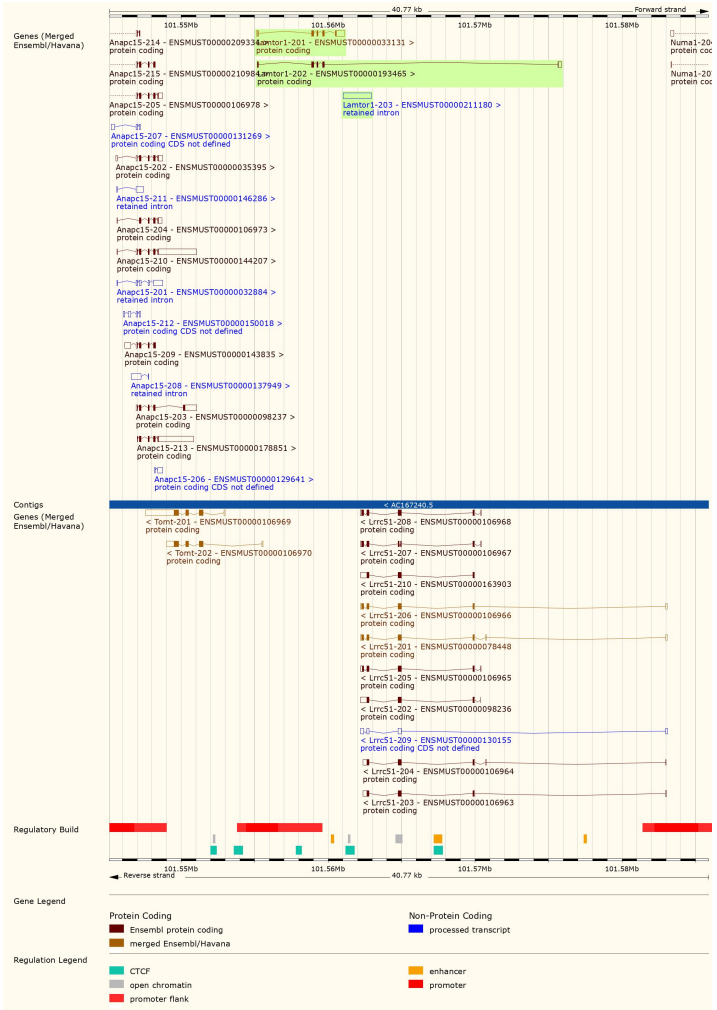
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000033131.12	Lamtor1-201	1119	161aa	Protein coding	CCDS21519	Q9CQ22	Ensembl Canonical, GENCODE basic, APPRIS P1, TSL:1
ENSMUST00000193465.2	Lamtor1-202	661	142aa	Protein coding		A0A0A6YX02	GENCODE basic, TSL:5
ENSMUST00000211180.2	Lamtor1-203	1936	No protein	Retained intron		-	TSL:NA

The strategy is based on the design of *Lamtor1*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org

Genomic Information



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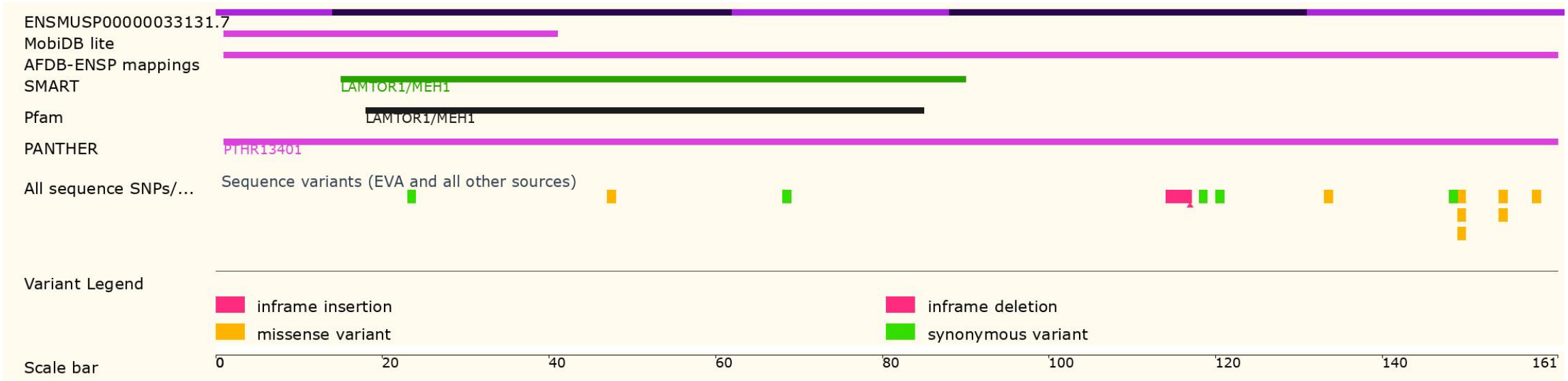
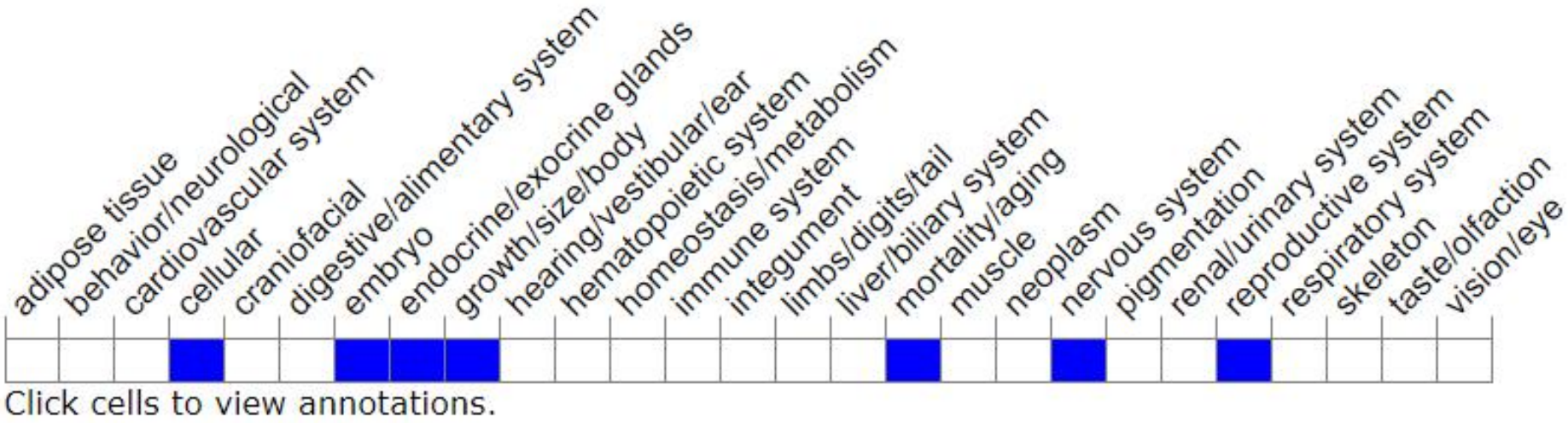
Source: : https://www.ensembl.org

Protein Information



Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Mice homozygous for a knock-out allele exhibit growth arrest and lethality at E7 and abnormal visceral endoderm with abnormal endosome-like organelles and small lysosomes.

Source: https://www.informatics.jax.org

Important Information

- According theMGI data, mice homozygous for a knock-out allele exhibit growth arrest and lethality at E7 and abnormal visceral endoderm with abnormal endosome-like organelles and small lysosomes.
- The effect of *Tomt* and *Anapc15* genes is unknown.
- There is a risk of identifying new ATG to form unknown proteins.
- *Lamtor1* is located on Chr7. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.

Reference

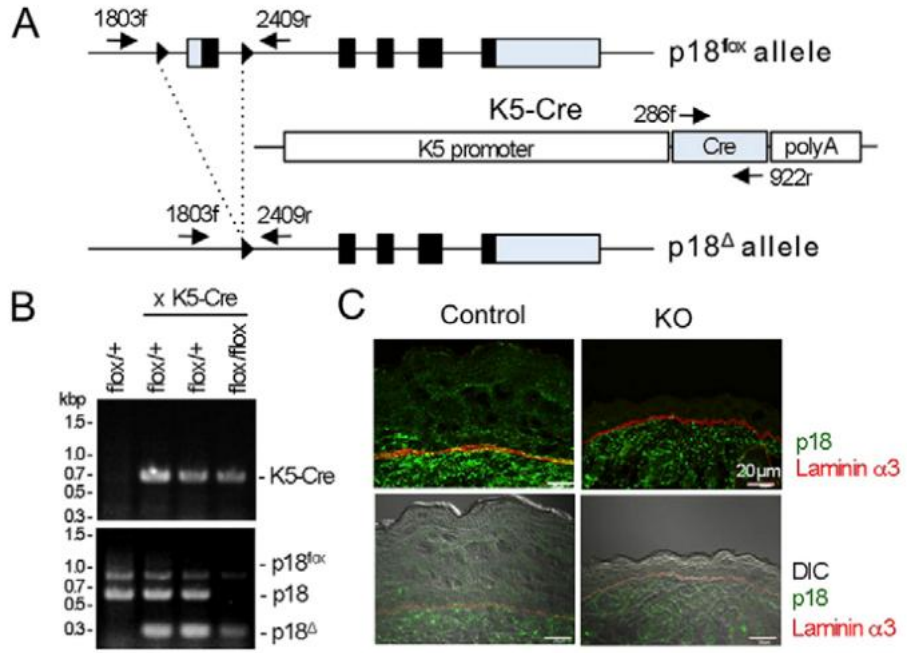


Fig. 1. Ablation of p18 in the epidermis. (**A**) The floxed and deleted *p18* alleles and the K5-Cre transgene construct are shown. Arrows indicate primers for genotyping. (**B**) PCR genotyping of tail DNA from E18.5 $p18^{flox/+}$, K5-Cre $p18^{flox/+}$ and K5-Cre $p18^{flox/flox}$ embryos. (**C**) Immunofluorescence

Reference:The lysosomal signaling anchor p18/LAMTOR1 controls epidermal development by regulating lysosome-mediated catabolic processes.