

Plin1 Cas9-KO Strategy

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Project Overview



Project Name

Plin1

Project type

Cas9-KO

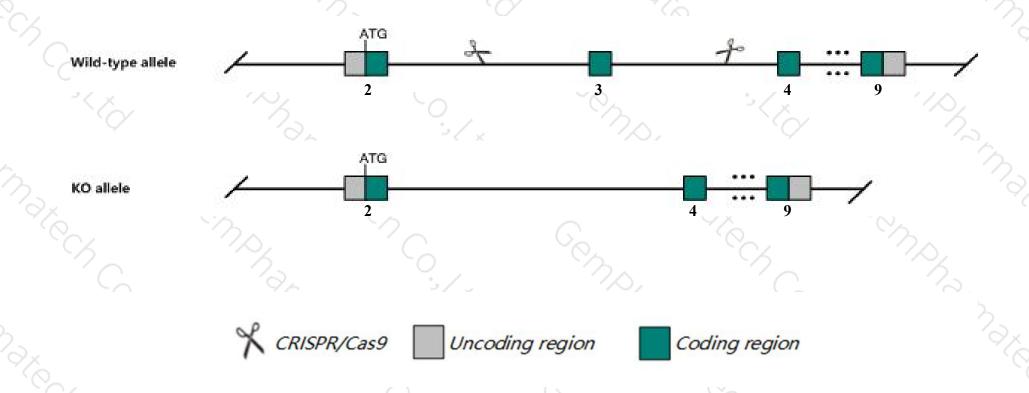
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Plin1* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Plin1* gene has 7 transcripts. According to the structure of *Plin1* gene, exon3 of *Plin1-201*(ENSMUST00000032762.13) transcript is recommended as the knockout region. The region contains 205bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Plin1* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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.

Notice



- ➤ According to the existing MGI data, Homozygous inactivation of this gene leads to increased lean body mass and altered adipocyte lipolysis, leptin production and susceptibility to diet-induced obesity. Increased oxygen and food consumption, impaired cold adaptation, and altered glucose and blood homeostasis have also been observed.
- \triangleright The 5'region of transcript *Plin1-204* is incomplete, so the effect on it is unknown.
- The *Plin1* gene is located on the Chr7. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)



Plin1 perilipin 1 [Mus musculus (house mouse)]

Gene ID: 103968, updated on 5-Mar-2019

Summary

☆ ?

Official Symbol Plin1 provided by MGI

Official Full Name perilipin 1 provided by MGI

Primary source MGI:MGI:1890505

See related Ensembl:ENSMUSG00000030546

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 6030432J05Rik, Peri, Plin

Expression Biased expression in subcutaneous fat pad adult (RPKM 403.0), mammary gland adult (RPKM 366.1) and 4 other tissuesSee more

Orthologs <u>human</u> all

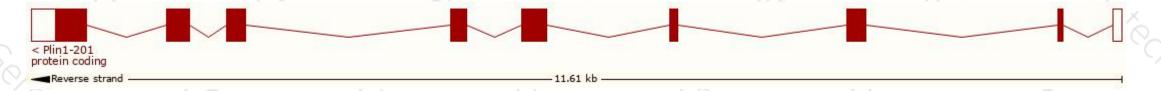
Transcript information (Ensembl)



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

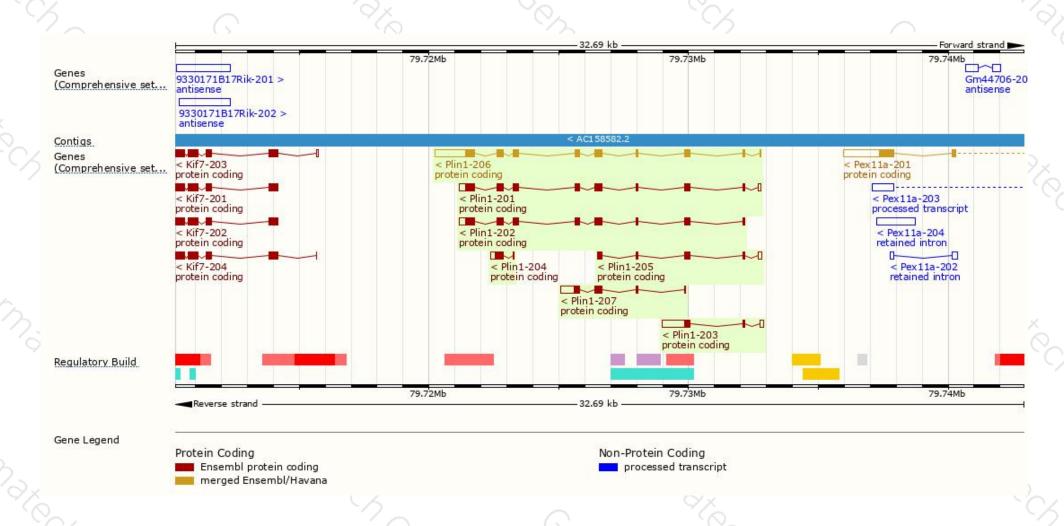
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|-----------------------|------|--------------|----------------|-----------|------------|-------------------------------|
| Plin1-206 | ENSMUST00000205915.1 | 2817 | <u>517aa</u> | Protein coding | CCDS21385 | Q8CGN5 | TSL:1 GENCODE basic APPRIS P1 |
| Plin1-201 | ENSMUST00000032762.13 | 1916 | <u>517aa</u> | Protein coding | CCDS21385 | Q8CGN5 | TSL:5 GENCODE basic APPRIS P1 |
| Plin1-202 | ENSMUST00000178257.2 | 1841 | 517aa | Protein coding | CCDS21385 | Q8CGN5 | TSL:1 GENCODE basic APPRIS P1 |
| Plin1-203 | ENSMUST00000205413.1 | 1294 | <u>87aa</u> | Protein coding | 62 | A0A0U1RNY2 | TSL:1 GENCODE basic |
| Plin1-207 | ENSMUST00000206083.1 | 1082 | <u>190aa</u> | Protein coding | 1.5 | A0A0U1RPJ3 | CDS 5' incomplete TSL:1 |
| Plin1-205 | ENSMUST00000205747.1 | 647 | <u>161aa</u> | Protein coding | - | A0A0U1RQ08 | CDS 3' incomplete TSL:2 |
| Plin1-204 | ENSMUST00000205553.1 | 511 | <u>111aa</u> | Protein coding | ŅL. | A0A0U1RNP7 | CDS 5' incomplete TSL:3 |

The strategy is based on the design of *Plin1-201* transcript, The transcription is shown below



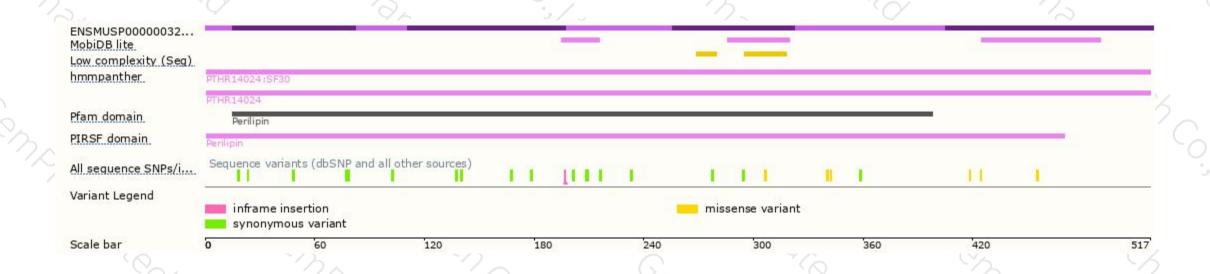
Genomic location distribution





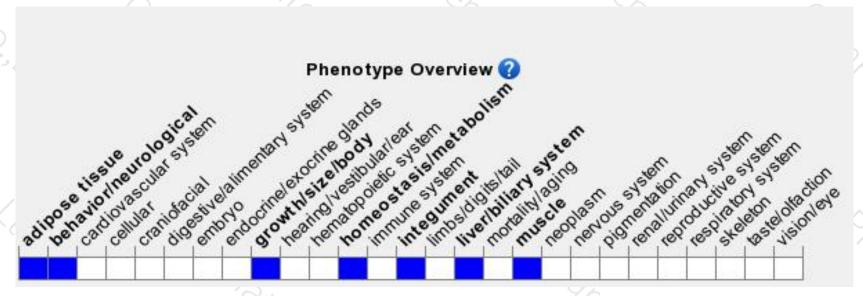
Protein domain





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, Homozygous inactivation of this gene leads to increased lean body mass and altered adipocyte lipolysis, leptin production and susceptibility to diet-induced obesity. Increased oxygen and food consumption, impaired cold adaptation, and altered glucose and blood homeostasis have also been observed.



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





