

Pqlc3 Cas9-CKO Strategy

Designer: Jia Yu

Reviewer: Xiaojing Li

Design Date: 2020-11-12

Project Overview



Project Name Pqlc3

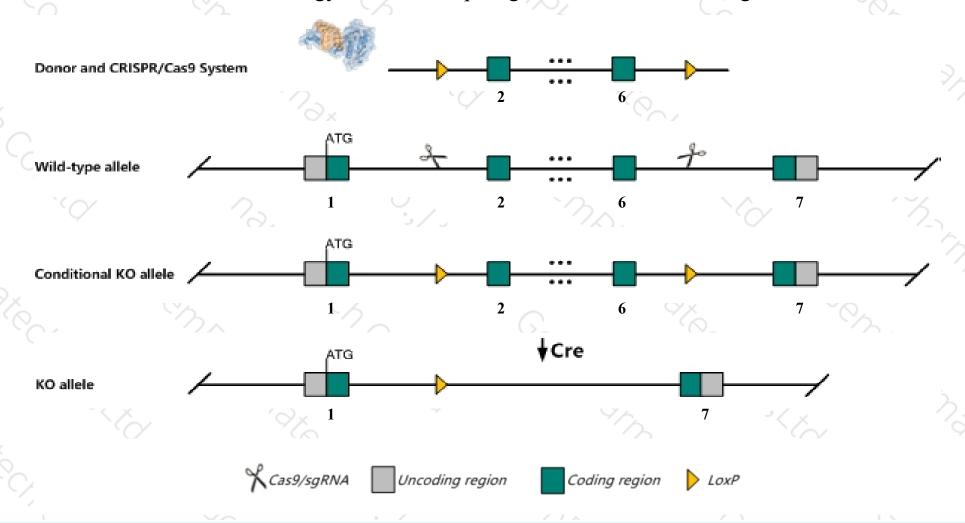
Project type Cas9-CKO

Strain background C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Pqlc3* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Pqlc3* gene has 8 transcripts. According to the structure of *Pqlc3* gene, exon2-exon6 of *Pqlc3*201(ENSMUST00000054536.10) transcript is recommended as the knockout region. The region contains 374bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Pqlc3* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was 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



- > The *Pqlc3* gene is located on the Chr12. 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.
- ➤ Transcript 203,204 CDS 3' incomplete the influences is unknown.
- 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)



Pqlc3 PQ loop repeat containing [Mus musculus (house mouse)]

Gene ID: 217430, updated on 13-Mar-2020

Summary

☆ ?

Official Symbol Pqlc3 provided by MGI

Official Full Name PQ loop repeat containing provided by MGI

Primary source MGI:MGI:2444067

See related Ensembl:ENSMUSG00000045679

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 C78076, E030024M05Rik, Slc66a3

Expression Broad expression in subcutaneous fat pad adult (RPKM 7.3), bladder adult (RPKM 5.8) and 25 other tissuesSee more

Orthologs <u>human</u> <u>all</u>

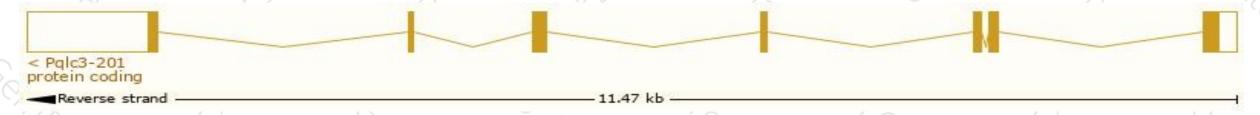
Transcript information (Ensembl)



The gene has 8 transcripts, all transcripts are shown below:

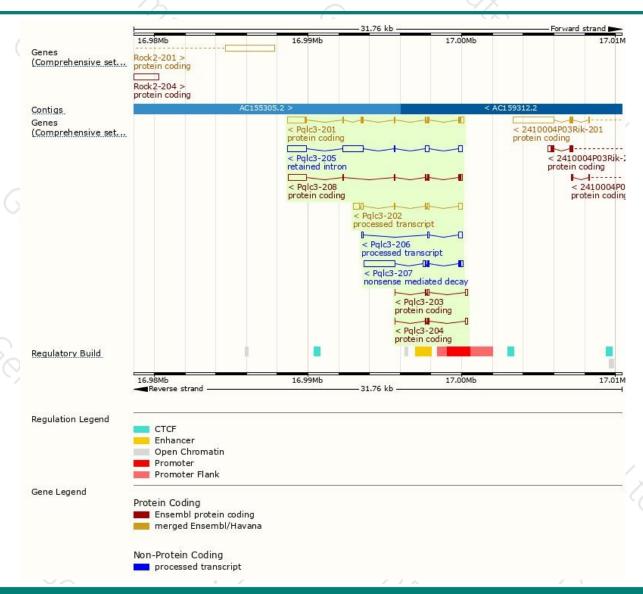
| Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------------------|---|---|---|--|--|---|
| ENSMUST00000054536.10 | 1928 | <u>202aa</u> | Protein coding | CCDS25824 | Q8C6U2 | TSL:1 GENCODE basic APPRIS P1 |
| ENSMUST00000222203.1 | 1706 | <u>120aa</u> | Protein coding | - | A0A1Y7VLY9 | TSL:5 GENCODE basic |
| ENSMUST00000134938.7 | 363 | <u>12aa</u> | Protein coding | - | A0A1Y7VIU4 | CDS 3' incomplete TSL:3 |
| ENSMUST00000137960.1 | 316 | <u>34aa</u> | Protein coding | - | A0A1Y7VMC5 | CDS 3' incomplete TSL:3 |
| ENSMUST00000156360.1 | 2585 | <u>104aa</u> | Nonsense mediated decay | - | <u>Q3UU83</u> | TSL:1 |
| ENSMUST00000067572.12 | 922 | No protein | Processed transcript | - | - | TSL:1 |
| ENSMUST00000141232.7 | 361 | No protein | Processed transcript | - | - | TSL:3 |
| ENSMUST00000140933.1 | 3045 | No protein | Retained intron | - | - | TSL:5 |
| | ENSMUST00000054536.10 ENSMUST00000134938.7 ENSMUST00000137960.1 ENSMUST00000156360.1 ENSMUST00000067572.12 ENSMUST00000141232.7 | ENSMUST00000054536.10 1928 ENSMUST000000222203.1 1706 ENSMUST00000134938.7 363 ENSMUST00000137960.1 316 ENSMUST00000156360.1 2585 ENSMUST00000067572.12 922 ENSMUST000000141232.7 361 | ENSMUST00000054536.10 1928 202aa ENSMUST000000222203.1 1706 120aa ENSMUST00000134938.7 363 12aa ENSMUST00000137960.1 316 34aa ENSMUST00000156360.1 2585 104aa ENSMUST00000067572.12 922 No protein ENSMUST000000141232.7 361 No protein | ENSMUST00000054536.10 1928 202aa Protein coding ENSMUST000000222203.1 1706 120aa Protein coding ENSMUST00000134938.7 363 12aa Protein coding ENSMUST00000137960.1 316 34aa Protein coding ENSMUST00000156360.1 2585 104aa Nonsense mediated decay ENSMUST00000067572.12 922 No protein Processed transcript ENSMUST00000141232.7 361 No protein Processed transcript | ENSMUST00000054536.10 1928 202aa Protein coding CCDS25824 ENSMUST00000222203.1 1706 120aa Protein coding - ENSMUST00000134938.7 363 12aa Protein coding - ENSMUST00000137960.1 316 34aa Protein coding - ENSMUST00000156360.1 2585 104aa Nonsense mediated decay - ENSMUST00000067572.12 922 No protein Processed transcript - ENSMUST000000141232.7 361 No protein Processed transcript - | ENSMUST00000054536.10 1928 202aa Protein coding CCDS25824 Q8C6U2 ENSMUST000000222203.1 1706 120aa Protein coding - A0A1Y7VLY9 ENSMUST00000134938.7 363 12aa Protein coding - A0A1Y7VIU4 ENSMUST00000137960.1 316 34aa Protein coding - A0A1Y7VMC5 ENSMUST000000156360.1 2585 104aa Nonsense mediated decay - Q3UU83 ENSMUST00000067572.12 922 No protein Processed transcript - - ENSMUST000000141232.7 361 No protein Processed transcript - - |

The strategy is based on the design of *Pqlc3-201* transcript, the transcription is shown below:



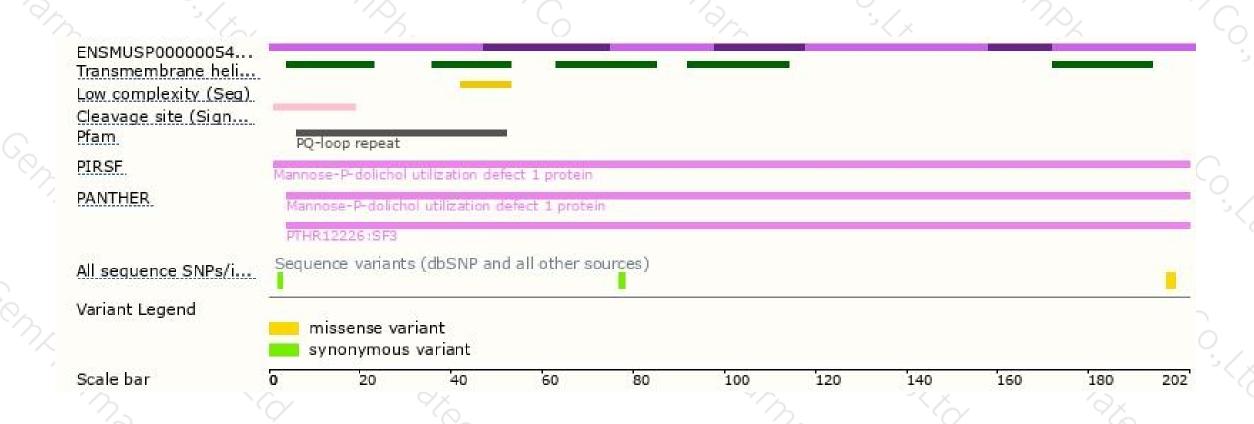
Genomic location distribution





Protein domain







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

Tel: 025-5864 1534





