

Pik3r4 Cas9-KO Strategy

Designer: Longyun Hu

Reviewer: Rui Xiong

Design Date: 2021-5-13

Project Overview

Project Name

Pik3r4

Project type

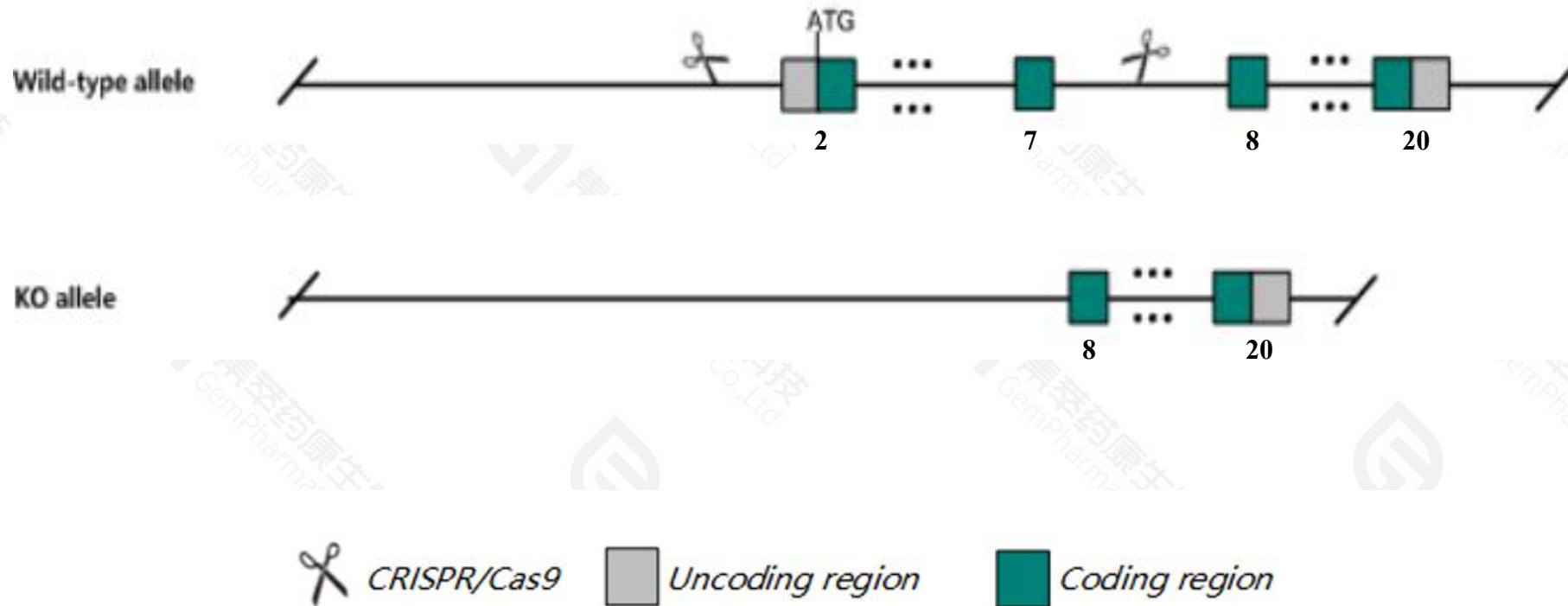
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pik3r4* gene. The schematic diagram is as follows:



- The *Pik3r4* gene has 11 transcripts. According to the structure of *Pik3r4* gene, exon2-exon7 of *Pik3r4-210*(ENSMUST00000191268.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pik3r4* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit early embryonic lethality before E7.5. Mice homozygous for a conditional allele activated in muscles exhibit symptoms of autophagic vacuolar myopathies.
- The *Pik3r4* gene is located on the Chr9. 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.

Pik3r4 phosphoinositide-3-kinase regulatory subunit 4 [Mus musculus (house mouse)]

Gene ID: 75669, updated on 26-Jan-2021

Summary



Official Symbol Pik3r4 provided by [MGI](#)

Official Full Name phosphoinositide-3-kinase regulatory subunit 4 provided by [MGI](#)

Primary source [MGI:MGI:1922919](#)

See related [Ensembl:ENSMUSG00000032571](#)

Gene type protein coding

RefSeq status PROVISIONAL

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 2210010O15Rik, C730038E05Rik, C85833, D9Ertd418e, Vp, Vps15, p15, p150

Expression Ubiquitous expression in ovary adult (RPKM 8.1), spleen adult (RPKM 7.8) and 28 other tissues [See more](#)

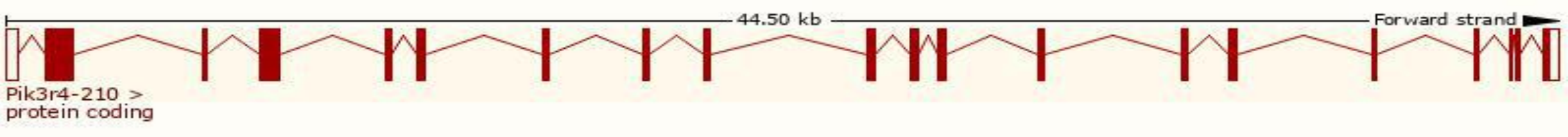
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

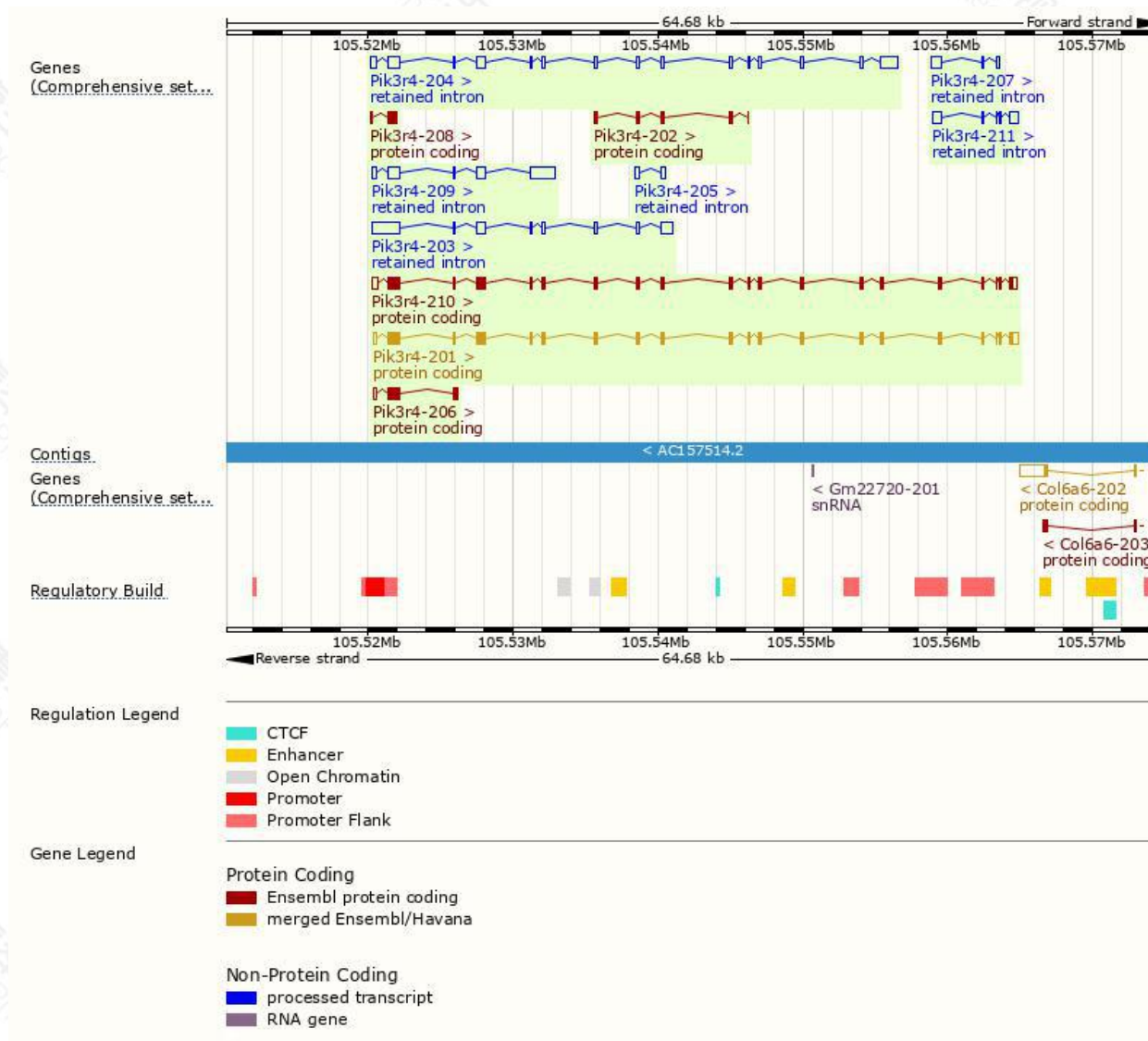
The gene has 11 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------------|---------------------------------------|------|------------------------|-----------------|---------------------------|---------|-------------------------------------|
| Pik3r4-210 | ENSMUST00000191268.7 | 4756 | 1358aa | Protein coding | CCDS40753 | | TSL:1 , GENCODE basic , APPRIS P1 , |
| Pik3r4-201 | ENSMUST00000065778.13 | 4711 | 1358aa | Protein coding | CCDS40753 | | TSL:1 , GENCODE basic , APPRIS P1 , |
| Pik3r4-206 | ENSMUST00000188784.2 | 1295 | 305aa | Protein coding | - | | TSL:1 , GENCODE basic , |
| Pik3r4-202 | ENSMUST00000186943.2 | 770 | 208aa | Protein coding | - | | CDS 3' incomplete , TSL:5 , |
| Pik3r4-208 | ENSMUST00000190358.2 | 611 | 174aa | Protein coding | - | | CDS 3' incomplete , TSL:2 , |
| Pik3r4-204 | ENSMUST00000187573.7 | 4929 | No protein | Retained intron | - | | TSL:1 , |
| Pik3r4-203 | ENSMUST00000187446.2 | 4124 | No protein | Retained intron | - | | TSL:1 , |
| Pik3r4-209 | ENSMUST00000191117.7 | 3613 | No protein | Retained intron | - | | TSL:1 , |
| Pik3r4-211 | ENSMUST00000214254.2 | 1358 | No protein | Retained intron | - | | TSL:1 , |
| Pik3r4-207 | ENSMUST00000189691.2 | 969 | No protein | Retained intron | - | | TSL:2 , |
| Pik3r4-205 | ENSMUST00000188385.2 | 634 | No protein | Retained intron | - | | TSL:3 , |

The strategy is based on the design of *Pik3r4-210* transcript,the transcription is shown below:



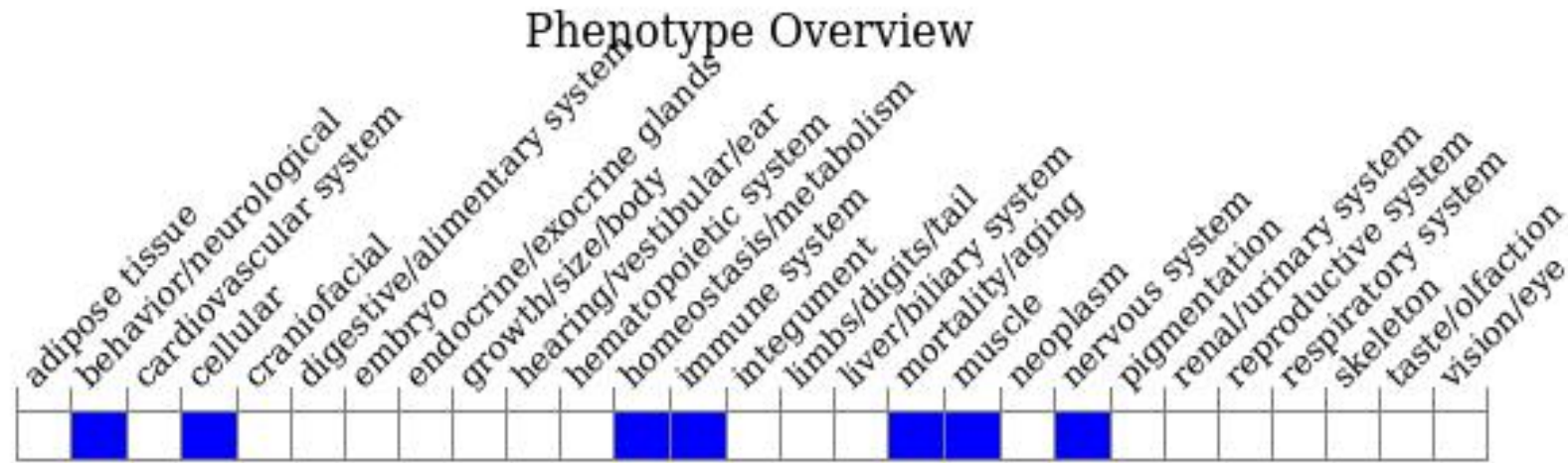
Genomic location distribution



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, mice homozygous for a knock-out allele exhibit early embryonic lethality before E7.5. Mice homozygous for a conditional allele activated in muscles exhibit symptoms of autophagic vacuolar myopathies.

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

