

Pik3r2 Cas9-KO Strategy

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Project Overview



Project Name

Pik3r2

Project type

Cas9-KO

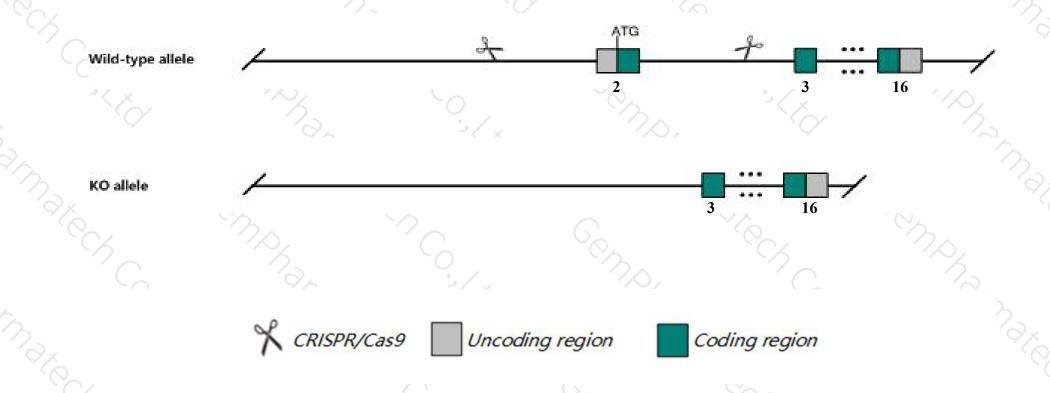
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Pik3r2* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Pik3r2* gene has 6 transcripts. According to the structure of *Pik3r2* gene, exon2 of *Pik3r2-201*(ENSMUST00000034296.14) 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 *Pik3r2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- ➤ According to the existing MGI data, Mice homozygous for disruptions in this gene have lower blood glucose levels both when fed and after fasting. Insulin sensitivity is improved as well.
- > There is a risk of recognizing a new ATG to form an unknown protein after knocking out ATG.
- > Transcripts 203, 204, 205 may not be affected.
- > The knockout region is about 1.3 kb away from the 5th end of the 2010320M18Rik gene, which may affect the 5-terminal regulation of the gene.
- The *Pik3r2* gene is located on the Chr8. 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)



Pik3r2 phosphoinositide-3-kinase regulatory subunit 2 [Mus musculus (house mouse)]

Gene ID: 18709, updated on 12-Aug-2019

Summary

☆ ?

Official Symbol Pik3r2 provided by MGI

Official Full Name phosphoinositide-3-kinase regulatory subunit 2 provided by MGI

Primary source MGI:MGI:1098772

See related Ensembl: ENSMUSG00000031834

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 p85beta

Expression Ubiquitous expression in ovary adult (RPKM 65.5), duodenum adult (RPKM 57.1) and 28 other tissues See more

Orthologs human all

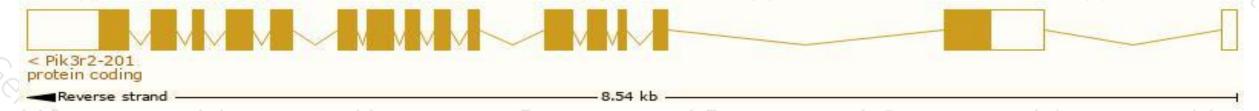
Transcript information (Ensembl)



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

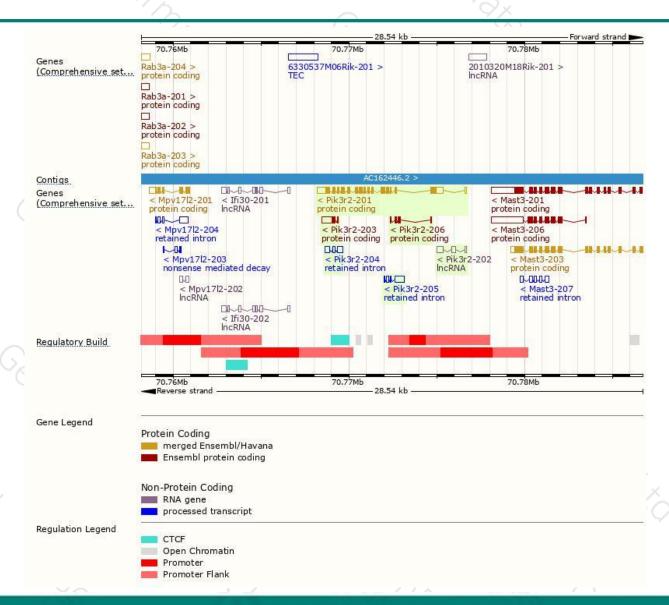
	T.		7	1 / / /			
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pik3r2-201	ENSMUST00000034296.14	3165	722aa	Protein coding	CCDS22381	008908	TSL:1 GENCODE basic APPRIS P1
Pik3r2-203	ENSMUST00000143785.1	813	<u>71aa</u>	Protein coding		F7CB91	CDS 5' incomplete TSL:3
Pik3r2-206	ENSMUST00000154685.1	250	<u>84aa</u>	Protein coding	9	F6R2V5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:
Pik3r2-202	ENSMUST00000142370.1	626	No protein	Processed transcript	2	100	TSL:3
Pik3r2-205	ENSMUST00000152545.1	783	No protein	Retained intron		1751	TSL:5
Pik3r2-204	ENSMUST00000146707.1	746	No protein	Retained intron			TSL:2
7.					1	/	

The strategy is based on the design of *Pik3r2-201* transcript, The transcription is shown below



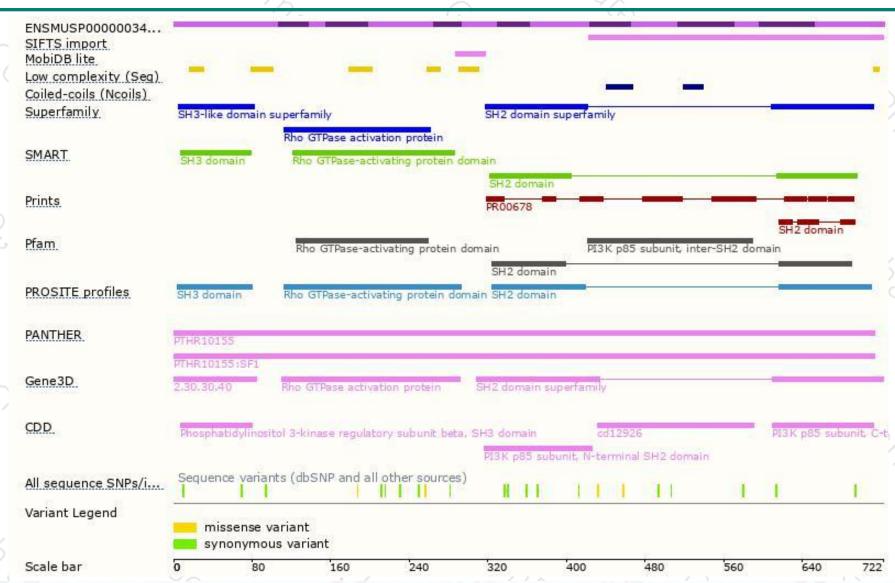
Genomic location distribution





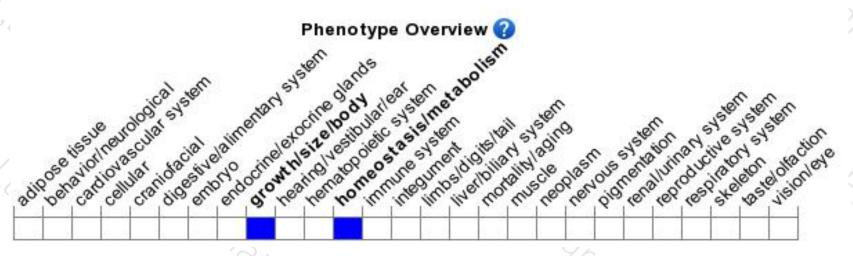
Protein domain





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, Mice homozygous for disruptions in this gene have lower blood glucose levels both when fed and after fasting. Insulin sensitivity is improved as well.



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





