

Grk5 Cas9-KO Strategy

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Project Overview



Project Name

Grk5

Project type

Cas9-KO

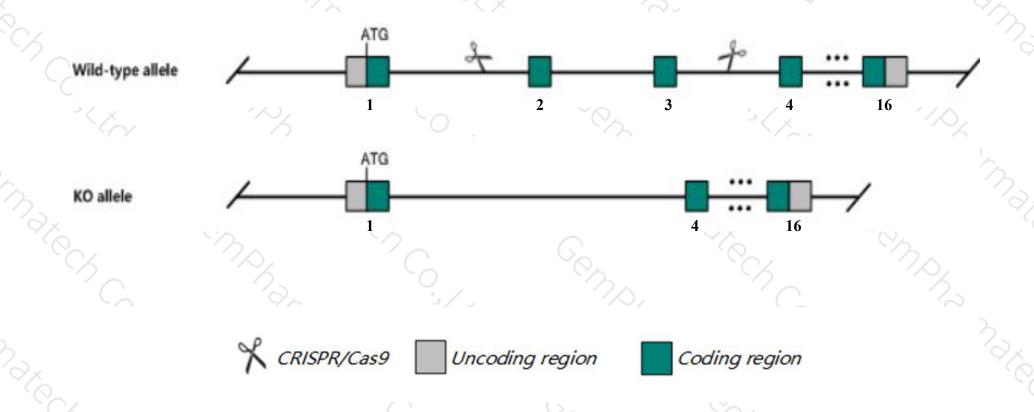
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Grk5* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Grk5* gene has 3 transcripts. According to the structure of *Grk5* gene, exon2-exon3 of *Grk5-201* (ENSMUST0000003313.9) transcript is recommended as the knockout region. The region contains 209bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Grk5* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- ➤ According to the existing MGI data, homozygous mutation of this gene results in a decrease in thermal pain sensation. mice homozygous for a knock-out allele exhibit decreased response of heart to induced stress.
- > *Gm22520* will be deleted.
- The *Grk5* gene is located on the Chr19. 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)



Grk5 G protein-coupled receptor kinase 5 [Mus musculus (house mouse)]

Gene ID: 14773, updated on 13-Mar-2020

Summary

☆ ?

Official Symbol Grk5 provided by MGI

Official Full Name G protein-coupled receptor kinase 5 provided by MGI

Primary source MGI:MGI:109161

See related Ensembl: ENSMUSG00000003228

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 Gprk5

Expression Ubiquitous expression in lung adult (RPKM 3.7), subcutaneous fat pad adult (RPKM 2.5) and 28 other tissuesSee more

Orthologs <u>human all</u>

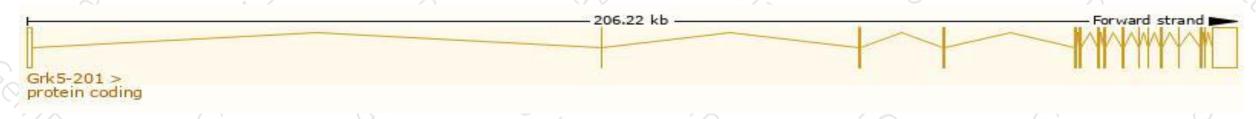
Transcript information (Ensembl)



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

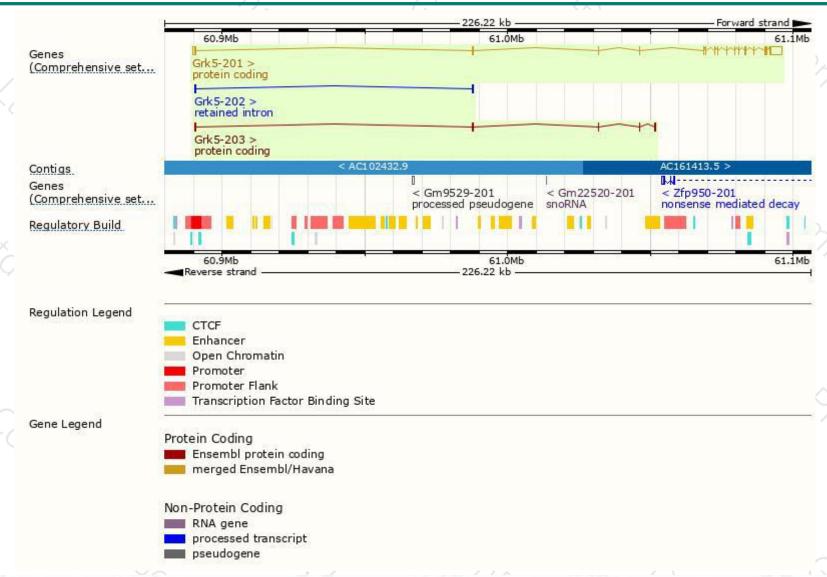
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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Grk5-201	ENSMUST00000003313.9	6580	590aa	Protein coding	CCDS29945	Q3TST4 Q8VEB1	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Grk5-203	ENSMUST00000236876.1	634	<u>125aa</u>	Protein coding	-	A0A494B9K8	GENCODE basic
Grk5-202	ENSMUST00000235623.1	568	No protein	Retained intron	12	928	

The strategy is based on the design of *Grk5-201* transcript, the transcription is shown below:



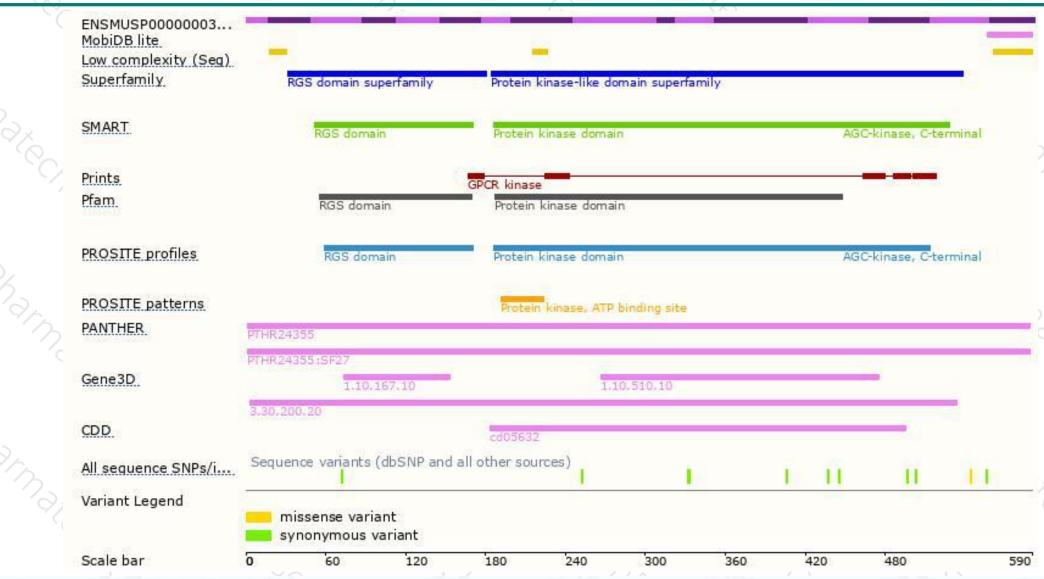
Genomic location distribution





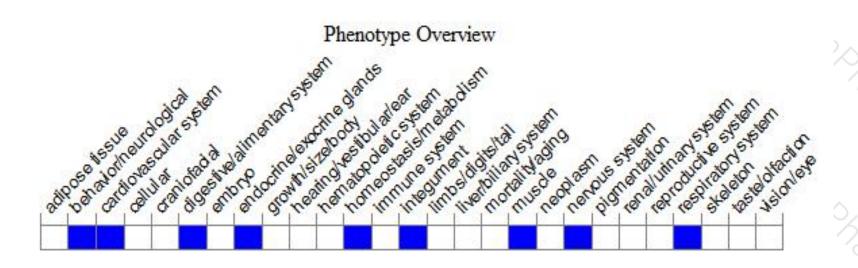
Protein domain





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 mutation of this gene results in a decrease in thermal pain sensation. Mice homozygous for a knock-out allele exhibit decreased response of heart to induced stress.



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





