

Kcne3 Cas9-KO Strategy

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Project Overview



Project Name

Kcne3

Project type

Cas9-KO

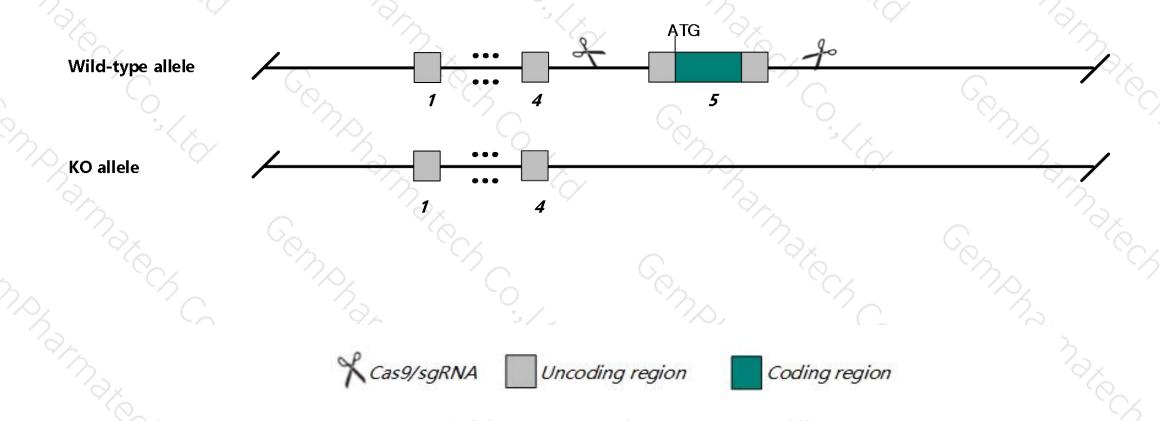
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Kcne3* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Kcne3* gene has 8 transcripts. According to the structure of *Kcne3* gene, exon5 of *Kcne3-203* (ENSMUST00000178946.8) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Kcne3* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased cAMP-stimulated electrogenic Cl- secretion across tracheal and intestinal epithelia. Another knock-out allele shows age-dependent alterations in action potential and firing properties of spiral ganglion neurons in the cochlea.
- ➤ The flox region is in the intron of the Gm34821 gene, which may affect the regulation of this gene.
- The *Kcne3* 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)



Kcne3 potassium voltage-gated channel, lsk-related subfamily, gene 3 [Mus musculus (house mouse)]

Gene ID: 57442, updated on 24-Oct-2019

Summary

☆ ?

Official Symbol Kcne3 provided by MGI

Official Full Name potassium voltage-gated channel, lsk-related subfamily, gene 3 provided by MGI

Primary source MGI:MGI:1891124

See related Ensembl: ENSMUSG00000035165

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 MiRP2: 2210017H05Rik

Expression Biased expression in colon adult (RPKM 22.2), testis adult (RPKM 22.1) and 7 other tissues See more

Orthologs human all

Transcript information (Ensembl)



The gene has 8 transcript, and the transcript is shown below:

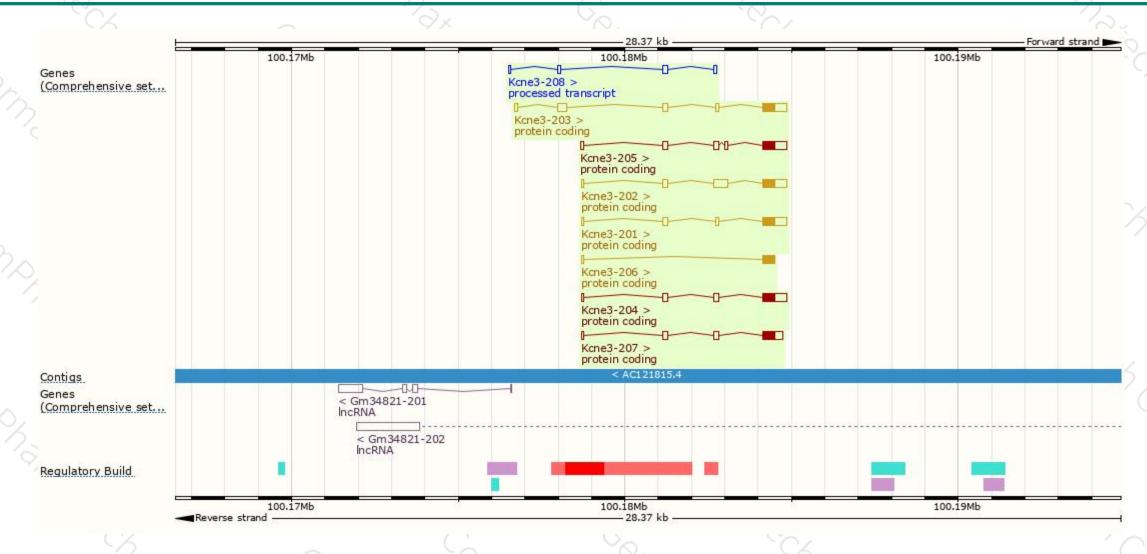
| Name | Transcript ID . | bp 🛊 | Protein 4 | Biotype | CCDS 🍦 | UniProt 4 | Flags |
|-----------|-----------------------|------|--------------|----------------------|------------|-----------------|-------------------------------|
| Kcne3-203 | ENSMUST00000178946.8 | 1323 | <u>103aa</u> | Protein coding | CCDS21495₽ | Q545H9& Q9WTW2& | TSL:1 GENCODE basic APPRIS P1 |
| Kcne3-202 | ENSMUST00000170954.9 | 1315 | 103aa | Protein coding | CCDS21495@ | Q545H9@Q9WTW2@ | TSL:1 GENCODE basic APPRIS P1 |
| Kcne3-205 | ENSMUST00000207358.1 | 1154 | 103aa | Protein coding | CCDS21495@ | Q545H9@Q9WTW2@ | TSL:5 GENCODE basic APPRIS P1 |
| Kcne3-204 | ENSMUST00000179842.2 | 1059 | 103aa | Protein coding | CCDS21495@ | Q545H9@Q9WTW2@ | TSL:1 GENCODE basic APPRIS P1 |
| Kcne3-201 | ENSMUST00000049333.12 | 1012 | <u>103aa</u> | Protein coding | CCDS21495@ | Q545H9@Q9WTW2@ | TSL:1 GENCODE basic APPRIS P1 |
| Kcne3-207 | ENSMUST00000208260.1 | 929 | 103aa | Protein coding | CCDS21495@ | Q545H9@Q9WTW2@ | TSL:3 GENCODE basic APPRIS P1 |
| Kcne3-206 | ENSMUST00000207995.1 | 439 | 103aa | Protein coding | CCDS21495@ | Q545H9@Q9WTW2@ | TSL:2 GENCODE basic APPRIS P1 |
| Kcne3-208 | ENSMUST00000208555.1 | 374 | No protein | Processed transcript | | | TSL:3 |
| | | | | | | | |

The strategy is based on the design of Kcne3-203 transcript, The transcription is shown below



Genomic location distribution





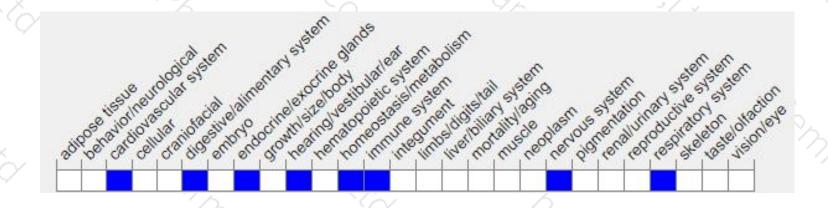
Protein domain





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 decreased cAMP-stimulated electrogenic Cl- secretion across tracheal and intestinal epithelia. Another knock-out allele shows age-dependent alterations in action potential and firing properties of spiral ganglion neurons in the cochlea.



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





