

Kcnk4 Cas9-KO Strategy

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Project Overview



Project Name

Kcnk4

Project type

Cas9-KO

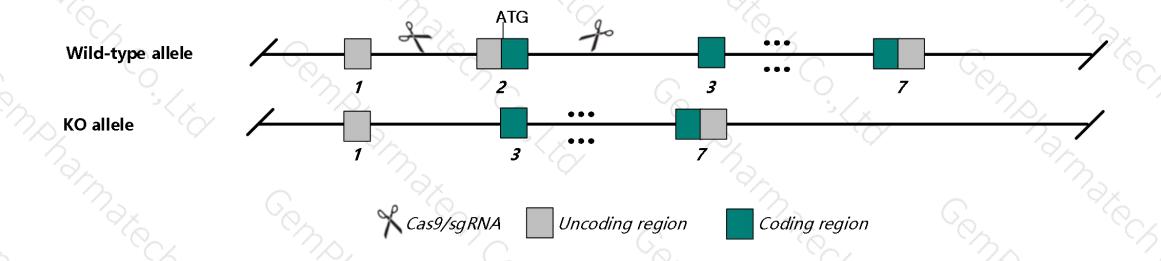
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Kcnk4 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Kcnk4* gene has 7 transcripts. According to the structure of *Kcnk4* gene, exon2 of *Kcnk4-201*(ENSMUST00000025908.7) 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 *Kcnk4* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > According to the existing MGI data, Mice homozygous for a null allele exhibit normal sensitivity to pharmacologically induced seizures.
- The Kcnk4 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)



Kcnk4 potassium channel, subfamily K, member 4 [Mus musculus (house mouse)]

Gene ID: 16528, updated on 13-Mar-2020

Summary

△ ?

Official Symbol Kcnk4 provided by MGI

Official Full Name potassium channel, subfamily K, member 4 provided by MGI

Primary source MGI:MGI:1298234

See related Ensembl: ENSMUSG00000024957

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 TRAAK; Tex40; TRAAKt; MLZ-622; Catsperz

Expression Biased expression in testis adult (RPKM 71.0) and cortex adult (RPKM 5.7) See more

Orthologs human all

Transcript information (Ensembl)



The gene has 7 transcripts, and the transcript is shown below:

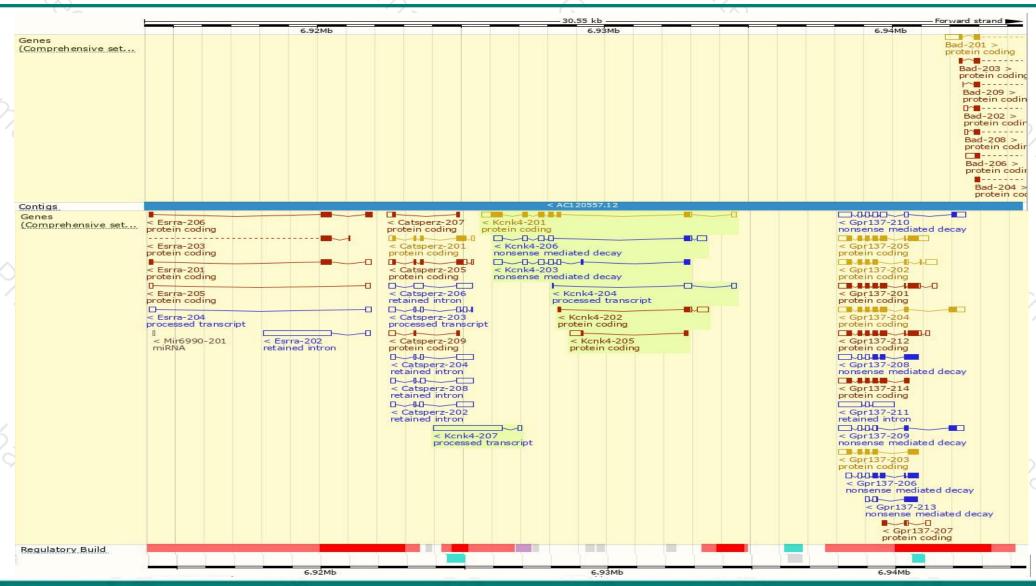
Name &	Transcript ID	bp 🌢	Protein &	Biotype	CCDS .	UniProt	Flags
Kcnk4-201	ENSMUST00000025908.7	1763	<u>398aa</u>	Protein coding	CCDS29511 ₺	<u>088454₽ Q0VD85</u> ₽	TSL:1 GENCODE basic APPRIS P1
Kcnk4-202	ENSMUST00000235248.1	780	<u>99aa</u>	Protein coding	-	<u>A0A494BA57</u> ₽	CDS 3' incomplete
Kcnk4-205	ENSMUST00000236443.1	600	<u>64aa</u>	Protein coding	- 5	A0A494B9F1 ₢	CDS 5' incomplete
Kcnk4-206	ENSMUST00000237484.1	1387	<u>67aa</u>	Nonsense mediated decay	- 5	<u>O88454</u> ₽	5
Kcnk4-203	ENSMUST00000235279.1	1175	<u>81aa</u>	Nonsense mediated decay	- 54	<u>A0A494B9Y6</u> ₽	CDS 5' incomplete
Kcnk4-207	ENSMUST00000237766.1	2537	No protein	Processed transcript	- 5	29	5
Kcnk4-204	ENSMUST00000235836.1	493	No protein	Processed transcript	- 5	79	5

The strategy is based on the design of Kcnk4-201 transcript, The transcription is shown below



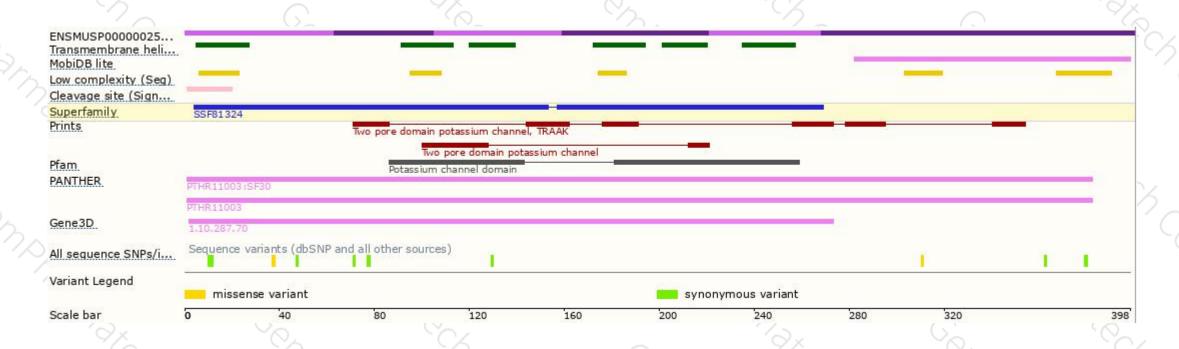
Genomic location distribution





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 a null allele exhibit normal sensitivity to pharmacologically induced seizures.



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





