

Kcnc2 Cas9-KO Strategy

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Project Overview

Project Name

Kcnc2

Project type

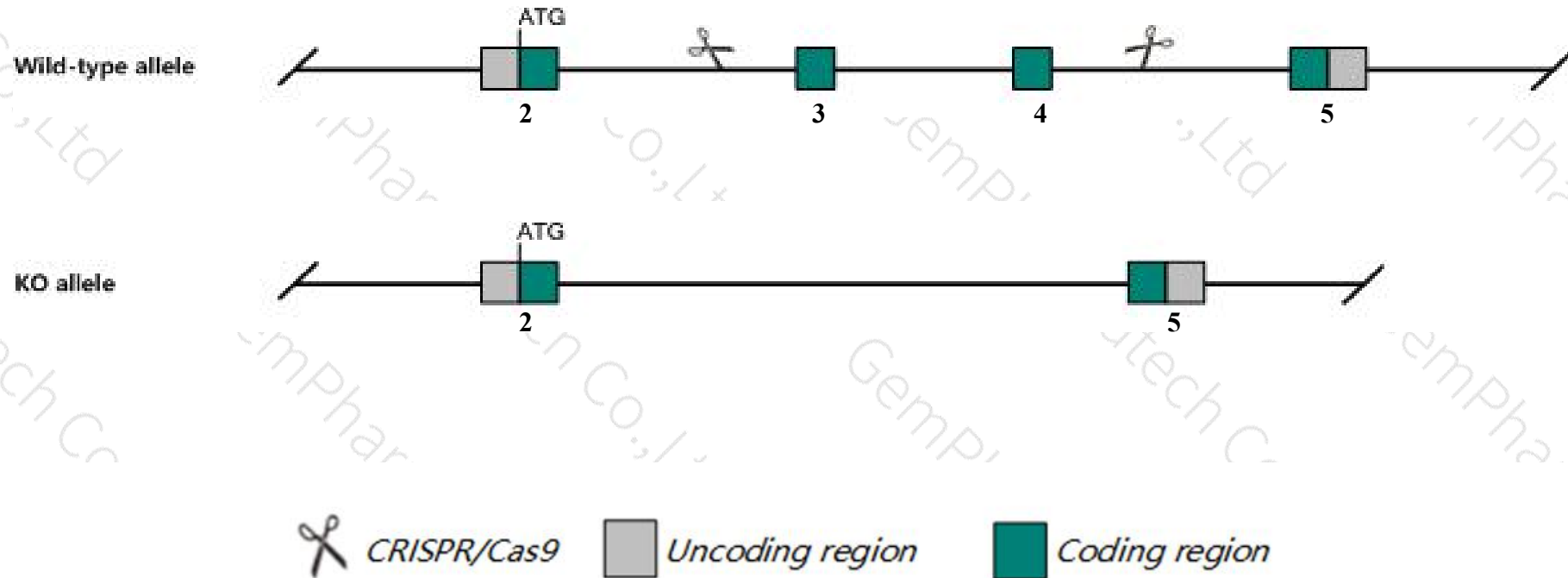
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnc2* gene. The schematic diagram is as follows:



- The *Kcnc2* gene has 5 transcripts. According to the structure of *Kcnc2* gene, exon3-exon4 of *Kcnc2-204* (ENSMUST00000219301.1) transcript is recommended as the knockout region. The region contains 1093bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnc2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele display impaired fast spiking in cortical interneurons, distorted cortical rhythmic activity, enhanced susceptibility to seizures, increased anxiety in the open field, and abnormal sleep patterns.
- The *Kcnc2* gene is located on the Chr10. 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)

Kcnc2 potassium voltage gated channel, Shaw-related subfamily, member 2 [Mus musculus (house mouse)]

Gene ID: 268345, updated on 31-Jan-2019

Summary



Official Symbol	Kcnc2 provided by MGI
Official Full Name	potassium voltage gated channel, Shaw-related subfamily, member 2 provided by MGI
Primary source	MGI:MGI:96668
See related	Ensembl:ENSMUSG00000035681
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	AW047325, B230117I07, KShIIIA, Kv3.2
Expression	Biased expression in cortex adult (RPKM 4.9), frontal lobe adult (RPKM 4.5) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

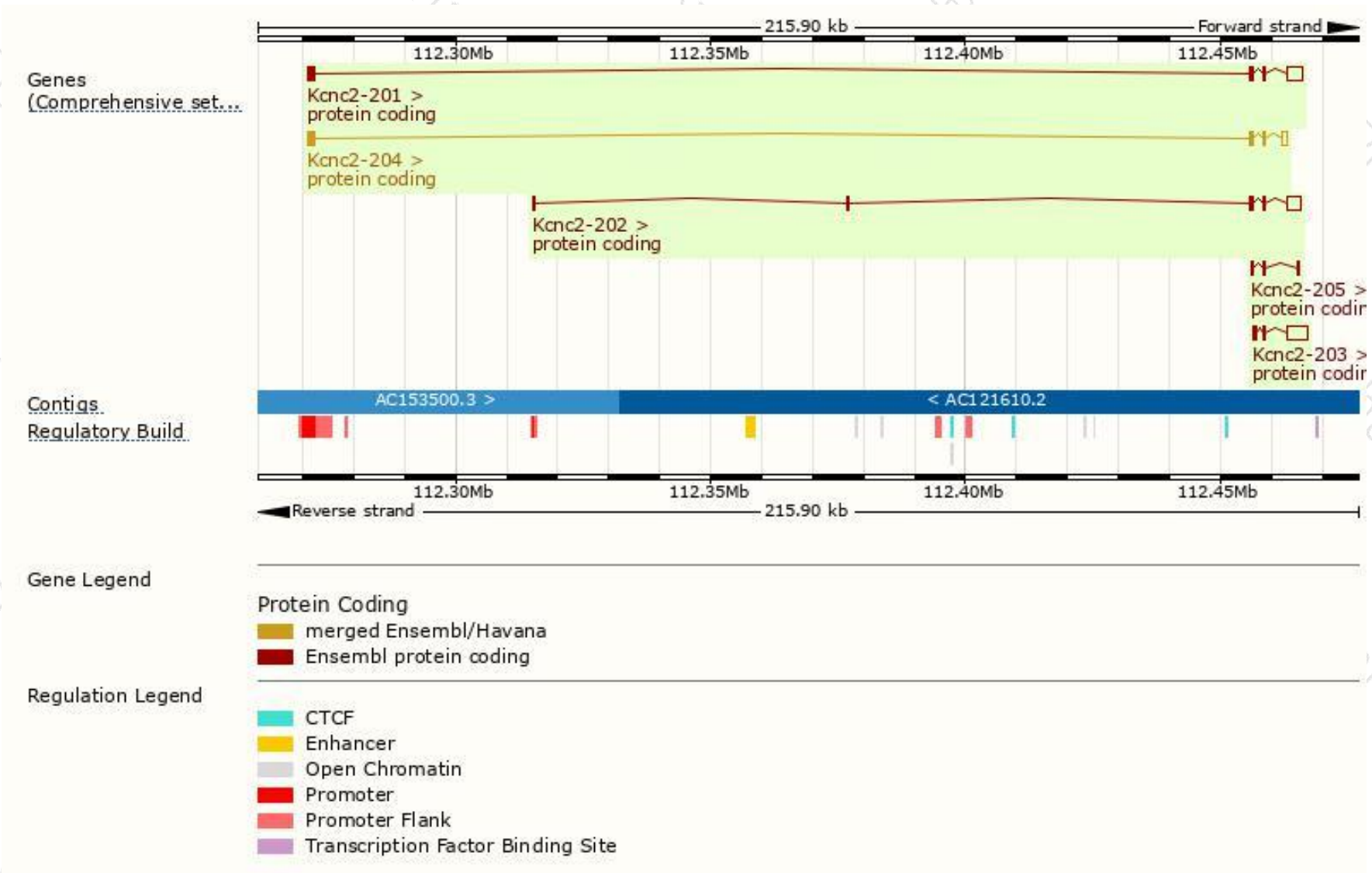
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnc2-204	ENSMUST00000219301.1	2944	639aa	Protein coding	CCDS24173	A0A1W2P796	TSL:1 GENCODE basic APPRIS P2
Kcnc2-201	ENSMUST00000092175.3	5046	642aa	Protein coding	-	E9QLW0 Q14B80	TSL:1 GENCODE basic APPRIS ALT2
Kcnc2-203	ENSMUST00000218827.1	4370	138aa	Protein coding	-	A0A1W2P8A0	CDS 5' incomplete TSL:1
Kcnc2-202	ENSMUST00000218445.1	4033	240aa	Protein coding	-	A0A1W2P7B9	TSL:1 GENCODE basic
Kcnc2-205	ENSMUST00000219607.1	596	198aa	Protein coding	-	A0A1W2P808	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3

The strategy is based on the design of *Kcnc2-204* transcript,The transcription is shown below



Genomic location distribution



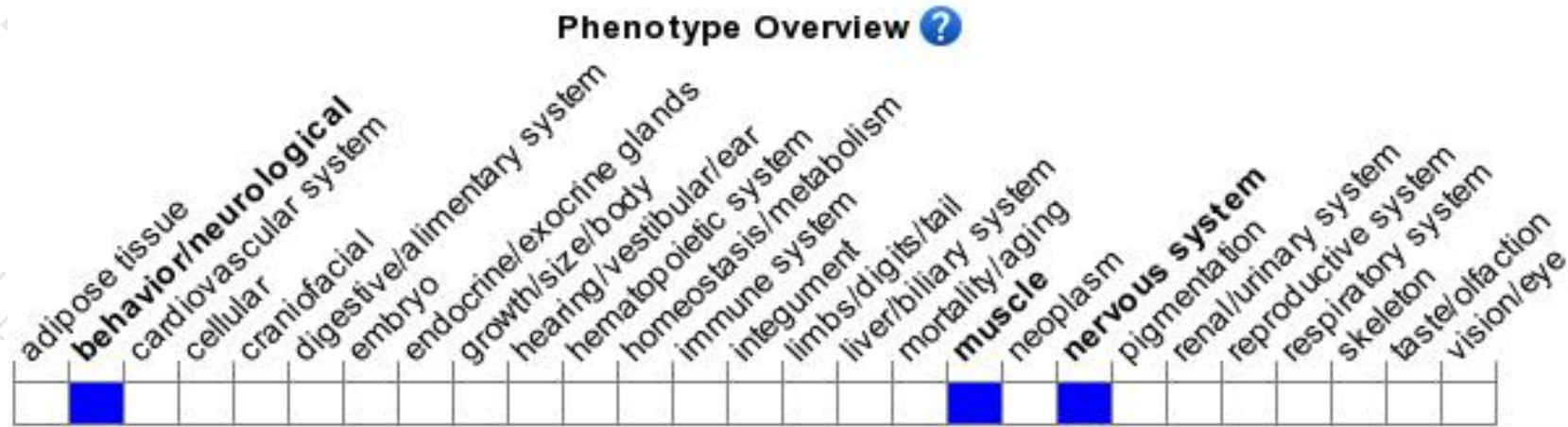
Protein domain



集萃药康
GemPharmatech



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 display impaired fast spiking in cortical interneurons, distorted cortical rhythmic activity, enhanced susceptibility to seizures, increased anxiety in the open field, and abnormal sleep patterns.

If you have any questions, you are welcome to inquire.

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