

Kcnq5 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Kcnq5

Project type

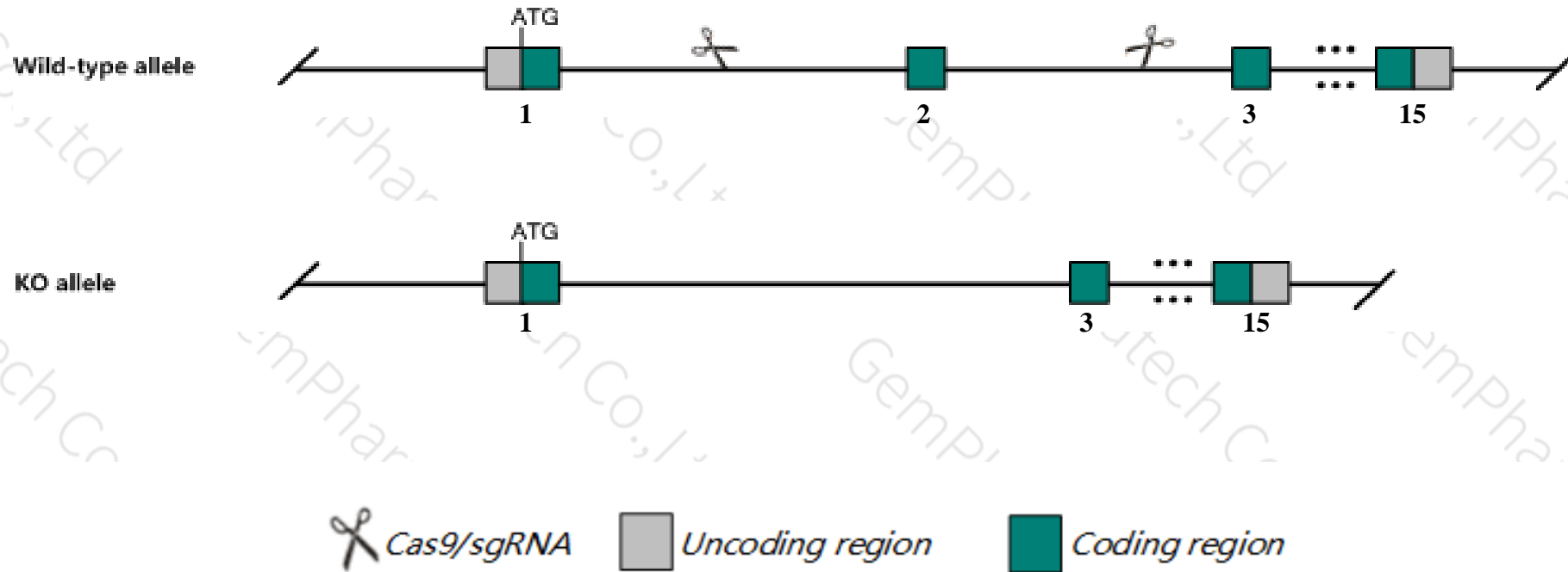
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnq5* gene. The schematic diagram is as follows:



- The *Kcnq5* gene has 7 transcripts. According to the structure of *Kcnq5* gene, exon2 of *Kcnq5-203* (ENSMUST00000115300.7) transcript is recommended as the knockout region. The region contains 91bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnq5* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, Mice homozygous for a dominant negative knock-in mutation in this gene exhibit partial prenatal lethality and abnormal afterhyperpolarization in the in the CA3 area of hippocampus.
- The *Kcnq5* gene is located on the Chr1. 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.

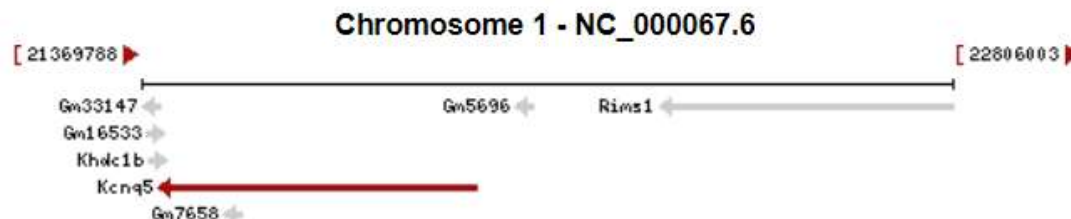
Gene information (NCBI)

Kcnq5 potassium voltage-gated channel, subfamily Q, member 5 [*Mus musculus* (house mouse)]

Gene ID: 226922, updated on 12-Aug-2019

Summary

Official Symbol	Kcnq5 provided by MGI
Official Full Name	potassium voltage-gated channel, subfamily Q, member 5 provided by MGI
Primary source	MGI:MGI:1924937
See related	Ensembl:ENSMUSG00000028033
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	D1Mgi1; AA589396; 7730402H11; 9230107O05Rik
Expression	Biased expression in cortex adult (RPKM 3.9), frontal lobe adult (RPKM 3.2) and 9 other tissues See more
Orthologs	human all



Transcript information (Ensembl)

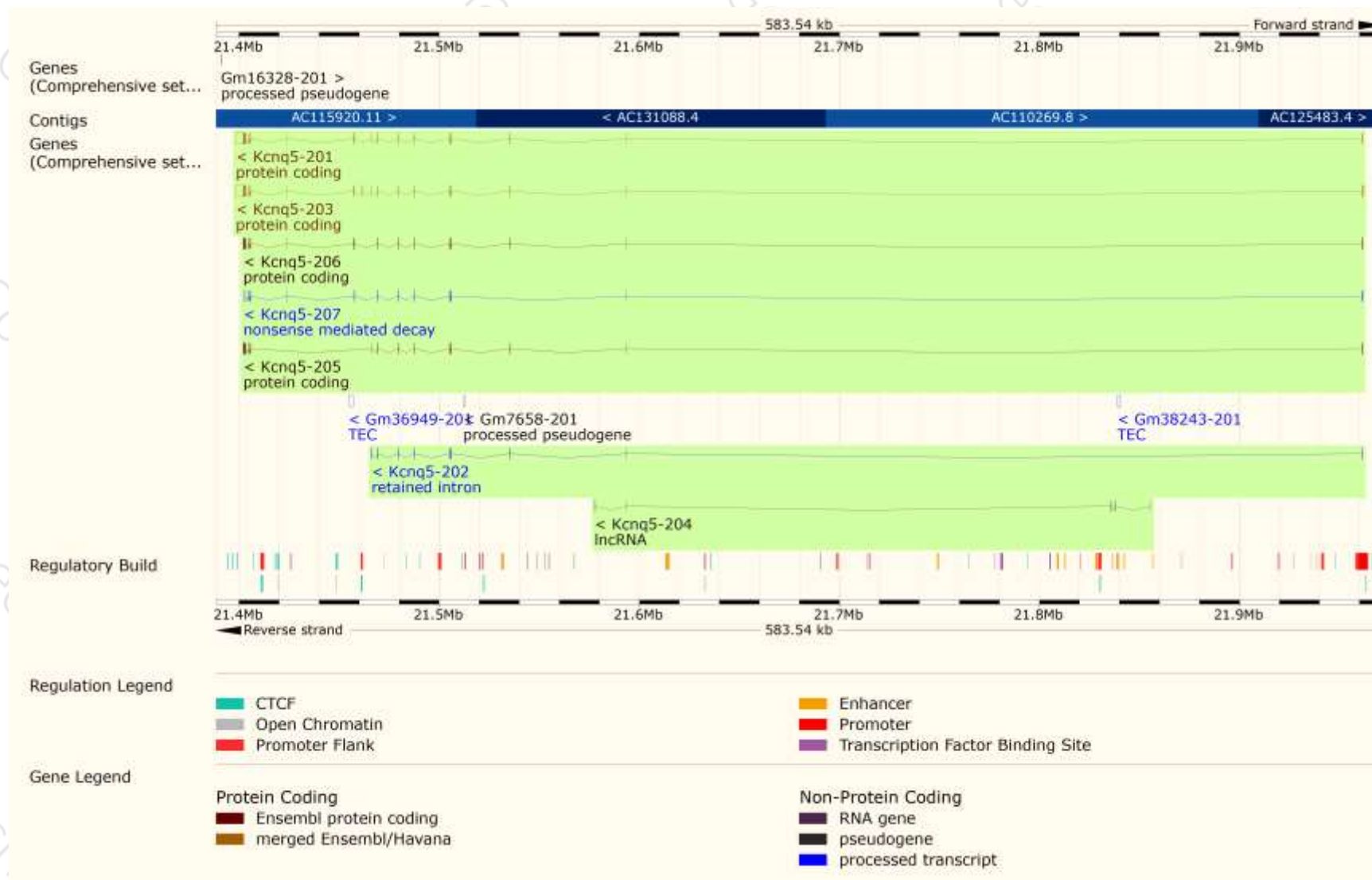
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Kcnq5-203	ENSMUST00000115300.7	6975	952aa	ENSMUSP00000110955.1	Protein coding	CCDS48230	E9Q9F1	TSL:1 GENCODE basic APPRIS ALT2
Kcnq5-201	ENSMUST00000029667.12	6562	933aa	ENSMUSP00000029667.6	Protein coding	CCDS35525	Q9JK45	TSL:1 GENCODE basic APPRIS P3
Kcnq5-206	ENSMUST00000173404.1	2775	924aa	ENSMUSP00000134076.1	Protein coding	CCDS78554	G3UYG5	TSL:5 GENCODE basic APPRIS ALT2
Kcnq5-205	ENSMUST00000173058.7	2472	823aa	ENSMUSP00000134166.1	Protein coding	-	G3UYP4	TSL:5 GENCODE basic
Kcnq5-207	ENSMUST00000174183.7	2648	172aa	ENSMUSP00000134389.1	Nonsense mediated decay	-	G3UZ84	TSL:5
Kcnq5-202	ENSMUST00000115299.7	1472	No protein	-	Retained intron	-	-	TSL:5
Kcnq5-204	ENSMUST00000134505.1	662	No protein	-	lncRNA	-	-	TSL:3

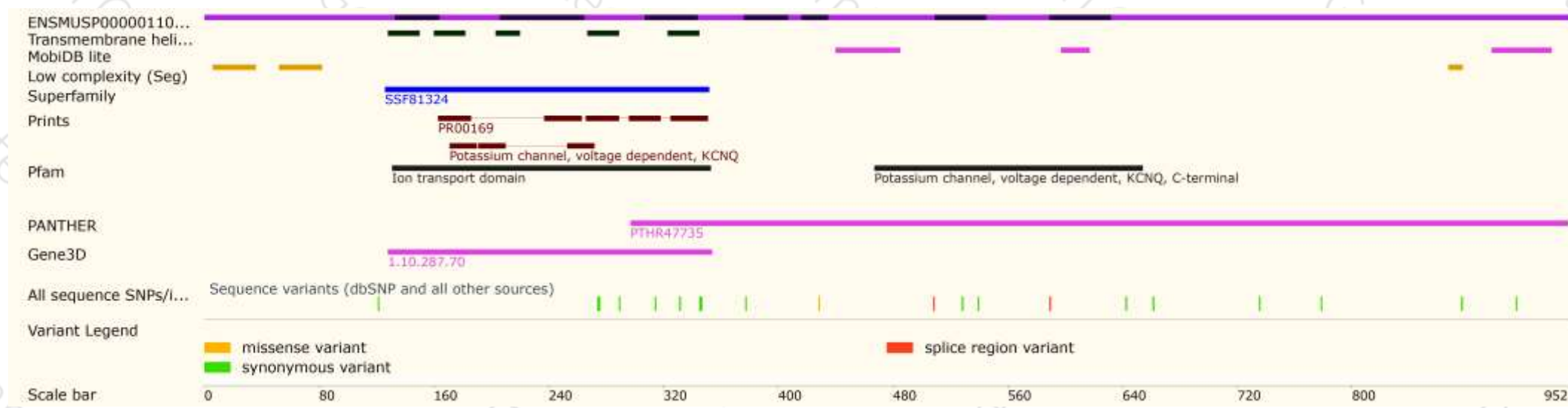
The strategy is based on the design of *Kcnq5-203* transcript,The transcription is shown below



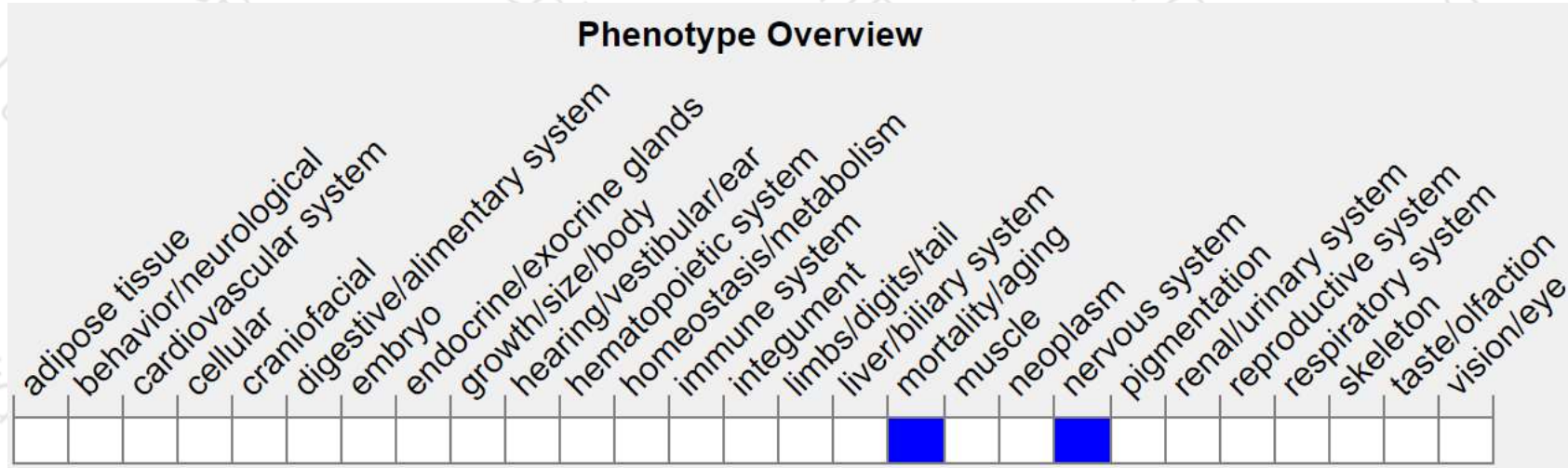
Genomic location distribution



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 dominant negative knock-in mutation in this gene exhibit partial prenatal lethality and abnormal afterhyperpolarization in the in the CA3 area of hippocampus.

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

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