

Kcnn1 Cas9-KO Strategy

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Project Overview

Project Name

Kcnn1

Project type

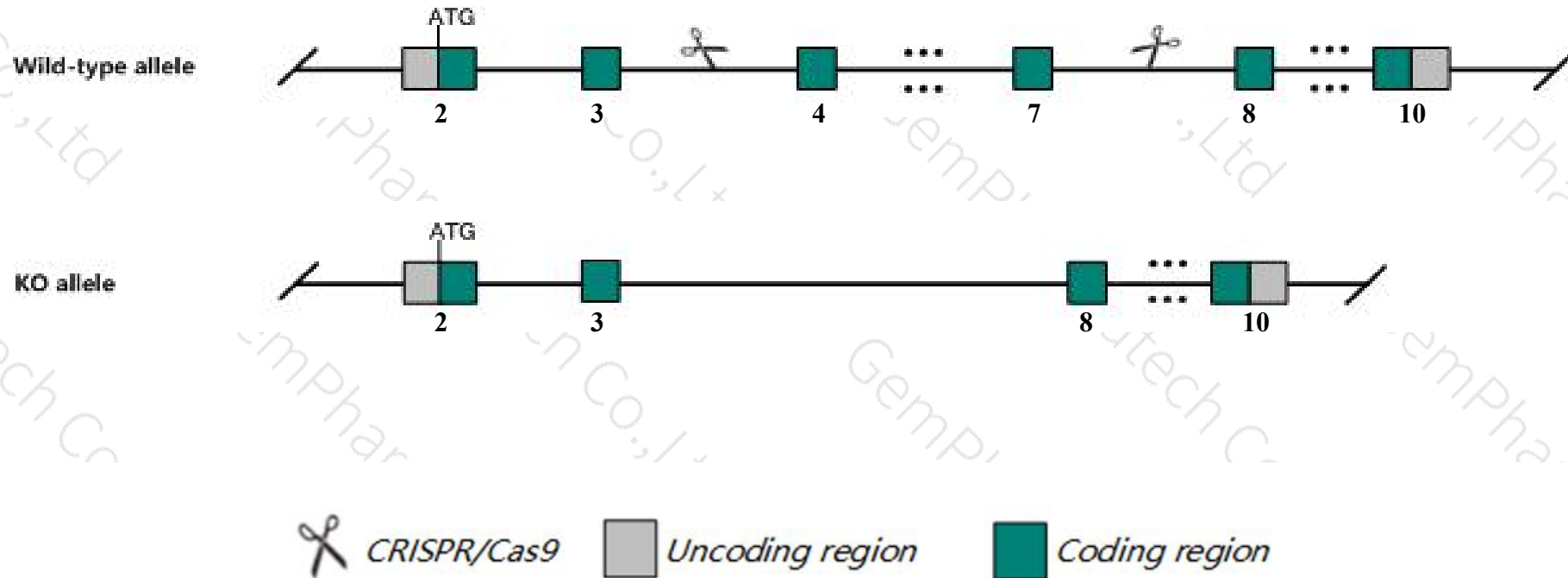
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnn1* gene. The schematic diagram is as follows:



- The *Kcnn1* gene has 8 transcripts. According to the structure of *Kcnn1* gene, exon4-exon7 of *Kcnn1-201* (ENSMUST00000110078.4) transcript is recommended as the knockout region. The region contains 800bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnn1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice display normal hippocampal morphology and afterhyperpolarization currents.
- Transcript Kcnn1-206 may not be affected.
- The *Kcnn1* gene is located on the Chr8. 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)

Kcnn1 potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1 [Mus musculus (house mouse)]

Gene ID: 84036, updated on 31-Jan-2019

Summary



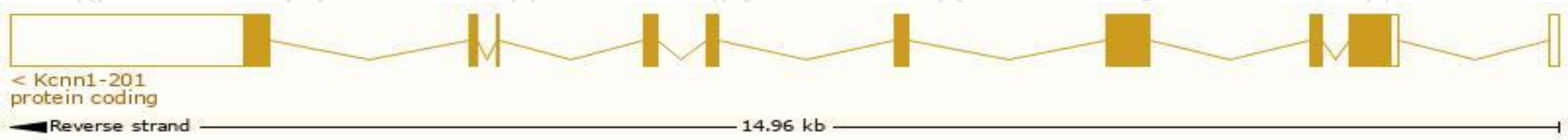
Official Symbol	Kcnn1 provided by MGI
Official Full Name	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1 provided by MGI
Primary source	MGI:MGI:1933993
See related	Ensembl:ENSMUSG000000002908
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Al854248, KCa2.1, SK1
Expression	Ubiquitous expression in whole brain E14.5 (RPKM 4.8), CNS E14 (RPKM 4.3) and 26 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

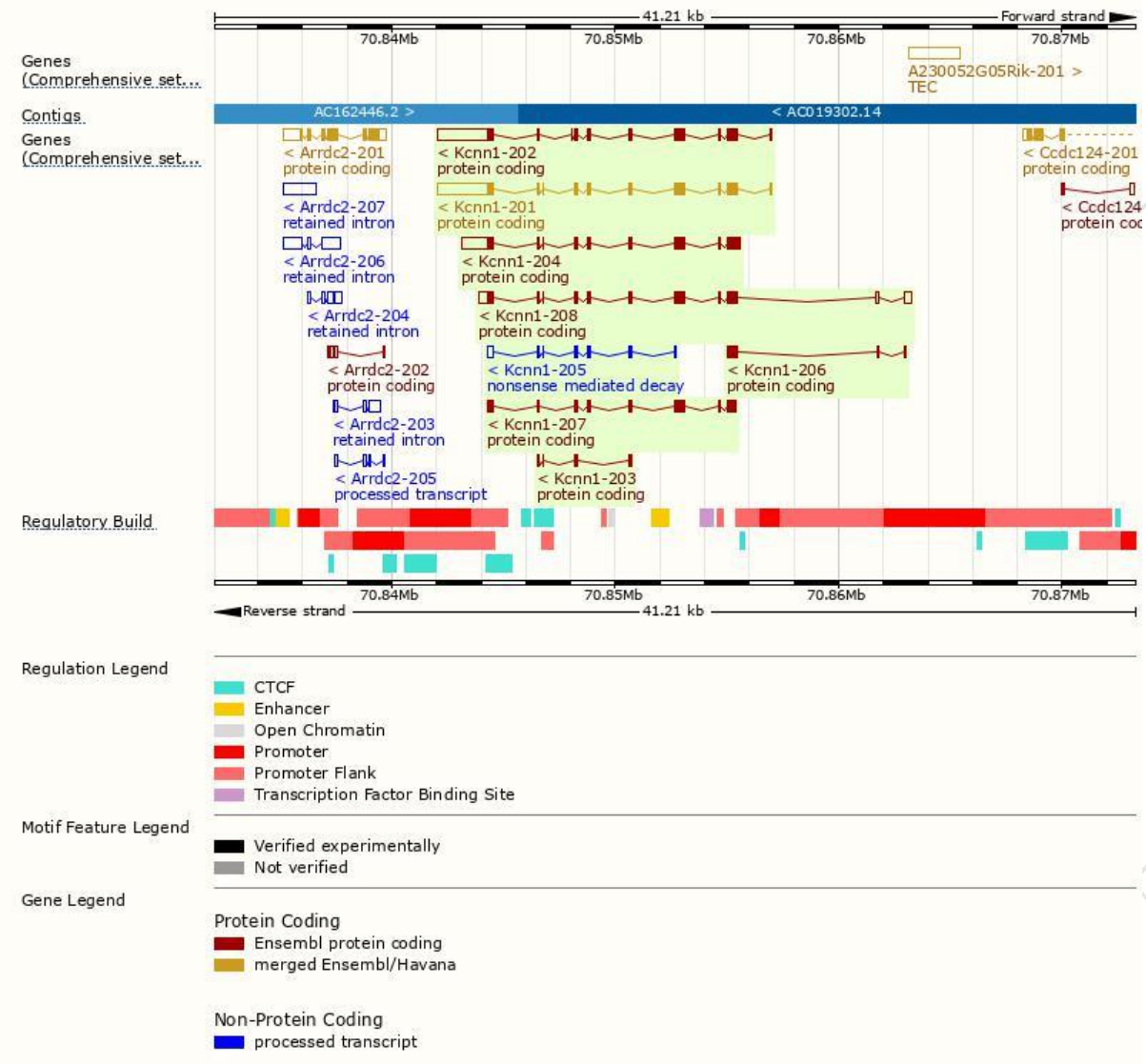
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnn1-201	ENSMUST00000110078.4	4047	538aa	Protein coding	CCDS52578	A0A140T8Q8	TSL:1 GENCODE basic APPRIS P2
Kcnn1-208	ENSMUST00000212611.1	2528	538aa	Protein coding	CCDS52578	A0A140T8Q8	TSL:1 GENCODE basic APPRIS P2
Kcnn1-202	ENSMUST00000110081.9	4045	539aa	Protein coding	-	Z4YL28	TSL:5 GENCODE basic APPRIS ALT2
Kcnn1-204	ENSMUST00000212086.1	2964	581aa	Protein coding	-	A0A1D5RM38	TSL:1 GENCODE basic APPRIS ALT2
Kcnn1-207	ENSMUST00000212509.2	1608	535aa	Protein coding	-	A0A1D5RMB2	TSL:5 GENCODE basic APPRIS ALT2
Kcnn1-206	ENSMUST00000212414.1	613	132aa	Protein coding	-	A0A1D5RMF8	CDS 3' incomplete TSL:1
Kcnn1-203	ENSMUST00000212084.1	338	113aa	Protein coding	-	A0A1D5RLS4	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
Kcnn1-205	ENSMUST00000212243.1	839	157aa	Nonsense mediated decay	-	A0A1D5RLR9	CDS 5' incomplete TSL:3

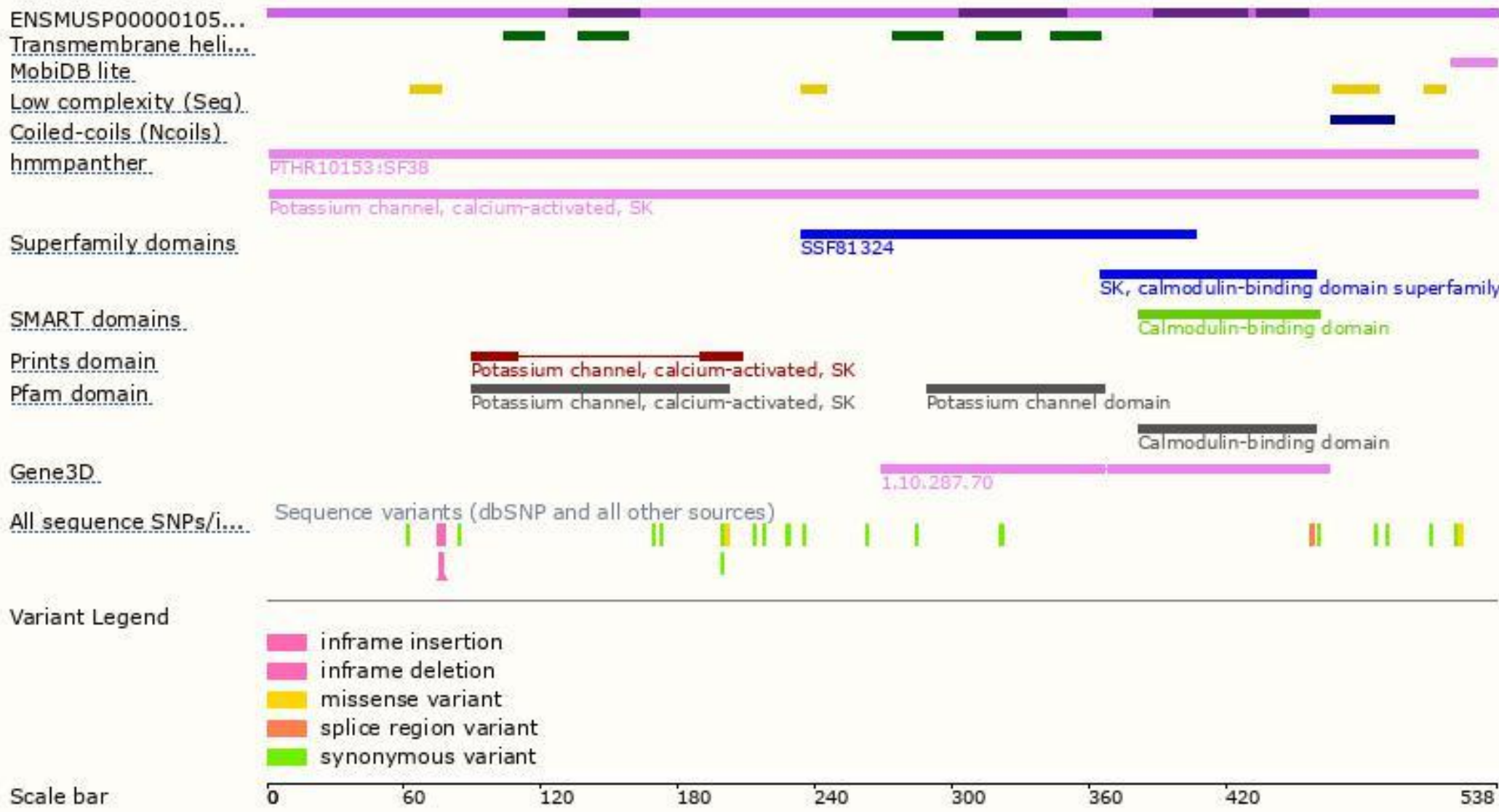
The strategy is based on the design of *Kcnn1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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