

Kcnt2 Cas9-KO Strategy

Designer:

JiaYu

Reviewer:

Xiaojing Li

Design Date:

2020-3-5

Project Overview

Project Name

Kcnt2

Project type

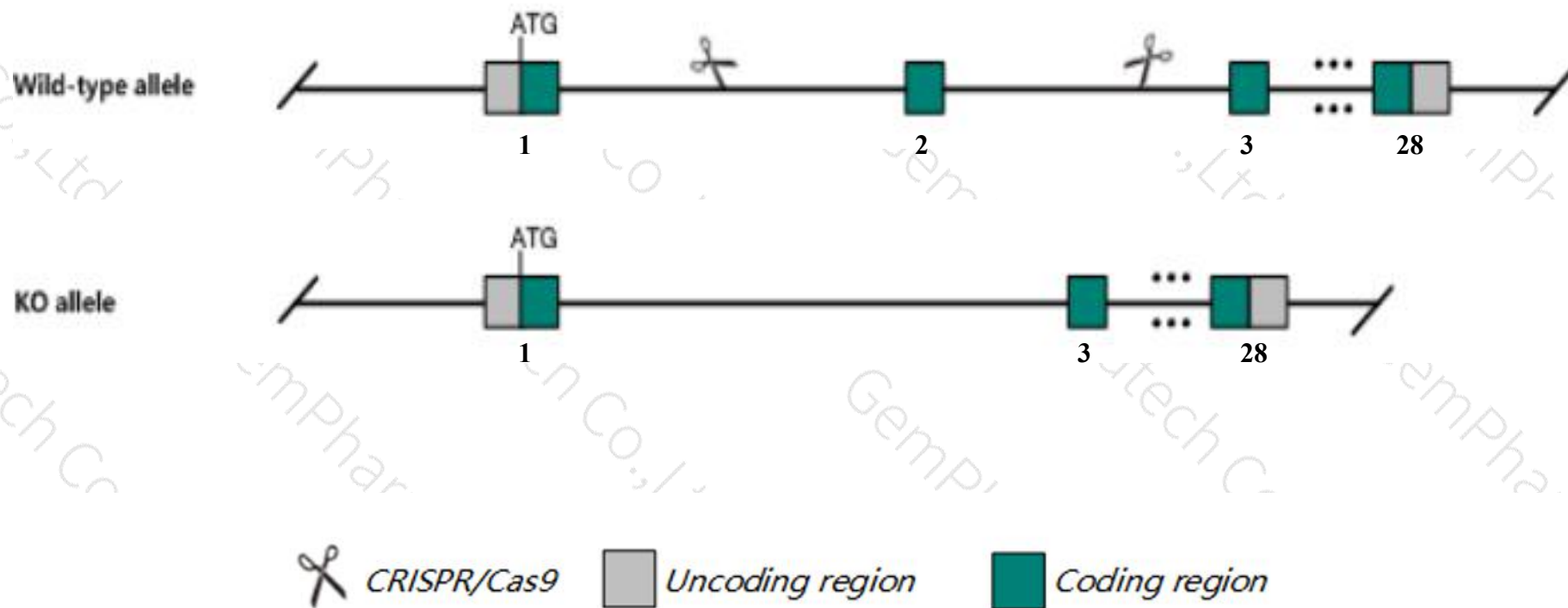
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnt2* gene. The schematic diagram is as follows:



- The *Kcnt2* gene has 6 transcripts. According to the structure of *Kcnt2* gene, exon2 of *Kcnt2-203* (ENSMUST00000120796.7) transcript is recommended as the knockout region. The region contains 80bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnt2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele are viable with normal pain and itch responses.
- The *Kcnt2* 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)

Kcnt2 potassium channel, subfamily T, member 2 [Mus musculus (house mouse)]

Gene ID: 240776, updated on 16-Feb-2019

Summary



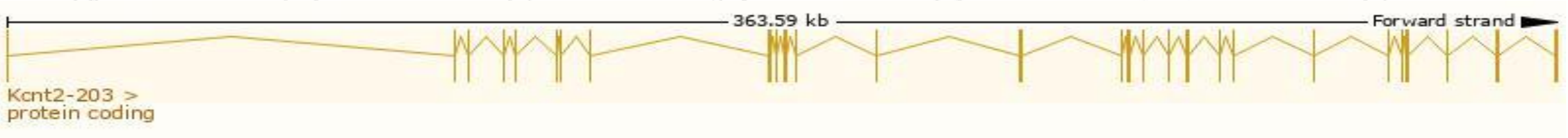
Official Symbol	Kcnt2 provided by MGI
Official Full Name	potassium channel, subfamily T, member 2 provided by MGI
Primary source	MGI:MGI:3036273
See related	Ensembl:ENSMUSG00000052726
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	E330038N15Rik, Slick
Expression	Biased expression in cortex adult (RPKM 2.5), frontal lobe adult (RPKM 1.6) and 9 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

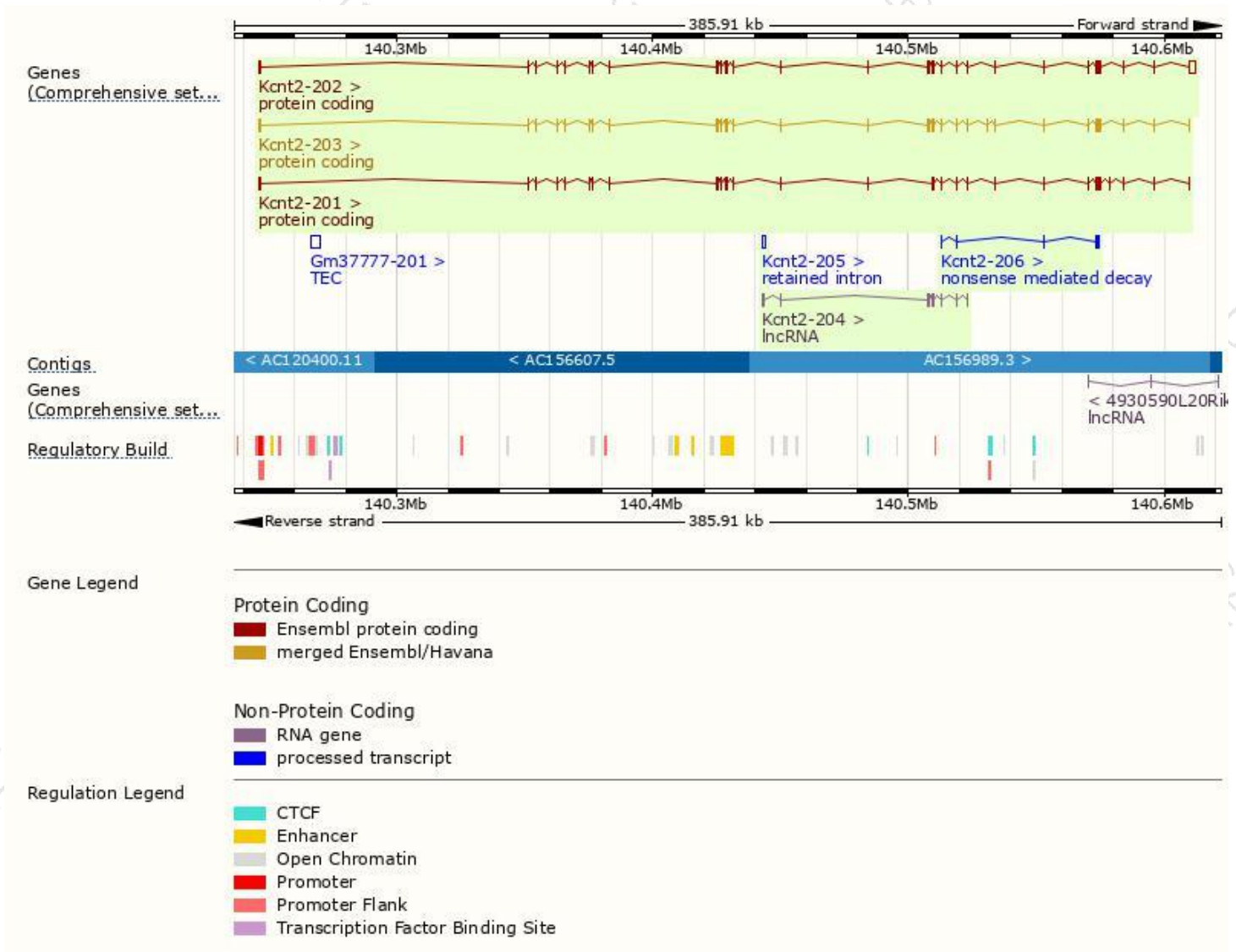
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnt2-203	ENSMUST00000120796.7	3540	1135aa	Protein coding	CCDS48389	D3Z649	TSL:5 GENCODE basic APPRIS P2
Kcnt2-202	ENSMUST00000120709.7	5790	1111aa	Protein coding	-	D3YTU6	TSL:5 GENCODE basic APPRIS ALT 1
Kcnt2-201	ENSMUST00000119786.7	3624	1068aa	Protein coding	-	D3Z592	TSL:5 GENCODE basic
Kcnt2-206	ENSMUST00000193606.1	442	71aa	Nonsense mediated decay	-	A0A0A6YXD8	CDS 5' incomplete TSL:3
Kcnt2-205	ENSMUST00000192840.1	1012	No protein	Retained intron	-	-	TSL:NA
Kcnt2-204	ENSMUST00000145077.2	1281	No protein	lncRNA	-	-	TSL:1

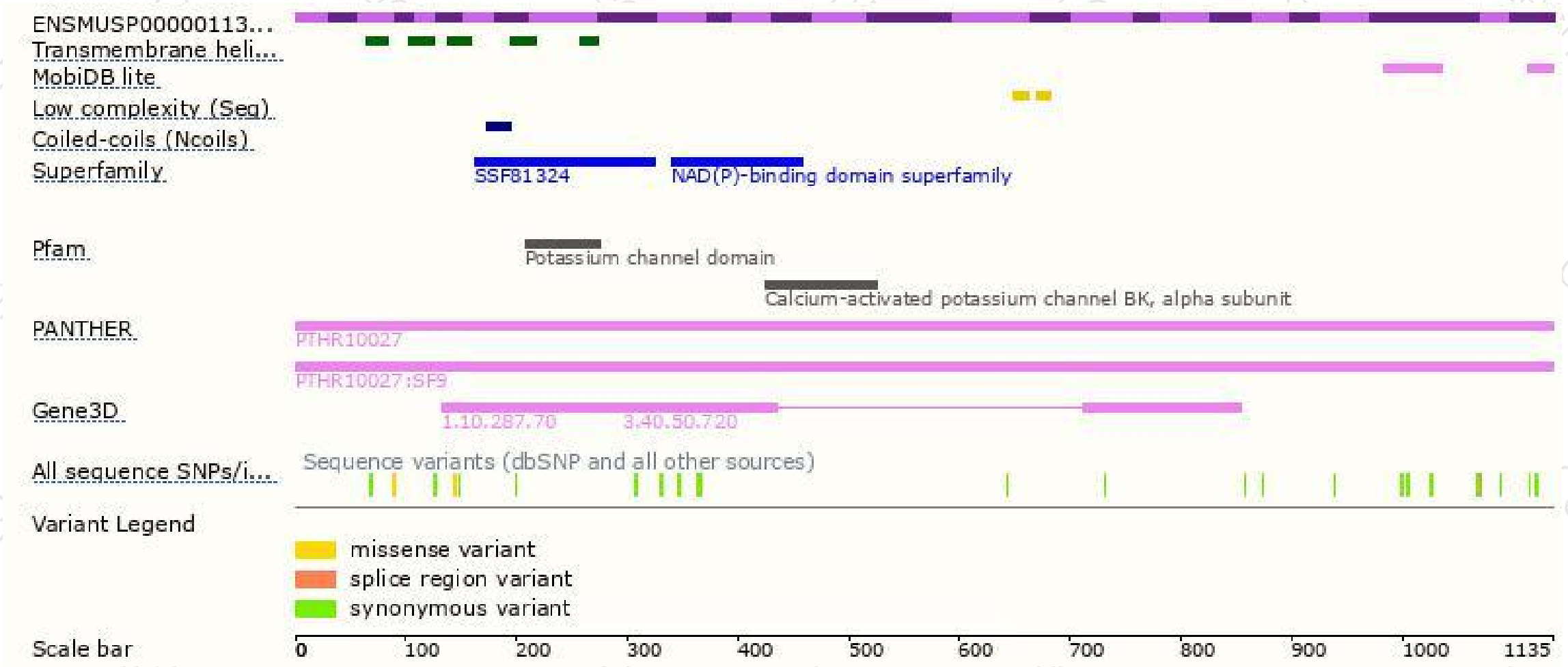
The strategy is based on the design of *Kcnt2-203* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

Tel: 400-9660890

