

***Kcnd3* Cas9-KO Strategy**

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Project Overview

Project Name

Kcnd3

Project type

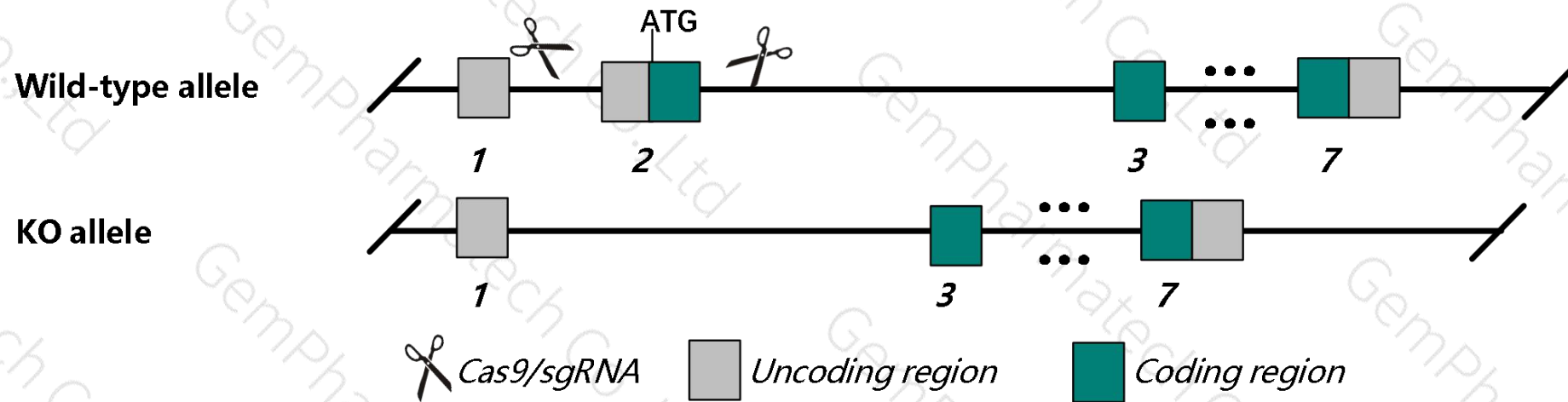
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnd3* gene. The schematic diagram is as follows:



- The *Kcnd3* gene has 5 transcripts. According to the structure of *Kcnd3* gene, exon2 of *Kcnd3-202* (ENSMUST00000098761.9) 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 *Kcnd3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a reporter (null) allele are viable and fertile and exhibit normal cardiac morphology and function.
- Transcript *Kcnd3*-205 may not be affected.
- The knockout region is near to the N-terminal of *Kcnd3os* gene, this strategy may influence the regulatory function of the N-terminal of *Kcnd3os* gene.
- The *Kcnd3* gene is located on the Chr3. 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)

Kcnd3 potassium voltage-gated channel, Shal-related family, member 3 [*Mus musculus* (house mouse)]

Gene ID: 56543, updated on 14-Aug-2019

Summary

- Official Symbol** Kcnd3 provided by [MGI](#)
- Official Full Name** potassium voltage-gated channel, Shal-related family, member 3 provided by [MGI](#)
- Primary source** [MGI:MGI:1928743](#)
- See related** [Ensembl:ENSMUSG00000040896](#)
- 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** Kcnd3; Kv4.3; AW045978
- Expression** Broad expression in frontal lobe adult (RPKM 8.1), cerebellum adult (RPKM 6.3) and 17 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 3; 3 F2.2 [See Kcnd3 in Genome Data Viewer](#)

Exon count: 9

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	3	NC_000069.6 (105451890..105674002)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	3	NC_000069.5 (105255248..105476920)

Transcript information (Ensembl)

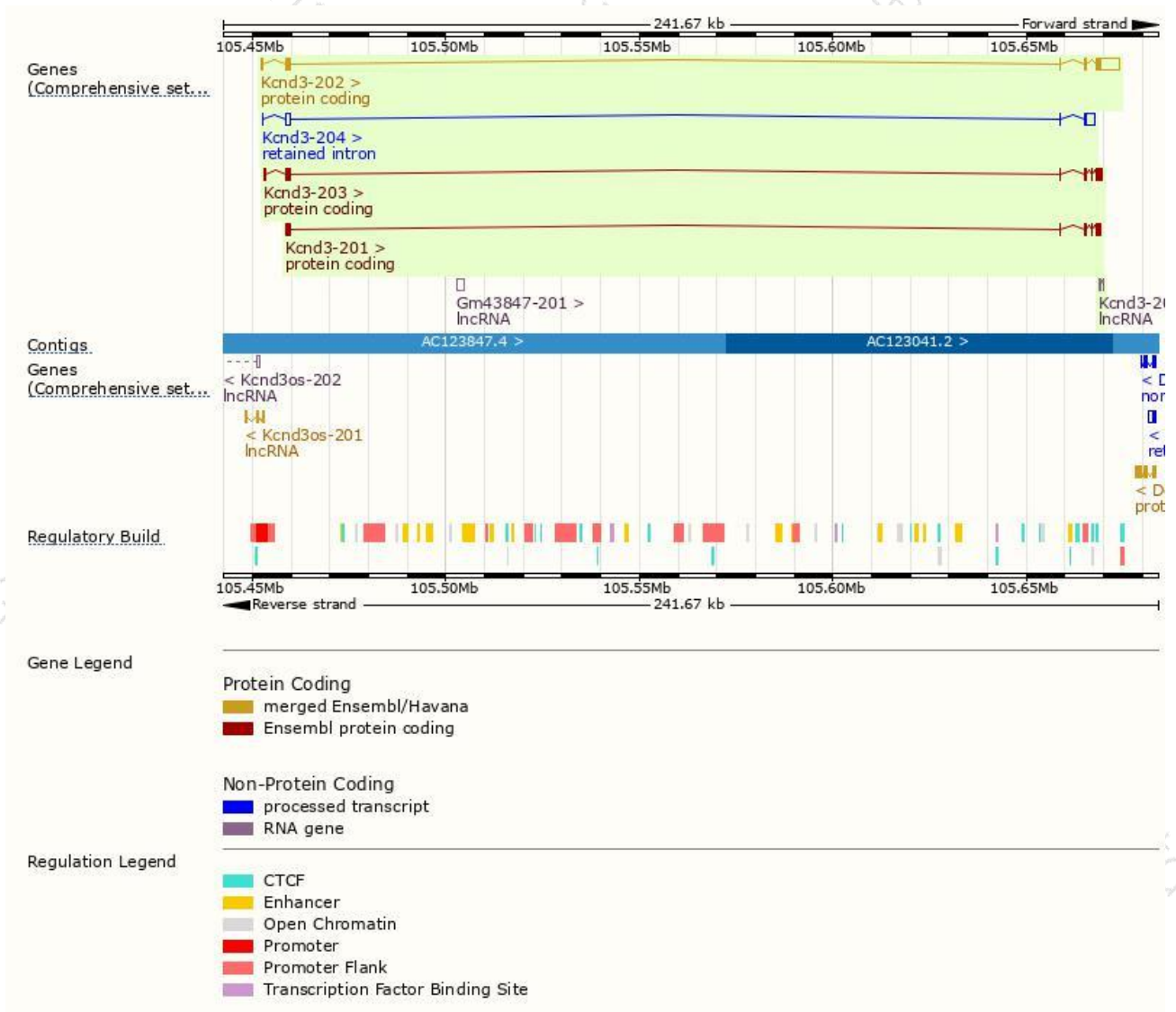
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnd3-202	ENSMUST00000098761.9	7169	636aa	Protein coding	CCDS17708	Q3UH54 Q9Z0V1	TSL:1 GENCODE basic APPRIS ALT1
Kcnd3-203	ENSMUST00000118360.7	2668	655aa	Protein coding	CCDS17709	B2RUE0 Q9Z0V1	TSL:5 GENCODE basic APPRIS P4
Kcnd3-201	ENSMUST00000079169.4	2102	655aa	Protein coding	CCDS17709	B2RUE0 Q9Z0V1	TSL:1 GENCODE basic APPRIS P4
Kcnd3-204	ENSMUST00000141694.1	3726	No protein	Retained intron	-	-	TSL:1
Kcnd3-205	ENSMUST00000147209.1	199	No protein	lncRNA	-	-	TSL:5

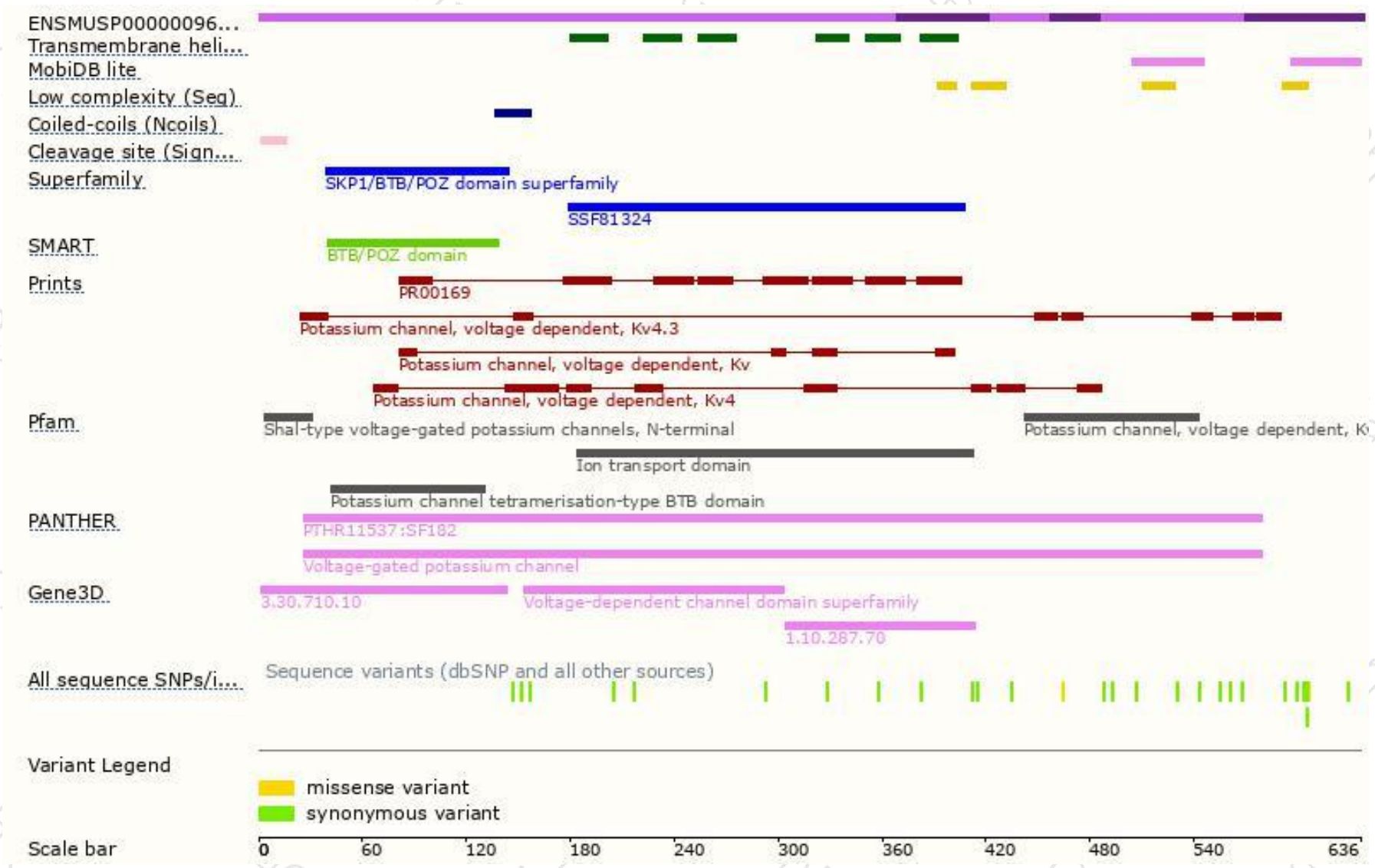
The strategy is based on the design of *Kcnd3-202* transcript,The transcription is shown below



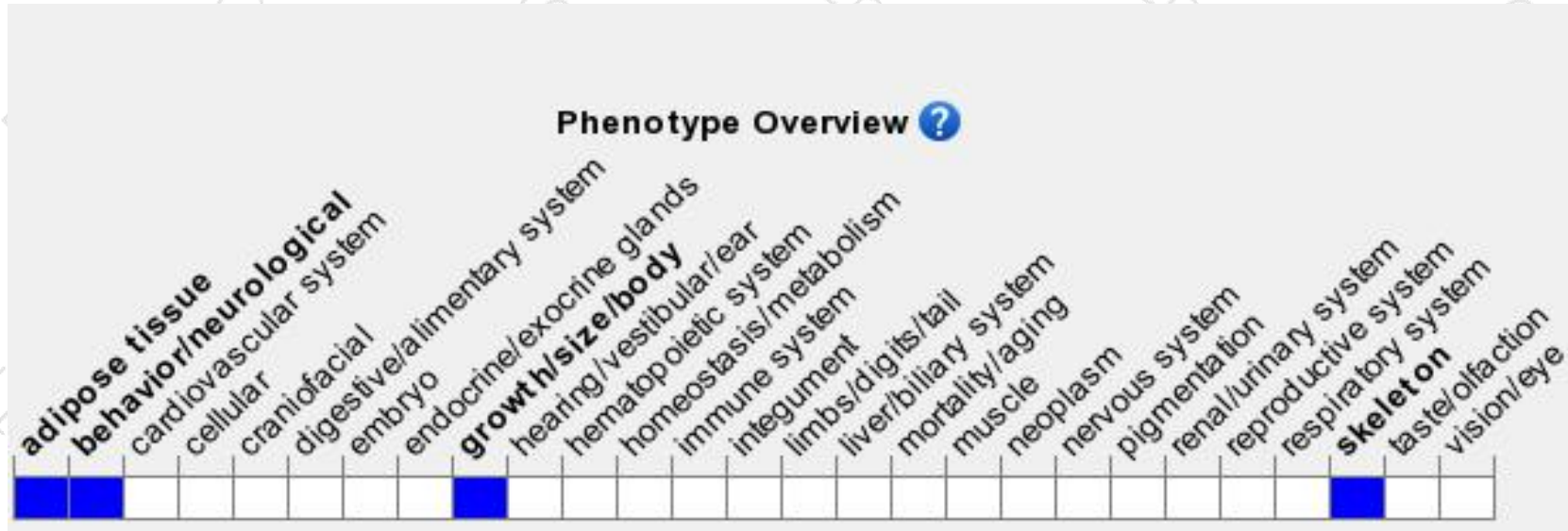
Genomic location distribution



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 reporter (null) allele are viable and fertile and exhibit normal cardiac morphology and function.

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

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