Kcnj6 Cas9-KO Strategy

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Reviewer: Daohua Xu

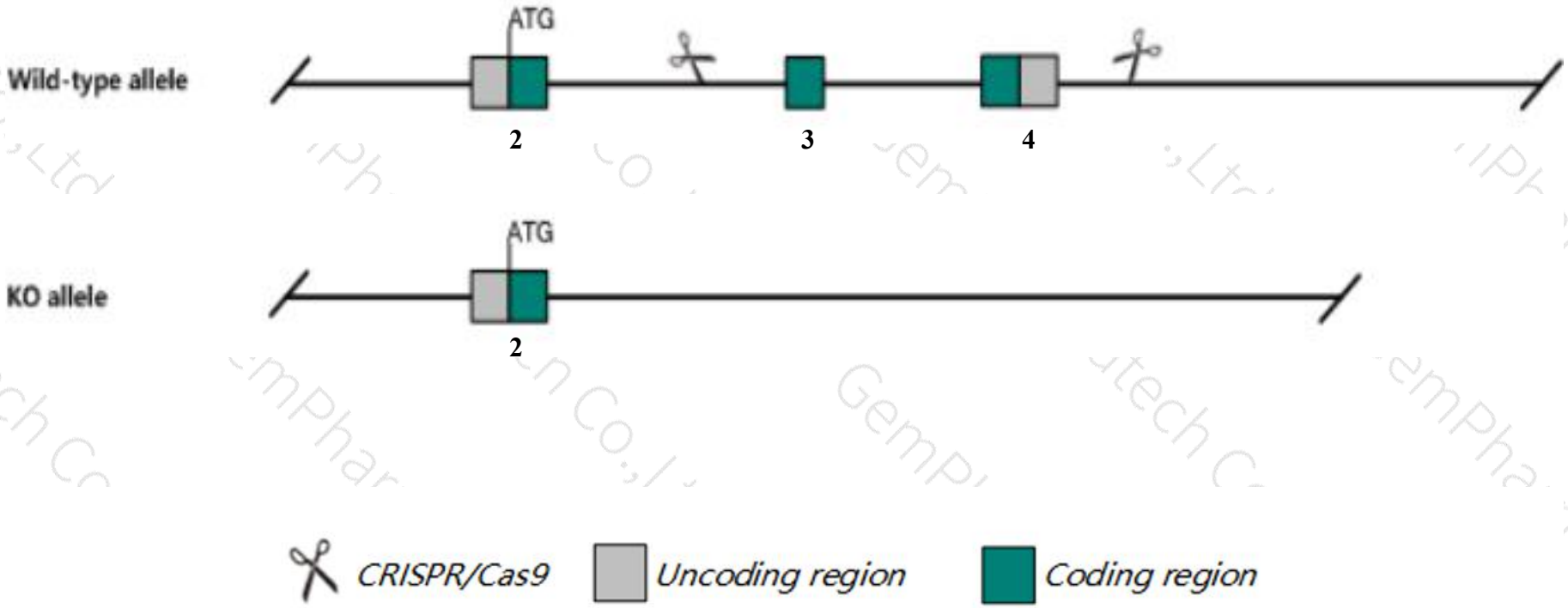
Design Date: 2020-4-21

Project Overview

Project Name	***Kcnj6***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnj6* gene. The schematic diagram is as follows:



Technical routes

➢ The *Kcnj6* gene has 7 transcripts. According to the structure of *Kcnj6* gene, exon3-exon4 of *Kcnj6-202* (ENSMUST00000099508.3) transcript is recommended as the knockout region.The region contains 1247bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Kcnj6* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,a spontaneous mutation exhibits small size, ataxia, hypotonia, high periweaning mortality, purkinje cell defects, and male sterility. homozygotes for a targeted null mutation exhibit increased susceptibility to spontaneous and drug-induced seizures.
- Transcript 204 may not be affected.
- The *Kcnj6* gene is located on the Chr16. 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）

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Kcnj6 potassium inwardly-rectifying channel, subfamily J, member 6 [Mus musculus (house mouse)]

Gene ID: 16522, updated on 20-Mar-2020

Summary

Official Symbol	Kcnj6 provided by MGI
Official Full Name	potassium inwardly-rectifying channel, subfamily J, member 6 provided byMGI
Primary source	MGI:MGI:104781
See related	Ensembl:ENSMUSG00000043301
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	BIR1, GIRK2, KATP2, KCNJ7, Kir3.2, weaver, wv
Expression	Biased expression in cortex adult (RPKM 1.9), testis adult (RPKM 1.8) and 5 other tissuesSee more
Orthologs	human all

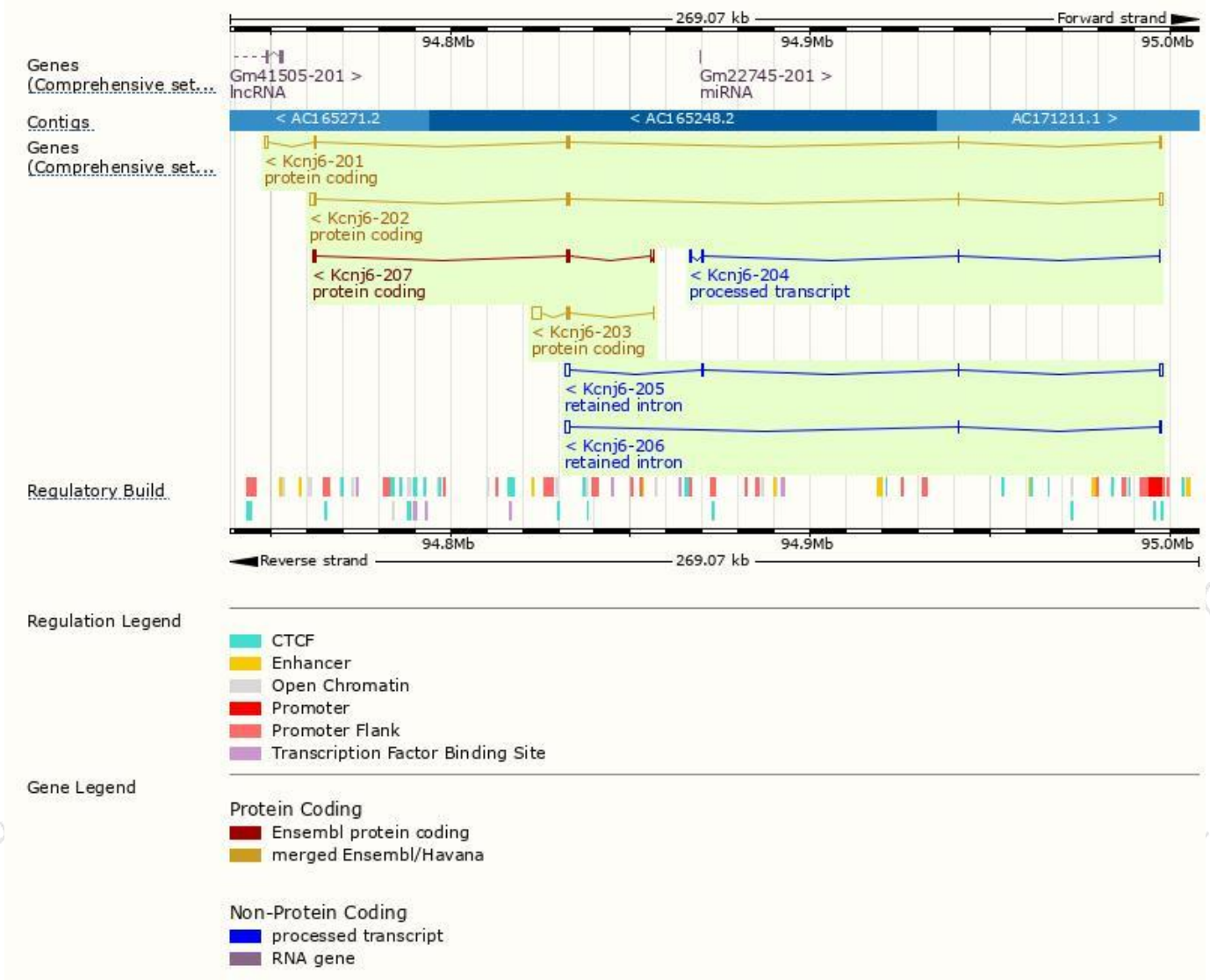
Transcript information（Ensembl）

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

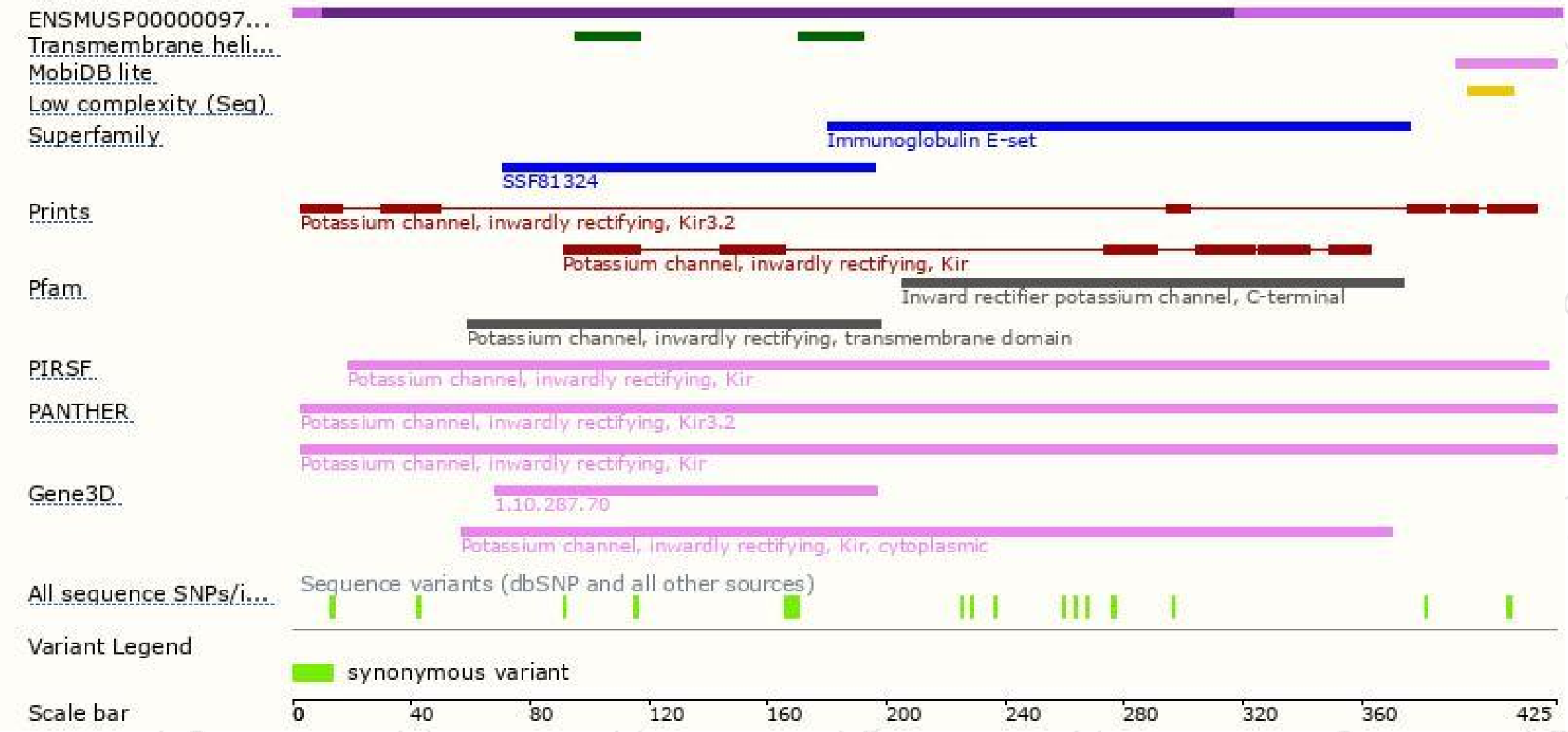
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnj6-203	ENSMUST00000165538.2	3627	302aa	Protein coding	CCDS49921	A0A0R4J239	TSL:1 GENCODE basic
Kcnj6-202	ENSMUST00000099508.3	3097	425aa	Protein coding	CCDS37409	Q0VB45	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Kcnj6-201	ENSMUST00000095873.11	2362	414aa	Protein coding	CCDS37408	Q8C4T8	TSL:1 GENCODE basic
Kcnj6-207	ENSMUST00000232562.1	2275	407aa	Protein coding	-	A0A338P6L0	GENCODE basic
Kcnj6-204	ENSMUST00000231744.1	631	No protein	Processed transcript	-	-	
Kcnj6-205	ENSMUST00000232128.1	2163	No protein	Retained intron	-	-	
Kcnj6-206	ENSMUST00000232403.1	1936	No protein	Retained intron	-	-	

The strategy is based on the design of *Kcnj6-202* transcript,The transcription is shown below

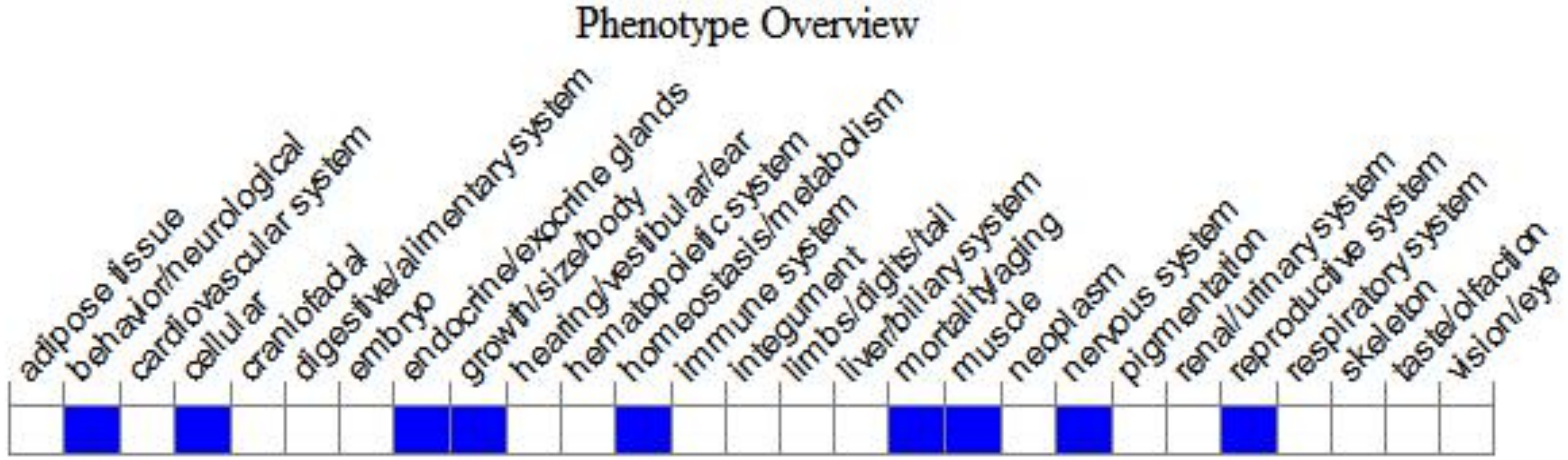
Genomic location distribution



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/).

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

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