Kcnj12 Cas9-KO Strategy

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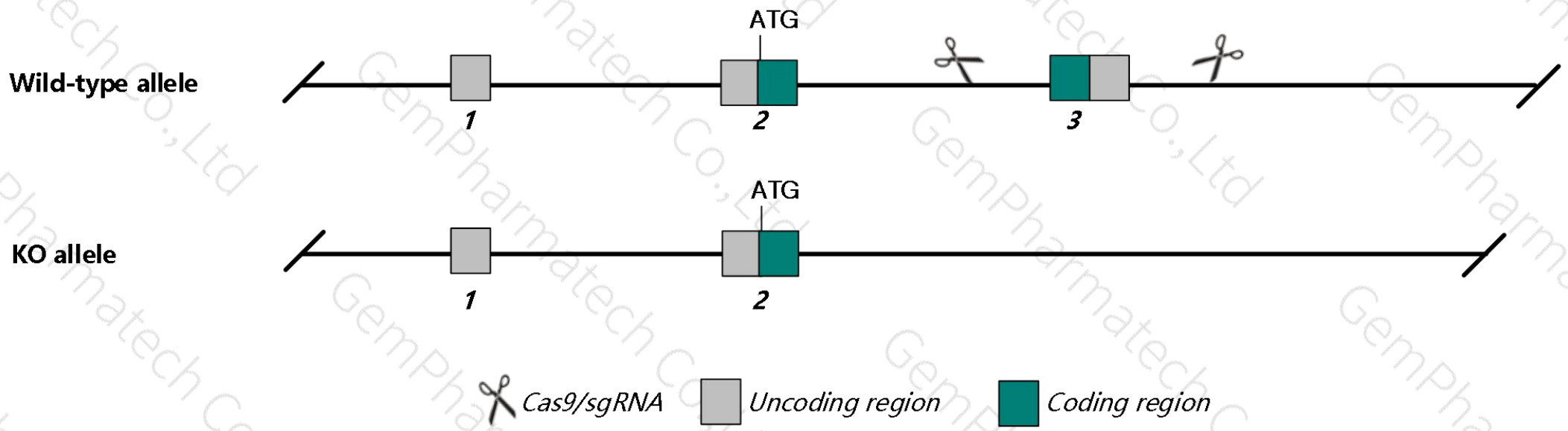
Project Overview

Project Name	***Kcnj12***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnj12* gene. The schematic diagram is as follows:



Technical routes

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- The *Kcnj12* gene has 3 transcripts. According to the structure of *Kcnj12* gene, exon3 of *Kcnj12-201* (ENSMUST00000041944.8) transcript is recommended as the knockout region.The region contains most of the coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Kcnj12* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

- According to the existing MGI data,Homozygotes for a targeted null mutation are viable and fertile with no detected abnormalities.

- The *Kcnj12* gene is located on the Chr11. 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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Kcnj12 potassium inwardly-rectifying channel, subfamily J, member 12 [*Mus musculus* (house mouse)]

Gene ID: 16515, updated on 12-Aug-2019

Summary

Official Symbol	Kcnj12 provided by MGI
Official Full Name	potassium inwardly-rectifying channel, subfamily J, member 12 provided by MGI
Primary source	MGI:MGI:108495
See related	Ensembl:ENSMUSG00000042529
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	IRK2; IRK-2; Kir2.2; MB-IRK2
Expression	Biased expression in cerebellum adult (RPKM 14.1), heart adult (RPKM 8.7) and 11 other tissues See more
Orthologs	human all

Chromosome 11 - NC_000077.6

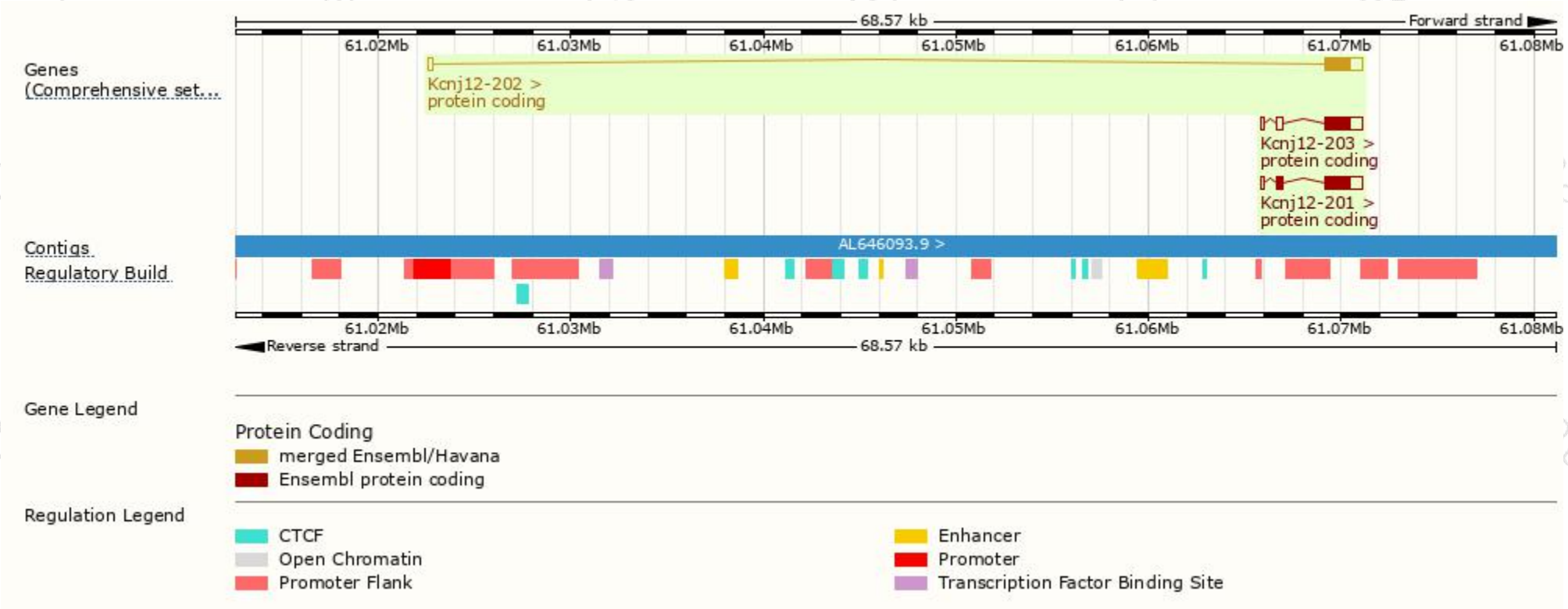
Transcript information（Ensembl）

The gene has 3 transcripts,all transcripts are shown below:

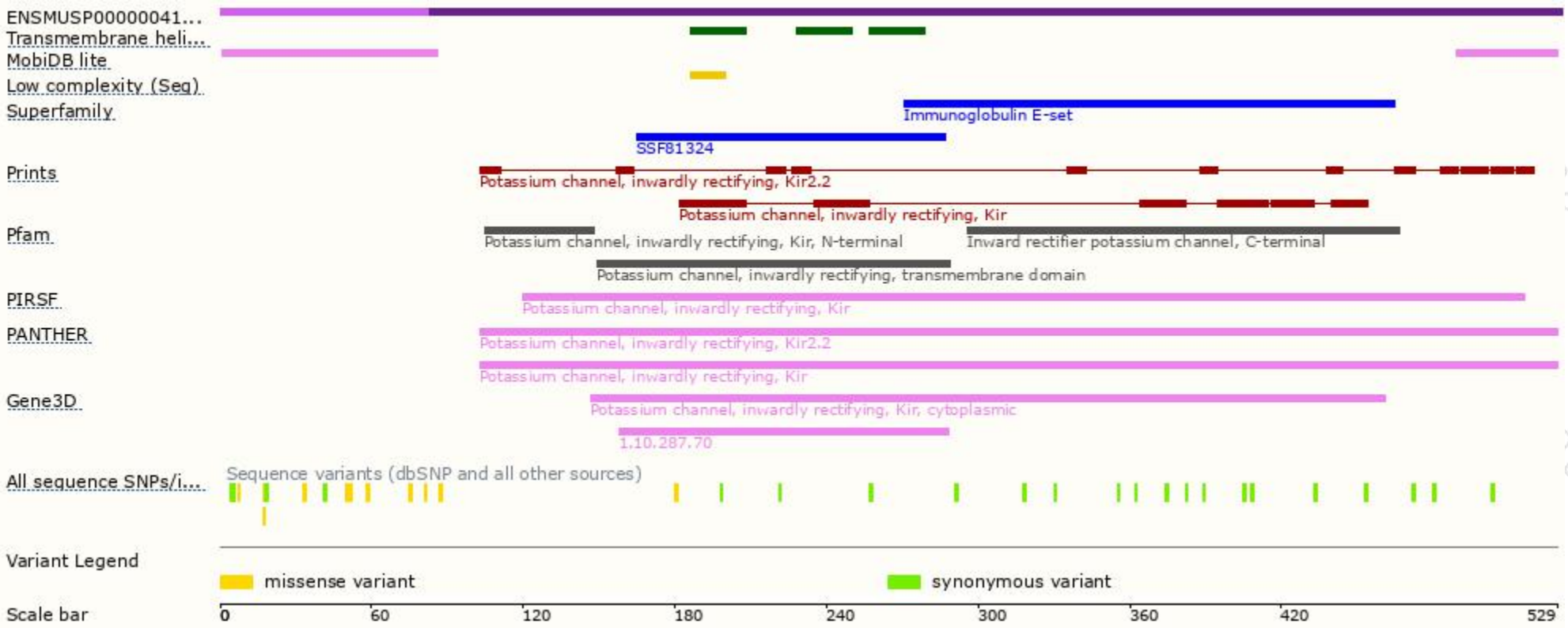
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnj12-203	ENSMUST00000108717.2	2463	427aa	Protein coding	CCDS24805	P52187	TSL:1 GENCODE basic APPRIS P3
Kcnj12-201	ENSMUST00000041944.8	2459	529aa	Protein coding	CCDS59563	B1ATI1	TSL:1 GENCODE basic APPRIS ALT2
Kcnj12-202	ENSMUST00000089184.10	2291	427aa	Protein coding	CCDS24805	P52187	TSL:1 GENCODE basic APPRIS P3

The strategy is based on the design of *Kcnj12-201* 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/).

Homozygotes for a targeted null mutation are viable and fertile with no detected abnormalities.

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