Kcnj13 Cas9-KO Strategy

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Reviewer: JiaYu

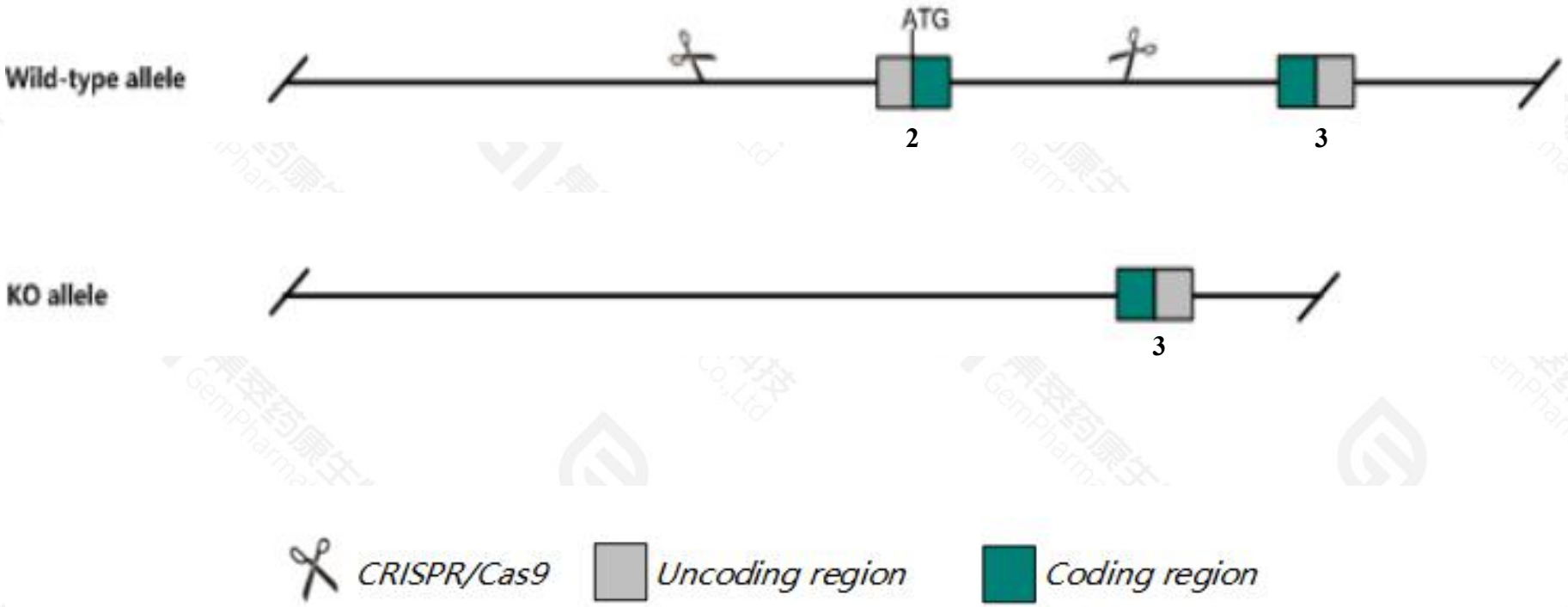
Design Date: 2021-9-28

Project Overview

Project Name	***Kcnj13***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnj13* gene. The schematic diagram is as follows:



Technical routes

➢ The *Kcnj13* gene has 2 transcripts. According to the structure of *Kcnj13* gene, exon2 of *Kcnj13-201*(ENSMUST00000113212.4) 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 *Kcnj13* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

Notice

➢ According to the existing MGI data,homozygous mutant null mice die shortly after birth, exhibit cleft palate and pulmonary abnormalities in embryonic lungs.

➢ Ko region of this strategy overlaps the intron of *Gigyf2* gene and may affect its normal splicing regulation function.

➢ The *Kcnj13* 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）

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Kcnj13 potassium inwardly-rectifying channel, subfamily J, member 13 [Mus musculus (house mouse)]

Gene ID: 100040591, updated on 16-Feb-2021

Summary

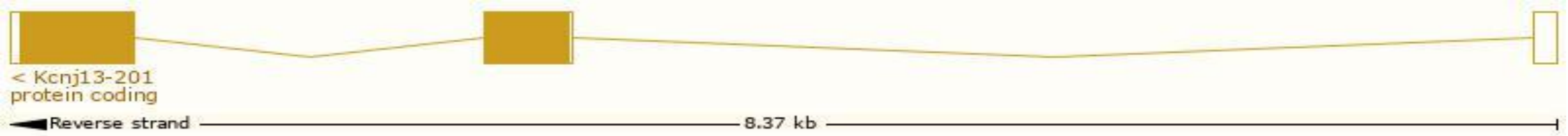
Official Symbol	Kcnj13 provided by MGI
Official Full Name	potassium inwardly-rectifying channel, subfamily J, member 13 provided by MGI
Primary source	MGI:MGI:3781032
See related	Ensembl:ENSMUSG00000079436
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Kir7.1
Expression	Biased expression in lung adult (RPKM 2.1), large intestine adult (RPKM 1.8) and 14 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

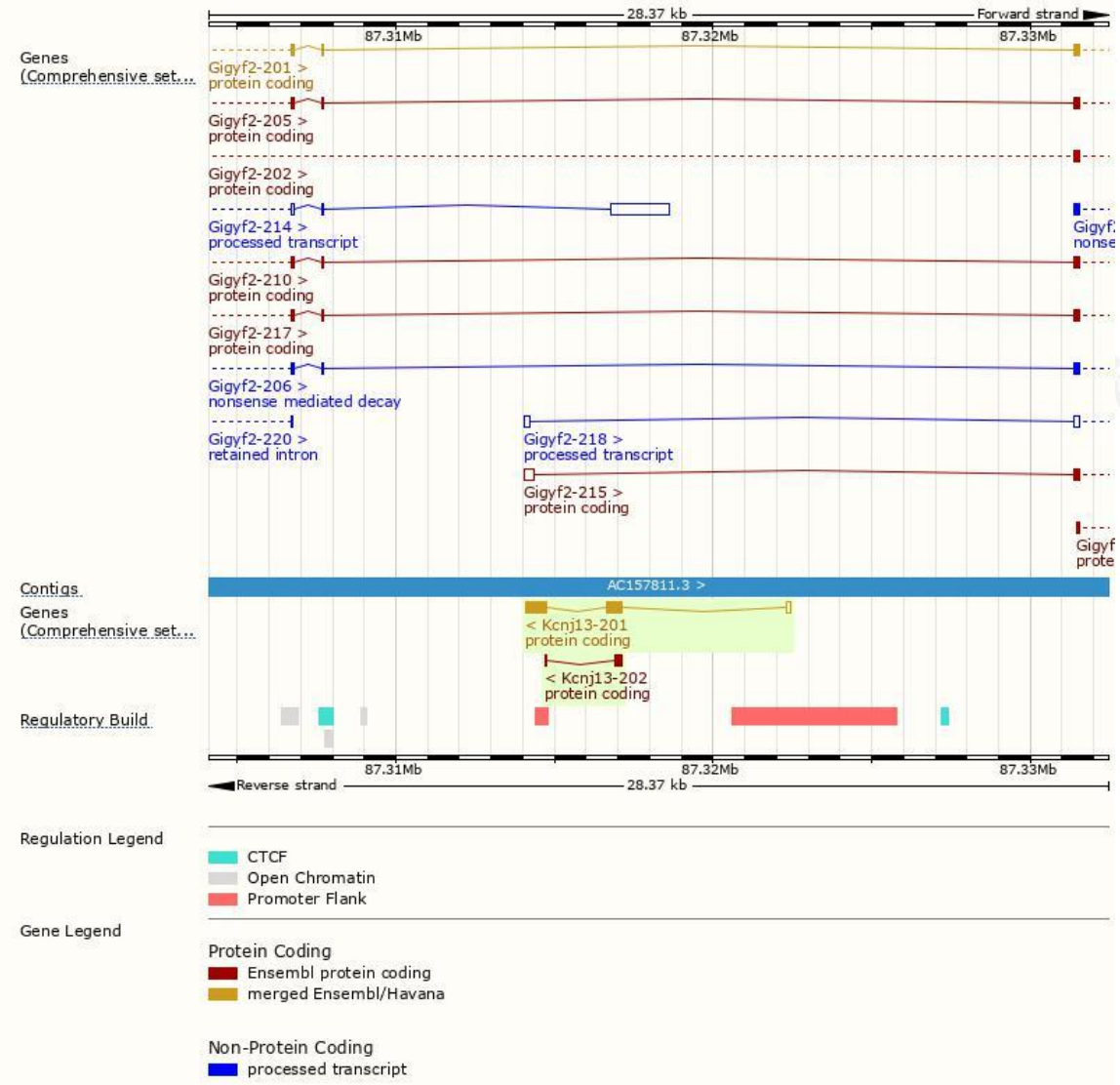
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnj13-201	ENSMUST00000113212.4	1270	360aa	Protein coding	CCDS35653		TSL:2 , GENCODE basic , APPRIS P1 ,
Kcnj13-202	ENSMUST00000174179.2	261	86aa	Protein coding	-		TSL:5 , GENCODE basic ,

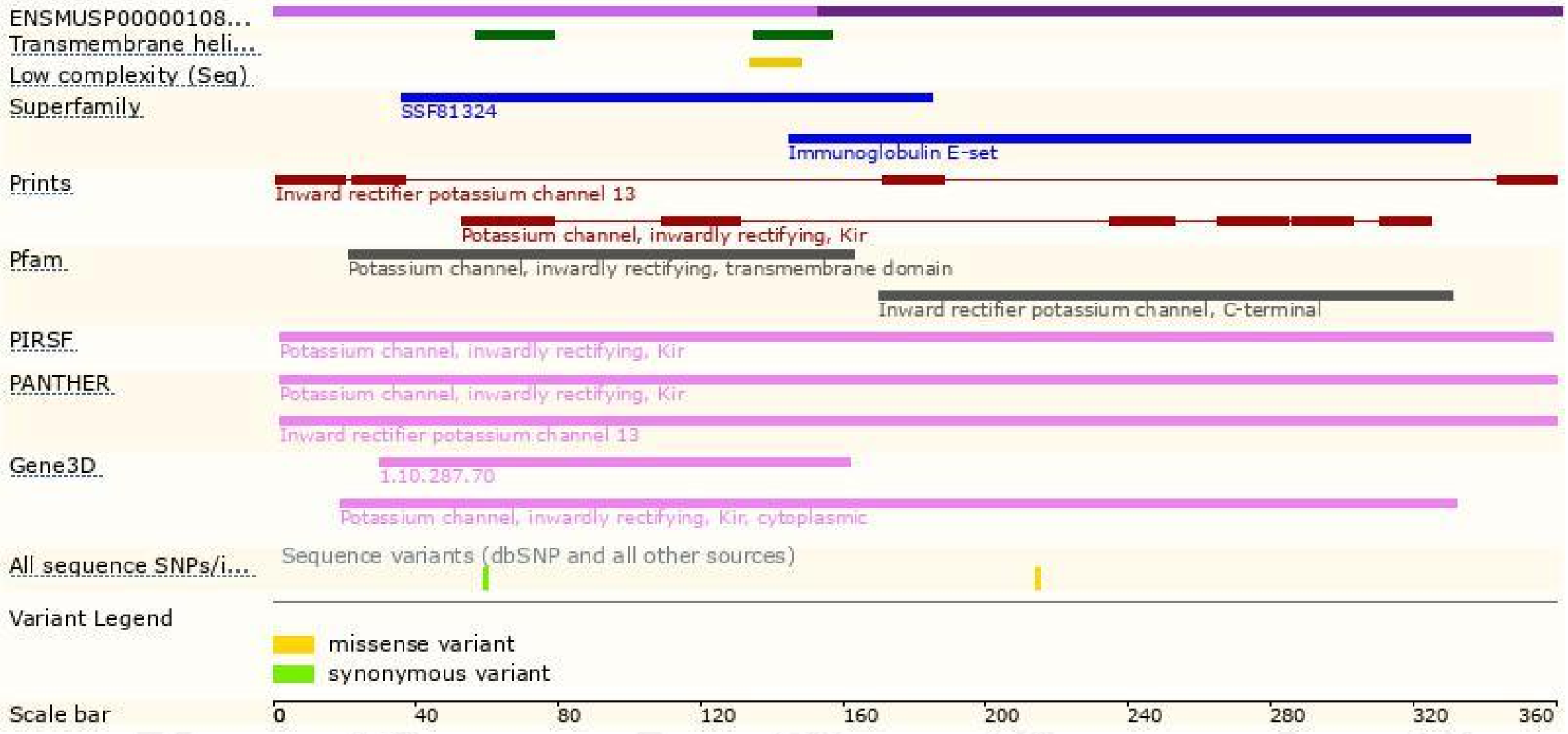
The strategy is based on the design of *Kcnj13-201* transcript,the transcription is shown below:



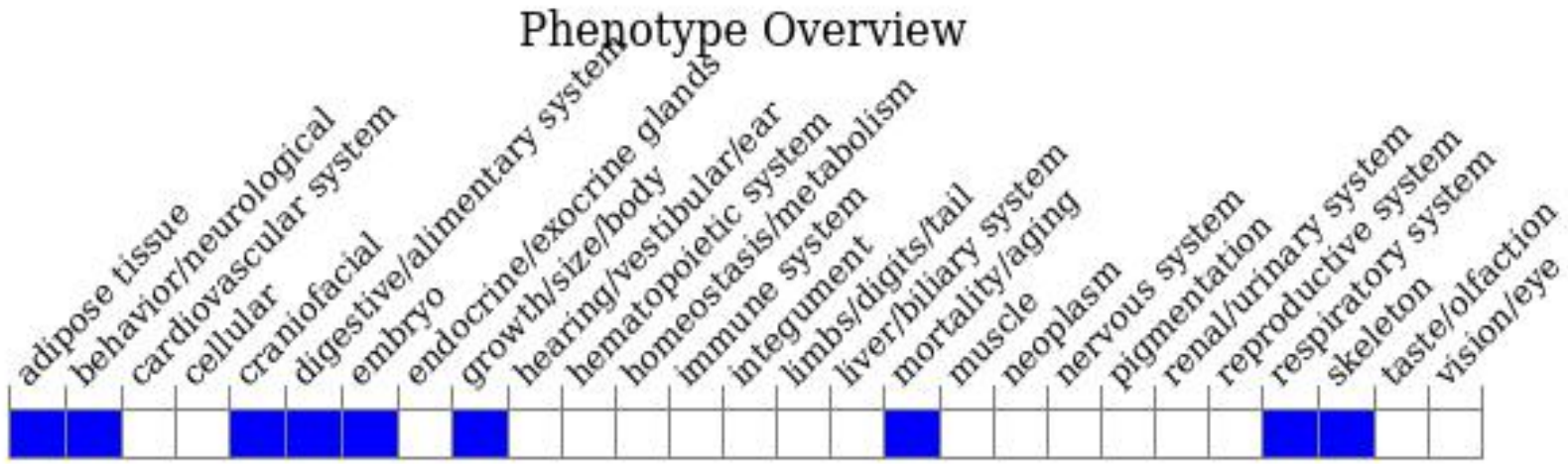
Genomic location distribution



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/).

According to the existing MGI data,homozygous mutant null mice die shortly after birth, exhibit cleft palate and pulmonary abnormalities in embryonic lungs.

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