

Jph2 Cas9-KO Strategy

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Project Overview

Project Name

Jph2

Project type

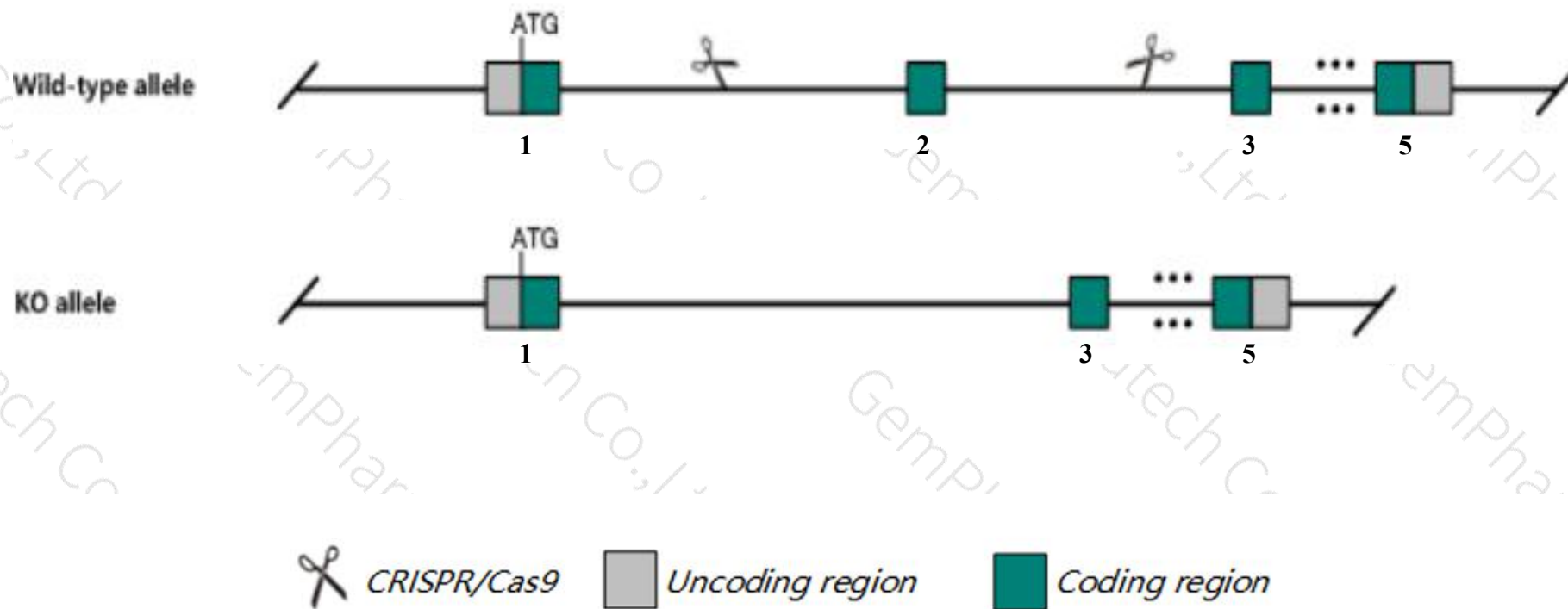
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Jph2* gene. The schematic diagram is as follows:



- The *Jph2* gene has 2 transcripts. According to the structure of *Jph2* gene, exon2 of *Jph2-201* (ENSMUST00000017961.10) transcript is recommended as the knockout region. The region contains 772bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Jph2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, homozygotes for a targeted null mutation exhibit a deficiency of junctional membrane complexes in cardiac myocytes and die by embryonic day 10.5.
- The *Jph2* gene is located on the Chr2. 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)

Jph2 junctophilin 2 [Mus musculus (house mouse)]

Gene ID: 59091, updated on 13-Mar-2020

Summary



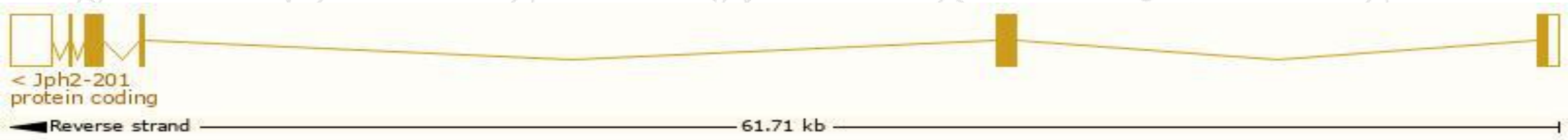
Official Symbol	Jph2 provided by MGI
Official Full Name	junctophilin 2 provided by MGI
Primary source	MGI:MGI:1891496
See related	Ensembl:ENSMUSG00000017817
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110002E14Rik, JP-2, Jp2
Expression	Biased expression in heart adult (RPKM 70.1), bladder adult (RPKM 48.2) and 10 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

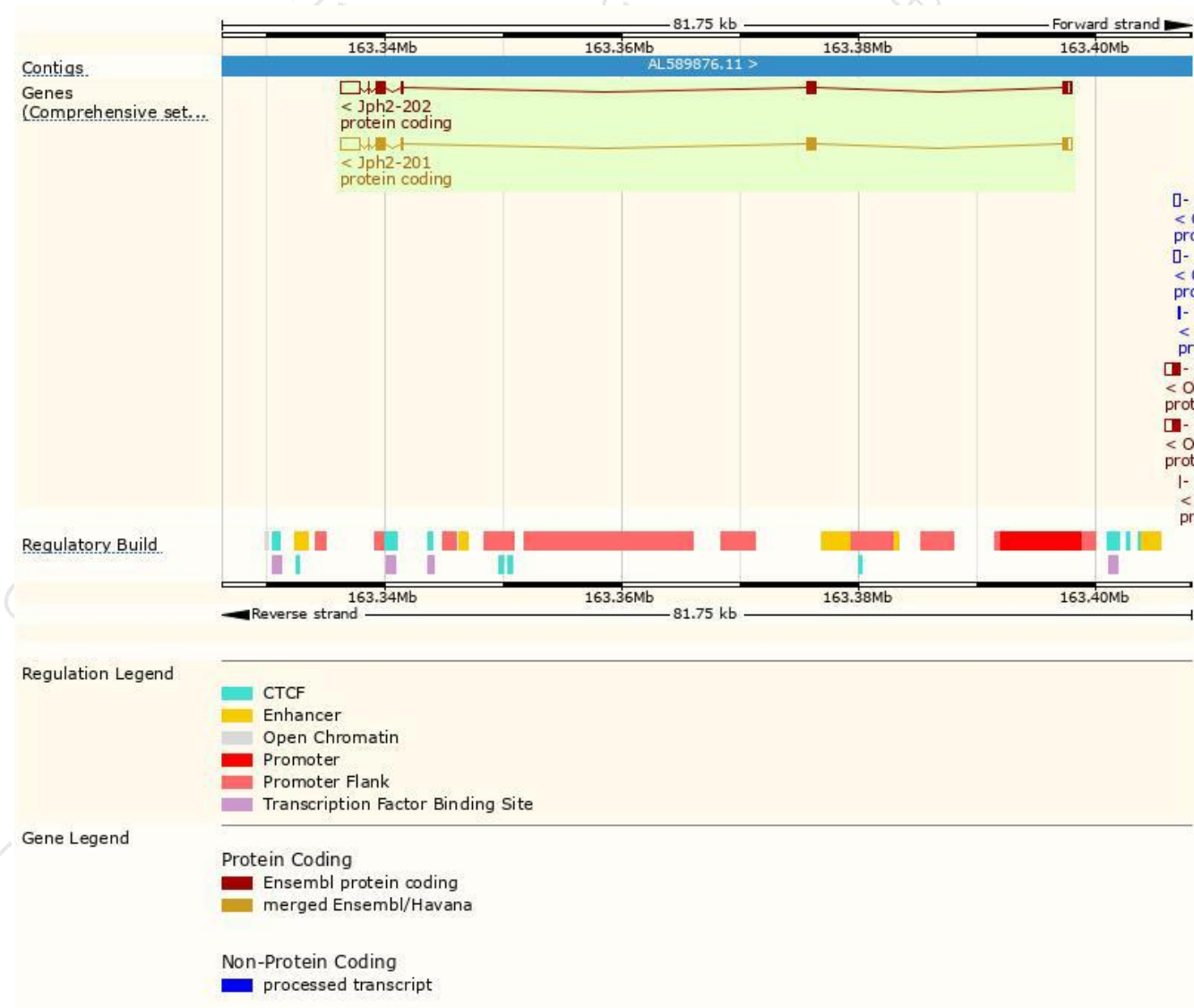
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Jph2-201	ENSMUST00000017961.10	4211	696aa	Protein coding	CCDS17008	Q9ET78	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
Jph2-202	ENSMUST00000109425.2	4155	696aa	Protein coding	CCDS17008	Q9ET78	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

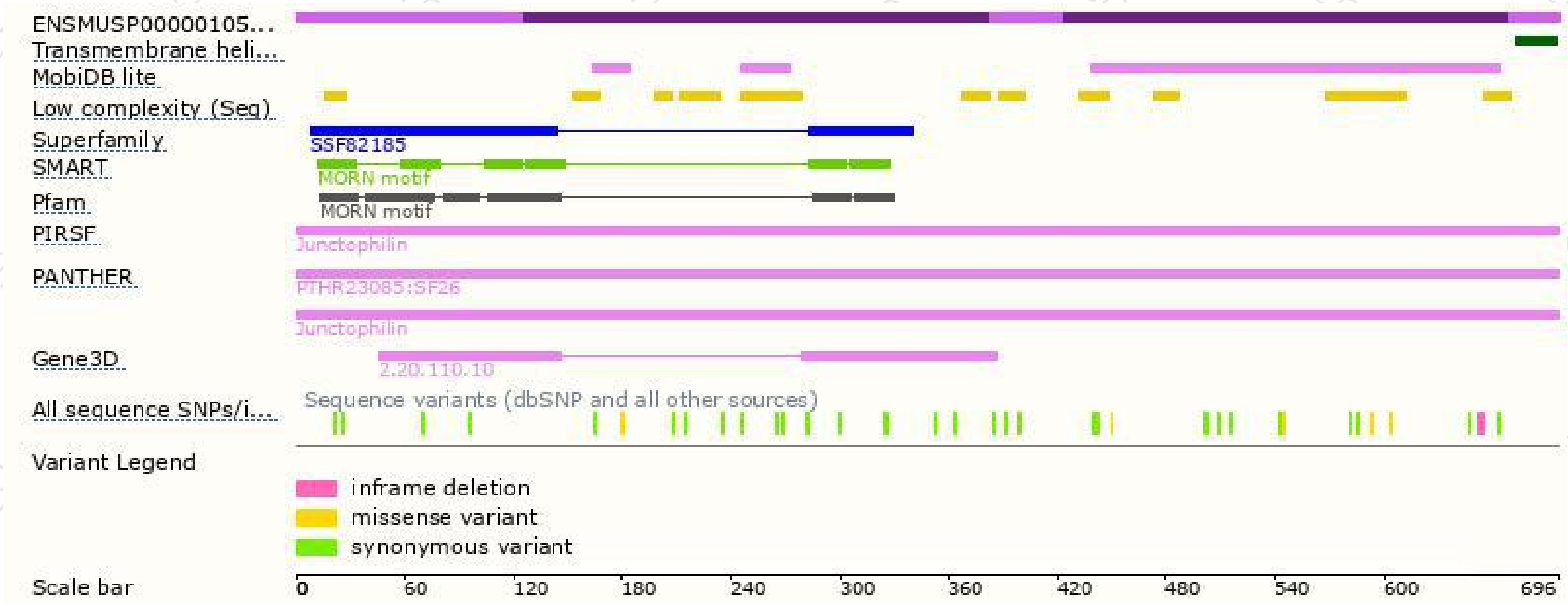
The strategy is based on the design of *Jph2-201* transcript,the transcription is shown below



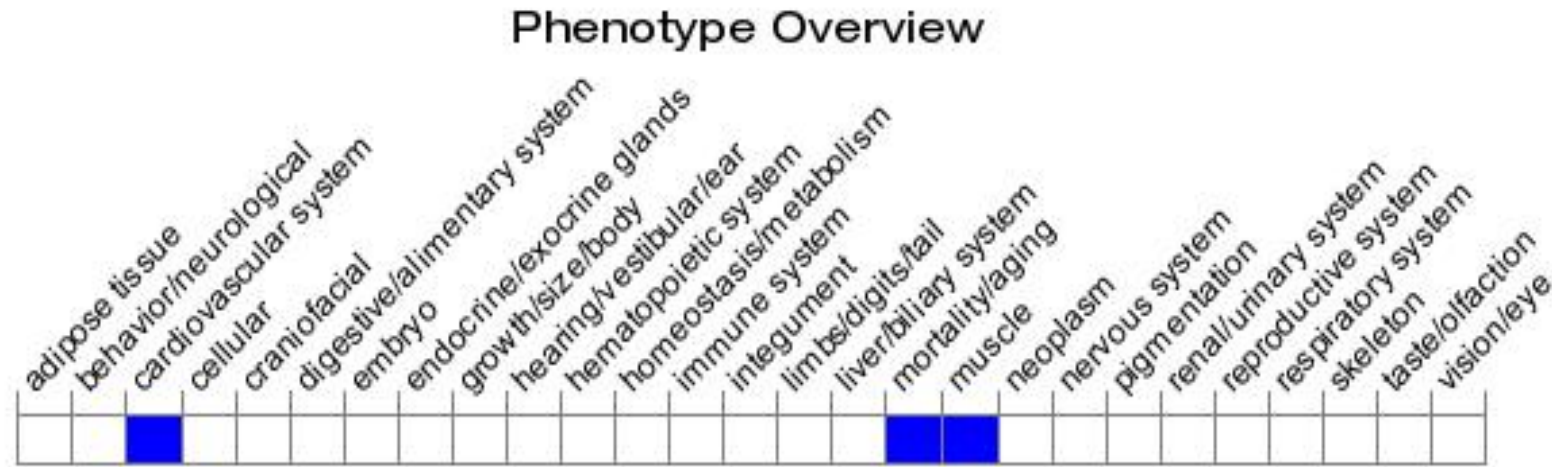
Genomic location distribution



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, homozygotes for a targeted null mutation exhibit a deficiency of junctional membrane complexes in cardiac myocytes and die by embryonic day 10.5.

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

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