

# Jrk Cas9-KO Strategy

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### Overview

#### Target Gene Name

• Jrk

#### Project Type

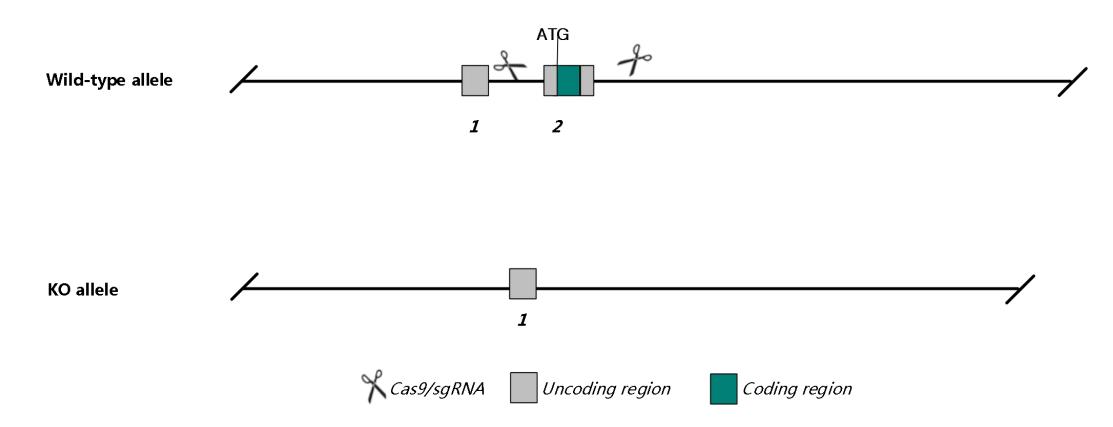
• Cas9-KO

#### Genetic Background

• C57BL/6JGpt



# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Jrk* gene.



#### Technical Information

- The *Jrk* gene has 1 transcript. According to the structure of *Jrk* gene, exon 2 of *Jrk*-201 (ENSMUST0000050234.4) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Jrk* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.



#### Gene Information

#### Jrk jerky [Mus musculus (house mouse)]

Gene ID: 16469, updated on 12-Apr-2023

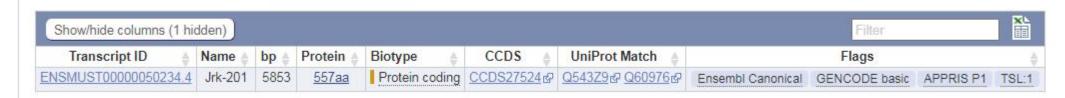


Source: https://www.ncbi.nlm.nih.gov/

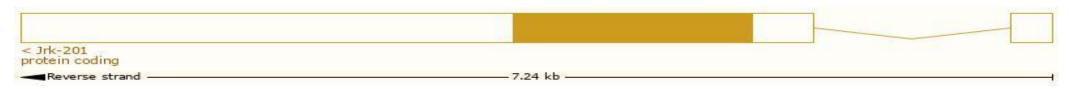


# Transcript Information

The gene has 1 transcript, and the transcript is shown below:



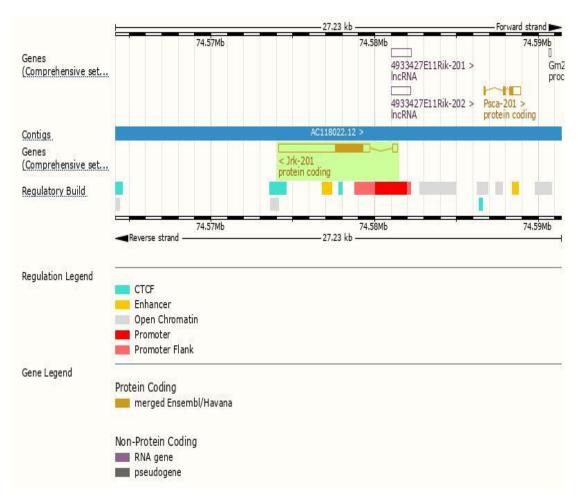
The strategy is based on the design of Jrk-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



## Genomic Information





Source: : https://www.ensembl.org

#### Protein Information





Source: : https://www.ensembl.org

# Important Information

- *Irk* is located on Chr15. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

