Prkd3 Cas9-KO Strategy

Designer: Huan Fan

Reviewer: Huan Wang

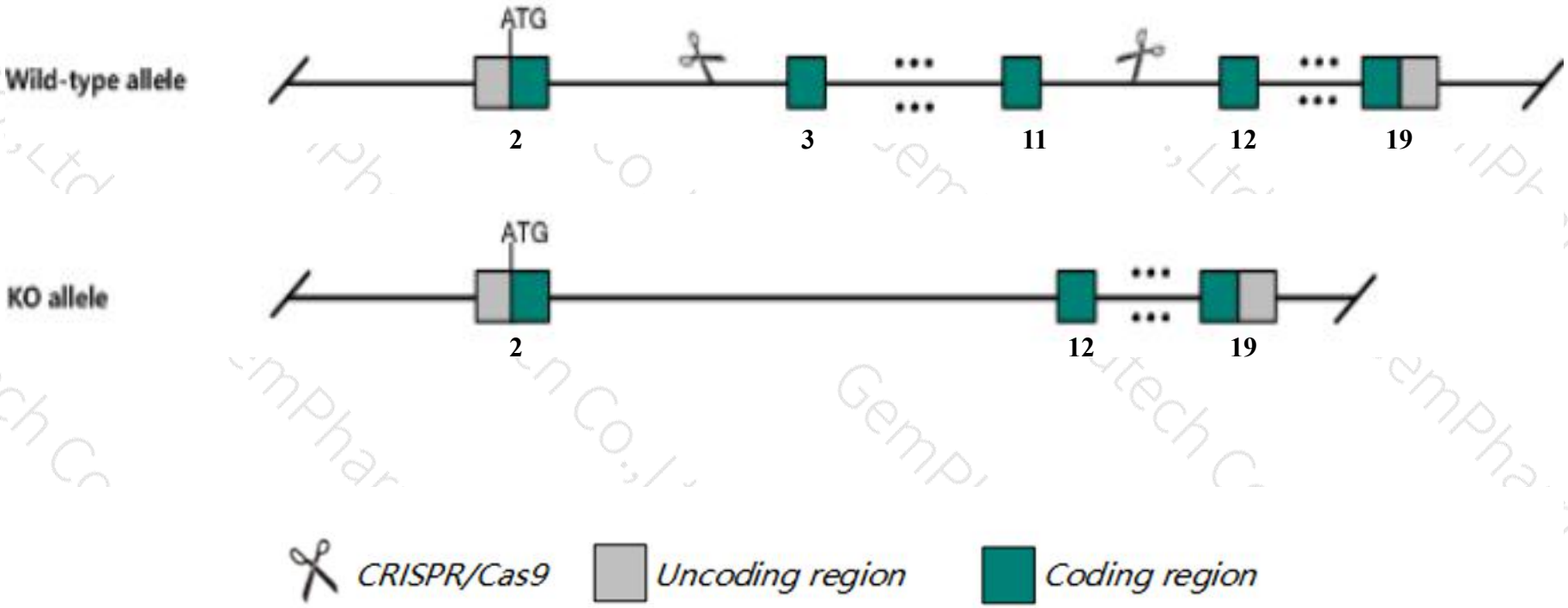
Design Date: 2020-4-16

Project Overview

Project Name	***Prkd3***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prkd3* gene. The schematic diagram is as follows:



Technical routes

➢ The *Prkd3* gene has 8 transcripts. According to the structure of *Prkd3* gene, exon3-exon11 of *Prkd3-204* (ENSMUST00000119284.7) transcript is recommended as the knockout region.The region contains 1363bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Prkd3* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,homozygous mutation of this gene results in abnormal vertebral trabecular bone morphology and abnormal femur morphology.
- The *Prkd3* gene is located on the Chr17. 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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Prkd3 protein kinase D3 [Mus musculus (house mouse)]

Gene ID: 75292, updated on 13-Mar-2020

Summary

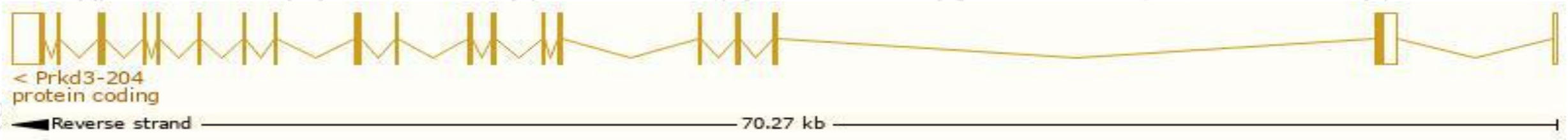
Official Symbol	Prkd3 provided by MGI
Official Full Name	protein kinase D3 provided byMGI
Primary source	MGI:MGI:1922542
See related	Ensembl:ENSMUSG00000024070
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930557O20Rik, 5730497N19Rik, PKD3, Pkcnu, Prkcn
Expression	Ubiquitous expression in CNS E11.5 (RPKM 13.1), limb E14.5 (RPKM 11.2) and 25 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

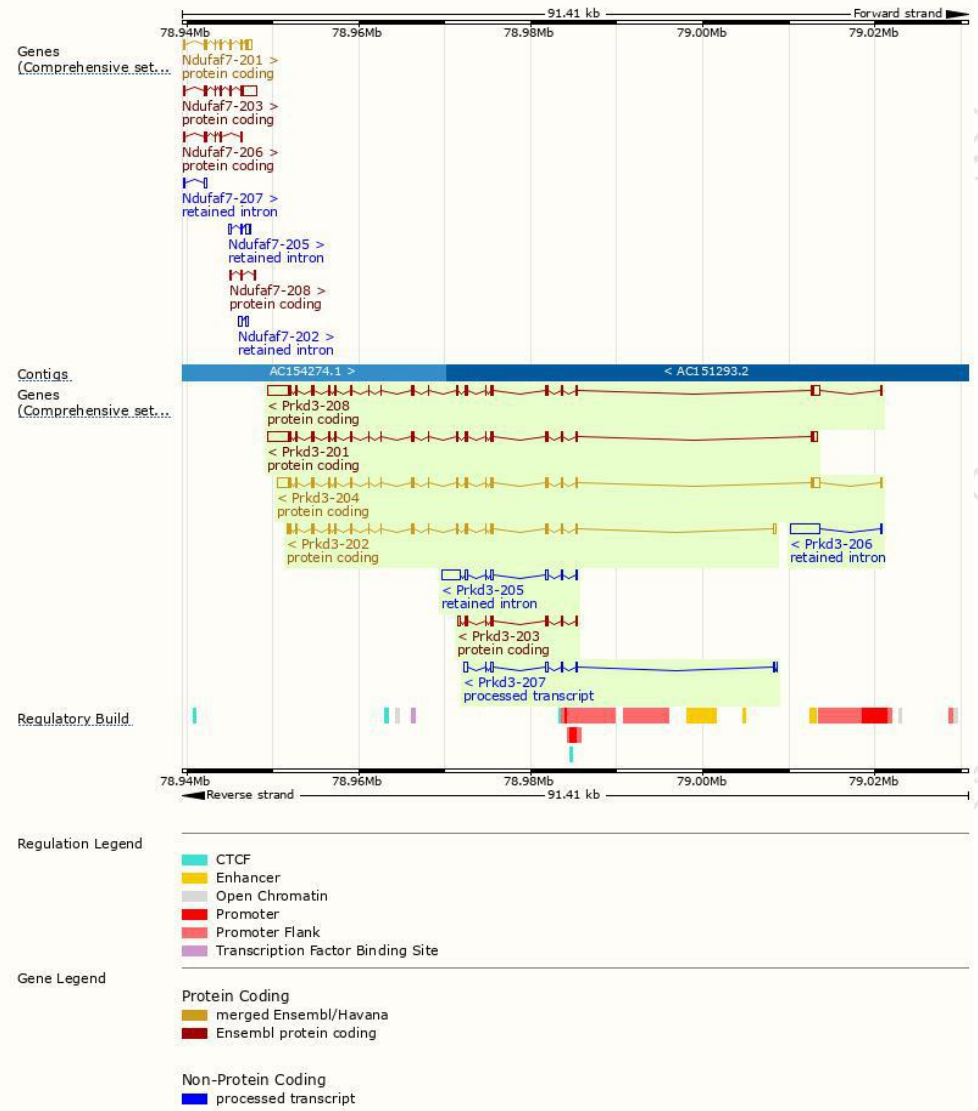
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prkd3-208	ENSMUST00000168887.7	5884	889aa	Protein coding	CCDS37699	Q8K1Y2	TSL:5 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 P3
Prkd3-201	ENSMUST00000003191.13	5517	889aa	Protein coding	CCDS37699	Q8K1Y2	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 P3
Prkd3-204	ENSMUST00000119284.7	4743	890aa	Protein coding	CCDS50185	Q5FWX6	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 ALT1
Prkd3-202	ENSMUST00000118768.7	2847	795aa	Protein coding	CCDS50184	D3Z6I0	TSL:1 GENCODE basic
Prkd3-203	ENSMUST00000118991.1	1265	297aa	Protein coding	-	D3YU02	TSL:2 GENCODE basic
Prkd3-207	ENSMUST00000146917.1	1214	No protein	Processed transcript	-	-	TSL:2
Prkd3-206	ENSMUST00000130070.1	3508	No protein	Retained intron	-	-	TSL:2
Prkd3-205	ENSMUST00000124229.7	3201	No protein	Retained intron	-	-	TSL:2

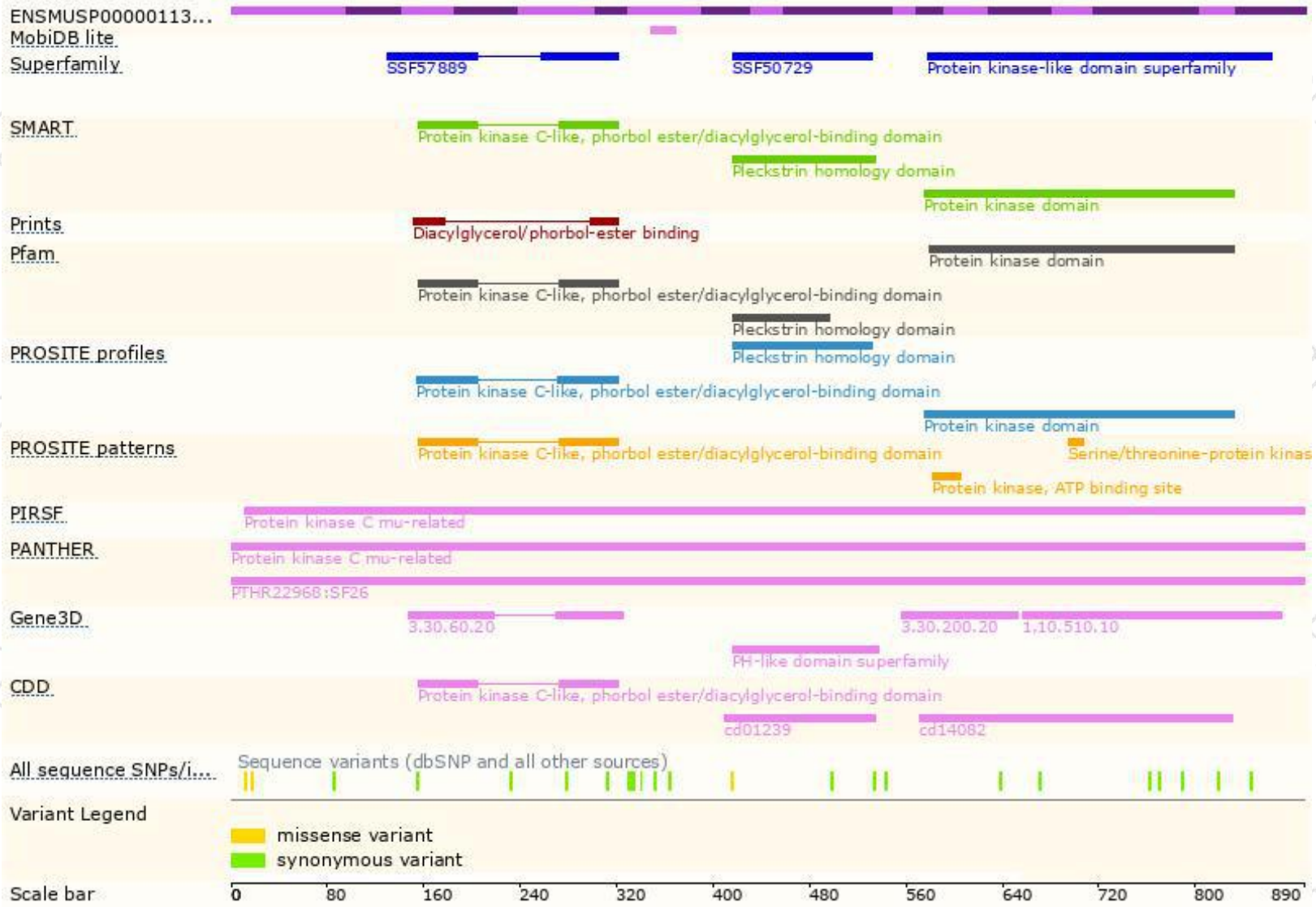
The strategy is based on the design of *Prkd3-204* transcript,the transcription is shown below



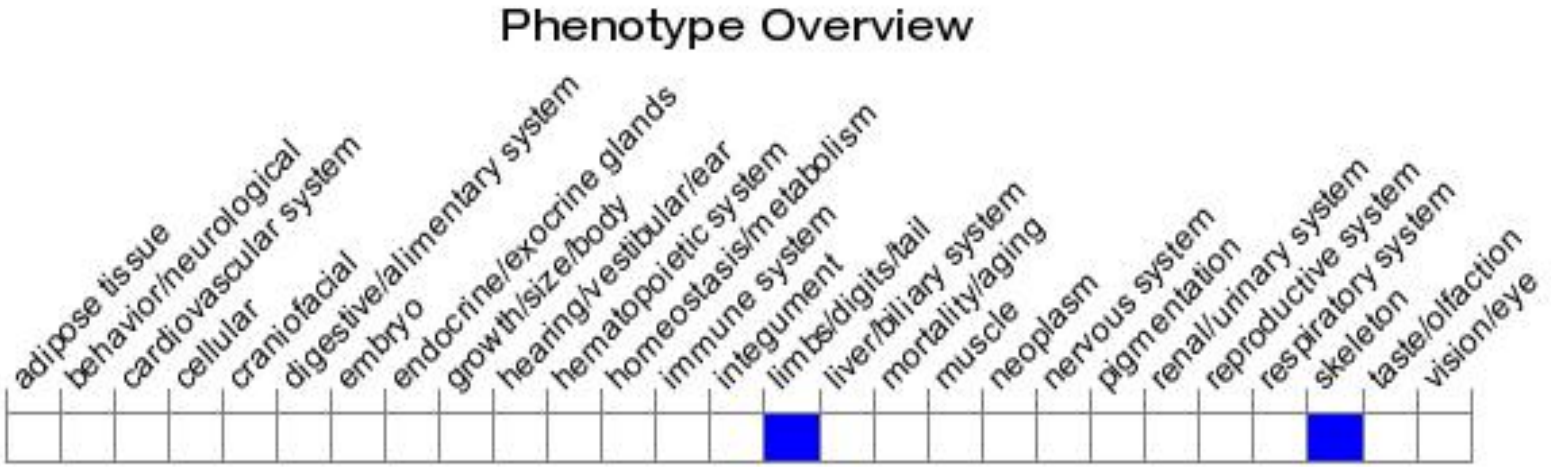
Genomic location distribution



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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集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd