

# *Pkn1* Cas9-KO Strategy

Designer:

# Project Overview

**Project Name**

***Pkn1***

**Project type**

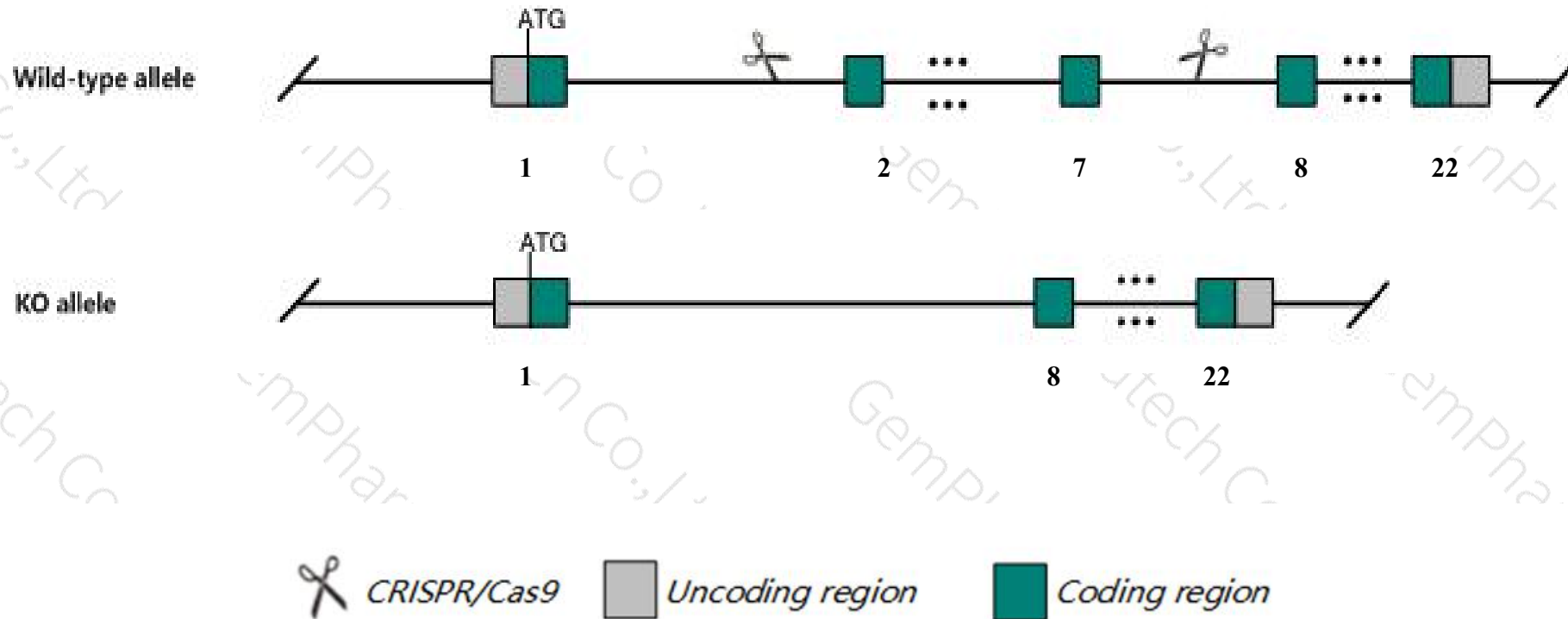
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pkn1* gene. The schematic diagram is as follows:



- The *Pkn1* gene has 9 transcripts. According to the structure of *Pkn1* gene, exon2-exon7 of *Pkn1*-208 (ENSMUST00000144258.7) transcript is recommended as the knockout region. The region contains 1153bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pkn1* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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.

- According to the existing MGI data, Homozygotes for a null allele show spontaneous germinal center formation and autoantibody production and develop glomerulonephritis. Homozygotes for a different null allele have mild systolic and diastolic dysfunction, and show increased myocardial infarction size after ischemia-reperfusion injury.
- The *Pkn1* gene is located on the Chr8. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.



# Gene information (NCBI)

## Pkn1 protein kinase N1 [Mus musculus (house mouse)]

Gene ID: 320795, updated on 2-Mar-2019

### Summary



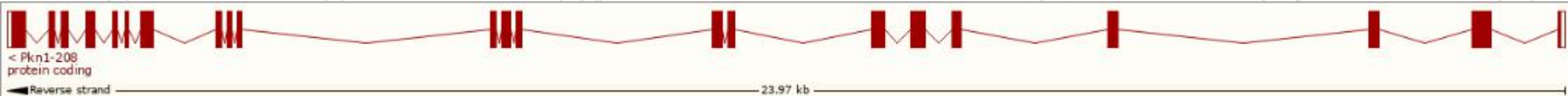
<b>Official Symbol</b>	Pkn1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	protein kinase N1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:108022</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000057672</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	DBK, F730027O18Rik, PAK1, PRK1, Pkn, Prkcl1, Stk3
<b>Expression</b>	Ubiquitous expression in thymus adult (RPKM 55.4), spleen adult (RPKM 49.1) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

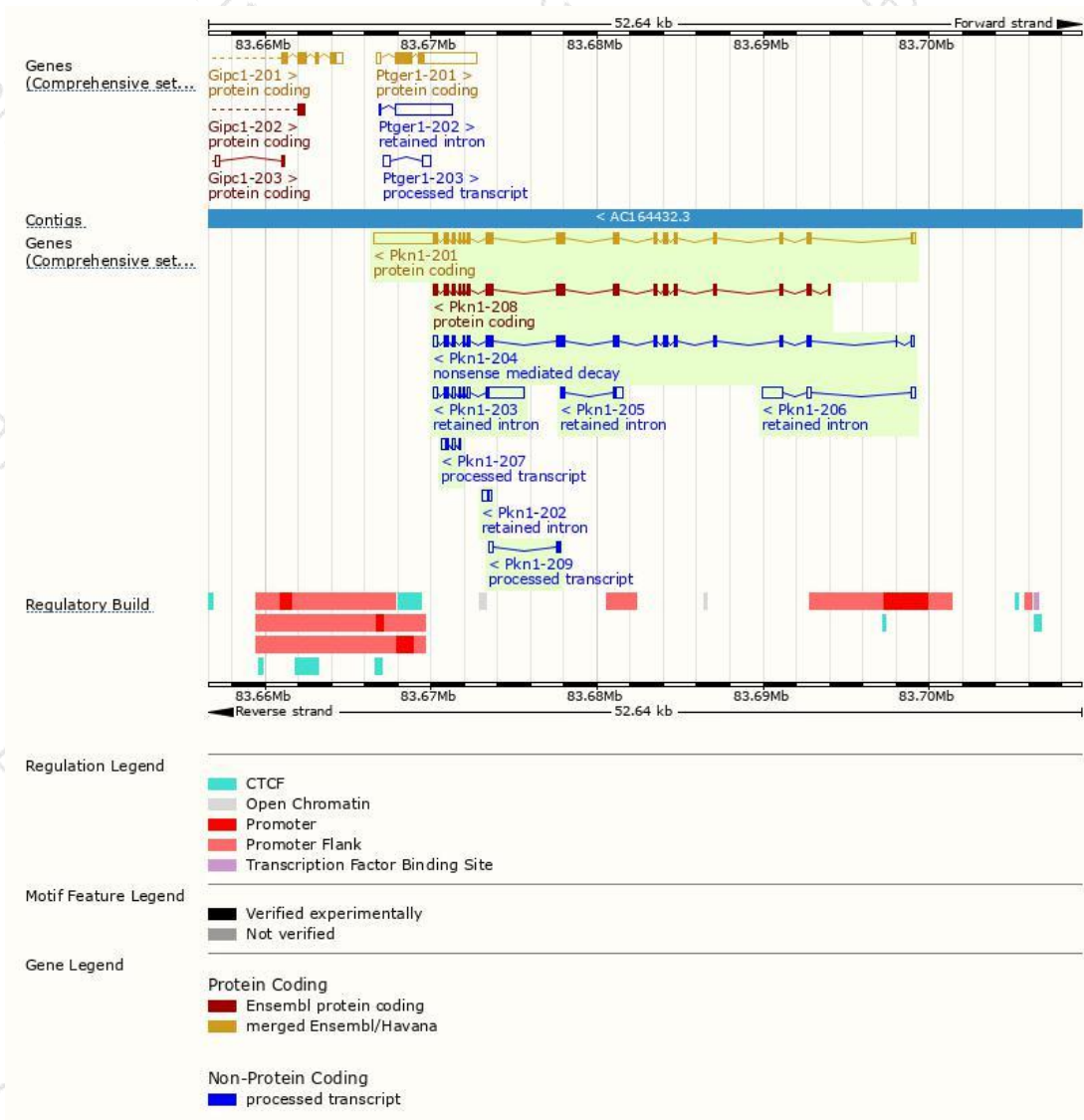
The gene has 9 transcript,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pkn1-201	<a href="#">ENSMUST00000005616.15</a>	6662	<a href="#">946aa</a>	Protein coding	<a href="#">CCDS22459</a>	<a href="#">P70268</a>	TSL:1 GENCODE basic APPRIS P3
Pkn1-208	<a href="#">ENSMUST00000144258.7</a>	2995	<a href="#">951aa</a>	Protein coding	<a href="#">CCDS57627</a>	<a href="#">P70268</a>	TSL:1 GENCODE basic APPRIS ALT 1
Pkn1-204	<a href="#">ENSMUST00000132945.7</a>	3005	<a href="#">796aa</a>	Nonsense mediated decay	-	<a href="#">D6RH37</a>	TSL:1
Pkn1-207	<a href="#">ENSMUST00000138898.1</a>	548	No protein	Processed transcript	-	-	TSL:2
Pkn1-209	<a href="#">ENSMUST00000146057.1</a>	450	No protein	Processed transcript	-	-	TSL:2
Pkn1-203	<a href="#">ENSMUST00000128523.7</a>	3070	No protein	Retained intron	-	-	TSL:1
Pkn1-206	<a href="#">ENSMUST00000135356.1</a>	1783	No protein	Retained intron	-	-	TSL:1
Pkn1-205	<a href="#">ENSMUST00000133195.1</a>	694	No protein	Retained intron	-	-	TSL:3
Pkn1-202	<a href="#">ENSMUST00000124946.1</a>	483	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Pkn1-208* transcript,The transcription is shown below

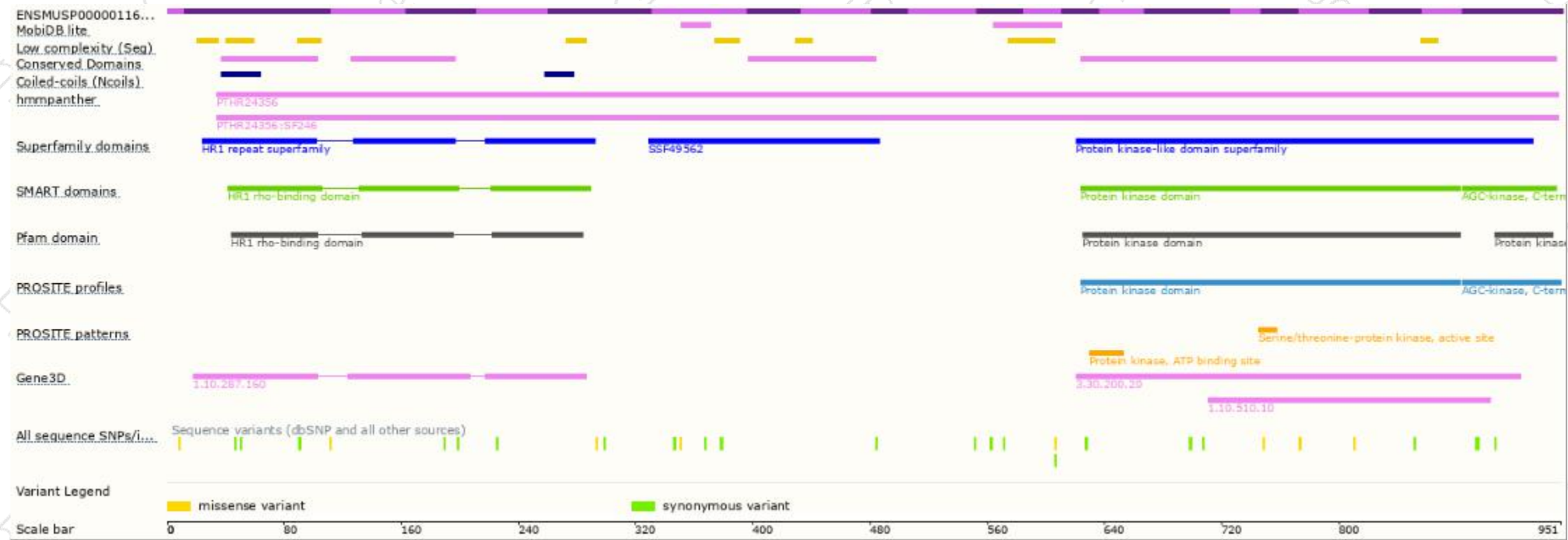


# Genomic location distribution

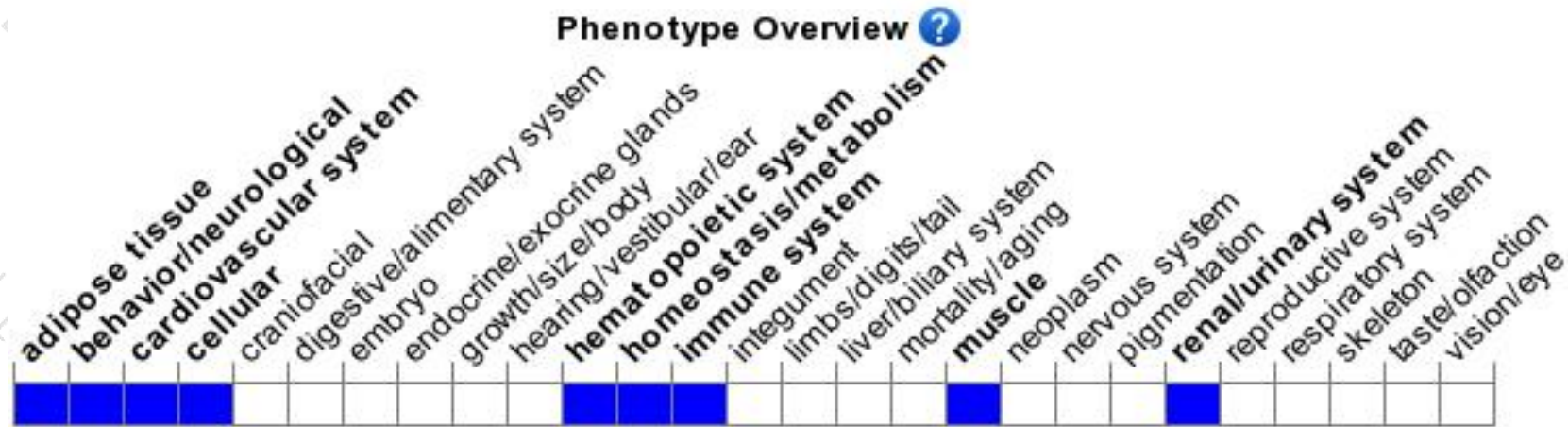




# Protein domain



# 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 null allele show spontaneous germinal center formation and autoantibody production and develop glomerulonephritis. Homozygotes for a different null allele have mild systolic and diastolic dysfunction, and show increased myocardial infarction size after ischemia-reperfusion injury.

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

Tel: 400-9660890

