

# ***Grk2* Cas9-KO Strategy**

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# Project Overview

**Project Name**

***Grk2***

**Project type**

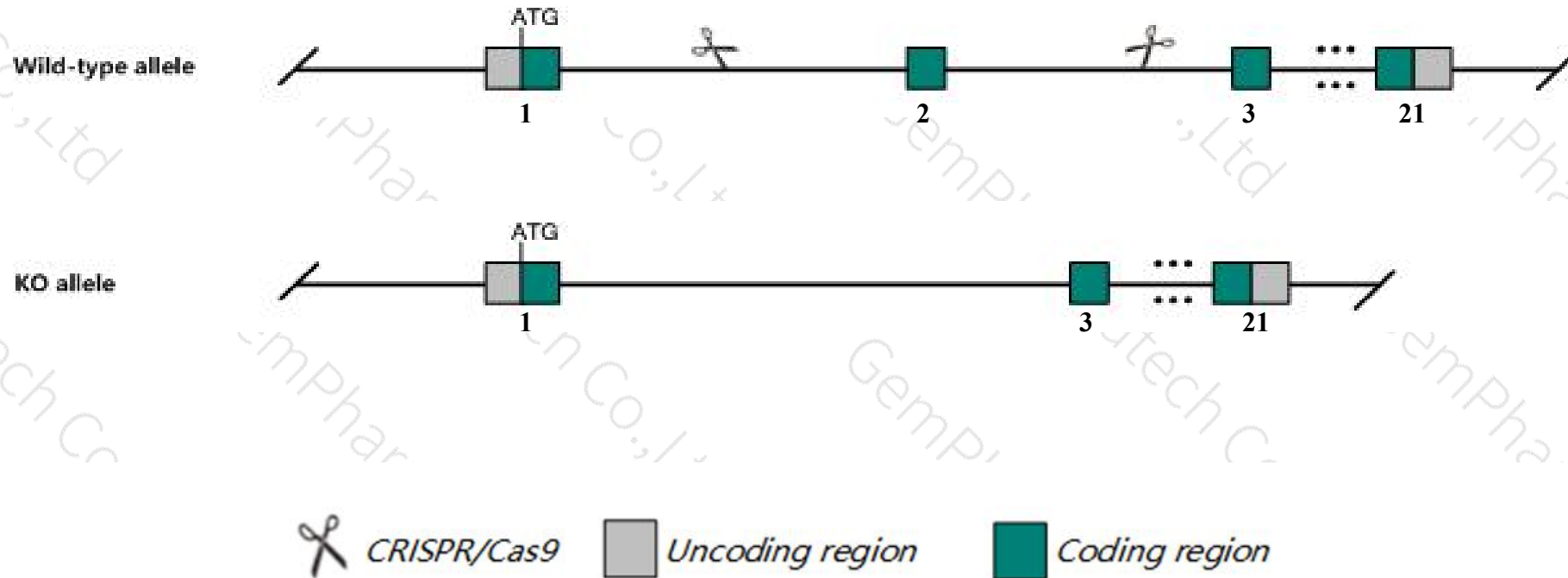
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Grk2* gene. The schematic diagram is as follows:



- The *Grk2* gene has 9 transcripts. According to the structure of *Grk2* gene, exon2 of *Grk2-202* (ENSMUST00000088737.10) transcript is recommended as the knockout region. The region contains 77bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Grk2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous mutation of this gene results in embryonic lethality likely due to heart failure. Homozygous mutant embryos are pale in appearance and exhibit ventricular hypoplasia.
- The *Grk2* gene is located on the Chr19. 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)

## Grk2 G protein-coupled receptor kinase 2 [Mus musculus (house mouse)]

Gene ID: 110355, updated on 2-Apr-2019

### Summary



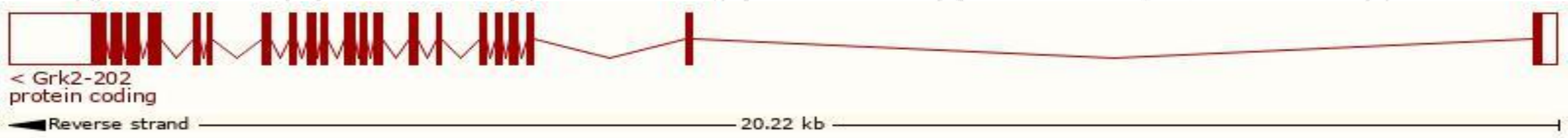
<b>Official Symbol</b>	Grk2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	G protein-coupled receptor kinase 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:87940</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000024858</a>
<b>Gene type</b>	protein coding
<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>	Adrbk-1, Adrbk1, Bark-1, beta ARK, betaARK1
<b>Expression</b>	Ubiquitous expression in spleen adult (RPKM 143.0), thymus adult (RPKM 142.5) and 27 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information（Ensembl）

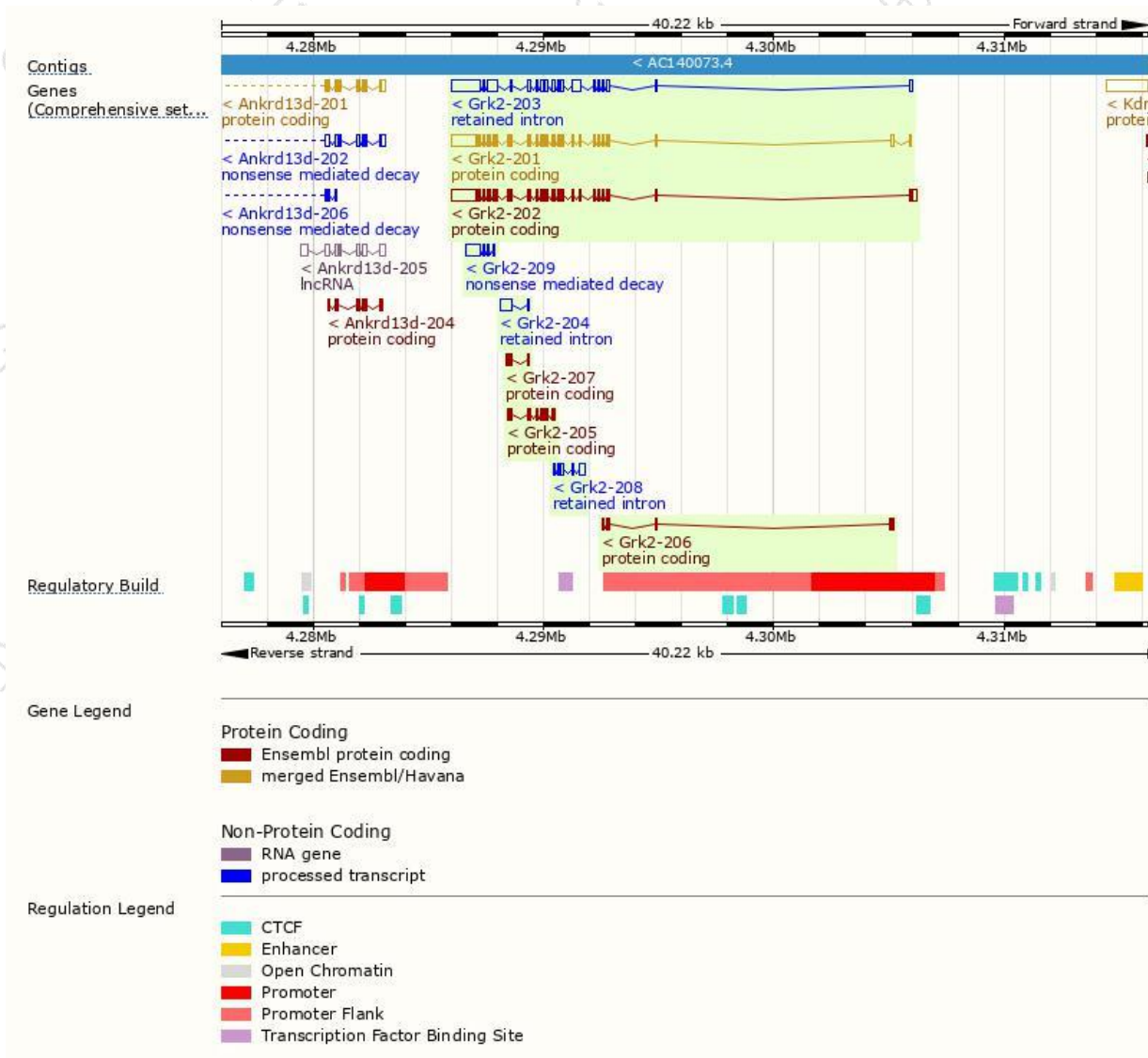
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Grk2-202	<a href="#">ENSMUST00000088737.10</a>	3376	<a href="#">689aa</a>	Protein coding	<a href="#">CCDS70915</a>	<a href="#">Q3U1V3 Q99MK8</a>	TSL:1 GENCODE basic APPRIS P1
Grk2-201	<a href="#">ENSMUST00000025791.11</a>	3182	<a href="#">647aa</a>	Protein coding	<a href="#">CCDS29426</a>	<a href="#">Q7TS64</a>	TSL:1 GENCODE basic
Grk2-205	<a href="#">ENSMUST00000165954.1</a>	624	<a href="#">208aa</a>	Protein coding	-	<a href="#">F6QY34</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Grk2-206	<a href="#">ENSMUST00000167511.2</a>	403	<a href="#">110aa</a>	Protein coding	-	<a href="#">F6Y9P3</a>	CDS 3' incomplete TSL:3
Grk2-207	<a href="#">ENSMUST00000168594.7</a>	261	<a href="#">87aa</a>	Protein coding	-	<a href="#">F7AEX1</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Grk2-209	<a href="#">ENSMUST00000235681.1</a>	853	<a href="#">26aa</a>	Nonsense mediated decay	-	-	CDS 5' incomplete
Grk2-203	<a href="#">ENSMUST00000113837.8</a>	3476	No protein	Retained intron	-	-	TSL:2
Grk2-204	<a href="#">ENSMUST00000164427.1</a>	608	No protein	Retained intron	-	-	TSL:3
Grk2-208	<a href="#">ENSMUST00000169991.1</a>	557	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Grk2-202* transcript,The transcription is shown below

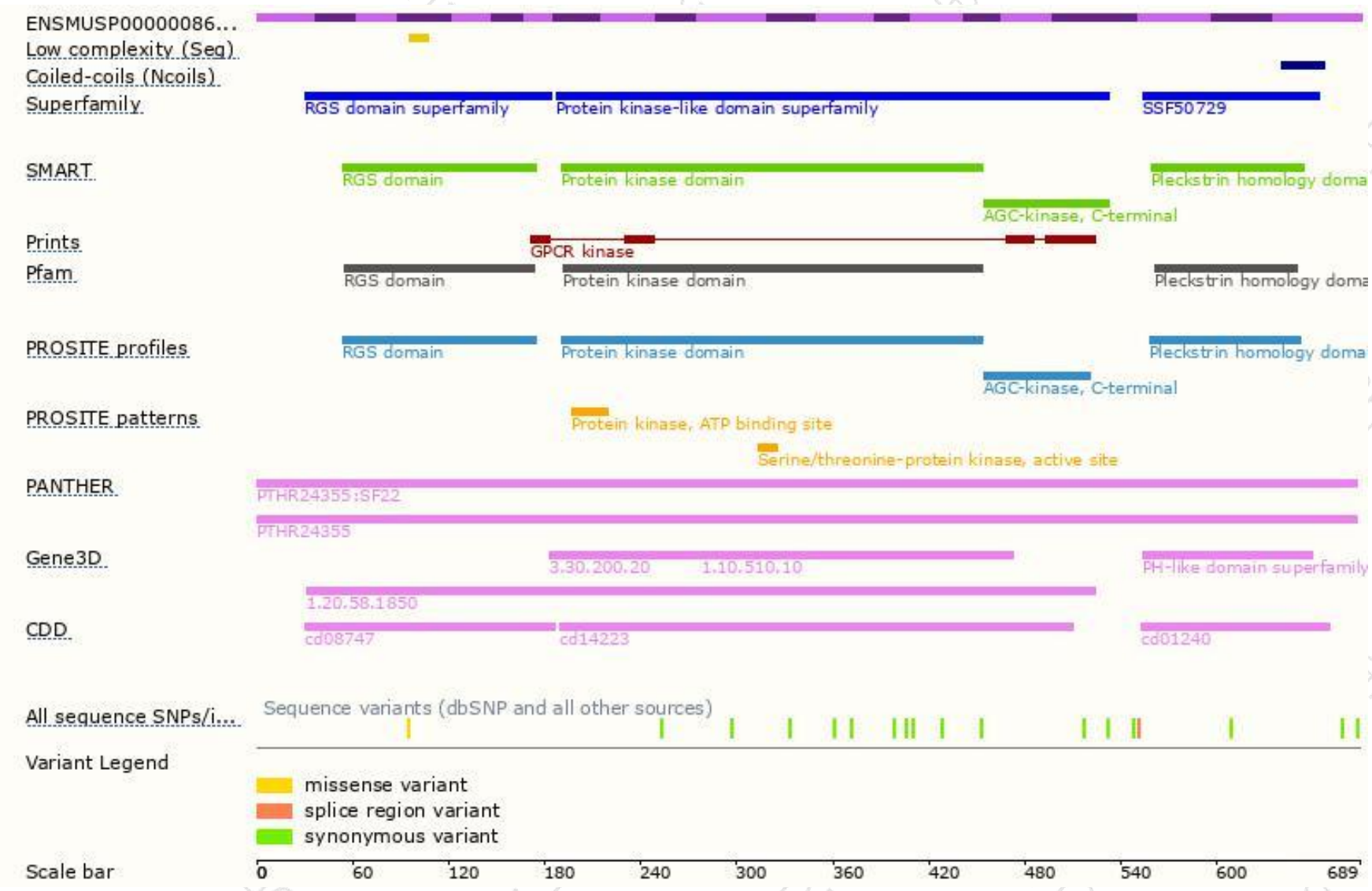


# Genomic location distribution

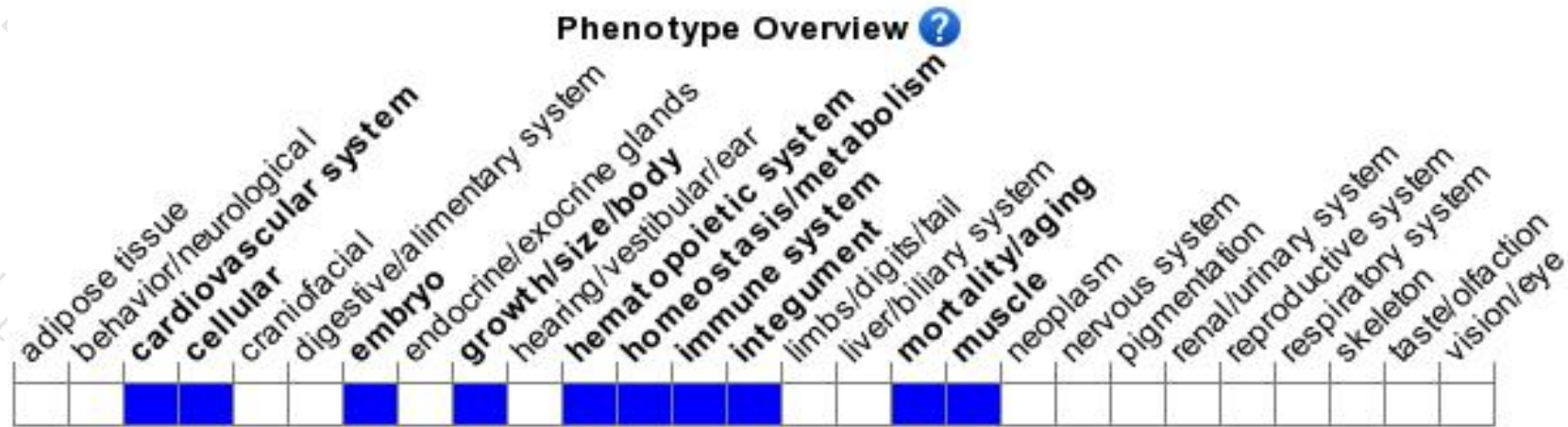




# Protein domain



# 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 mutation of this gene results in embryonic lethality likely due to heart failure. Homozygous mutant embryos are pale in appearance and exhibit ventricular hypoplasia.

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

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