

Pde9a Cas9-KO Strategy

Designer:

Huimin Su

Reviewer:

Ruirui Zhang

Design Date:

2020-2-19

Project Overview

Project Name

Pde9a

Project type

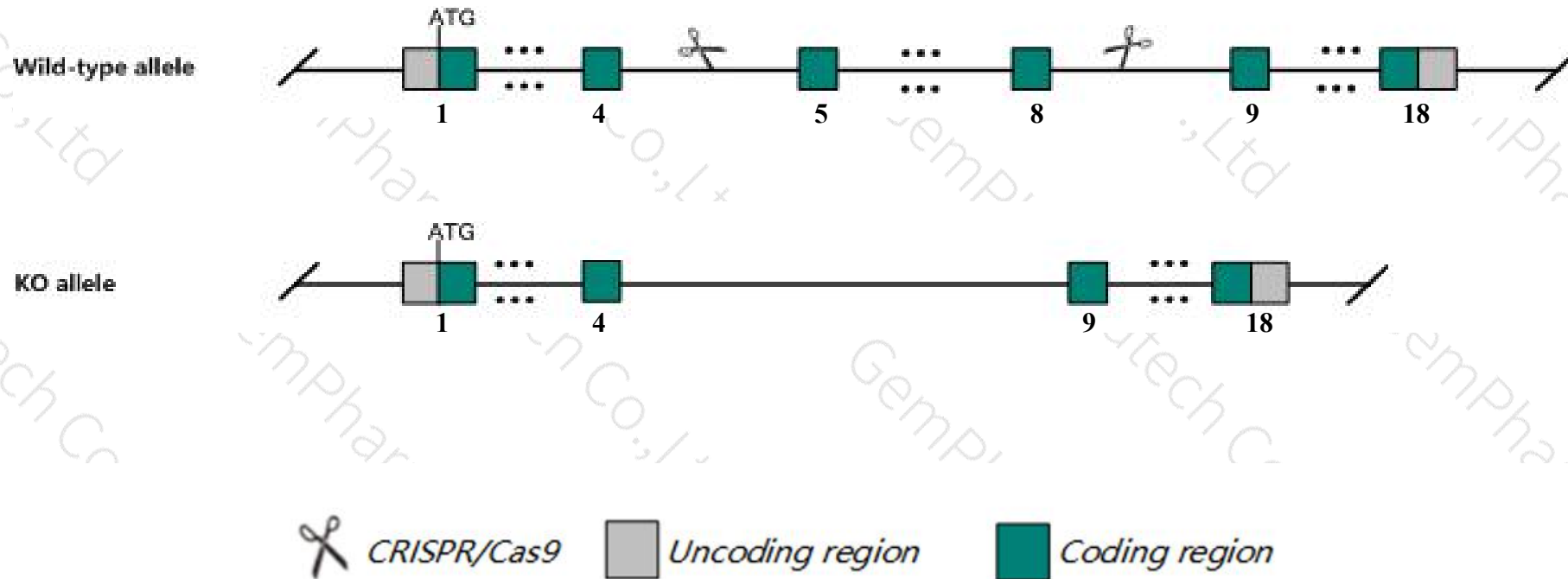
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pde9a* gene. The schematic diagram is as follows:



- The *Pde9a* gene has 28 transcripts. According to the structure of *Pde9a* gene, exon5-exon8 of *Pde9a-201* (ENSMUST00000047168.12) transcript is recommended as the knockout region. The region contains 290bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pde9a* gene. The brief process is as follows: CRISPR/Cas9 system will

- According to the existing MGI data, Mice homozygous for a null allele exhibit suppressed pressure-overload-induced cardiac pathobiology.
- The *Gm50138* gene may be affected.
- The *Pde9a* 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)

Pde9a phosphodiesterase 9A [*Mus musculus* (house mouse)]

Gene ID: 18585, updated on 12-Aug-2019

Summary

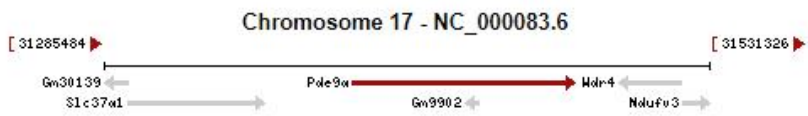
Official Symbol Pde9a provided by [MGI](#)
Official Full Name phosphodiesterase 9A provided by [MGI](#)
Primary source [MGI: MGI:1277179](#)
See related [Ensembl: ENSMUSG00000041119](#)
Gene type protein coding
RefSeq status VALIDATED
Organism [Mus musculus](#)
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as PDE9A1
Expression Broad expression in colon adult (RPKM 62.7), large intestine adult (RPKM 61.1) and 19 other tissues [See more](#)
Orthologs [human](#) [all](#)

Genomic context

Location: 17; 17 B1 [See Pde9a in Genome Data Viewer](#)

Exon count: 20

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	17	NC_000083.6 (31386105..31476309)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	17	NC_000083.5 (31523179..31613254)

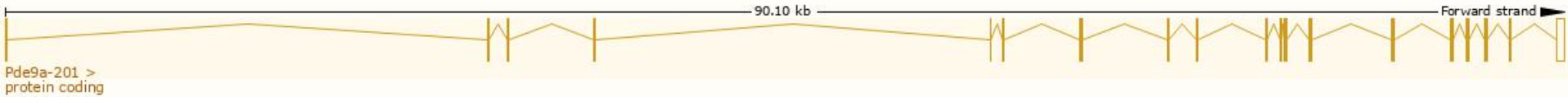


Transcript information (Ensembl)

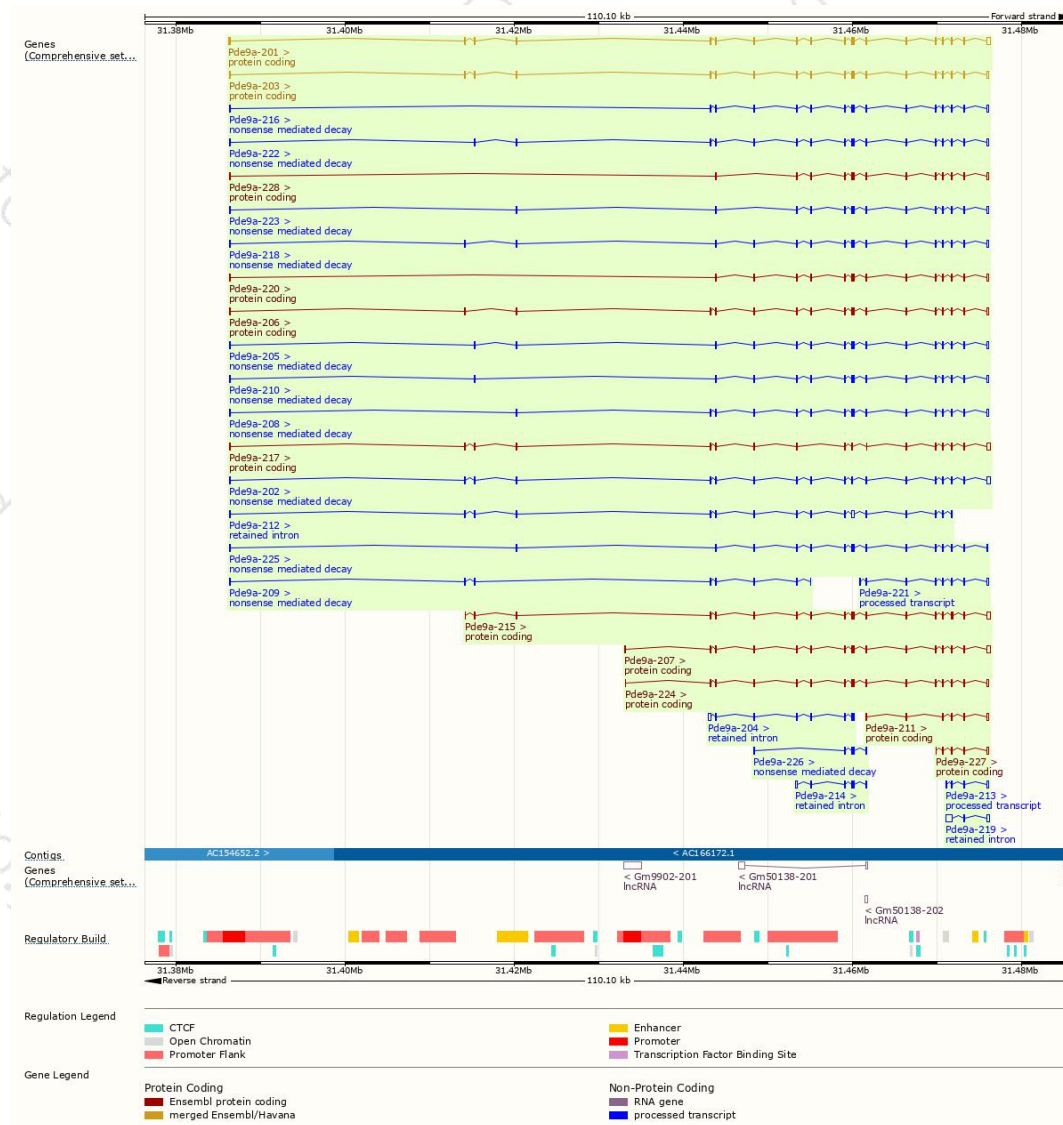
The gene has 28 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pde9a-201	ENSMUST00000047168.12	2089	534aa	Protein coding	CCDS28605.6	Q70628.6	TSL:1 GENCODE basic APPRIS P2
Pde9a-203	ENSMUST00000127929.7	1891	534aa	Protein coding	CCDS28605.6	Q70628.6	TSL:1 GENCODE basic APPRIS P2
Pde9a-215	ENSMUST00000235639.1	1913	495aa	Protein coding	-	A0A494BAJ0.6	CDS 5' incomplete
Pde9a-207	ENSMUST00000136384.8	1887	387aa	Protein coding	-	D3Z408.6	TSL:2 GENCODE basic
Pde9a-206	ENSMUST00000134525.8	1810	508aa	Protein coding	-	D3YTQ4.6	TSL:5 GENCODE basic APPRIS ALT2
Pde9a-217	ENSMUST00000235719.1	1787	452aa	Protein coding	-	A0A494BAI4.6	GENCODE basic
Pde9a-224	ENSMUST00000237363.1	1660	383aa	Protein coding	-	A0A494BBD2.6	GENCODE basic
Pde9a-220	ENSMUST00000236454.1	1640	387aa	Protein coding	-	D3Z408.6	GENCODE basic
Pde9a-228	ENSMUST00000238091.1	1555	377aa	Protein coding	-	A0A494B9U5.6	GENCODE basic
Pde9a-211	ENSMUST00000154392.1	778	180aa	Protein coding	-	F6ZAU1.6	CDS 5' incomplete TSL:3
Pde9a-227	ENSMUST00000238006.1	591	115aa	Protein coding	-	A0A494BAI3.6	CDS 5' incomplete
Pde9a-202	ENSMUST00000124902.8	1904	102aa	Nonsense mediated decay	-	D6RH57.6	TSL:5
Pde9a-222	ENSMUST00000236850.1	1817	63aa	Nonsense mediated decay	-	D6RGP8.6	-
Pde9a-205	ENSMUST00000131417.8	1762	63aa	Nonsense mediated decay	-	D6RGP8.6	TSL:5
Pde9a-218	ENSMUST00000236077.1	1755	68aa	Nonsense mediated decay	-	A0A494BAR7.6	-
Pde9a-208	ENSMUST00000137927.8	1737	37aa	Nonsense mediated decay	-	D6RFN9.6	TSL:5
Pde9a-210	ENSMUST00000143549.8	1718	51aa	Nonsense mediated decay	-	D6REE8.6	TSL:5
Pde9a-216	ENSMUST00000235644.1	1695	48aa	Nonsense mediated decay	-	A0A494B907.6	-
Pde9a-223	ENSMUST00000236874.1	1599	37aa	Nonsense mediated decay	-	D6RFN9.6	-
Pde9a-225	ENSMUST00000237406.1	1585	37aa	Nonsense mediated decay	-	D6RFN9.6	-
Pde9a-209	ENSMUST00000141314.7	571	91aa	Nonsense mediated decay	-	F7APE3.6	CDS 5' incomplete TSL:3
Pde9a-226	ENSMUST00000237698.1	517	30aa	Nonsense mediated decay	-	A0A494B9M2.6	CDS 5' incomplete
Pde9a-221	ENSMUST00000236675.1	1042	No protein	Processed transcript	-	-	-
Pde9a-213	ENSMUST00000155113.2	607	No protein	Processed transcript	-	-	TSL:3
Pde9a-212	ENSMUST00000154567.7	1629	No protein	Retained intron	-	-	TSL:2
Pde9a-219	ENSMUST00000236367.1	1290	No protein	Retained intron	-	-	-
Pde9a-204	ENSMUST00000130547.8	809	No protein	Retained intron	-	-	TSL:5
Pde9a-214	ENSMUST00000155395.2	638	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Pde9a-201* transcript,The transcription is shown below



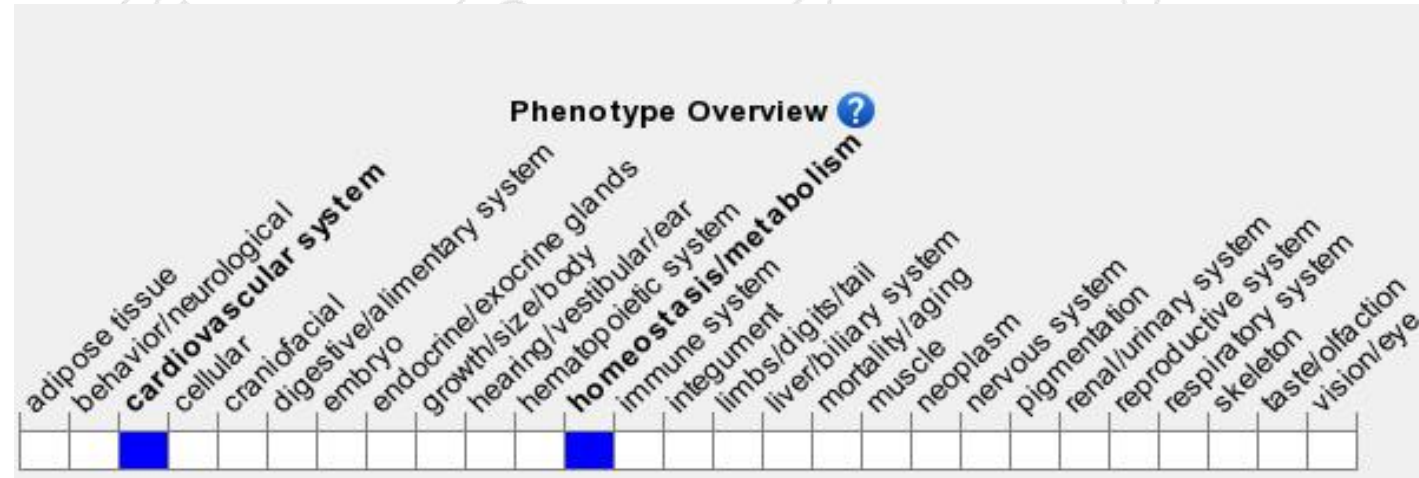
Genomic location distribution



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, Mice homozygous for a null allele exhibit suppressed pressure-overload-induced cardiac pathobiology.

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

Tel: 400-9660890

