

Pde6a Cas9-KO Strategy

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Project Overview

Project Name

Pde6a

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pde6a* gene. The schematic diagram is as follows:



- The *Pde6a* gene has 2 transcripts. According to the structure of *Pde6a* gene, exon2-exon6 of *Pde6a-201* (ENSMUST00000025468.14) transcript is recommended as the knockout region. The region contains 524bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pde6a* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutant mice have retinal degeneration.
- The effect on transcript *Pde6a*-202 is unknown.
- The N-terminal of *Pde6a* gene will remain 158aa, it may remain the partial function of *Pde6a* gene.
- The *Pde6a* gene is located on the Chr18. 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)

Pde6a phosphodiesterase 6A, cGMP-specific, rod, alpha [*Mus musculus* (house mouse)]

Gene ID: 225600, updated on 12-Aug-2019

Summary

Official Symbol	Pde6a provided by MGI
Official Full Name	phosphodiesterase 6A, cGMP-specific, rod, alpha provided by MGI
Primary source	MGI:MGI:97524
See related	Ensembl:ENSMUSG00000024575
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	Pdea; nmf282
Expression	Low expression observed in reference dataset See more
Orthologs	human all

Genomic context

Location: 18 E1; 18 34.41 cM

See Pde6a in [Genome Data Viewer](#)

Exon count: 23

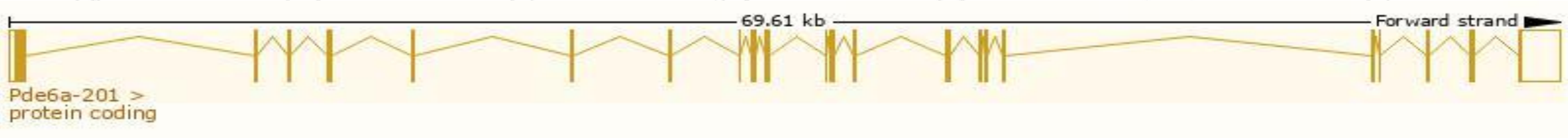
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (61220474..61289750)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (61380153..61449404)

Transcript information (Ensembl)

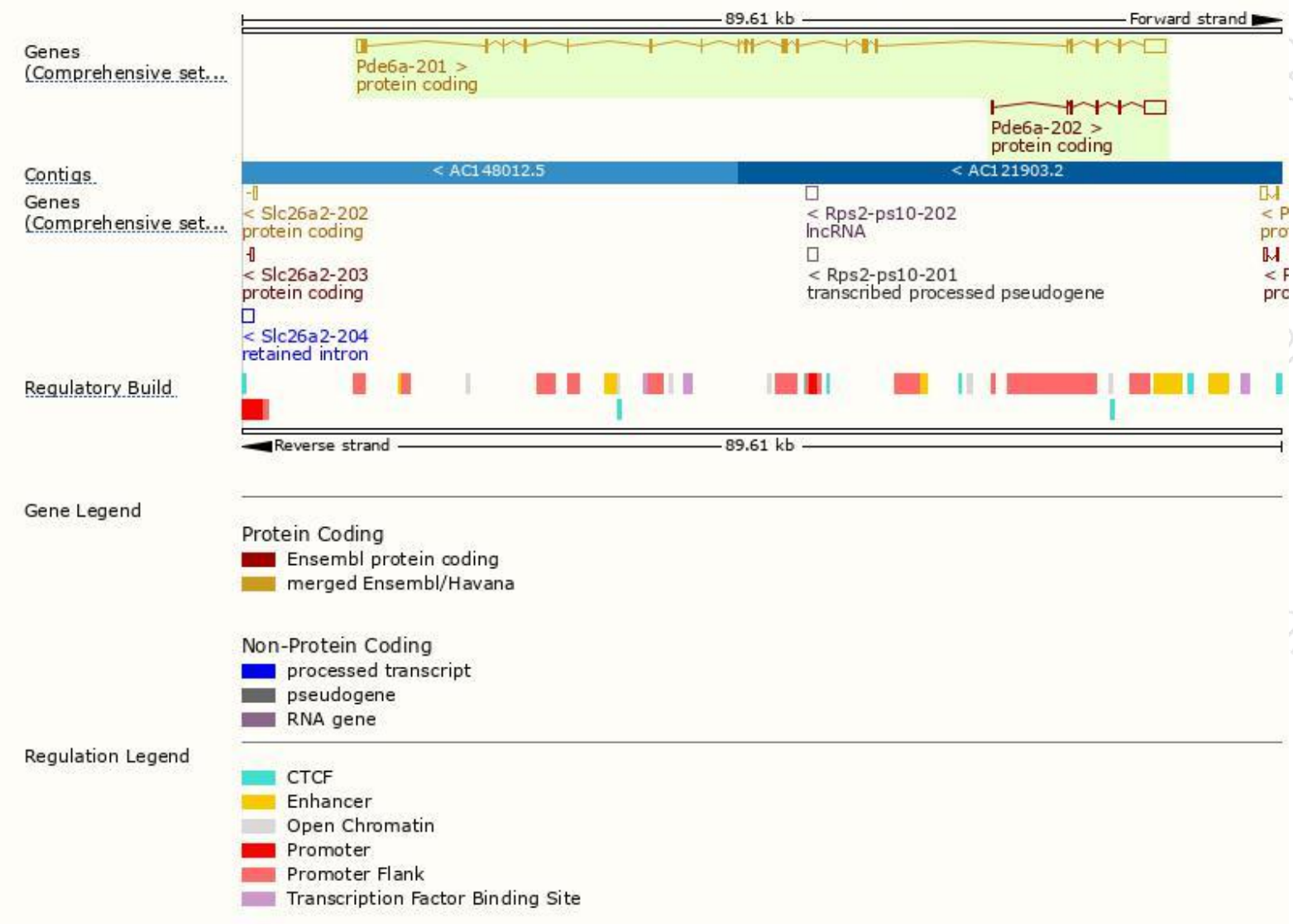
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pde6a-201	ENSMUST00000025468.14	4588	860aa	Protein coding	CCDS29283	Q8K0A8	TSL:1 GENCODE basic APPRIS P1
Pde6a-202	ENSMUST00000135688.1	2263	182aa	Protein coding	-	F6UDG9	CDS 5' incomplete TSL:1

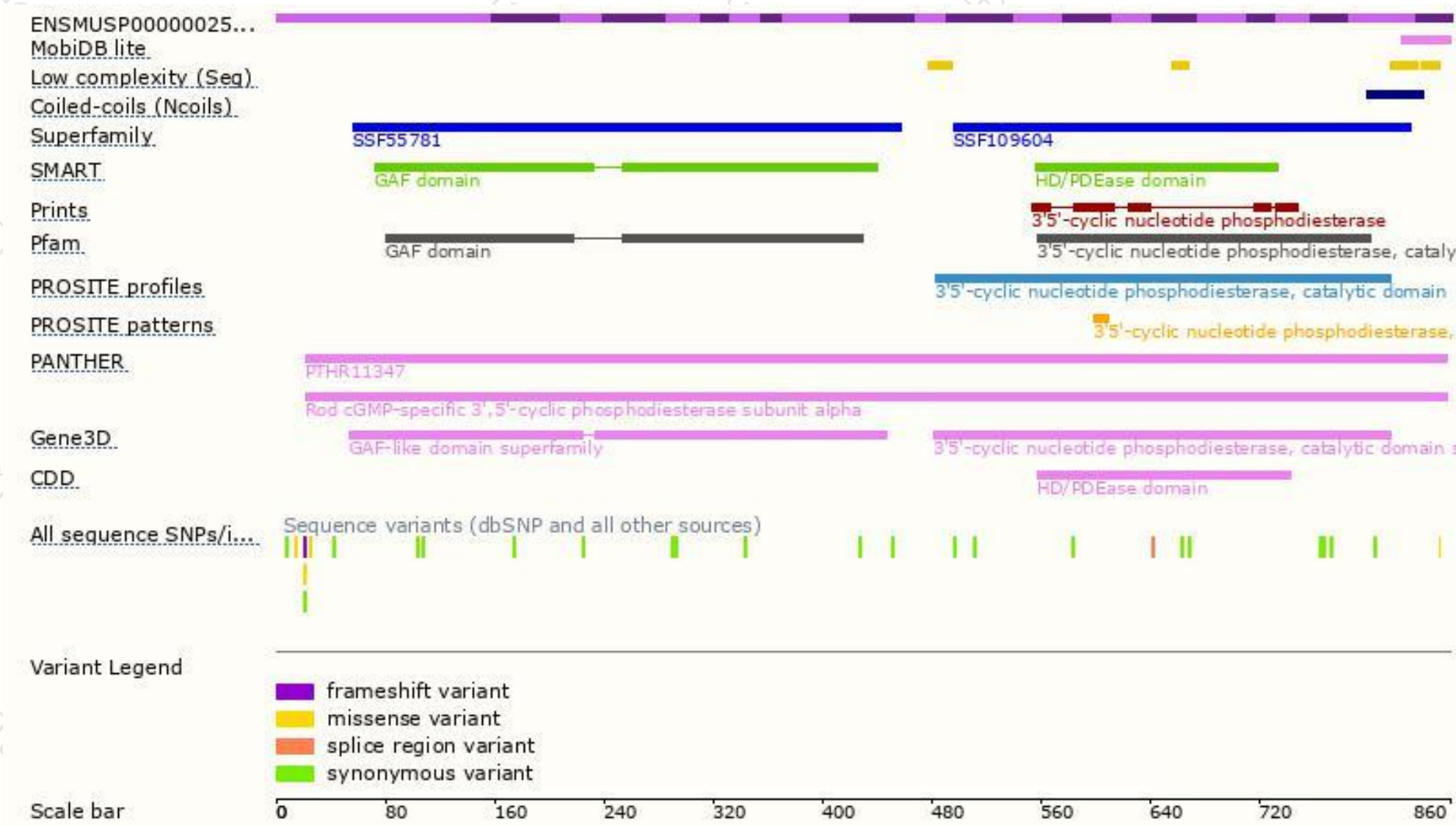
The strategy is based on the design of *Pde6a-201* transcript,The transcription is shown below



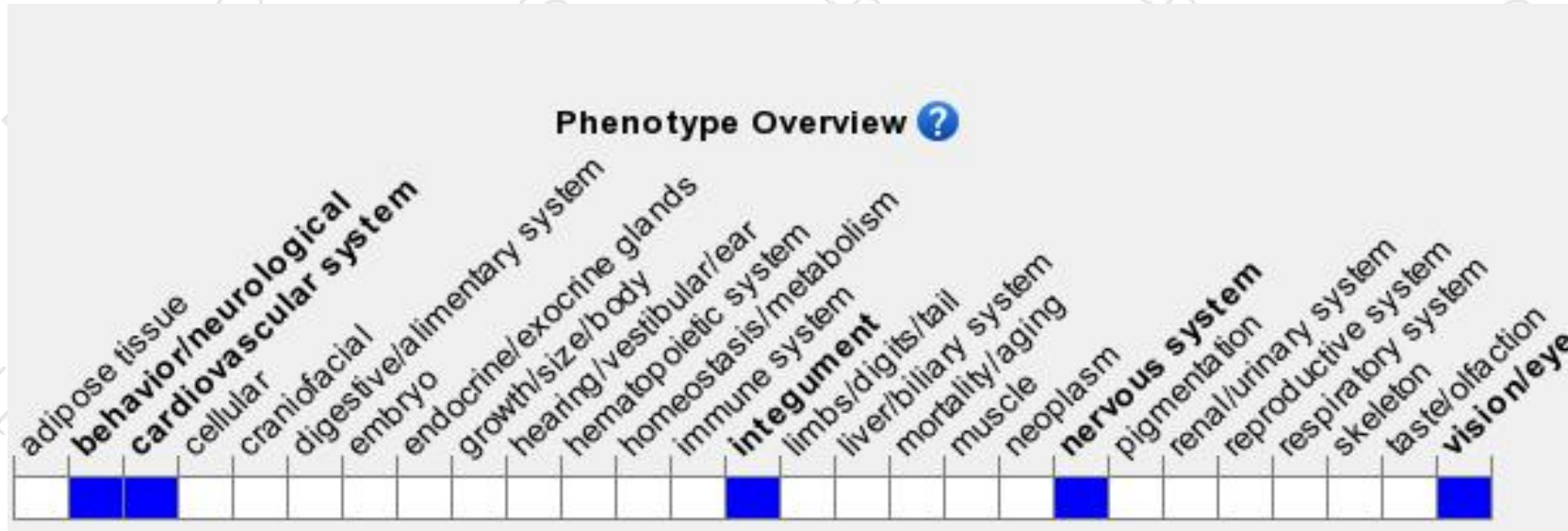
Genomic location distribution



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, Homozygous mutant mice have retinal degeneration.

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

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