

Pde1a Cas9-KO Strategy

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Project Overview

Project Name

Pde1a

Project type

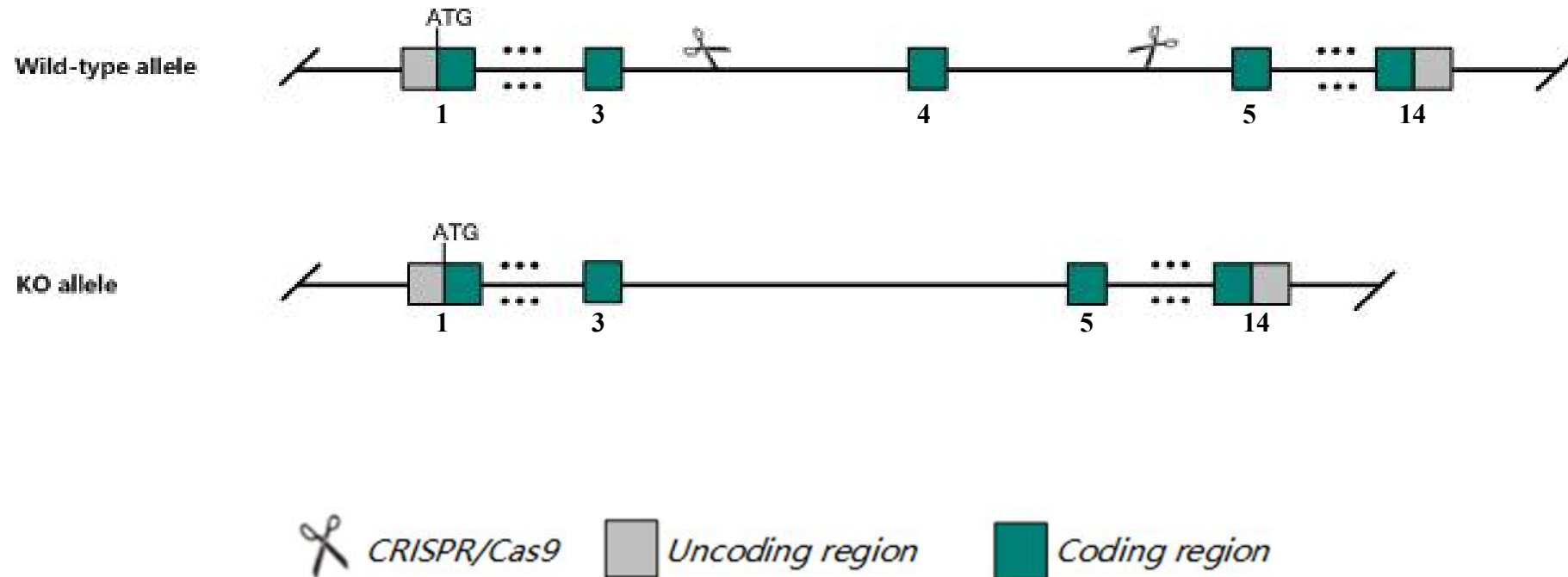
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pde1a* gene. The schematic diagram is as follows:



The *Pde1a* gene has 10 transcripts. According to the structure of *Pde1a* gene, exon4 of *Pde1a-206* (ENSMUST00000102655.9) transcript is recommended as the knockout region. The region contains 67bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Pde1a* gene. The brief process is as follows: CRISPR/Cas9 system

The *Pde1a* gene is located on the Chr2. 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.

Pde1a phosphodiesterase 1A, calmodulin-dependent [Mus musculus (house mouse)]

Gene ID: 18573, updated on 31-Jan-2019

Summary



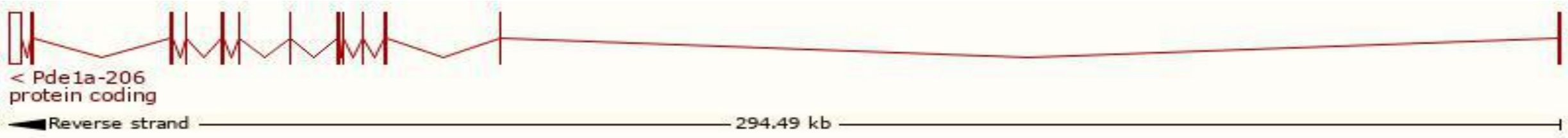
Official Symbol	Pde1a provided by MGI
Official Full Name	phosphodiesterase 1A, calmodulin-dependent provided by MGI
Primary source	MGI:MGI:1201792
See related	Ensembl:ENSMUSG00000059173
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI987702, AW125737
Expression	Biased expression in cortex adult (RPKM 19.1), frontal lobe adult (RPKM 12.1) and 8 other tissues See more
Orthologs	human all

Transcript information Ensembl

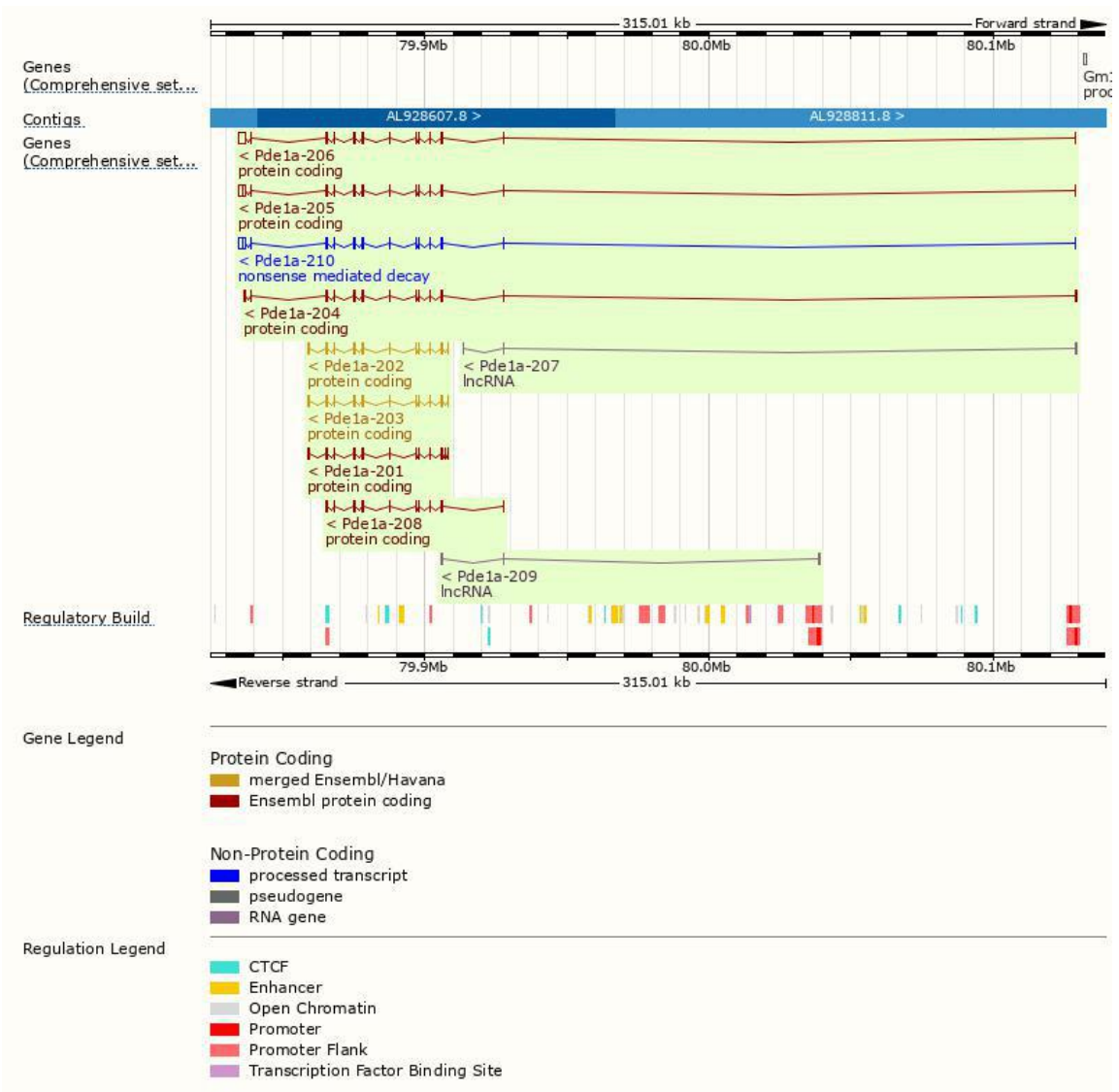
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pde1a-206	ENSMUST00000102655.9	4258	545aa	Protein coding	CCDS16172	Q8BRR9	TSL:1 GENCODE basic APPRIS P4
Pde1a-205	ENSMUST00000102654.10	4122	545aa	Protein coding	CCDS16172	Q8BRR9	TSL:5 GENCODE basic APPRIS P4
Pde1a-204	ENSMUST00000102653.7	2439	545aa	Protein coding	CCDS16172	Q8BRR9	TSL:1 GENCODE basic APPRIS P4
Pde1a-202	ENSMUST00000102651.9	1673	465aa	Protein coding	CCDS16174	Q5I7S8	TSL:1 GENCODE basic APPRIS ALT2
Pde1a-203	ENSMUST00000102652.9	1646	456aa	Protein coding	CCDS16173	Q9JLL9	TSL:1 GENCODE basic
Pde1a-201	ENSMUST00000090756.10	1661	420aa	Protein coding	-	A2ASF9	TSL:1 GENCODE basic
Pde1a-208	ENSMUST00000134739.1	1426	476aa	Protein coding	-	F6X0V1	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
Pde1a-210	ENSMUST00000183775.7	4178	545aa	Nonsense mediated decay	CCDS16172	Q8BRR9	TSL:5
Pde1a-207	ENSMUST00000125887.1	1029	No protein	lncRNA	-	-	TSL:1
Pde1a-209	ENSMUST00000146076.7	869	No protein	lncRNA	-	-	TSL:2

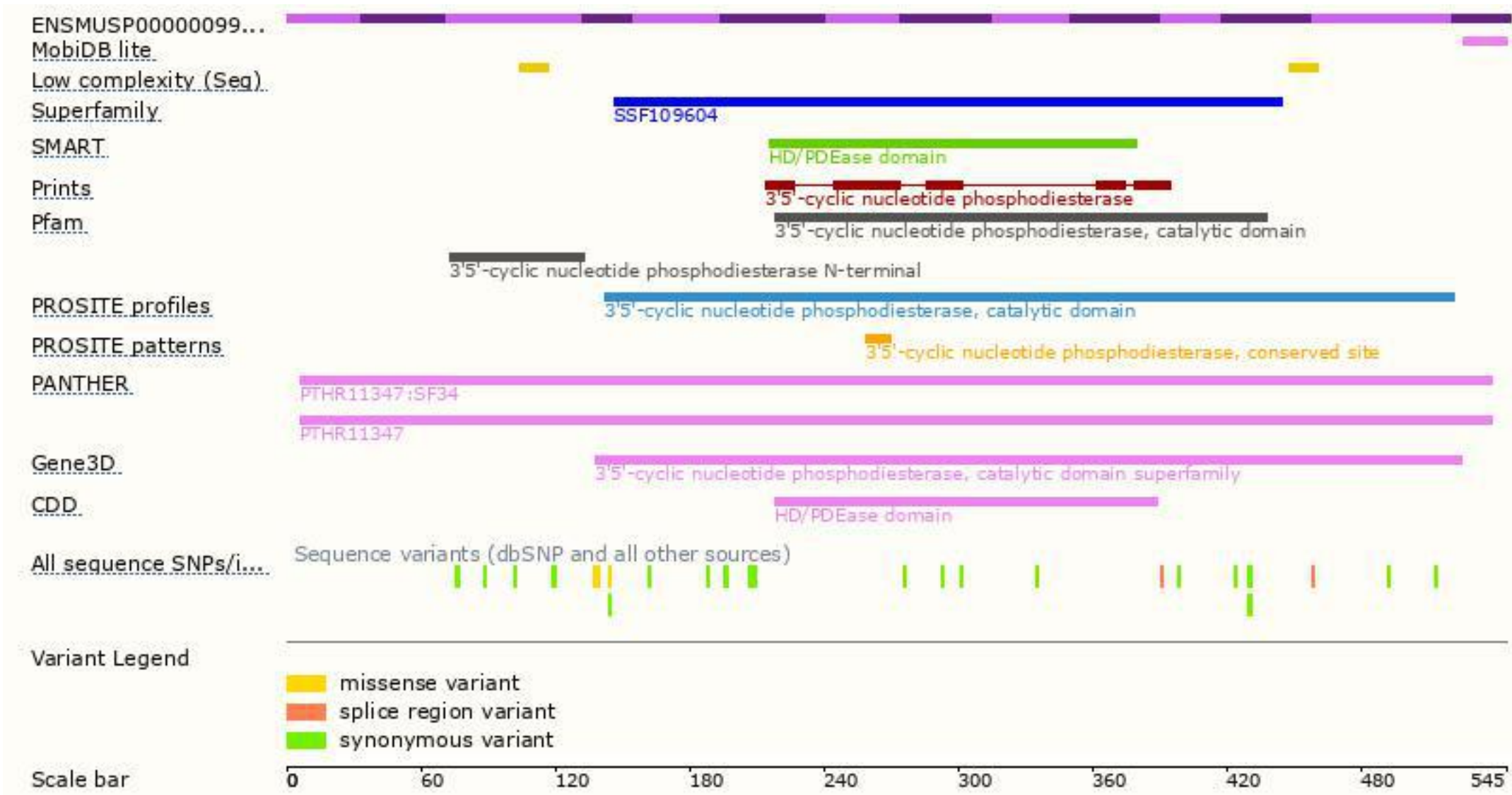
The strategy is based on the design of *Pde1a-206* transcript,The transcription is shown below



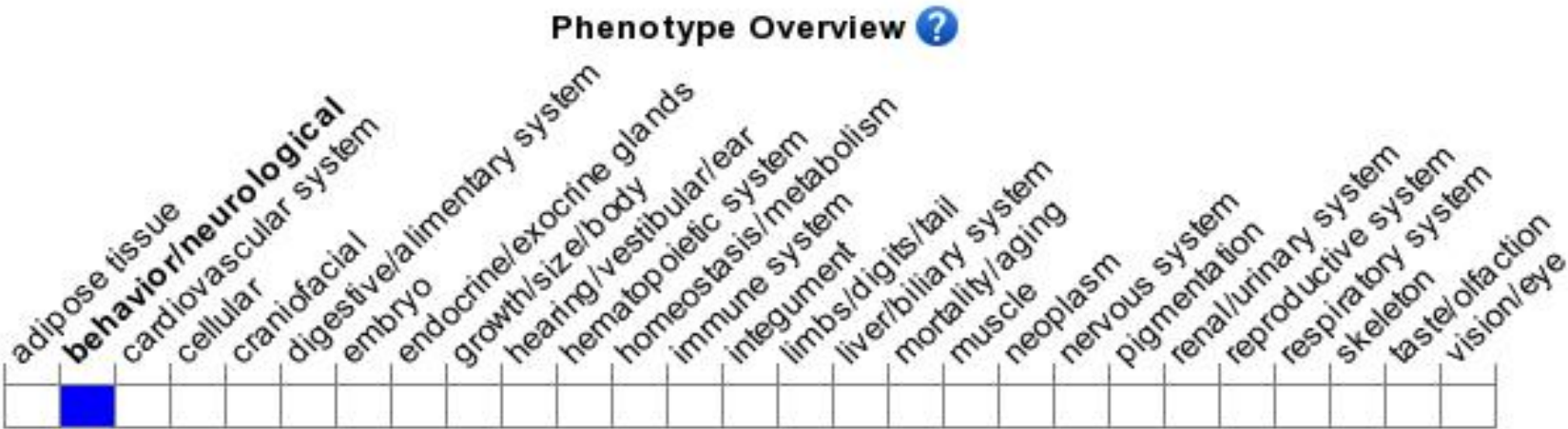
Genomic location distribution



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/>).

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