Pds5a Cas9-KO Strategy

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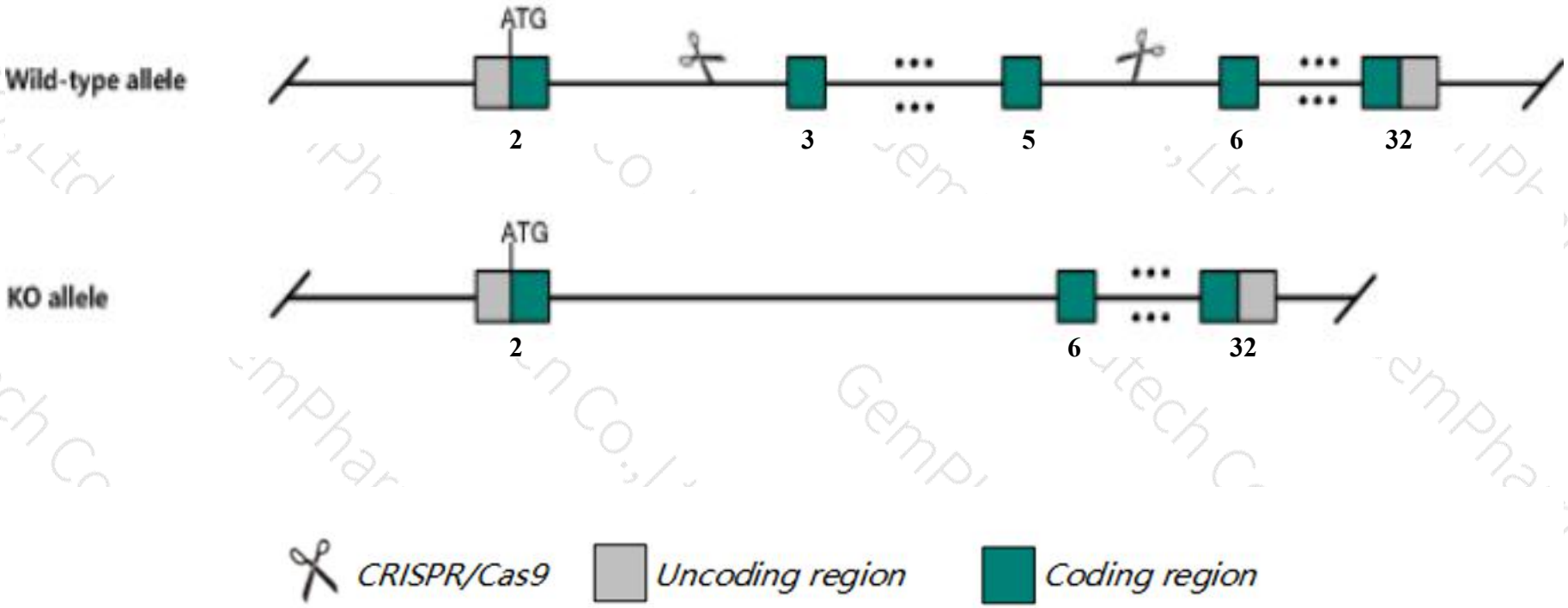
Project Overview

Project Name	***Pds5a***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pds5a* gene. The schematic diagram is as follows:



Technical routes

➢ The *Pds5a* gene has 14 transcripts. According to the structure of *Pds5a* gene, exon3-exon5 of *Pds5a-209* (ENSMUST00000201948.3) transcript is recommended as the knockout region.The region contains 389bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Pds5a* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,mice homozygous for a null allele exhibit neonatal lethality associated with respiratory distress, abnormal heart development, abnormal skeletal development, kidney agenesis, and delayed enteric nervous system development.
- Transcript *Pds5a-212* may not be affected.
- The *Pds5a* gene is located on the Chr5. 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）

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Pds5a PDS5 cohesin associated factor A [Mus musculus (house mouse)]

Gene ID: 71521, updated on 13-Mar-2020

Summary

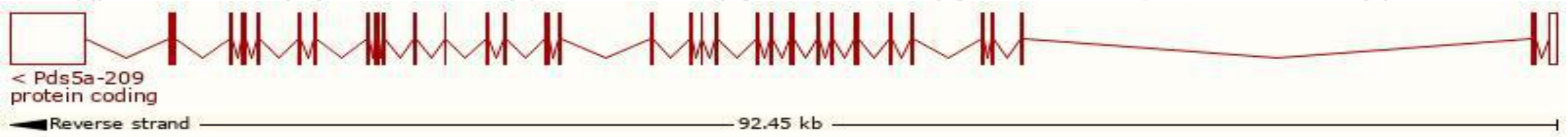
Official Symbol	Pds5a provided by MGI
Official Full Name	PDS5 cohesin associated factor A provided by MGI
Primary source	MGI:MGI:1918771
See related	Ensembl:ENSMUSG00000029202
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9030416H16Rik, B230308N11Rik, E230024D05Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 19.5), limb E14.5 (RPKM 12.4) and 24 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

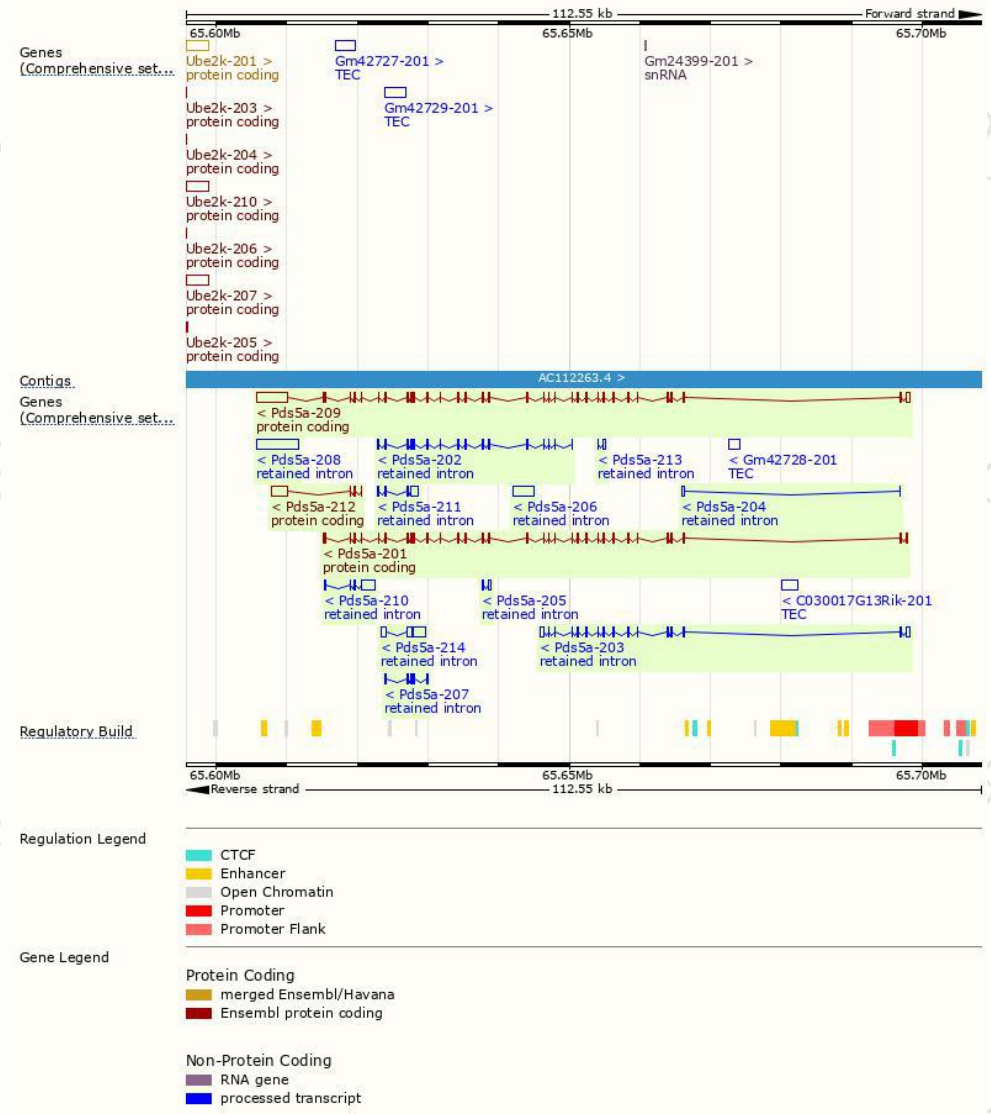
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pds5a-209	ENSMUST00000201948.3	8934	1332aa	Protein coding	CCDS39099	E9QPI5	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Pds5a-201	ENSMUST00000031104.6	4146	1332aa	Protein coding	CCDS39099	E9QPI5	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Pds5a-212	ENSMUST00000202648.3	2725	140aa	Protein coding	-	A0A0J9YV33	CDS 5' incomplete TSL:3
Pds5a-208	ENSMUST00000201673.1	6051	No protein	Retained intron	-	-	TSL:NA
Pds5a-206	ENSMUST00000201109.1	3021	No protein	Retained intron	-	-	TSL:NA
Pds5a-214	ENSMUST00000202910.1	3008	No protein	Retained intron	-	-	TSL:1
Pds5a-203	ENSMUST00000200790.1	2705	No protein	Retained intron	-	-	TSL:5
Pds5a-210	ENSMUST00000201987.1	2443	No protein	Retained intron	-	-	TSL:1
Pds5a-202	ENSMUST00000200766.3	1974	No protein	Retained intron	-	-	TSL:5
Pds5a-211	ENSMUST00000202107.3	1504	No protein	Retained intron	-	-	TSL:1
Pds5a-207	ENSMUST00000201420.1	800	No protein	Retained intron	-	-	TSL:2
Pds5a-205	ENSMUST00000201046.1	521	No protein	Retained intron	-	-	TSL:3
Pds5a-204	ENSMUST00000201034.1	462	No protein	Retained intron	-	-	TSL:2
Pds5a-213	ENSMUST00000202698.1	461	No protein	Retained intron	-	-	TSL:5

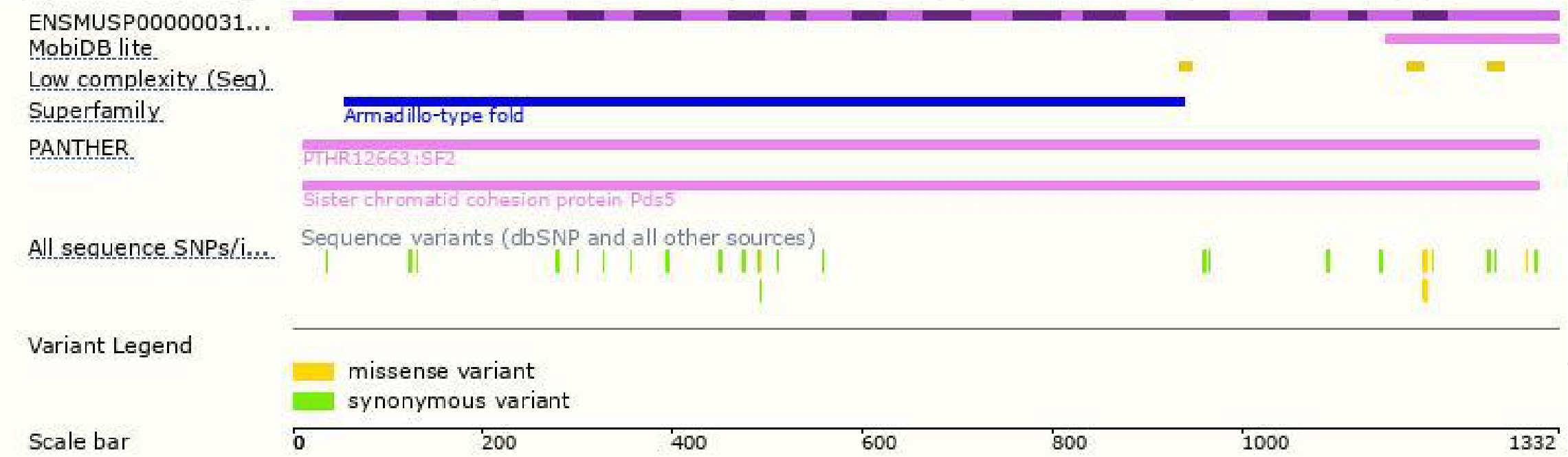
The strategy is based on the design of *Pds5a-209* transcript,the transcription is shown below:



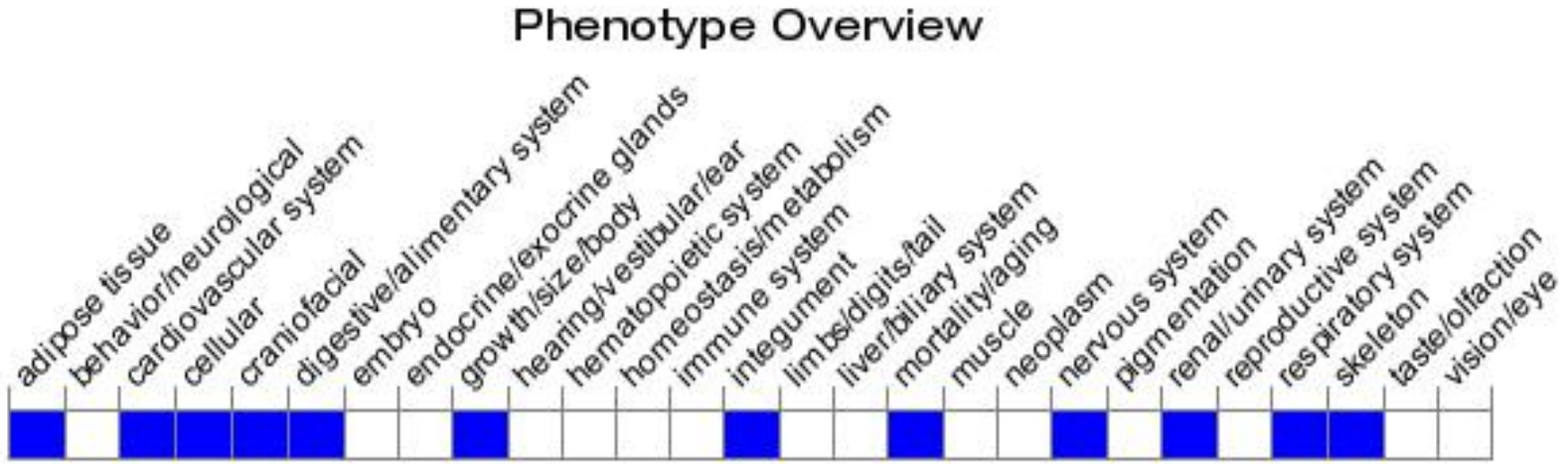
Genomic location distribution



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/).

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

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