Pds5b Cas9-KO Strategy

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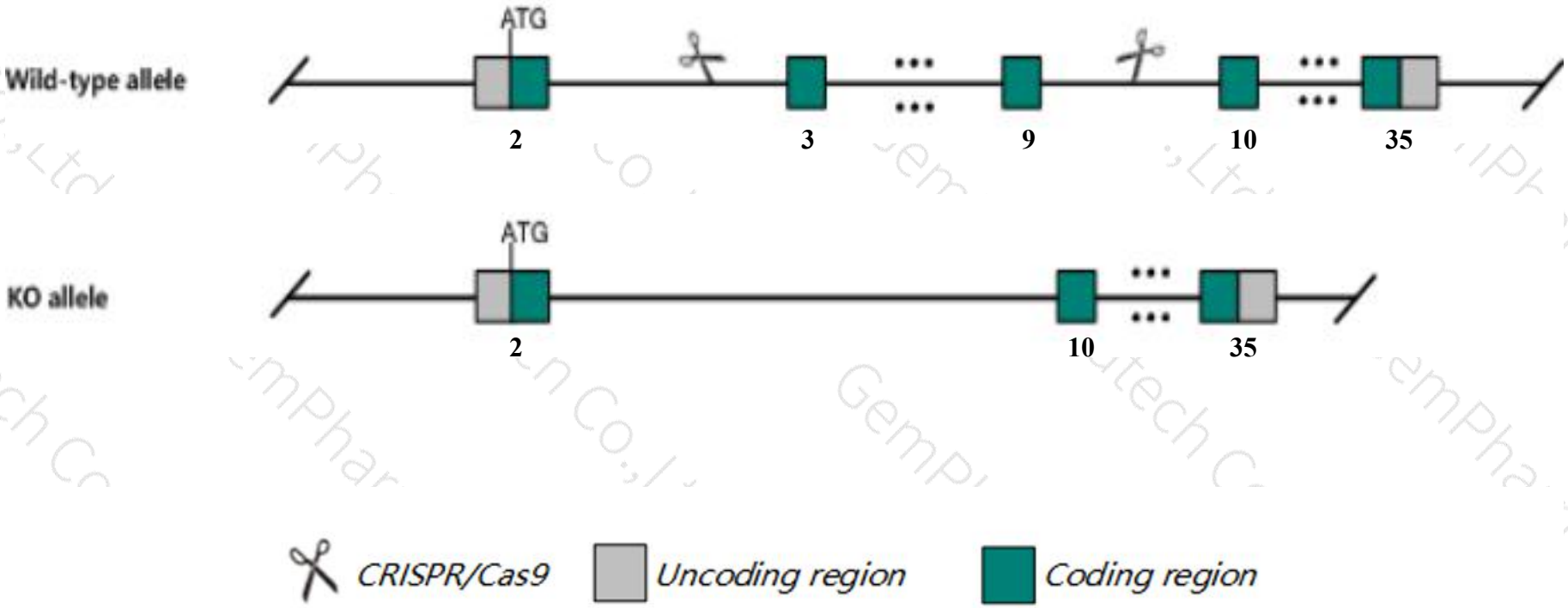
Project Overview

Project Name	***Pds5b***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pds5b* gene. The schematic diagram is as follows:



Technical routes

➢ The *Pds5b* gene has 8 transcripts. According to the structure of *Pds5b* gene, exon3-exon9 of *Pds5b-208* (ENSMUST00000202170.3) transcript is recommended as the knockout region.The region contains 854bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Pds5b* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,mice homozygous for a null allele exhibit embryonic and neonatal lethality with cardiac defects, craniofacial abnormalities, axial skeletal defects, shortening of most of the long bones, abnormal enteric nervous system morphology, and decreased germ cells.
- Transcript *Pds5b-203* may not be affected.
- The *Pds5b* 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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Pds5b PDS5 cohesin associated factor B [Mus musculus (house mouse)]

Gene ID: 100710, updated on 13-Mar-2020

Summary

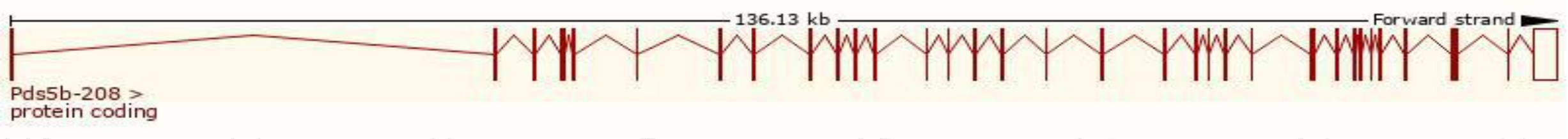
Official Symbol	Pds5b provided by MGI
Official Full Name	PDS5 cohesin associated factor B provided by MGI
Primary source	MGI:MGI:2140945
See related	Ensembl:ENSMUSG00000034021
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI646570, AS3, AW212954, Aprin, Tg(Wap-ERBB2)229Wzw, WAP-Her-2, mKIAA0979
Expression	Broad expression in CNS E11.5 (RPKM 11.8), limb E14.5 (RPKM 9.2) and 22 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

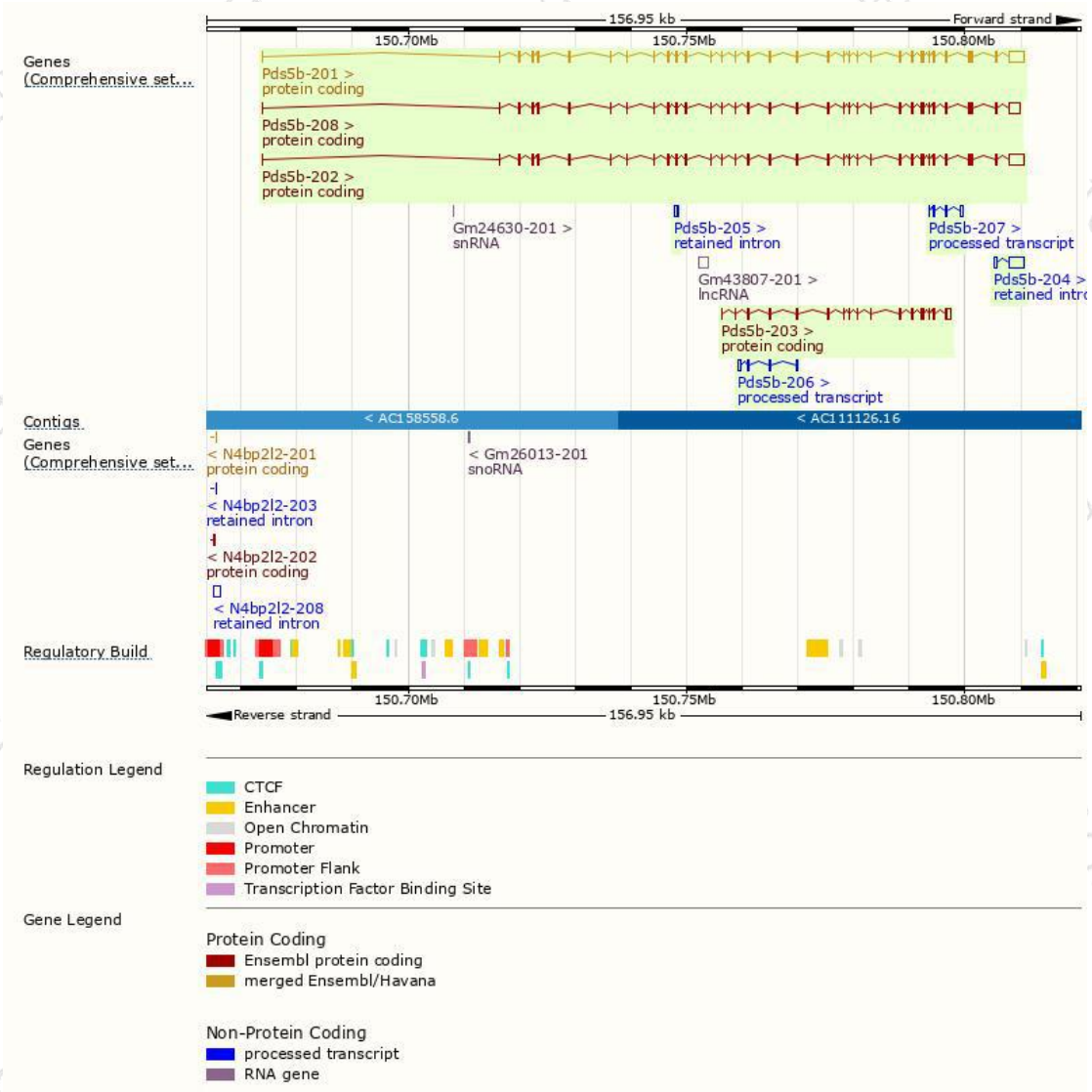
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pds5b-201	ENSMUST00000016569.10	7417	1446aa	Protein coding	CCDS39412	Q4VA53	TSL:1 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 P3
Pds5b-208	ENSMUST00000202170.3	6598	1448aa	Protein coding	CCDS85012	Q4VA53	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 ALT2
Pds5b-202	ENSMUST00000038900.14	7315	1449aa	Protein coding	-	F8WHU5	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 ALT2
Pds5b-203	ENSMUST00000110486.1	2900	701aa	Protein coding	-	Q4VA53	TSL:1 GENCODE basic
Pds5b-207	ENSMUST00000201920.1	723	No protein	Processed transcript	-	-	TSL:3
Pds5b-206	ENSMUST00000154083.1	668	No protein	Processed transcript	-	-	TSL:3
Pds5b-204	ENSMUST00000132947.1	3152	No protein	Retained intron	-	-	TSL:1
Pds5b-205	ENSMUST00000133738.1	584	No protein	Retained intron	-	-	TSL:3

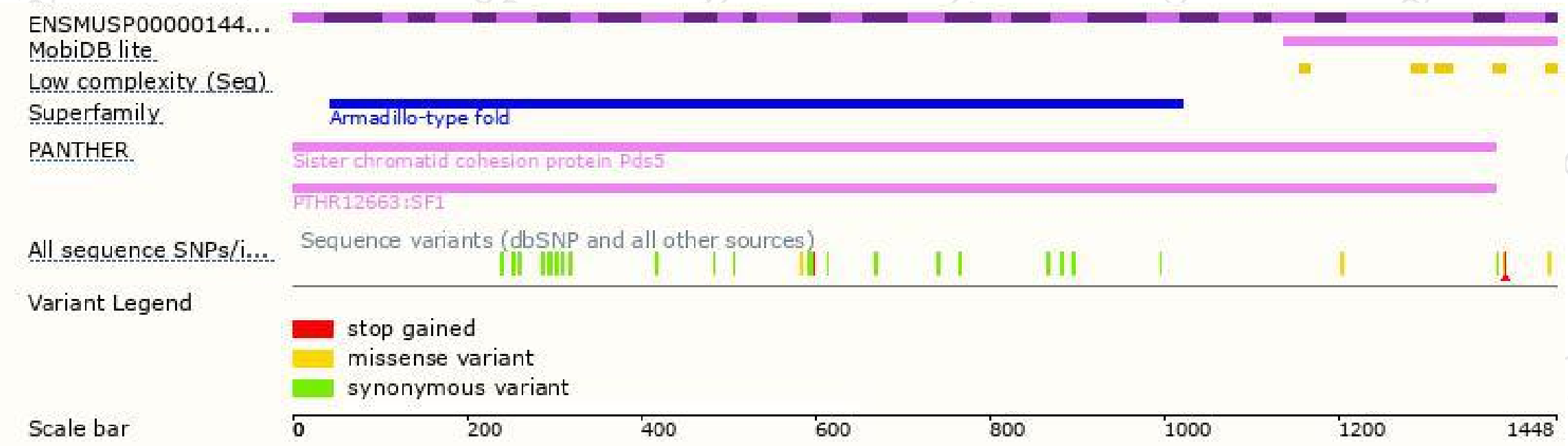
The strategy is based on the design of *Pds5b-208* transcript,the transcription is shown below:



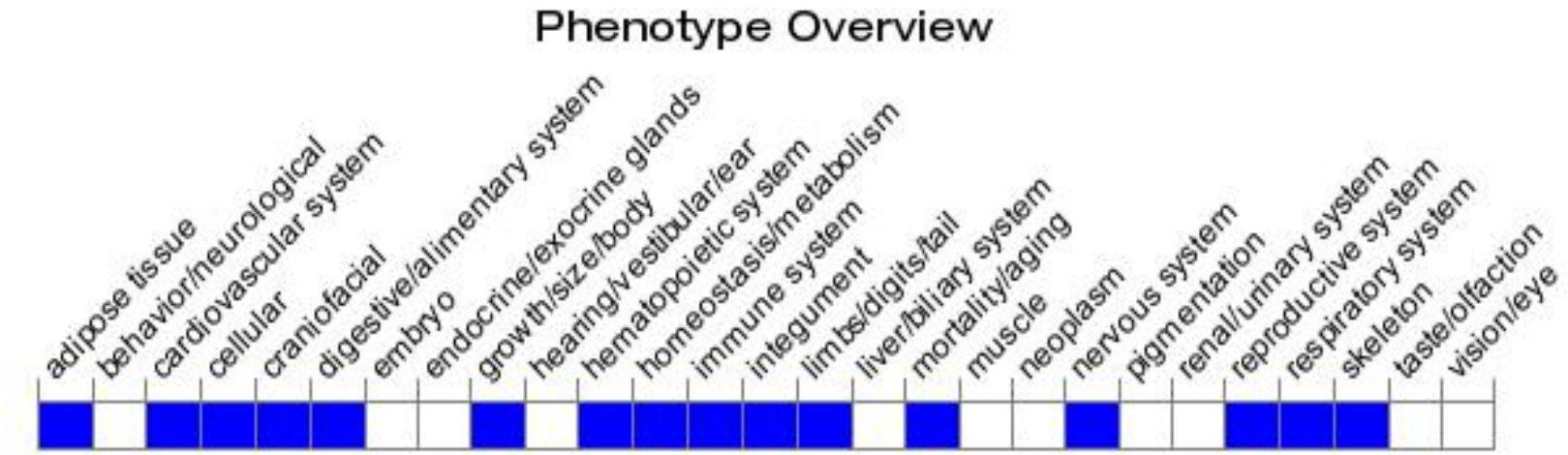
Genomic location distribution



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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