Prdm8 Cas9-KO Strategy

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Reviewer: Huimin Su

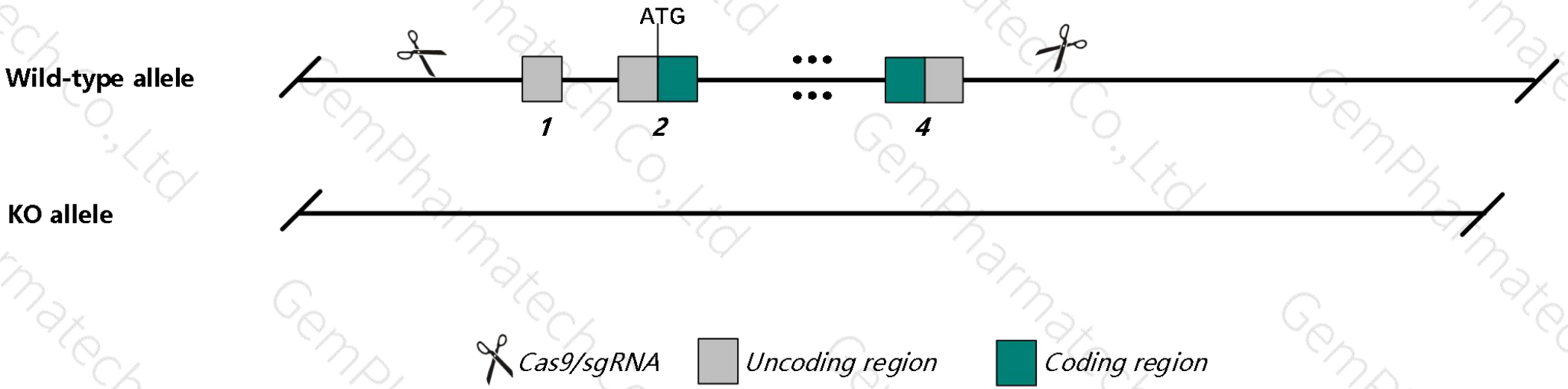
Design Date: 2020-3-10

Project Overview

Project Name	***Prdm8***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prdm8* gene. The schematic diagram is as follows:



Technical routes

➢ The *Prdm8* gene has 2 transcripts. According to the structure of *Prdm8* gene, exon1-exon4 of *Prdm8-201* (ENSMUST00000112959.3) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Prdm8* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele exhibit premature termination of corticopsinal motor neuron axons, absent corpus callosum and hippocampal commissure, excessive scratching, skin lesions, and contraction of hindpaws resulting a handstand phenotype.

➢The KO region contains functional region of the *A730035I17Rik* gene.Knockout the region may affect the function of *A730035I17Rik* gene.

➢ The *Prdm8* 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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Prdm8 PR domain containing 8 [Mus musculus (house mouse)]

Gene ID: 77630, updated on 13-Mar-2020

Summary

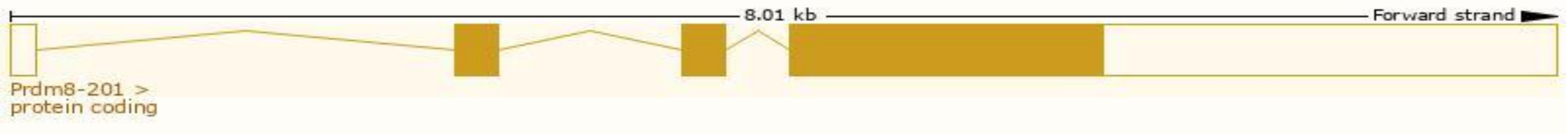
Official Symbol	Prdm8 provided by MGI
Official Full Name	PR domain containing 8 provided by MGI
Primary source	MGI:MGI:1924880
See related	Ensembl:ENSMUSG00000035456
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930565F05Rik, PFM5
Expression	Biased expression in testis adult (RPKM 13.3), CNS E18 (RPKM 8.4) and 9 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

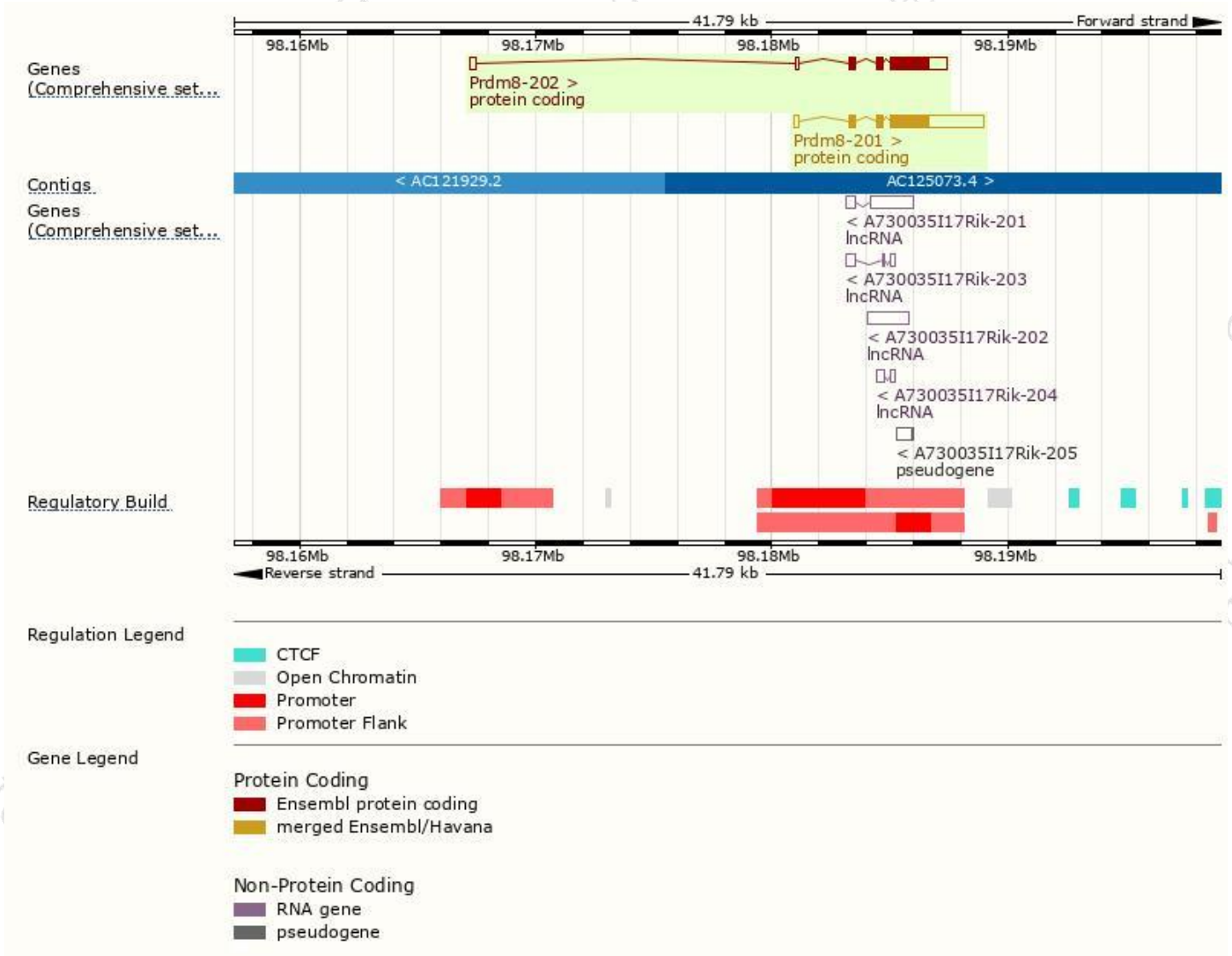
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prdm8-201	ENSMUST00000112959.3	4553	688aa	Protein coding	CCDS39178	B2RU90	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 P1
Prdm8-202	ENSMUST00000210477.1	3316	688aa	Protein coding	CCDS39178	B2RU90	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

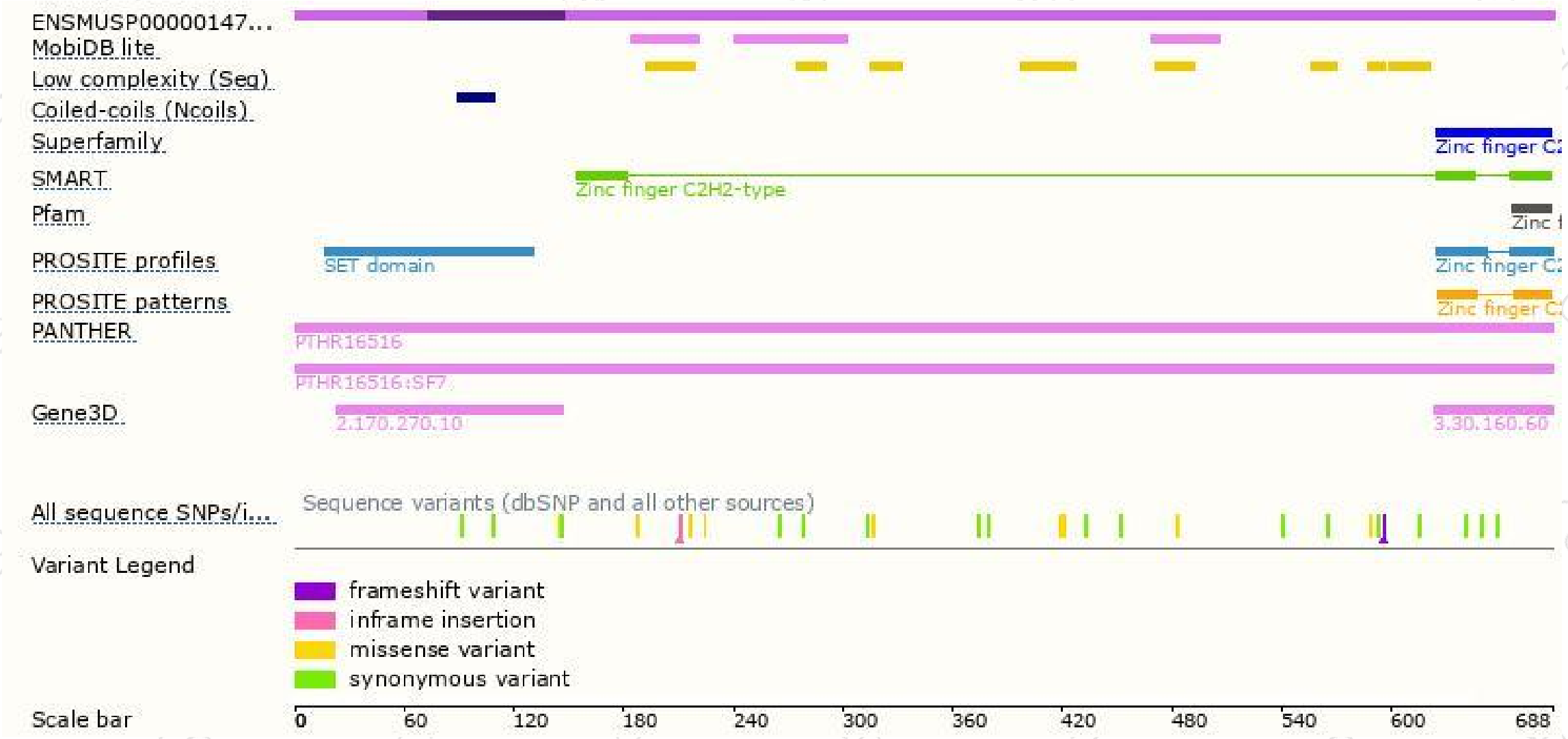
The strategy is based on the design of *Prdm8-201* transcript,The transcription is shown below



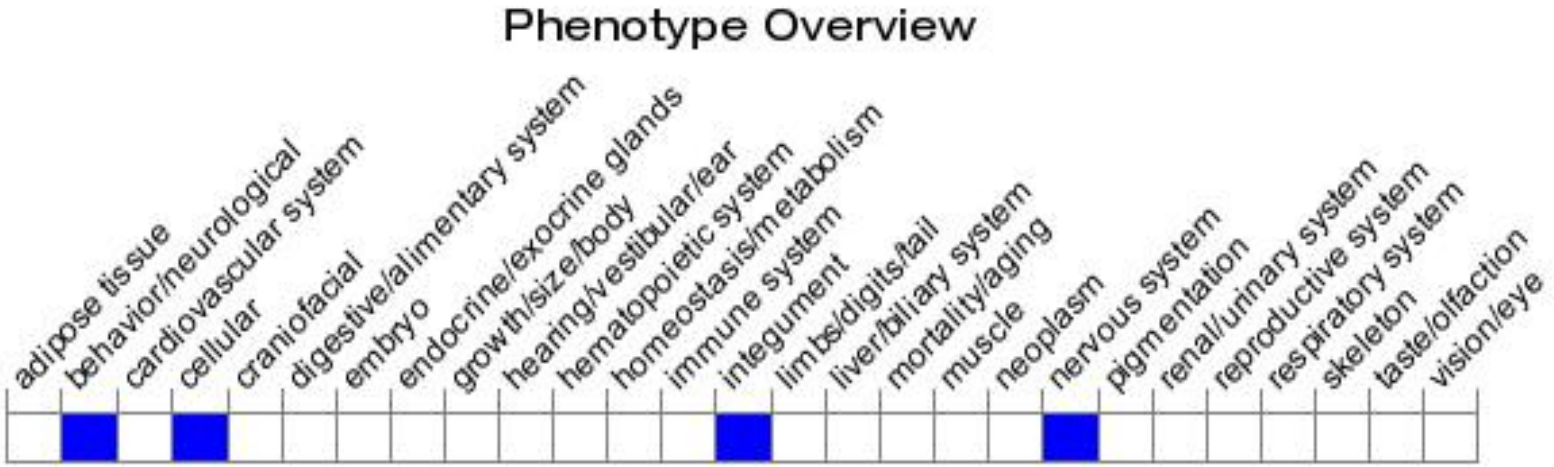
Genomic location distribution



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/).

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

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