

Prmt9 Cas9-KO Strategy

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Project Overview

Project Name

Prmt9

Project type

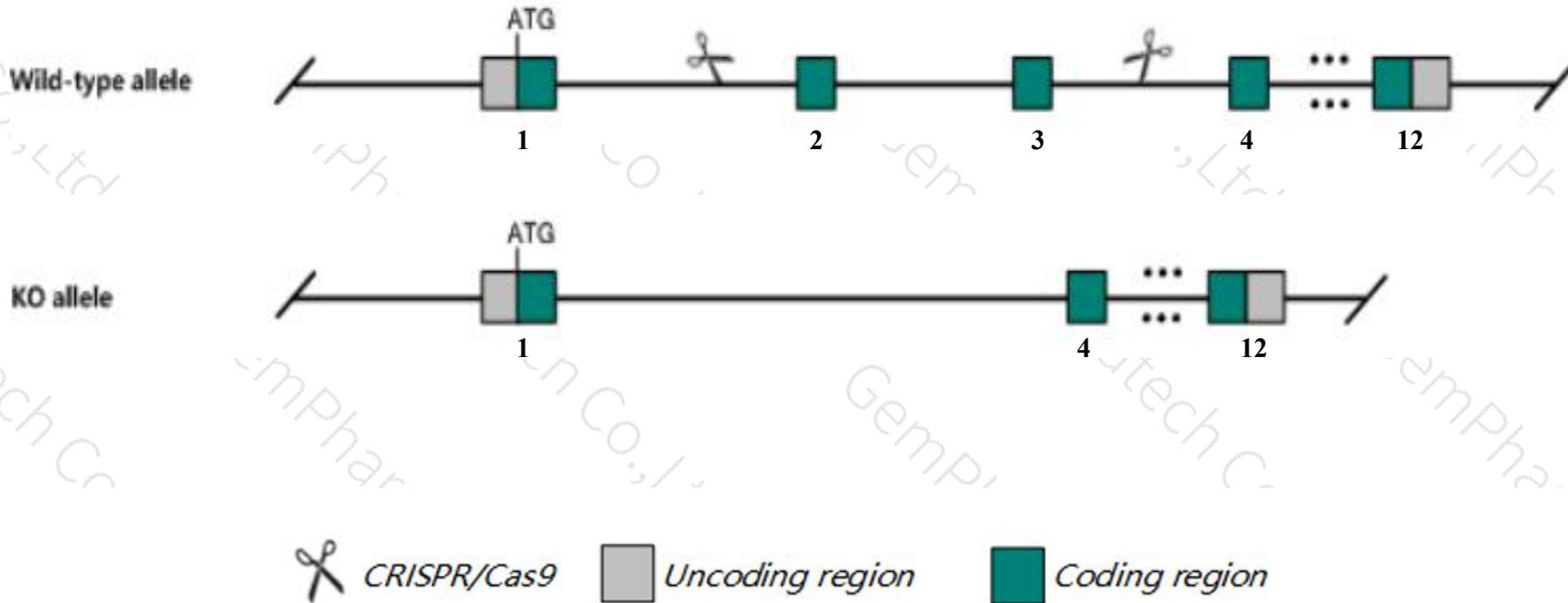
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prmt9* gene. The schematic diagram is as follows:



- The *Prmt9* gene has 5 transcripts. According to the structure of *Prmt9* gene, exon2-exon3 of *Prmt9-201* (ENSMUST00000056237.14) transcript is recommended as the knockout region. The region contains 386bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Prmt9* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Prmt9* gene is located on the Chr8. 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)

Prmt9 protein arginine methyltransferase 9 [Mus musculus (house mouse)]

Gene ID: 102182, updated on 13-Mar-2020

Summary



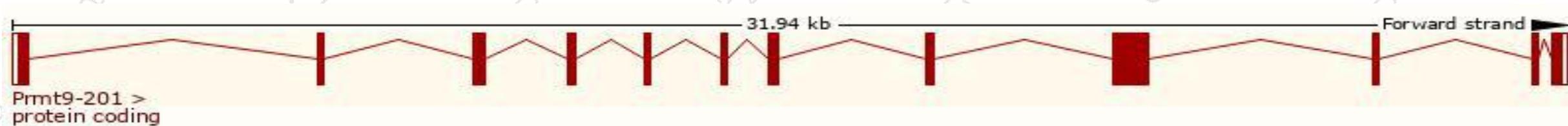
| | |
|---------------------------|---|
| Official Symbol | Prmt9 provided by MGI |
| Official Full Name | protein arginine methyltransferase 9 provided by MGI |
| Primary source | MGI:MGI:2142651 |
| See related | Ensembl:ENSMUSG00000037134 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | AI931714, Prmt10 |
| Expression | Ubiquitous expression in CNS E11.5 (RPKM 7.2), CNS E18 (RPKM 6.7) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

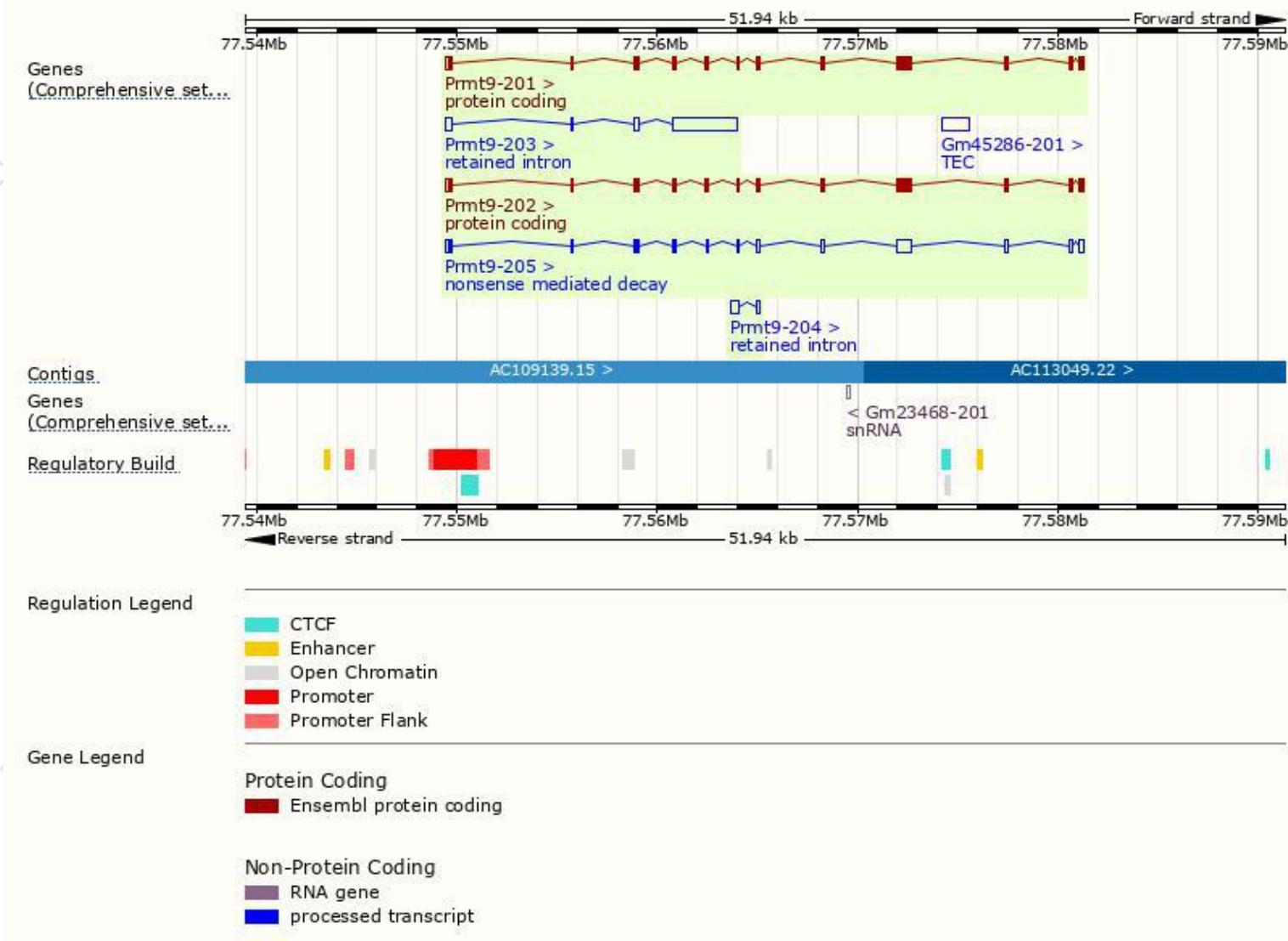
The gene has 5 transcripts, all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|----------------------------|---|
| Prmt9-201 | ENSMUST00000056237.14 | 2781 | 846aa | Protein coding | CCDS40394 | F8WIU7 | 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 P2 |
| Prmt9-202 | ENSMUST00000118622.1 | 2768 | 846aa | Protein coding | - | Q3U3W5 | 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 |
| Prmt9-205 | ENSMUST00000210040.1 | 2688 | 305aa | Nonsense mediated decay | - | A0A1B0GT44 | TSL:1 |
| Prmt9-203 | ENSMUST00000142824.1 | 3888 | No protein | Retained intron | - | - | TSL:1 |
| Prmt9-204 | ENSMUST00000156753.1 | 561 | No protein | Retained intron | - | - | TSL:3 |

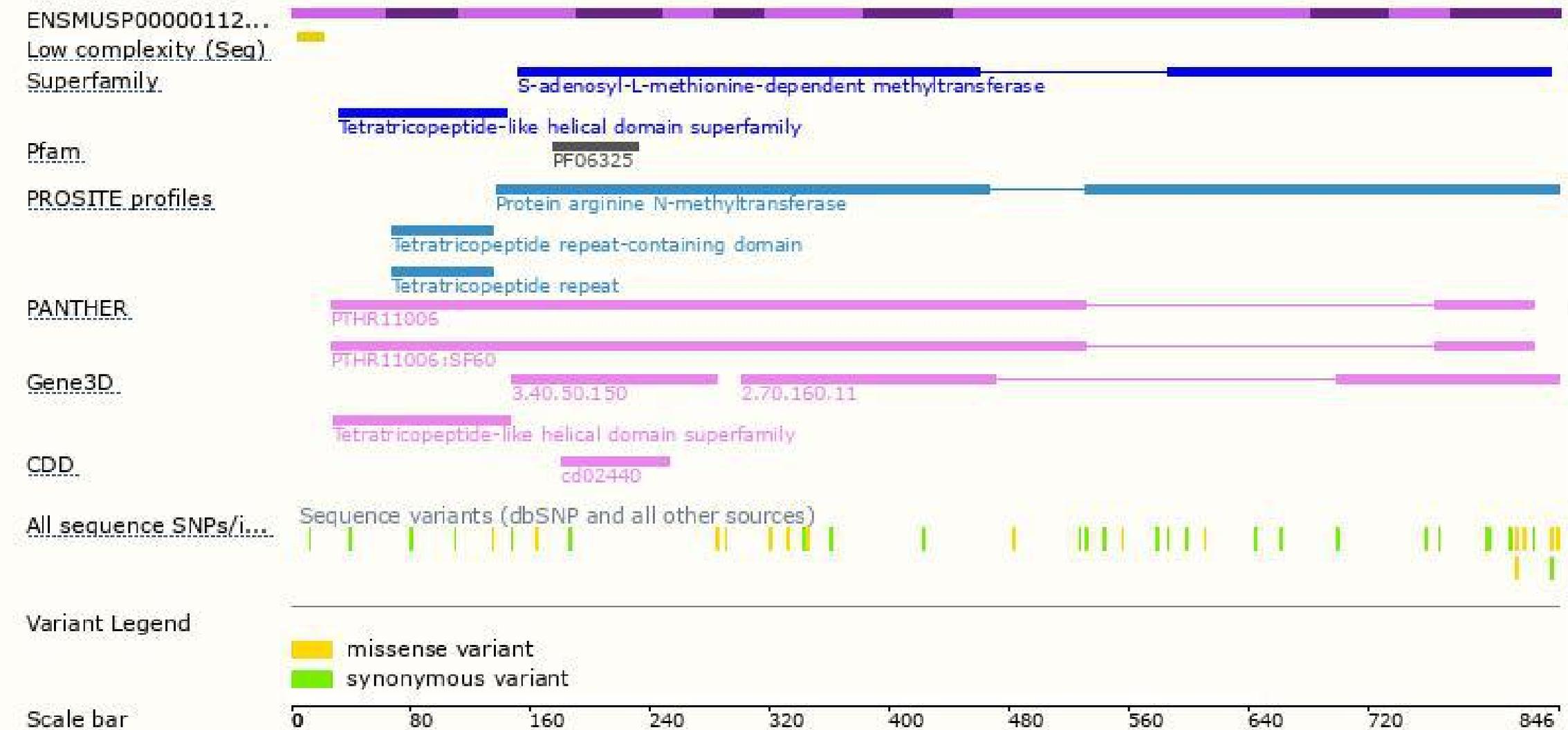
The strategy is based on the design of *Prmt9-201* transcript, the transcription is shown below:



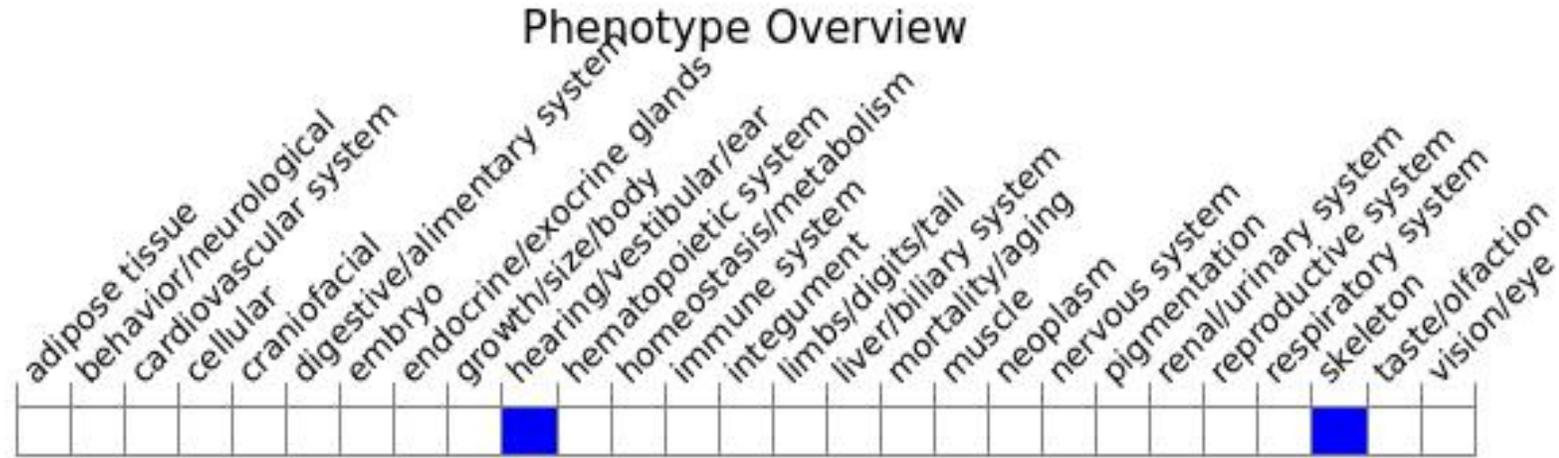
Genomic location distribution



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/>).

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

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