

Prmt5 Cas9-KO Strategy

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Project Overview

Project Name

Prmt5

Project type

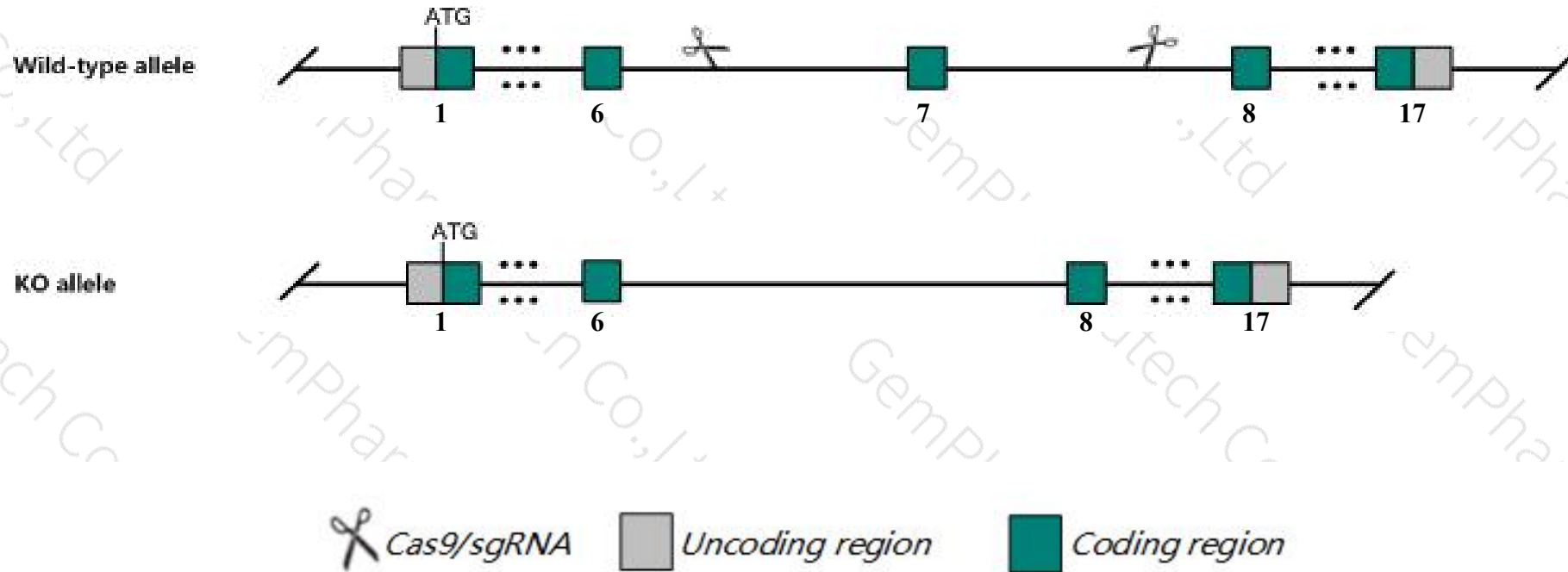
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prmt5* gene. The schematic diagram is as follows:



- The *Prmt5* gene has 7 transcripts. According to the structure of *Prmt5* gene, exon7 of *Prmt5-201* (ENSMUST00000023873.11) transcript is recommended as the knockout region. The region contains 164bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Prmt5* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. The stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6J mice.

- According to the existing MGI data, mice homozygous for a null allele display embryonic lethality before somite formation with failure of inner cell mass proliferation.
- The *Prmt5* gene is located on the Chr14. 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)

Prmt5 protein arginine N-methyltransferase 5 [Mus musculus (house mouse)]

Gene ID: 27374, updated on 26-Mar-2019

Summary



Official Symbol Prmt5 provided by [MGI](#)

Official Full Name protein arginine N-methyltransferase 5 provided by [MGI](#)

Primary source [MGI:MGI:1351645](#)

See related [Ensembl:ENSMUSG00000023110](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as Jbp1, Skb1

Summary This gene encodes an enzyme that belongs to the methyltransferase family. The encoded protein catalyzes the transfer of methyl groups to the amino acid arginine, in target proteins that include histones, transcriptional elongation factors and the tumor suppressor p53. This gene plays a role in several cellular processes, including transcriptional regulation and the assembly of small nuclear ribonucleoproteins. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Sep 2015]

Expression Ubiquitous expression in CNS E11.5 (RPKM 31.6), CNS E14 (RPKM 26.3) and 28 other tissues [See more](#)

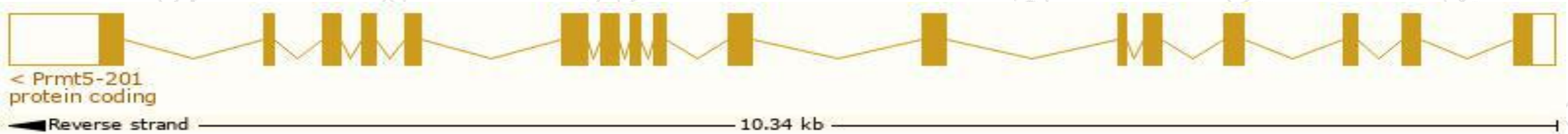
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

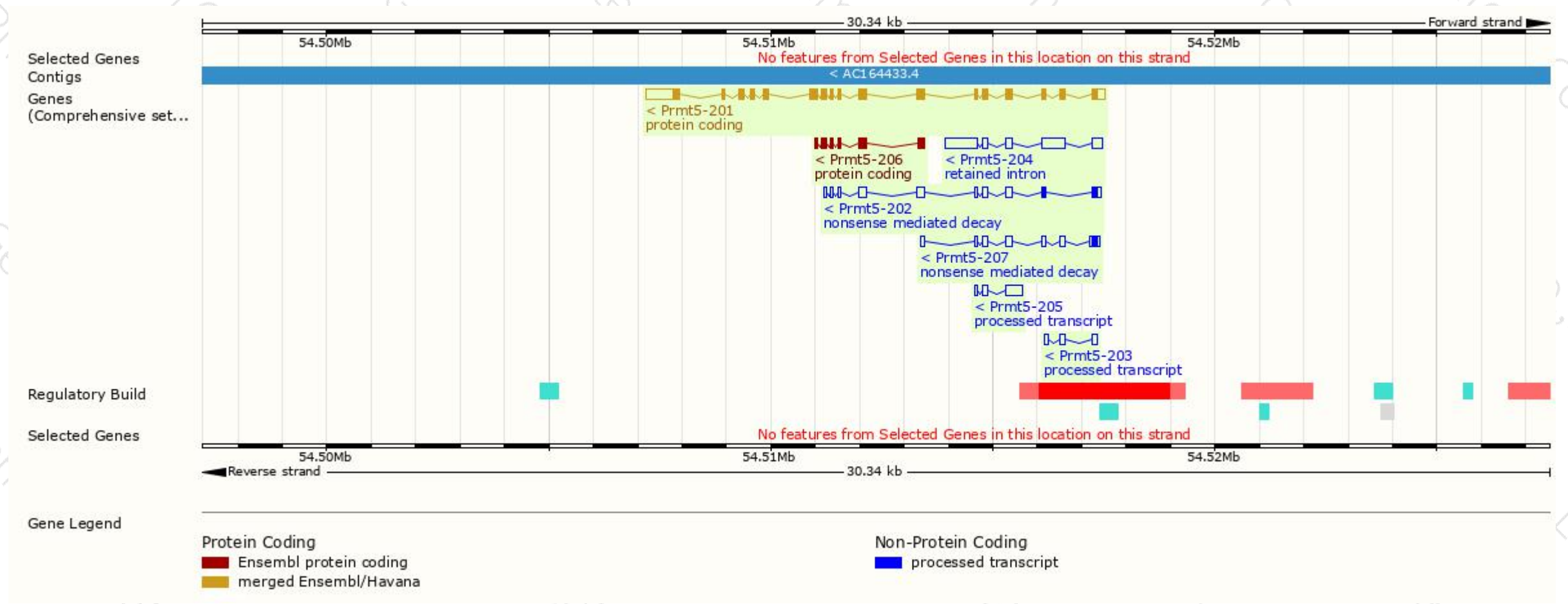
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prmt5-201	ENSMUST00000023873.11	2691	637aa	Protein coding	CCDS27091	A0A0R4J049	TSL:1 GENCODE basic APPRIS P1
Prmt5-206	ENSMUST00000139964.1	609	203aa	Protein coding	-	F6QQQ6	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Prmt5-202	ENSMUST00000132227.8	1094	63aa	Nonsense mediated decay	-	S4R295	TSL:5
Prmt5-207	ENSMUST00000147214.7	811	37aa	Nonsense mediated decay	-	A0A2I3BRG2	TSL:3
Prmt5-205	ENSMUST00000138367.1	521	No protein	Processed transcript	-	-	TSL:2
Prmt5-203	ENSMUST00000132801.1	338	No protein	Processed transcript	-	-	TSL:5
Prmt5-204	ENSMUST00000133552.7	1692	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Prmt5-201* transcript, the transcription is shown below:



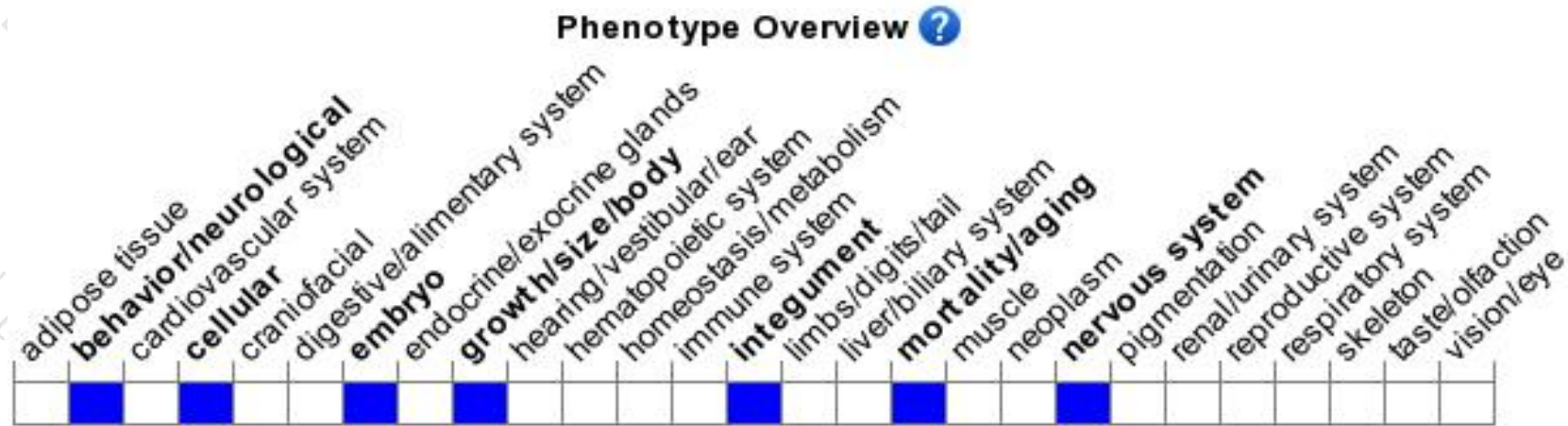
Genomic location distribution



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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