

Trmt11 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Trmt11

Project type

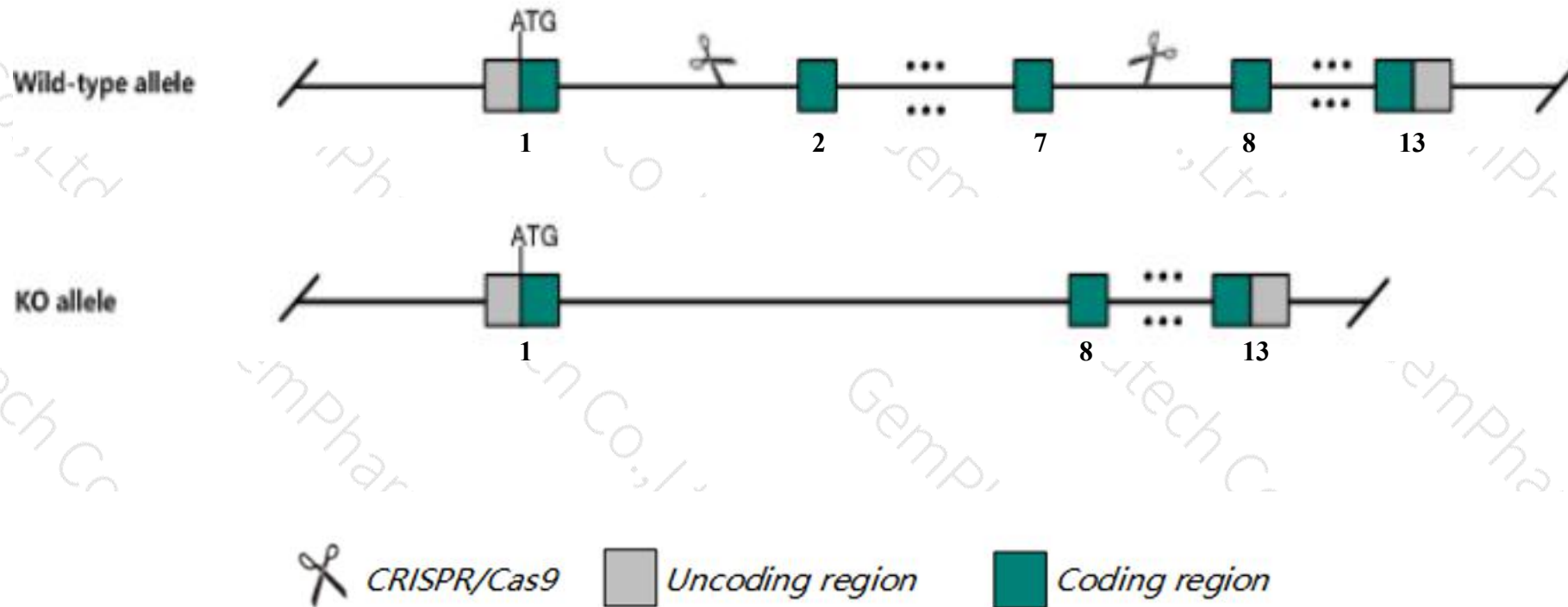
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Trmt11* gene. The schematic diagram is as follows:



- The *Trmt11* gene has 6 transcripts. According to the structure of *Trmt11* gene, exon2-exon7 of *Trmt11-201* (ENSMUST00000019927.6) transcript is recommended as the knockout region. The region contains 607bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Trmt11* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Trmt11* gene is located on the Chr10. 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)

Trmt11 tRNA methyltransferase 11 [Mus musculus (house mouse)]

Gene ID: 73681, updated on 13-Mar-2020

Summary



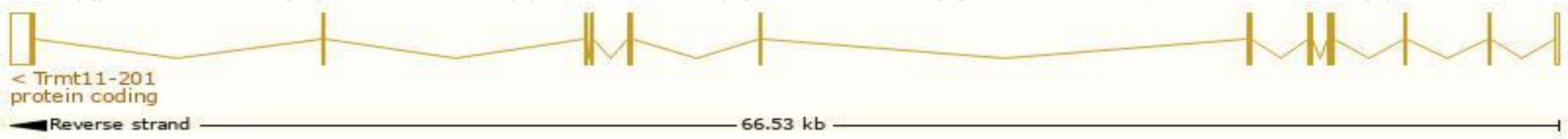
Official Symbol	Trmt11 provided by MGI
Official Full Name	tRNA methyltransferase 11 provided by MGI
Primary source	MGI:MGI:1920931
See related	Ensembl:ENSMUSG00000019792
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410075D05Rik, 3110045I18Rik, AW213713
Expression	Broad expression in liver E14 (RPKM 1.8), CNS E11.5 (RPKM 1.6) and 23 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

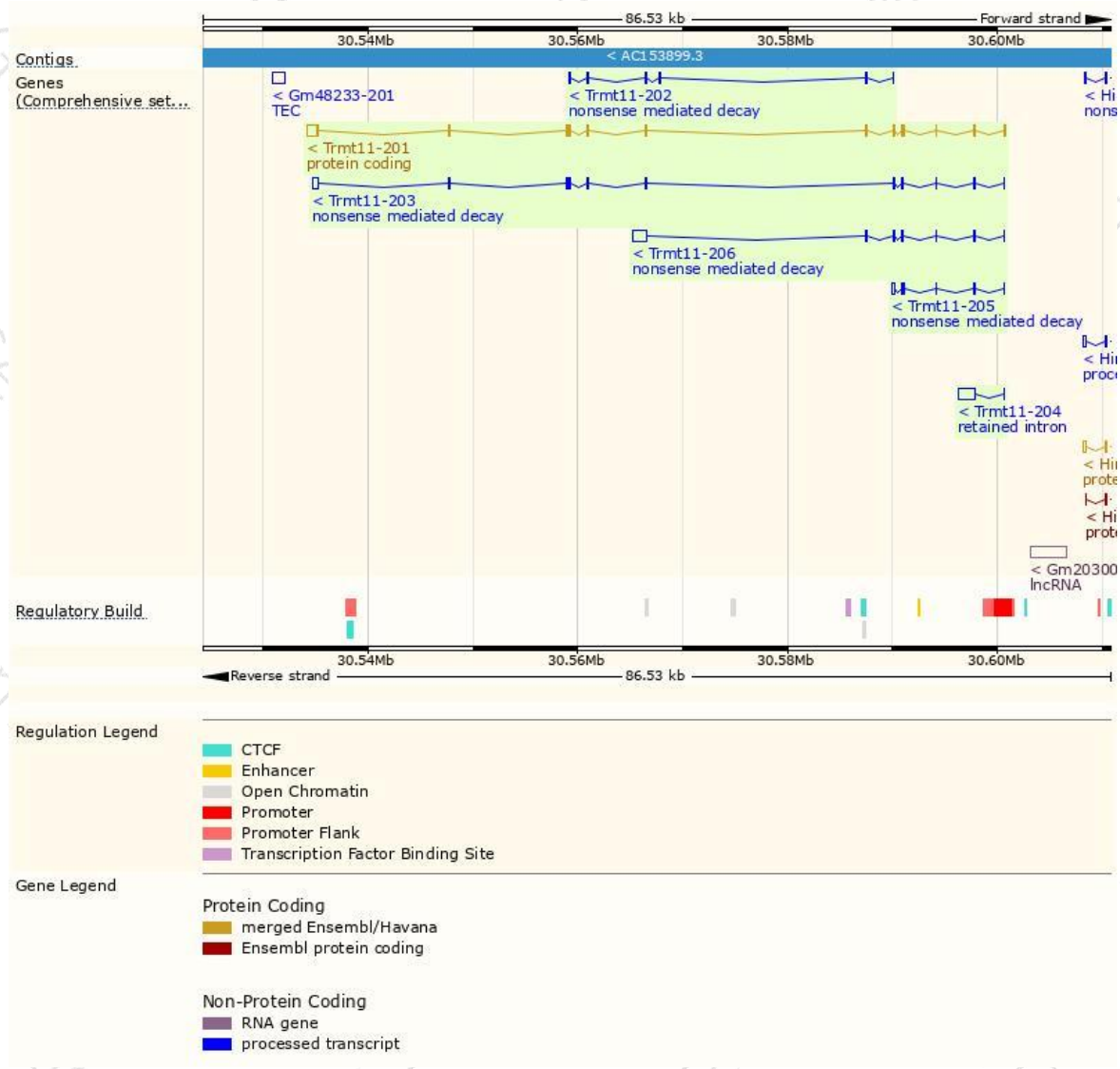
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Trmt11-201	ENSMUST00000019927.6	2359	460aa	Protein coding	CCDS23763	E9QKG3	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
Trmt11-206	ENSMUST00000216790.1	1921	82aa	Nonsense mediated decay	-	A0A1L1SSB7	TSL:1
Trmt11-203	ENSMUST00000215595.1	1576	82aa	Nonsense mediated decay	-	A0A1L1SSB7	TSL:1
Trmt11-202	ENSMUST00000215041.1	715	112aa	Nonsense mediated decay	-	A0A1L1SVA9	CDS 5' incomplete TSL:5
Trmt11-205	ENSMUST00000216705.1	666	100aa	Nonsense mediated decay	-	A0A1L1SQZ0	CDS 5' incomplete TSL:3
Trmt11-204	ENSMUST00000216638.1	1585	No protein	Retained intron	-	-	TSL:1

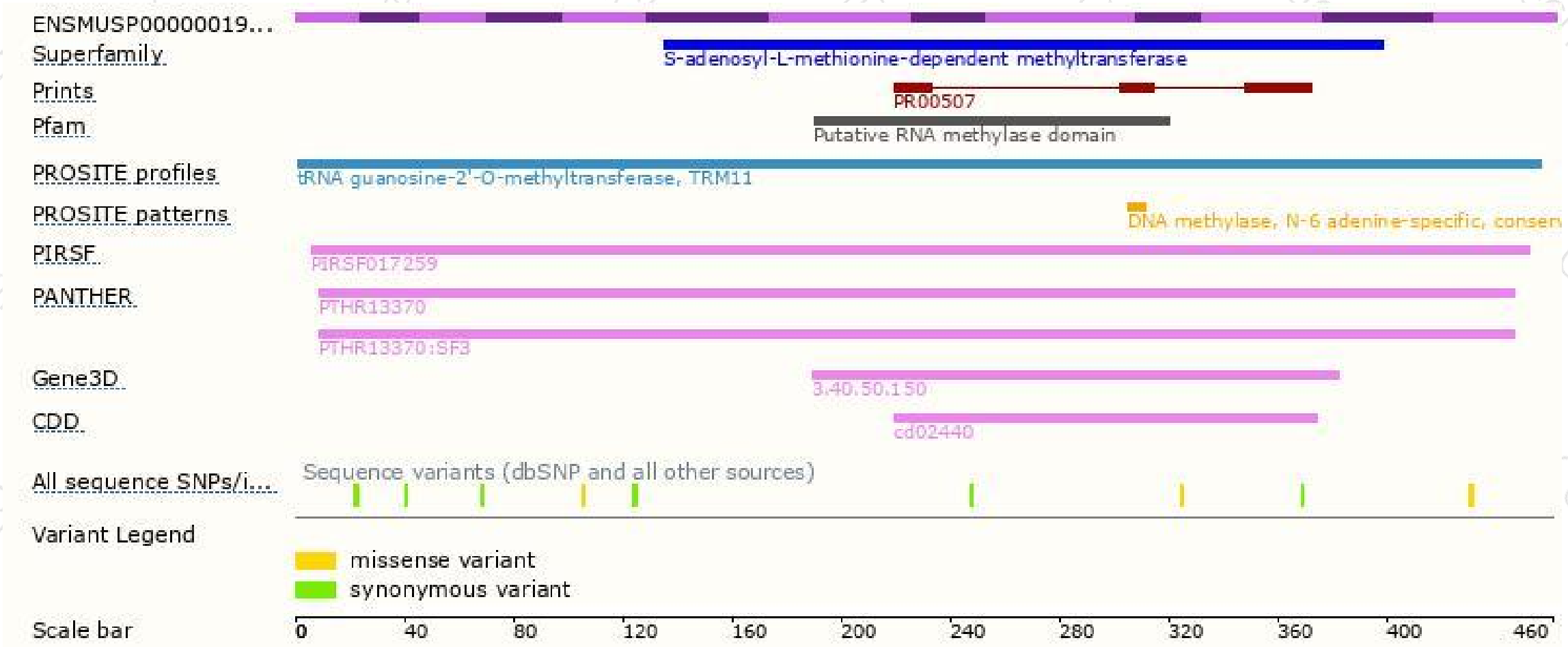
The strategy is based on the design of *Trmt11-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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