

Dimt1 Cas9-KO Strategy

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Project Overview

Project Name

Dimt1

Project type

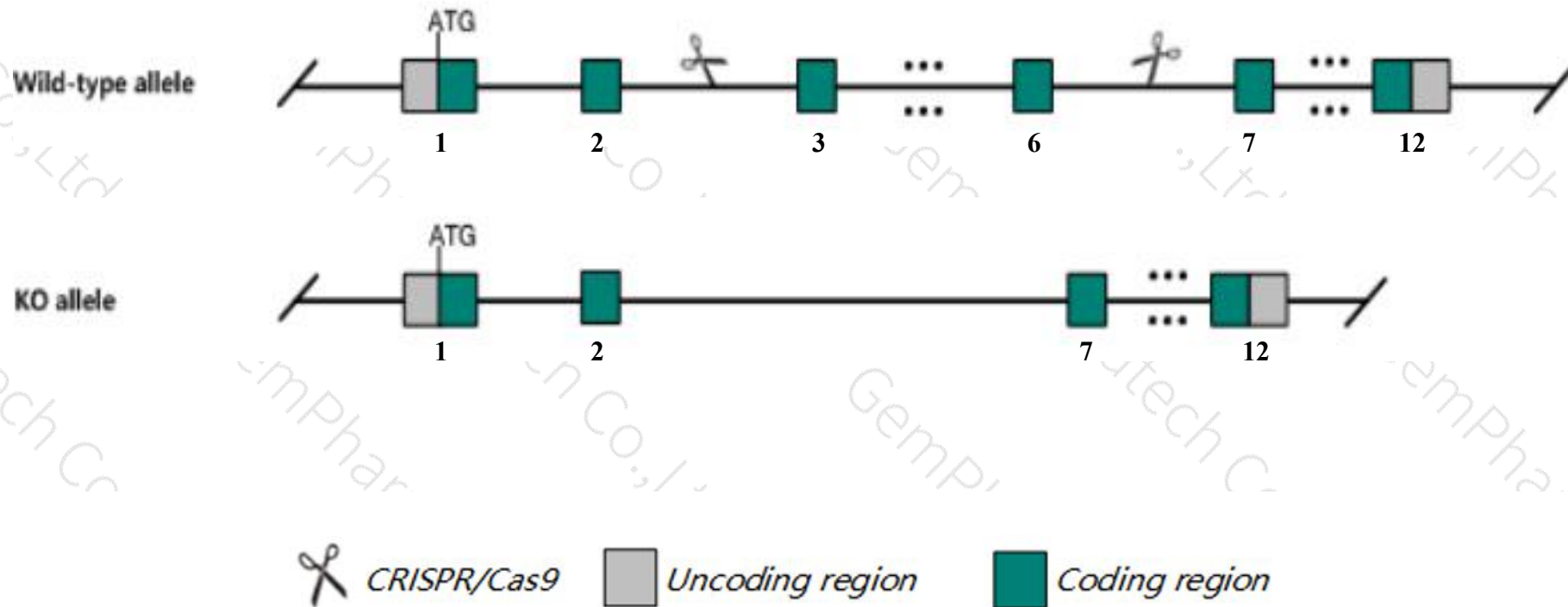
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dimt1* gene. The schematic diagram is as follows:



- The *Dimt1* gene has 4 transcripts. According to the structure of *Dimt1* gene, exon3-exon6 of *Dimt1-201* (ENSMUST00000022203.9) transcript is recommended as the knockout region. The region contains 293bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dimt1* gene. The brief process is as follows: CRISPR/Cas9 system we

- Some amino acids will remain at the N-terminus and some functions may be retained.
- The transcript 202 may not be affected.
- The *Dimt1* gene is located on the Chr13. 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)

Dimt1 DIM1 dimethyladenosine transferase 1-like (*S. cerevisiae*) [Mus musculus (house mouse)]

Gene ID: 66254, updated on 13-Mar-2020

Summary



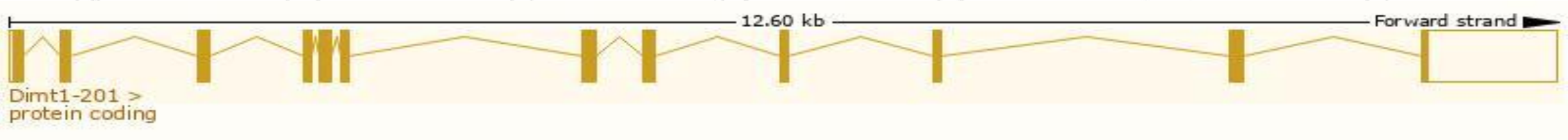
Official Symbol	Dimt1 provided by MGI
Official Full Name	DIM1 dimethyladenosine transferase 1-like (<i>S. cerevisiae</i>) provided by MGI
Primary source	MGI:MGI:1913504
See related	Ensembl:ENSMUSG000000021692
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1500031M22Rik, AV111347, Dimt1l
Expression	Broad expression in CNS E18 (RPKM 7.5), limb E14.5 (RPKM 6.9) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

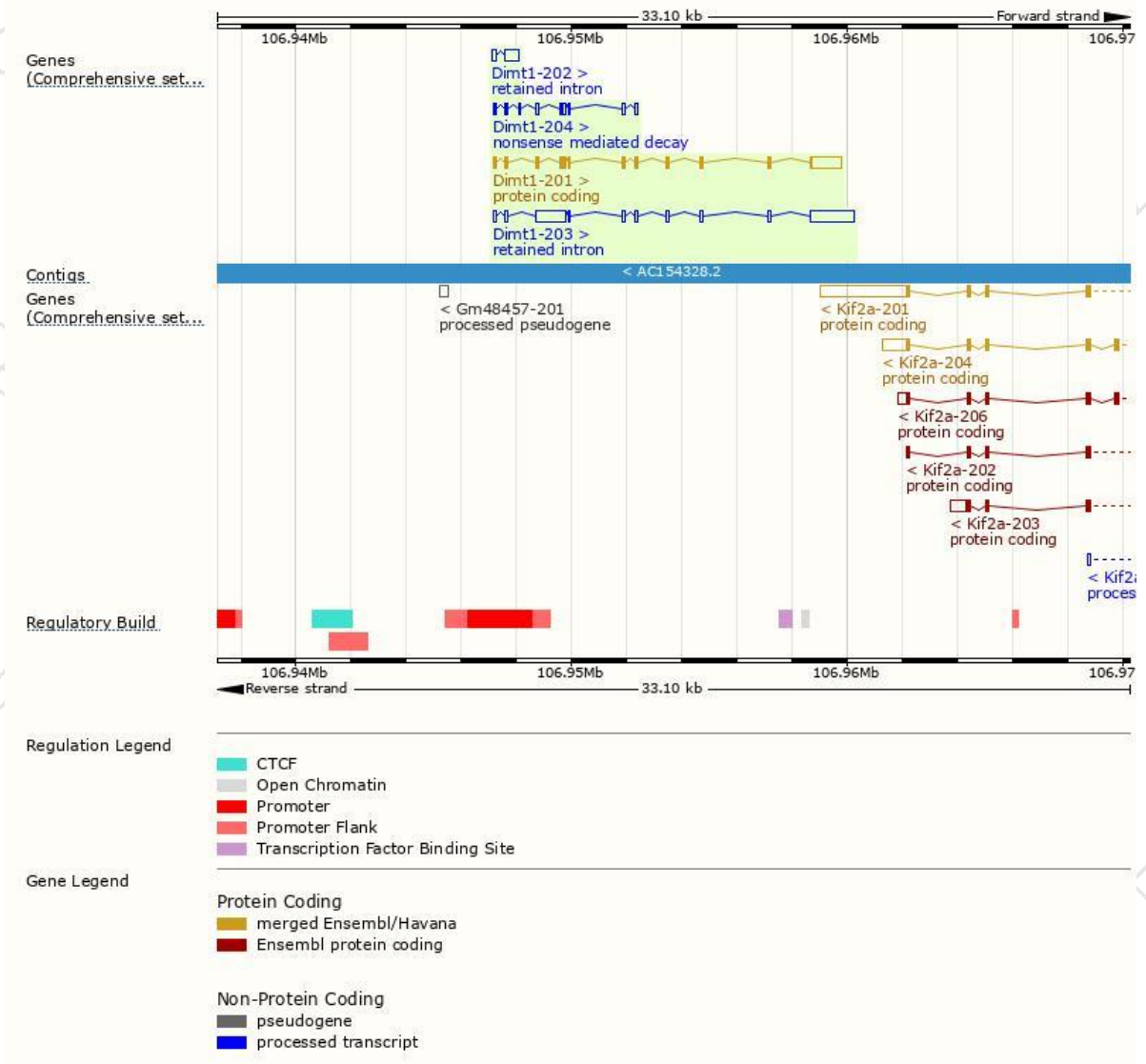
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dimt1-201	ENSMUST0000022203.9	2051	313aa	Protein coding	CCDS26758	Q9D0D4	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
Dimt1-204	ENSMUST00000224052.1	767	71aa	Nonsense mediated decay	-	A0A286YCE5	
Dimt1-203	ENSMUST00000223870.1	3338	No protein	Retained intron	-	-	
Dimt1-202	ENSMUST00000223851.1	644	No protein	Retained intron	-	-	

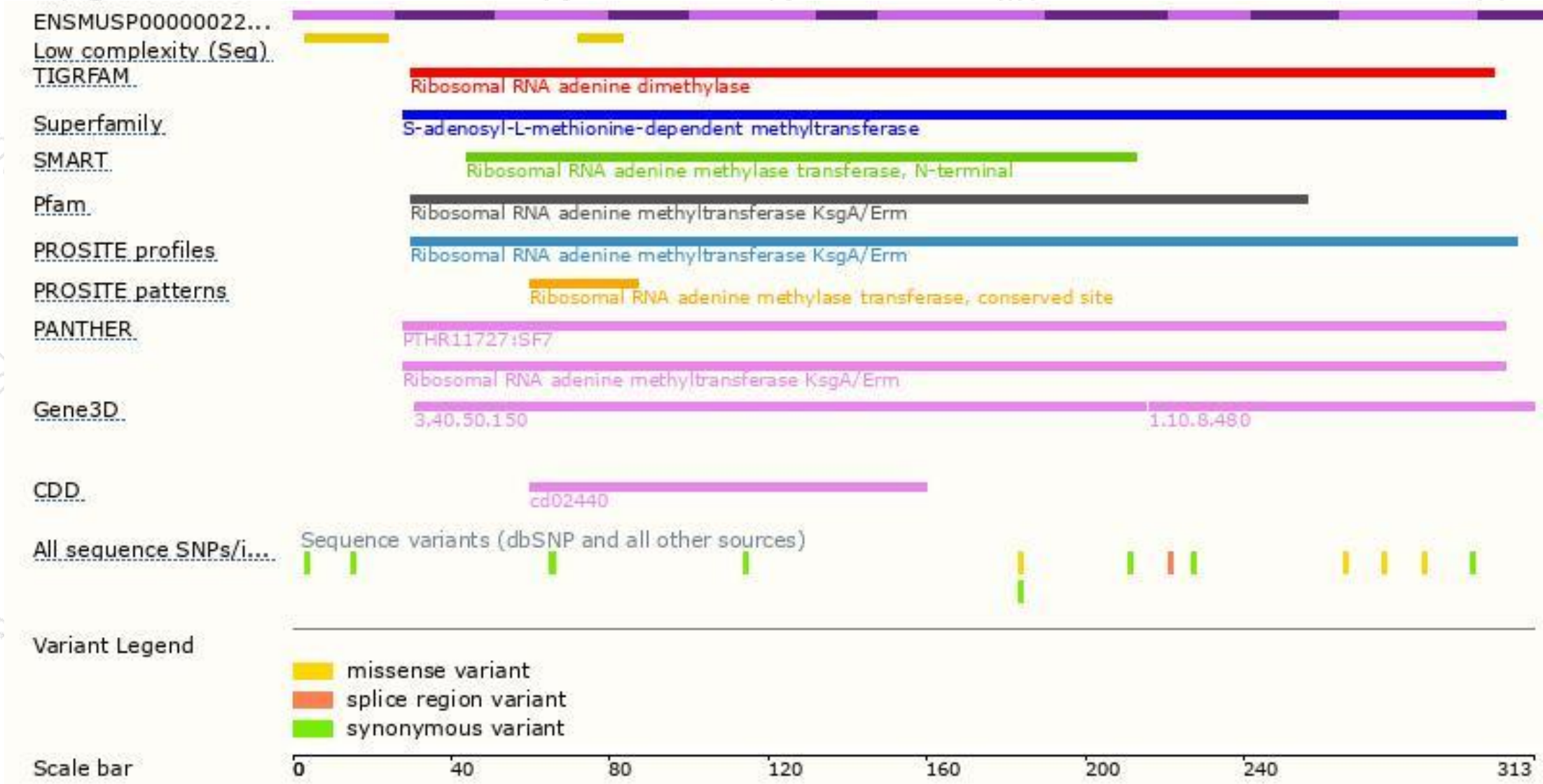
The strategy is based on the design of *Dimt1-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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