

***Cmtm5* Cas9-KO Strategy**

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Reviewer:

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Design Date:

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Project Overview

Project Name

Cmtm5

Project type

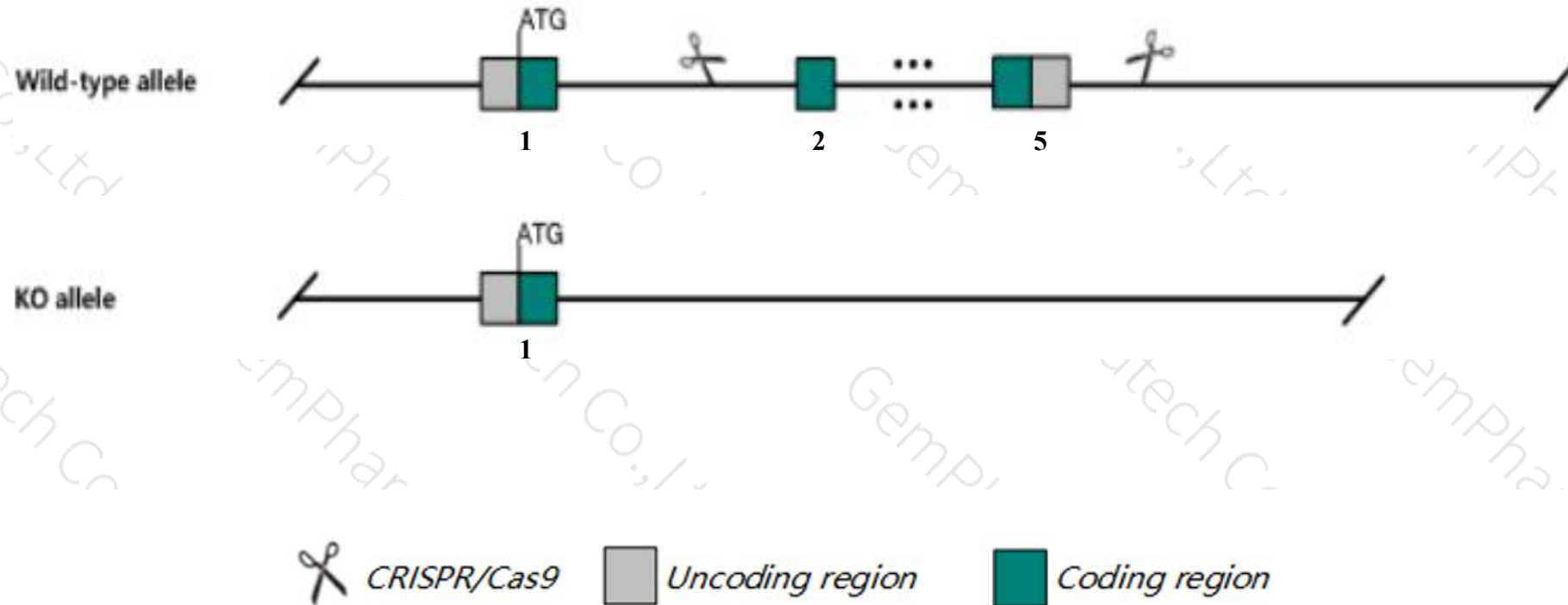
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cmtm5* gene. The schematic diagram is as follows:



- The *Cmtm5* gene has 3 transcripts. According to the structure of *Cmtm5* gene, exon2-exon5 of *Cmtm5-201* (ENSMUST00000037814.7) transcript is recommended as the knockout region. The region contains most 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 *Cmtm5* gene. The brief process is as follows: CRISPR/Cas9 system

- The knockout region is about 1.0 kb away from the 5th end of the *Gm49430-201* gene, and its effect is unknown.
- The *Cmtm5* 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)

Cmtm5 CKLF-like MARVEL transmembrane domain containing 5 [Mus musculus (house mouse)]

Gene ID: 67272, updated on 13-Mar-2020

Summary



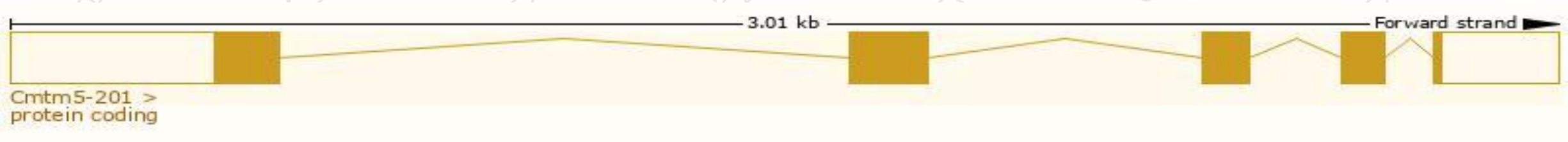
Official Symbol	Cmtm5 provided by MGI
Official Full Name	CKLF-like MARVEL transmembrane domain containing 5 provided by MGI
Primary source	MGI:MGI:2447164
See related	Ensembl:ENSMUSG00000040759
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1500005P16Rik, 2900052H21Rik, Cklfsf5
Expression	Biased expression in heart adult (RPKM 55.6), cerebellum adult (RPKM 11.4) and 2 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

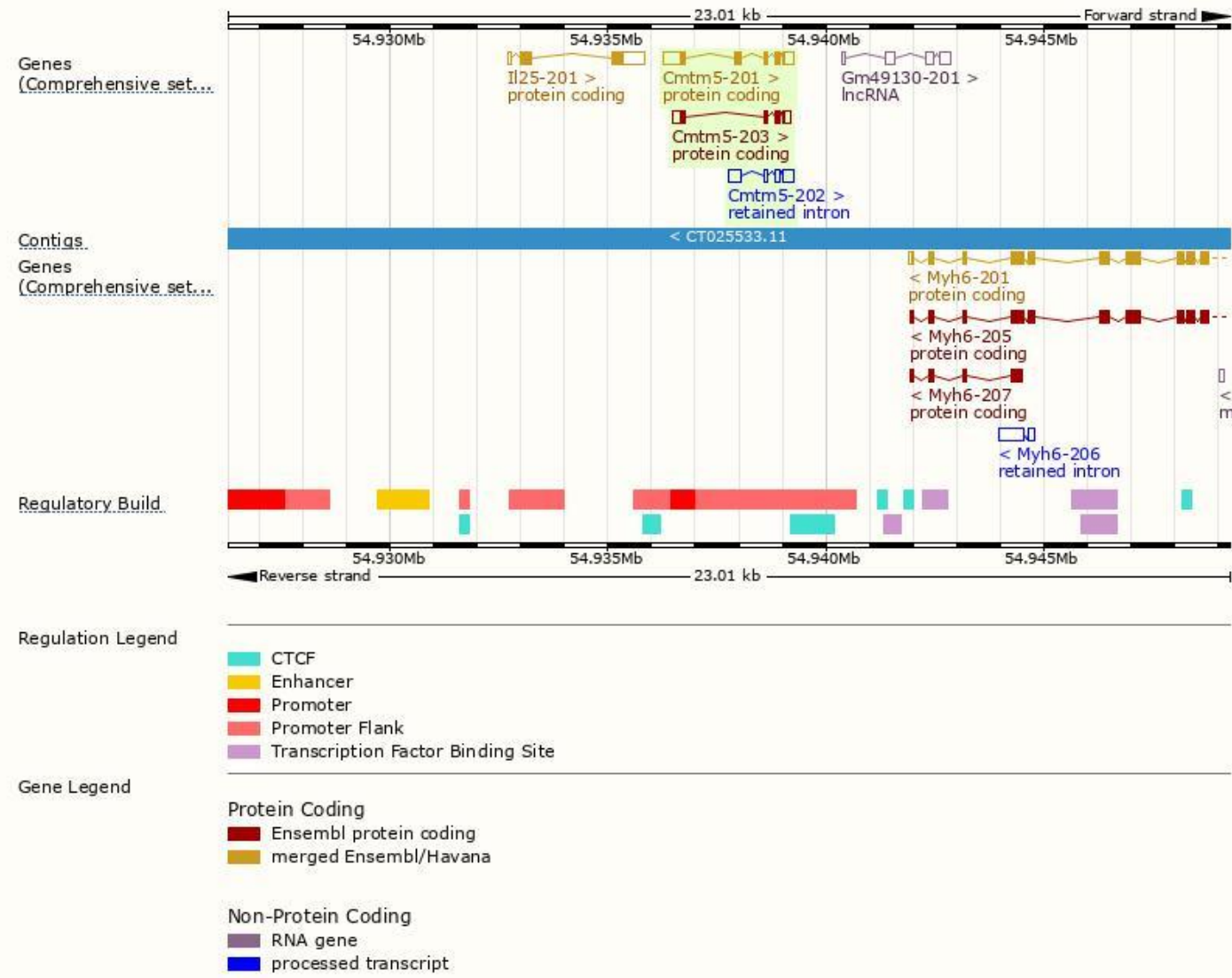
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cmtm5-201	ENSMUST00000037814.7	1095	156aa	Protein coding	CCDS27105	Q9D6G9	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
Cmtm5-203	ENSMUST00000227441.1	610	105aa	Protein coding	-	Q45TP8	GENCODE basic
Cmtm5-202	ENSMUST00000226807.1	687	No protein	Retained intron	-	-	

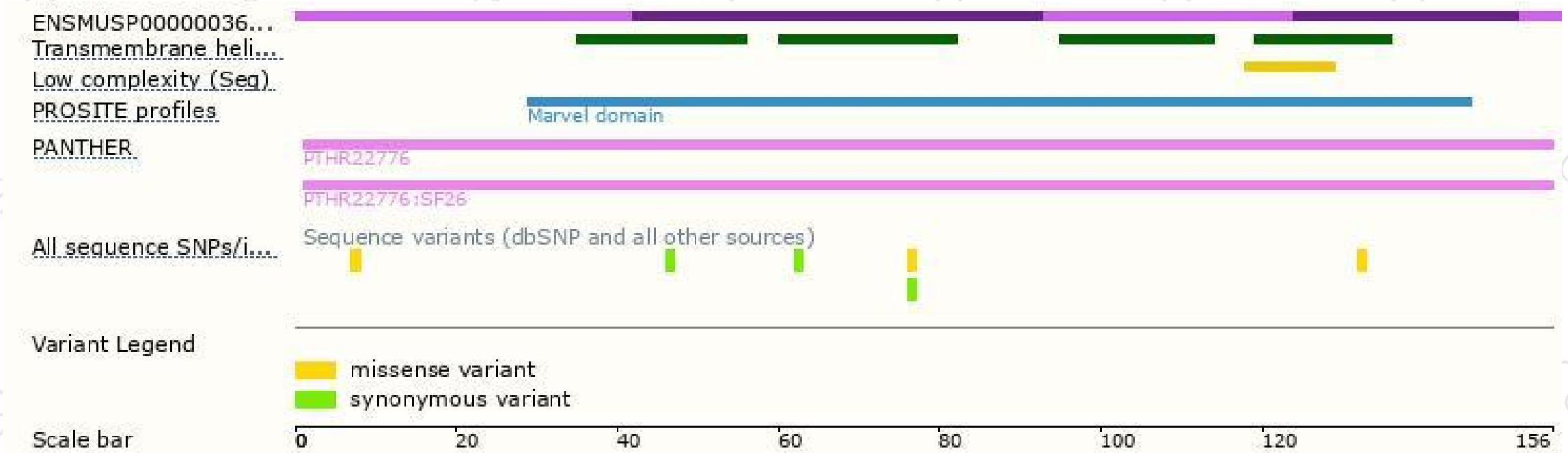
The strategy is based on the design of *Cmtm5-201* transcript,the transcription is shown below:



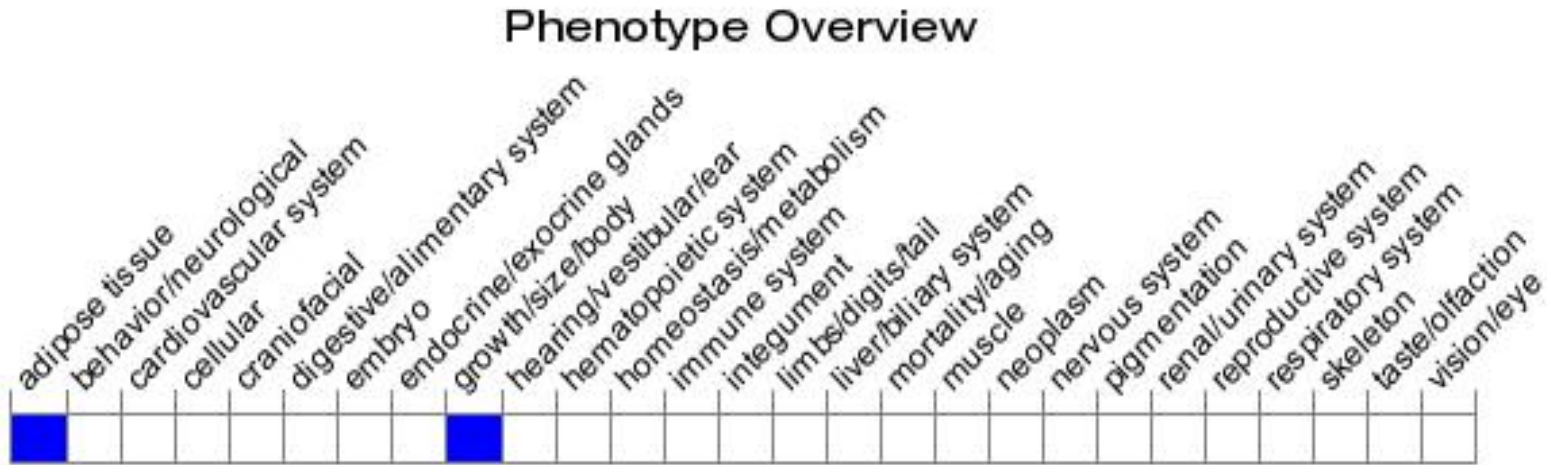
Genomic location distribution



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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