

# *Cmtm7* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Cmtm7***

**Project type**

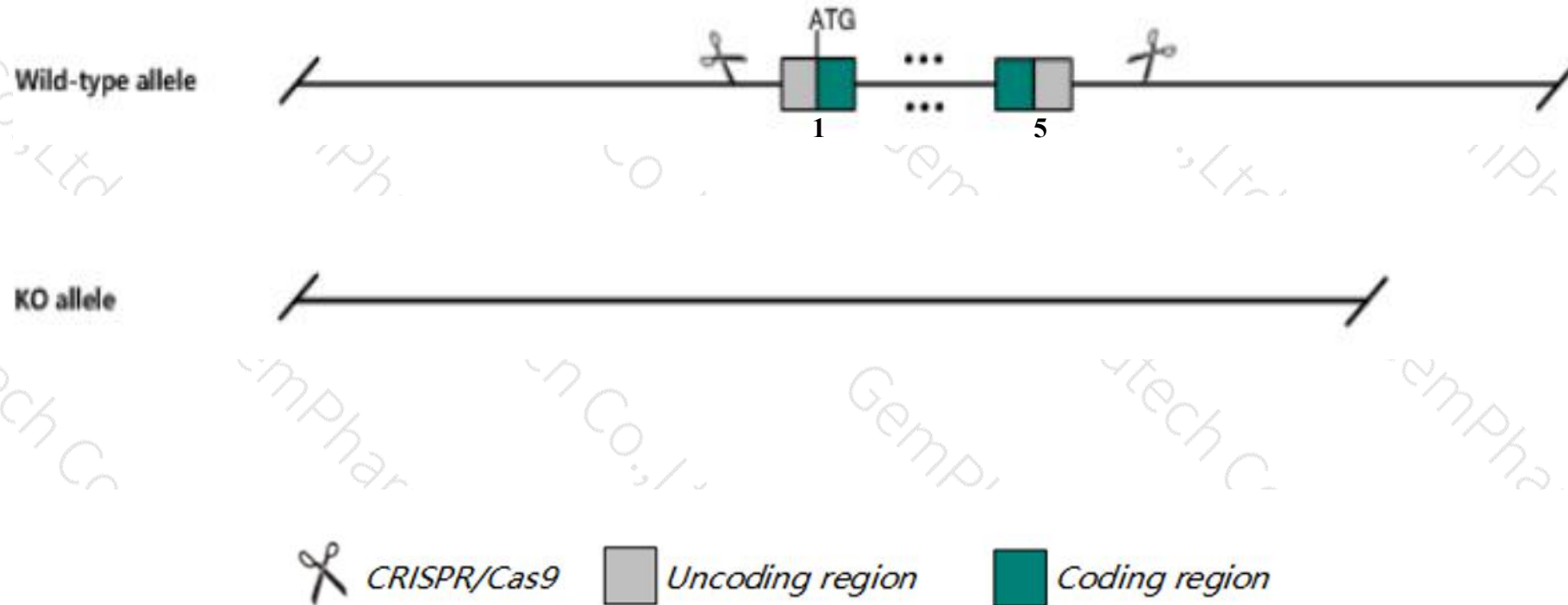
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cmtm7* gene. The schematic diagram is as follows:



- The *Cmtm7* gene has 5 transcripts. According to the structure of *Cmtm7* gene, exon1-exon5 of *Cmtm7-201* (ENSMUST00000035009.15) transcript is recommended as the knockout region. The region contains all 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 *Cmtm7* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, heterozygous mice die shortly after birth. Null mutations in this gene are haploinsufficient. a chimeric mouse showed defects in b-1a cell numbers and physiology.
- *Gm9888-201* gene may be destroyed.
- The *Cmtm7* gene is located on the Chr9. 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)

## Cmtm7 CKLF-like MARVEL transmembrane domain containing 7 [Mus musculus (house mouse)]

Gene ID: 102545, updated on 13-Mar-2020

### Summary



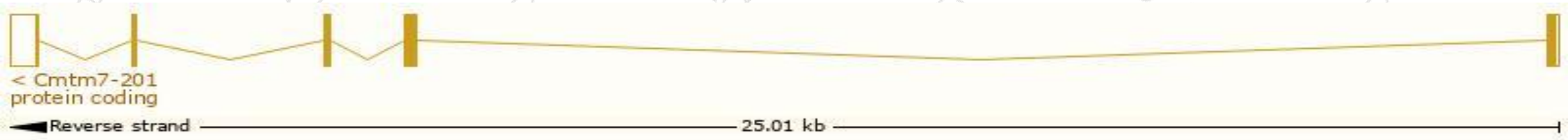
<b>Official Symbol</b>	Cmtm7 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	CKLF-like MARVEL transmembrane domain containing 7 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2447166</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000032436</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	AI481279, Cklfsf7, LNV
<b>Expression</b>	Broad expression in thymus adult (RPKM 190.5), stomach adult (RPKM 118.3) and 20 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information（Ensembl）

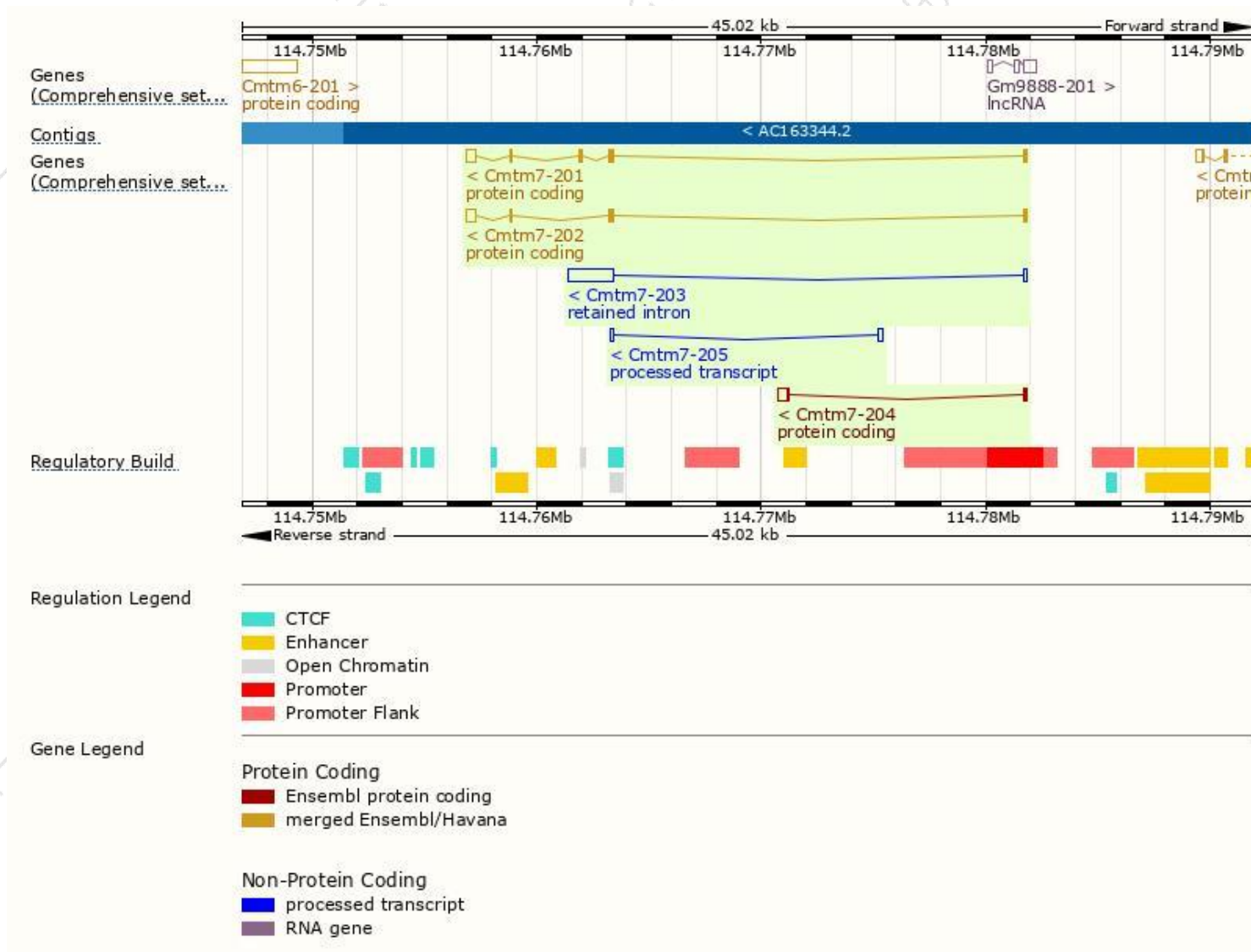
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cmtm7-201	<a href="#">ENSMUST00000035009.15</a>	993	<a href="#">167aa</a>	Protein coding	<a href="#">CCDS57710</a>	<a href="#">Q9ESD6</a>	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
Cmtm7-202	<a href="#">ENSMUST00000084867.8</a>	874	<a href="#">134aa</a>	Protein coding	<a href="#">CCDS57709</a>	<a href="#">Q9ESD6</a>	TSL:1 GENCODE basic
Cmtm7-204	<a href="#">ENSMUST00000216760.1</a>	665	<a href="#">63aa</a>	Protein coding	-	<a href="#">A0A1L1SRR1</a>	TSL:1 GENCODE basic
Cmtm7-205	<a href="#">ENSMUST00000217056.1</a>	345	No protein	Processed transcript	-	-	TSL:3
Cmtm7-203	<a href="#">ENSMUST00000214604.1</a>	2183	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Cmtm7-201* transcript,the transcription is shown below:

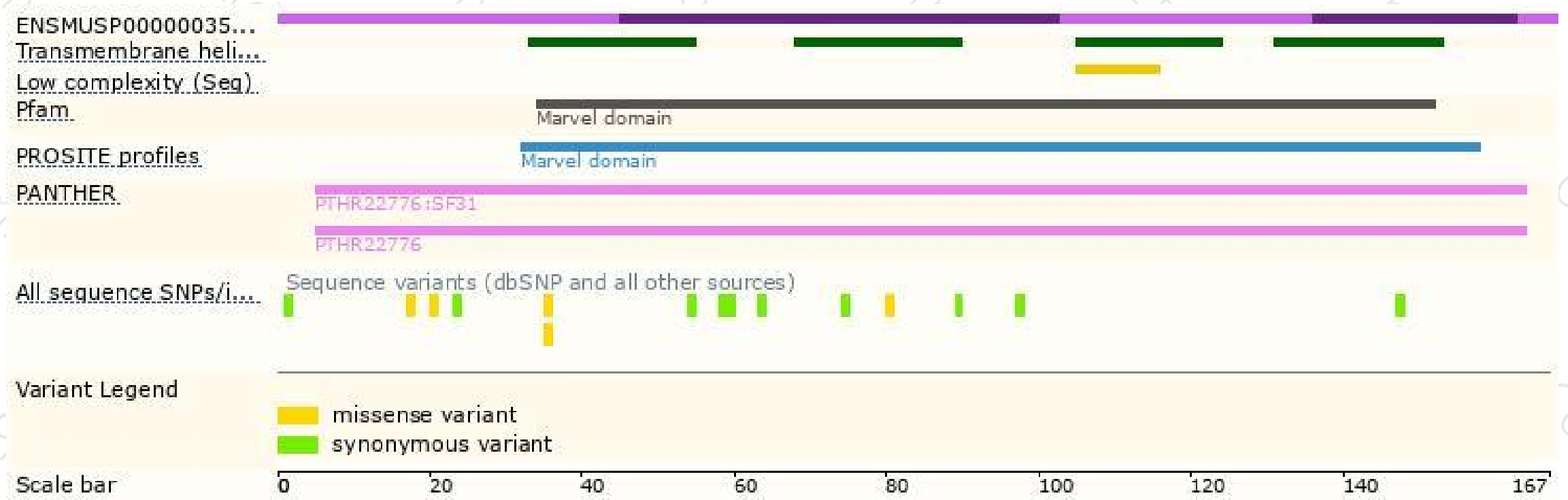


# Genomic location distribution

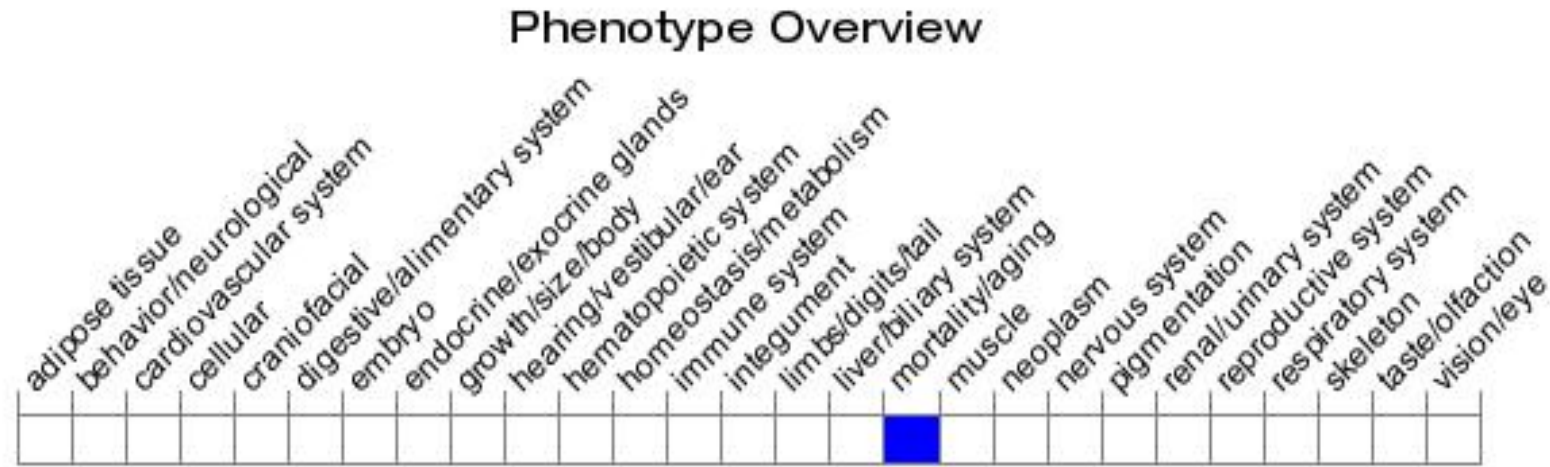




# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, heterozygous mice die shortly after birth. Null mutations in this gene are haploinsufficient. A chimeric mouse showed defects in B-1a cell numbers and physiology.

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

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