

# *Tmc7* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

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**Project Name**

***Tmc7***

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**Project type**

**Cas9-KO**

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**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tmc7* gene. The schematic diagram is as follows:



- The *Tmc7* gene has 4 transcripts. According to the structure of *Tmc7* gene, exon2-exon5 of *Tmc7-201* (ENSMUST00000044195.5) transcript is recommended as the knockout region. The region contains 641bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tmc7* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Tmc7* gene is located on the Chr7. 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)

## Tmc7 transmembrane channel-like gene family 7 [Mus musculus (house mouse)]

Gene ID: 209760, updated on 19-Mar-2019

### Summary



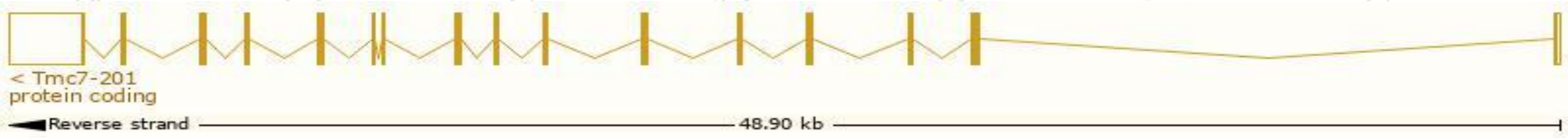
<b>Official Symbol</b>	Tmc7 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	transmembrane channel-like gene family 7 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2443317</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000042246</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	PROVISIONAL
<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>	1700030H01Rik, C230064B05, C630024K23Rik
<b>Expression</b>	Biased expression in testis adult (RPKM 39.3), cerebellum adult (RPKM 4.2) and 7 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

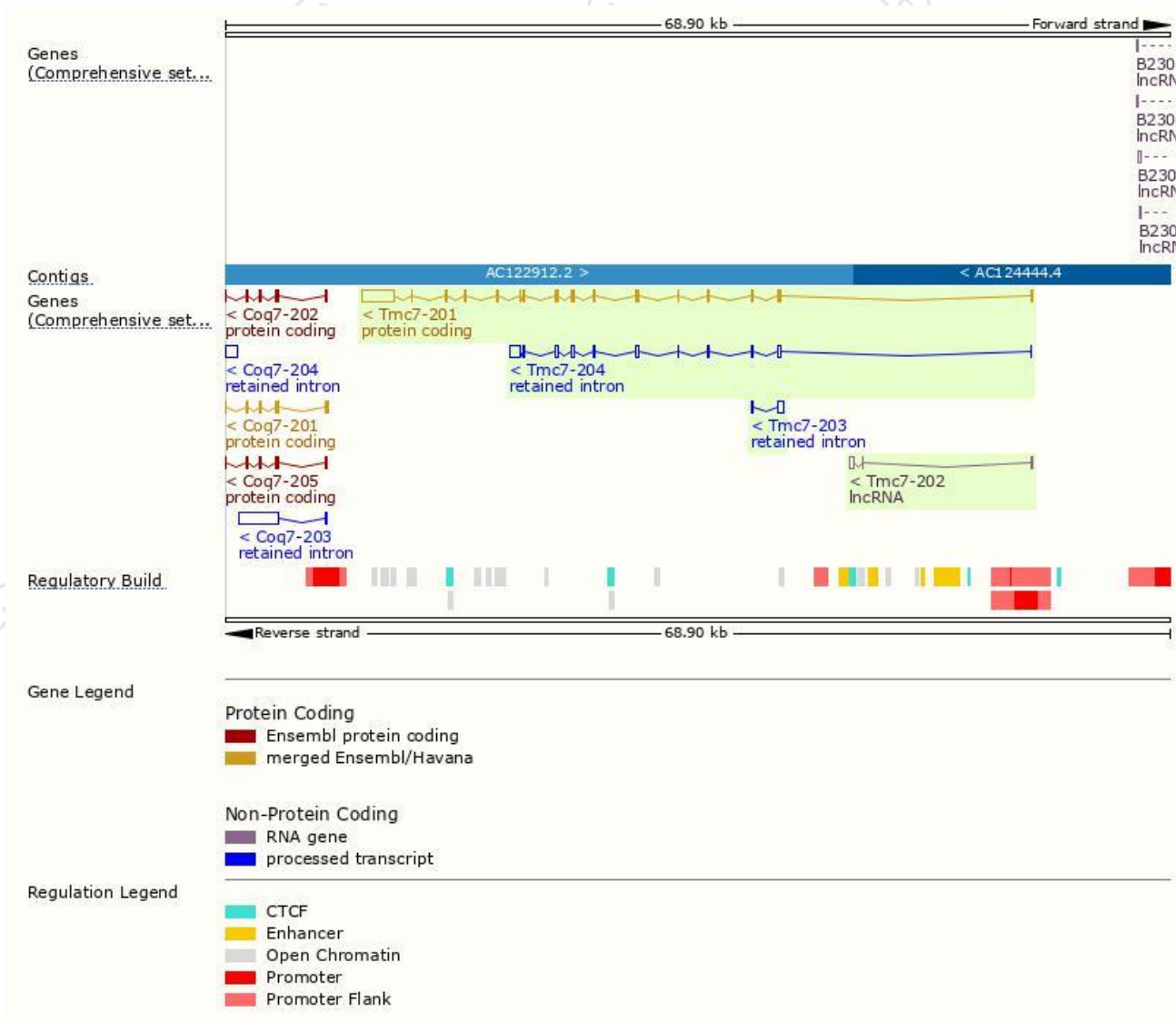
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tmc7-201	<a href="#">ENSMUST00000044195.5</a>	4546	<a href="#">726aa</a>	Protein coding	<a href="#">CCDS21772</a>	<a href="#">Q8C428</a>	TSL:1 GENCODE basic APPRIS P1
Tmc7-204	<a href="#">ENSMUST00000153635.1</a>	2298	No protein	Retained intron	-	-	TSL:1
Tmc7-203	<a href="#">ENSMUST00000145989.1</a>	570	No protein	Retained intron	-	-	TSL:3
Tmc7-202	<a href="#">ENSMUST00000139693.1</a>	389	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Tmc7-201* transcript,The transcription is shown below

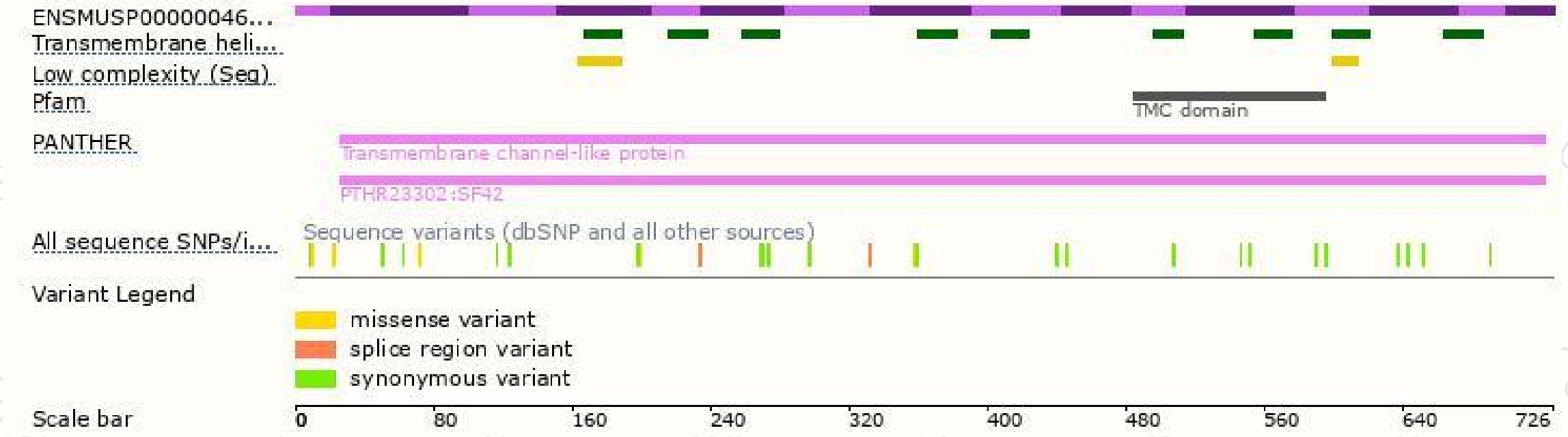


# Genomic location distribution

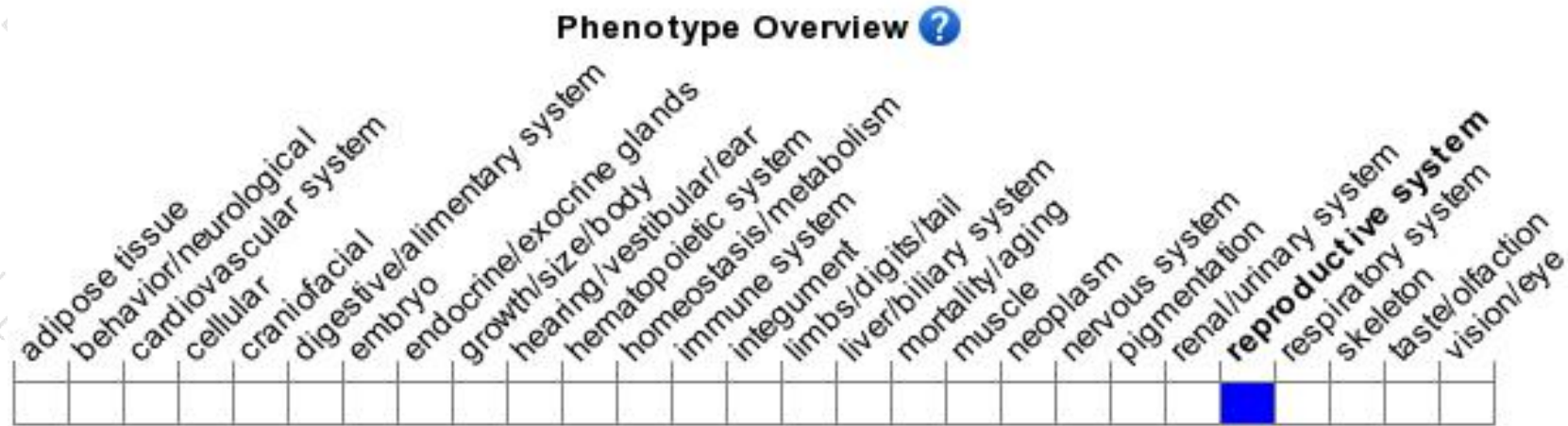




# Protein domain



# 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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