

Tpm2 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Tpm2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tpm2* gene. The schematic diagram is as follows:



- The *Tpm2* gene has 6 transcripts. According to the structure of *Tpm2* gene, exon3-exon8 of *Tpm2-202* (ENSMUST00000107913.9) transcript is recommended as the knockout region. The region contains 532bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tpm2* gene. The brief process is as follows: CRISPR/Cas9 system w

- The *Tpm2* gene is located on the Chr4. 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)

Tpm2 tropomyosin 2, beta [*Mus musculus* (house mouse)]

Gene ID: 22004, updated on 14-Nov-2019

Summary

Official Symbol Tpm2 provided by MGI

Official Full Name tropomyosin 2, beta provided by MGI

Primary source MGI:MGI:98810

See related [Ensembl:ENSMUSG00000028464](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

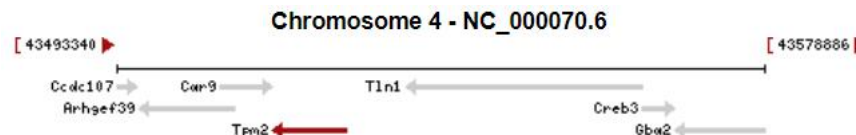
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as Tpm-2; Trop-2

Summary This gene belongs to the tropomyosin family which encodes proteins that bind to actin filaments and stabilize them by regulating access to actin modifying proteins. The encoded protein is a high molecular weight tropomyosin expressed in slow skeletal muscle. In humans, mutations in this gene are associated with nemaline myopathy, cap disease and distal arthrogryposis syndromes. Alternative splicing of this gene results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Apr 2013]

Expression Biased expression in bladder adult (RPKM 555.0), mammary gland adult (RPKM 100.5) and 4 other tissues [See more](#)

Orthologs [human](#) [all](#)

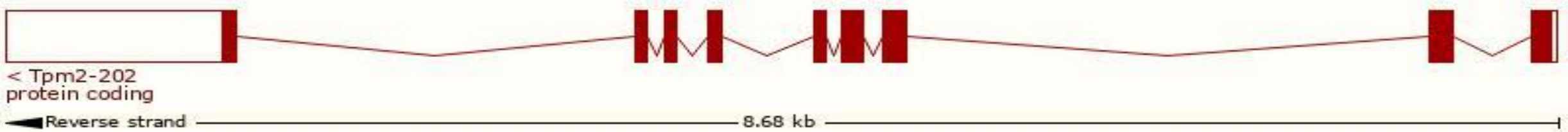


Transcript information (Ensembl)

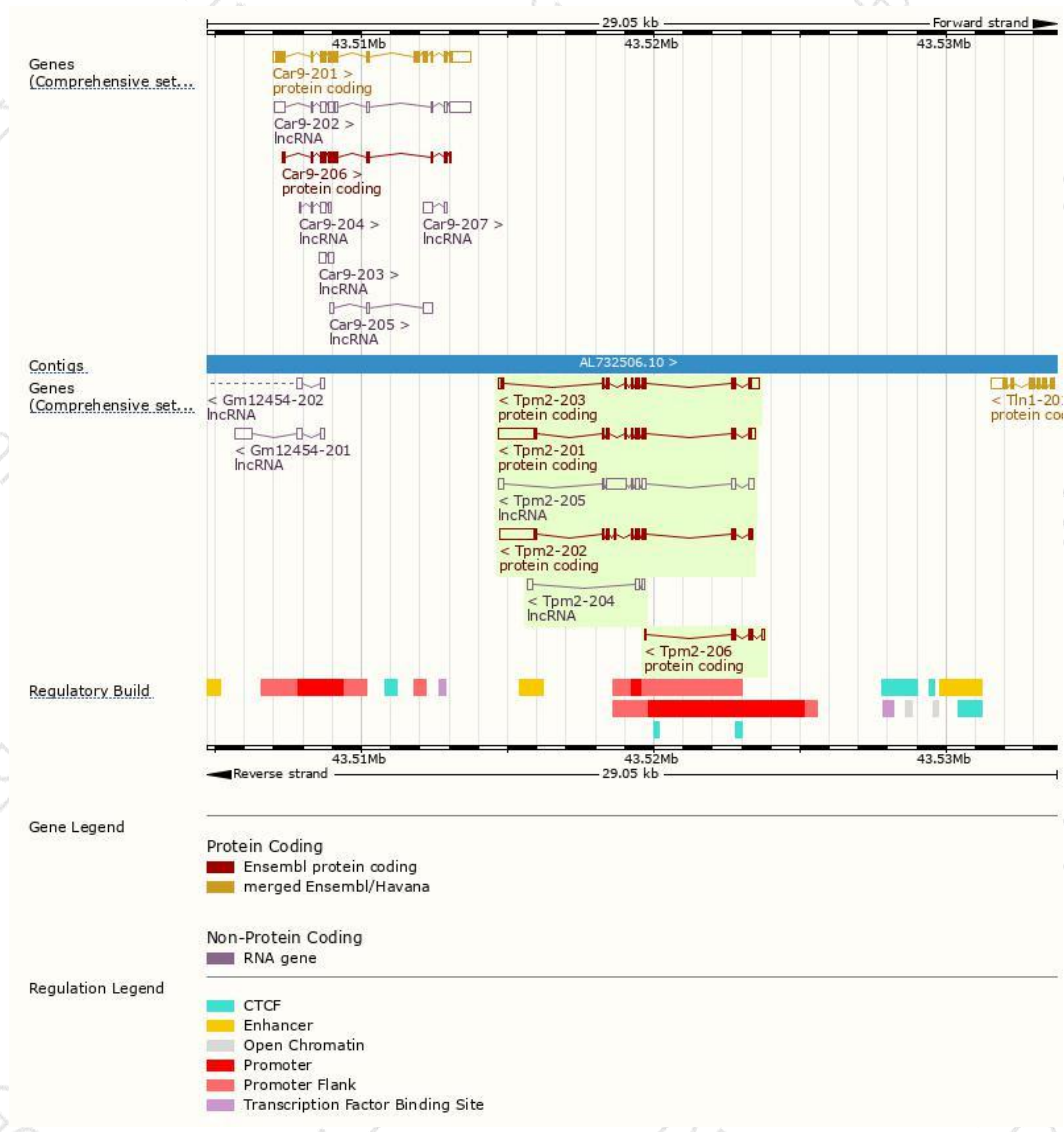
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Tpm2-202	ENSMUST00000107913.9	2098	284aa	ENSMUSP00000103546.3	Protein coding	CCDS18100	P58774	TSL:1 GENCODE basic APPRIS P3
Tpm2-203	ENSMUST00000107914.9	1164	284aa	ENSMUSP00000103547.3	Protein coding	CCDS71374	P58774 Q6PJ18	TSL:1 GENCODE basic APPRIS ALT1
Tpm2-201	ENSMUST00000030184.11	2175	284aa	ENSMUSP00000030184.5	Protein coding	-	A2AIM4	TSL:5 GENCODE basic APPRIS ALT1
Tpm2-206	ENSMUST00000150592.1	401	105aa	ENSMUSP00000119908.1	Protein coding	-	A2AIM5	CDS 3' incomplete TSL:3
Tpm2-205	ENSMUST00000150262.7	1545	No protein	-	lncRNA	-	-	TSL:2
Tpm2-204	ENSMUST00000133355.1	337	No protein	-	lncRNA	-	-	TSL:5

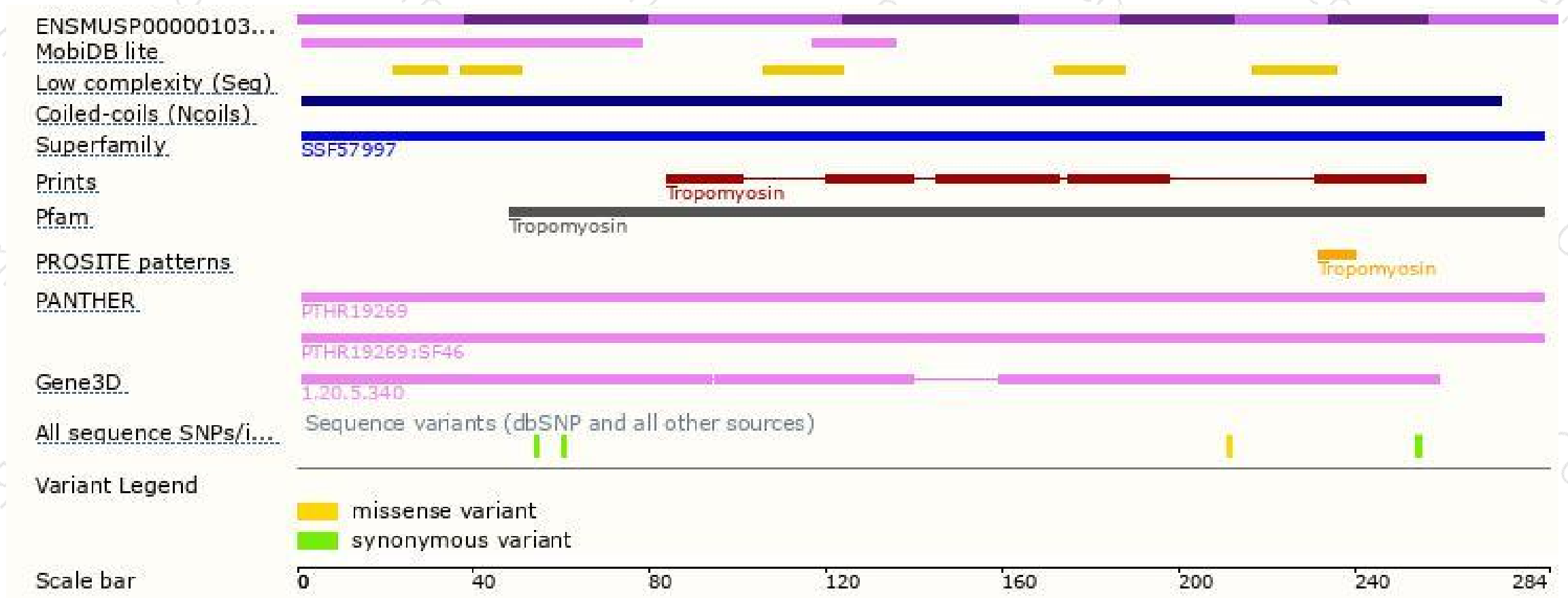
The strategy is based on the design of *Tpm2-202* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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