

Tmtc3 Cas9-KO Strategy

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Project Overview

Project Name

Tmtc3

Project type

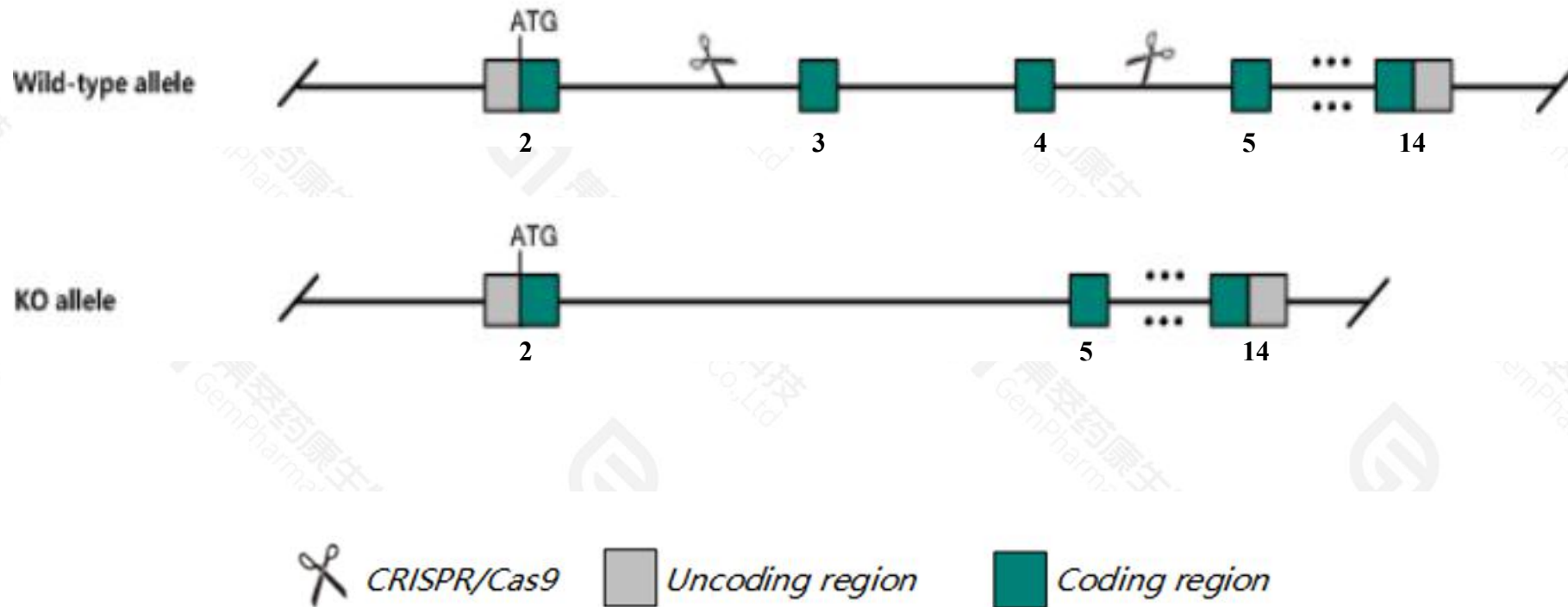
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tmtc3* gene. The schematic diagram is as follows:



- The *Tmtc3* gene has 5 transcripts. According to the structure of *Tmtc3* gene, exon3-exon4 of *Tmtc3-201*(ENSMUST00000058154.15) transcript is recommended as the knockout region. The region contains 319bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tmtc3* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, mice homozygous for a gene trap allele exhibit impaired bronchial smooth muscle and alveolar myofibroblast development that leads to cyanosis and postnatal lethality in some mice.
- Transcript *Tmtc3* -205 may not be affected.
- The *Tmtc3* gene is located on the Chr10. 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.

Tmtc3 transmembrane and tetratricopeptide repeat containing 3 [Mus musculus (house mouse)]

Gene ID: 237500, updated on 17-Dec-2020

Summary



Official Symbol Tmtc3 provided by [MGI](#)

Official Full Name transmembrane and tetratricopeptide repeat containing 3 provided by [MGI](#)

Primary source [MGI:MGI:3036255](#)

See related [Ensembl:ENSMUSG00000036676](#)

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 9130014E20Rik, B130008E12Rik, mSm, mSmile

Expression Ubiquitous expression in limb E14.5 (RPKM 3.8), bladder adult (RPKM 3.8) and 28 other tissues [See more](#)

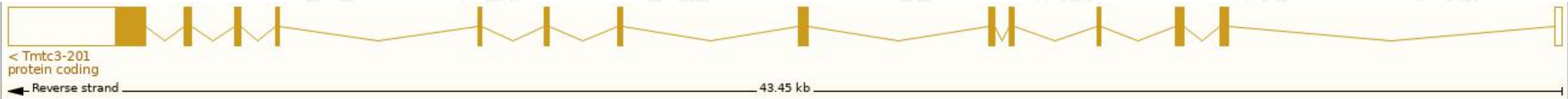
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

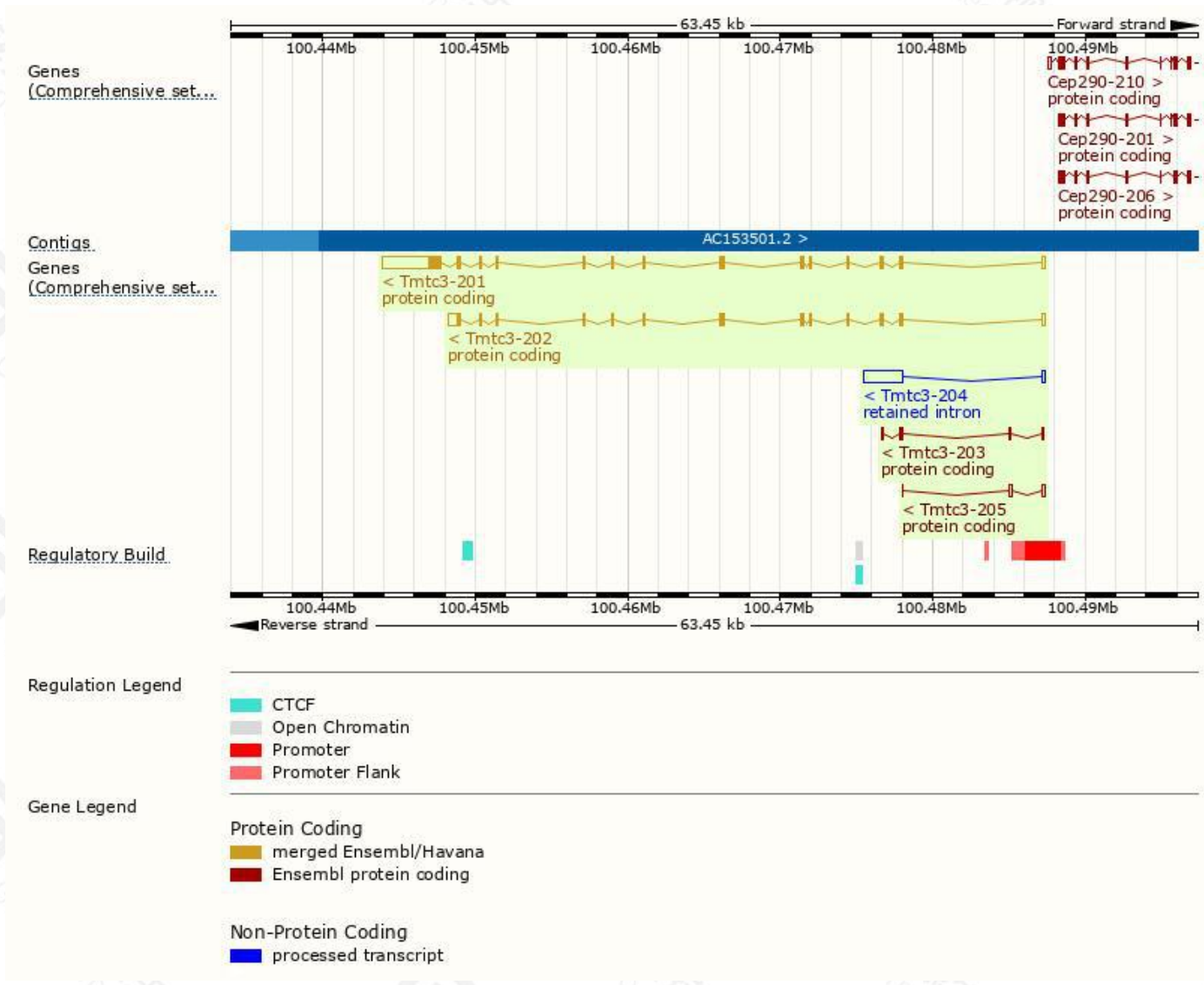
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tmtc3-201	ENSMUST00000058154.15	5993	920aa	Protein coding	CCDS48684		TSL:1 , GENCODE basic , APPRIS P1 ,
Tmtc3-202	ENSMUST00000099318.10	2794	658aa	Protein coding	CCDS24150		TSL:1 , GENCODE basic ,
Tmtc3-203	ENSMUST00000128009.2	535	113aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Tmtc3-205	ENSMUST00000134477.2	347	11aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Tmtc3-204	ENSMUST00000130883.2	2780	No protein	Retained intron	-		TSL:1 ,

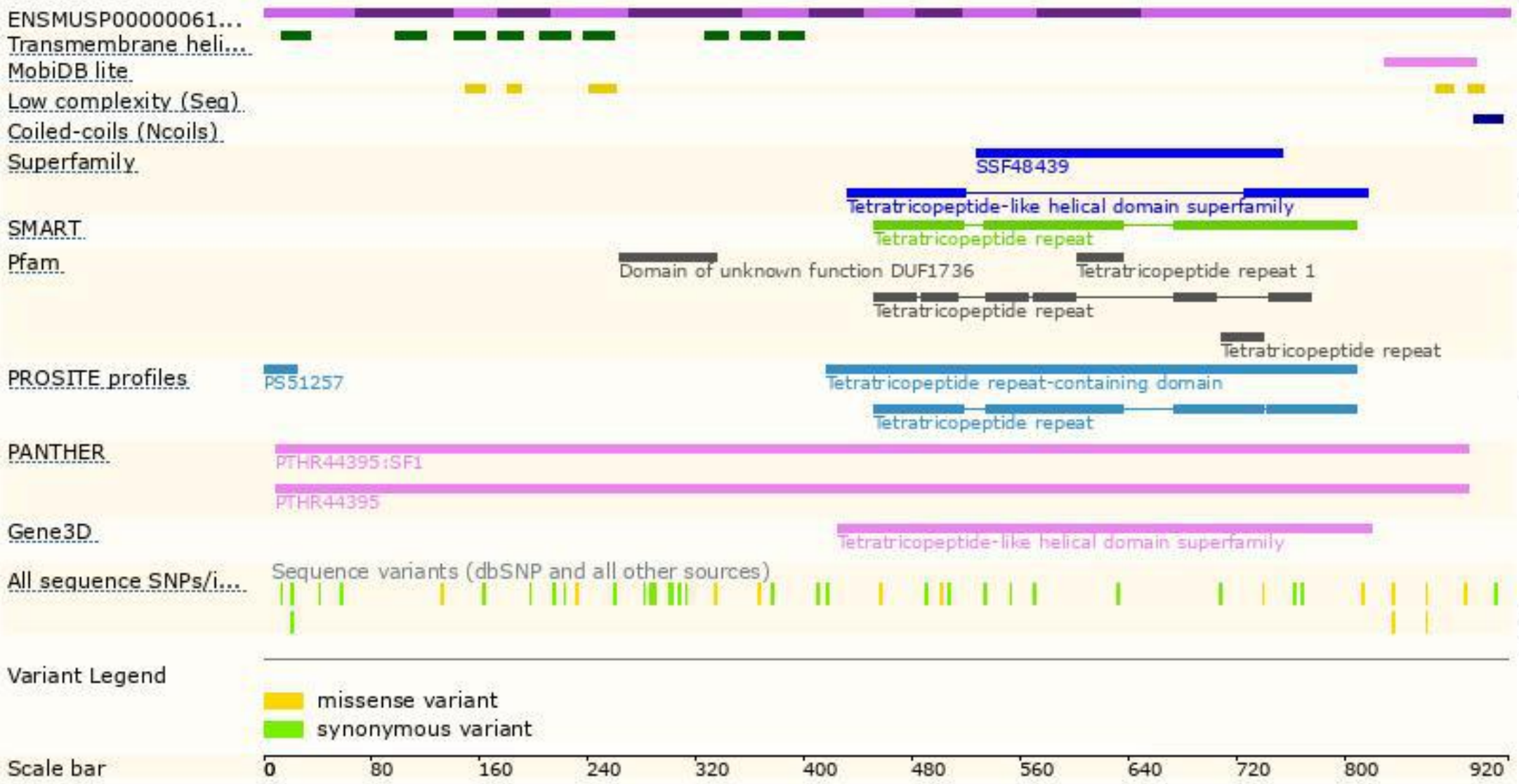
The strategy is based on the design of *Tmtc3-201* transcript,the transcription is shown below:



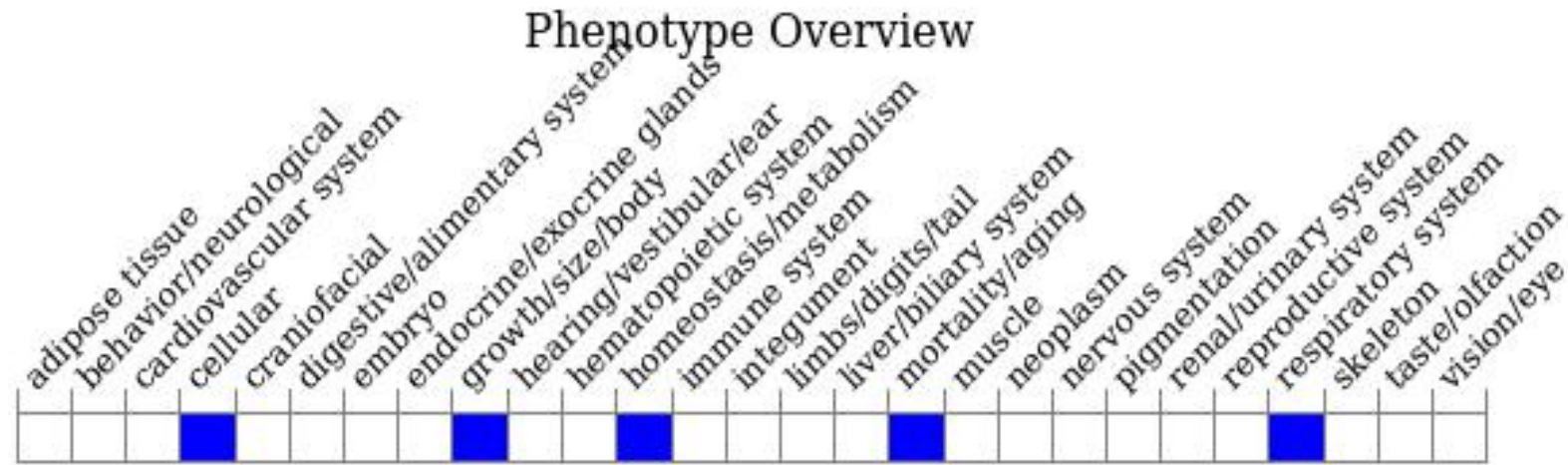
Genomic location distribution



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, mice homozygous for a gene trap allele exhibit impaired bronchial smooth muscle and alveolar myofibroblast development that leads to cyanosis and postnatal lethality in some mice.

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