

***Mtmr14* Cas9-KO Strategy**

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Project Overview

Project Name

Mtmr14

Project type

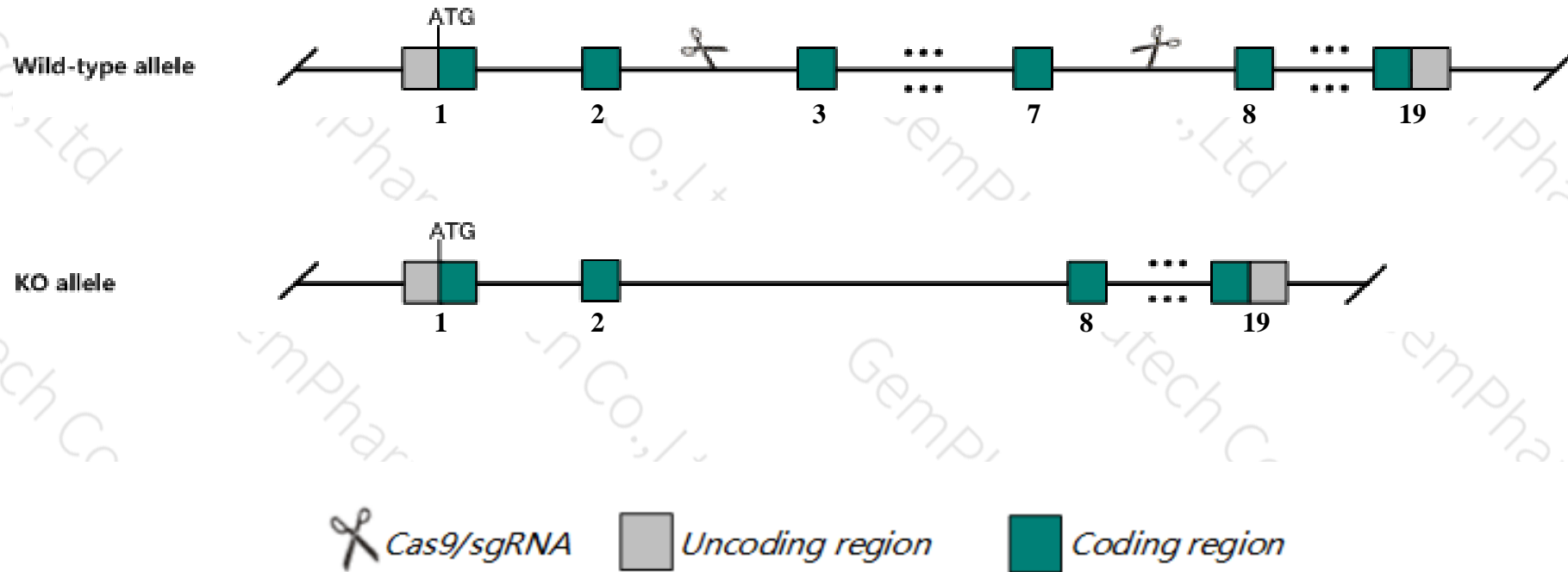
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mtmr14* gene. The schematic diagram is as follows:



- The *Mtmr14* gene has 10 transcripts. According to the structure of *Mtmr14* gene, exon3-exon7 of *Mtmr14-201* (ENSMUST00000113146.8) transcript is recommended as the knockout region. The region contains 443bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mtmr14* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 knock-out allele exhibit impaired coordination, decreased exercise endurance, increased muscle fatigue, and muscle atrophy associated with impaired muscular calcium homeostasis.
- The effect on transcript *Mtmt14*-203&204&206&207&208&209&210 is unknown.
- The *Mtmt14* gene is located on the Chr6. 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)

Mtmr14 myotubularin related protein 14 [*Mus musculus* (house mouse)]

Gene ID: 97287, updated on 14-Aug-2019

Summary

- Official Symbol** Mtmr14 provided by [MGI](#)
- Official Full Name** myotubularin related protein 14 provided by [MGI](#)
- Primary source** [MGI:MGI:1916075](#)
- See related** [Ensembl:ENSMUSG00000030269](#)
- 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** C76151; AW553738; 1110061O04Rik
- Expression** Ubiquitous expression in ovary adult (RPKM 18.6), thymus adult (RPKM 14.9) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 6; 6 E3 See Mtmr14 in [Genome Data Viewer](#)

Exon count: 20

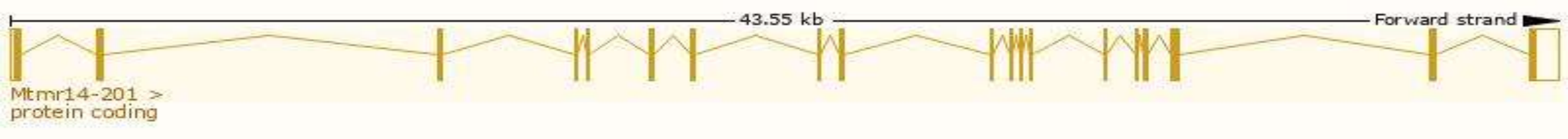
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	6	NC_000072.6 (113237635..113281392)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	6	NC_000072.5 (113187837..113231386)

Transcript information (Ensembl)

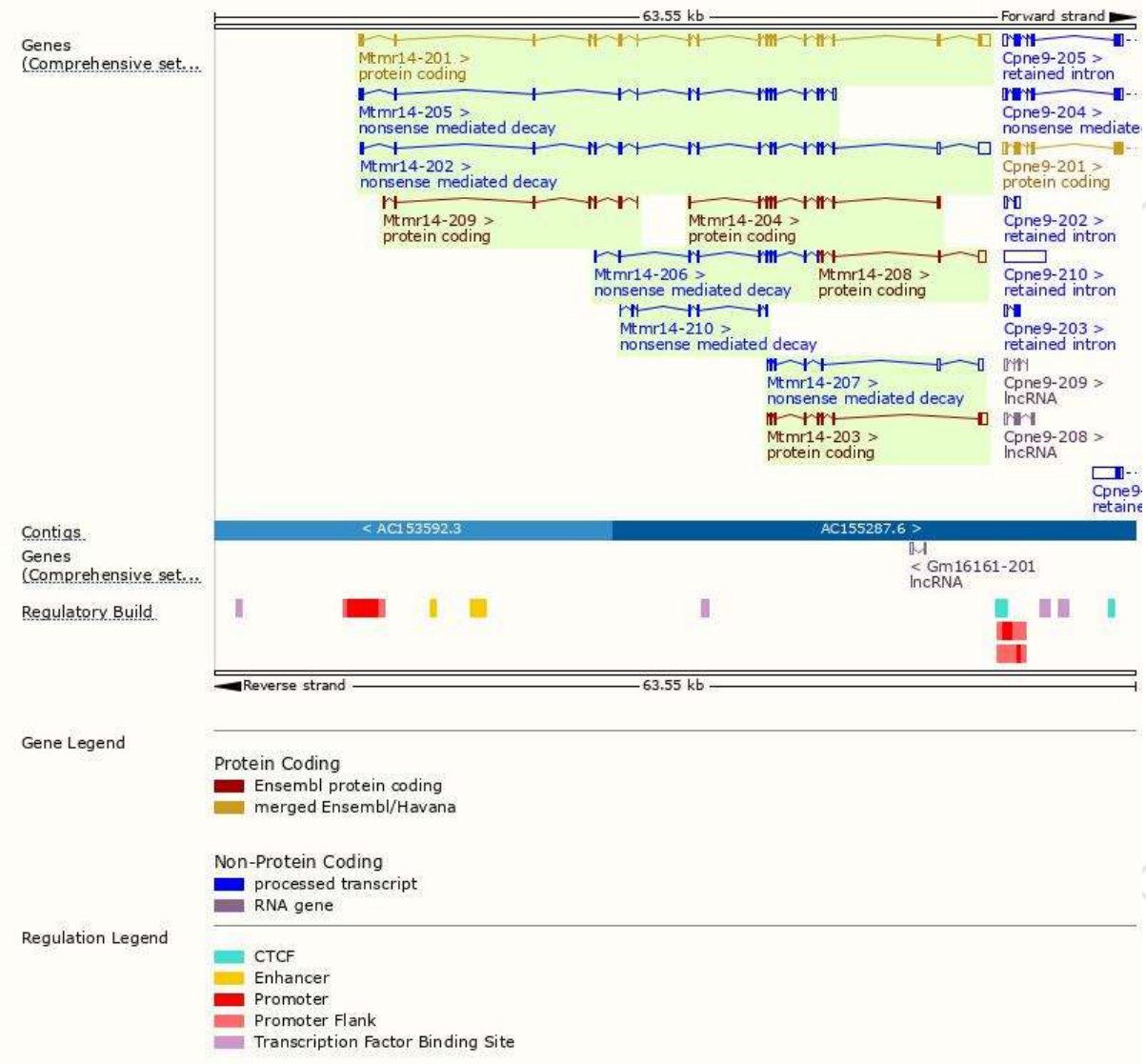
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mtmr14-201	ENSMUST00000113146.8	2676	648aa	Protein coding	CCDS20412	Q8VEL2	TSL:1 GENCODE basic APPRIS P2
Mtmr14-203	ENSMUST00000134945.7	1205	264aa	Protein coding	-	F6W741	CDS 5' incomplete TSL:1
Mtmr14-208	ENSMUST00000151149.1	930	142aa	Protein coding	-	F7BA73	CDS 5' incomplete TSL:3
Mtmr14-204	ENSMUST00000137772.7	893	298aa	Protein coding	-	F6RV41	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 APPRIS ALT2
Mtmr14-209	ENSMUST00000156141.2	642	189aa	Protein coding	-	D3Z1C1	CDS 3' incomplete TSL:5
Mtmr14-202	ENSMUST00000129883.7	2531	331aa	Nonsense mediated decay	-	D6RDS6	TSL:1
Mtmr14-205	ENSMUST00000142938.7	1661	140aa	Nonsense mediated decay	-	D6RFN8	TSL:2
Mtmr14-207	ENSMUST00000148523.7	876	119aa	Nonsense mediated decay	-	F6SBM1	CDS 5' incomplete TSL:5
Mtmr14-210	ENSMUST00000203385.1	575	73aa	Nonsense mediated decay	-	A0A0N4SV39	CDS 5' incomplete TSL:5
Mtmr14-206	ENSMUST00000144976.3	570	57aa	Nonsense mediated decay	-	F6YA17	CDS 5' incomplete TSL:5

The strategy is based on the design of *Mtmr14-201* transcript,The transcription is shown below



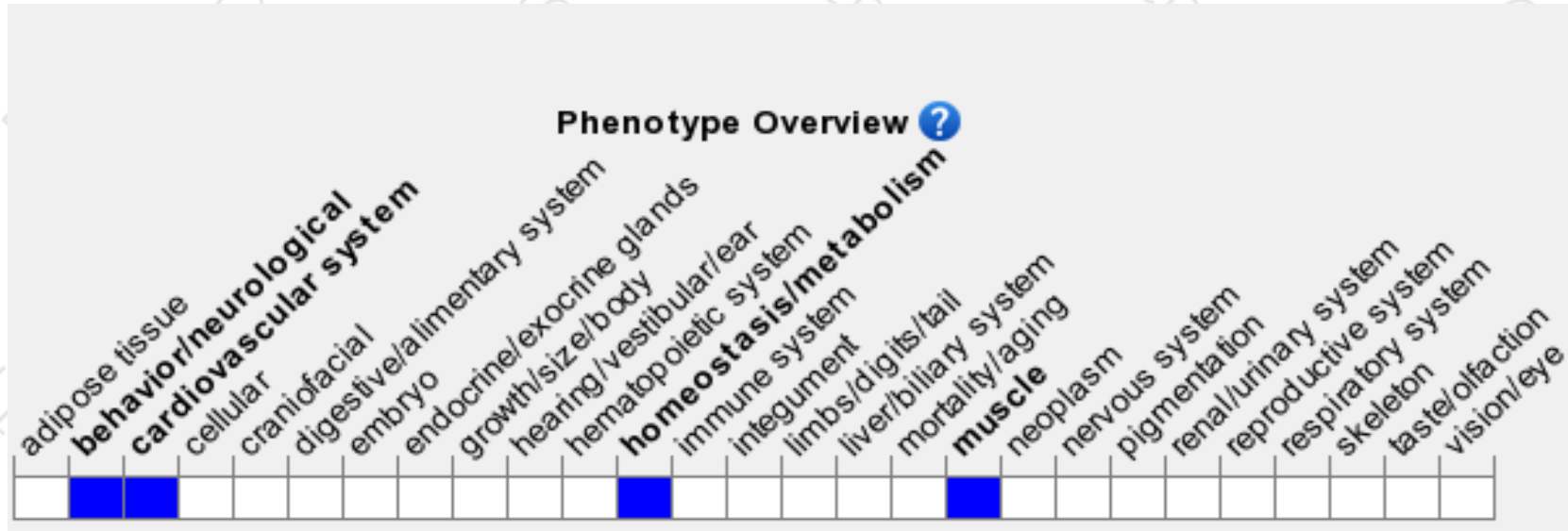
Genomic location distribution



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 knock-out allele exhibit impaired coordination, decreased exercise endurance, increased muscle fatigue, and muscle atrophy associated with impaired muscular calcium homeostasis.

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

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