

***Mtmr1* Cas9-KO Strategy**

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Project Overview

Project Name

Mtmr1

Project type

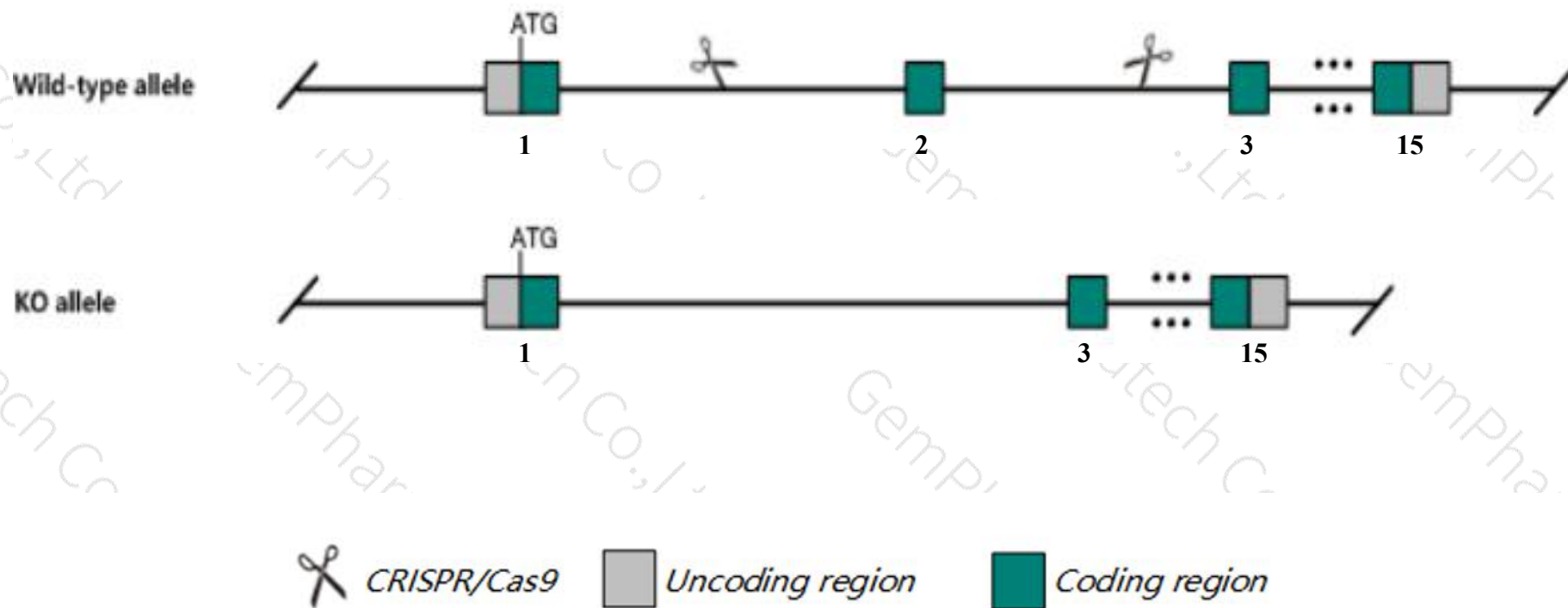
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mtmr1* gene. The schematic diagram is as follows:



- The *Mtmr1* gene has 10 transcripts. According to the structure of *Mtmr1* gene, exon2 of *Mtmr1-201* (ENSMUST00000015358.7) transcript is recommended as the knockout region. The region contains 106bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mtmr1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, female mice homozygous and male mice hemizygous for a gene disruption display normal morphology, clinical chemistry, hematology, and behavior.
- Transcript *Mtmr1-203&206&209* may not be affected.
- The *Mtmr1* gene is located on the ChrX. 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)

Mtmr1 myotubularin related protein 1 [Mus musculus (house mouse)]

Gene ID: 53332, updated on 13-Mar-2020

Summary



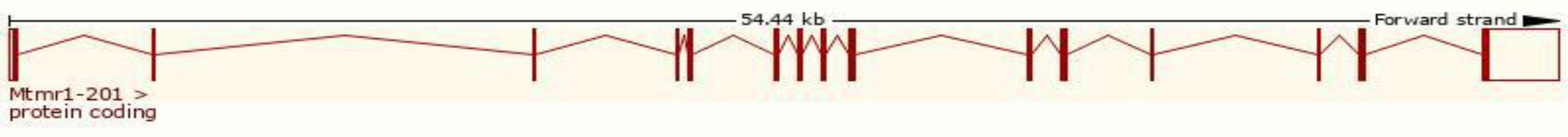
Official Symbol	Mtmr1 provided by MGI
Official Full Name	myotubularin related protein 1 provided by MGI
Primary source	MGI:MGI:1858271
See related	Ensembl:ENSMUSG00000015214
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW049210
Expression	Ubiquitous expression in bladder adult (RPKM 7.3), frontal lobe adult (RPKM 4.3) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

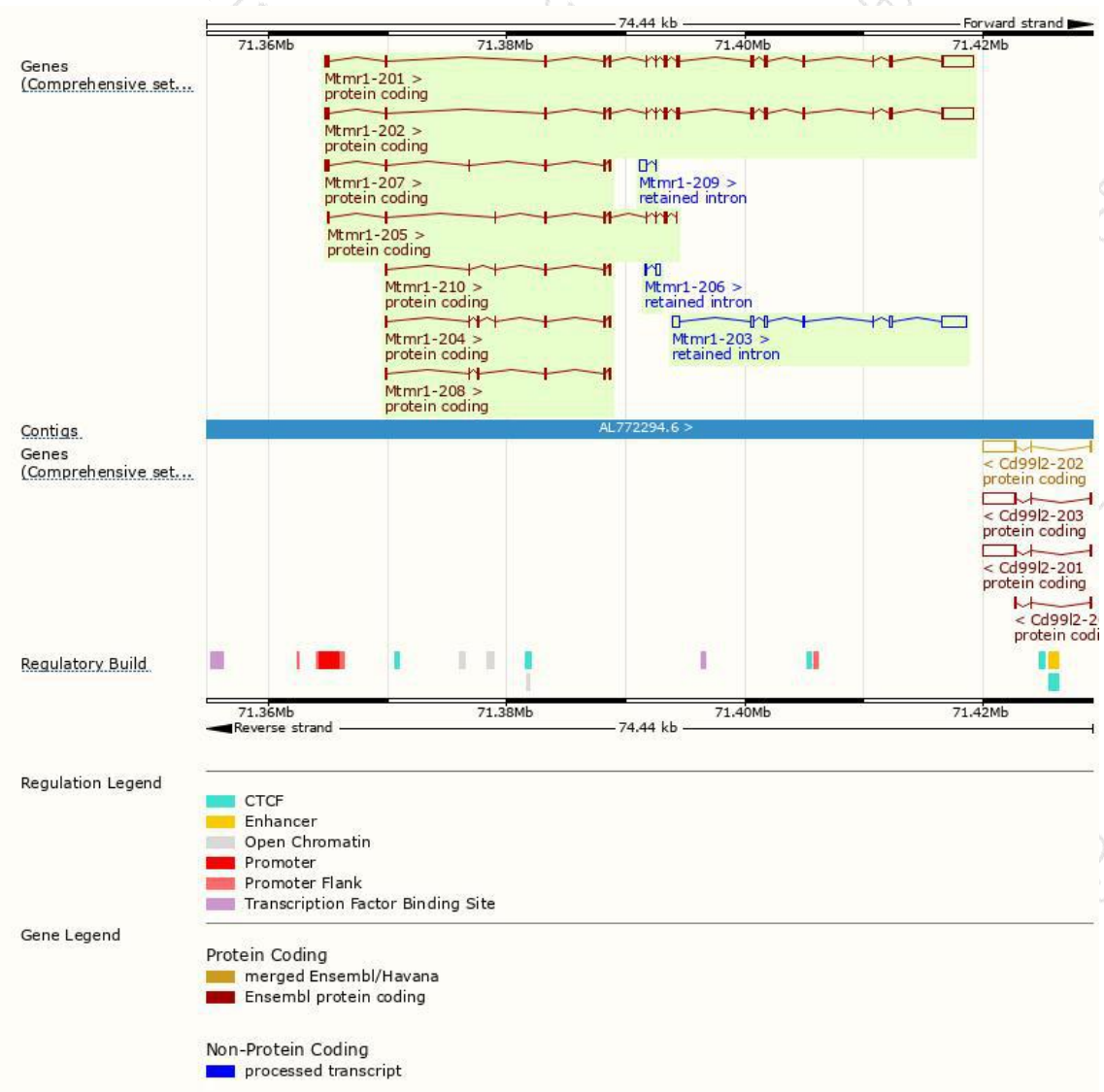
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mtmr1-201	ENSMUST00000015358.7	4634	669aa	Protein coding	CCDS30178	Q9Z2C4	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 P2
Mtmr1-202	ENSMUST00000114601.7	4640	671aa	Protein coding	-	I7HJQ9	TSL:5 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 ALT2
Mtmr1-205	ENSMUST00000132837.4	928	309aa	Protein coding	-	F6T9H9	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
Mtmr1-207	ENSMUST00000146213.7	718	187aa	Protein coding	-	I7HPV7	CDS 3' incomplete TSL:2
Mtmr1-204	ENSMUST00000130909.7	448	149aa	Protein coding	-	Q8CIU5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1
Mtmr1-210	ENSMUST00000156756.2	421	140aa	Protein coding	-	Q8CIU3	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1
Mtmr1-208	ENSMUST00000149323.7	397	132aa	Protein coding	-	Q8CIU6	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1
Mtmr1-203	ENSMUST00000130179.1	3355	No protein	Retained intron	-	-	TSL:5
Mtmr1-209	ENSMUST00000156307.1	679	No protein	Retained intron	-	-	TSL:2
Mtmr1-206	ENSMUST00000138565.1	515	No protein	Retained intron	-	-	TSL:2

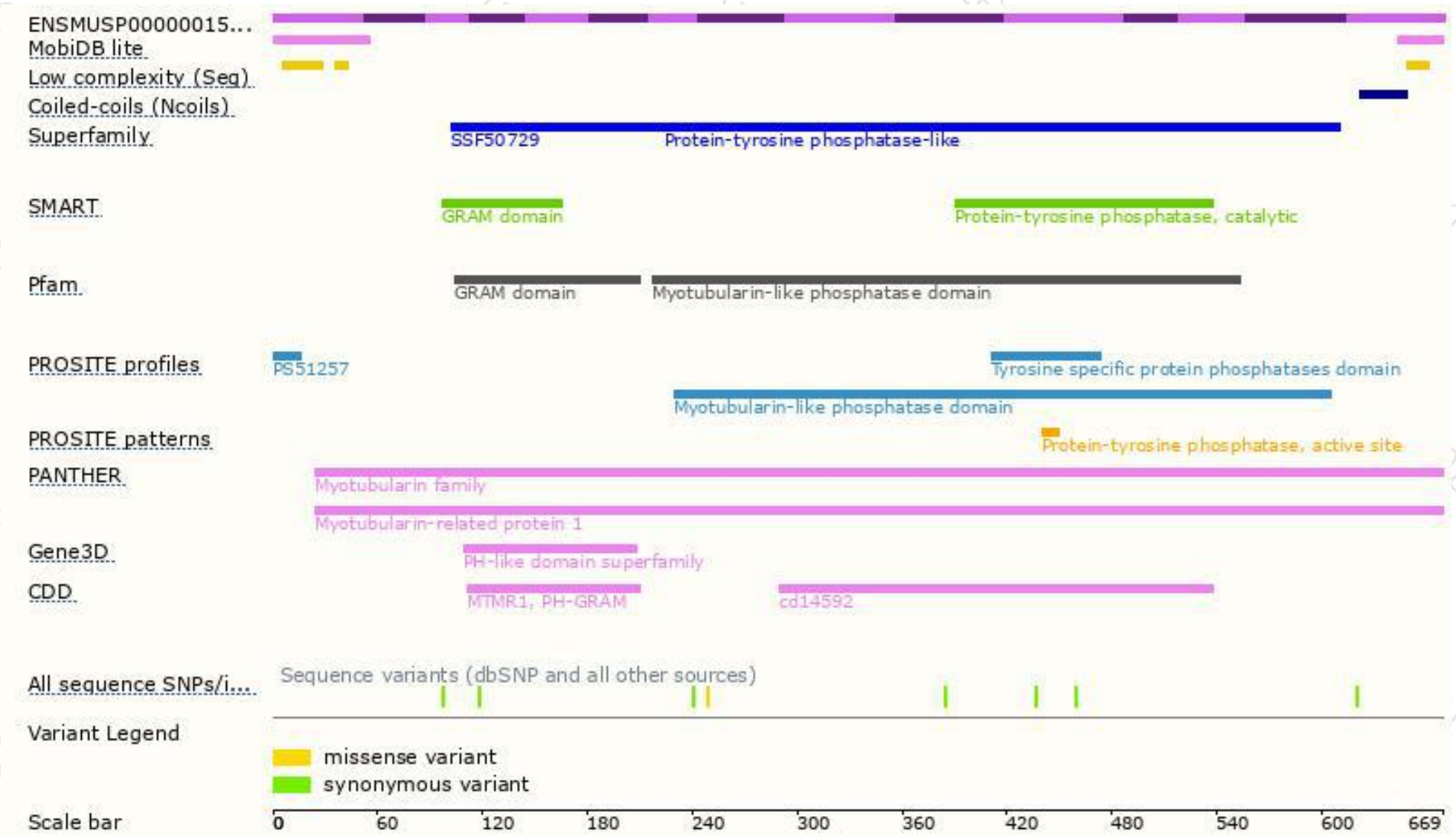
The strategy is based on the design of *Mtmr1-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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