

***Mtmr6* Cas9-KO Strategy**

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Project Overview

Project Name

Mtmr6

Project type

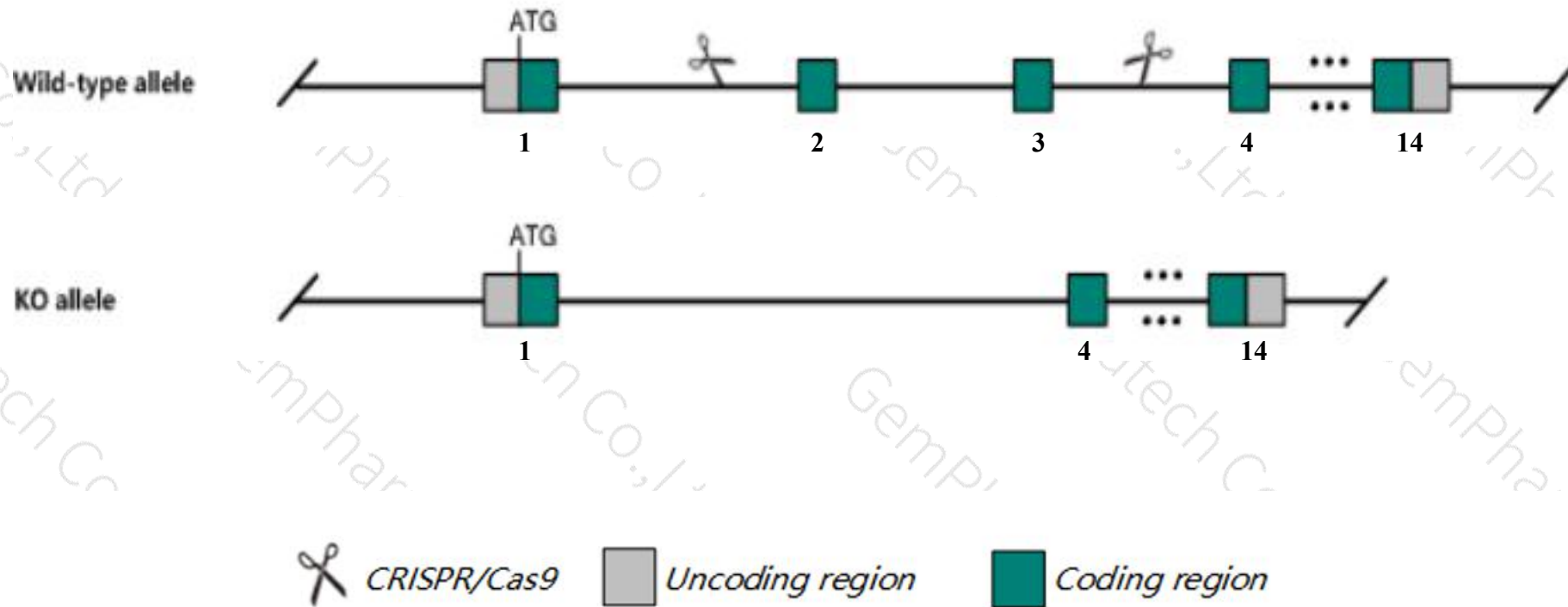
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mtmr6* gene. The schematic diagram is as follows:



- The *Mtmr6* gene has 4 transcripts. According to the structure of *Mtmr6* gene, exon2-exon3 of *Mtmr6-201* (ENSMUST00000022563.8) transcript is recommended as the knockout region. The region contains 280bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mtmr6* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Mtmr6-202* may not be affected.
- The *Mtmr6* gene is located on the Chr14. 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)

Mtmr6 myotubularin related protein 6 [Mus musculus (house mouse)]

Gene ID: 219135, updated on 13-Mar-2020

Summary



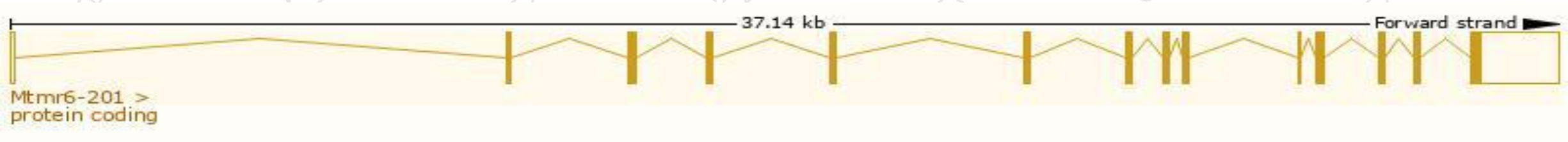
Official Symbol	Mtmr6 provided by MGI
Official Full Name	myotubularin related protein 6 provided by MGI
Primary source	MGI:MGI:2145637
See related	Ensembl:ENSMUSG000000021987
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4022440C11Rik, AI428804, AU041072
Expression	Ubiquitous expression in testis adult (RPKM 32.5), cerebellum adult (RPKM 18.2) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

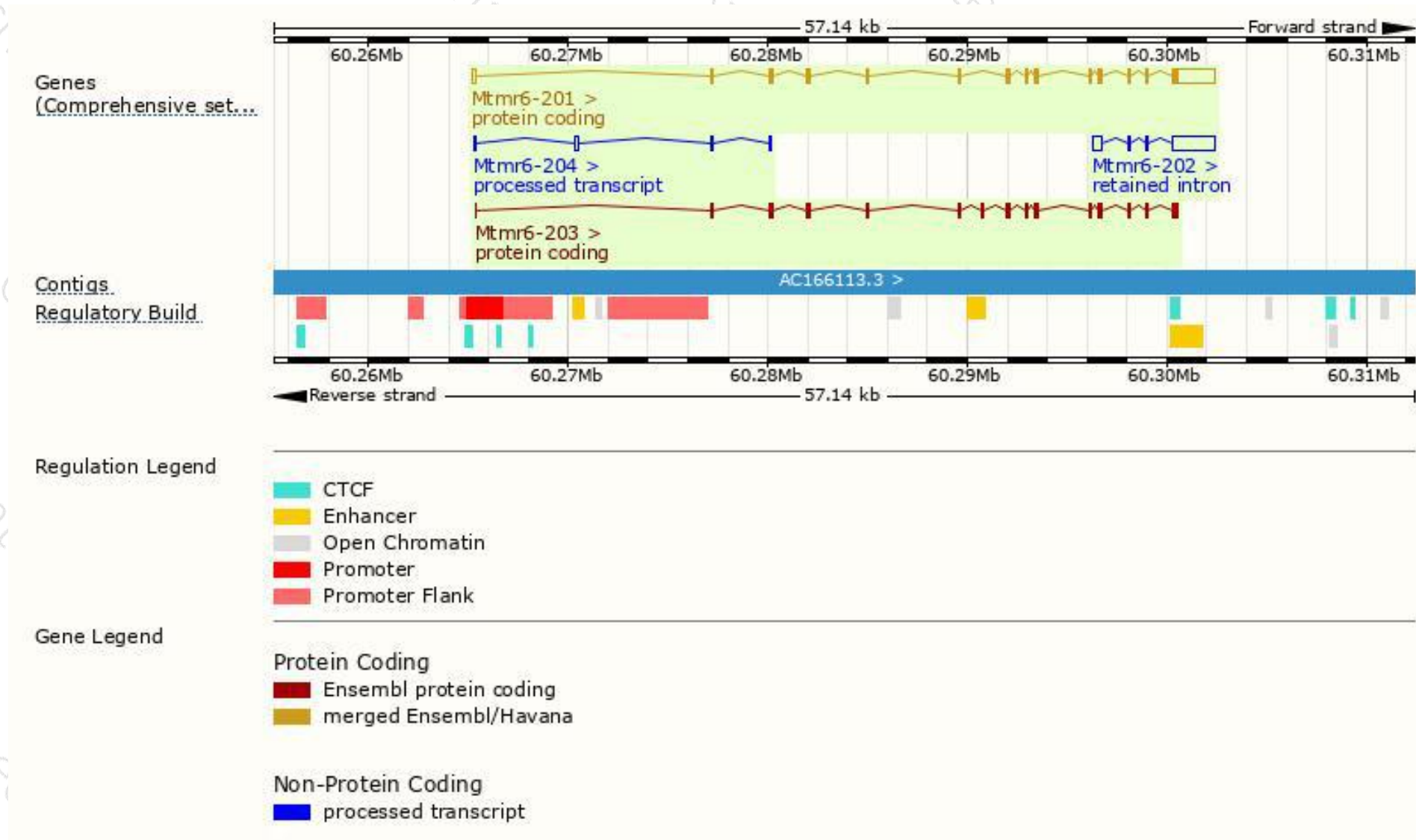
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mtmr6-201	ENSMUST00000022563.8	3813	617aa	Protein coding	CCDS27176	Q8VE11	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
Mtmr6-203	ENSMUST00000224366.1	1968	655aa	Protein coding	-	Q8VE11	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
Mtmr6-204	ENSMUST00000225574.1	487	No protein	Processed transcript	-	-	
Mtmr6-202	ENSMUST00000224164.1	2877	No protein	Retained intron	-	-	

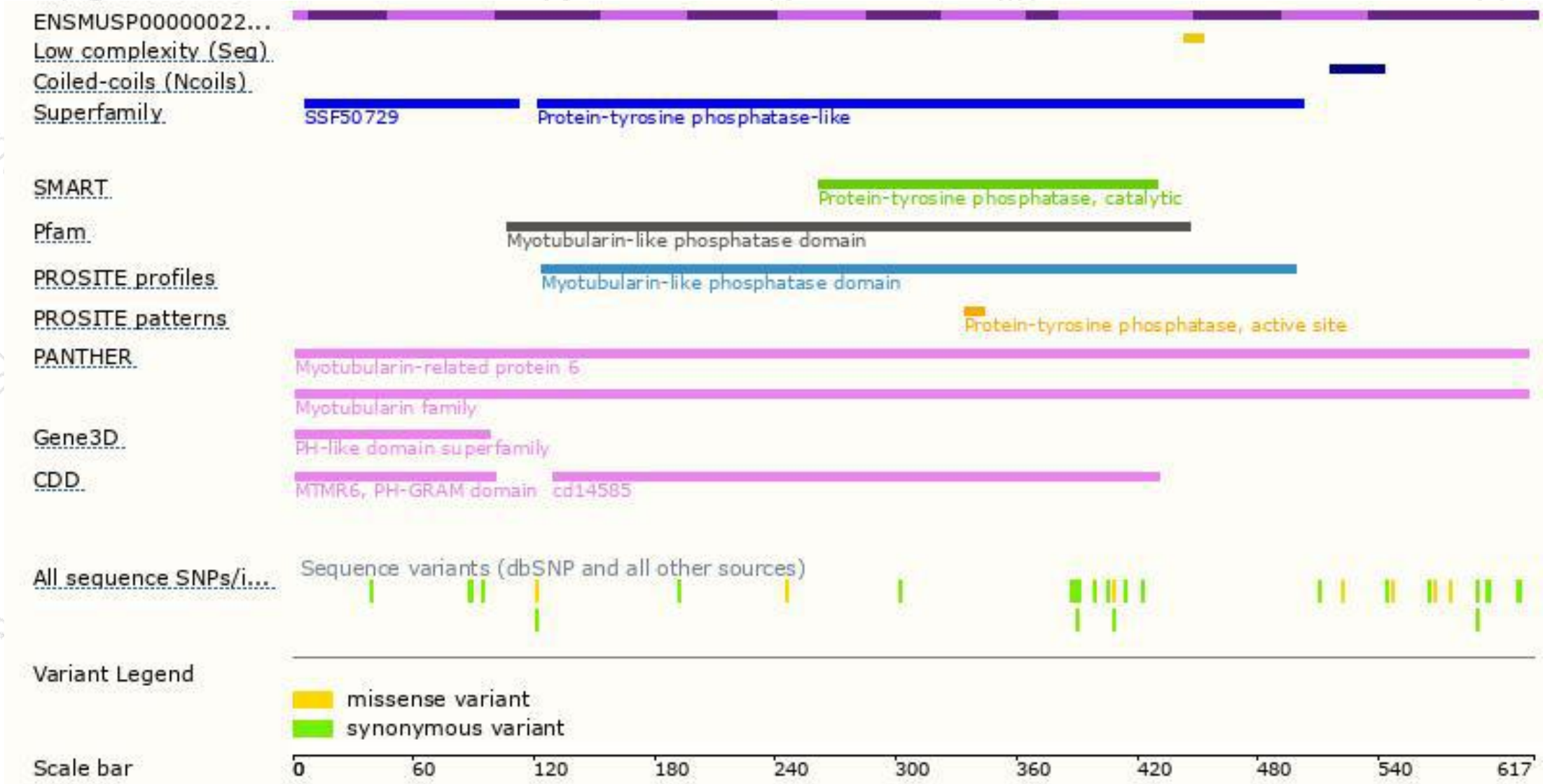
The strategy is based on the design of *Mtmr6-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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