Mtmr4 Cas9-KO Strategy

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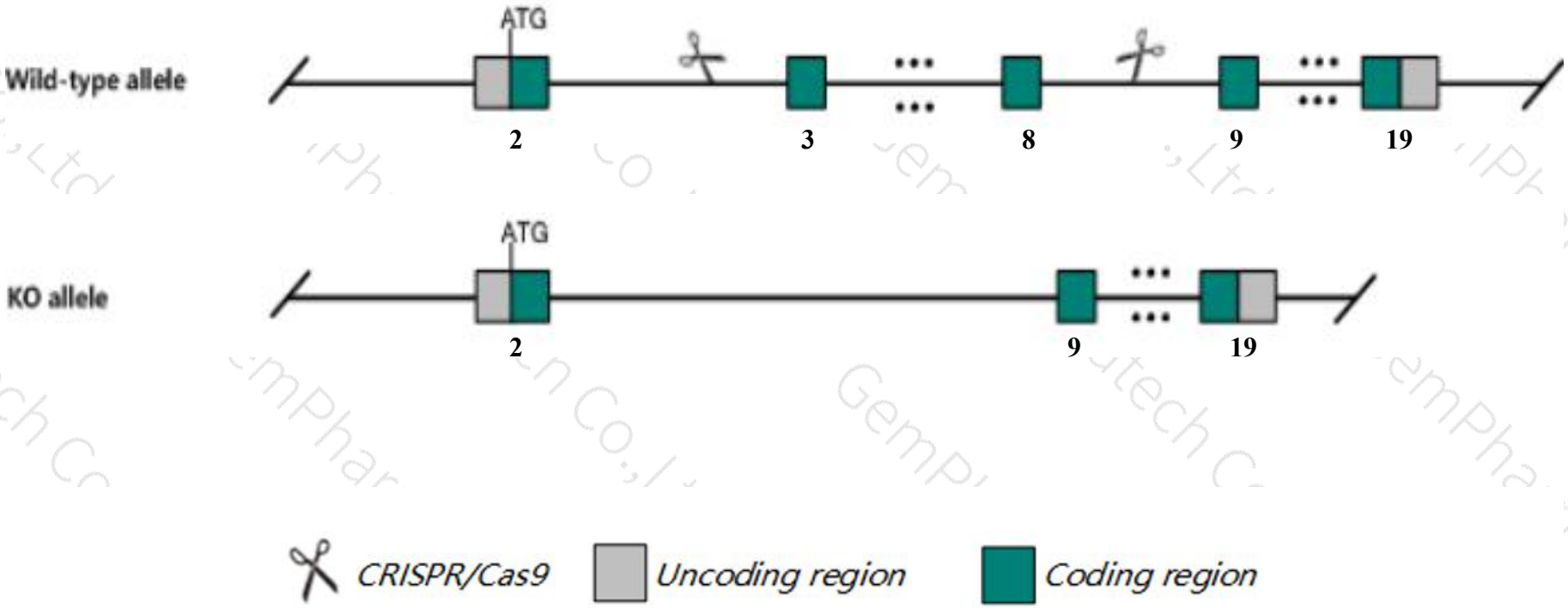
Project Overview

Project Name	***Mtmr4***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mtmr4* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mtmr4* gene has 6 transcripts. According to the structure of *Mtmr4* gene, exon3-exon8 of *Mtmr4-202* (ENSMUST00000103179.9) transcript is recommended as the knockout region.The region contains 662bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mtmr4* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- The *Mtmr4* gene is located on the Chr11. 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）

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Mtmr4 myotubularin related protein 4 [Mus musculus (house mouse)]

Gene ID: 170749, updated on 13-Mar-2020

Summary

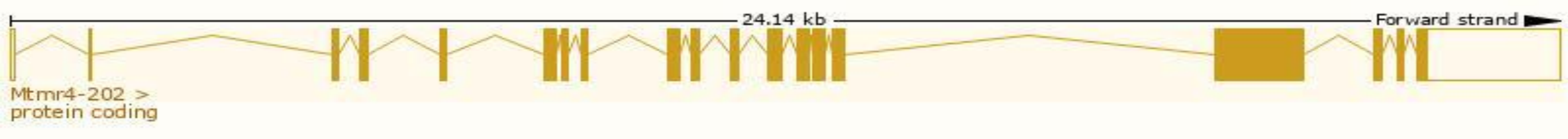
Official Symbol	Mtmr4 provided by MGI
Official Full Name	myotubularin related protein 4 provided by MGI
Primary source	MGI:MGI:2180699
See related	Ensembl:ENSMUSG00000018401
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA596759, ESTM44, FYVE-DSP2, ZFYVE11, mKIAA0647
Expression	Ubiquitous expression in whole brain E14.5 (RPKM 12.2), CNS E18 (RPKM 11.6) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

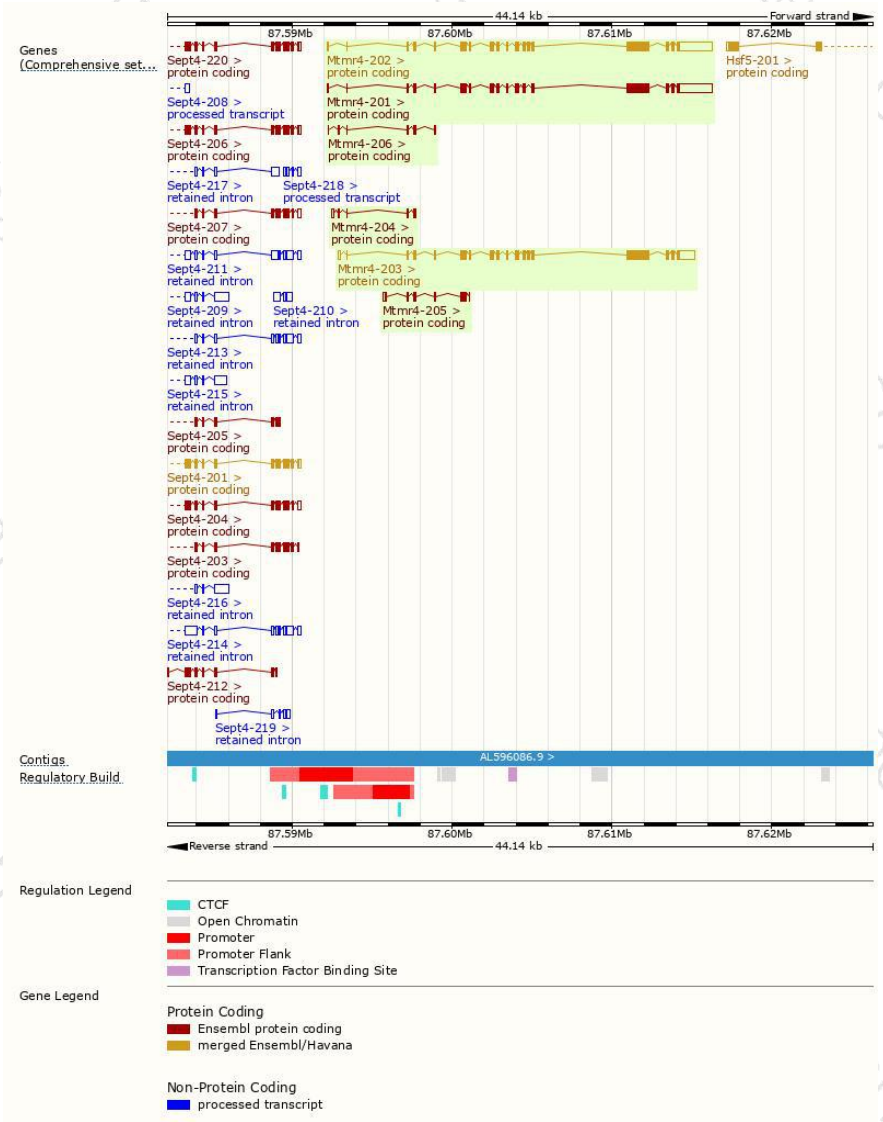
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mtmr4-202	ENSMUST00000103179.9	5753	1190aa	Protein coding	CCDS25214	Q91XS1	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 P1
Mtmr4-203	ENSMUST00000119628.7	4664	1190aa	Protein coding	CCDS25214	Q91XS1	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 P1
Mtmr4-201	ENSMUST00000092802.11	5525	1133aa	Protein coding	-	Q91XS1	TSL:1 GENCODE basic
Mtmr4-205	ENSMUST00000134216.2	792	204aa	Protein coding	-	Q5ND05	CDS 3' incomplete TSL:2
Mtmr4-204	ENSMUST00000123105.7	437	70aa	Protein coding	-	A7M7R0	CDS 3' incomplete TSL:5
Mtmr4-206	ENSMUST00000146871.7	418	97aa	Protein coding	-	A7M7R1	CDS 3' incomplete TSL:3

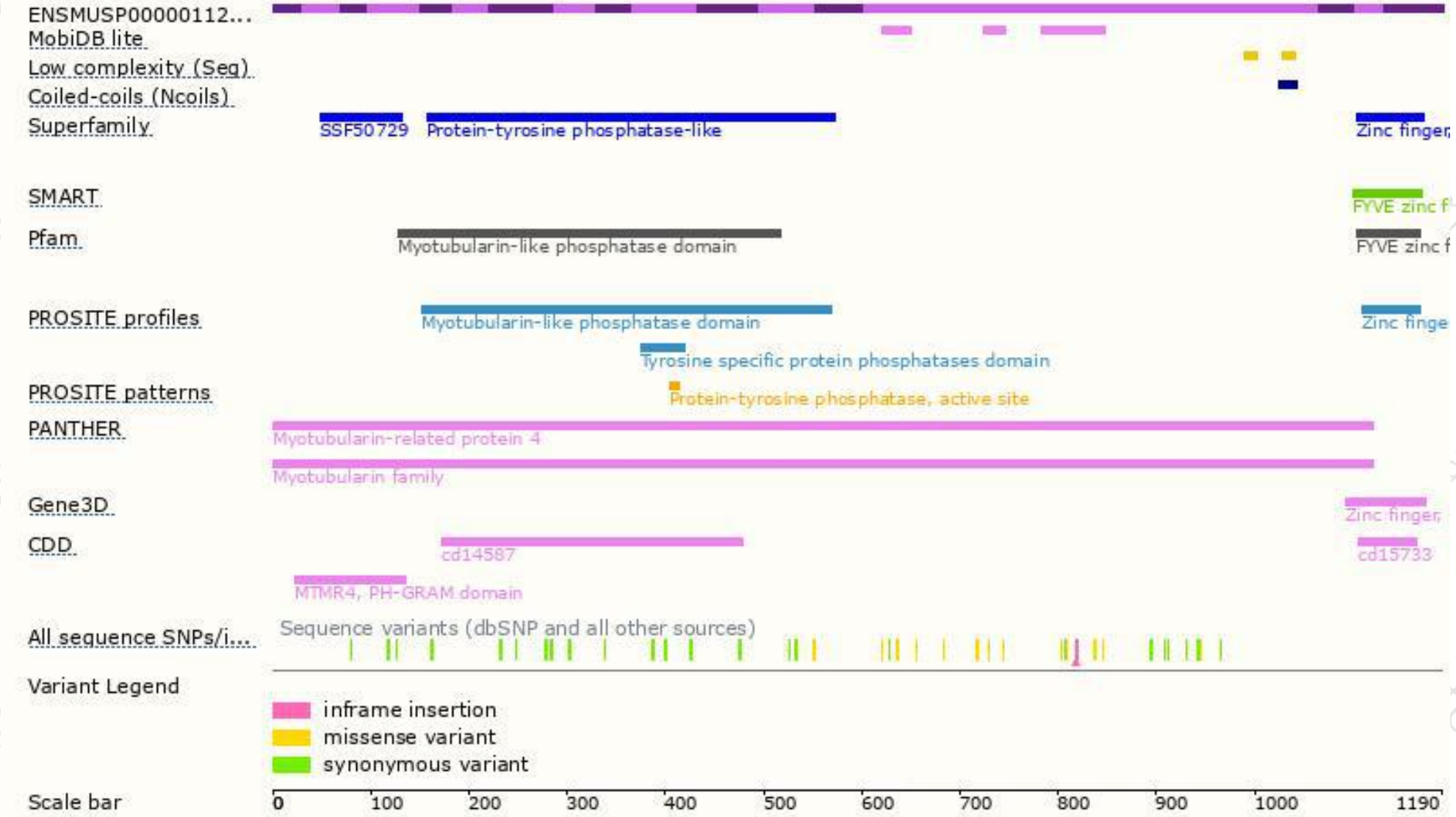
The strategy is based on the design of *Mtmr4-202* transcript,the transcription is shown below:



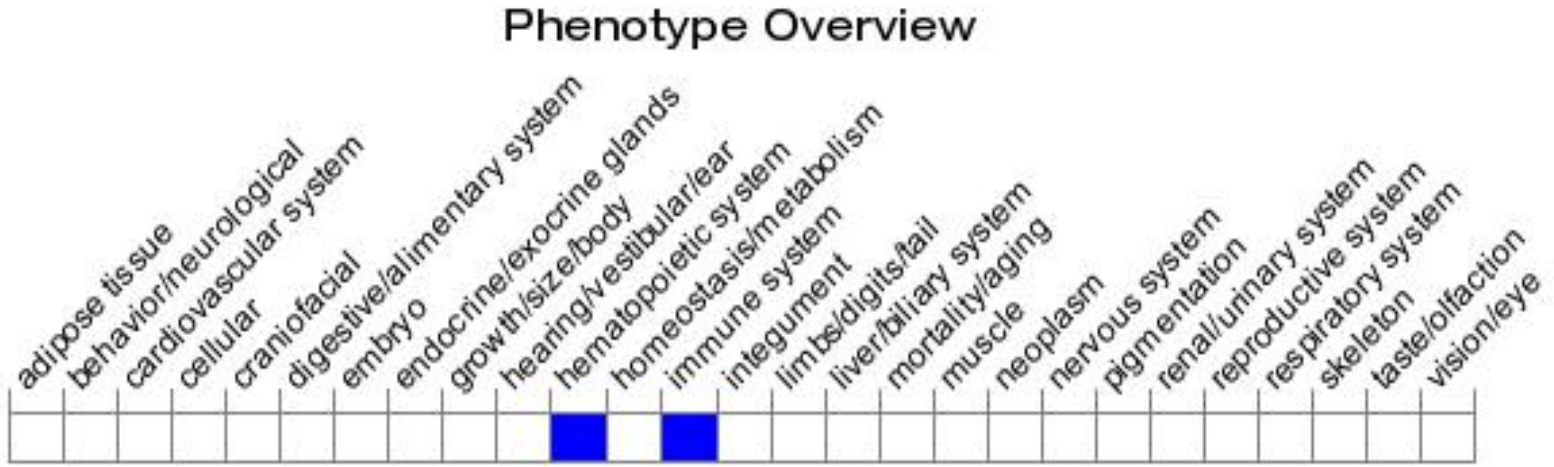
Genomic location distribution



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/).

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

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