Mtmr2 Cas9-KO Strategy

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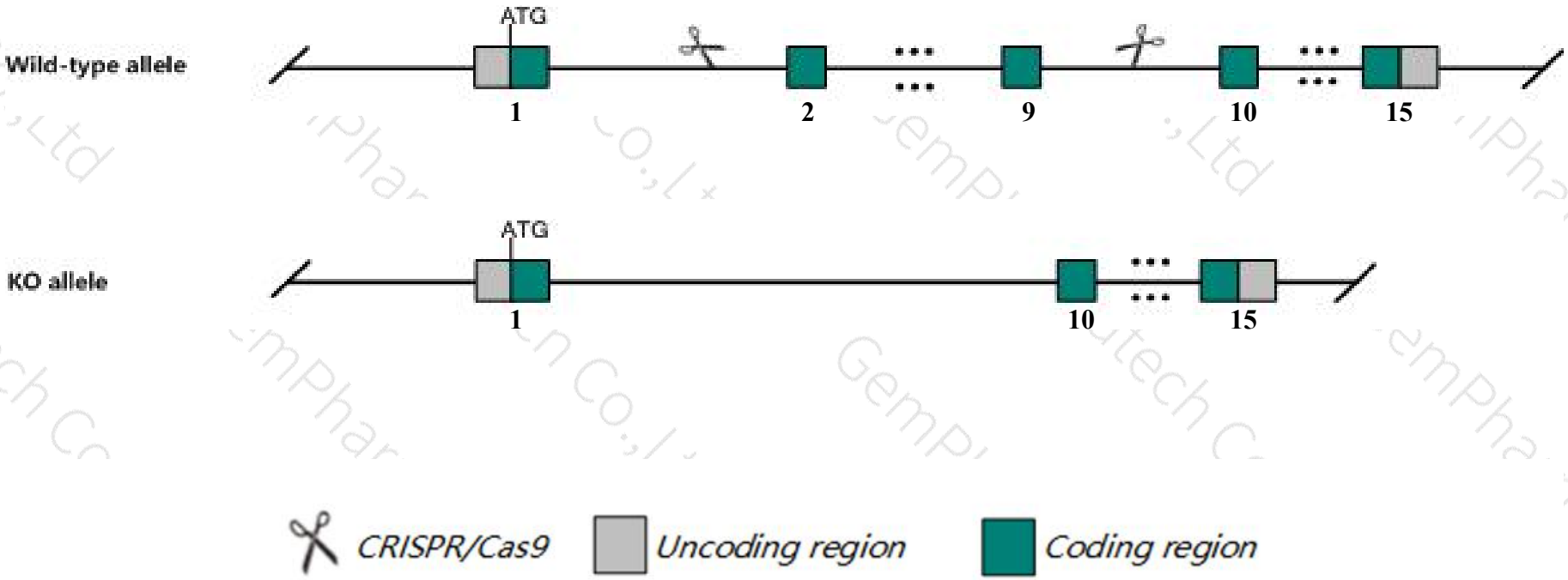
Design Date: 2020-1-16

Project Overview

Project Name	***Mtmr2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mtmr2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mtmr2* gene has 9 transcripts. According to the structure of *Mtmr2* gene, exon2-exon9 of *Mtmr2-201* (ENSMUST00000034396.13) transcript is recommended as the knockout region.The region contains 913bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mtmr2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Homozygous null mutants develop progressive neuropathy characterized by myelin outfolding and recurrent loops and depletion of spermatids and spermatocytes from the seminiferous epithelium.

- The *Mtmr2* gene is located on the Chr9. 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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Mtmr2 myotubularin related protein 2 [Mus musculus (house mouse)]

Gene ID: 77116, updated on 19-Mar-2019

Summary

Official Symbol	Mtmr2 provided by MGI
Official Full Name	myotubularin related protein 2 provided by MGI
Primary source	MGI:MGI:1924366
See related	Ensembl:ENSMUSG00000031918
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	6030445P13Rik
Expression	Ubiquitous expression in adrenal adult (RPKM 8.9), cerebellum adult (RPKM 7.0) and 28 other tissues See more
Orthologs	human all

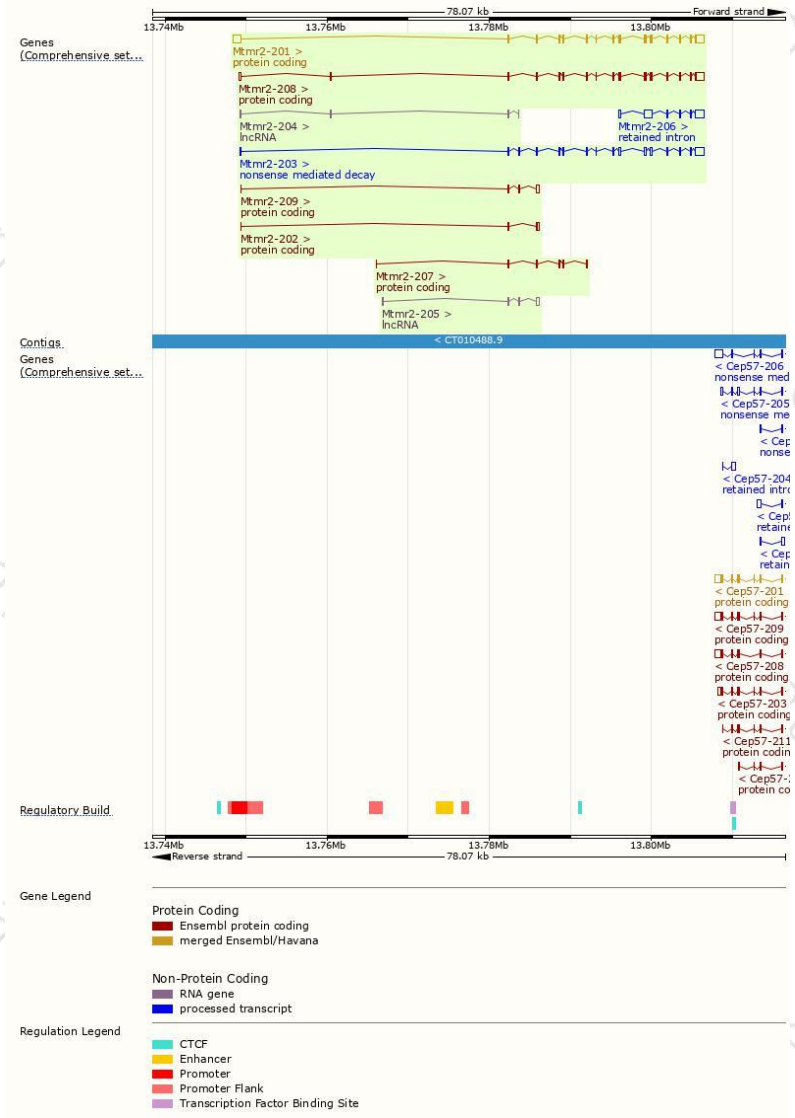
Transcript information（Ensembl）

The gene has 9 transcripts,all transcripts are shown below:

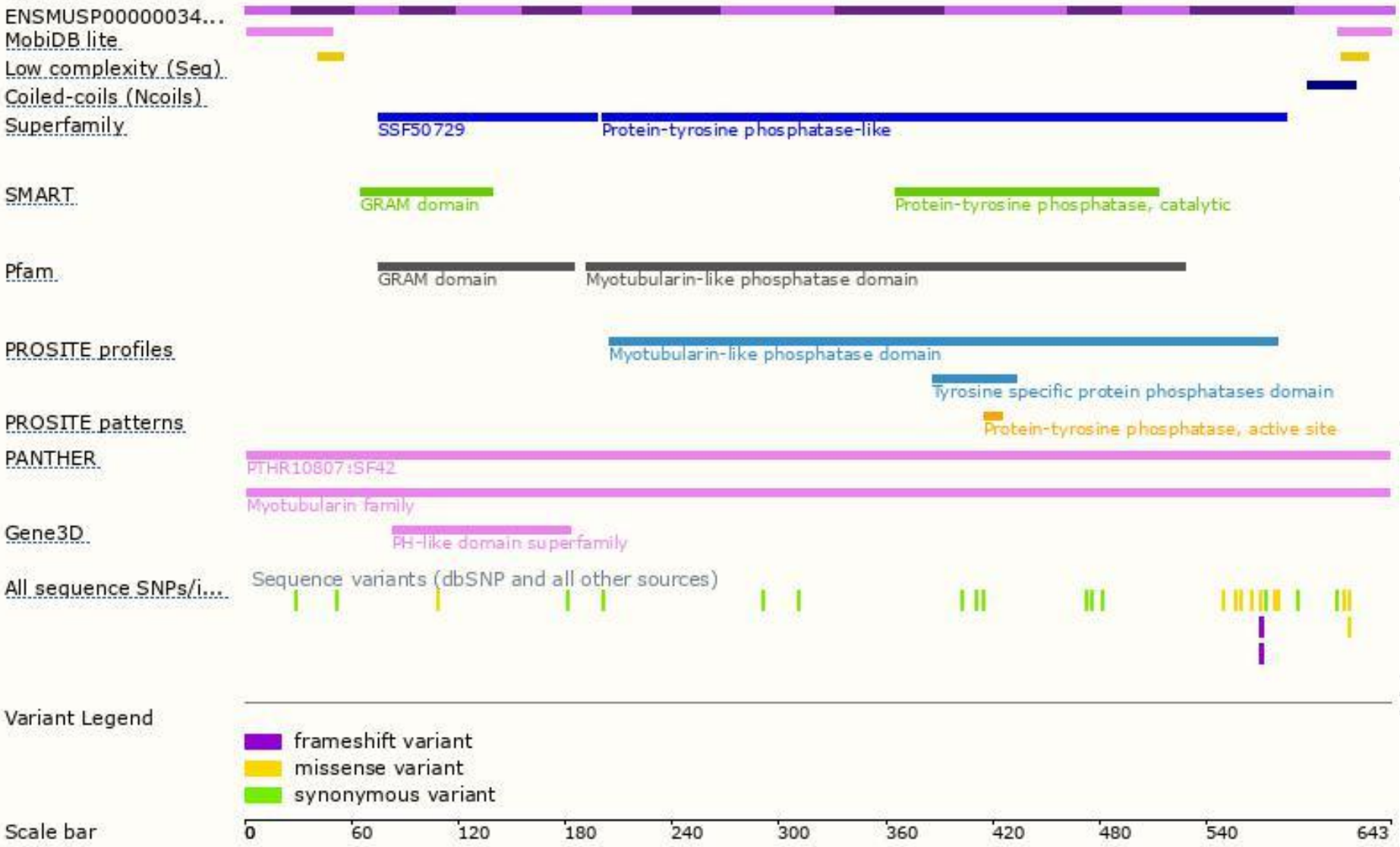
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mtmr2-201	ENSMUST00000034396.13	3788	643aa	Protein coding	CCDS22818	Q9Z2D1	TSL:1 GENCODE basic APPRIS P1
Mtmr2-208	ENSMUST00000155679.7	3088	571aa	Protein coding	-	Q6P572	TSL:5 GENCODE basic
Mtmr2-209	ENSMUST00000156801.7	617	82aa	Protein coding	-	B8JJF6	TSL:5 GENCODE basic
Mtmr2-207	ENSMUST00000152532.7	535	105aa	Protein coding	-	B8JJF3	CDS 3' incomplete TSL:5
Mtmr2-202	ENSMUST00000134530.1	442	67aa	Protein coding	-	F6T2Q0	CDS 5' incomplete TSL:2
Mtmr2-203	ENSMUST00000134674.7	3106	82aa	Nonsense mediated decay	-	B8JJF6	TSL:1
Mtmr2-206	ENSMUST00000146901.1	2593	No protein	Retained intron	-	-	TSL:2
Mtmr2-205	ENSMUST00000143002.1	612	No protein	lncRNA	-	-	TSL:3
Mtmr2-204	ENSMUST00000136735.7	453	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Mtmr2-201* transcript,The transcription is shown below

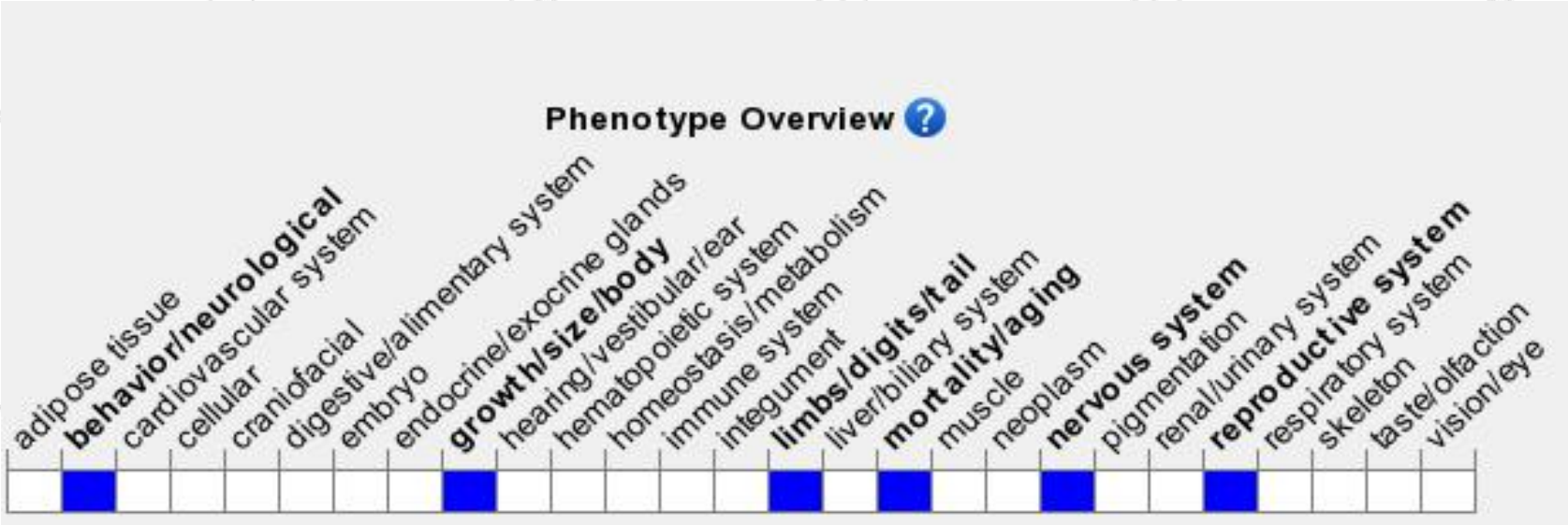
Genomic location distribution



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,Homozygous null mutants develop progressive neuropathy characterized by myelin outfolding and recurrent loops and depletion of spermatids and spermatocytes from the seminiferous epithelium.

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

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