

Pmm2 Cas9-KO Strategy

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Project Overview

Project Name

Pmm2

Project type

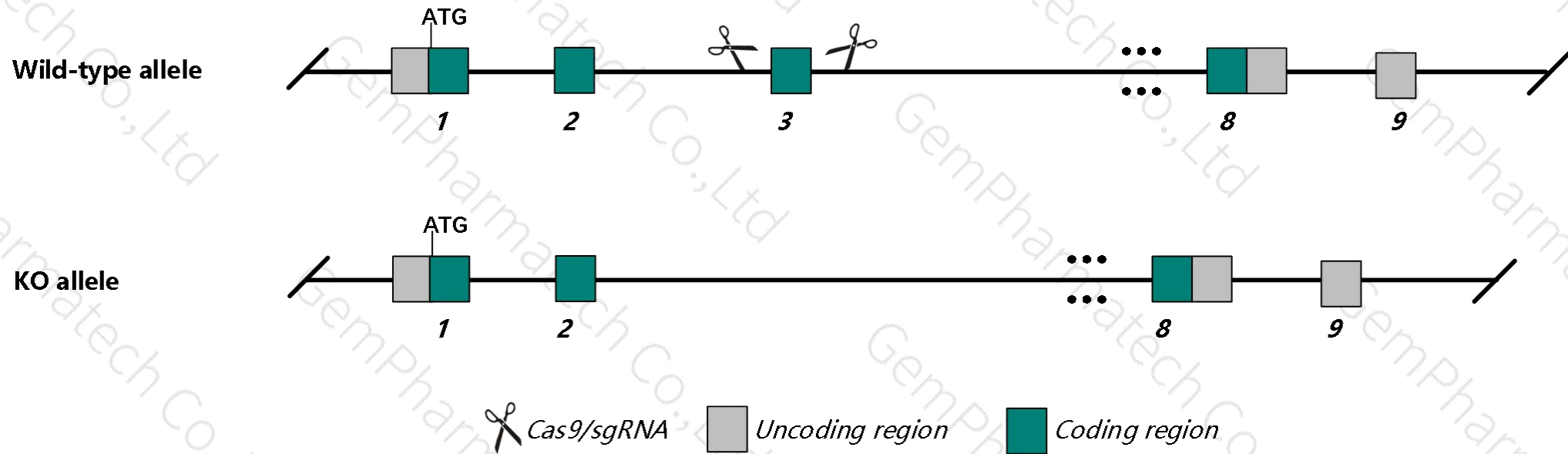
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pmm2* gene. The schematic diagram is as follows:



- The *Pmm2* gene has 7 transcripts. According to the structure of *Pmm2* gene, exon3 of *Pmm2-201* (ENSMUST00000023396.9) transcript is recommended as the knockout region. The region contains 77bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pmm2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit early embryonic lethality around E2.5. Transmission of the maternal null allele is severely impaired.
- The *Pmm2* gene is located on the Chr16. 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)

Pmm2 phosphomannomutase 2 [Mus musculus (house mouse)]

Gene ID: 54128, updated on 31-Jan-2019

Summary



Official Symbol	Pmm2 provided by MGI
Official Full Name	phosphomannomutase 2 provided by MGI
Primary source	MGI:MGI:1859214
See related	Ensembl:ENSMUSG00000022711
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	AI585868, C86848
Expression	Broad expression in duodenum adult (RPKM 113.6), large intestine adult (RPKM 102.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

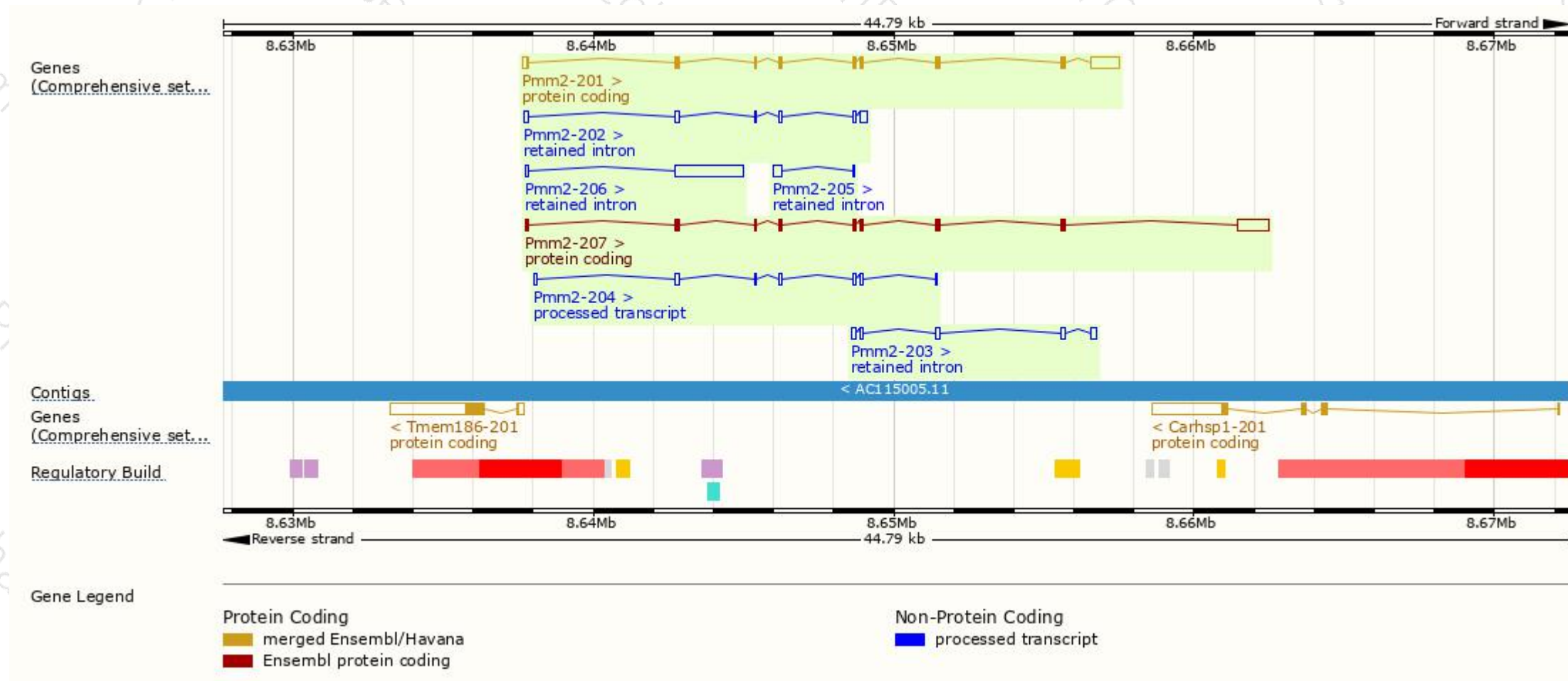
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pmm2-201	ENSMUST00000023396.9	1842	242aa	Protein coding	CCDS27941	Q545N8 Q9Z2M7	TSL:1 GENCODE basic APPRIS P1
Pmm2-207	ENSMUST00000230828.1	1796	242aa	Protein coding	CCDS27941	Q545N8 Q9Z2M7	GENCODE basic APPRIS P1
Pmm2-204	ENSMUST00000134975.7	569	No protein	Processed transcript	-	-	TSL:5
Pmm2-206	ENSMUST00000143174.1	2370	No protein	Retained intron	-	-	TSL:1
Pmm2-202	ENSMUST00000130885.7	721	No protein	Retained intron	-	-	TSL:1
Pmm2-203	ENSMUST00000131385.1	673	No protein	Retained intron	-	-	TSL:3
Pmm2-205	ENSMUST00000142935.1	357	No protein	Retained intron	-	-	TSL:3

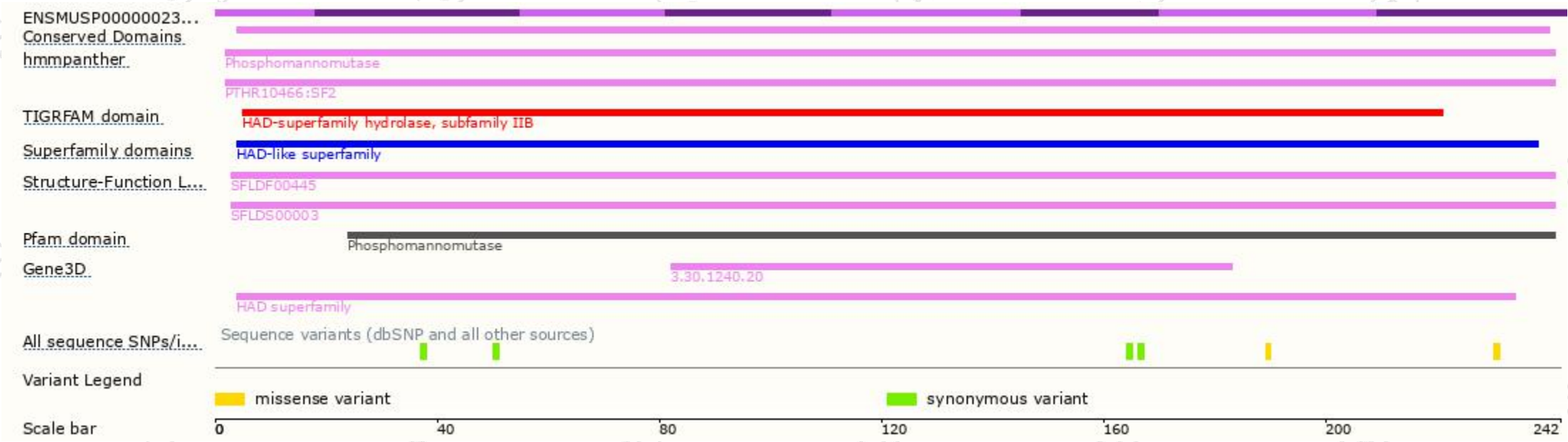
The strategy is based on the design of *Pmm2-201* transcript,The transcription is shown below



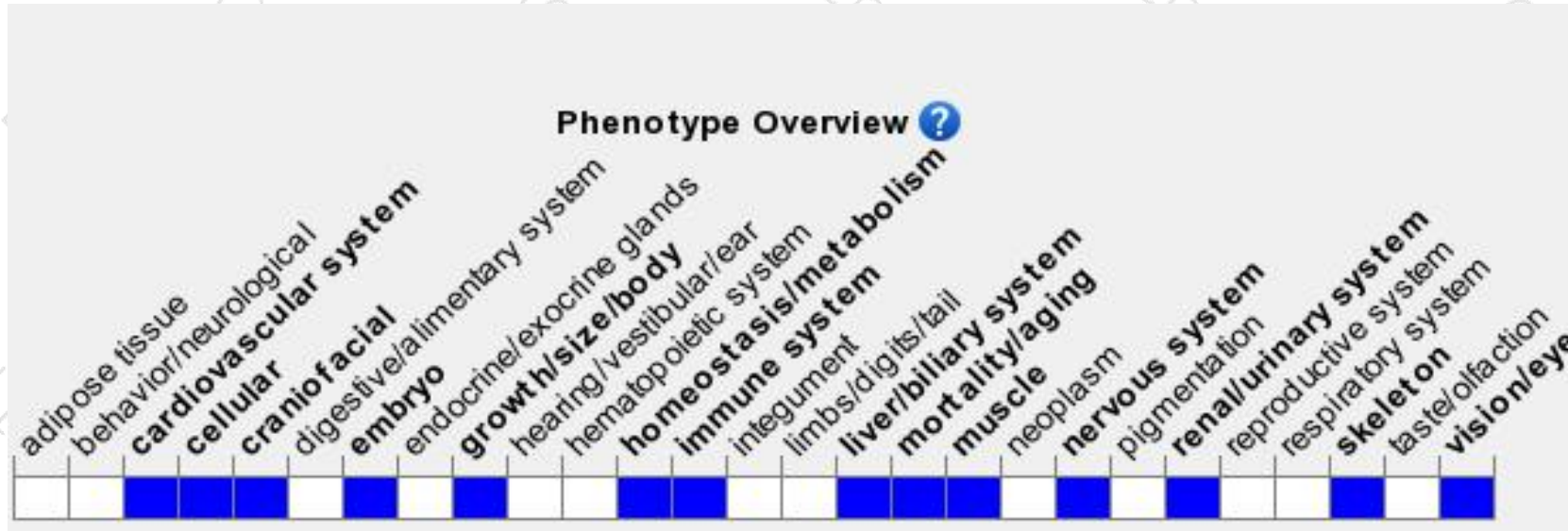
Genomic location distribution



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 early embryonic lethality around E2.5. Transmission of the maternal null allele is severely impaired.

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

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