

***Mmrn1* Cas9-KO Strategy**

Designer: Daohua Xu

Reviewer: Huimin Su

Design Date: 2020-3-31

Project Overview

Project Name

Mmrn1

Project type

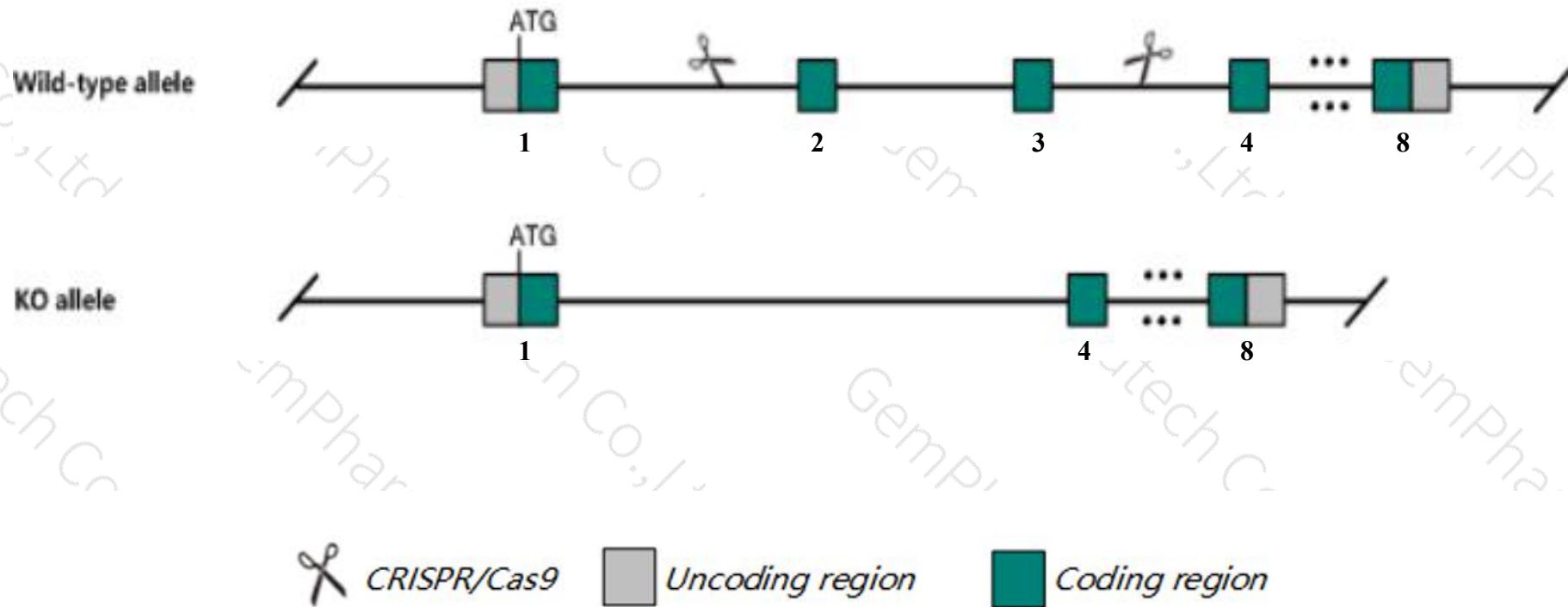
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mmrn1* gene. The schematic diagram is as follows:



- The *Mmrn1* gene has 3 transcripts. According to the structure of *Mmrn1* gene, exon2-exon3 of *Mmrn1-201* (ENSMUST00000129603.3) transcript is recommended as the knockout region. The region contains 227bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mmrn1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Mmrn1* gene is located on the Chr6. 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)

Mmrn1 multimerin 1 [Mus musculus (house mouse)]

Gene ID: 70945, updated on 13-Mar-2020

Summary



Official Symbol	Mmrn1 provided by MGI
Official Full Name	multimerin 1 provided by MGI
Primary source	MGI:MGI:1918195
See related	Ensembl:ENSMUSG000000054641
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	4921530G03Rik, Emilin4, Mmm
Expression	Broad expression in bladder adult (RPKM 3.6), liver E14 (RPKM 2.2) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

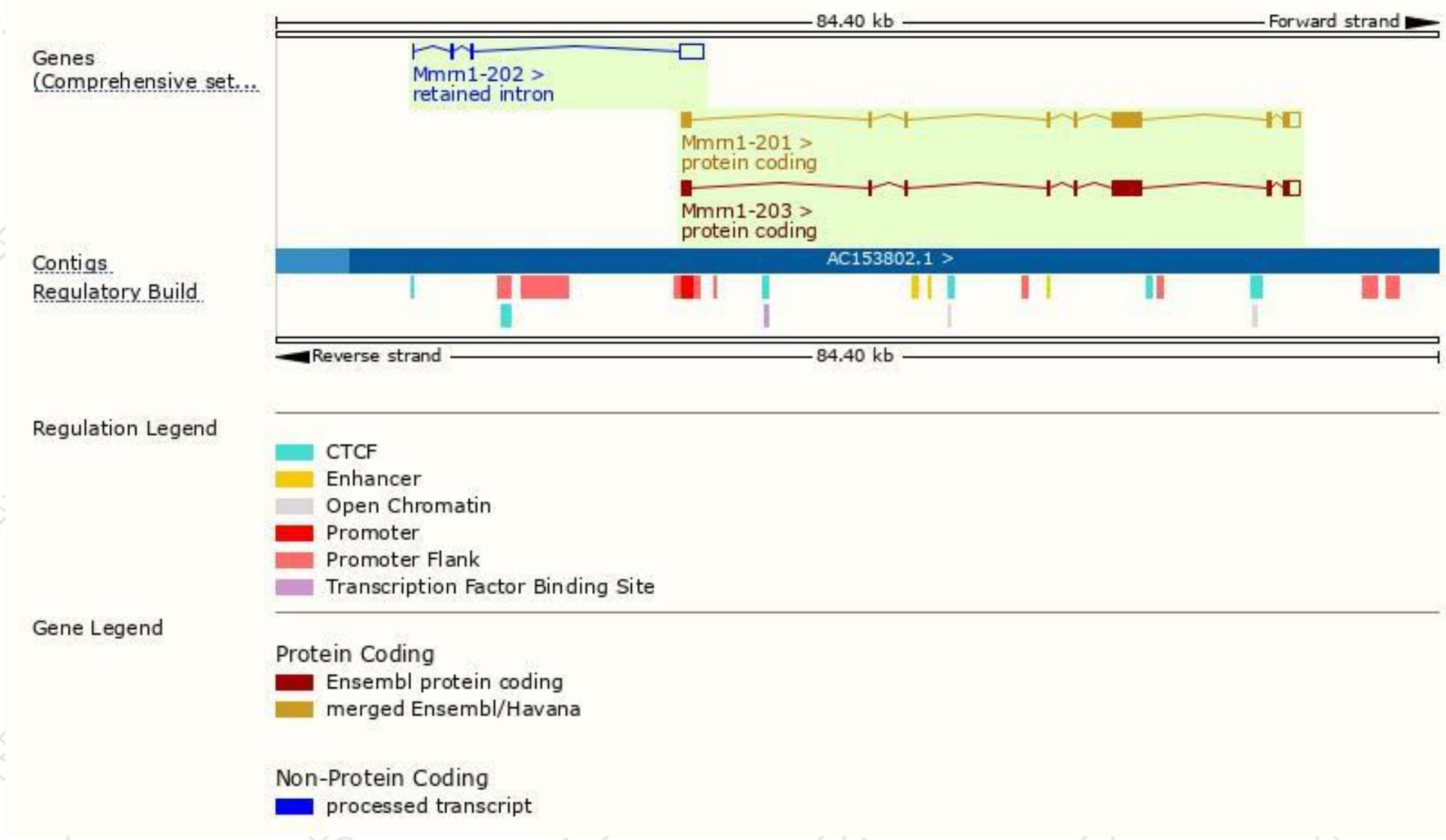
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mmrn1-201	ENSMUST00000129603.3	4477	1210aa	Protein coding	CCDS51799	G3UVV6	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 P3
Mmrn1-203	ENSMUST00000204333.1	4472	1209aa	Protein coding	CCDS85058	A0A0N4SVL8	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 ALT2
Mmrn1-202	ENSMUST00000145763.1	2054	No protein	Retained intron	-	-	TSL:2

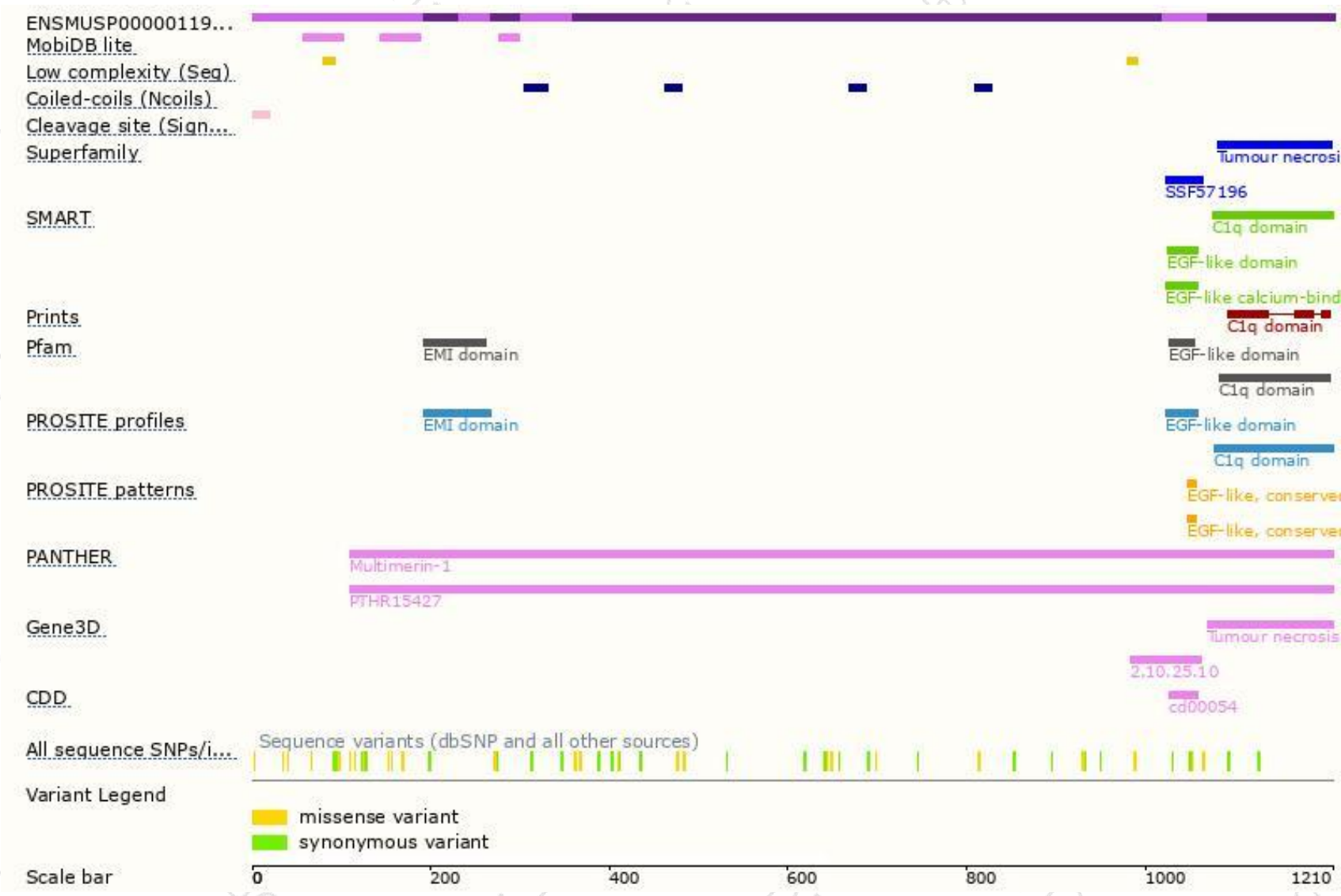
The strategy is based on the design of *Mmrn1-201* transcript,The transcription is shown below



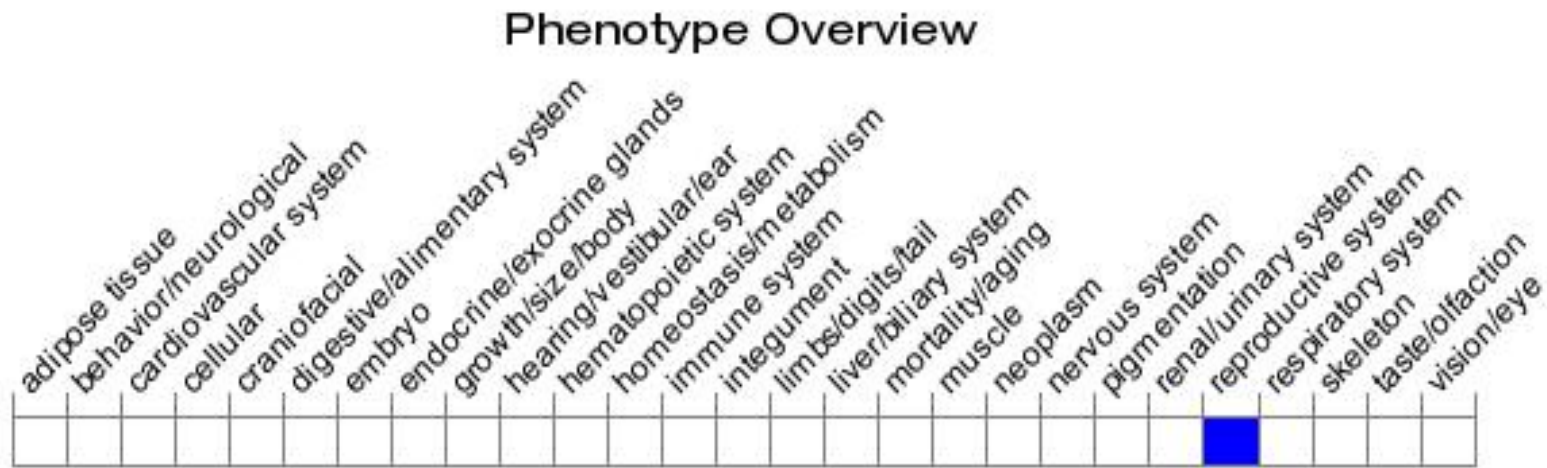
Genomic location distribution



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/>).

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

Tel: 400-9660890

