

Mmel1 Cas9-KO Strategy

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Design Date:

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Project Overview

Project Name

Mmel1

Project type

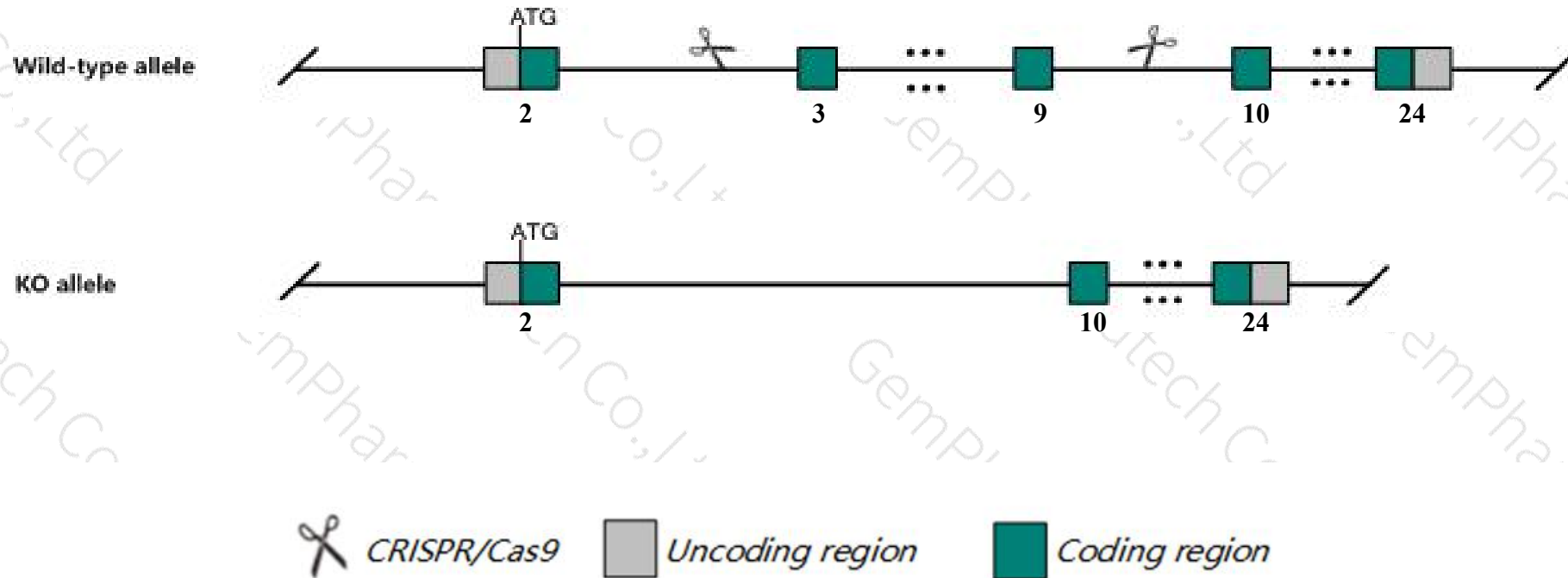
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Mmel1* gene has 7 transcripts. According to the structure of *Mmel1* gene, exon3-exon9 of *Mmel1*-207 (ENSMUST00000163732.7) transcript is recommended as the knockout region. The region contains 653bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mmel1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice display impaired male fertility. Female fertility is not affected.
- The *Mmell* gene is located on the Chr4. 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)

Mmel1 membrane metallo-endopeptidase-like 1 [Mus musculus (house mouse)]

Gene ID: 27390, updated on 3-Apr-2019

Summary



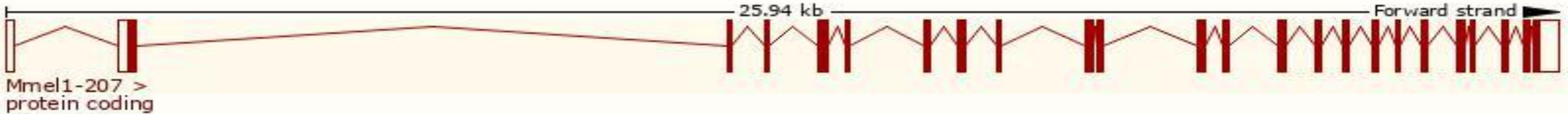
Official Symbol	Mmel1 provided by MGI
Official Full Name	membrane metallo-endopeptidase-like 1 provided by MGI
Primary source	MGI:MGI:1351603
See related	Ensembl:ENSMUSG00000058183
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mell1, NEP2, NEP2(m), NEPII, NL-1, NL2, NI1, SEP
Expression	Biased expression in testis adult (RPKM 51.8) and ovary adult (RPKM 4.3) See more
Orthologs	human all

Transcript information (Ensembl)

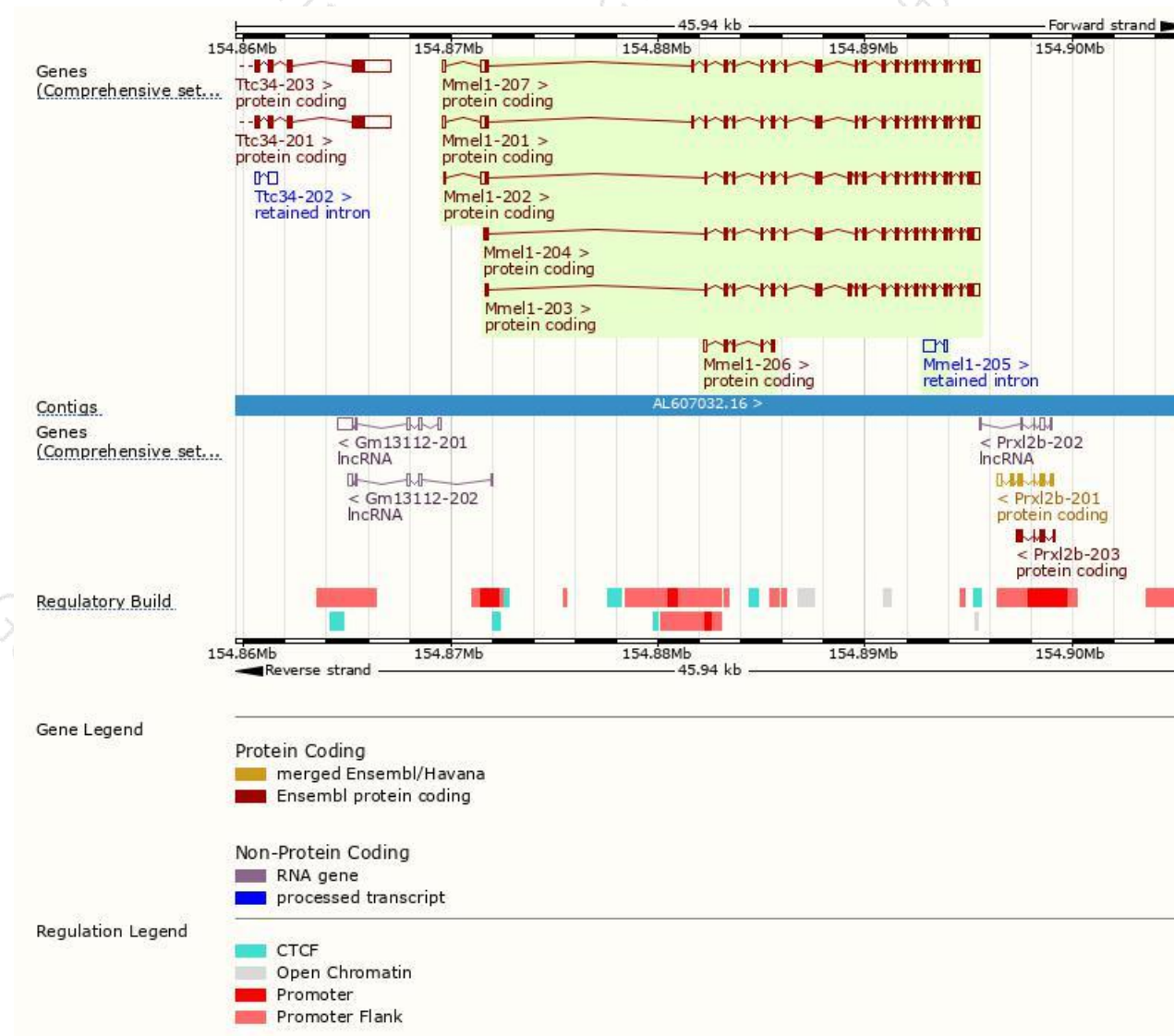
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mmel1-207	ENSMUST00000163732.7	2935	766aa	Protein coding	CCDS51401	E9PVK7	TSL:1 GENCODE basic APPRIS P2
Mmel1-201	ENSMUST00000079269.13	2934	768aa	Protein coding	-	B1AS15	TSL:5 GENCODE basic APPRIS ALT2
Mmel1-202	ENSMUST00000080559.12	2926	780aa	Protein coding	-	E9QPA9	TSL:5 GENCODE basic APPRIS ALT2
Mmel1-203	ENSMUST00000105634.7	2669	782aa	Protein coding	-	B1AS17	TSL:5 GENCODE basic APPRIS ALT2
Mmel1-204	ENSMUST00000105635.7	2592	745aa	Protein coding	-	B1AS16	TSL:5 GENCODE basic APPRIS ALT2
Mmel1-206	ENSMUST00000131758.1	592	150aa	Protein coding	-	B1AS18	CDS 3' incomplete TSL:3
Mmel1-205	ENSMUST00000129623.1	652	No protein	Retained intron	-	-	TSL:3

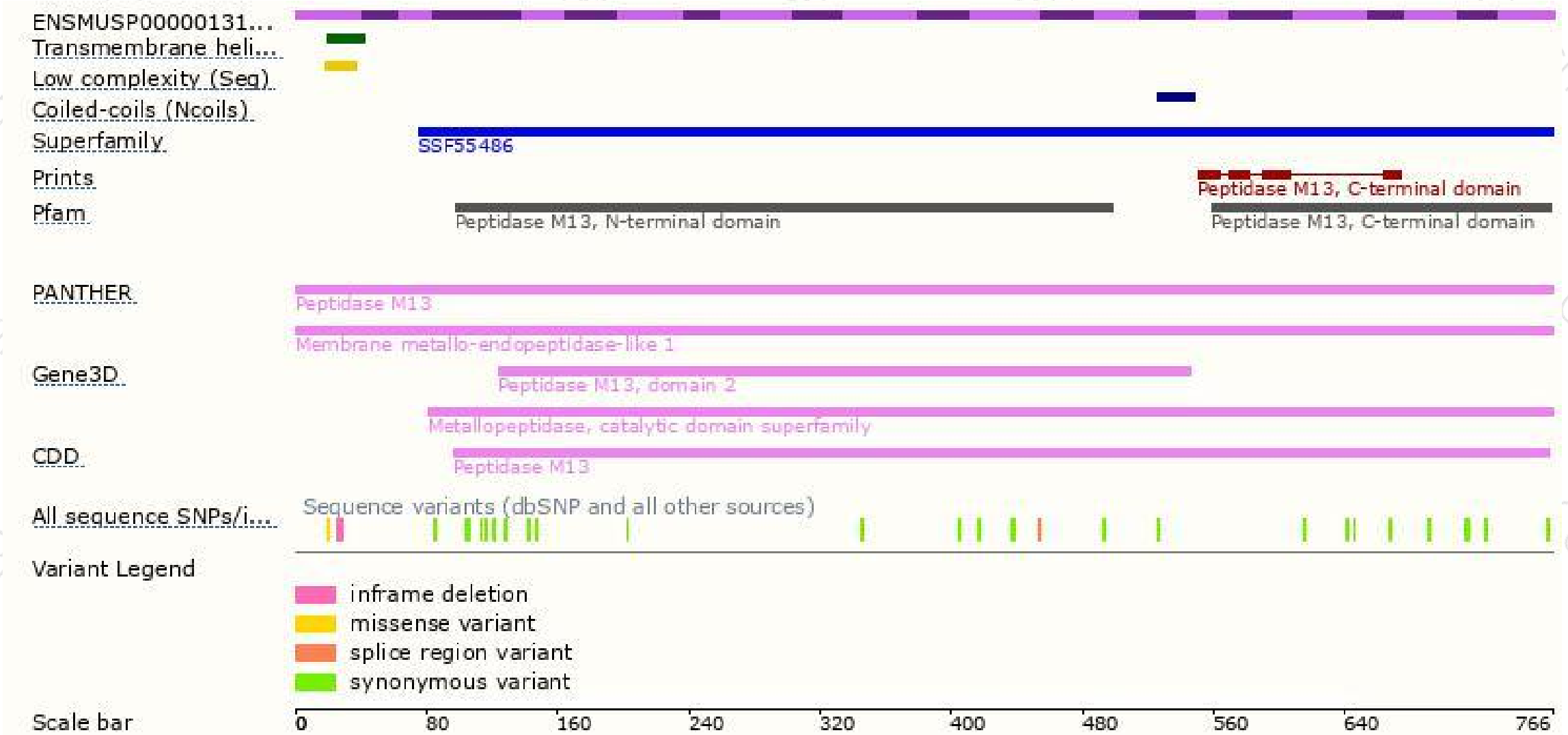
The strategy is based on the design of *Mmel1-207* transcript,The transcription is shown below



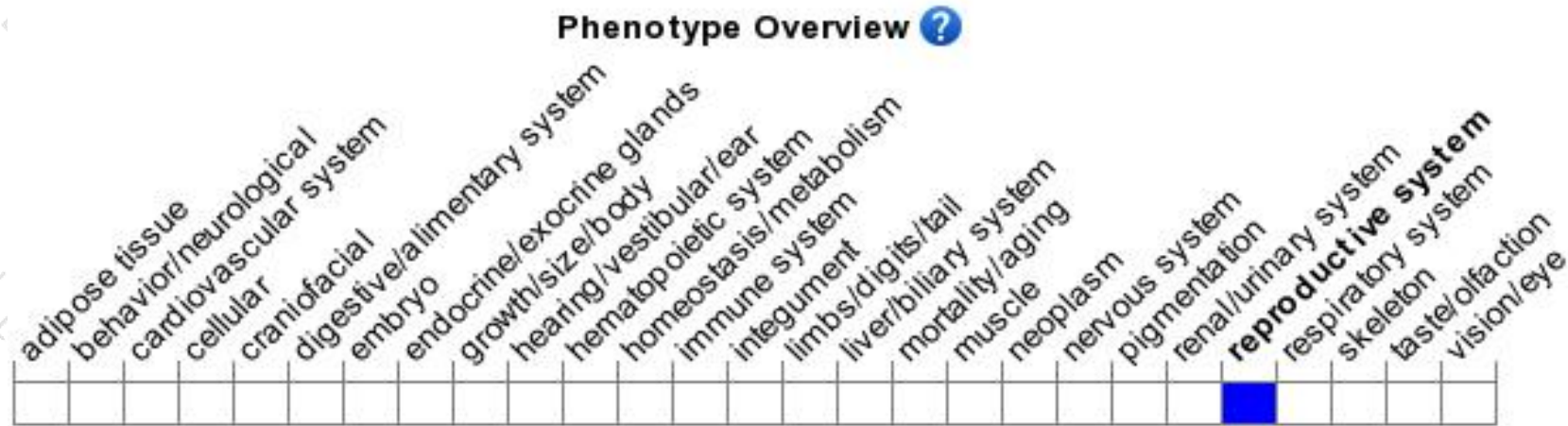
Genomic location distribution



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 mice display impaired male fertility. Female fertility is not affected.

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

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