



Mmd Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Mmd

Project type

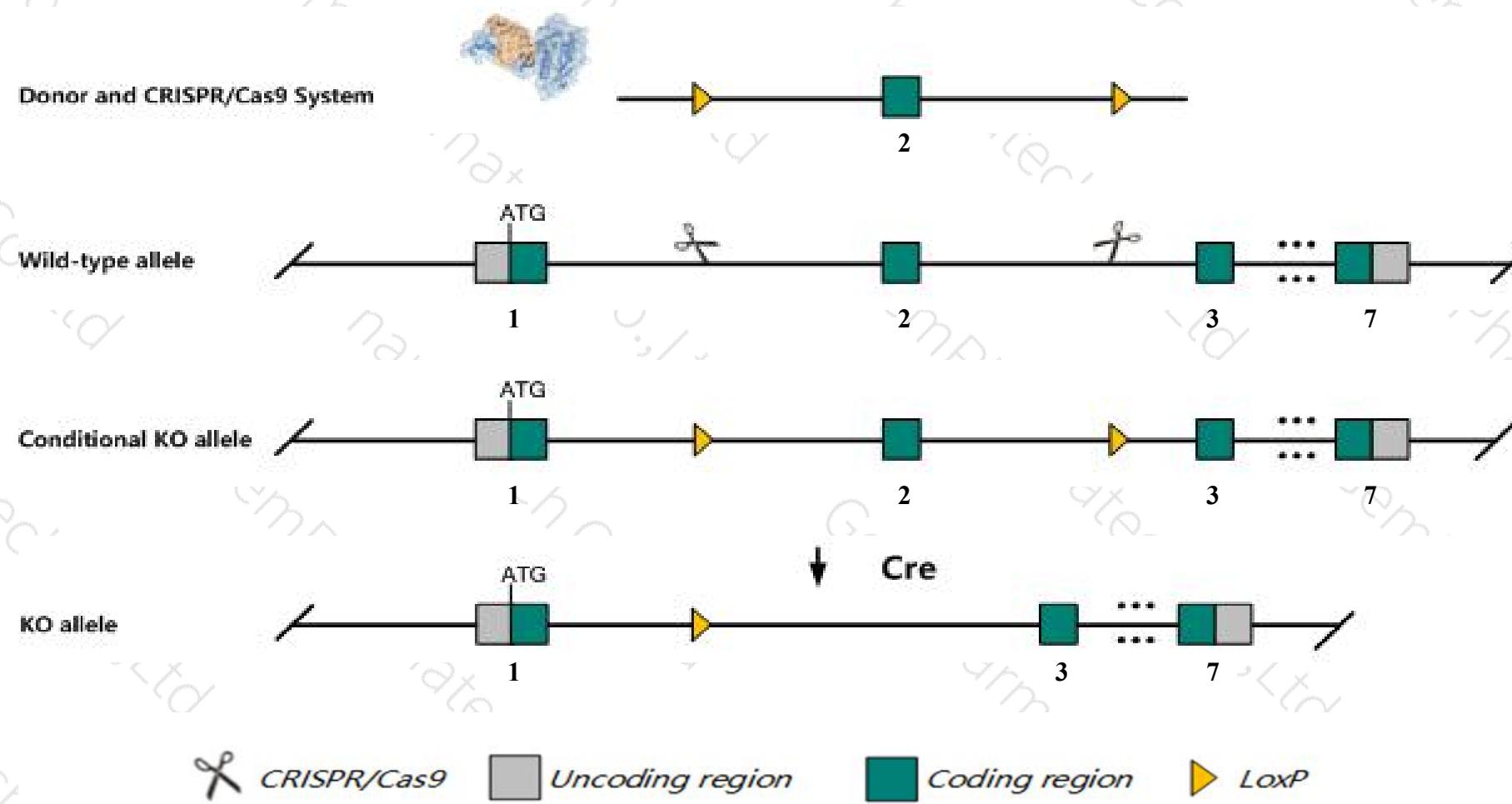
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Mmd* gene has 2 transcripts. According to the structure of *Mmd* gene, exon2 of *Mmd-201* (ENSMUST00000004050.6) transcript is recommended as the knockout region. The region contains 82bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mmd* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



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Notice

- The KO region contains one exon of *Gm45883*, so *Gm45883* gene may be affected.
- The *Mmd* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



Gene information (NCBI)

Mmd monocyte to macrophage differentiation-associated [Mus musculus (house mouse)]

Gene ID: 67468, updated on 13-Mar-2020

Summary



Official Symbol Mmd provided by [MGI](#)

Official Full Name monocyte to macrophage differentiation-associated provided by [MGI](#)

Primary source [MGI:MGI:1914718](#)

See related [Ensembl:ENSMUSG00000003948](#)

Gene type protein coding

RefSeq status PROVISIONAL

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 1200017E07Rik, 1810073C06Rik, AA690185

Expression Broad expression in subcutaneous fat pad adult (RPKM 114.9), genital fat pad adult (RPKM 66.5) and 16 other tissues [See more](#)

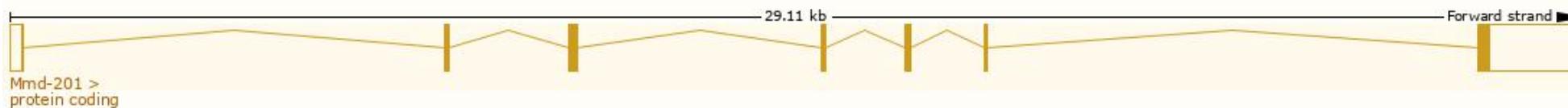
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

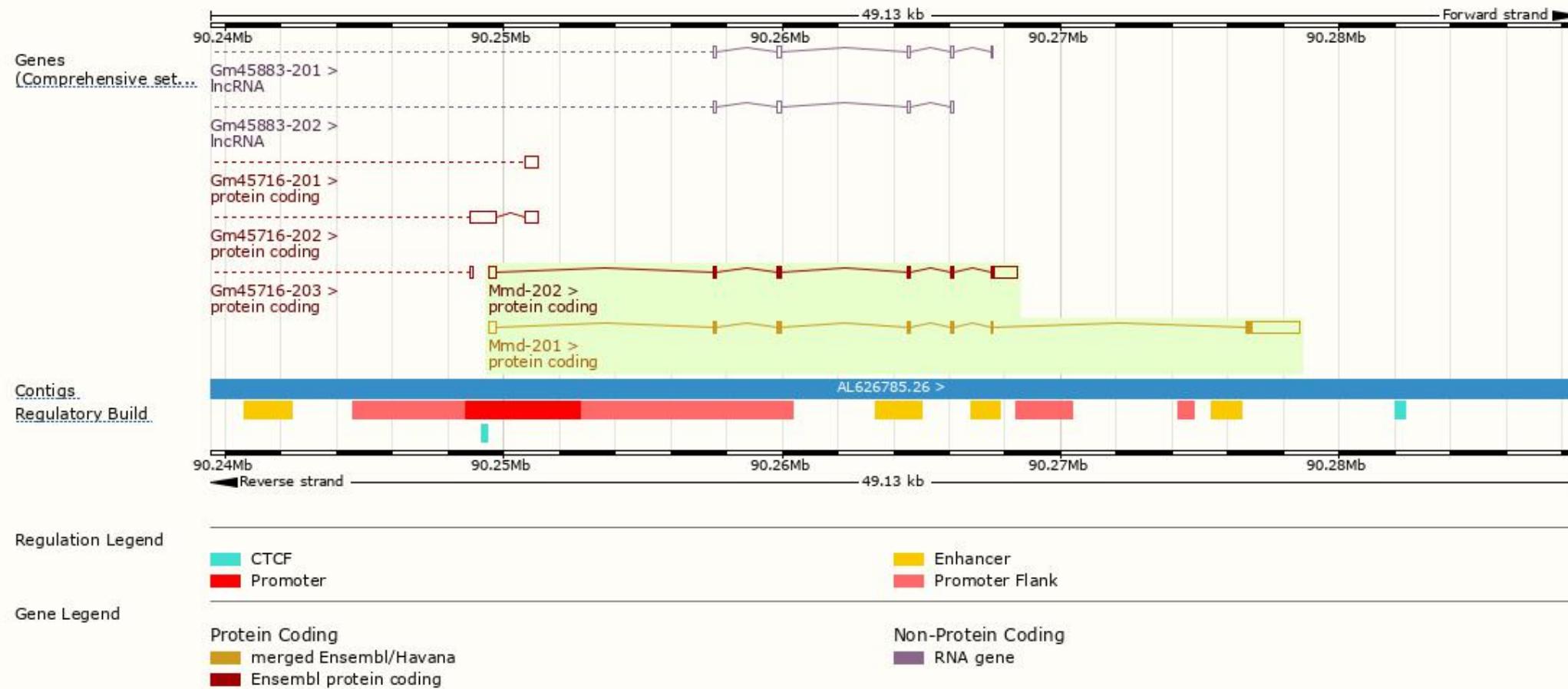
The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mmd-201	ENSMUST00000004050.6	2677	238aa	Protein coding	CCDS25240	Q9CQY7	TSL:1 GENCODE basic APPRIS P1
Mmd-202	ENSMUST00000107887.7	1654	187aa	Protein coding	-	Z4YKP7	TSL:1 GENCODE basic

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



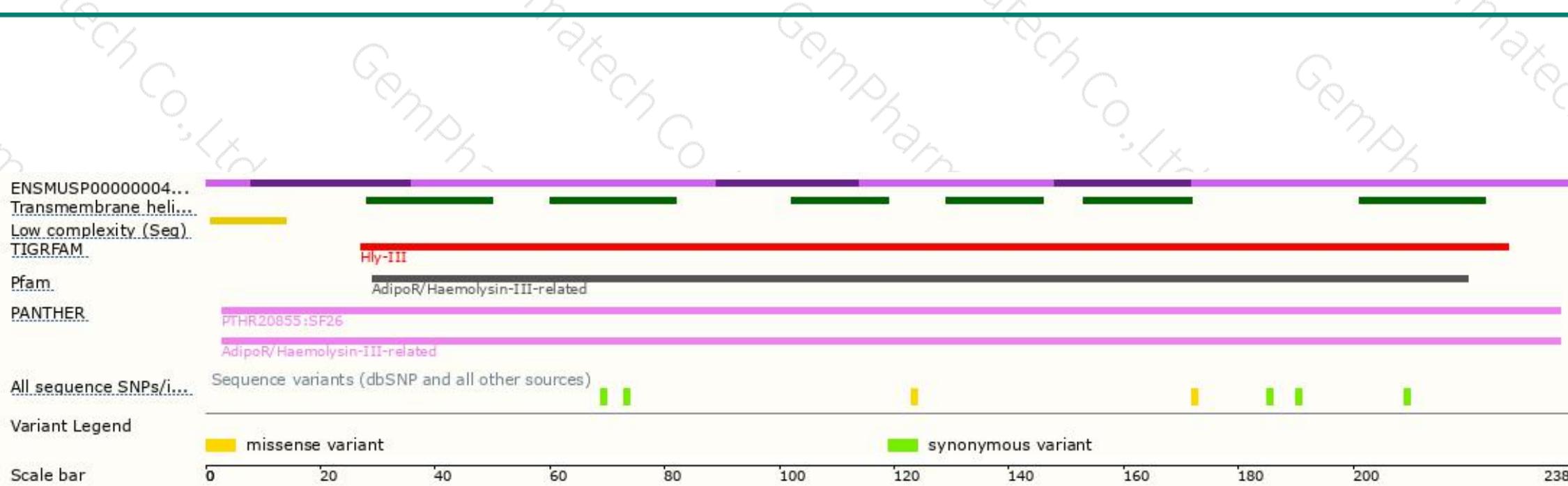
Genomic location distribution





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Protein domain





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

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