

Mmd2 Cas9-KO Strategy

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Project Overview

Project Name

Mmd2

Project type

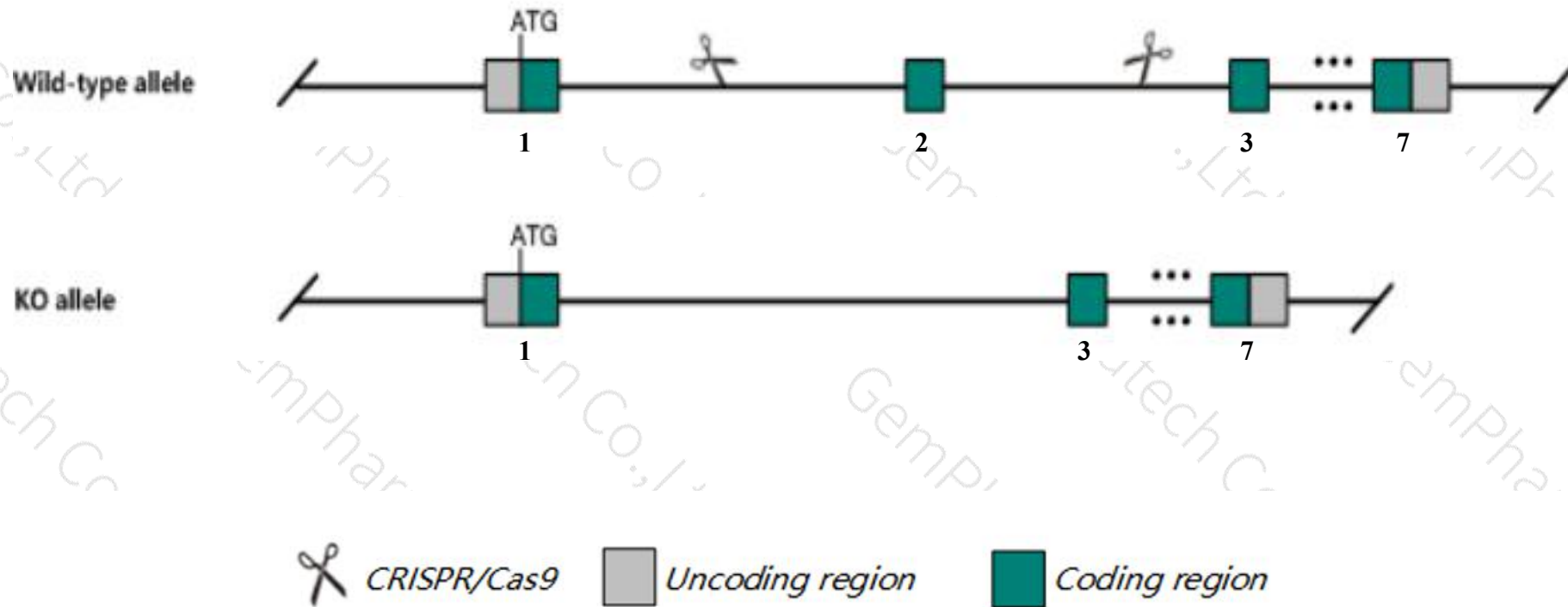
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mmd2* gene. The schematic diagram is as follows:



- The *Mmd2* gene has 3 transcripts. According to the structure of *Mmd2* gene, exon2 of *Mmd2-201* (ENSMUST00000037048.8) 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 *Mmd2* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Mmd2* gene is located on the Chr5. 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)

Mmd2 monocyte to macrophage differentiation-associated 2 [Mus musculus (house mouse)]

Gene ID: 75104, updated on 13-Mar-2020

Summary



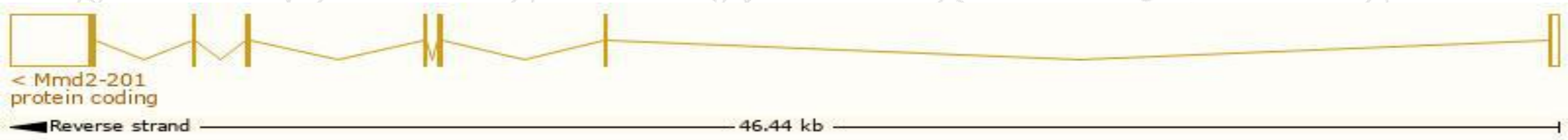
Official Symbol	Mmd2 provided by MGI
Official Full Name	monocyte to macrophage differentiation-associated 2 provided by MGI
Primary source	MGI:MGI:1922354
See related	Ensembl:ENSMUSG00000039533
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930518M15Rik, C88001
Expression	Biased expression in frontal lobe adult (RPKM 31.8), cortex adult (RPKM 26.0) and 13 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

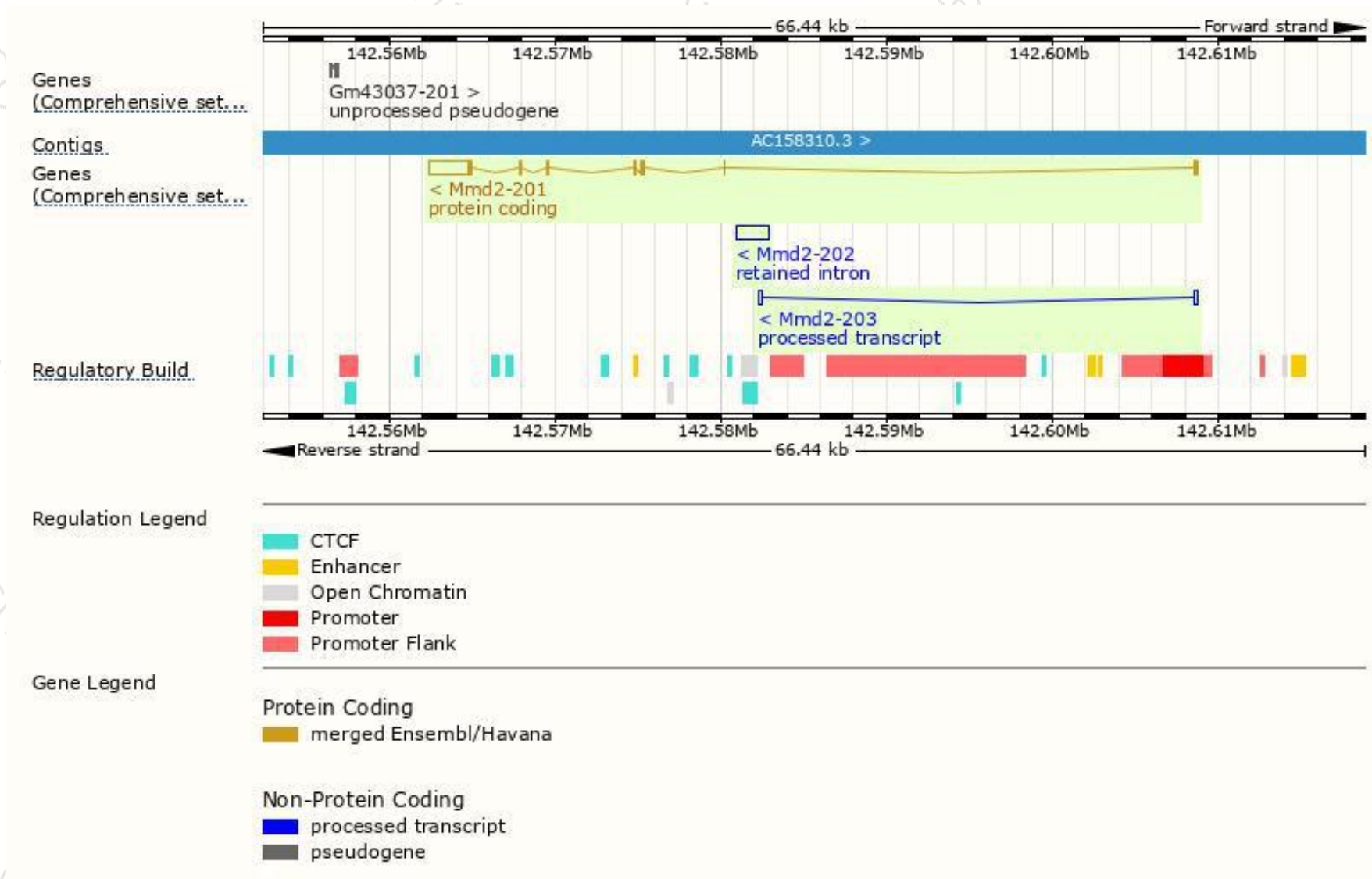
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mmd2-201	ENSMUST00000037048.8	3317	247aa	Protein coding	CCDS39363	Q3V1Z9 Q8R189	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 P1
Mmd2-203	ENSMUST00000196972.1	465	No protein	Processed transcript	-	-	TSL:2
Mmd2-202	ENSMUST00000195947.1	1876	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Mmd2-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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