

Cma1 Cas9-KO Strategy

Designer:

Huimin Su

Reviewer:

Ruirui Zhang

Design Date:

2019/9/23

Project Overview

Project Name

Cma1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cma1* gene. The schematic diagram is as follows:



- The *Cma1* gene has 2 transcripts. According to the structure of *Cma1* gene, exon2 of *Cma1-201* (ENSMUST00000022834.6) transcript is recommended as the knockout region. The region contains 151bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cma1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele display a reduction in mast cell-mediated ischemia reperfusion injury of skeletal muscle.
- The *Cma1* gene is located on the Chr14. 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)

Cma1 chymase 1, mast cell [*Mus musculus* (house mouse)]

Gene ID: 17228, updated on 12-Aug-2019

Summary

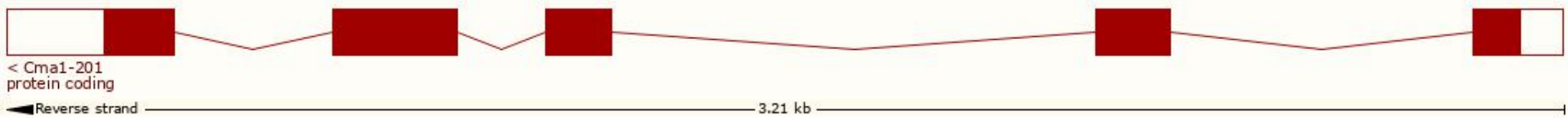
Official Symbol	Cma1 provided by MGI
Official Full Name	chymase 1, mast cell provided by MGI
Primary source	MGI:MGI:96941
See related	Ensembl:ENSMUSG00000022225
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mcp5; Mcp-5; Mcpt5; MMCP-5
Summary	This gene encodes a serine protease that belongs to the peptidase family S1. It is expressed in mast cells and is thought to function in the degradation of the extracellular matrix, the regulation of submucosal gland secretion, and the generation of vasoactive peptides. The encoded preproprotein undergoes proteolytic processing to generate a functional enzyme with elastase-like activity. Mice lacking the encoded protein exhibit significant attenuation of ischemia-reperfusion injury of the skeletal muscle. This gene is located in a cluster of related mast cell protease genes on chromosome 14. [provided by RefSeq, Nov 2015]
Expression	Biased expression in limb E14.5 (RPKM 20.7), mammary gland adult (RPKM 10.9) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

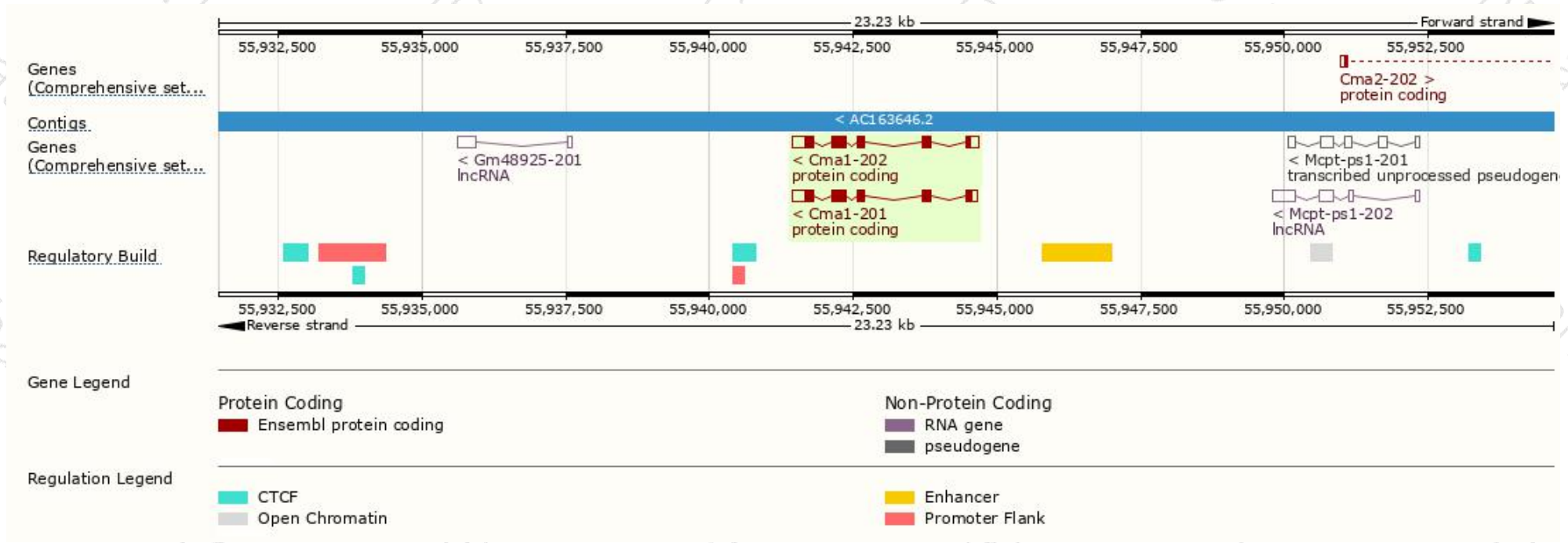
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cma1-201	ENSMUST00000022834.6	1074	260aa	Protein coding	CCDS27135	A4QPC5	TSL:1 GENCODE basic APPRIS P2
Cma1-202	ENSMUST000000226280.1	1090	247aa	Protein coding	-	P21844	GENCODE basic APPRIS ALT2

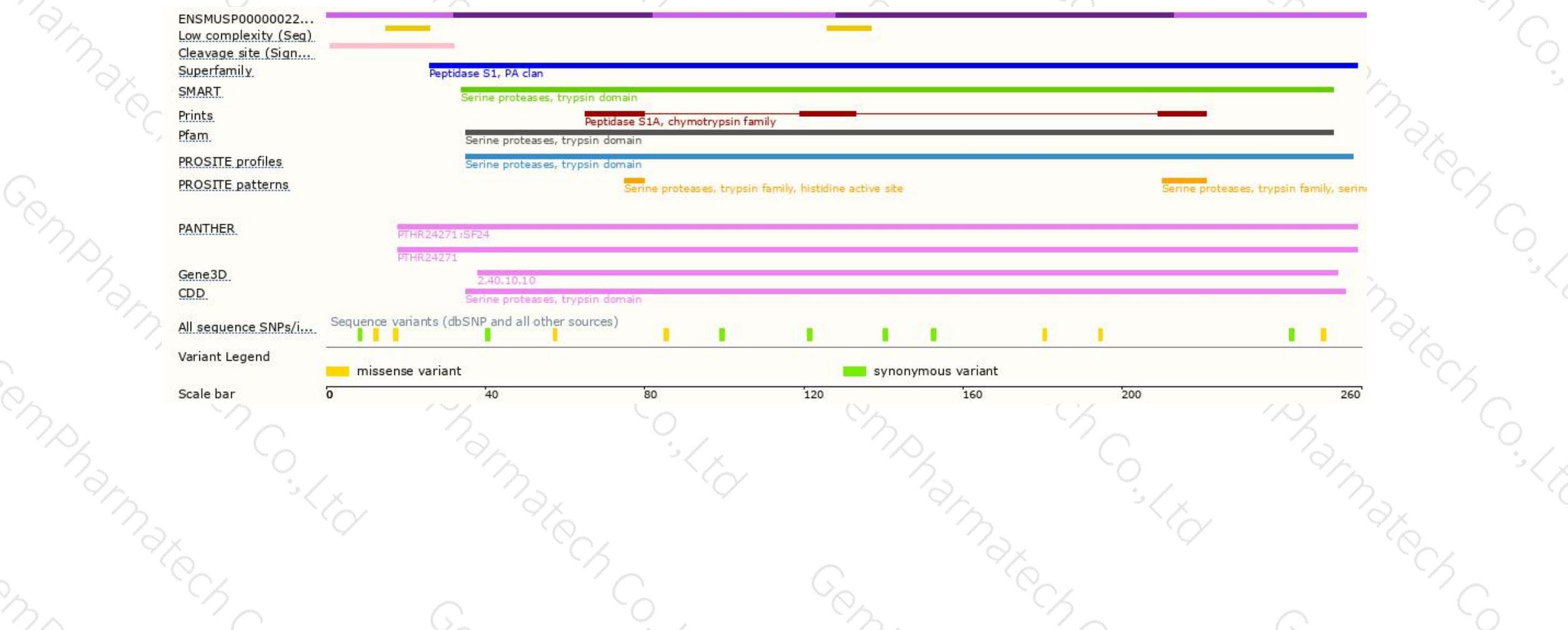
The strategy is based on the design of *Cma1-201* transcript,The transcription is shown below



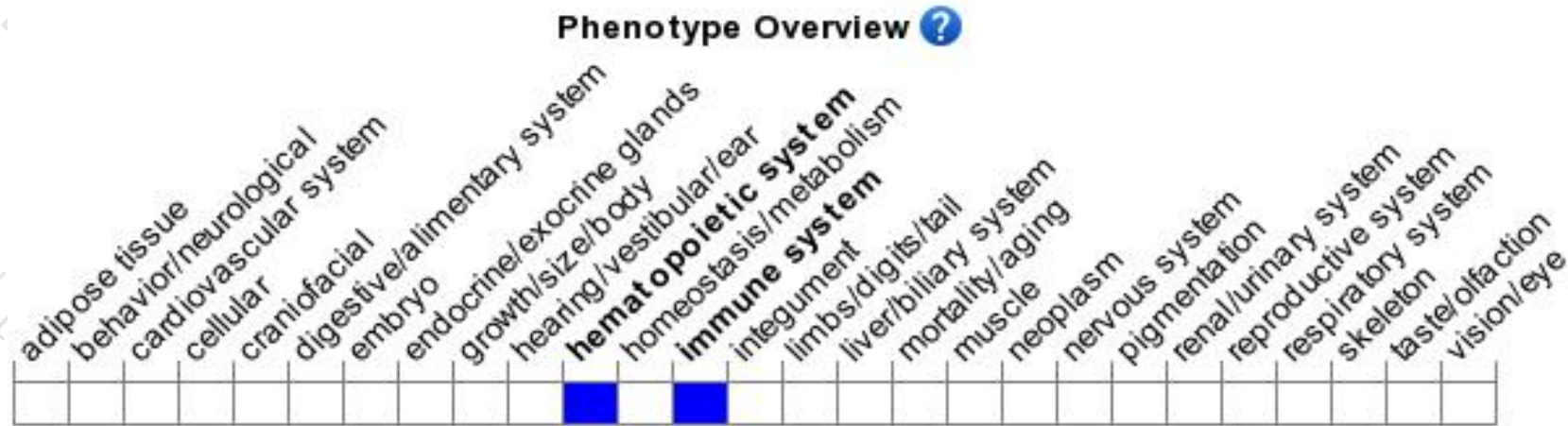
Genomic location distribution



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 display a reduction in mast cell-mediated ischemia reperfusion injury of skeletal muscle.

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

Tel: 400-9660890

