

Cpm Cas9-CKO Strategy

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Project Overview

Project Name

Cpm

Project type

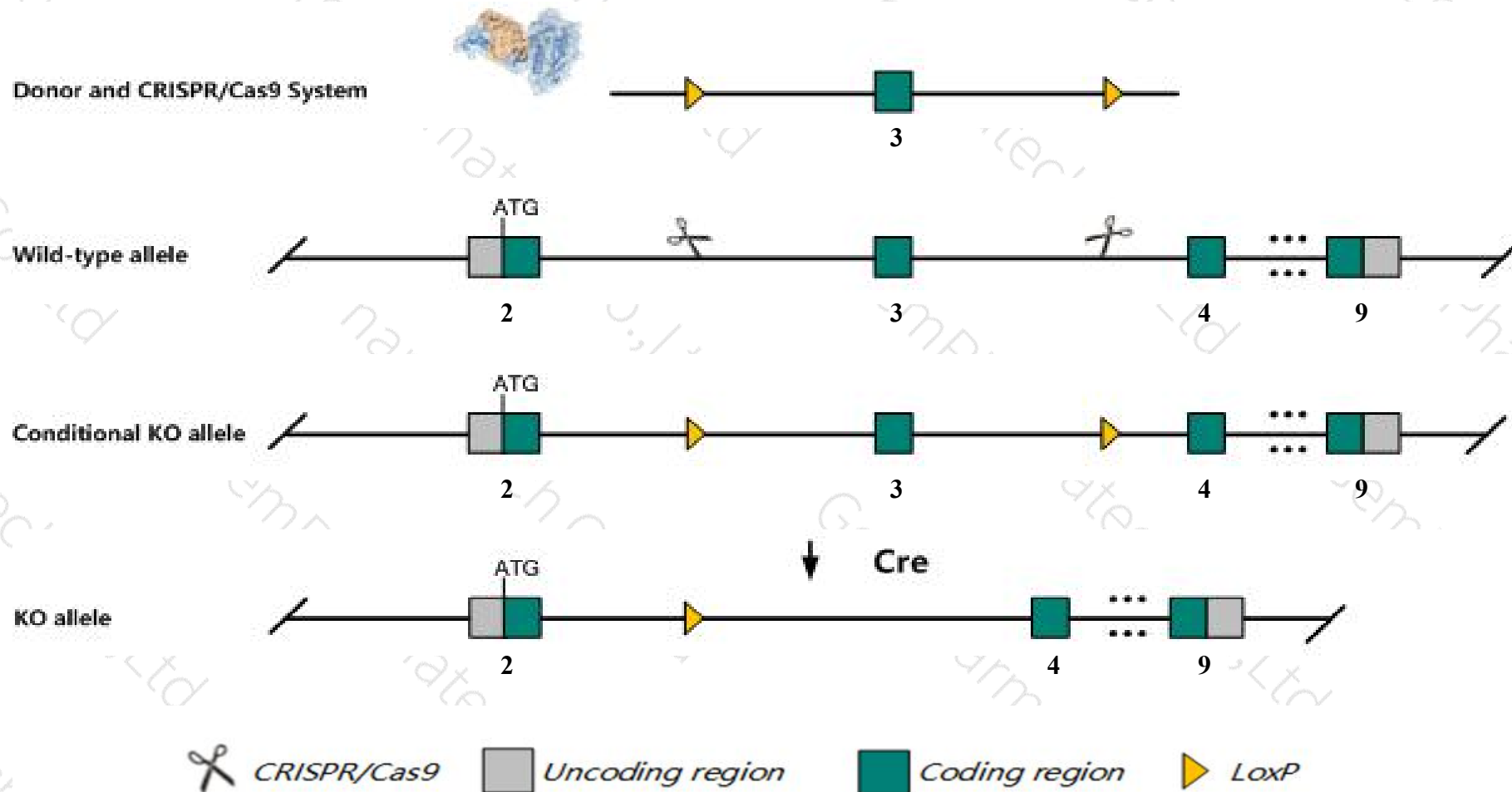
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Cpm* gene has 4 transcripts. According to the structure of *Cpm* gene, exon3 of *Cpm-201* (ENSMUST00000020399.5) transcript is recommended as the knockout region. The region contains 98bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cpm* 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.

Notice

- The *Cpm* gene is located on the Chr10. 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)

Cpm carboxypeptidase M [Mus musculus (house mouse)]

Gene ID: 70574, updated on 13-Mar-2020

Summary



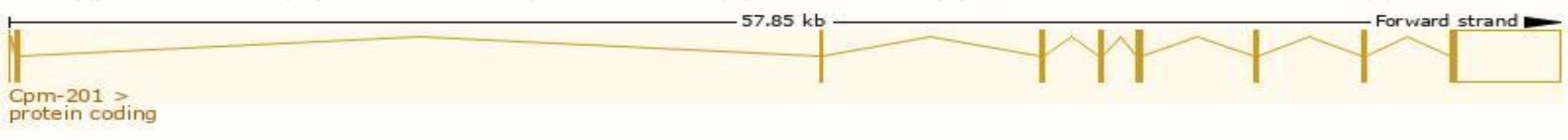
Official Symbol	Cpm provided by MGI
Official Full Name	carboxypeptidase M provided by MGI
Primary source	MGI:MGI:1917824
See related	Ensembl:ENSMUSG00000020183
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110060I01Rik, 5730456K23Rik, AA589379, E030045M14Rik
Expression	Broad expression in lung adult (RPKM 24.8), kidney adult (RPKM 7.5) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

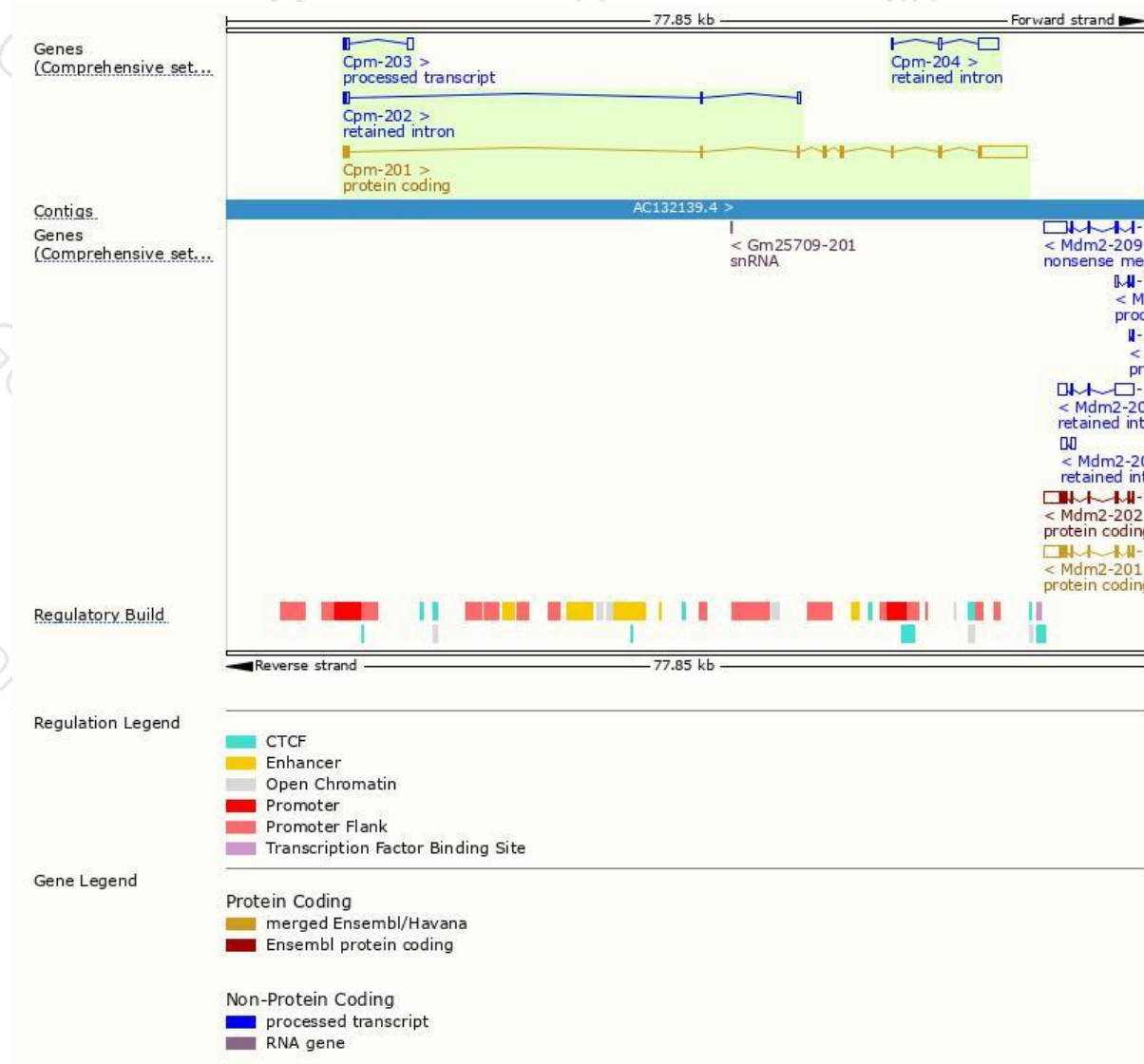
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cpm-201	ENSMUST00000020399.5	5195	443aa	Protein coding	CCDS48696	Q80V42	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
Cpm-203	ENSMUST00000138020.7	798	No protein	Processed transcript	-	-	TSL:3
Cpm-204	ENSMUST00000141991.1	2006	No protein	Retained intron	-	-	TSL:1
Cpm-202	ENSMUST00000123374.7	573	No protein	Retained intron	-	-	TSL:3

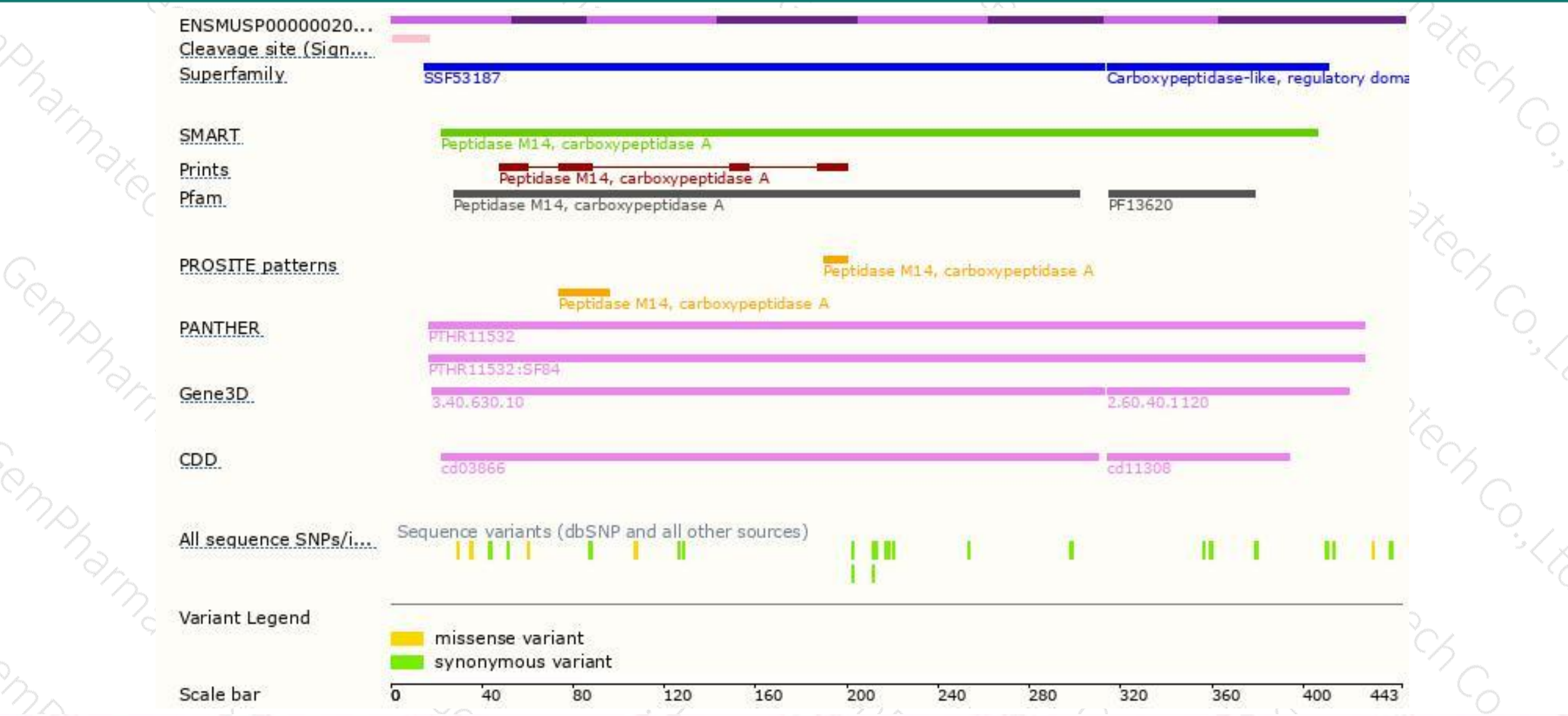
The strategy is based on the design of *Cpm-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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