GemPharmatech™

Metap1 Cas9-CKO Strategy

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Overview

Target Gene Name

- Metap1

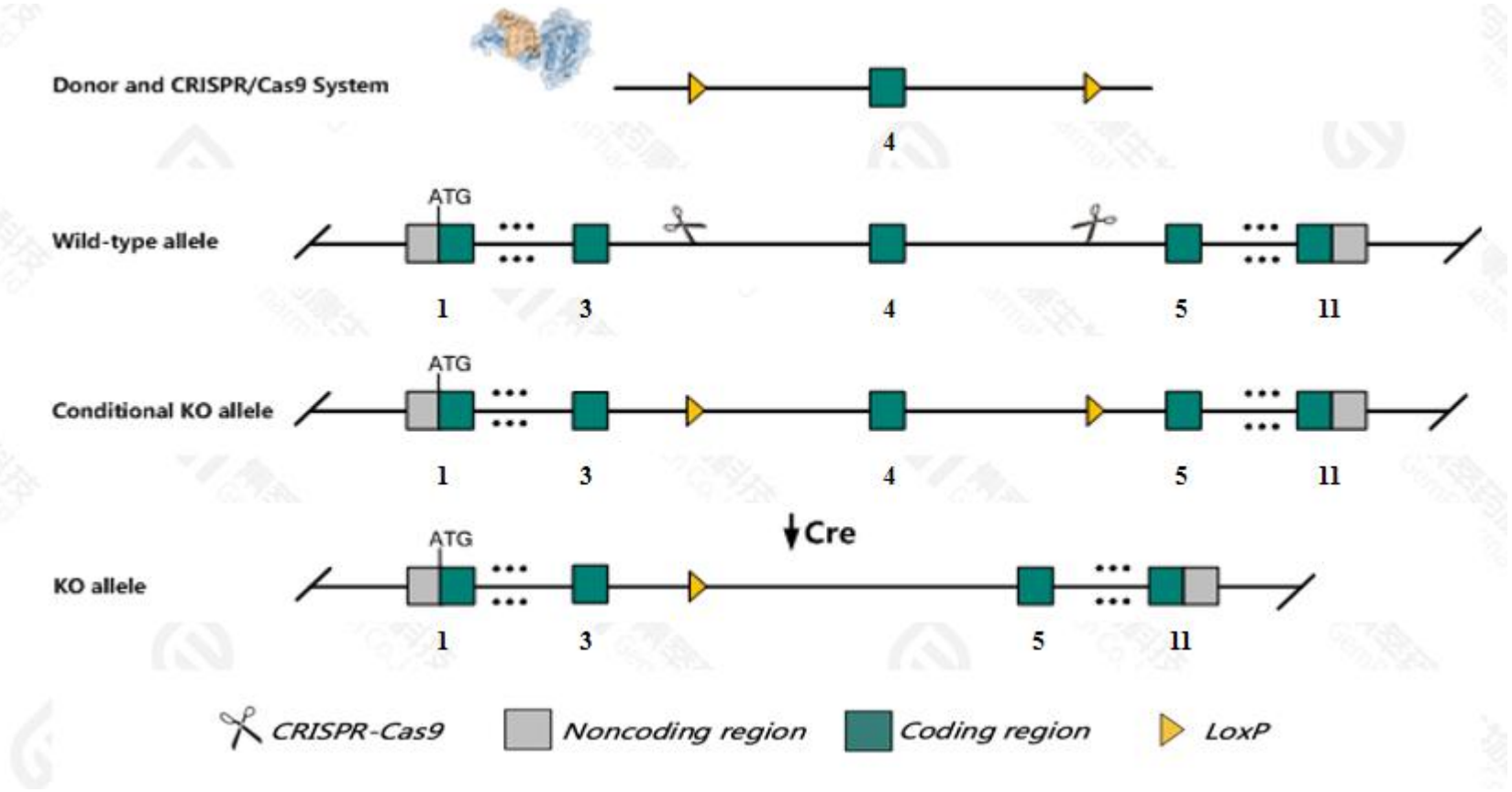
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Metap1* gene.

Technical Information

- The *Metap1* gene has 7 transcripts. According to the structure of *Metap1* gene, exon4 of *Metap1-201*(ENSMUST00000029804.13) transcript is recommended as the knockout region.The region contains 61bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Metap1* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Metap1 methionyl aminopeptidase 1 [Mus musculus (house mouse)]

Gene ID: 75624, updated on 12-Jul-2022

Summary

Official Symbol	Metap1 provided by MGI
Official Full Name	methionyl aminopeptidase 1 provided byMGI
Primary source	MGI:MGI:1922874
See related	Ensembl:ENSMUSG00000005813
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	1700029C17Rik, AW047992, mKIAA0094
Expression	Ubiquitous expression in placenta adult (RPKM 27.6), CNS E11.5 (RPKM 21.6) and 28 other tissuesSee more
Orthologs	human all

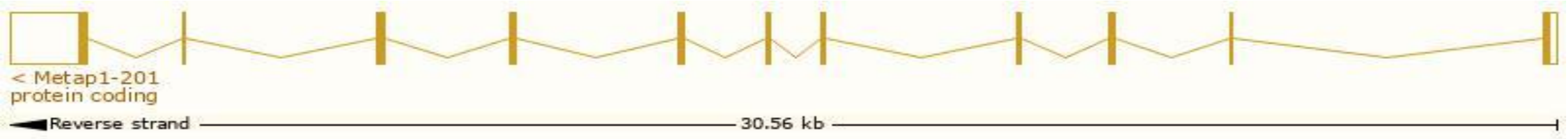
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

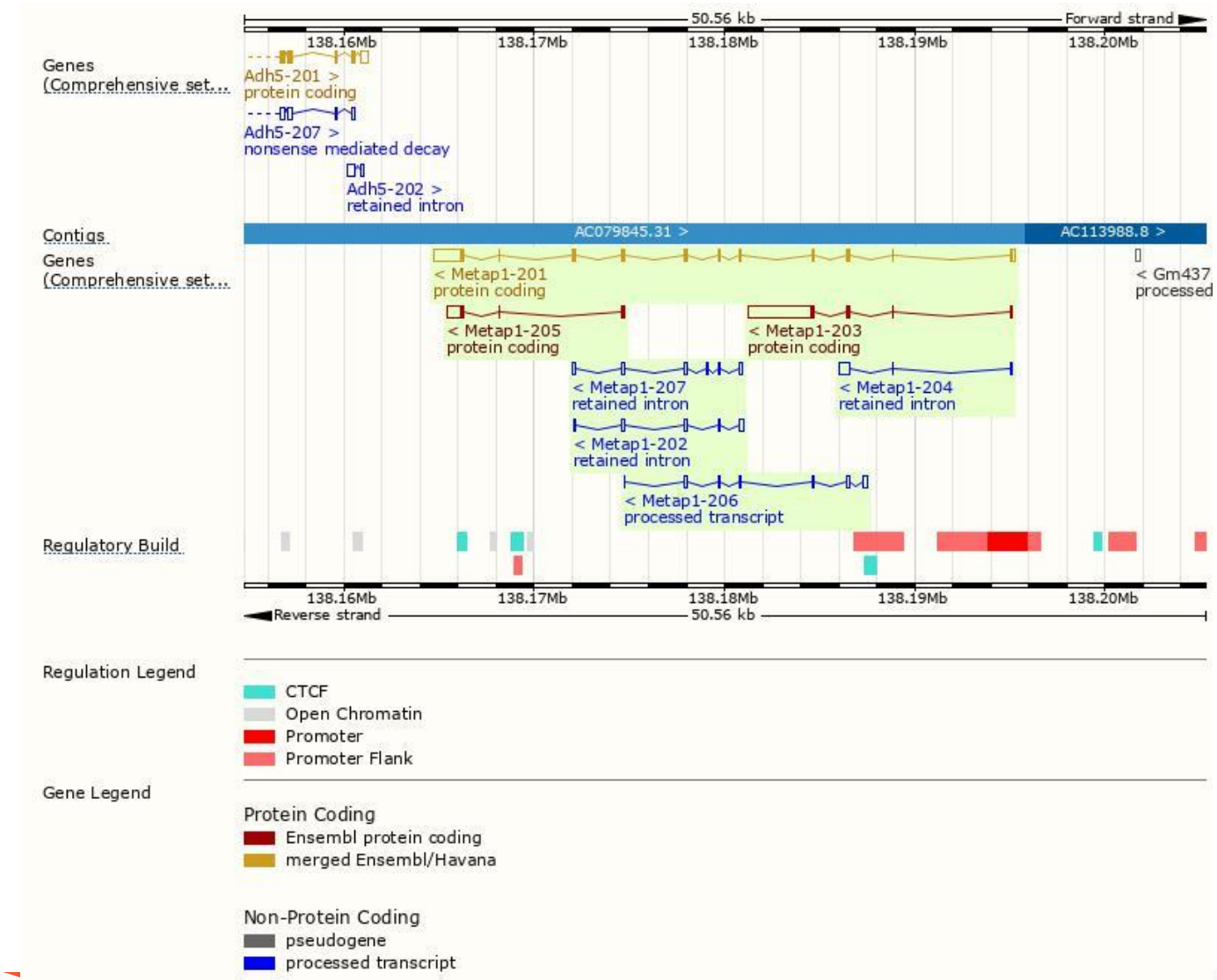
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Metap1-201	ENSMUST00000029804.13	2686	386aa	Protein coding	CCDS17869		TSL:1 , GENCODE basic , APPRIS P1 ,
Metap1-203	ENSMUST00000197531.2	3708	142aa	Protein coding	-		TSL:1 , GENCODE basic ,
Metap1-205	ENSMUST00000198700.2	1007	116aa	Protein coding	-		CDS 5' incomplete , TSL:5 ,
Metap1-206	ENSMUST00000199303.2	763	No protein	Processed transcript	-		TSL:5 ,
Metap1-207	ENSMUST00000200365.5	731	No protein	Retained intron	-		TSL:3 ,
Metap1-204	ENSMUST00000198492.2	716	No protein	Retained intron	-		TSL:2 ,
Metap1-202	ENSMUST00000195910.5	681	No protein	Retained intron	-		TSL:2 ,

The strategy is based on the design of *Metap1*-201 transcript, the transcription is shown below:

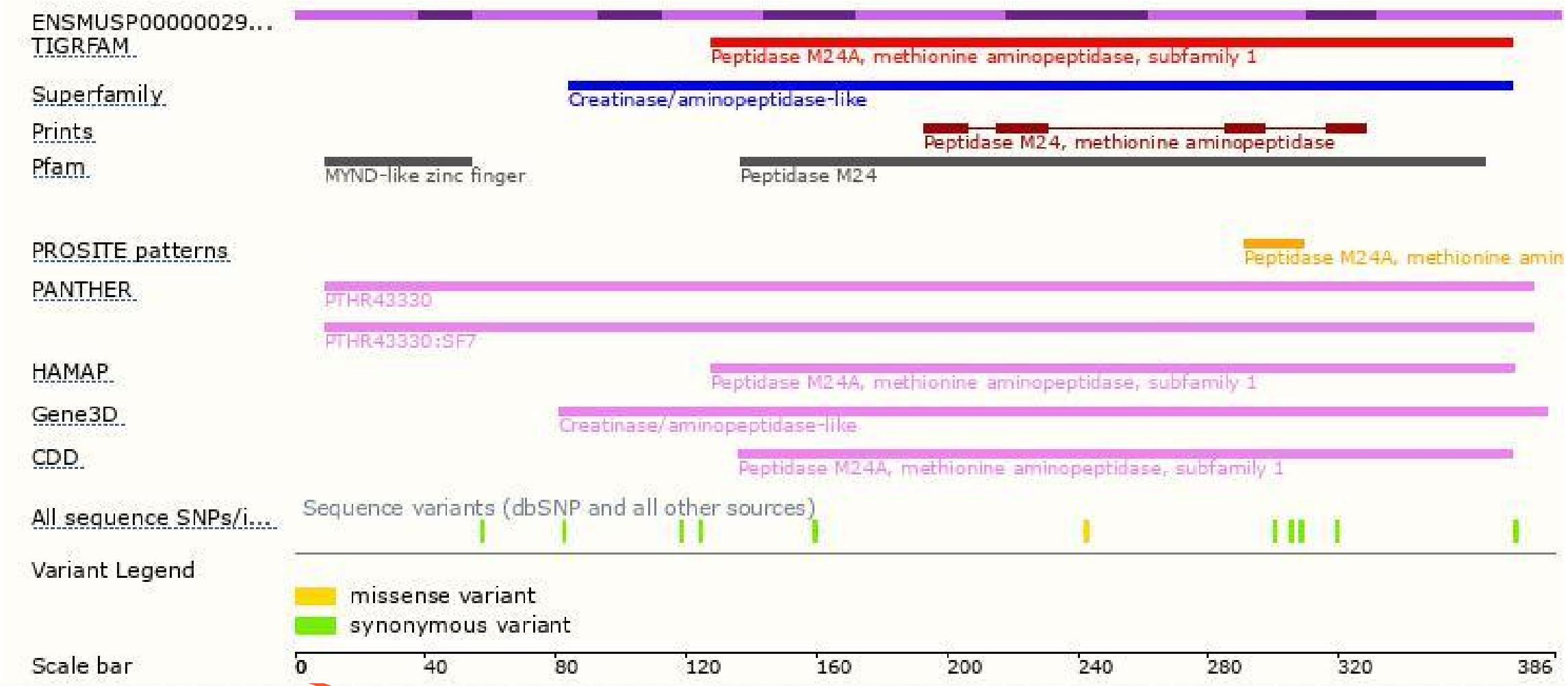


Genomic Information



Source: : https://www.ensembl.org

Protein Information



Source: : https://www.ensembl.org

Important Information

- The effect of Metap1-205 gene is unknown.
- *Metap1* is located on Chr3. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.