

# *Mmp12* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview



**Project Name**

***Mmp12***

**Project type**

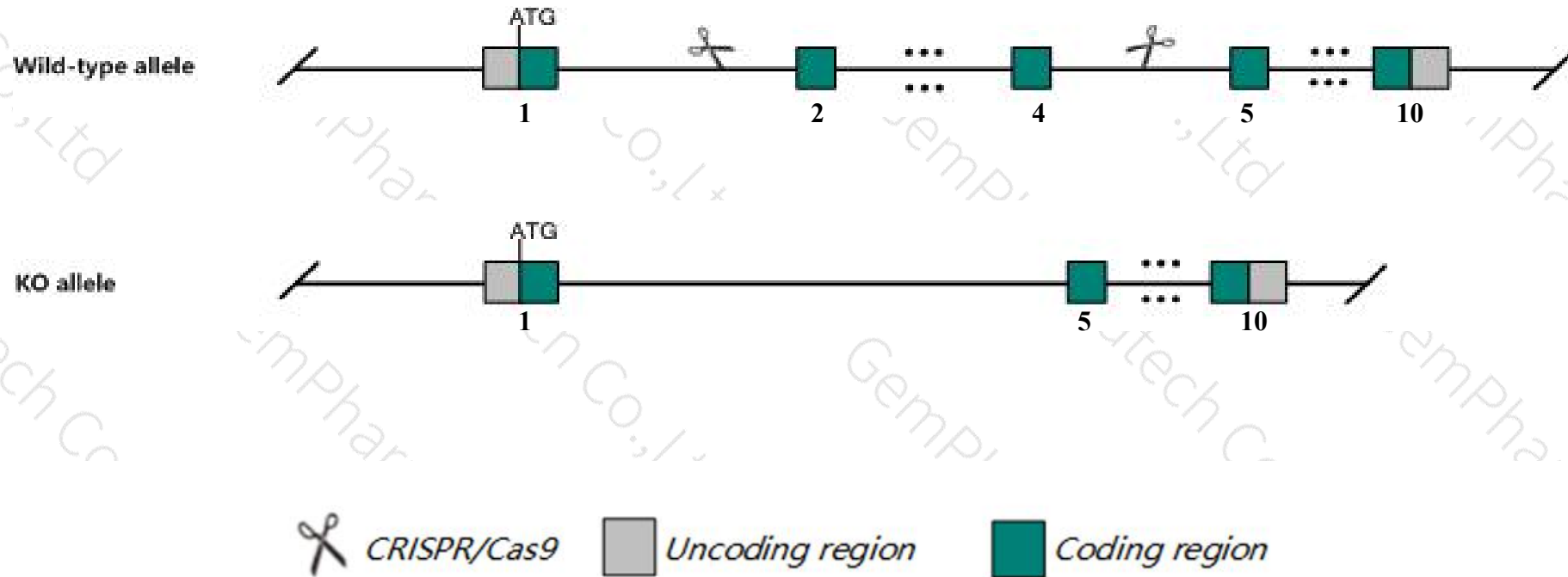
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mmp12* gene. The schematic diagram is as follows:



- The *Mmp12* gene has 7 transcripts. According to the structure of *Mmp12* gene, exon2-exon4 of *Mmp12-201* (ENSMUST00000005950.11) transcript is recommended as the knockout region. The region contains 523bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mmp12* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased sensitivity to cigarette smoke, decreased litter size, abnormal myelination, abnormal macrophage physiology, and decreased oligodendrocytes.
- The *Mmp12* gene is located on the Chr9. 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)

## Mmp12 matrix metalloproteinase 12 [ *Mus musculus* (house mouse) ]

Gene ID: 17381, updated on 10-Oct-2019

### Summary



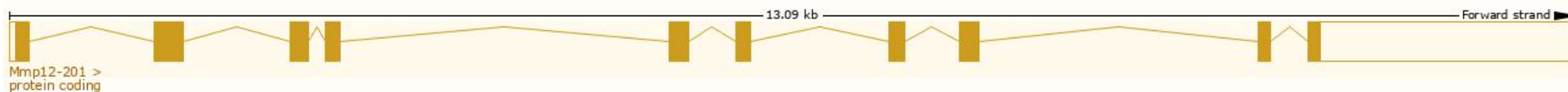
Official Symbol	Mmp12 provided by <a href="#">MGI</a>
Official Full Name	matrix metalloproteinase 12 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:97005</a>
See related	<a href="#">Ensembl:ENSMUSG00000049723</a>
Gene type	protein coding
RefSeq status	REVIEWED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MME; Mmel; AV378681
Summary	This gene encodes a member of the matrix metalloproteinase family of extracellular matrix-degrading enzymes that are involved in tissue remodeling, wound repair, progression of atherosclerosis and tumor invasion. The encoded preproprotein undergoes proteolytic processing to generate a mature, zinc-dependent endopeptidase enzyme. Mice lacking the encoded protein have a diminished capacity to degrade extracellular matrix components, do not develop emphysema in response to long-term exposure to cigarette smoke, and exhibit impaired clearance and increased mortality upon bacterial infection. This gene is located in a cluster of other matrix metalloproteinase genes on chromosome 9. Alternate splicing generates multiple transcript variants encoding distinct isoforms. [provided by RefSeq, Feb 2016]
Expression	Low expression observed in reference dataset <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

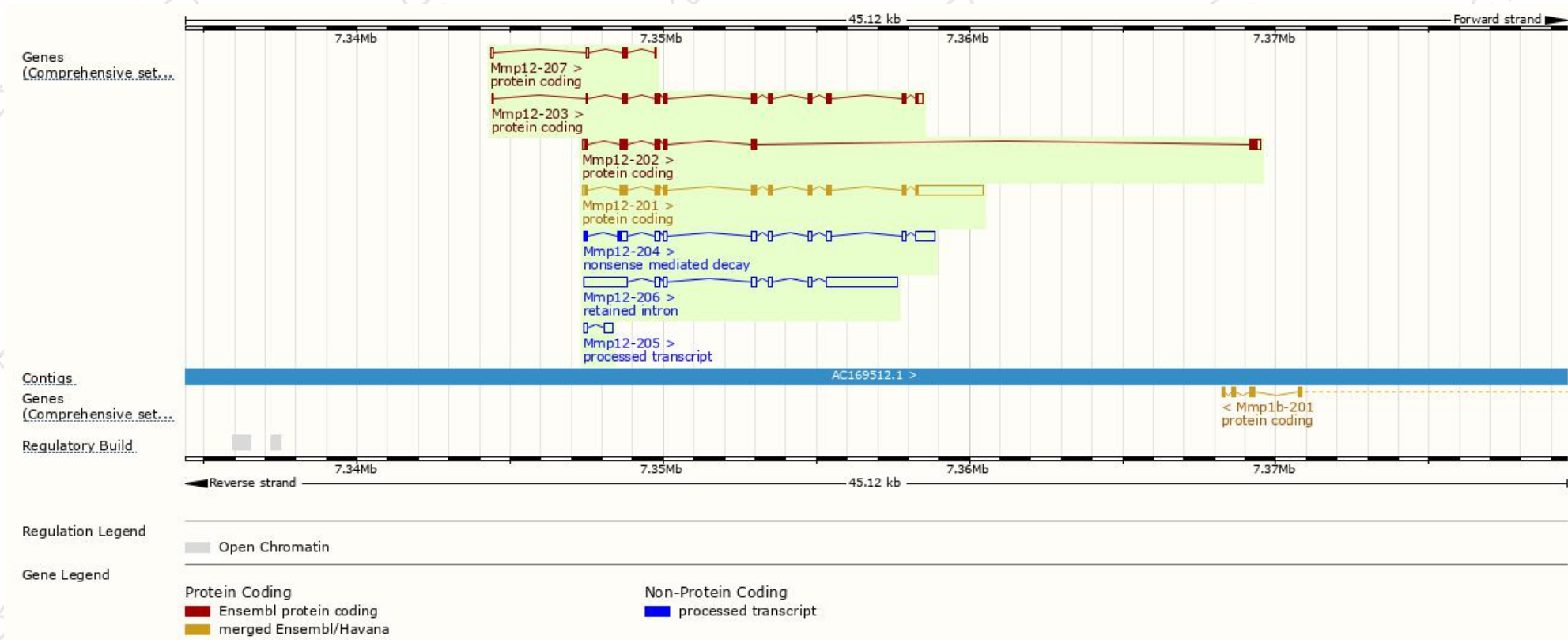
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mmp12-201	<a href="#">ENSMUST00000005950.11</a>	3607	<a href="#">473aa</a>	Protein coding	<a href="#">CCDS22804</a>	<a href="#">P34960</a>	TSL:1 GENCODE basic APPRIS P3
Mmp12-203	<a href="#">ENSMUST00000120655.7</a>	1452	<a href="#">403aa</a>	Protein coding	<a href="#">CCDS85639</a>	<a href="#">Q3TCW6</a>	TSL:1 GENCODE basic APPRIS ALT2
Mmp12-202	<a href="#">ENSMUST00000065079.5</a>	1185	<a href="#">339aa</a>	Protein coding	-	<a href="#">Q8BJC0</a>	TSL:1 GENCODE basic
Mmp12-207	<a href="#">ENSMUST00000150167.1</a>	362	<a href="#">72aa</a>	Protein coding	-	<a href="#">D3Z705</a>	CDS 3' incomplete TSL:5
Mmp12-204	<a href="#">ENSMUST00000127722.1</a>	2060	<a href="#">64aa</a>	Nonsense mediated decay	-	<a href="#">D6RJI9</a>	TSL:1
Mmp12-205	<a href="#">ENSMUST00000138220.1</a>	410	No protein	Processed transcript	-	-	TSL:2
Mmp12-206	<a href="#">ENSMUST00000148005.7</a>	4474	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Mmp12-201* transcript, The transcription is shown below



# Genomic location distribution

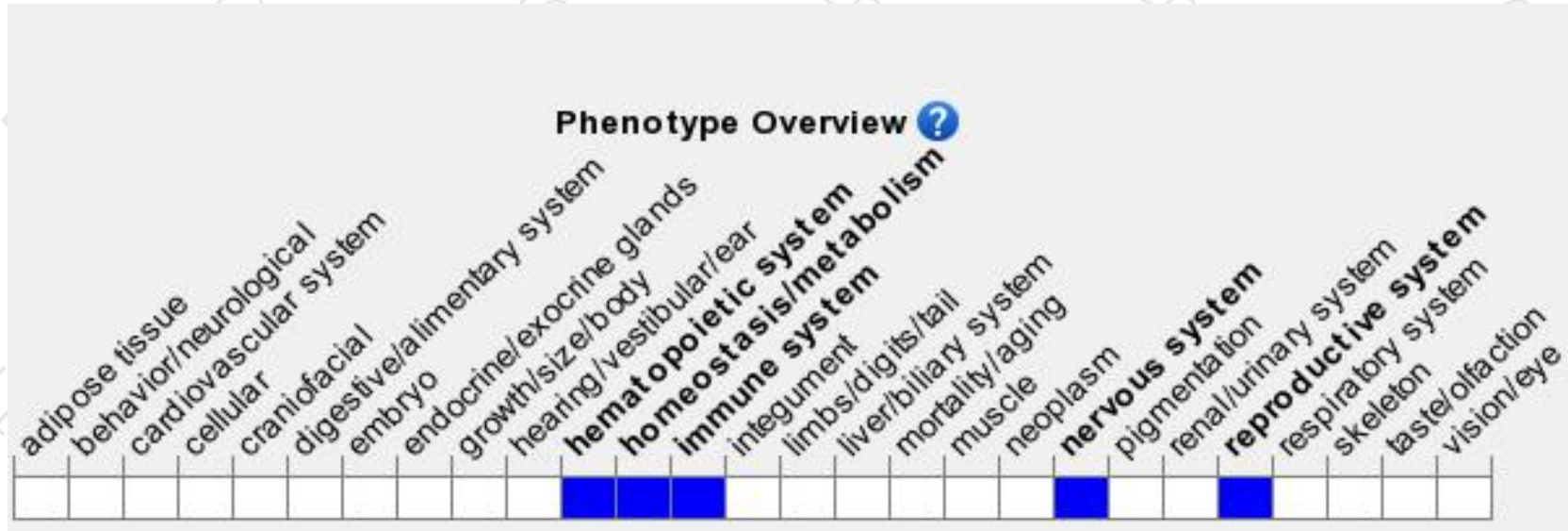




# Protein domain



# 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 exhibit decreased sensitivity to cigarette smoke, decreased litter size, abnormal myelination, abnormal macrophage physiology, and decreased oligodendrocytes.

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

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