

# *Masp1* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Masp1*

**Project type**

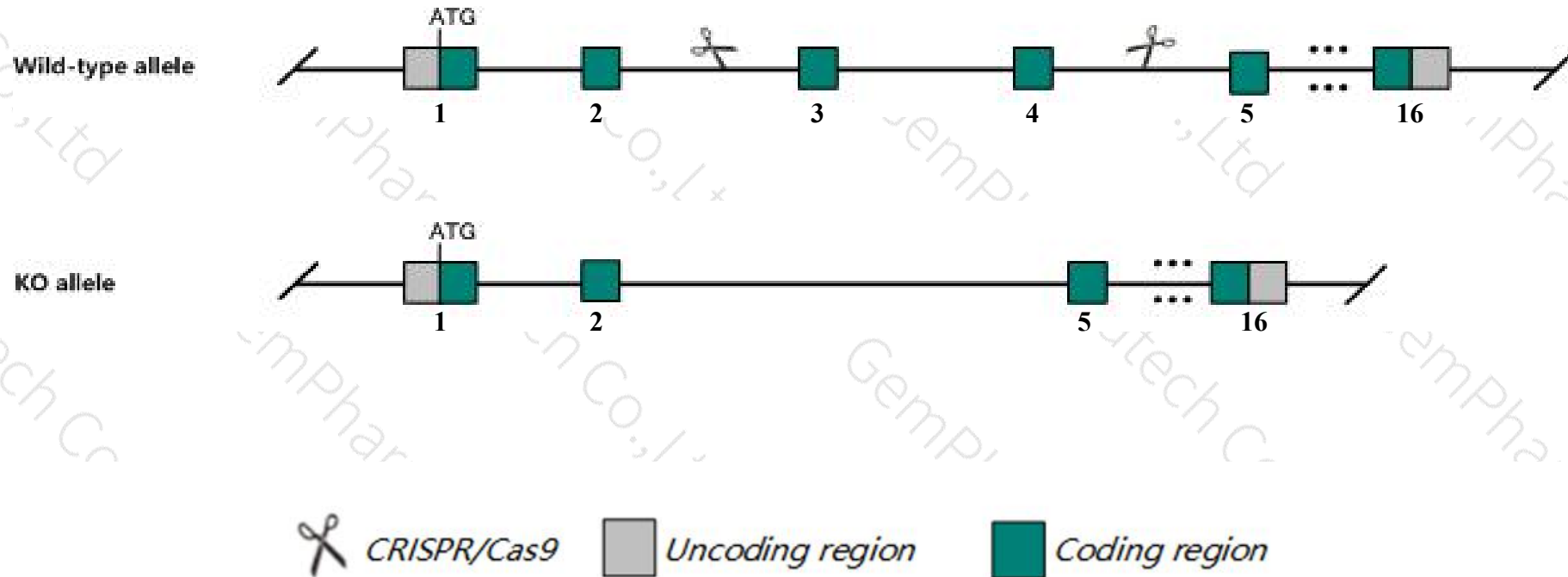
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Masp1* gene. The schematic diagram is as follows:



- The *Masp1* gene has 4 transcripts. According to the structure of *Masp1* gene, exon3-exon4 of *Masp1-201* (ENSMUST00000089883.6) transcript is recommended as the knockout region. The region contains 310bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Masp1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knockout allele display decreased survivor rate, reduced body weight, and impaired activation of the lectin and alternative complement pathways.
- The *Masp1* gene is located on the Chr16. 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)

## Masp1 mannan-binding lectin serine peptidase 1 [ *Mus musculus* (house mouse) ]

Gene ID: 17174, updated on 24-Oct-2019

### Summary

<b>Official Symbol</b>	Masp1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	mannan-binding lectin serine peptidase 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:88492</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000022887</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	CCPII; Crarf; Masp1/3; AW048060
<b>Expression</b>	Broad expression in adrenal adult (RPKM 13.8), liver adult (RPKM 12.9) and 16 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

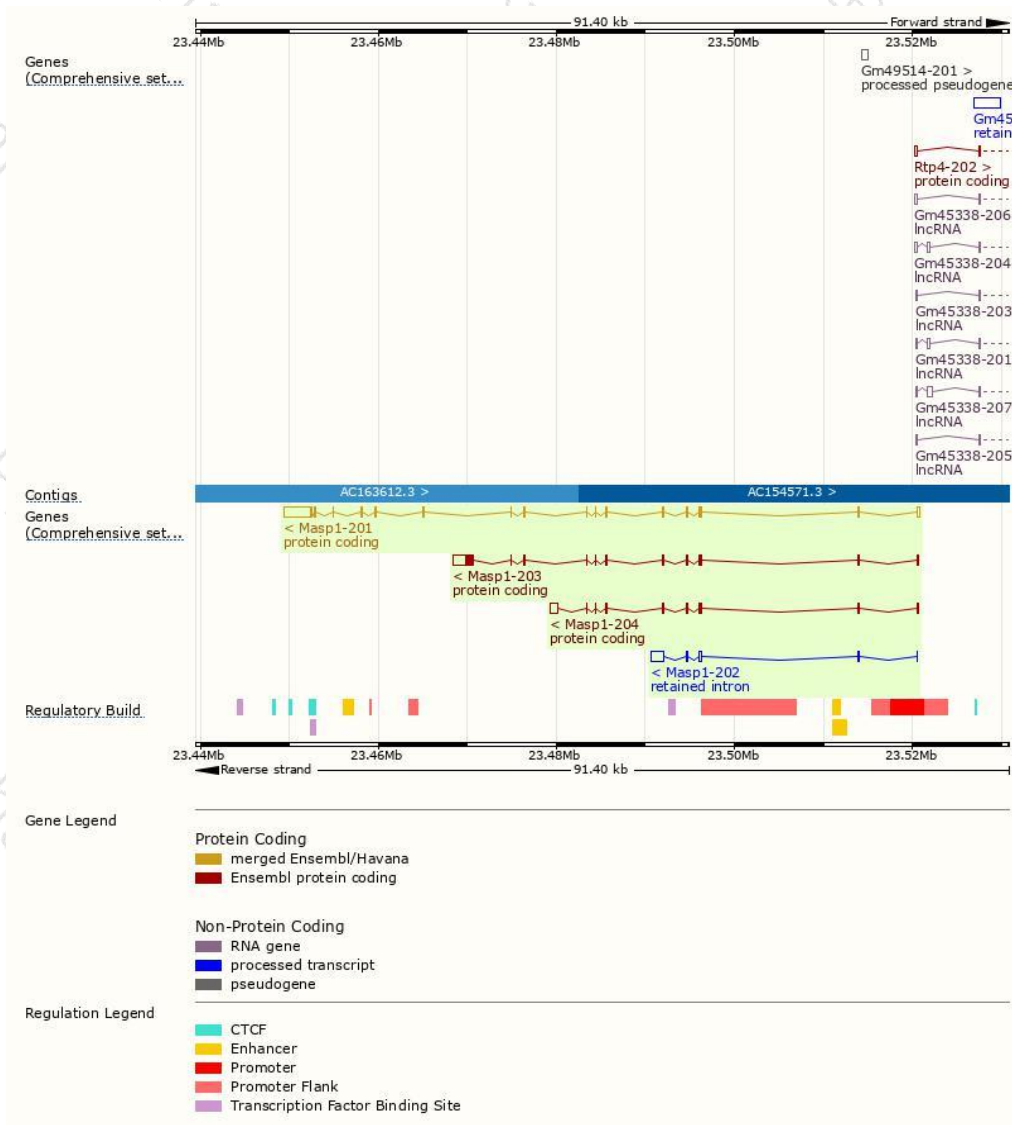
The gene has 4 transcripts,all transcripts are shown below:

Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Masp1-201	<a href="#">ENSMUST00000089883.6</a>	5345	<a href="#">704aa</a>	Protein coding	<a href="#">CCDS37303</a>	<a href="#">P98064</a>	TSL:1 GENCODE basic APPRIS P1
Masp1-202	<a href="#">ENSMUST00000229152.1</a>	2093	No protein	Retained intron	-	-	-
Masp1-203	<a href="#">ENSMUST00000229619.1</a>	3786	<a href="#">733aa</a>	Protein coding	-	<a href="#">P98064</a>	GENCODE basic
Masp1-204	<a href="#">ENSMUST00000230040.1</a>	2035	<a href="#">385aa</a>	Protein coding	-	<a href="#">A0A2R8VHR3</a>	GENCODE basic

The strategy is based on the design of *Masp1-201* transcript, the transcription is shown below:



# Genomic location distribution

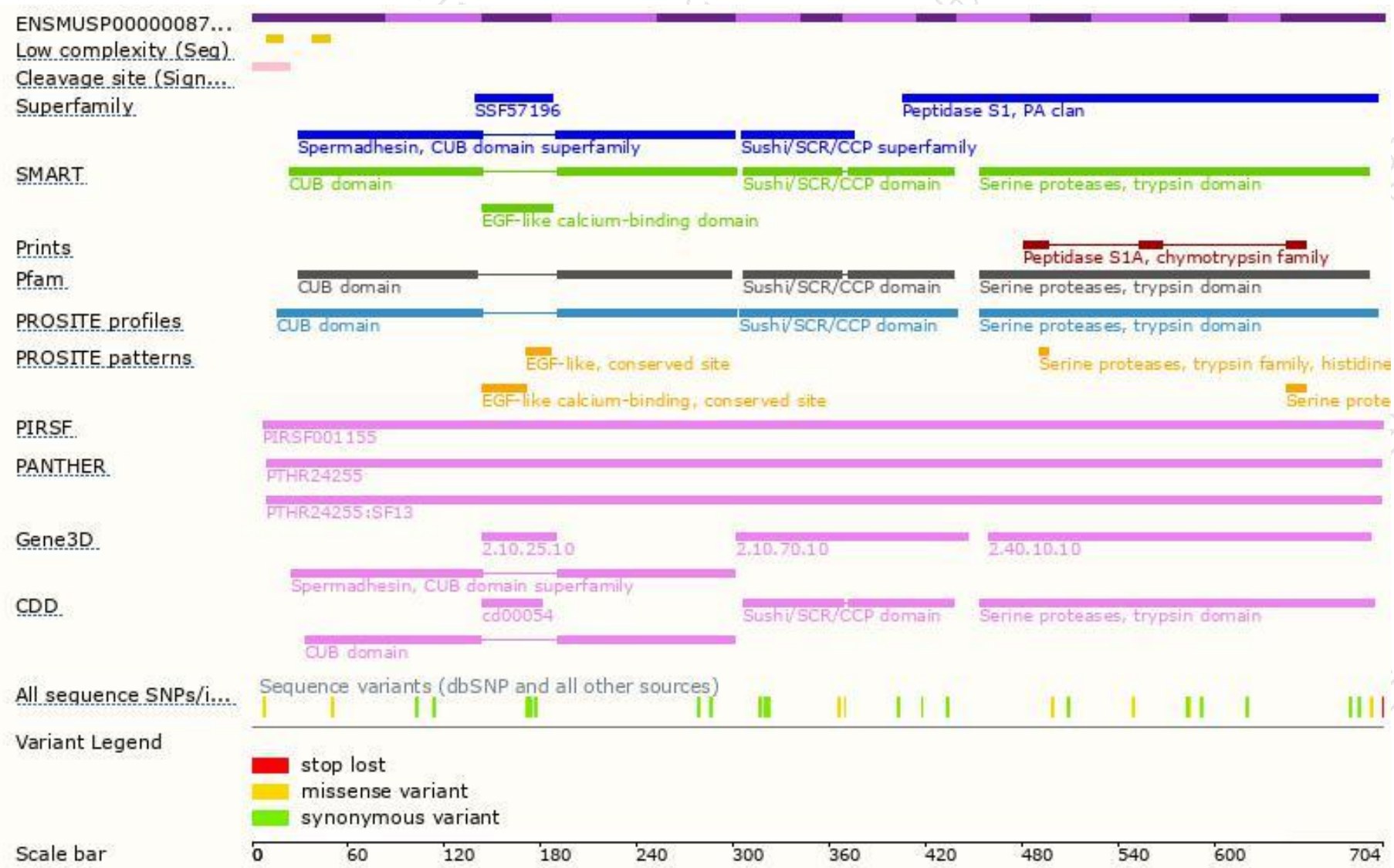




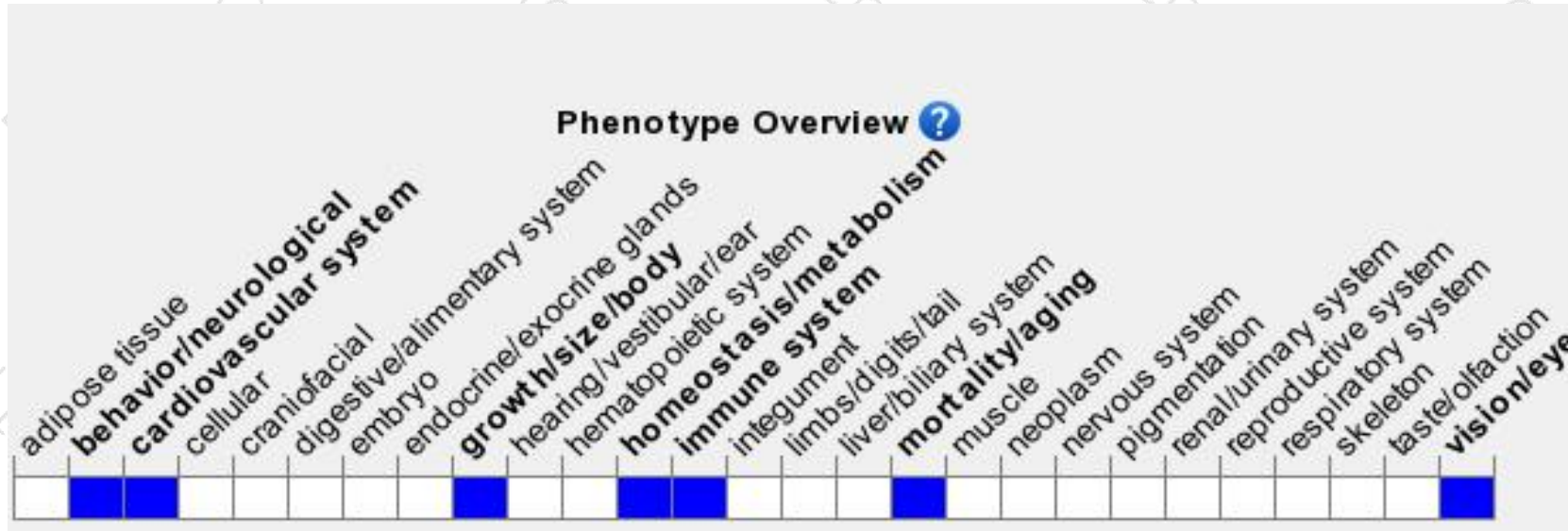
# Protein domain



集萃药康  
GemPharmatech



# 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 knockout allele display decreased survivor rate, reduced body weight, and impaired activation of the lectin and alternative complement pathways.

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

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