

# *Psmb8* Cas9-KO Strategy

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**Reviewer: Jia Yu**

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# Project Overview

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**Project Name**

***Psmb8***

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**Project type**

**Cas9-KO**

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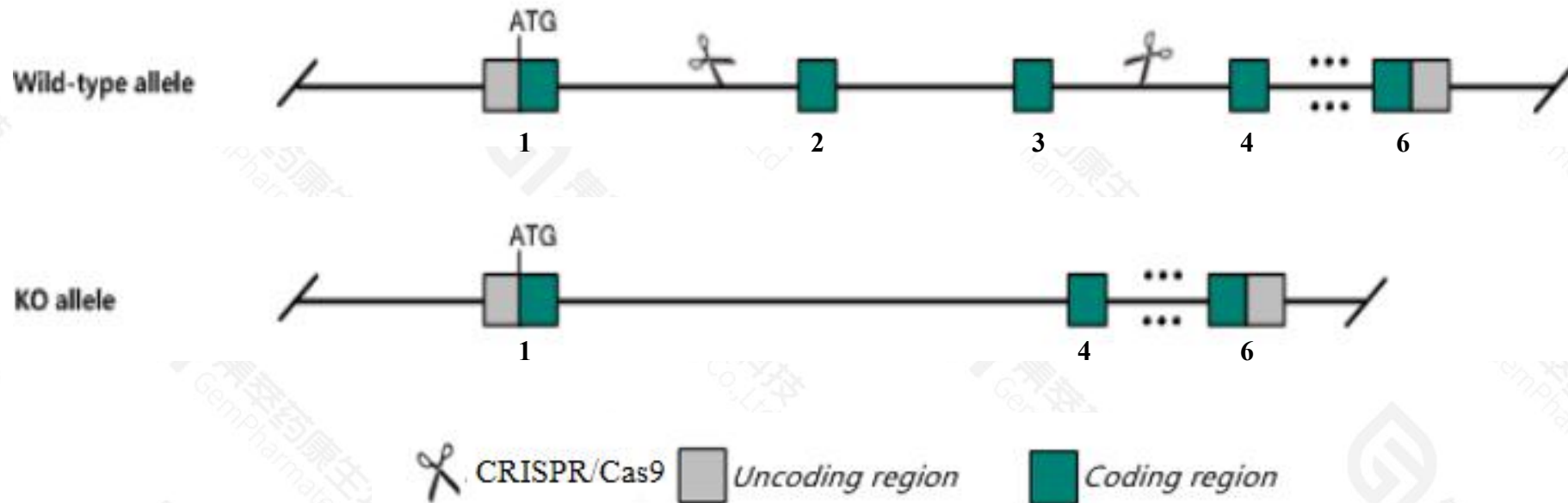
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Psmb8* gene. The schematic diagram is as follows:



- The *Psmb8* gene has 7 transcripts. According to the structure of *Psmb8* gene, exon2-exon3 of *Psmb8-201*(ENSMUST00000025196.9) transcript is recommended as the knockout region. The region contains 260bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Psmb8* gene. The brief process is as follows: CRISPR/Cas9 system 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.



- According to the existing MGI data, mice homozygous for disruptions in this gene display an essentially normal phenotype. However they have a reduced ability to process MHC class I restricted antigens.
- The effect of this strategy on *Psmb8-204* is unknown because the 5-terminus of the *Psmb8-204* is incomplete.
- The knockout region is about 3.6 kb in the 5-terminal of *Tap2*, which may affect the 5-terminal regulation function of *Tap2*.
- This strategy also knocked out *Gm20496* gene.
- The *Psmb8* gene is located on the Chr17. 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)

## Psmb8 proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7) [Mus musculus (house mouse)]

Gene ID: 16913, updated on 13-Mar-2020

### Summary



**Official Symbol** Psmb8 provided by [MGI](#)

**Official Full Name** proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7) provided by [MGI](#)

**Primary source** [MGI:MGI:1346527](#)

**See related** [Ensembl:ENSMUSG00000024338](#)

**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** Lmp-7, Lmp7

**Expression** Broad expression in thymus adult (RPKM 141.3), large intestine adult (RPKM 117.3) and 15 other tissues [See more](#)

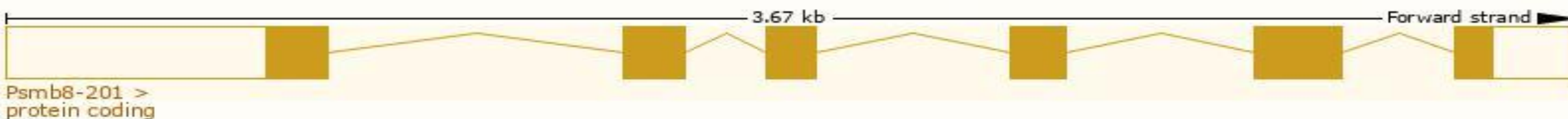
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

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

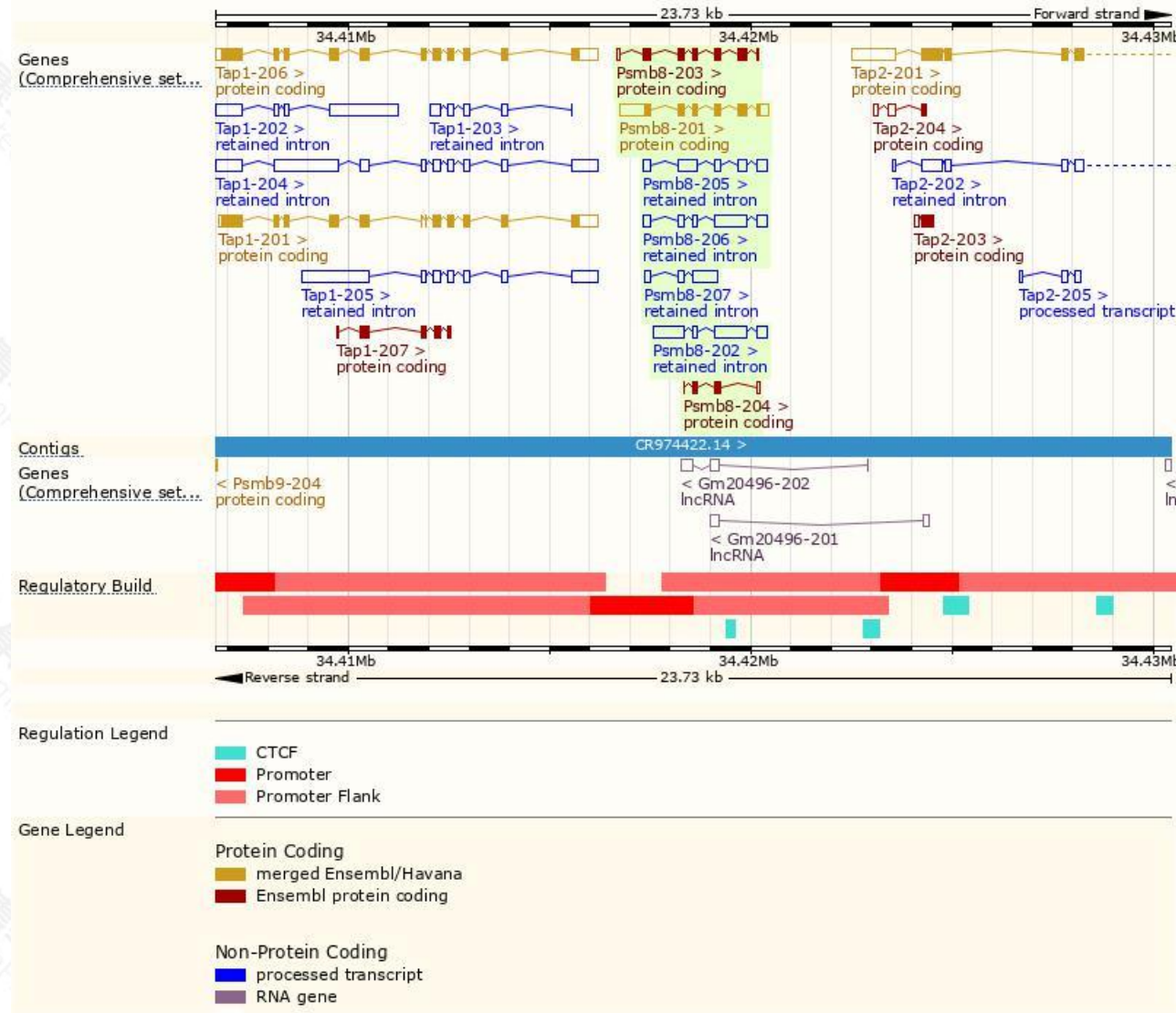
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt Match	Flags
Psmb8-201	<a href="#">ENSMUST00000025196.9</a>	1628	<a href="#">276aa</a>	Protein coding	<a href="#">CCDS50073</a>	<a href="#">P28063</a>	GENCODE basic APPRIS P1 TSL:1
Psmb8-202	<a href="#">ENSMUST00000172960.2</a>	1907	No protein	Retained intron	-	-	TSL:2
Psmb8-203	<a href="#">ENSMUST00000173441.9</a>	840	<a href="#">256aa</a>	Protein coding	-	<a href="#">G3UZW8</a>	TSL:5 CDS 3' incomplete
Psmb8-204	<a href="#">ENSMUST00000236331.2</a>	358	<a href="#">93aa</a>	Protein coding	-	<a href="#">A0A494BAB6</a>	CDS 5' incomplete
Psmb8-205	<a href="#">ENSMUST00000236557.2</a>	1234	No protein	Retained intron	-	-	-
Psmb8-206	<a href="#">ENSMUST00000237106.2</a>	1484	No protein	Retained intron	-	-	-
Psmb8-207	<a href="#">ENSMUST00000238071.2</a>	968	No protein	Retained intron	-	-	-

The strategy is based on the design of *Psmb8-201* transcript, the transcription is shown below:



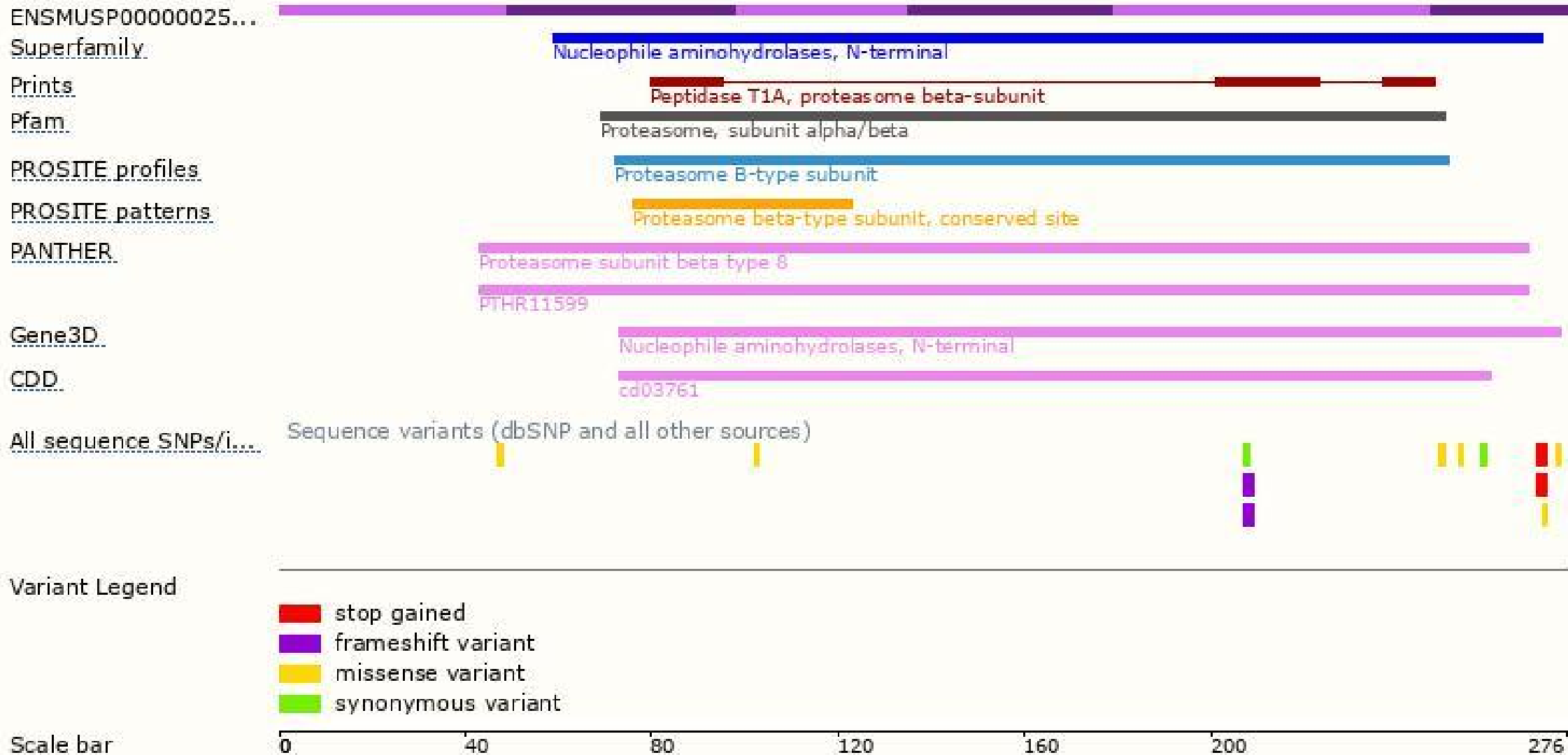


# Genomic location distribution

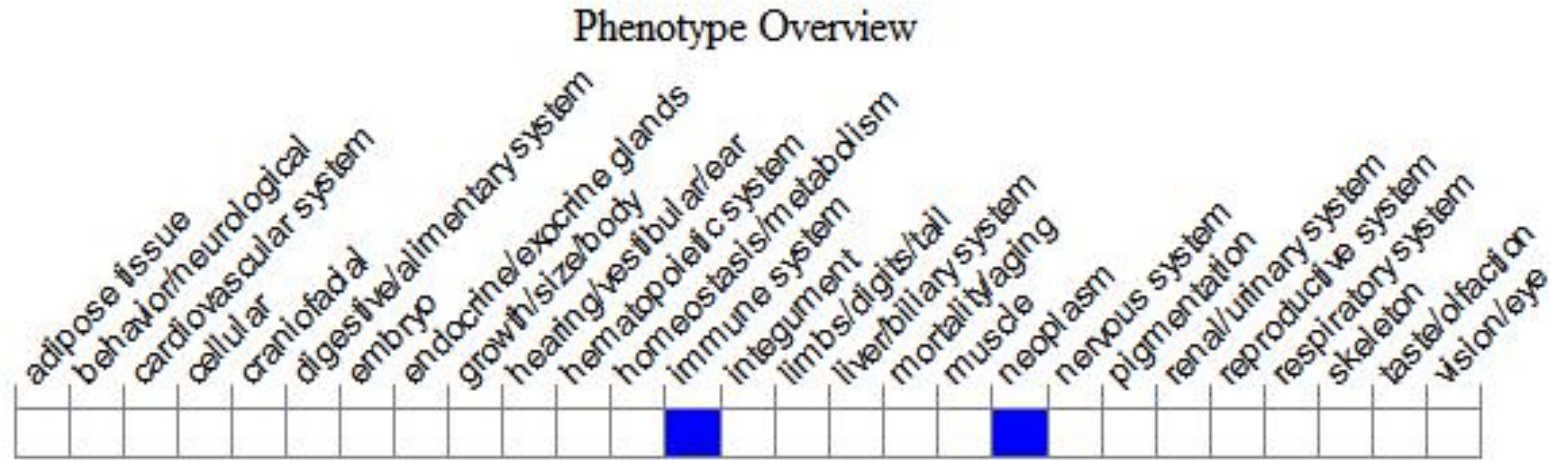




# Protein domain



# 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 disruptions in this gene display an essentially normal phenotype. However they have a reduced ability to process MHC class I restricted antigens.

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

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