

# *Psmd1* Cas9-CKO Strategy

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**Reviewer:**

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**Design Date:**

**2020-2-17**

# Project Overview

**Project Name**

***Psm $\alpha$ 1***

**Project type**

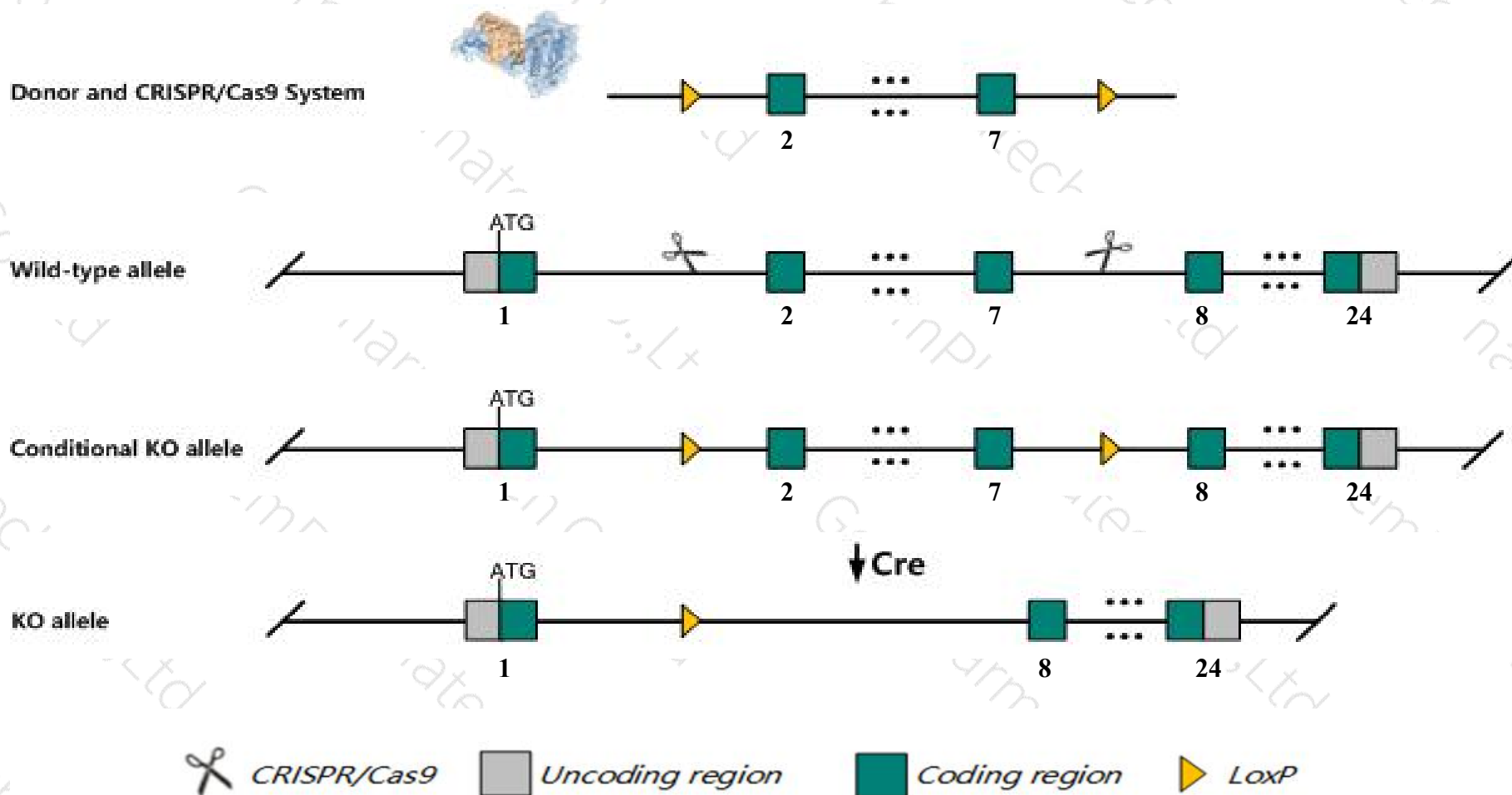
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Psmd1* gene. The schematic diagram is as follows:



- The *Psmcl* gene has 9 transcripts. According to the structure of *Psmcl* gene, exon2-exon7 of *Psmcl*-201 (ENSMUST00000027432.8) transcript is recommended as the knockout region. The region contains 865bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Psmcl* 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 *Psmcl* gene is located on the Chr1. 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)

## Psmd1 proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 [Mus musculus (house mouse)]

Gene ID: 70247, updated on 31-Jan-2019

### Summary



**Official Symbol** Psmd1 provided by [MGI](#)

**Official Full Name** proteasome (prosome, macropain) 26S subunit, non-ATPase, 1 provided by [MGI](#)

**Primary source** [MGI:MGI:1917497](#)

**See related** [Ensembl:ENSMUSG000000026229](#)

**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** 2410026J11Rik, P112, S1

**Summary** In eukaryotic cells, most proteins in the cytosol and nucleus are degraded via the ubiquitin-proteasome pathway. The 26S proteasome is a self-compartmentalizing protease comprised of approximately 31 different subunits. It contains a barrel-shaped proteolytic core complex (the 20S proteasome), capped at one or both ends by 19S regulatory complexes, which recognize ubiquitinated proteins. Protein degradation by proteasomes is the source of most antigenic peptides presented on MHC class I molecules. This gene encodes a non-ATPase subunit of the 26S proteasome. [provided by RefSeq, Jul 2008]

**Expression** Ubiquitous expression in CNS E11.5 (RPKM 41.0), placenta adult (RPKM 37.7) and 28 other tissues [See more](#)

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

# Transcript information (Ensembl)

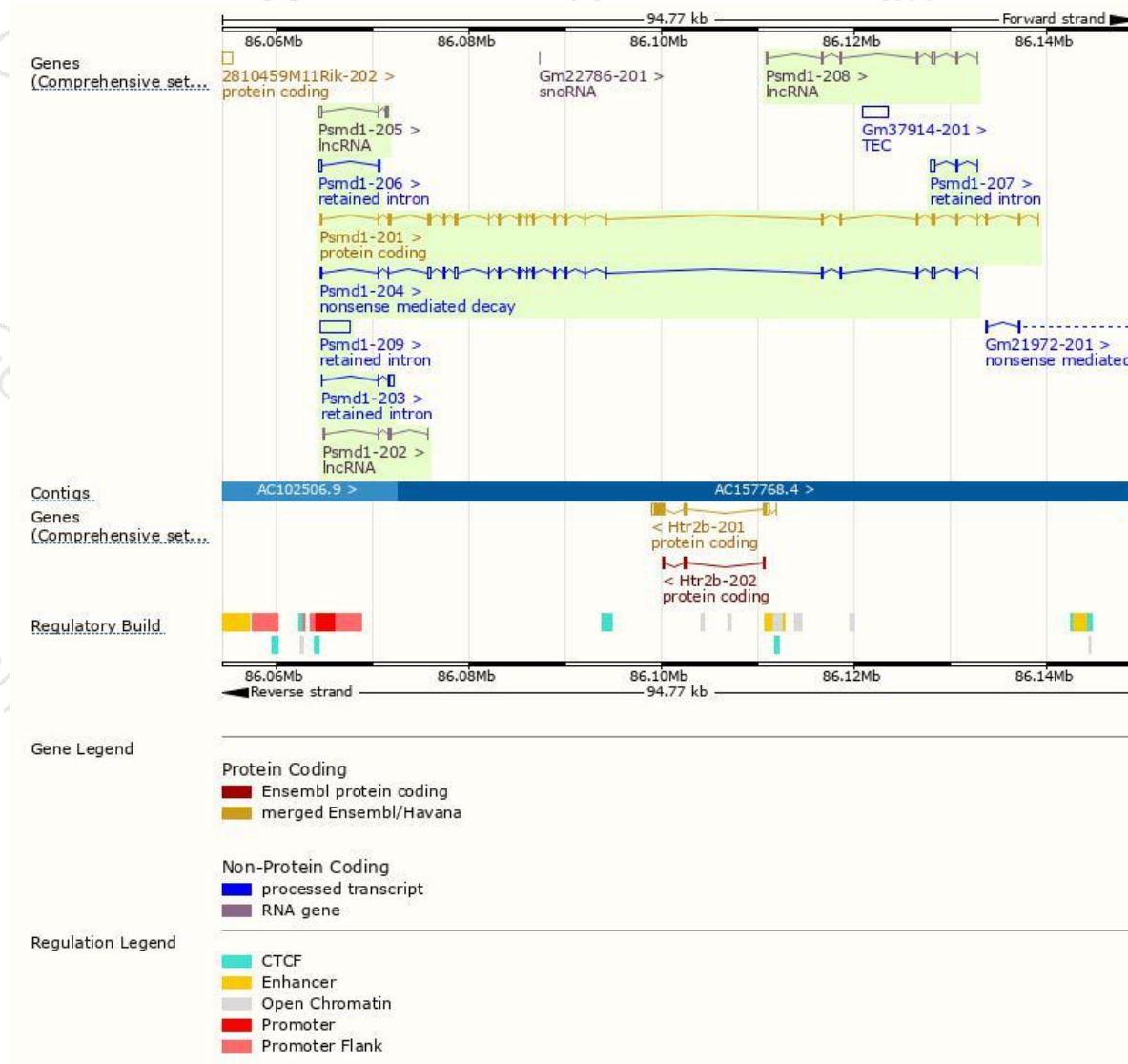
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psmc1-201	<a href="#">ENSMUST00000027432.8</a>	3112	<a href="#">953aa</a>	Protein coding	<a href="#">CCDS15117</a>	<a href="#">Q3TXS7</a>	TSL:1 GENCODE basic APPRIS P1
Psmc1-204	<a href="#">ENSMUST00000139715.7</a>	2518	<a href="#">48aa</a>	Nonsense mediated decay	-	<a href="#">D6RGR5</a>	TSL:5
Psmc1-209	<a href="#">ENSMUST00000189234.1</a>	3022	No protein	Retained intron	-	-	TSL:NA
Psmc1-203	<a href="#">ENSMUST00000133480.7</a>	690	No protein	Retained intron	-	-	TSL:2
Psmc1-206	<a href="#">ENSMUST00000147807.7</a>	613	No protein	Retained intron	-	-	TSL:2
Psmc1-207	<a href="#">ENSMUST00000149946.1</a>	586	No protein	Retained intron	-	-	TSL:2
Psmc1-208	<a href="#">ENSMUST00000152184.1</a>	939	No protein	lncRNA	-	-	TSL:5
Psmc1-205	<a href="#">ENSMUST00000143200.7</a>	613	No protein	lncRNA	-	-	TSL:3
Psmc1-202	<a href="#">ENSMUST00000127104.1</a>	445	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Psmc1-201* transcript,The transcription is shown below

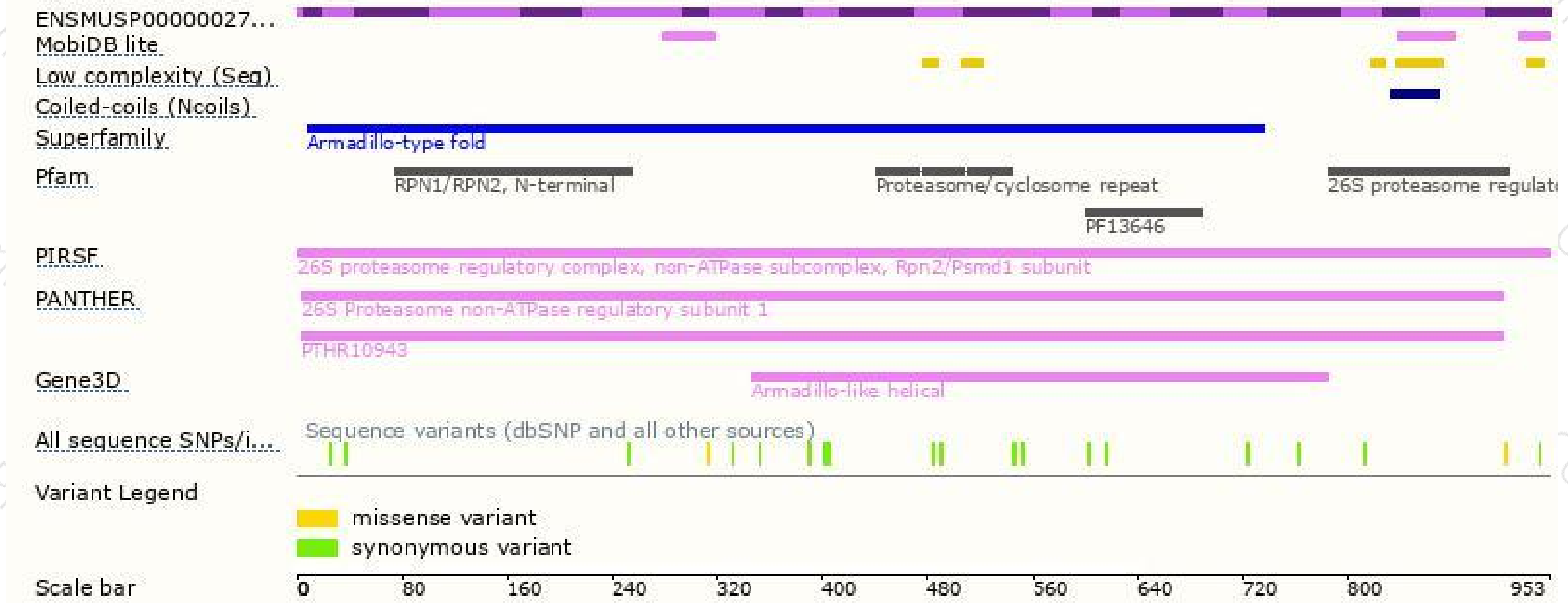


# Genomic location distribution





# Protein domain



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

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