

# ***Psm*****d11 Cas9-KO Strategy**

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**Reviewer:**

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**Design Date:**

**2020-8-4**

# Project Overview

**Project Name**

***Psm $\alpha$ 11***

**Project type**

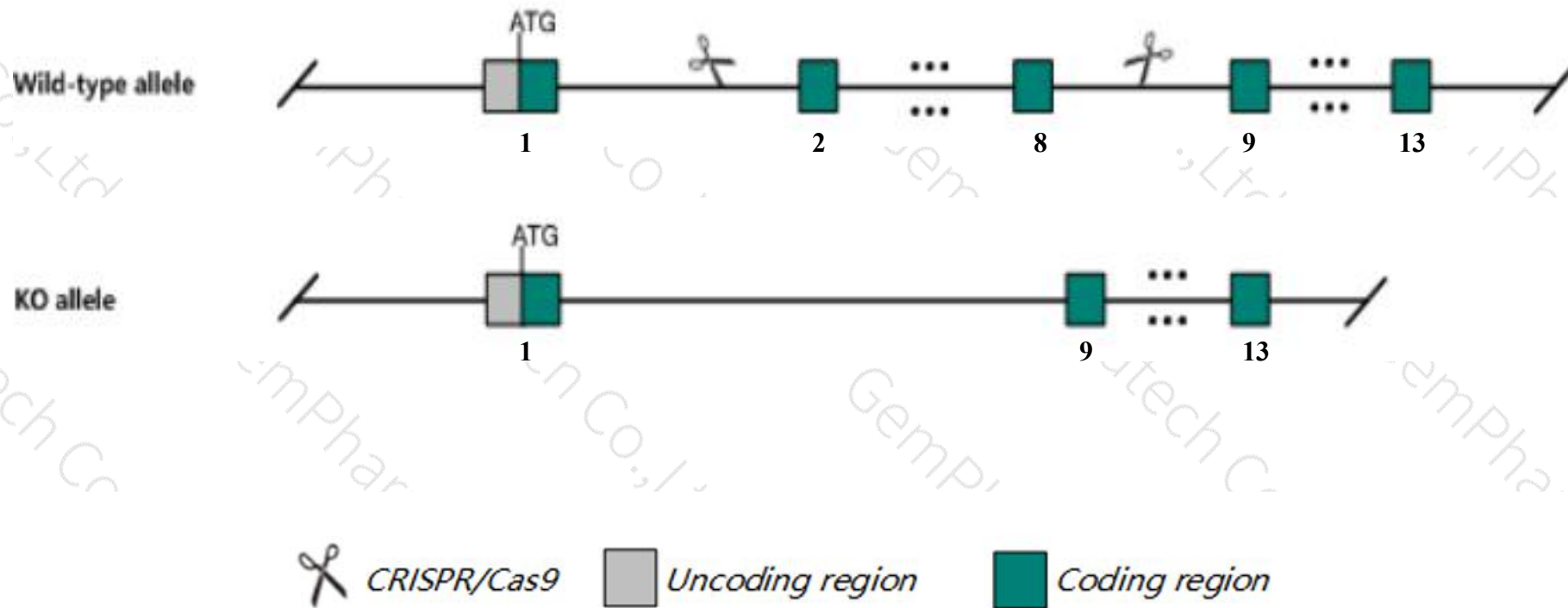
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Psm $\alpha$ 11* gene. The schematic diagram is as follows:



- The *Psmc11* gene has 15 transcripts. According to the structure of *Psmc11* gene, exon2-exon8 of *Psmc11-201* (ENSMUST00000017572.13) transcript is recommended as the knockout region. The region contains 758bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Psmc11* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Psmc11* gene is located on the Chr11. 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)

## Psmd11 proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 [Mus musculus (house mouse)]

Gene ID: 69077, updated on 13-Mar-2020

### Summary



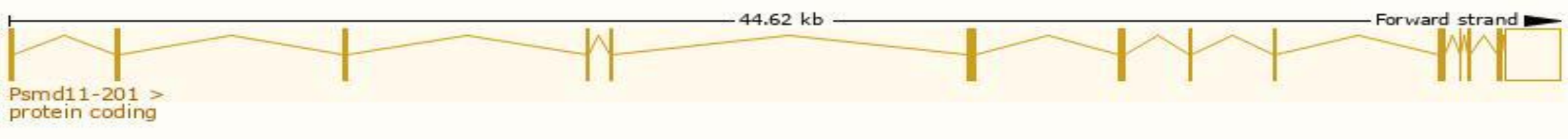
<b>Official Symbol</b>	Psmd11 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1916327</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000017428</a>
<b>Gene 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>	1700089D09Rik, 1810019E17Rik, 2610024G20Rik, 2810055C24Rik, C78232, P44.5, S9
<b>Expression</b>	Ubiquitous expression in CNS E11.5 (RPKM 25.8), liver E14 (RPKM 25.4) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information（Ensembl）

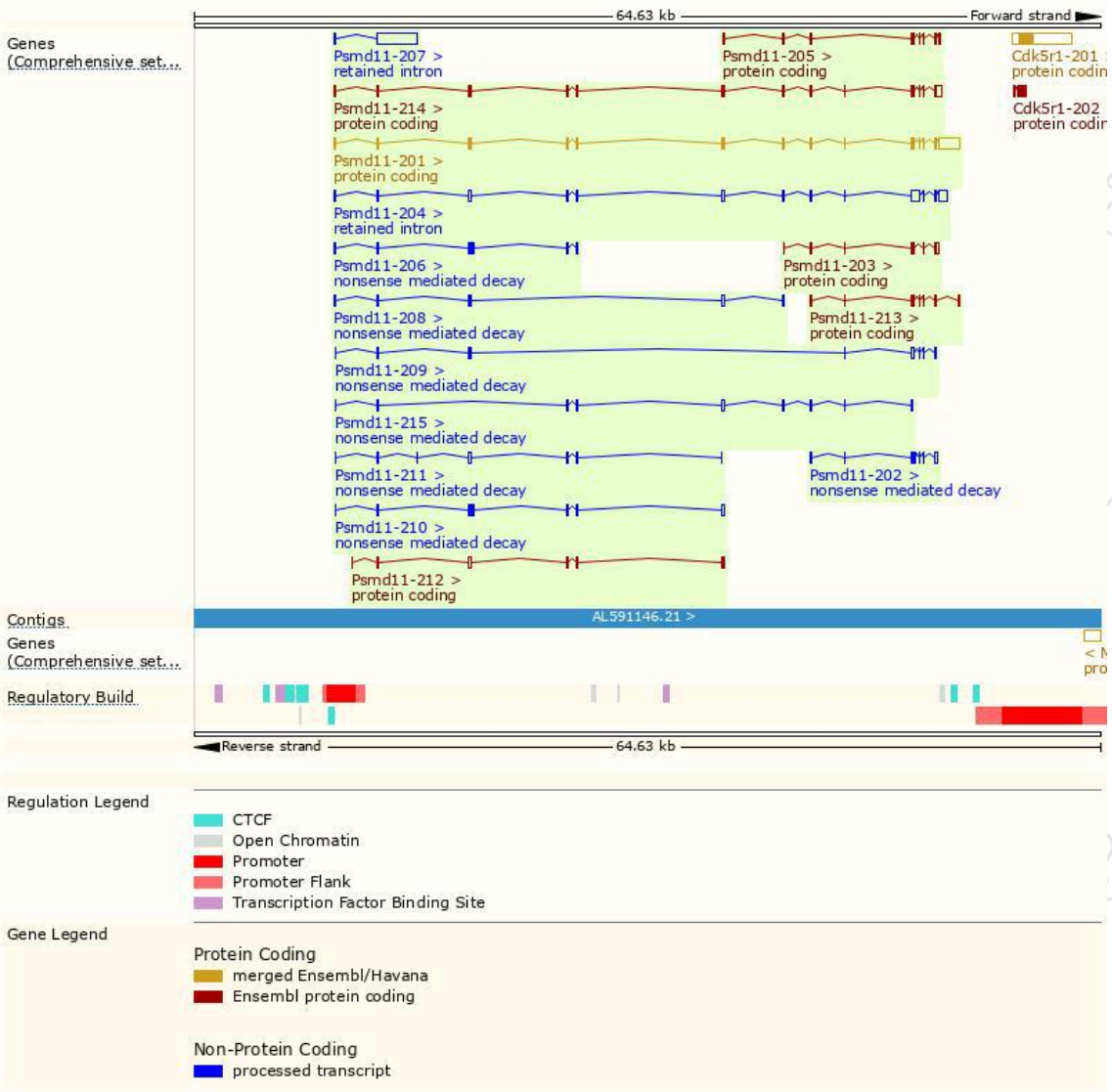
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psmid11-201	<a href="#">ENSMUST00000017572.13</a>	2848	<a href="#">422aa</a>	Protein coding	<a href="#">CCDS25133</a>	<a href="#">Q5BKQ9_Q8BG32</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Psmid11-214	<a href="#">ENSMUST000000173938.7</a>	1626	<a href="#">422aa</a>	Protein coding	<a href="#">CCDS25133</a>	<a href="#">Q5BKQ9_Q8BG32</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Psmid11-205	<a href="#">ENSMUST000000148895.8</a>	796	<a href="#">209aa</a>	Protein coding	-	<a href="#">G3UYH2</a>	CDS 5' incomplete TSL:5
Psmid11-213	<a href="#">ENSMUST000000173797.7</a>	637	<a href="#">160aa</a>	Protein coding	-	<a href="#">G3UXL5</a>	CDS 5' incomplete TSL:5
Psmid11-212	<a href="#">ENSMUST000000173565.1</a>	600	<a href="#">114aa</a>	Protein coding	-	<a href="#">G3UZ33</a>	CDS 3' incomplete TSL:3
Psmid11-203	<a href="#">ENSMUST000000129500.7</a>	597	<a href="#">158aa</a>	Protein coding	-	<a href="#">G3UWW7</a>	CDS 5' incomplete TSL:3
Psmid11-215	<a href="#">ENSMUST000000174743.7</a>	847	<a href="#">89aa</a>	Nonsense mediated decay	-	<a href="#">G3UWV7</a>	CDS 5' incomplete TSL:5
Psmid11-210	<a href="#">ENSMUST000000173060.1</a>	717	<a href="#">100aa</a>	Nonsense mediated decay	-	<a href="#">G3UX15</a>	CDS 5' incomplete TSL:5
Psmid11-209	<a href="#">ENSMUST000000172847.7</a>	655	<a href="#">100aa</a>	Nonsense mediated decay	-	<a href="#">G3UYL8</a>	CDS 5' incomplete TSL:5
Psmid11-202	<a href="#">ENSMUST000000125591.2</a>	627	<a href="#">95aa</a>	Nonsense mediated decay	-	<a href="#">G3UZ28</a>	CDS 5' incomplete TSL:2
Psmid11-208	<a href="#">ENSMUST000000172773.7</a>	609	<a href="#">113aa</a>	Nonsense mediated decay	-	<a href="#">G3UYI4</a>	TSL:5
Psmid11-206	<a href="#">ENSMUST000000172615.7</a>	581	<a href="#">116aa</a>	Nonsense mediated decay	-	<a href="#">G3UYL3</a>	TSL:5
Psmid11-211	<a href="#">ENSMUST000000173186.7</a>	493	<a href="#">67aa</a>	Nonsense mediated decay	-	<a href="#">G3UX67</a>	CDS 5' incomplete TSL:5
Psmid11-207	<a href="#">ENSMUST000000172641.1</a>	2975	No protein	Retained intron	-	-	TSL:2
Psmid11-204	<a href="#">ENSMUST000000147898.7</a>	2342	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Psmid11-201* 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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