

# **Psmd11** Cas9-KO Strategy

2020-8-4

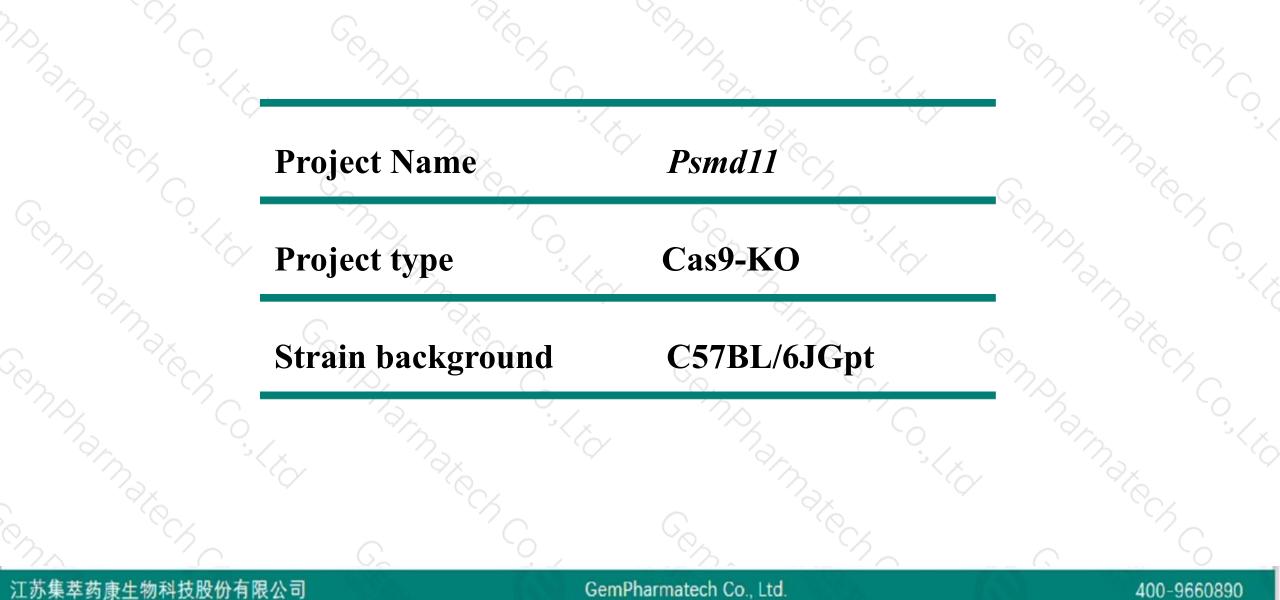
Designer: Reviewer:

**Design Date:** 

Huan Wang Shanhong Tao

### **Project Overview**

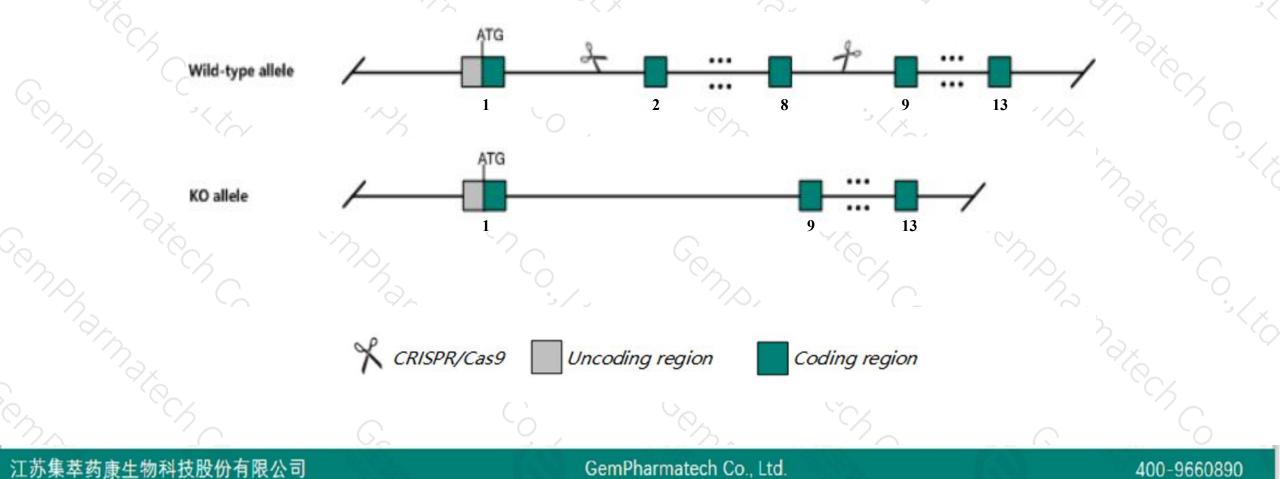




# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Psmd11* gene. The schematic diagram is as follows:





- The Psmd11 gene has 15 transcripts. According to the structure of Psmd11 gene, exon2-exon8 of Psmd11-201 (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 *Psmd11* gene. The brief process is as follows: CRISPR/Cas9 system

- The Psmd11 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.

Notice

# **Gene information** (NCBI)



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

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

#### Summary

Psmd11 provided by MGI
proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 provided by MGI
MGI:MGI:1916327
Ensembl:ENSMUSG0000017428
protein coding
VALIDATED
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muroidea; Muridae; Murinae; Mus; Mus
1700089D09Rik, 1810019E17Rik, 2610024G20Rik, 2810055C24Rik, C78232, P44.5, S9
Ubiquitous expression in CNS E11.5 (RPKM 25.8), liver E14 (RPKM 25.4) and 28 other tissues See more
human all

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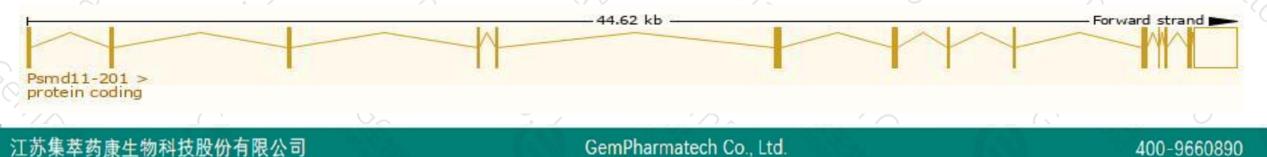
## **Transcript information (Ensembl)**



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

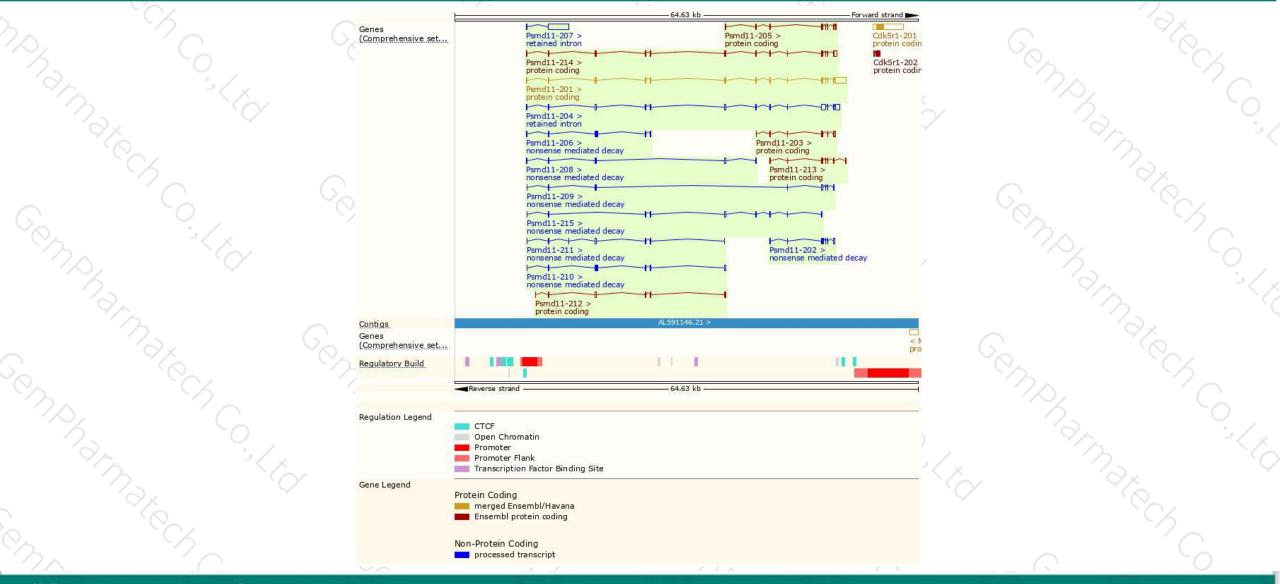
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags			
ENSMUST00000017572.13	2848	<u>422aa</u>	Protein coding	CCDS25133	Q5BKQ9 Q8BG32	IG32 TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APP			
ENSMUST00000173938.7	1626	<u>422aa</u>	Protein coding	CCDS25133	<u>058KQ9 088G32</u>	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.			
ENSMUST00000148895.8	796	<u>209aa</u>	Protein coding	2	G3UYH2	CDS 5' incomplete TSL:5			
ENSMUST00000173797.7	637	<u>160aa</u>	Protein coding	-	G3UXL5	CDS 5' incomplete TSL:5			
ENSMUST00000173565.1	600	<u>114aa</u>	Protein coding	-	<u>G3UZ33</u>	CDS 3' incomplete TSL:3			
ENSMUST00000129500.7	597	<u>158aa</u>	Protein coding	-	<u>G3UWW7</u>	CDS 5' incomplete TSL:3			
ENSMUST00000174743.7	847	<u>89aa</u>	Nonsense mediated decay	2	G3UWV7	CDS 5' incomplete TSL:5			
ENSMUST00000173060.1	717	<u>100aa</u>	Nonsense mediated decay	-	G3UX15	CDS 5' incomplete TSL:5			
ENSMUST00000172847.7	655	<u>100aa</u>	Nonsense mediated decay	-	G3UYL8	CDS 5' incomplete TSL:5			
ENSMUST00000125591.2	627	<u>95aa</u>	Nonsense mediated decay	-	<u>G3UZ28</u>	CDS 5' incomplete TSL:2			
ENSMUST00000172773.7	609	<u>113aa</u>	Nonsense mediated decay	-	G3UYI4	TSL:5			
ENSMUST00000172615.7	581	<u>116aa</u>	Nonsense mediated decay	-	G3UYL3	TSL:5			
ENSMUST00000173186.7	493	<u>67aa</u>	Nonsense mediated decay		<u>G3UX67</u>	CDS 5' incomplete TSL:5			
ENSMUST00000172641.1	2975	No protein	Retained intron	-		TSL:2			
ENSMUST00000147898.7	2342	No protein	Retained intron	-	-	TSL1			
	ENSMUST0000017572.13 ENSMUST00000173938.7 ENSMUST00000173938.7 ENSMUST00000173797.7 ENSMUST00000173797.7 ENSMUST00000173565.1 ENSMUST00000174743.7 ENSMUST00000174743.7 ENSMUST00000172847.7 ENSMUST00000172659.12 ENSMUST00000172615.7 ENSMUST00000173186.7 ENSMUST00000173186.7	ENSMUST0000017572.13 2848   ENSMUST00000173938.7 1626   ENSMUST00000173938.7 637   ENSMUST00000173797.7 637   ENSMUST00000173797.7 637   ENSMUST0000017356.1 600   ENSMUST0000012550.7 597   ENSMUST00000174743.7 847   ENSMUST00000174743.7 655   ENSMUST00000172847.7 655   ENSMUST00000125591.2 627   ENSMUST0000017273.7 609   ENSMUST00000173186.7 493   ENSMUST00000173186.7 493	ENSMUST0000017572.13 2848 422aa   ENSMUST0000173938.7 1626 422aa   ENSMUST0000173938.7 1604 209aa   ENSMUST0000173797.7 637 160aa   ENSMUST0000173797.7 637 158aa   ENSMUST0000173797.7 597 158aa   ENSMUST0000174743.7 647 89aa   ENSMUST000017366.1 717 100aa   ENSMUST0000172847.7 655 100aa   ENSMUST000017277.7 609 113aa   ENSMUST0000172615.7 581 116aa   ENSMUST0000173186.7 493 67aa	ENSMUST0000017572.132848422aaProtein codingENSMUST00000173938.71626422aaProtein codingENSMUST00000148895.8796209aaProtein codingENSMUST00000173797.7637160aaProtein codingENSMUST00000173565.1600114aaProtein codingENSMUST00000129500.7597158aaProtein codingENSMUST00000174743.784789aaNonsense mediated decayENSMUST00000172847.7655100aaNonsense mediated decayENSMUST00000125591.262795aaNonsense mediated decayENSMUST0000017273.7609113aaNonsense mediated decayENSMUST00000172615.7581116aaNonsense mediated decayENSMUST00000173186.749367aaNonsense mediated decayENSMUST00000172641.12975No proteinRetained intron	ENSMUST0000017572.132848422aaProtein codingCCDS25133ENSMUST00000173938.71626422aaProtein codingCCDS25133ENSMUST00000148895.8796209aaProtein coding-ENSMUST00000173797.7637160aaProtein coding-ENSMUST00000173565.1600114aaProtein coding-ENSMUST00000129500.7597158aaProtein coding-ENSMUST00000174743.784789aaNonsense mediated decay-ENSMUST00000172847.7655100aaNonsense mediated decay-ENSMUST00000125591.262795aaNonsense mediated decay-ENSMUST0000017273.7609113aaNonsense mediated decay-ENSMUST00000172615.7581116aaNonsense mediated decay-ENSMUST00000173186.749367aaNonsense mediated decay-ENSMUST00000172641.12976No proteinRetained intron-	ENSMUST0000017572.132848422aaProtein codingCCDS25133Q5BKQ9 Q8BG32ENSMUST00000173938.71626422aaProtein codingCCDS25133Q5BKQ9 Q8BG32ENSMUST0000173938.71626422aaProtein codingCCDS25133Q5BKQ9 Q8BG32ENSMUST0000148895.8796209aaProtein codingG3UYH2ENSMUST0000173797.7637160aaProtein codingG3UXL5ENSMUST0000173565.1600114aaProtein codingG3UWY7ENSMUST0000172500.7597158aaProtein codingG3UWY7ENSMUST0000174743.764789aaNonsense mediated decayG3UWY7ENSMUST0000172847.7655100aaNonsense mediated decayG3UYL8ENSMUST0000017273.7609113aaNonsense mediated decayG3UY14ENSMUST00000172615.7581116aaNonsense mediated decayG3UY13ENSMUST00000173186.749367aaNonsense mediated decayG3UY13ENSMUST00000172641.1297Non orteinRetained intronG3UX67			

The strategy is based on the design of Psmd11-201 transcript, the transcription is shown below



### **Genomic location distribution**





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### **Protein domain**



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If you have any questions, you are welcome to inquire. Tel: 400-9660890



