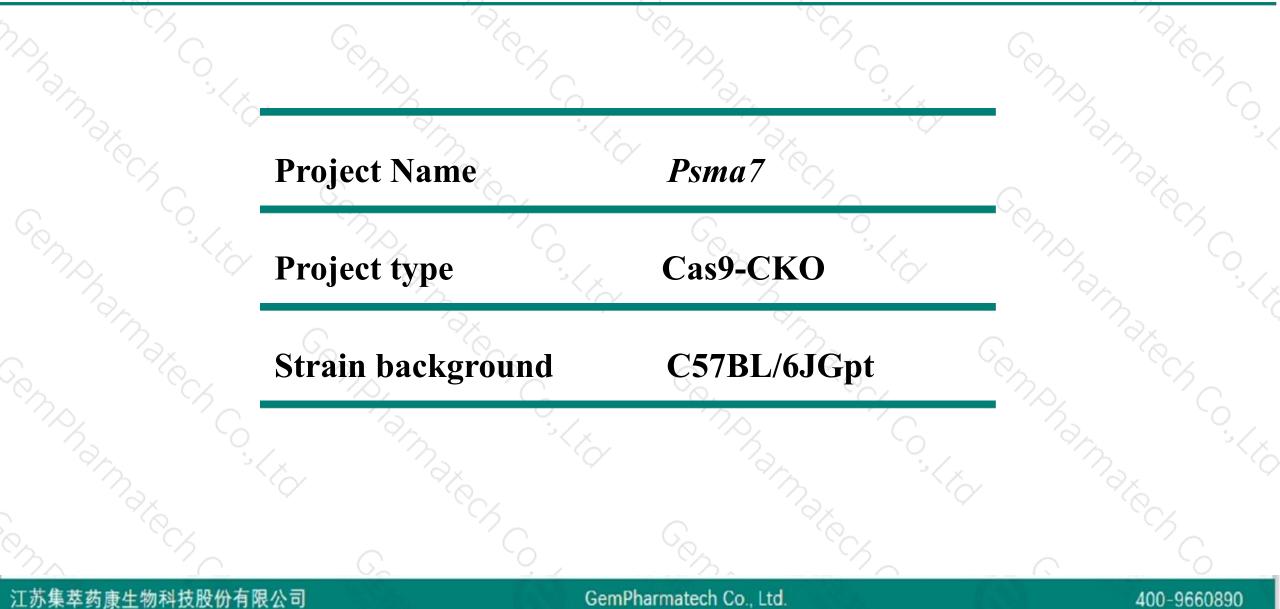


# Psma7 Cas9-CKO Strategy

Designer:Xueting Zhang Reviewer:Yanhua Shen Date:2019-10-20

### **Project Overview**

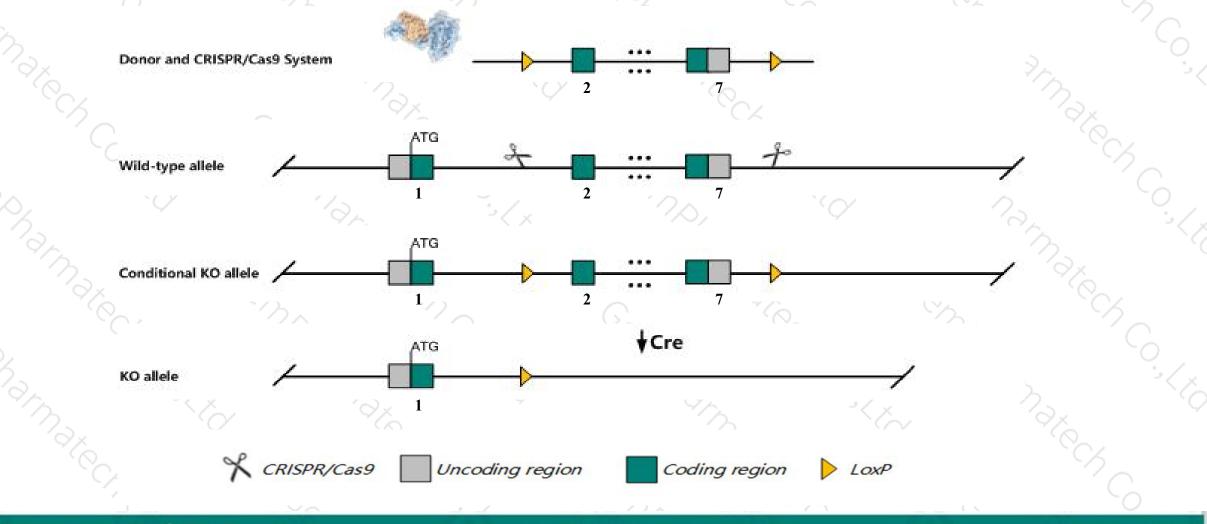




### **Conditional Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Psma7* gene. The schematic diagram is as follows:



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The Psma7 gene has 7 transcripts. According to the structure of Psma7 gene, exon2-exon7 of Psma7-201 (ENSMUST00000029082.8) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Psma7* 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.

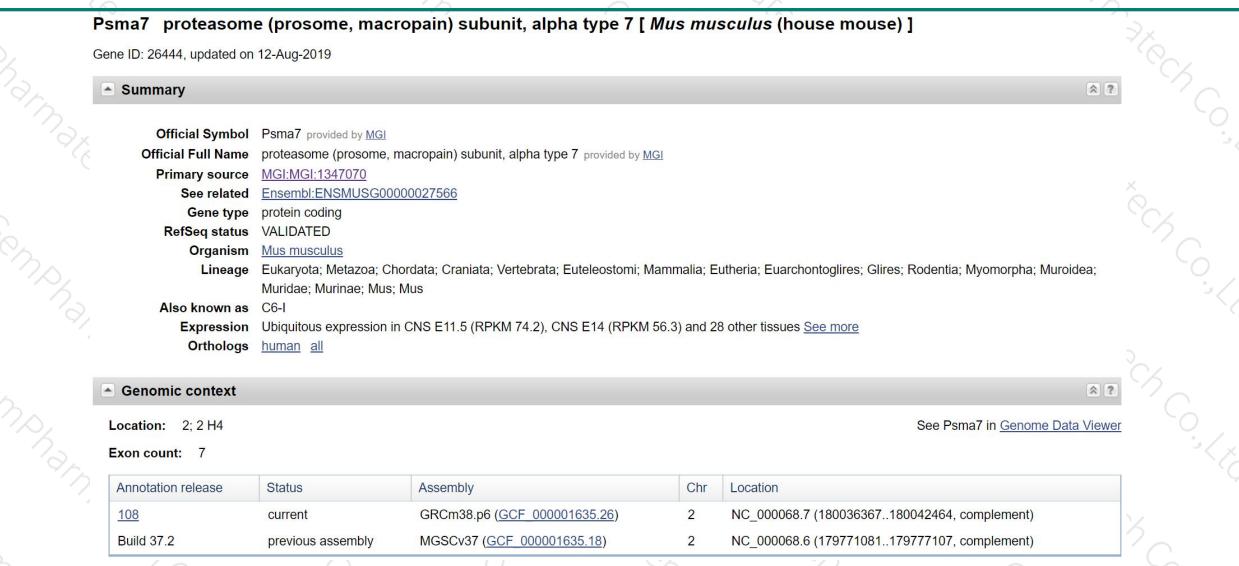
The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



- The floxed region is near to the N-terminal of Ss1811 gene and C-terminal of Lsm14b gene, this strategy may influence the regulatory function of the N-terminal of Ss1811 gene and C-terminal of Lsm14b gene.
- The Psma7 gene is located on the Chr2. 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)





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## **Transcript information (Ensembl)**



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

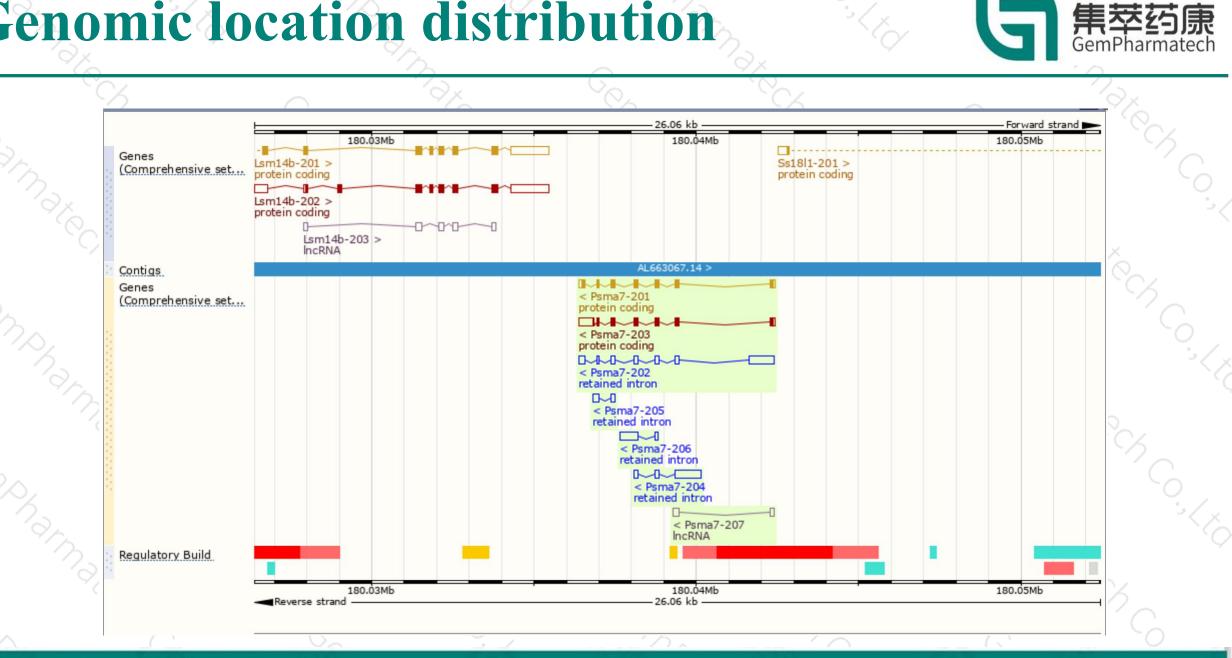
	1 1 1						(			
	Name 🍦	Transcript ID 🝦 bp 🖕 Protein 🧅		Biotype 🍦	CCDS	UniProt 🍦	Flags 🍦			
	Psma7-201	ENSMUST0000029082.8	914	<u>248aa</u>	Protein coding	<u>CCDS17166</u> &	<u>Q542H2</u> & <u>Q9Z2U0</u> &	TSL:1 GENCODE basic APPRIS P1		
	Psma7-203	ENSMUST00000129529.8	1157	<u>223aa</u>	Protein coding	-	<u>A0A338P7D7</u> &	TSL:5 GENCODE basic		
	Psma7-202	ENSMUST00000126021.7	1515	No protein	Retained intron	-	-	TSL:1		
5	Psma7-204	ENSMUST00000132431.1	1037	No protein	Retained intron	-	-	TSL:2		
	Psma7-206	ENSMUST00000142042.1	651	No protein	Retained intron	-		TSL:3		
	Psma7-205	ENSMUST00000135650.1	288	No protein	Retained intron	-		TSL:3		
	Psma7-207	ENSMUST00000155898.1	292	No protein	IncRNA	-		TSL:2		

The strategy is based on the design of Psma7-201 transcript, The transcription is shown below

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### **Genomic location distribution**



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### **Protein domain**



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	ENSMUSP00000029 PDB-ENSP mappings Low complexity (Seg) Coiled-coils (Ncoils)							_		
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Ò	<u>Pfam</u>		a-subunit, N-terminal do Proteasome, subunit alph						~~~~	
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	PROSITE patterns		a-subunit, N-terminal do						~~~	
-	PANTHER	Proteasome subur	it alpha 7							
1	-	PTHR11599								
	Gene3D	Nucleophile aminohydrolases, N-terminal								
5	CDD	cd03755								
2	All sequence SNPs/i	Sequence variar	ts (dbSNP and all othe	r sources)	1 11	1.1	п.	1.1	0	
	Variant Legend	synonymou	s variant							
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



