

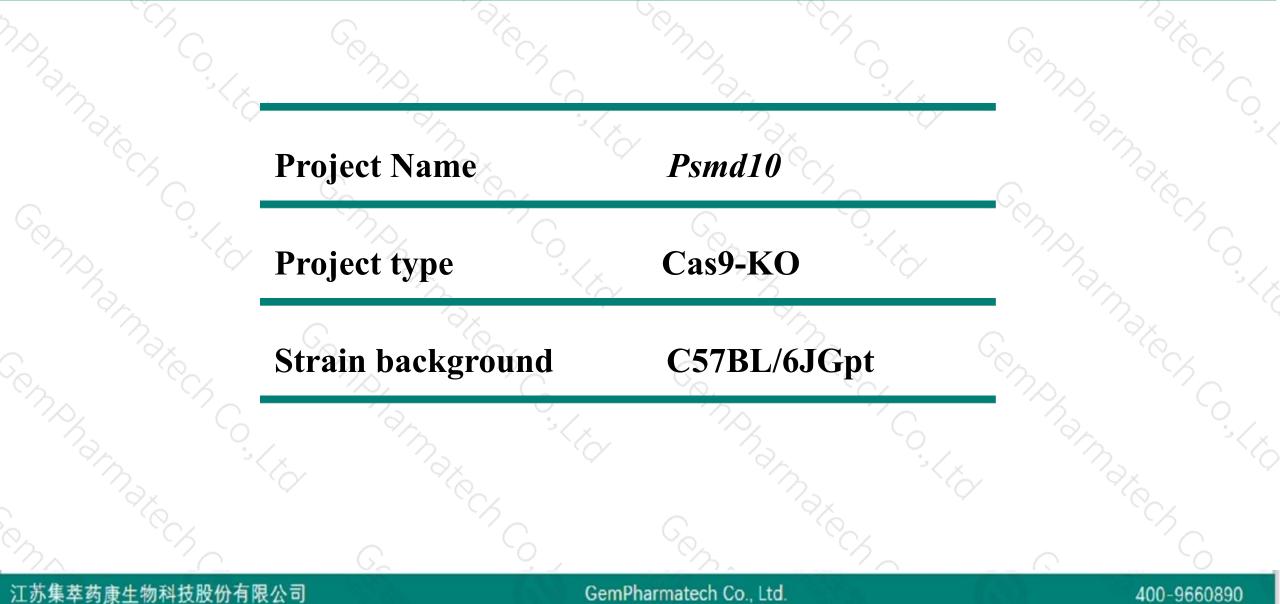
# Companyated .... **Psmd10** Cas9-KO Strategy Romphamater Control

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## **Project Overview**

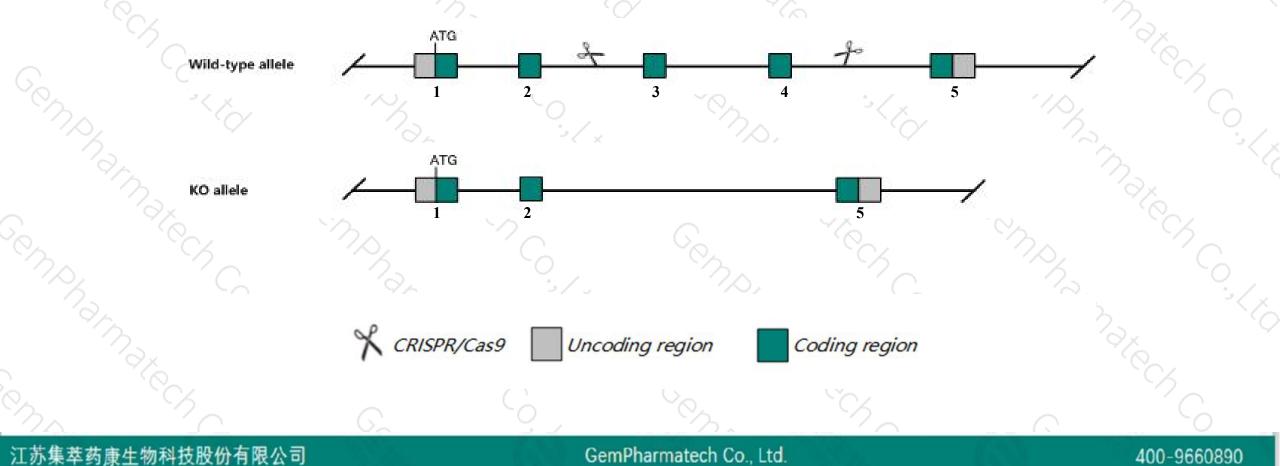




# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Psmd10* gene. The schematic diagram is as follows:





- The Psmd10 gene has 2 transcripts. According to the structure of Psmd10 gene, exon3-exon4 of Psmd10-201 (ENSMUST00000033805.14) transcript is recommended as the knockout region. The region contains 314bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Psmd10* gene. The brief process is as follows: CRISPR/Cas9 syste

- The Psmd10 gene is located on the ChrX. 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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#### Psmd10 proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 [Mus musculus (house mouse)]

Gene ID: 53380, updated on 31-Jan-2019

#### Summary

Official Symbol	Psmd10 provided by MGI
Official Full Name	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 provided by MGI
Primary source	MGI:MGI:1858898
See related	Ensembl:ENSMUSG00000031429
Gene type	protein coding
<b>RefSeq status</b>	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	AW554874
Expression	Ubiquitous expression in liver E14 (RPKM 11.2), placenta adult (RPKM 10.3) and 24 other tissues See more
Orthologs	human all

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# **Transcript information (Ensembl)**



The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psmd10-201	ENSMUST0000033805.14	1430	<u>231aa</u>	Protein coding	CCDS30444	<u>Q9Z2X2</u>	TSL:1 GENCODE basic APPRIS P3
Psmd10-202	ENSMUST00000112978.1	1390	<u>151aa</u>	Protein coding	CCDS53207	A2AG83	TSL:2 GENCODE basic APPRIS ALT1

The strategy is based on the design of *Psmd10-201* transcript, The transcription is shown below

< Psmd	
protein	coding

leverse strand

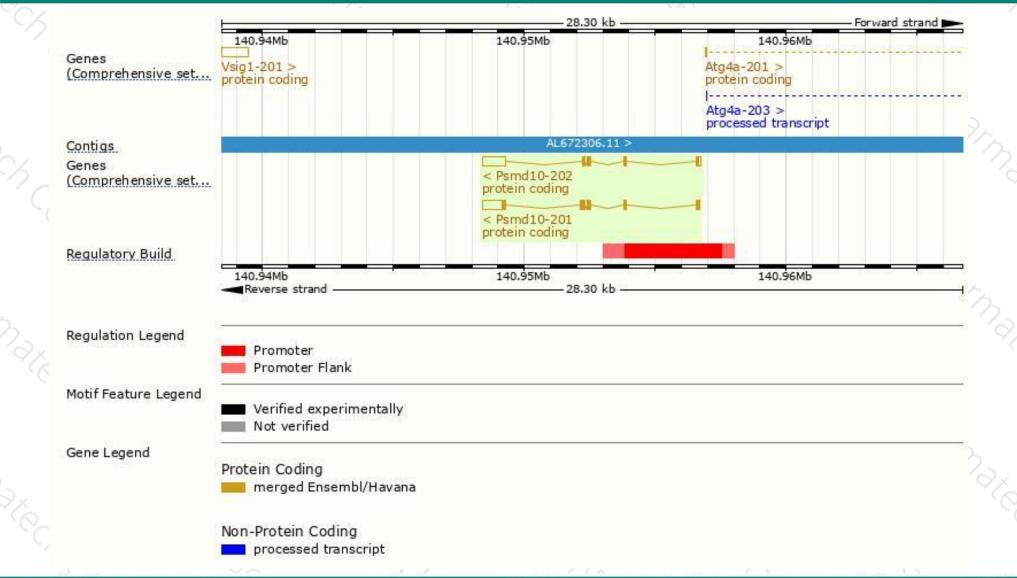
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### **Genomic location distribution**





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## **Protein domain**



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ENSMUSP00000033 Conserved Domains		ifference and the second se				
hmmpanther	26S proteasome no	n-ATPase regulatory subun	iit 10-like			-
Superfamily domains	Ankyrin repe	at-containing domain super	rfamily			
SMART domains		Ankyrin repeat				
Prints domain	32	Ankyrin repeat			1010	
Pfam domain	Ап	nkyrin repeat-containing do	imain		Ankyrin repeat	$\sim$
PROSITE profiles		Ankyrin repeat				
		Ankyrin repeat-containin	ig domain			
PIRSF domain	PIRSF000654					
Gene3D	Ankyrin repeat-cont	taining domain superfamily				
All sequence SNPs/i	Sequence variant	s (dbSNP and all other s	ources)			
Variant Legend						
variant Legenu	missense va	riant				
	synonymous	s variant				
Scale bar	0 20	40 60 8	80 100 1	20 140 160	180 200	231
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



