

Psm**d1 Cas9-KO Strategy**

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Reviewer:

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Project Overview

Project Name

Psm α 1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Psmc1* gene has 9 transcripts. According to the structure of *Psmc1* gene, exon2-exon7 of *Psmc1-201* (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 *Psmc1* gene. The brief process is as follows: CRISPR/Cas9 system

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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)

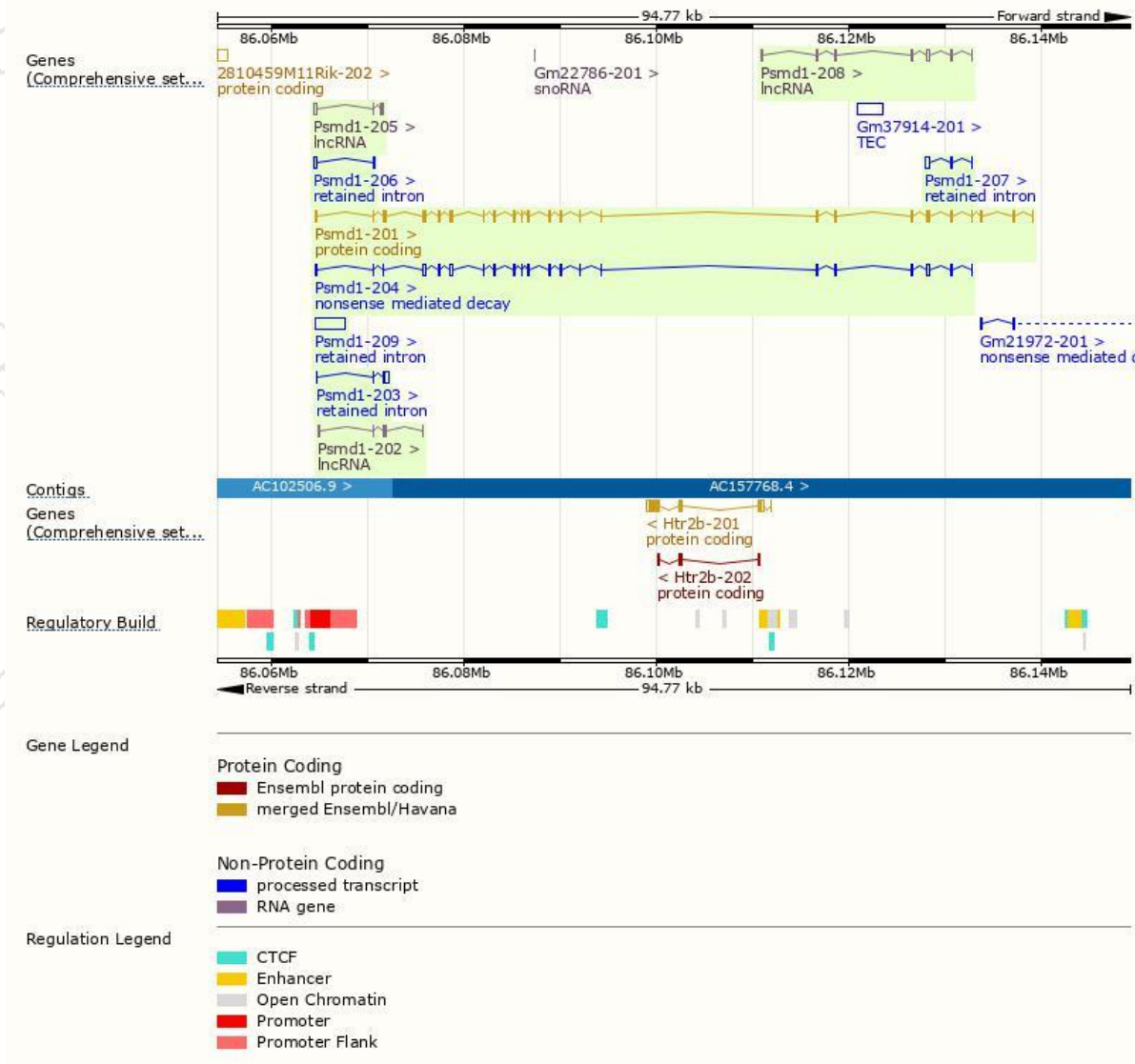
The gene has 9 transcripts,all transcripts are shown below:

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

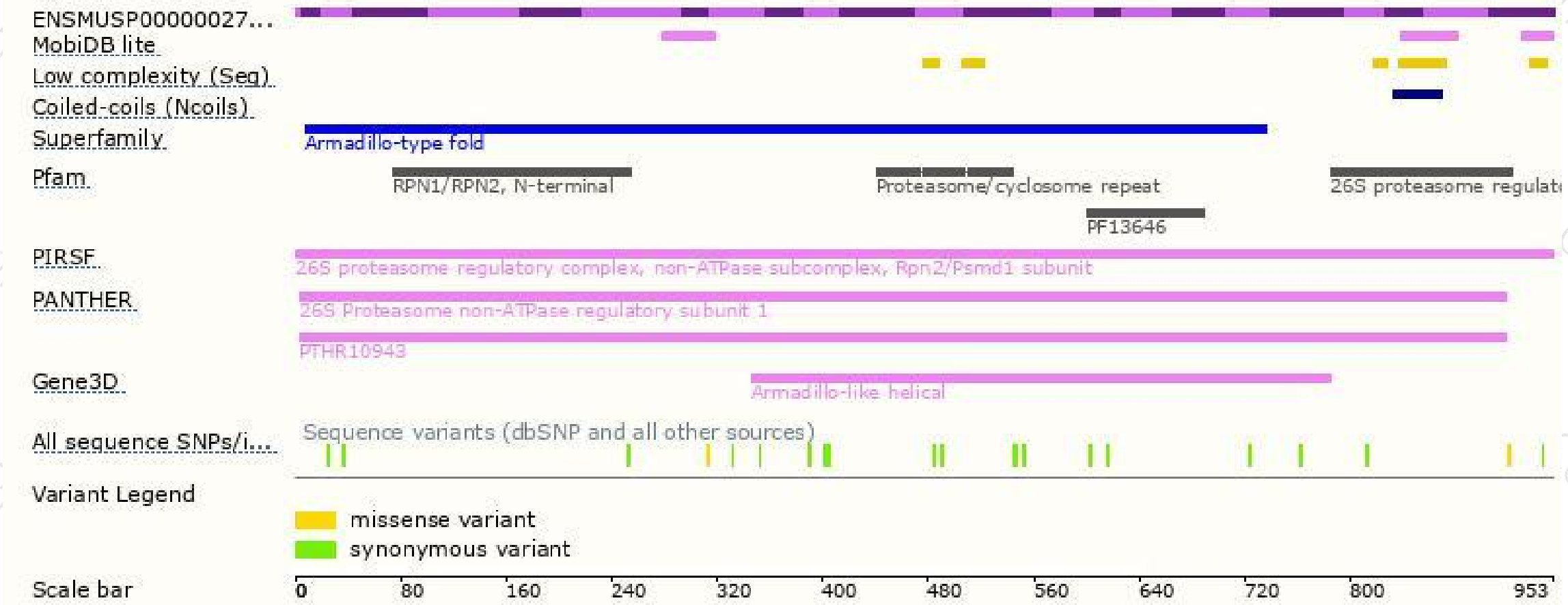
The strategy is based on the design of *Psmc1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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