

Psmf1 Cas9-KO Strategy

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Project Overview

Project Name

Psmf1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Psmf1* gene. The schematic diagram is as follows:



- The *Psmf1* gene has 6 transcripts. According to the structure of *Psmf1* gene, exon2-exon6 of *Psmf1-201* (ENSMUST00000042452.10) transcript is recommended as the knockout region. The region contains 635bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Psmf1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Psmf1* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Psmf1 proteasome (prosome, macropain) inhibitor subunit 1 [*Mus musculus* (house mouse)]

Gene ID: 228769, updated on 12-Aug-2019

Summary

Official Symbol Psmf1 provided by [MGI](#)

Official Full Name proteasome (prosome, macropain) inhibitor subunit 1 provided by [MGI](#)

Primary source [MGI:MGI:1346072](#)

See related [Ensembl:ENSMUSG00000032869](#)

Gene type protein coding

RefSeq status 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 PI31; AW048666; BC012260

Expression Broad expression in testis adult (RPKM 115.5), ovary adult (RPKM 10.6) and 25 other tissues [See more](#)

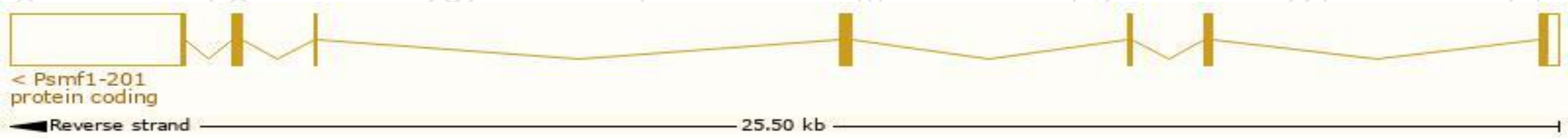
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

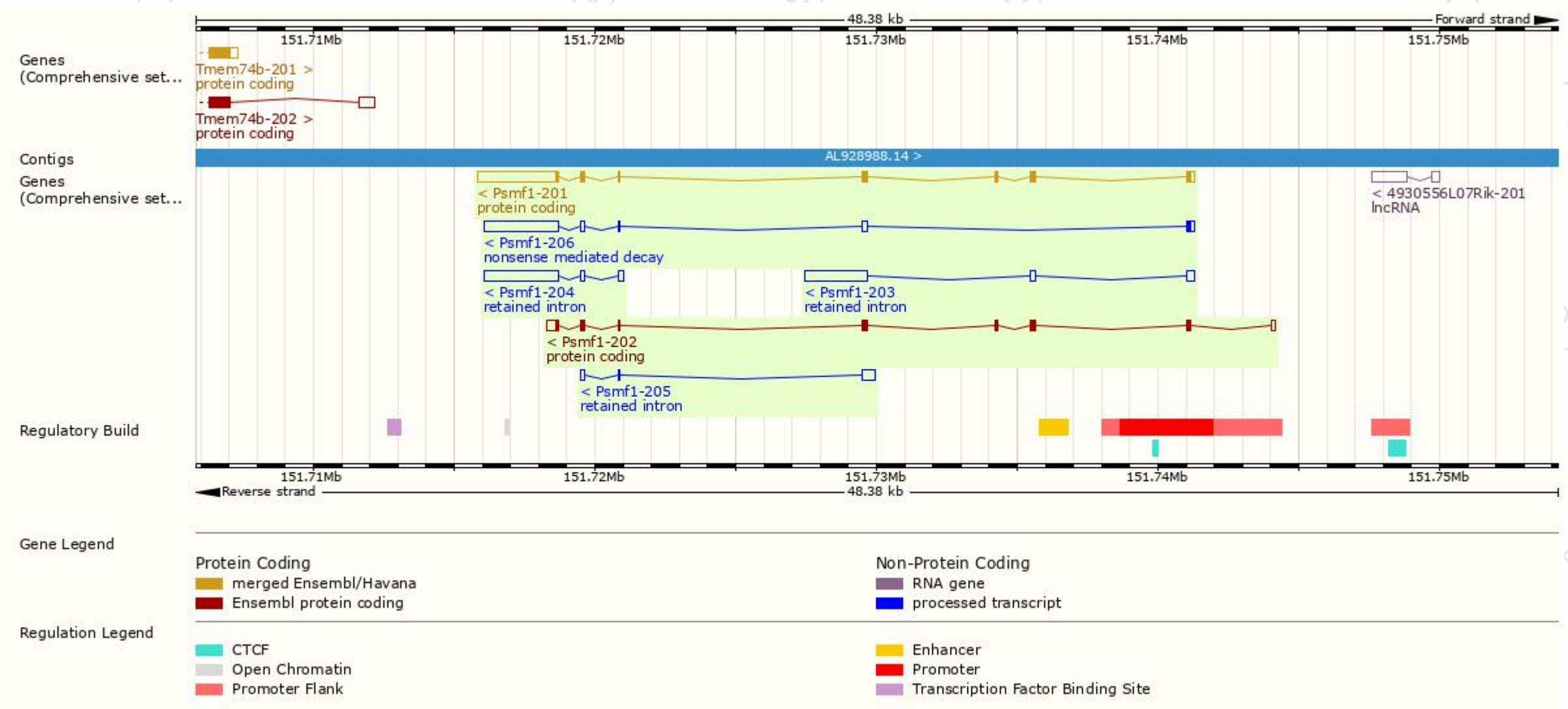
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psmf1-201	ENSMUST00000042452.10	3809	271aa	Protein coding	CCDS16872	A2AU35 Q8BHL8	TSL:1 GENCODE basic APPRIS P1
Psmf1-202	ENSMUST00000109869.1	1384	271aa	Protein coding	CCDS16872	A2AU35 Q8BHL8	TSL:5 GENCODE basic APPRIS P1
Psmf1-206	ENSMUST00000155939.7	3306	45aa	Nonsense mediated decay	-	D6REH2	TSL:1
Psmf1-204	ENSMUST00000125977.7	2956	No protein	Retained intron	-	-	TSL:2
Psmf1-203	ENSMUST00000123449.1	2667	No protein	Retained intron	-	-	TSL:1
Psmf1-205	ENSMUST00000151656.1	683	No protein	Retained intron	-	-	TSL:2

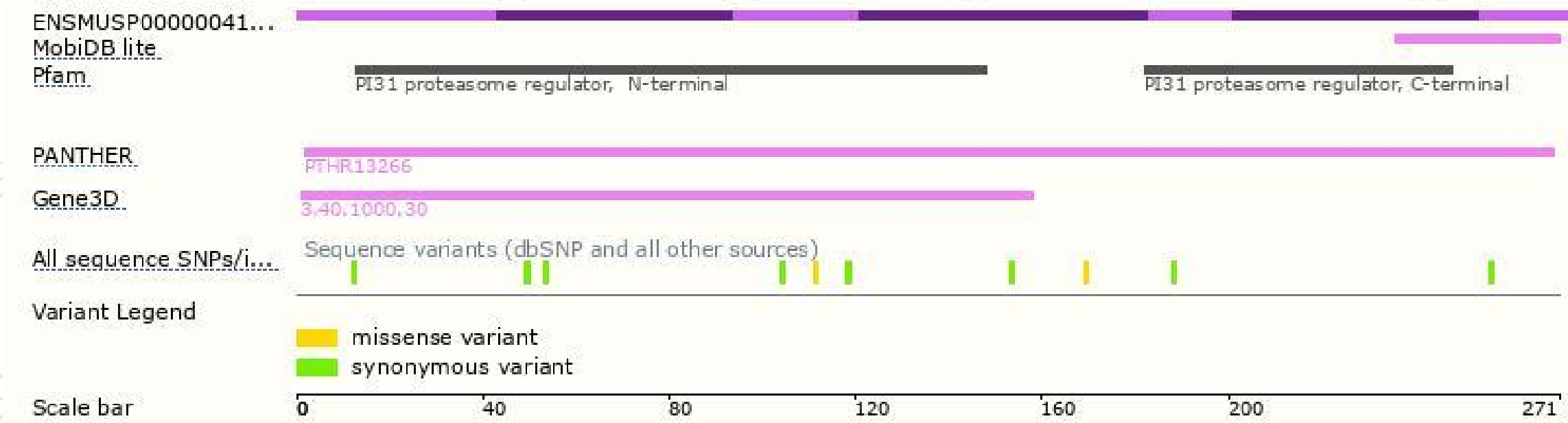
The strategy is based on the design of *Psmf1-201* transcript,The transcription is shown below



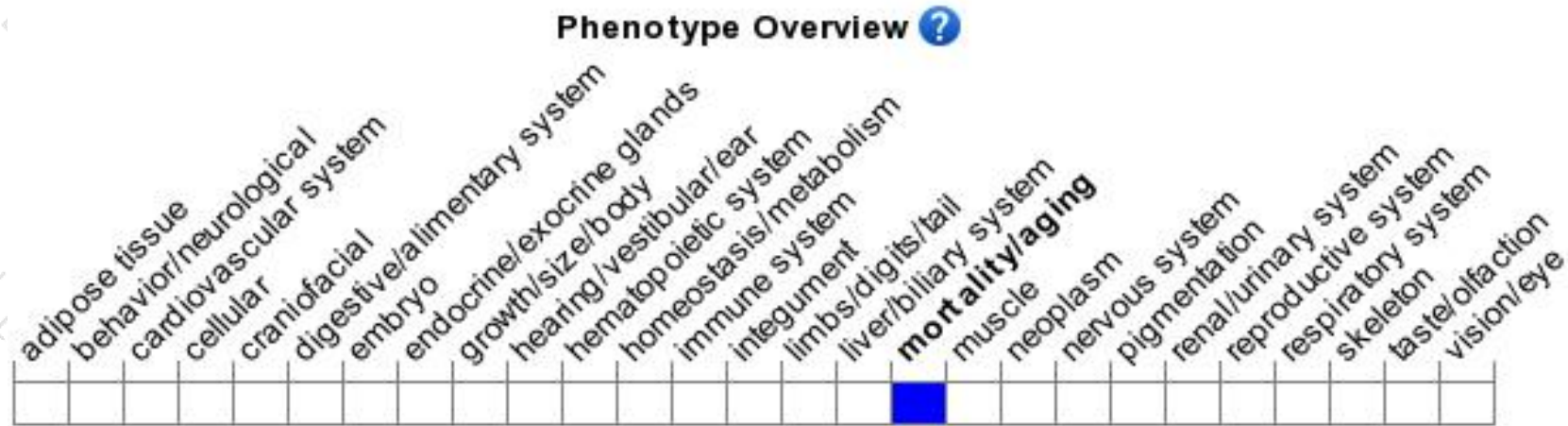
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

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

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