

Psme3 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Psme3

Project type

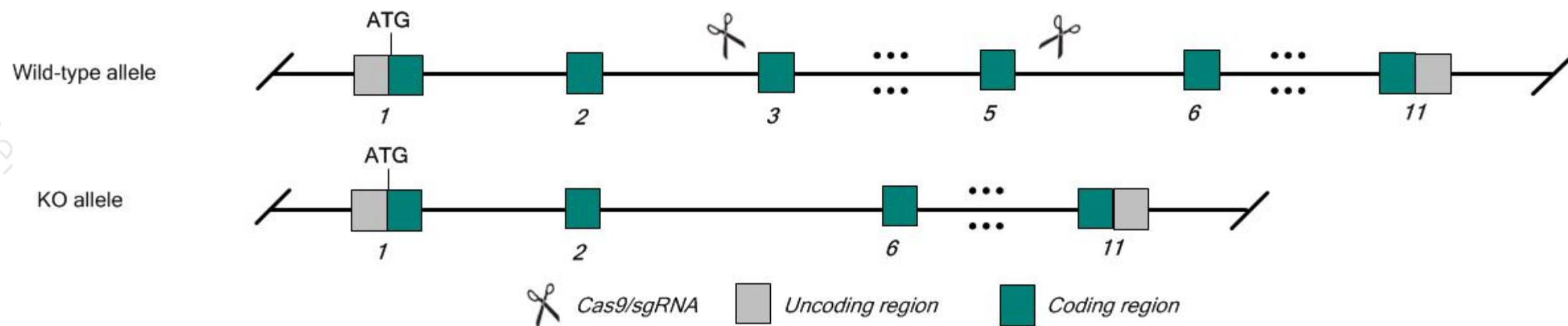
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Psme3* gene. The schematic diagram is as follows:



- The *Psme3* gene has 5 transcripts. According to the structure of *Psme3* gene, exon3-5 of *Psme3*-201 (ENSMUST00000019470.13) transcript is recommended as the knockout region. The region contains 217bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Psme3* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Homozygous null mutants are smaller than normal with a defect in cell proliferation and increased susceptibility to fungal infection.
- The *Psme3* 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.

Psme3 proteasome (prosome, macropain) activator subunit 3 (PA28 gamma, Ki) [*Mus musculus* (house mouse)]






Gene ID: 19192, updated on 4-Jun-2019

Summary

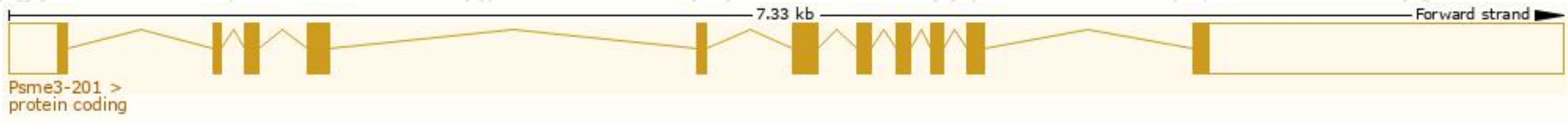
Official Symbol	Psme3 provided by MGI
Official Full Name	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma, Ki) provided by MGI
Primary source	MGI:MGI:1096366
See related	Ensembl:ENSMUSG000000078652
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ki; pa28g; AA410043; AU020960; REGgamma; PA28gamma
Expression	Ubiquitous expression in liver E14.5 (RPKM 81.8), liver E14 (RPKM 74.6) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

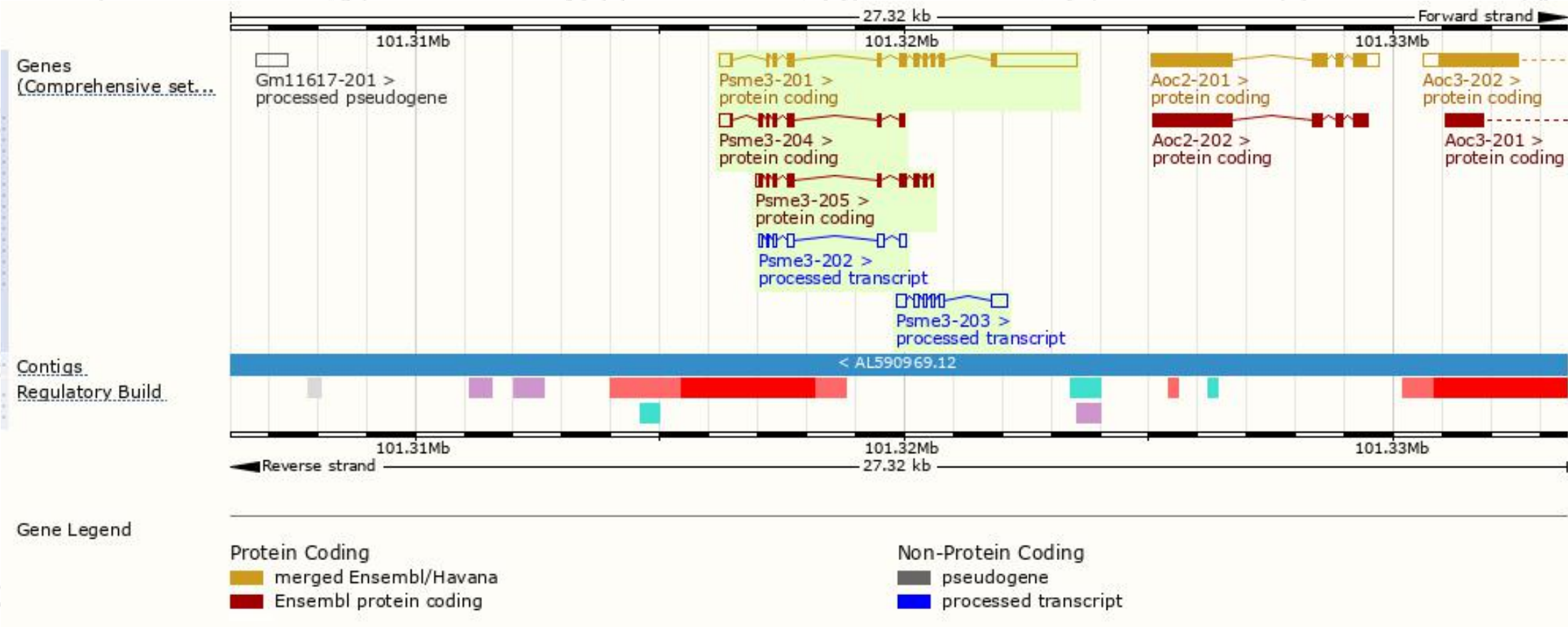
The gene has 5 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psme3-201	ENSMUST00000019470.13	2664	254aa	 Protein coding	CCDS25463	P61290 Q4FK54	TSL:1 Gencode basic APPRIS P1
Psme3-204	ENSMUST000000142640.7	698	154aa	 Protein coding	-	A2A4J3	CDS 3' incomplete TSL:3
Psme3-205	ENSMUST000000151385.1	653	203aa	 Protein coding	-	A2A4J1	CDS 3' incomplete TSL:5
Psme3-203	ENSMUST000000131170.1	778	No protein	 Processed transcript	-	-	TSL:2
Psme3-202	ENSMUST000000127998.1	524	No protein	 Processed transcript	-	-	TSL:5

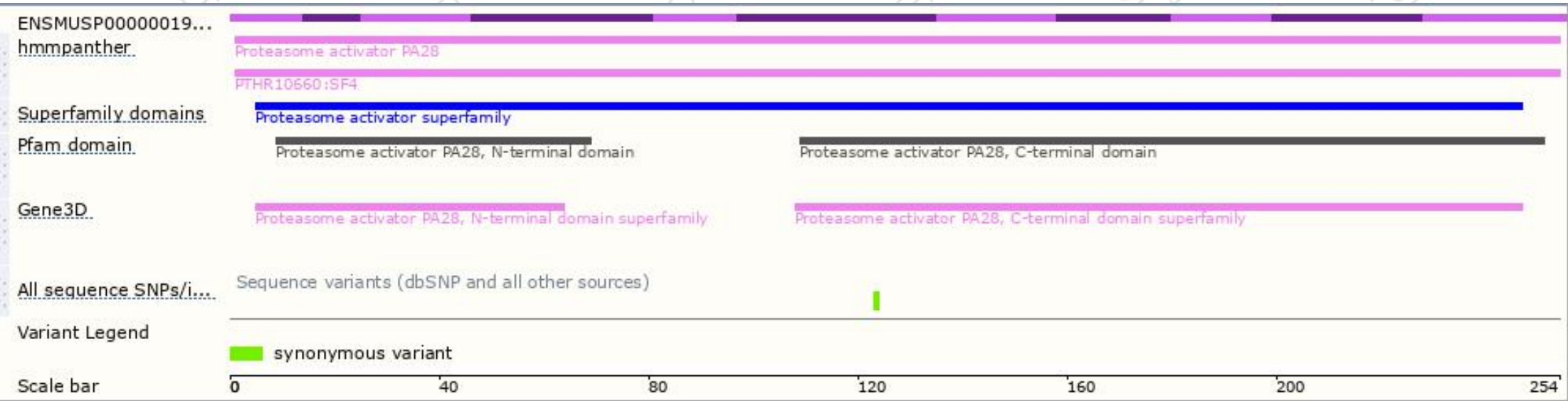
The strategy is based on the design of *Psme3-201* transcript, The transcription is shown below



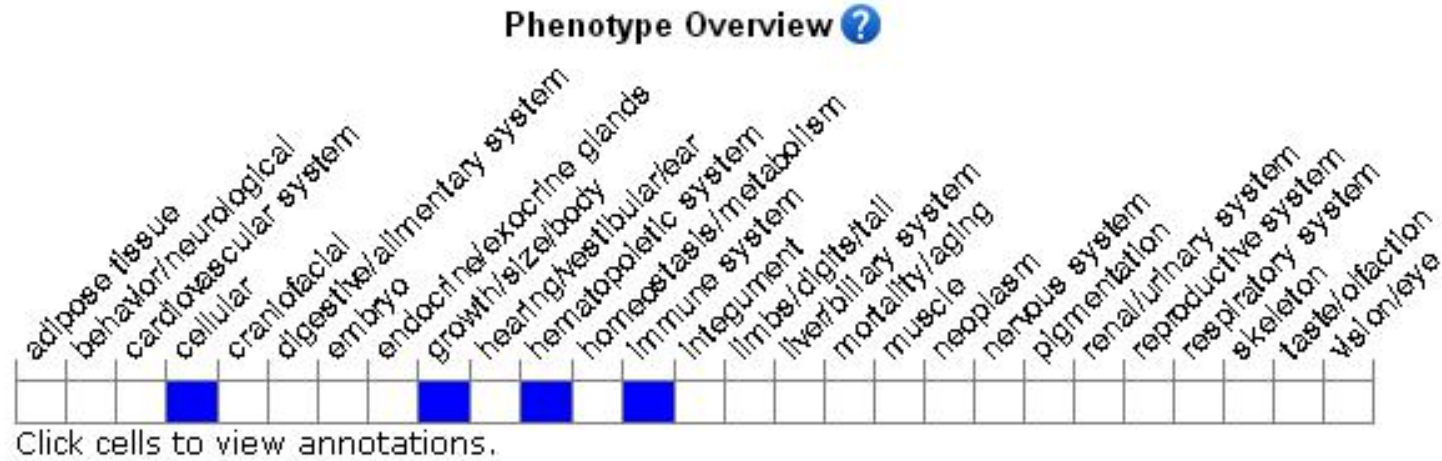
Genomic location (Ensembl)



Protein domain (Ensembl)



Mouse phenotype description(MGI)



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

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

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