

Psmc3 Cas9-CKO Strategy

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Design Date:

2019-8-30

Project Overview



Project Name

Psme3

Project type

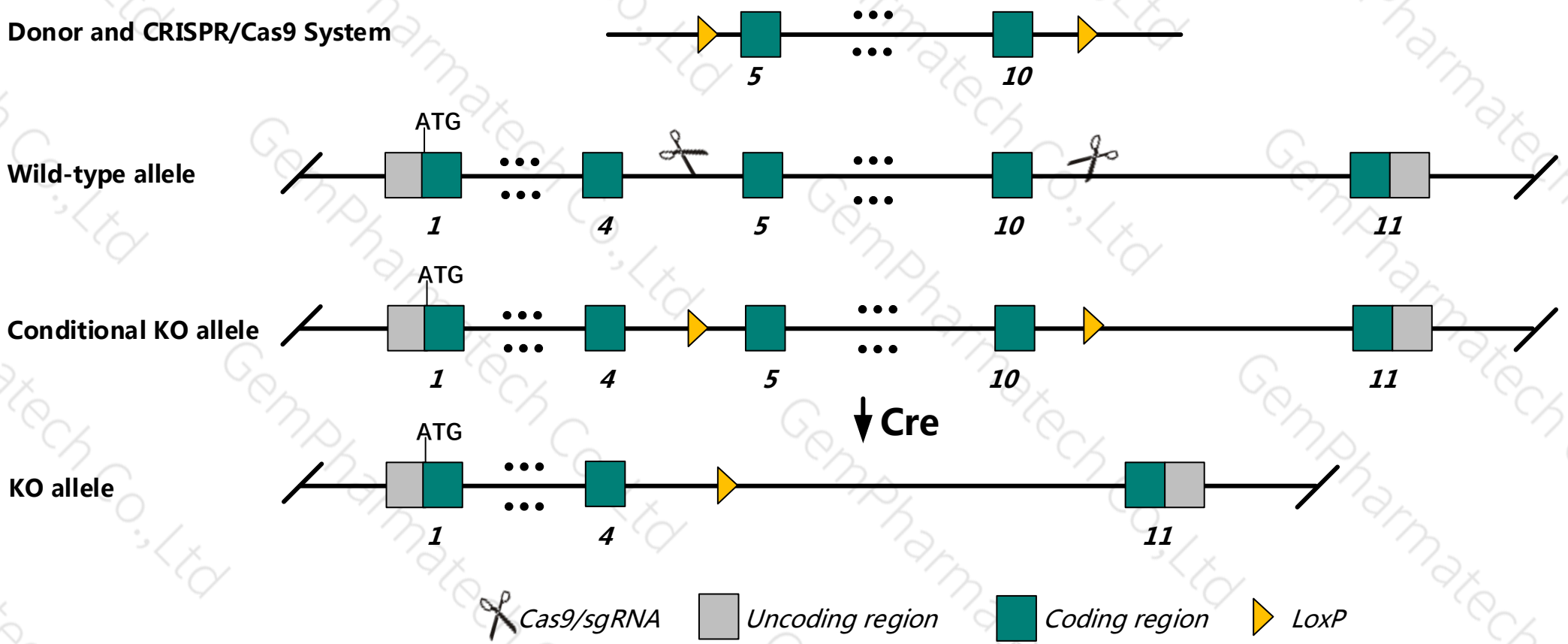
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional 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 transcript. According to the structure of *Psme3* gene, exon5~10 of *Psme3*-201 (ENSMUST00000019470.13) transcript is recommended as the knockout region. The region contains 441bp 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, donor vector was constructed. Cas9, sgRNA 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 was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

- 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.
- This strategy may affect the 5 terminal regulatory function of the *Aoc2* gene.
- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

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

Gene ID: 19192, updated on 12-Aug-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:ENSMUSG00000078652](#)

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](#)

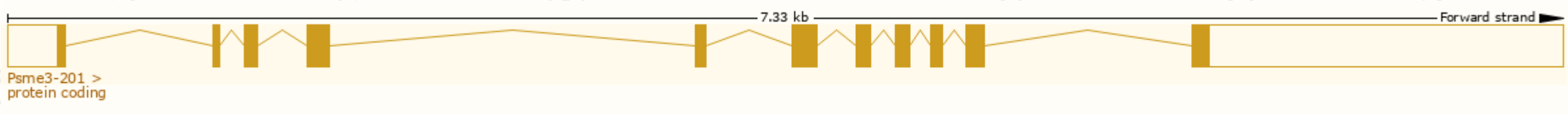
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

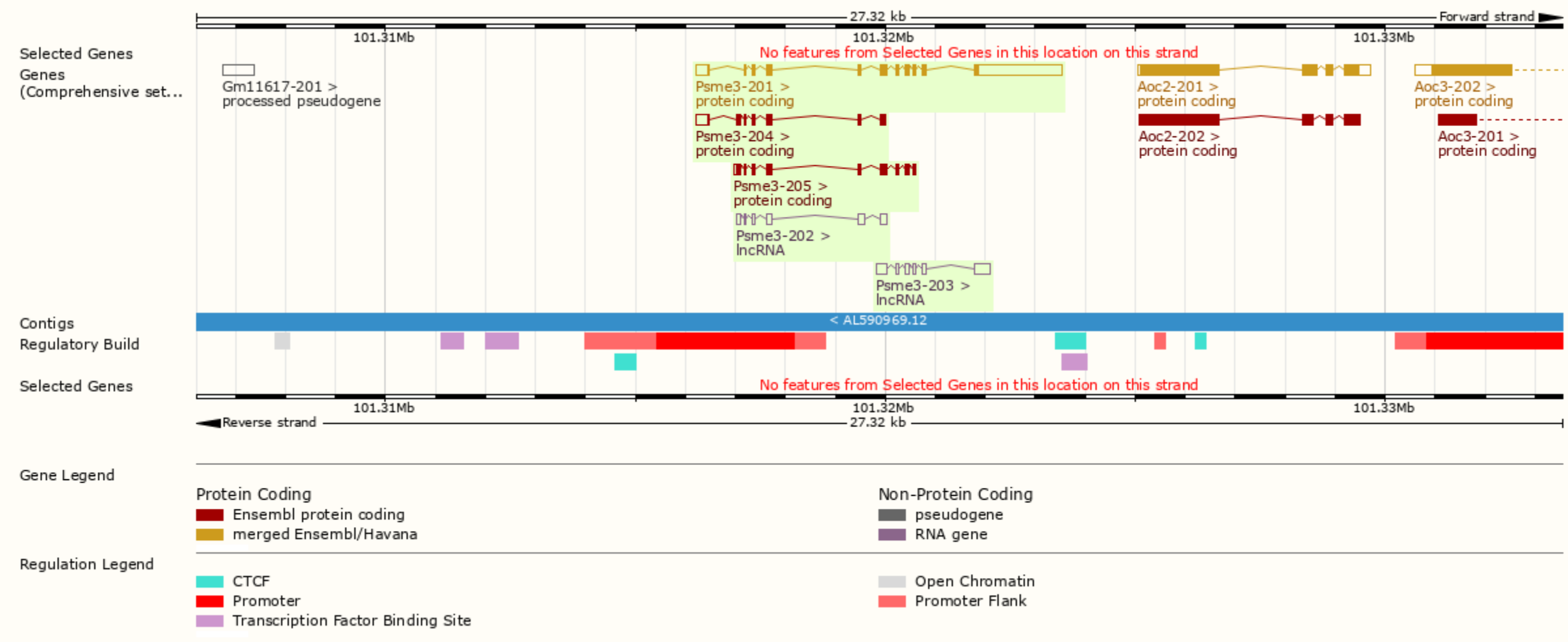
The gene has 5 transcripts, and all transcripts are shown below:

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	ENSMUST00000142640.7	698	154aa	Protein coding	-	A2A4J3	CDS 3' incomplete TSL:3
Psme3-205	ENSMUST00000151385.1	653	203aa	Protein coding	-	A2A4J1	CDS 3' incomplete TSL:5
Psme3-203	ENSMUST00000131170.1	778	No protein	lncRNA	-	-	TSL:2
Psme3-202	ENSMUST00000127998.1	524	No protein	lncRNA	-	-	TSL:5

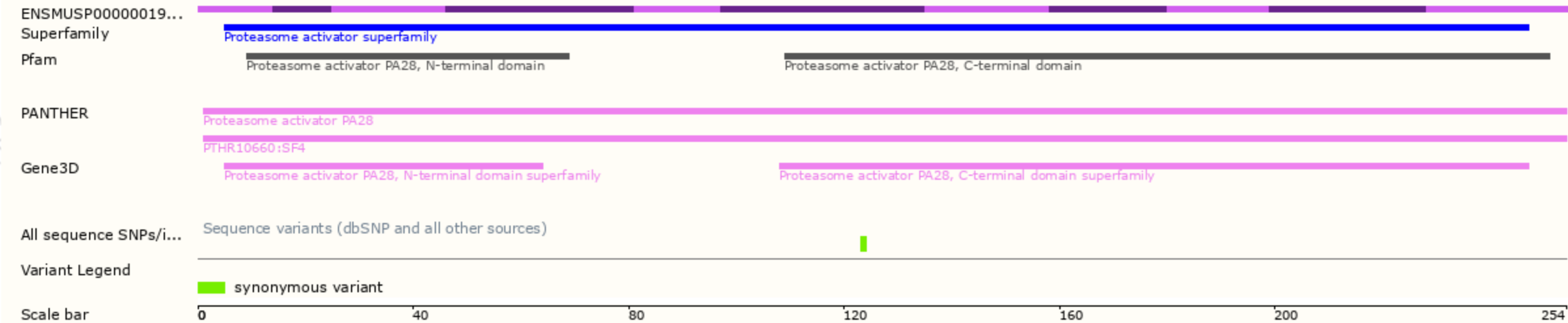
The strategy is based on the design of *Psme3-201* transcript, The transcription is shown below:



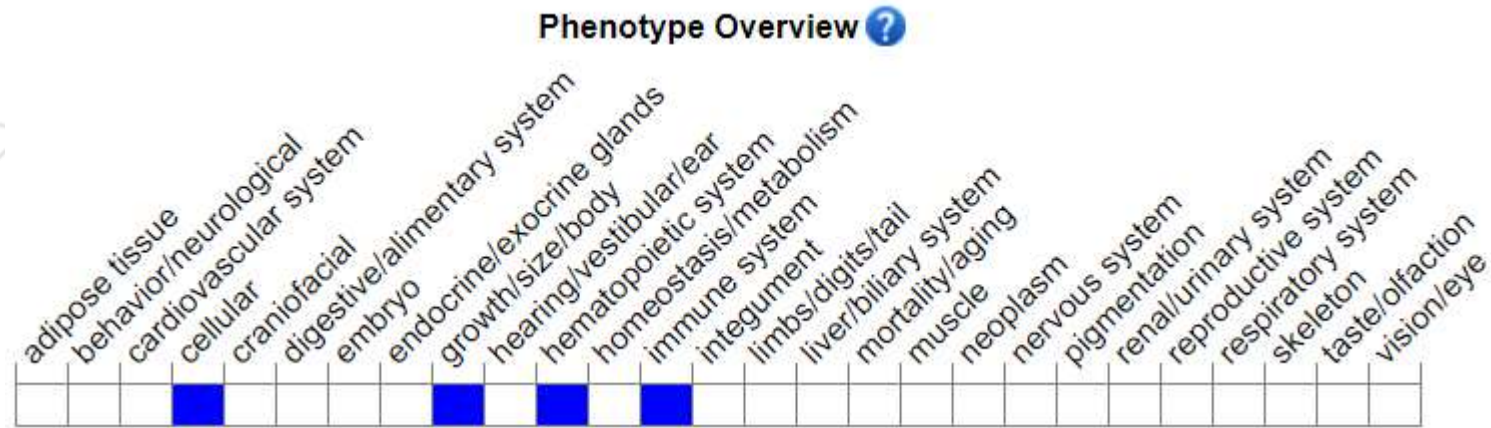
Genomic location distribution



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/>).

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.

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