

Psmc6 Cas9-CKO Strategy

Project Overview

Project Name

Psmc6

Project type

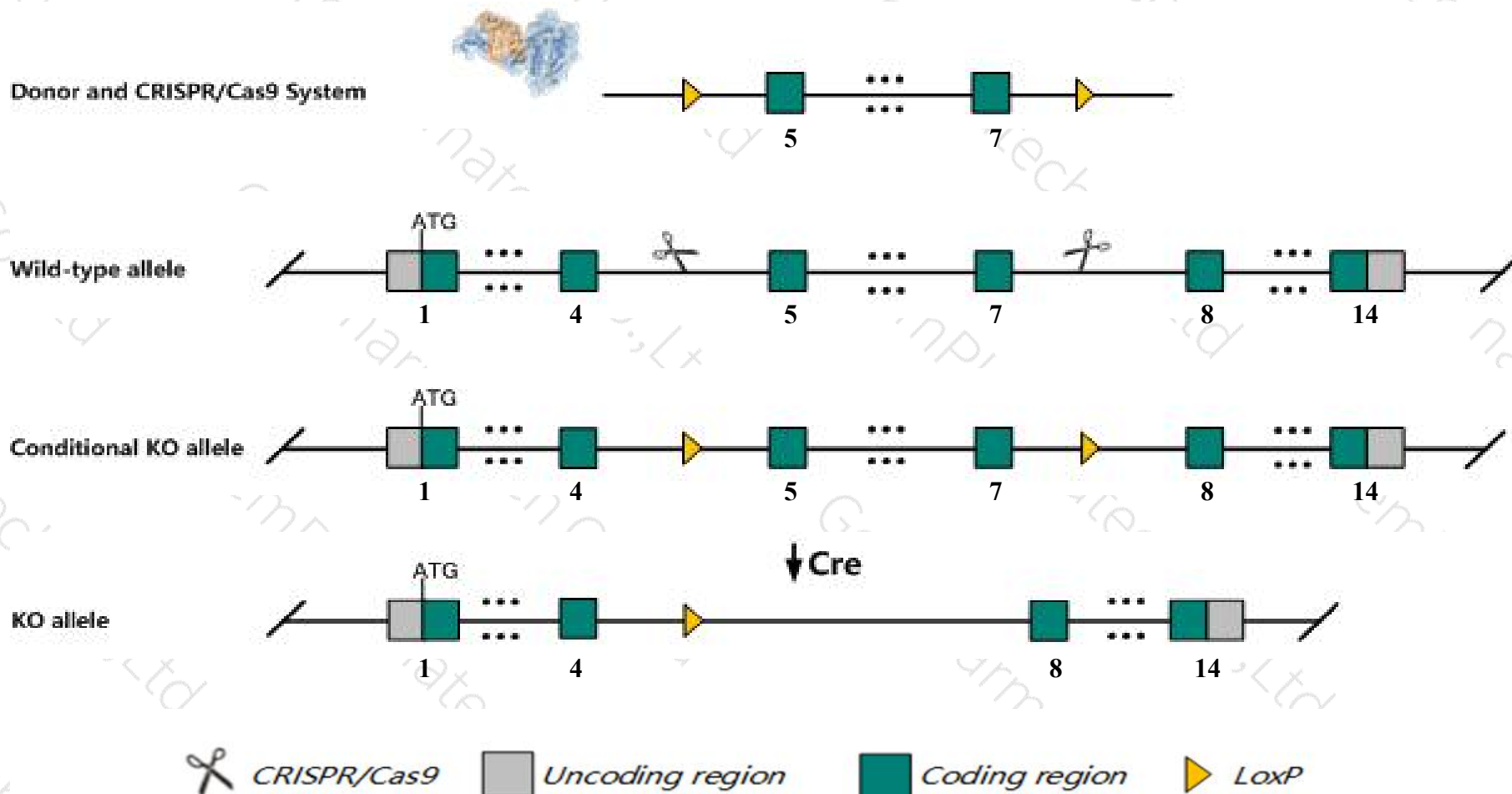
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Psmc6* gene. The schematic diagram is as follows:



- The *Psmc6* gene has 10 transcripts. According to the structure of *Psmc6* gene, exon5-exon7 of *Psmc6-201* (ENSMUST00000022380.8) transcript is recommended as the knockout region. The region contains 271bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Psmc6* gene. The brief process is as follows: CRISPR/Cas9 system 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 will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- The *Psmc6* gene is located on the Chr14. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Psmc6 proteasome (prosome, macropain) 26S subunit, ATPase, 6 [*Mus musculus* (house mouse)]

Gene ID: 67089, updated on 12-Aug-2019

Summary

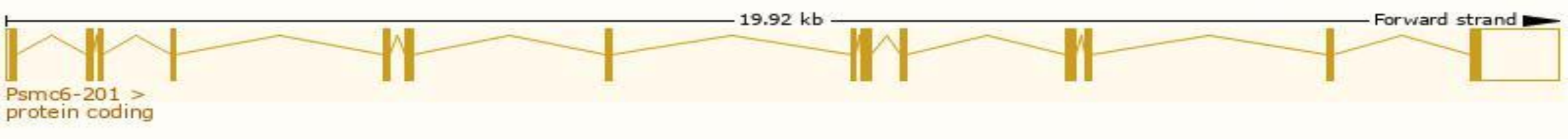
Official Symbol	Psmc6 provided by MGI
Official Full Name	proteasome (prosome, macropain) 26S subunit, ATPase, 6 provided by MGI
Primary source	MGI:MGI:1914339
See related	Ensembl:ENSMUSG00000021832
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI451058; 2300001E01Rik
Expression	Broad expression in CNS E11.5 (RPKM 59.8), liver E14 (RPKM 50.8) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

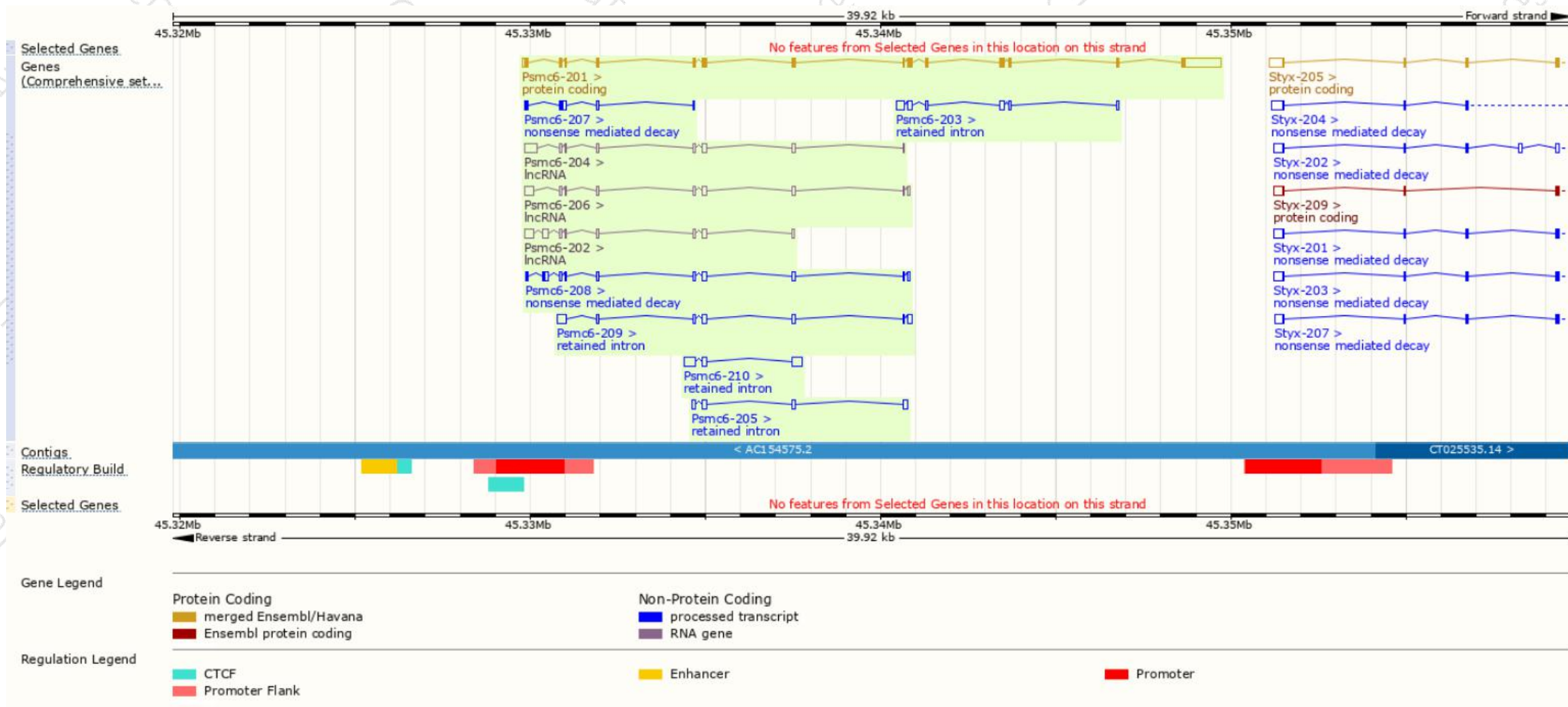
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psmc6-201	ENSMUST00000022380.8	2234	389aa	Protein coding	CCDS26974	P62334 Q14AQ1	TSL:1 GENCODE basic APPRIS P1
Psmc6-208	ENSMUST00000228479.1	813	45aa	Nonsense mediated decay	-	A0A2I3BQ49	CDS 5' incomplete
Psmc6-207	ENSMUST00000228300.1	383	60aa	Nonsense mediated decay	-	A0A2I3BQ79	
Psmc6-206	ENSMUST00000228026.1	844	No protein	Processed transcript	-	-	
Psmc6-204	ENSMUST00000227148.1	830	No protein	Processed transcript	-	-	
Psmc6-202	ENSMUST00000226431.1	812	No protein	Processed transcript	-	-	
Psmc6-209	ENSMUST00000228831.1	777	No protein	Retained intron	-	-	
Psmc6-210	ENSMUST00000228870.1	724	No protein	Retained intron	-	-	
Psmc6-203	ENSMUST00000226739.1	680	No protein	Retained intron	-	-	
Psmc6-205	ENSMUST00000227385.1	432	No protein	Retained intron	-	-	

The strategy is based on the design of *Psmc6-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000022...

[Low complexity \(Seq\)](#)

[Conserved Domains](#)

[Coiled-coils \(Ncoils\)](#)

[hmmpanther](#)

[TIGRFAM domain](#)

[Superfamily domains](#)

[SMART domains](#)

[Pfam domain](#)

[PROSITE patterns](#)

[Gene3D](#)

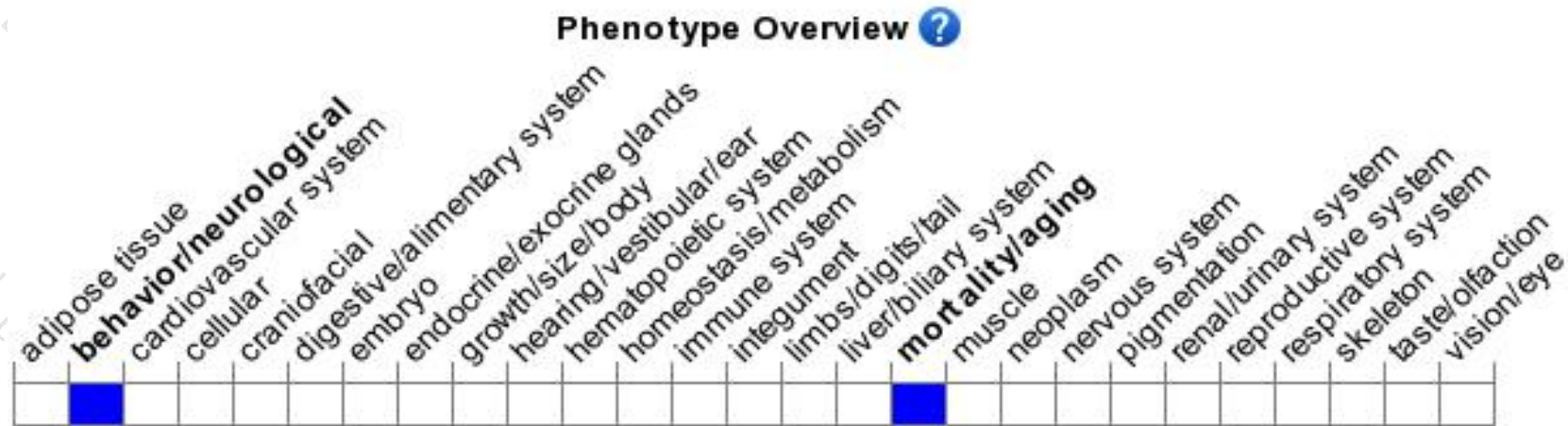
[All sequence SNPs/i...](#)

[Variant Legend](#)

[Scale bar](#)



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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