Psmd2 Cas9-KO Strategy

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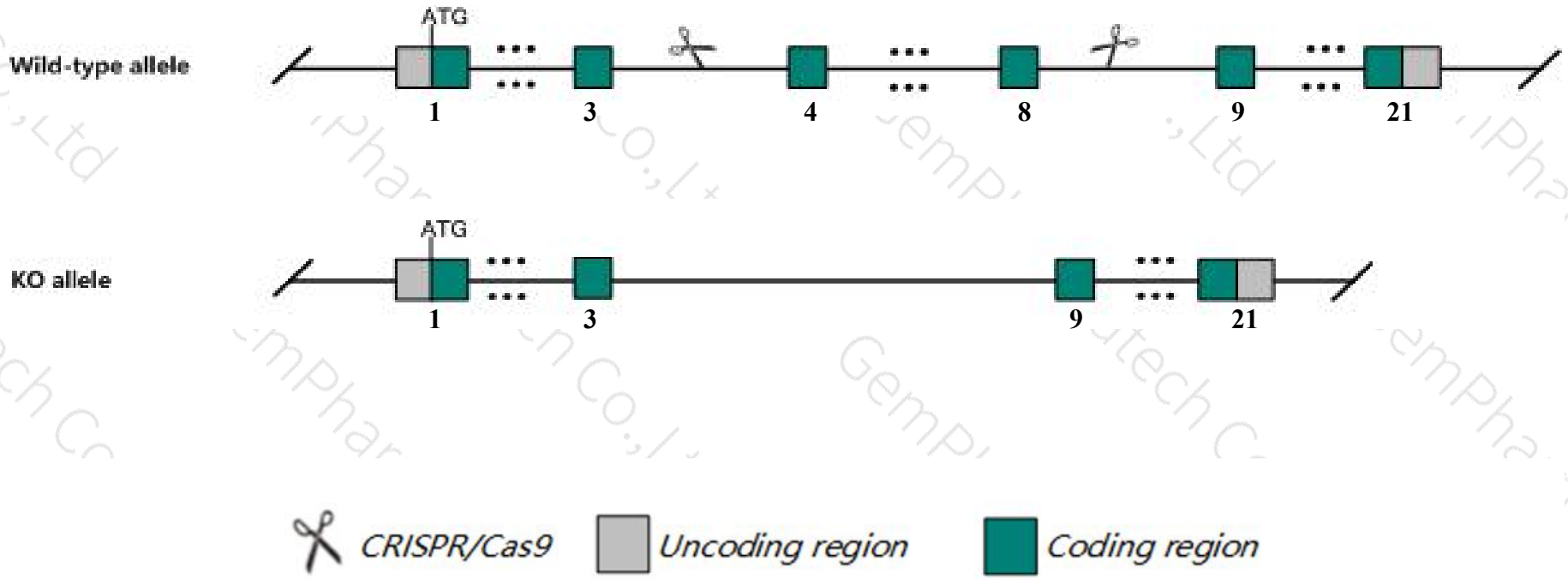
Project Overview

Project Name	***Psmd2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Psmd2* gene. The schematic diagram is as follows:



Technical routes

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- The *Psmd2* gene has 9 transcripts. According to the structure of *Psmd2* gene, exon4-exon8 of *Psmd2-201* (ENSMUST00000007212.8) transcript is recommended as the knockout region.The region contains 712bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Psmd2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- The *Psmd2* gene is located on the Chr16. 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）

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Psmd2 proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 [Mus musculus (house mouse)]

Gene ID: 21762, updated on 31-Jan-2019

Summary

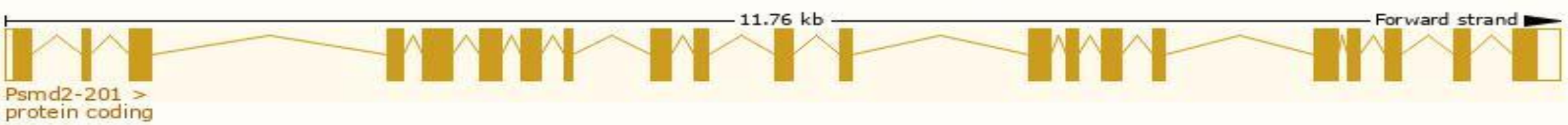
Official Symbol	Psmd2 provided by MGI
Official Full Name	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 provided by MGI
Primary source	MGI:MGI:1096584
See related	Ensembl:ENSMUSG00000006998
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9430095H01Rik, AA407121, TEG-190, Tex190
Expression	Ubiquitous expression in testis adult (RPKM 102.9), CNS E11.5 (RPKM 75.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

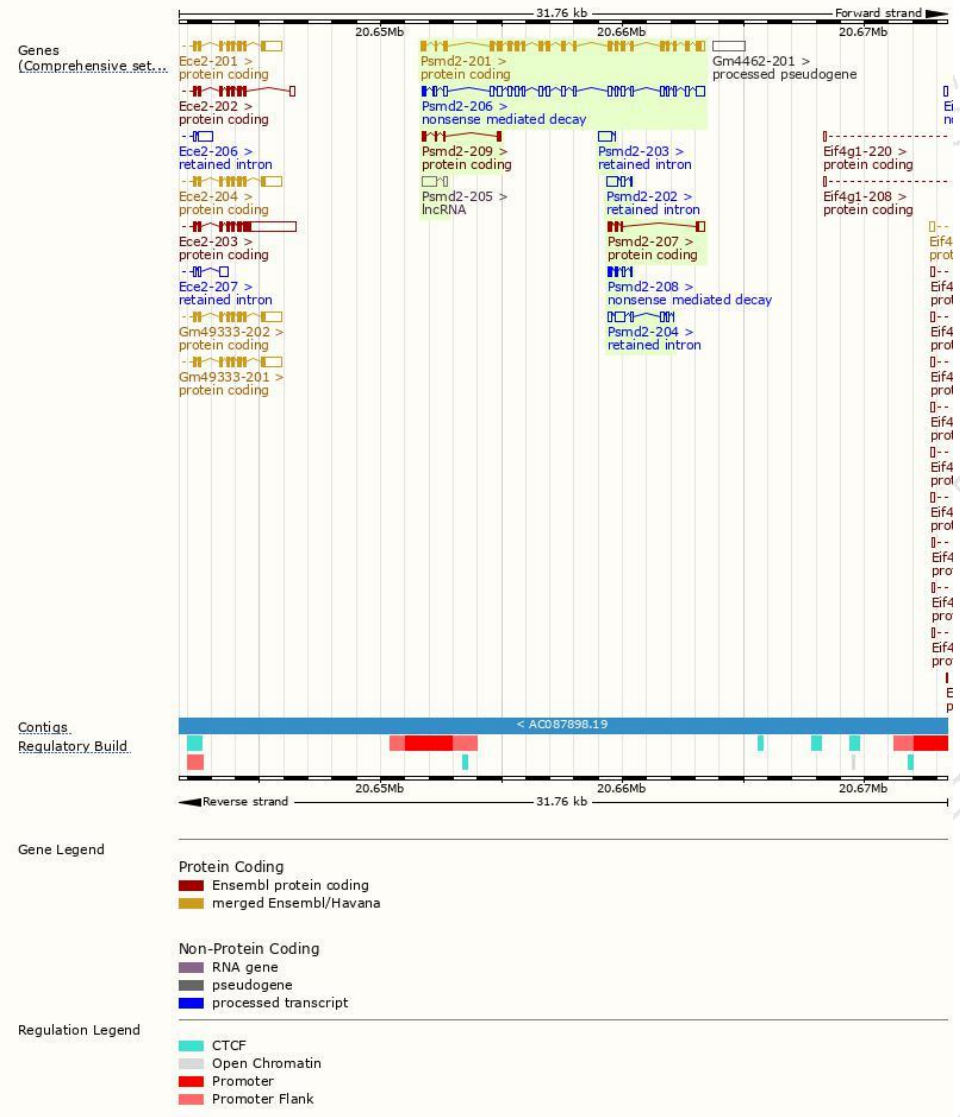
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psmd2-201	ENSMUST00000007212.8	2961	908aa	Protein coding	CCDS28053	Q3TKV1 Q8VDM4	TSL:1 GENCODE basic APPRIS P1
Psmd2-207	ENSMUST00000231897.1	659	139aa	Protein coding	-	A0A338P7H4	CDS 5' incomplete
Psmd2-209	ENSMUST00000232629.1	441	142aa	Protein coding	-	A0A338P6M5	CDS 3' incomplete
Psmd2-206	ENSMUST00000172207.7	3001	60aa	Nonsense mediated decay	-	E9Q2S8	TSL:1
Psmd2-208	ENSMUST00000232513.1	433	97aa	Nonsense mediated decay	-	A0A338P6S9	CDS 5' incomplete
Psmd2-204	ENSMUST00000169184.1	939	No protein	Retained intron	-	-	TSL:5
Psmd2-202	ENSMUST00000166071.1	601	No protein	Retained intron	-	-	TSL:2
Psmd2-203	ENSMUST00000167869.1	600	No protein	Retained intron	-	-	TSL:3
Psmd2-205	ENSMUST00000169195.1	747	No protein	lncRNA	-	-	TSL:2

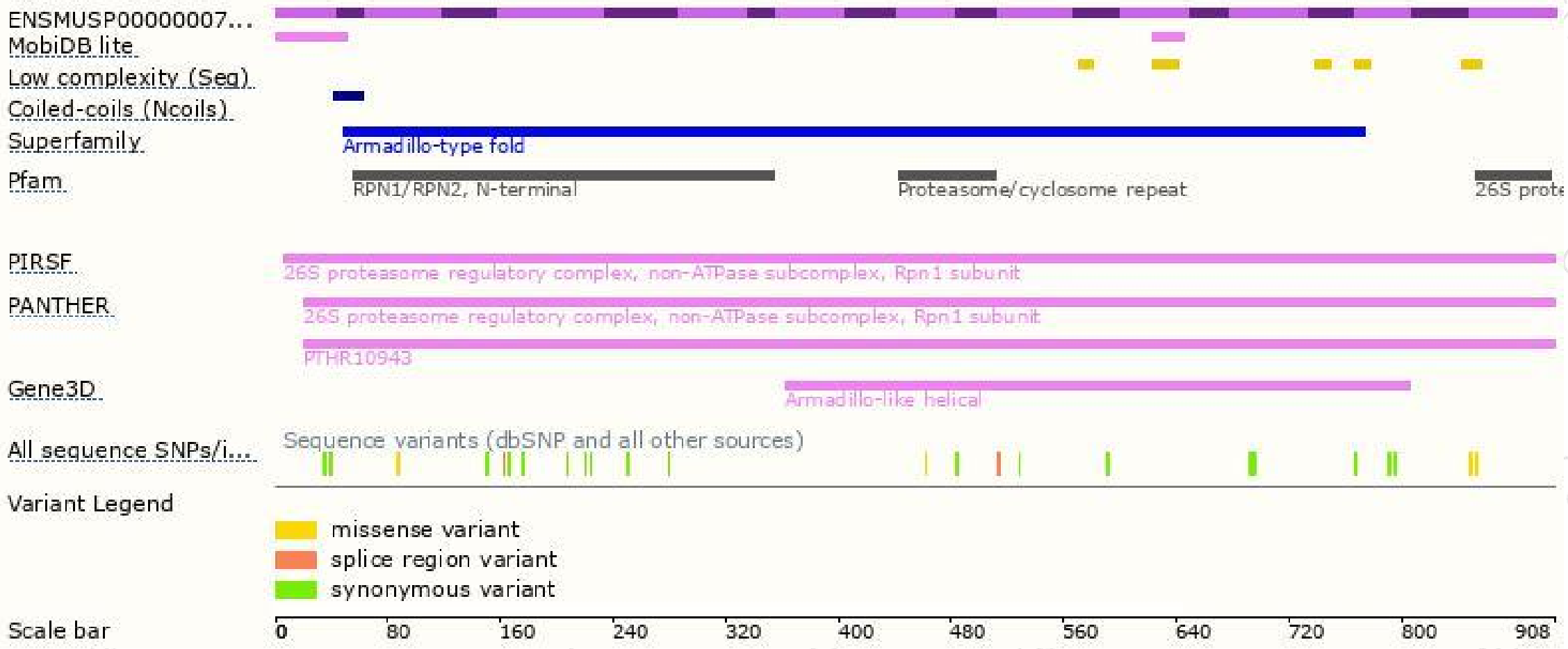
The strategy is based on the design of *Psmd2-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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