

Psmb9 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Psmb9

Project type

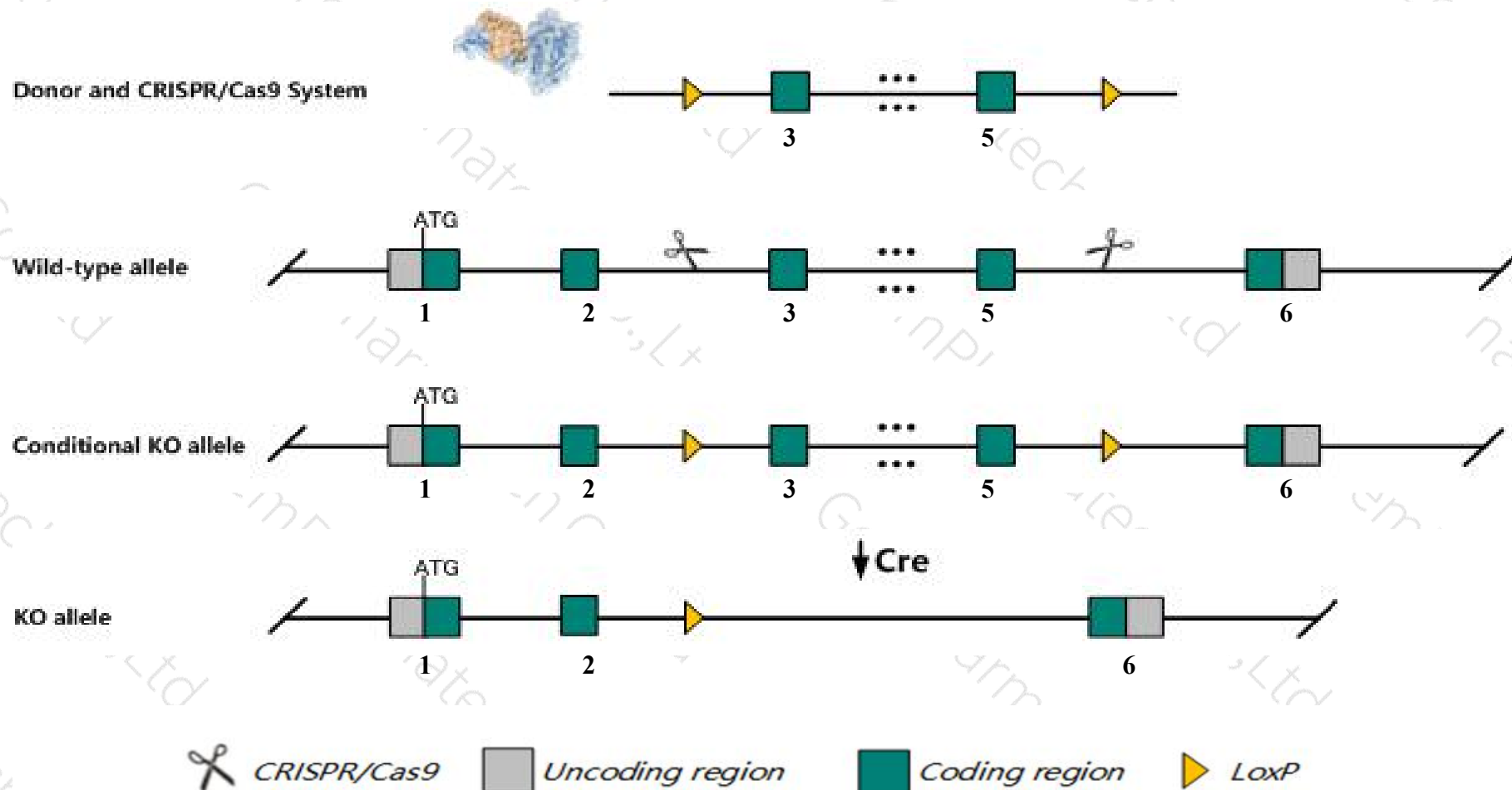
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Psmb9* gene. The schematic diagram is as follows:



- The *Psmb9* gene has 7 transcripts. According to the structure of *Psmb9* gene, exon3-exon5 of *Psmb9*-204 (ENSMUST00000174576.3) transcript is recommended as the knockout region. The region contains 404bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Psmb9* 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.

- According to the existing MGI data, Mice homozygous for disruptions in this gene have a grossly normal phenotype but suffer from increased susceptibility to some viruses and have an increased risk of tumor development.
- Knockout the region may affect the 5 terminal regulation function of *Tap1* gene.
- The *Psmb9* gene is located on the Chr17. 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)

Psmb9 proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) [*Mus musculus* (house mouse)]

Gene ID: 16912, updated on 12-Aug-2019

Summary

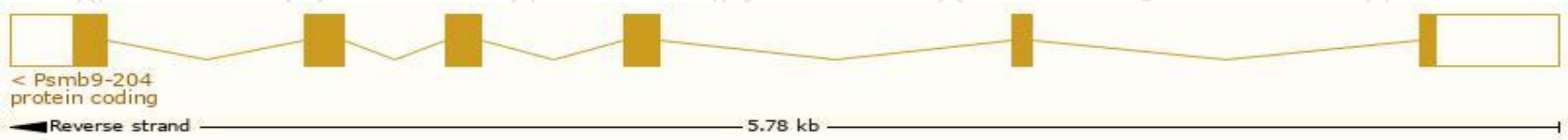
Official Symbol	Psmb9 provided by MGI
Official Full Name	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) provided by MGI
Primary source	MGI:MGI:1346526
See related	Ensembl:ENSMUSG00000096727
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Lmp2; Lmp-2
Expression	Broad expression in large intestine adult (RPKM 97.4), thymus adult (RPKM 90.4) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

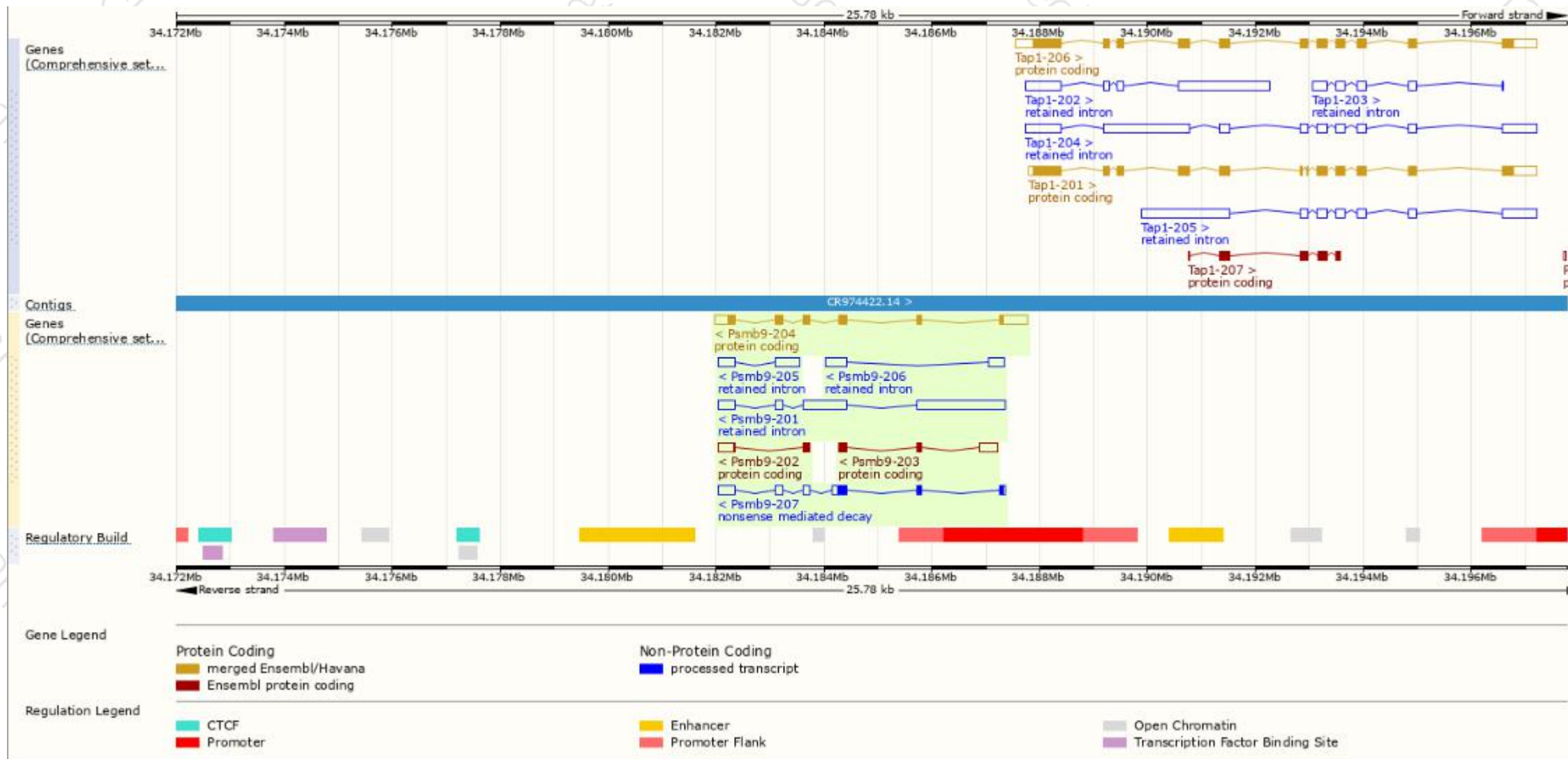
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psemb9-204	ENSMUST00000174576.3	1352	219aa	Protein coding	CCDS28642	A0A0R4J256	TSL:1 GENCODE basic APPRIS P1
Psemb9-203	ENSMUST00000173831.2	529	63aa	Protein coding	-	G3UYK5	CDS 3' incomplete TSL:3
Psemb9-202	ENSMUST00000171321.1	433	44aa	Protein coding	-	F6QXK7	CDS 5' incomplete TSL:2
Psemb9-207	ENSMUST00000237228.1	1025	93aa	Nonsense mediated decay	-	-	-
Psemb9-201	ENSMUST00000114230.2	2884	No protein	Retained intron	-	-	TSL:2
Psemb9-205	ENSMUST00000178857.1	783	No protein	Retained intron	-	-	TSL:2
Psemb9-206	ENSMUST00000179593.1	665	No protein	Retained intron	-	-	TSL:3

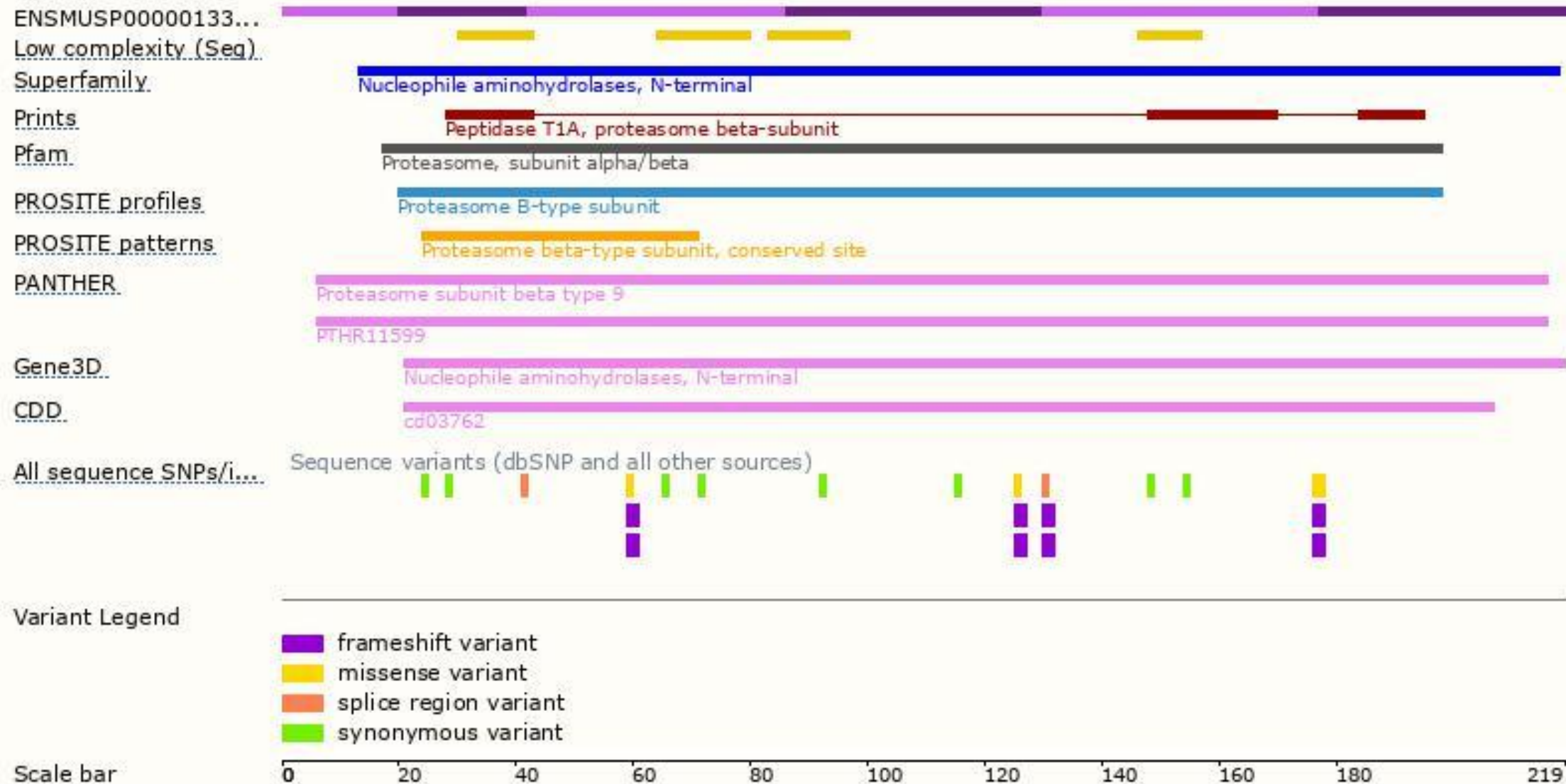
The strategy is based on the design of *Psemb9-204* transcript,The transcription is shown below



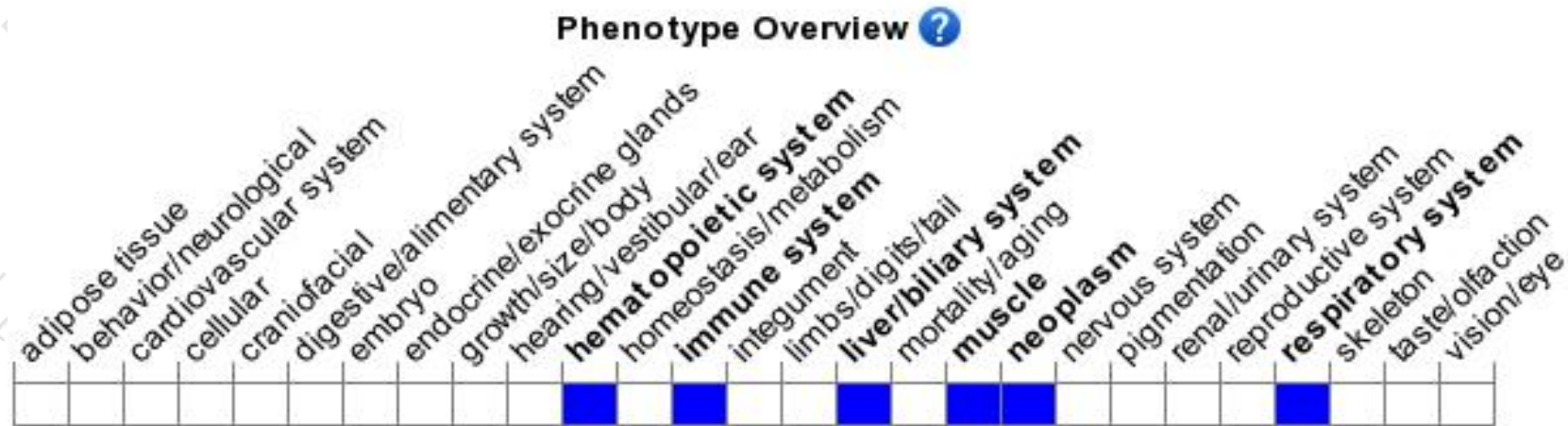
Genomic location distribution



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/>).

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

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