

# *Psmb9* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Psmb9***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# 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

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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

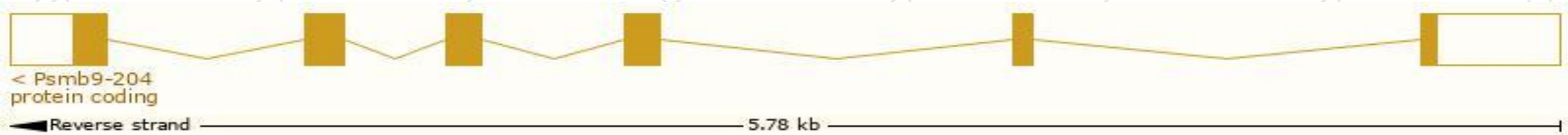
<b>Official Symbol</b>	Psmb9 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2) provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1346526</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000096727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

# Transcript information (Ensembl)

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

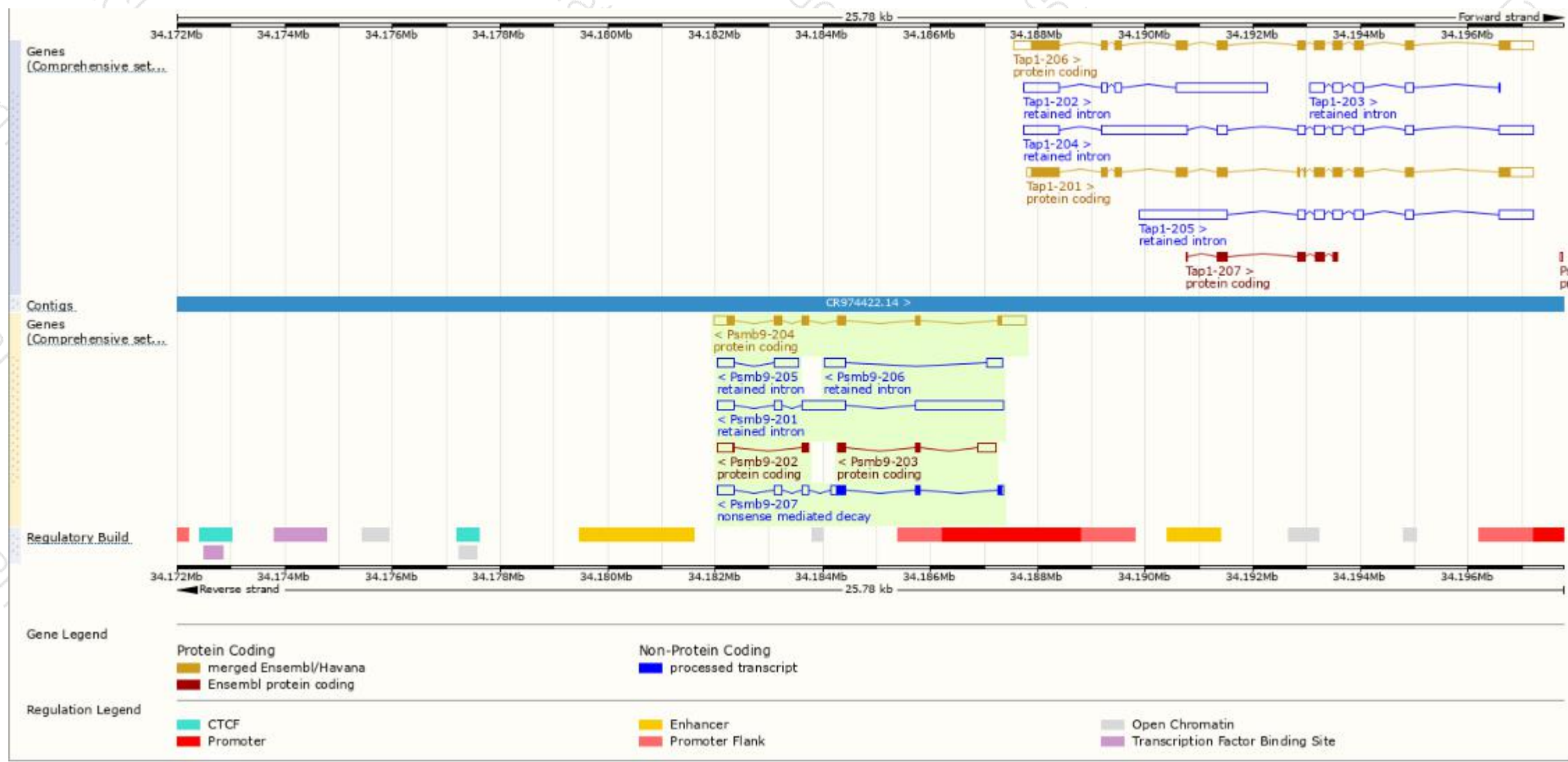
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psemb9-204	<a href="#">ENSMUST00000174576.3</a>	1352	<a href="#">219aa</a>	Protein coding	<a href="#">CCDS28642</a>	<a href="#">A0A0R4J256</a>	TSL:1 GENCODE basic APPRIS P1
Psemb9-203	<a href="#">ENSMUST00000173831.2</a>	529	<a href="#">63aa</a>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

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



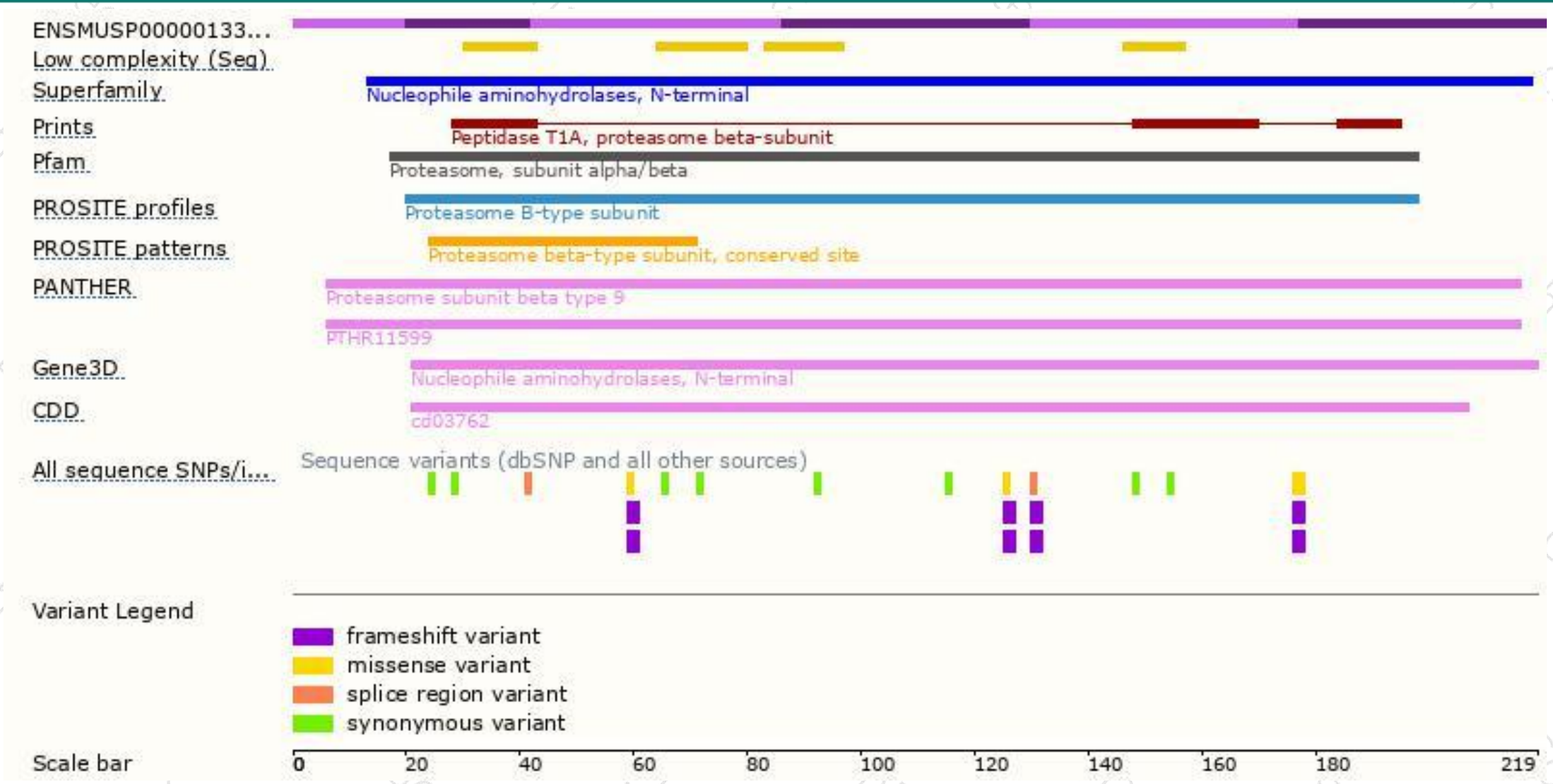


# Genomic location distribution

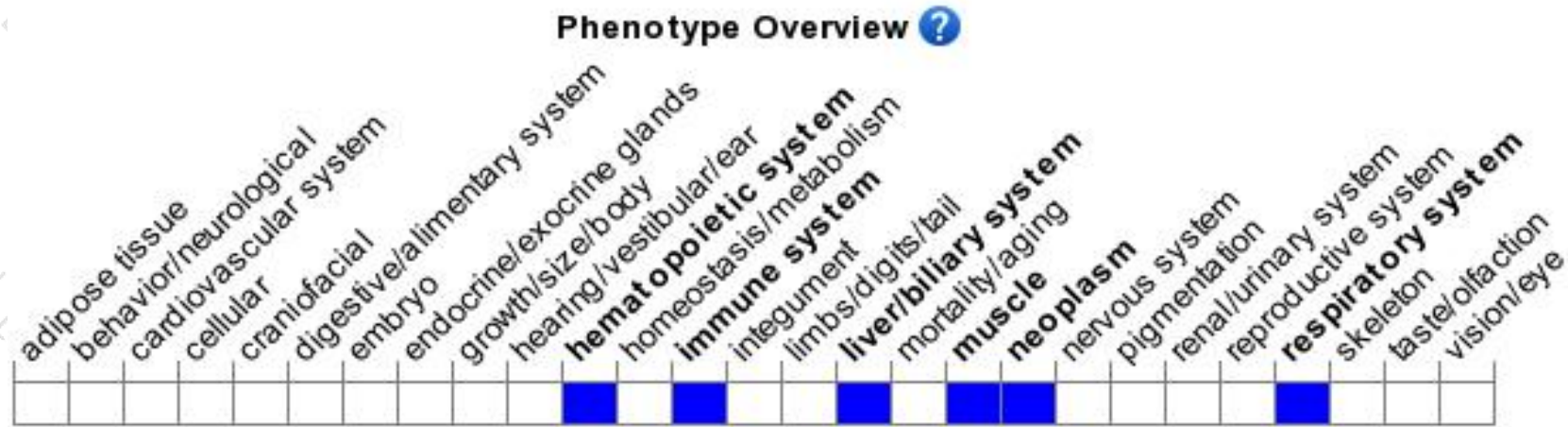




# Protein domain



# Mouse phenotype description(MGI )



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

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.

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

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