

# *Sacs* Cas9-CKO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Sacs*

**Project type**

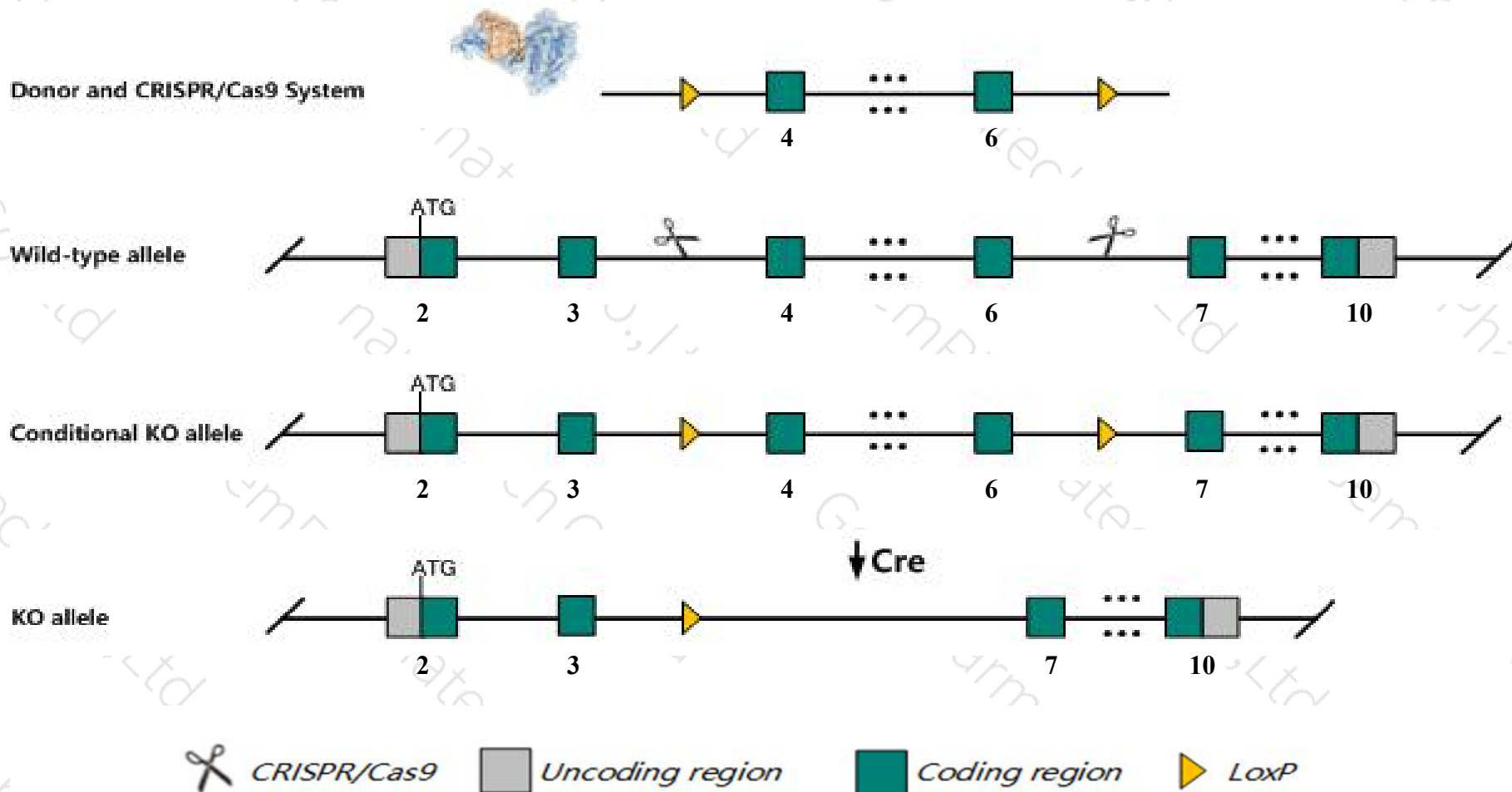
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



- The *Sacs* gene has 7 transcripts. According to the structure of *Sacs* gene, exon4-exon6 of *Sacs*-201 (ENSMUST00000089394.9) transcript is recommended as the knockout region. The region contains 286bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sacs* 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

- According to the existing MGI data, Mice homozygous for a knockout allele exhibit Purkinje cell degeneration with thickened tortuous dendrites and altered mitochondrial dysfunction.
- Transcript *Sacs*-207 may not be affected.
- The *Sacs* 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)

## Sacs *sacsin* [ *Mus musculus* (house mouse) ]

Gene ID: 50720, updated on 13-Mar-2020

### Summary

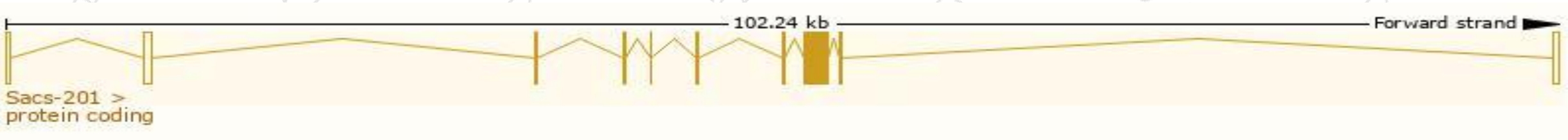
Official Symbol	Sacs provided by MGI
Official Full Name	sacsin provided by MGI
Primary source	MGI:MGI:1354724
See related	Ensembl:ENSMUSG00000048279
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	DNAJC29; A230052M14; E130115J16Rik
Expression	Broad expression in CNS E18 (RPKM 4.2), cerebellum adult (RPKM 4.2) and 18 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

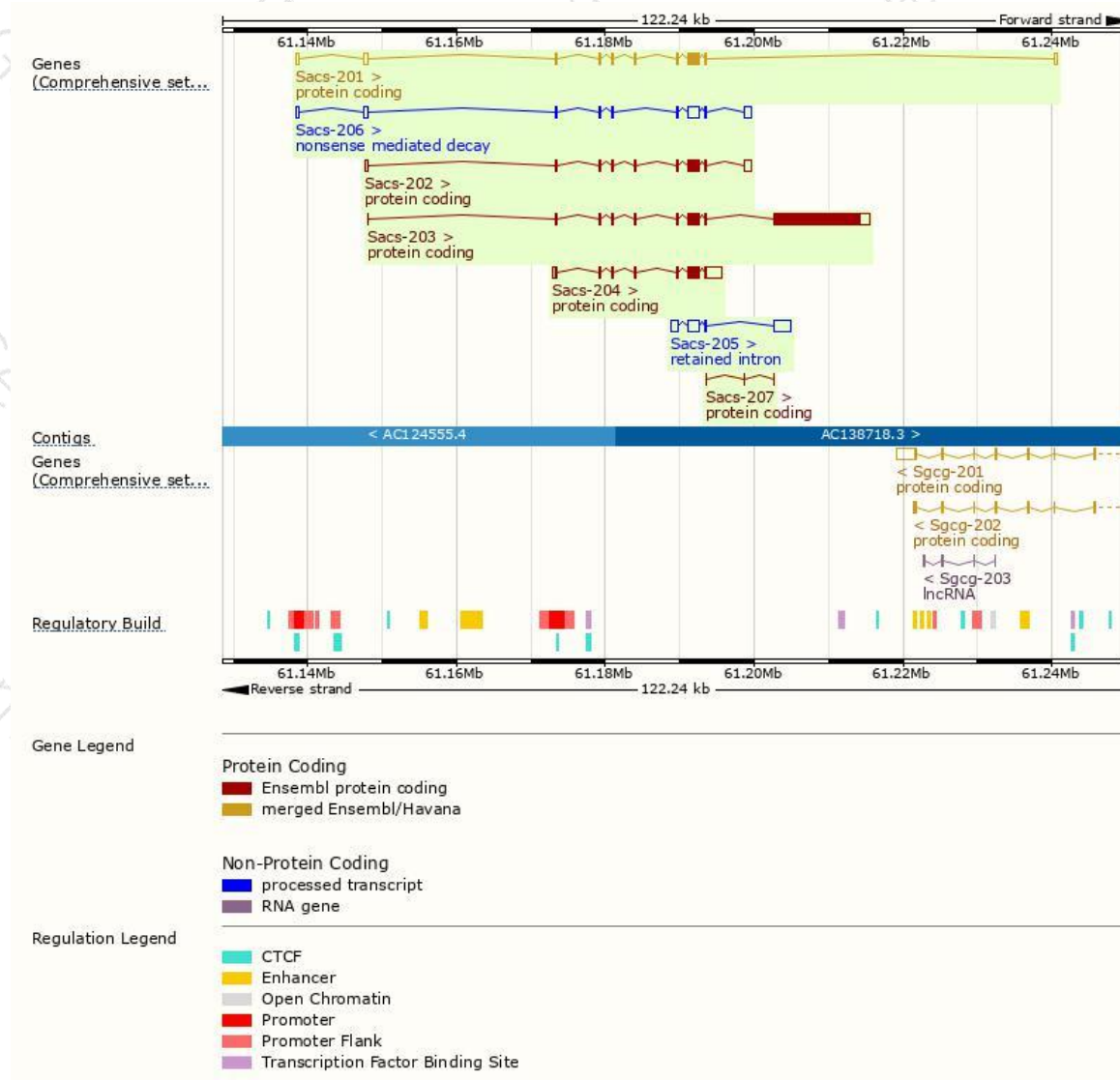
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sacs-201	<a href="#">ENSMUST00000089394.9</a>	3345	<a href="#">768aa</a>	Protein coding	<a href="#">CCDS27180</a>	<a href="#">A0A0R4J125</a>	TSL:1 GENCODE basic APPRIS P2
Sacs-203	<a href="#">ENSMUST00000119943.7</a>	14991	<a href="#">4582aa</a>	Protein coding	-	<a href="#">E9QNY8</a>	TSL:5 GENCODE basic APPRIS ALT2
Sacs-204	<a href="#">ENSMUST00000121091.1</a>	4581	<a href="#">745aa</a>	Protein coding	-	<a href="#">D3Z3H1</a>	TSL:1 GENCODE basic APPRIS ALT2
Sacs-202	<a href="#">ENSMUST00000119509.8</a>	3468	<a href="#">744aa</a>	Protein coding	-	<a href="#">B2RRL5</a>	TSL:5 GENCODE basic APPRIS ALT2
Sacs-207	<a href="#">ENSMUST00000229692.1</a>	42	<a href="#">14aa</a>	Protein coding	-	<a href="#">A0A2R8VKQ1</a>	CDS 5' and 3' incomplete
Sacs-206	<a href="#">ENSMUST00000227570.1</a>	3884	<a href="#">137aa</a>	Nonsense mediated decay	-	<a href="#">A0A2I3BR28</a>	-
Sacs-205	<a href="#">ENSMUST00000150222.1</a>	4752	No protein	Retained intron	-	-	TSL:1

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

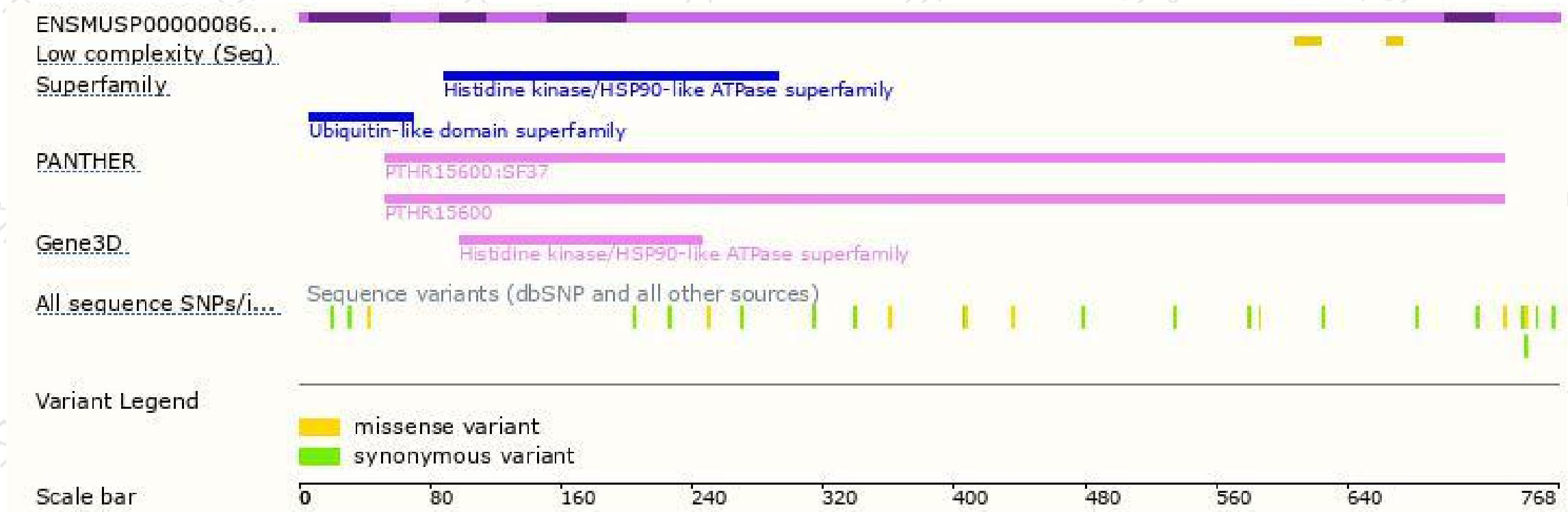


# Genomic location distribution

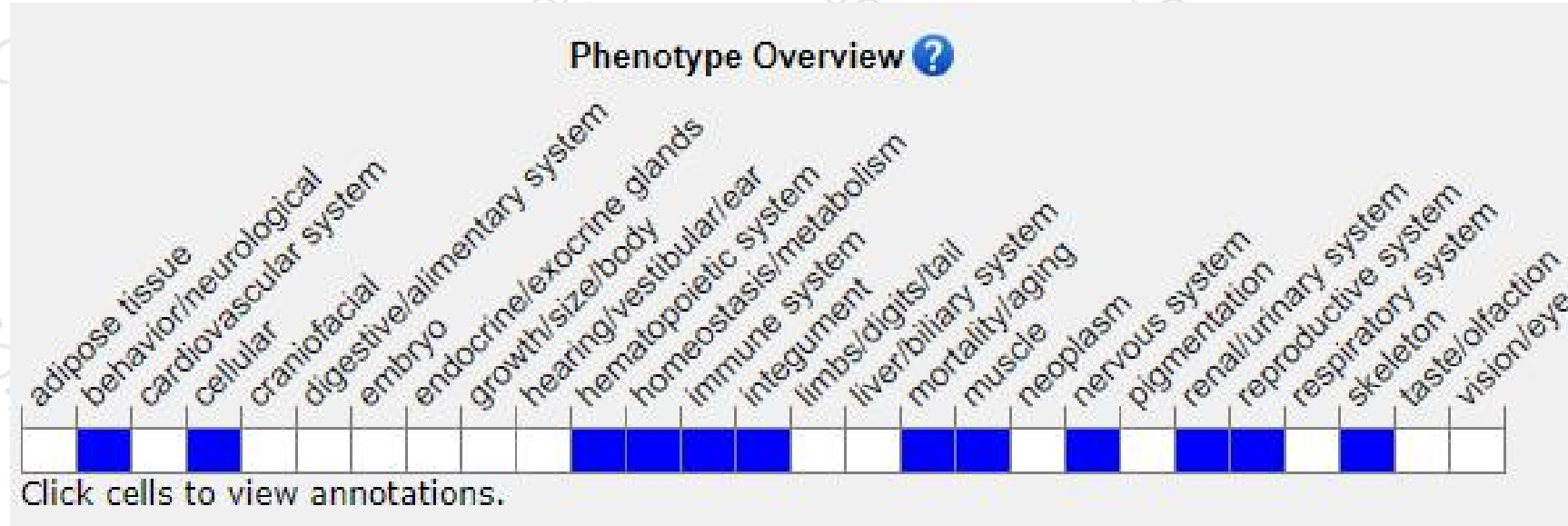




# Protein domain



# 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, Mice homozygous for a knockout allele exhibit Purkinje cell degeneration with thickened tortuous dendrites and altered mitochondrial dysfunction.

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

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