

# ***Hdac6*** Cas9-KO Strategy

**Designer:**

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**Design Date:**

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# Project Overview

**Project Name**

*Hdac6*

**Project type**

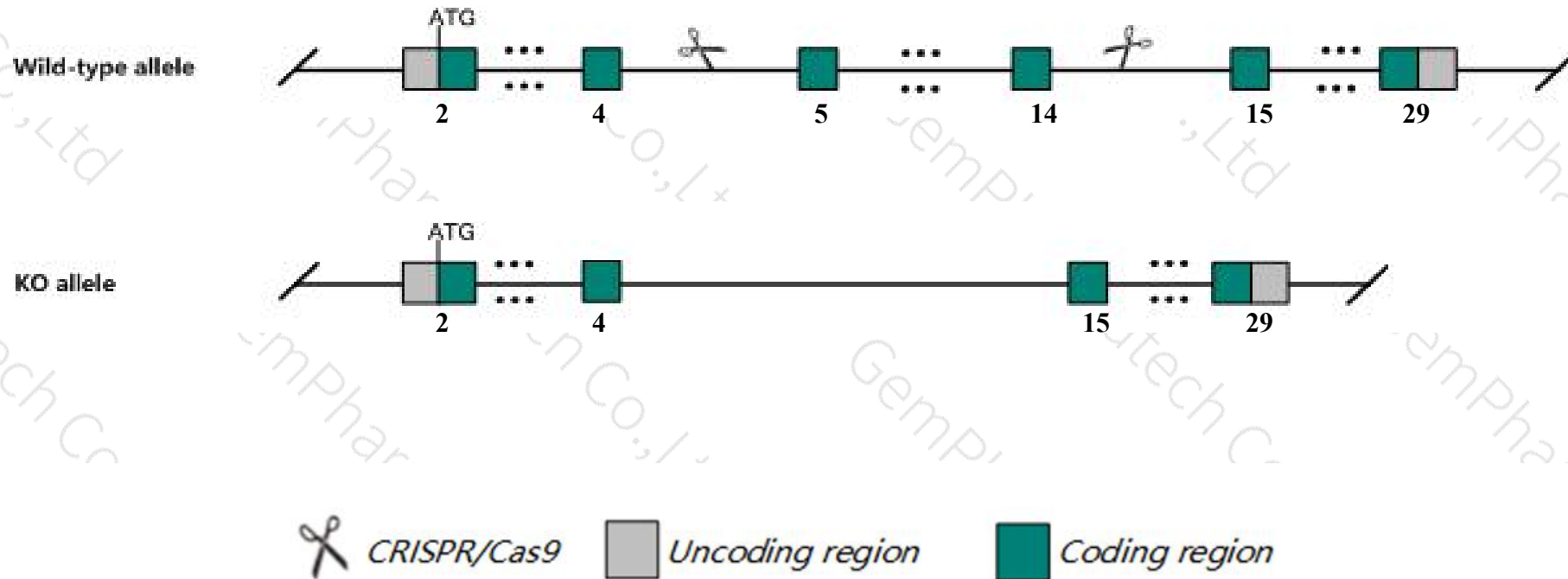
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hdac6* gene. The schematic diagram is as follows:



- The *Hdac6* gene has 10 transcripts. According to the structure of *Hdac6* gene, exon5-exon14 of *Hdac6-201* (ENSMUST00000033501.14) transcript is recommended as the knockout region. The region contains 838bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hdac6* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Although mice homozygous for a knock-out allele exhibit global tubulin hyperacetylation, they are viable and fertile and display only a moderately impaired immune response and a minor increase in cancellous bone mineral density.
- The *Hdac6* gene is located on the ChrX. 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)

## Hdac6 histone deacetylase 6 [Mus musculus (house mouse)]

Gene ID: 15185, updated on 9-Apr-2019

### Summary



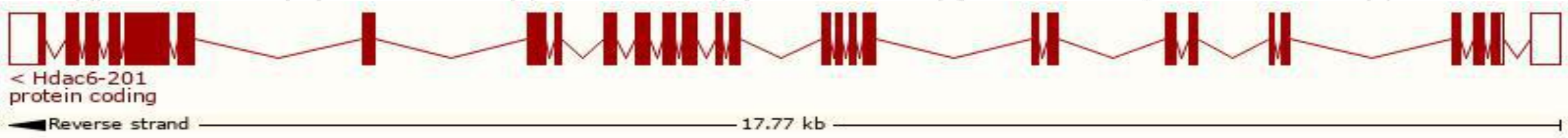
<b>Official Symbol</b>	Hdac6 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	histone deacetylase 6 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1333752</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000031161</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</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>	Hd6, Hdac5, Sfc6, mHDA2
<b>Expression</b>	Ubiquitous expression in genital fat pad adult (RPKM 65.5), whole brain E14.5 (RPKM 26.3) and 27 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

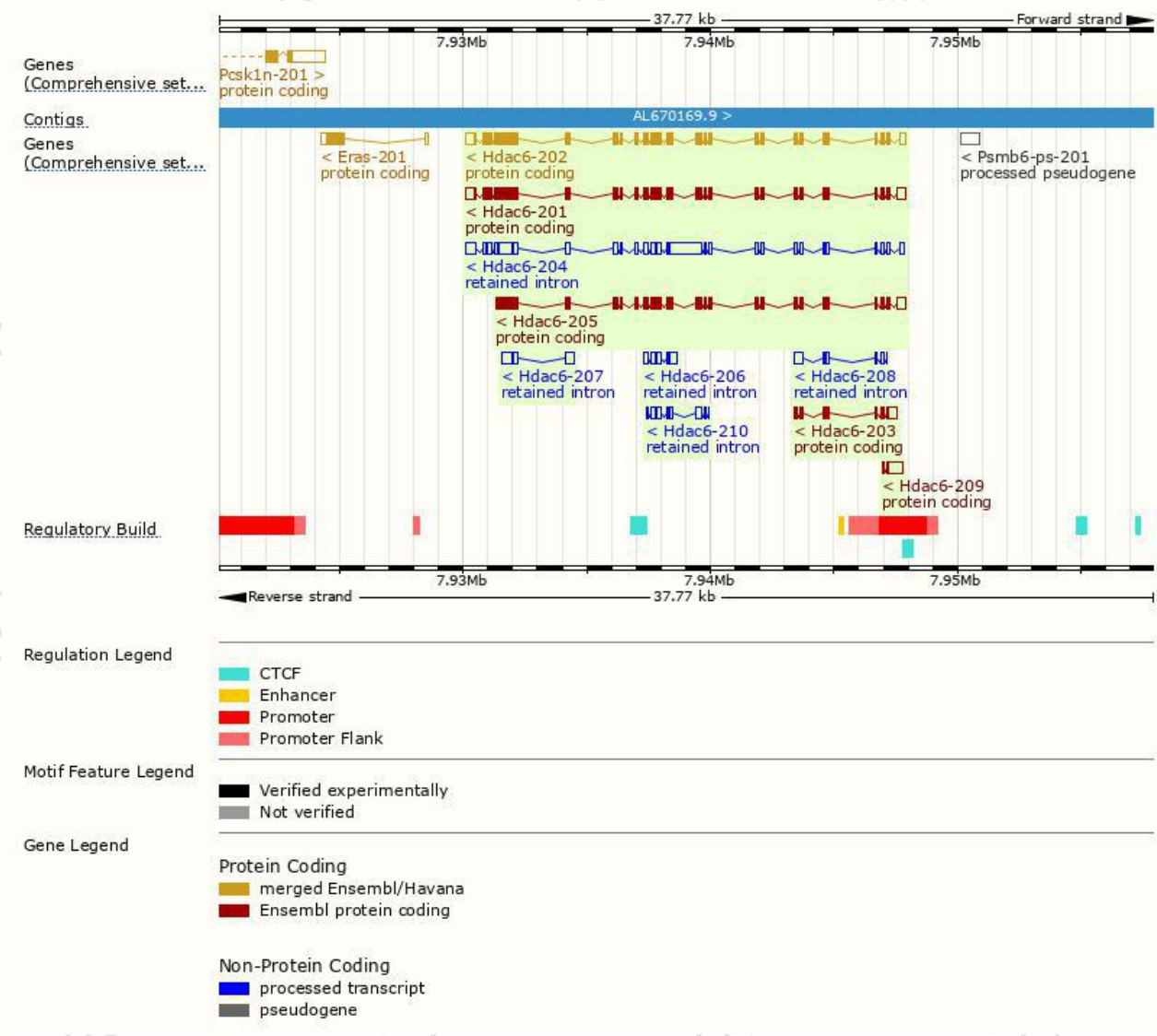
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hdac6-201	<a href="#">ENSMUST00000033501.14</a>	4142	<a href="#">1149aa</a>	Protein coding	<a href="#">CCDS40845</a>	<a href="#">Q9Z2V5</a>	TSL:5 GENCODE basic APPRIS P1
Hdac6-202	<a href="#">ENSMUST00000115642.7</a>	4069	<a href="#">1149aa</a>	Protein coding	<a href="#">CCDS40845</a>	<a href="#">Q9Z2V5</a>	TSL:1 GENCODE basic APPRIS P1
Hdac6-205	<a href="#">ENSMUST00000145675.7</a>	3371	<a href="#">1008aa</a>	Protein coding	-	<a href="#">A0A1B0GX25</a>	CDS 3' incomplete TSL:1
Hdac6-203	<a href="#">ENSMUST00000133349.1</a>	932	<a href="#">197aa</a>	Protein coding	-	<a href="#">B1AUA8</a>	CDS 3' incomplete TSL:3
Hdac6-209	<a href="#">ENSMUST00000154244.1</a>	678	<a href="#">41aa</a>	Protein coding	-	<a href="#">B1AUA9</a>	CDS 3' incomplete TSL:3
Hdac6-204	<a href="#">ENSMUST00000137499.7</a>	5037	No protein	Retained intron	-	-	TSL:2
Hdac6-207	<a href="#">ENSMUST00000153788.1</a>	894	No protein	Retained intron	-	-	TSL:5
Hdac6-210	<a href="#">ENSMUST00000156127.1</a>	853	No protein	Retained intron	-	-	TSL:5
Hdac6-206	<a href="#">ENSMUST00000151916.7</a>	804	No protein	Retained intron	-	-	TSL:5
Hdac6-208	<a href="#">ENSMUST00000154200.1</a>	718	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Hdac6-201* transcript,The transcription is shown below

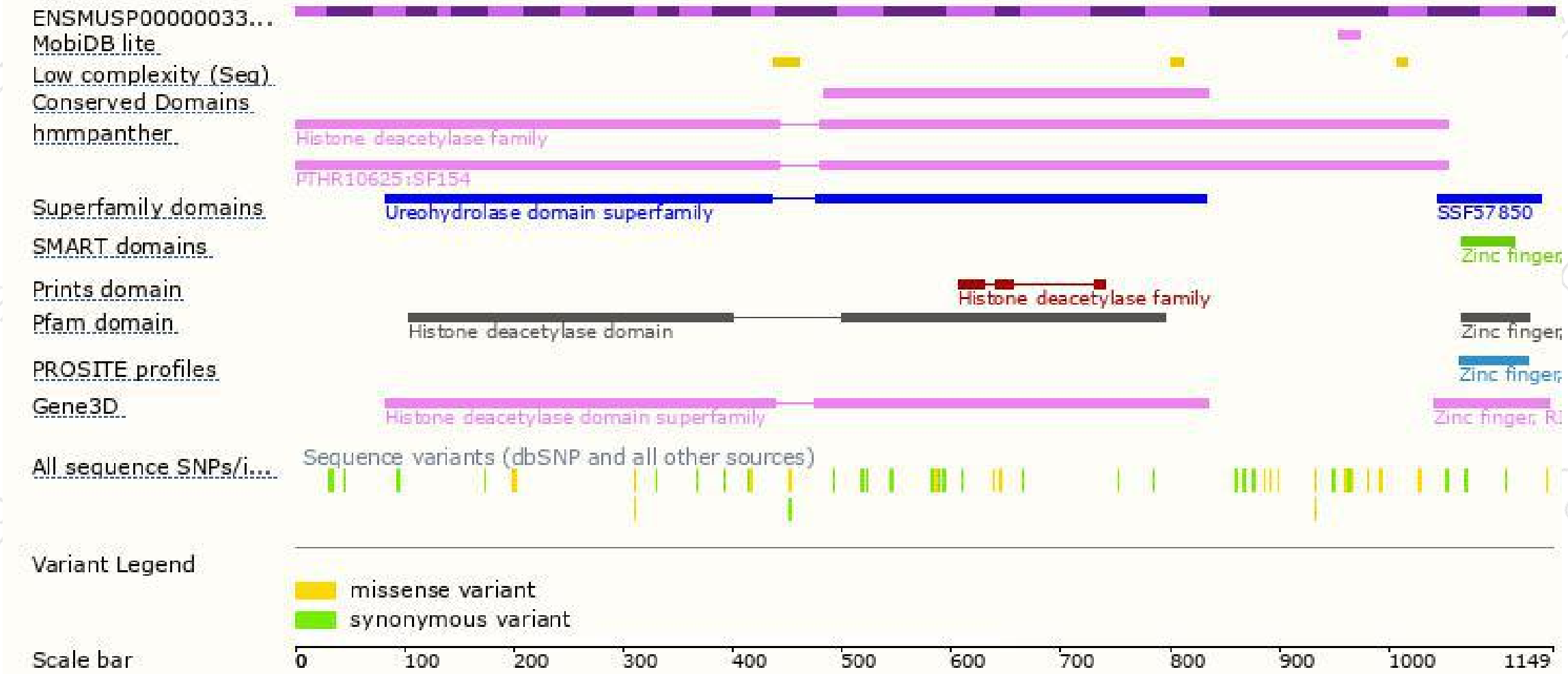


# Genomic location distribution

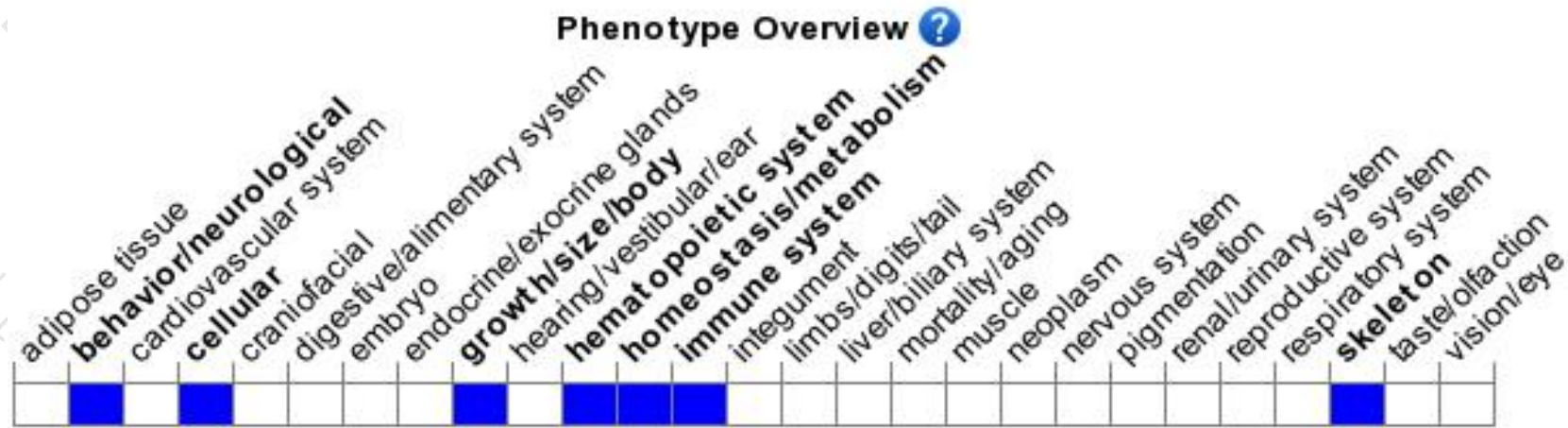




# Protein domain



# 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, Although mice homozygous for a knock-out allele exhibit global tubulin hyperacetylation, they are viable and fertile and display only a moderately impaired immune response and a minor increase in cancellous bone mineral density.

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

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