

# ***Pltp Cas9-KO Strategy***

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**Reviewer :**

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# Project Overview

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**Project Name**

*Pltp*

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**Project type**

Cas9-KO

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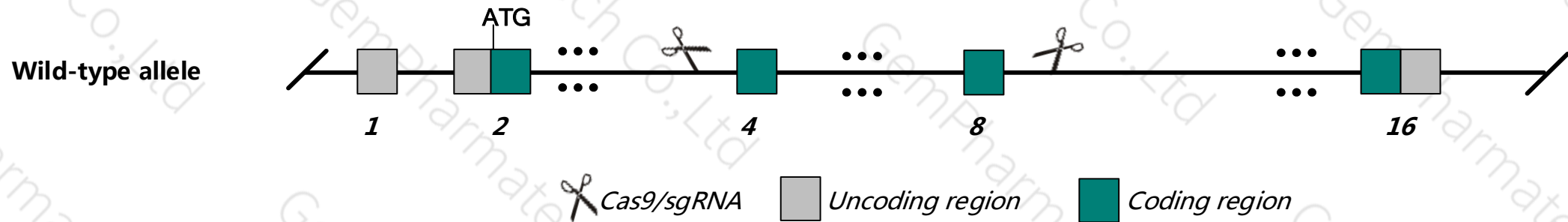
**Animal background**

C57BL/6JGpt

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# Knockout strategy

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



# Technical routes

- The *Pltp* gene has 7 transcripts, According to the structure of *Pltp* gene, exon4-exon8 of *Pltp-201* transcript is recommended as the knockout region. The region contains the 505bp coding sequence. Knock out the region, result in destruction of protein.
- This project uses CRISPR/Cas9 technology to modify *Pltp* gene. The brief process is as follows: sgRNA was transcribed in vitro, Cas9, sgRNA were microinjected into fertilized eggs of C57BL/6JGpt mice and homologous recombination was carried out to obtain F0 mice. A stable and hereditary F1 generation mouse model was obtained by mating F0 generation mice with C57BL/6JGpt mice which were confirmed positive by PCR-sequencing.

- According to the existing MGI data , Mice homozygous for disruptions in this gene have lower levels of circulating HDL and exhibit symptoms of dry eye syndrome such as corneal epithelial damage.
- The *Pltp* gene is located in the Chr2. If the knockout mice are mixed with other mice, two target genes are avoided on the same chromosome as possible, otherwise the offspring of mice with double gene positive and homozygous gene knockout can not be obtained.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of gene transcription and translation processes, all risks cannot be predicted under existing information.

# Gene information ( NCBI )

## Pltp phospholipid transfer protein [ *Mus musculus* (house mouse) ]

Gene ID: 18830, updated on 22-Jan-2019

### Summary

Official Symbol	Pltp provided by <a href="#">MGI</a>
Official Full Name	phospholipid transfer protein provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:103151</a>
See related	<a href="#">Ensembl:ENSMUSG00000017754</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Bpife; OD107
Expression	Broad expression in lung adult (RPKM 368.4), subcutaneous fat pad adult (RPKM 153.5) and 18 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

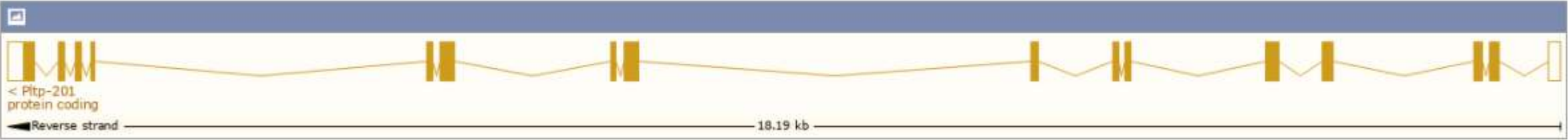


# Transcript information ( Ensembl )

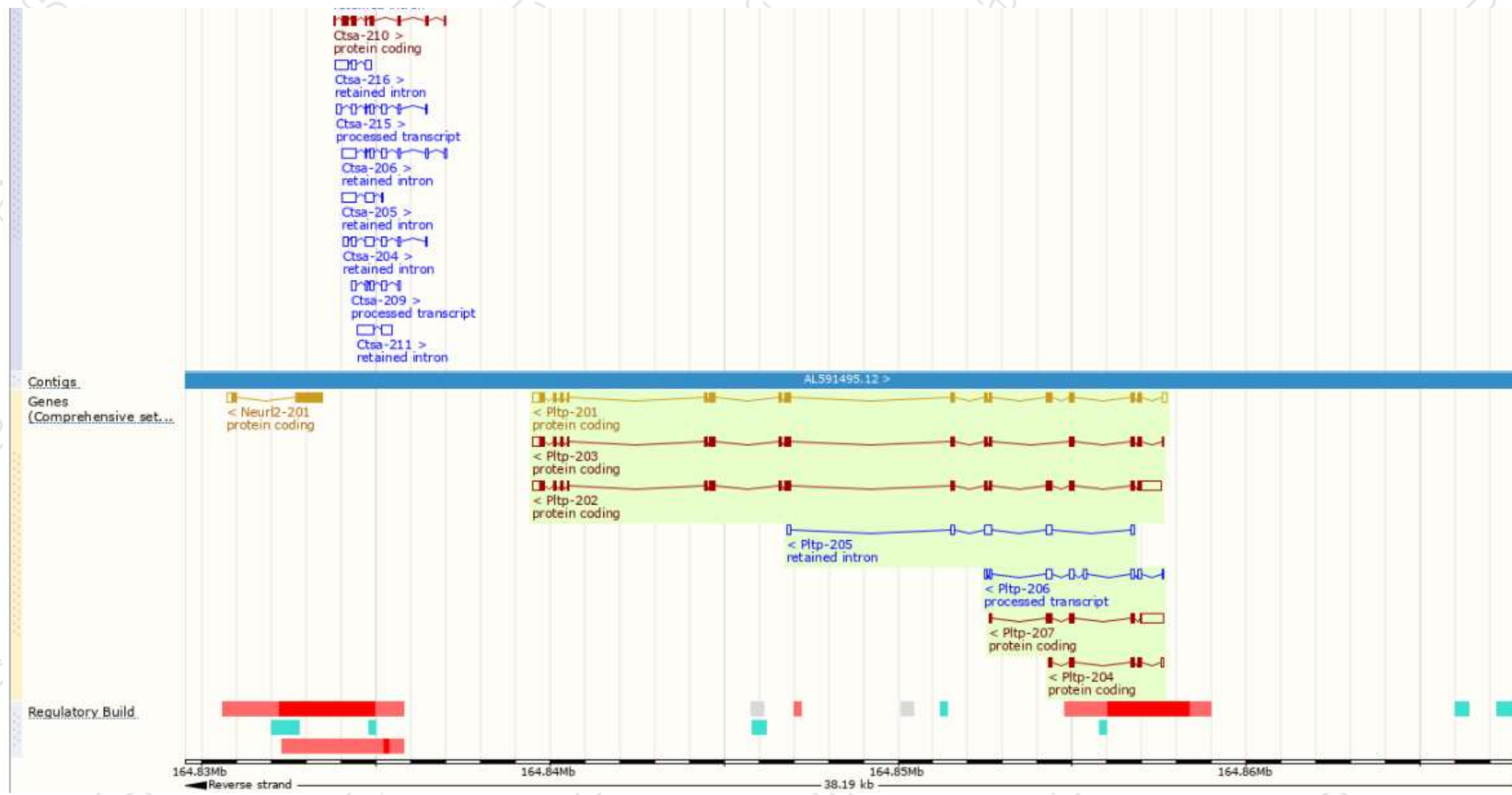
The gene has 7 transcripts, and all transcripts are shown below :

Show/hide columns (1 hidden)								Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags	
Pltp-202	<a href="#">ENSMUST00000109316.7</a>	2226	<a href="#">493aa</a>	Protein coding	<a href="#">CCDS17063</a>	<a href="#">P55065</a> <a href="#">Q3UFS5</a>	-	TSL:1	GENCODE basic APPRIS P1
Pltp-201	<a href="#">ENSMUST00000059954.13</a>	1809	<a href="#">493aa</a>	Protein coding	<a href="#">CCDS17063</a>	<a href="#">P55065</a> <a href="#">Q3UFS5</a>	<a href="#">NM_011125</a> <a href="#">NP_035255</a>	TSL:1	GENCODE basic APPRIS P1
Pltp-203	<a href="#">ENSMUST00000109317.9</a>	1575	<a href="#">441aa</a>	Protein coding	-	<a href="#">A2A5K2</a>	-	TSL:5	GENCODE basic
Pltp-207	<a href="#">ENSMUST00000156255.7</a>	1130	<a href="#">165aa</a>	Protein coding	-	<a href="#">A2A5K4</a>	-	CDS 3' incomplete	TSL:5
Pltp-204	<a href="#">ENSMUST00000128110.1</a>	538	<a href="#">147aa</a>	Protein coding	-	<a href="#">A2A5K3</a>	-	CDS 3' incomplete	TSL:2
Pltp-206	<a href="#">ENSMUST00000148912.1</a>	754	No protein	Processed transcript	-	-	-	TSL:5	
Pltp-205	<a href="#">ENSMUST00000142603.7</a>	653	No protein	Retained intron	-	-	-	TSL:3	

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

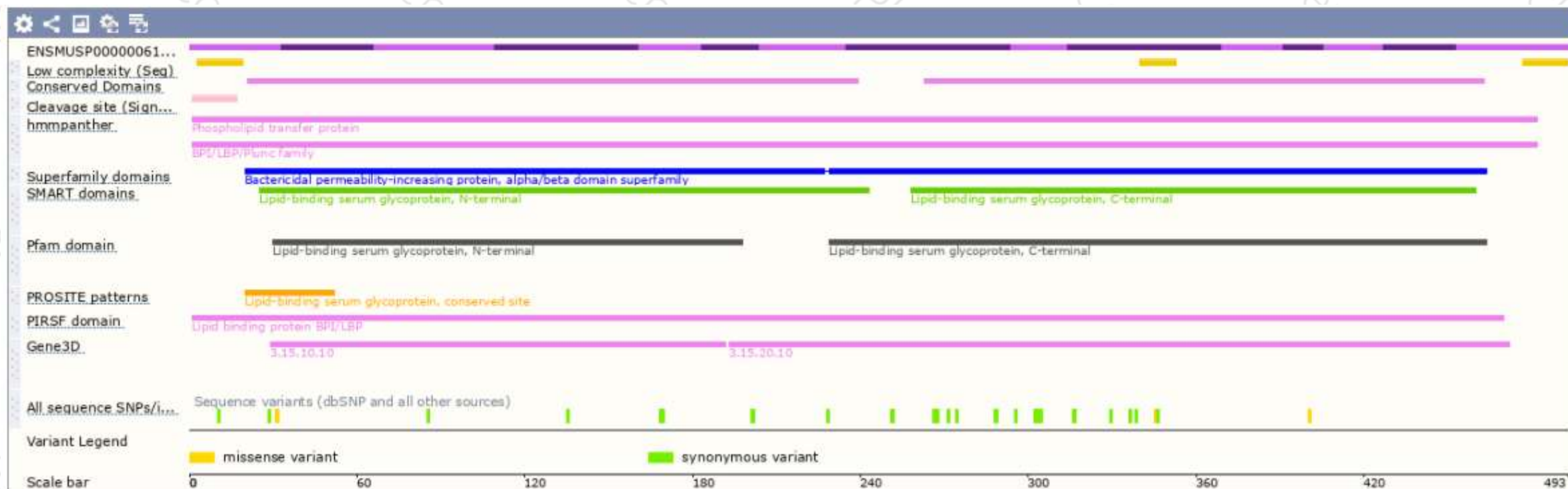


# Genomic location distribution

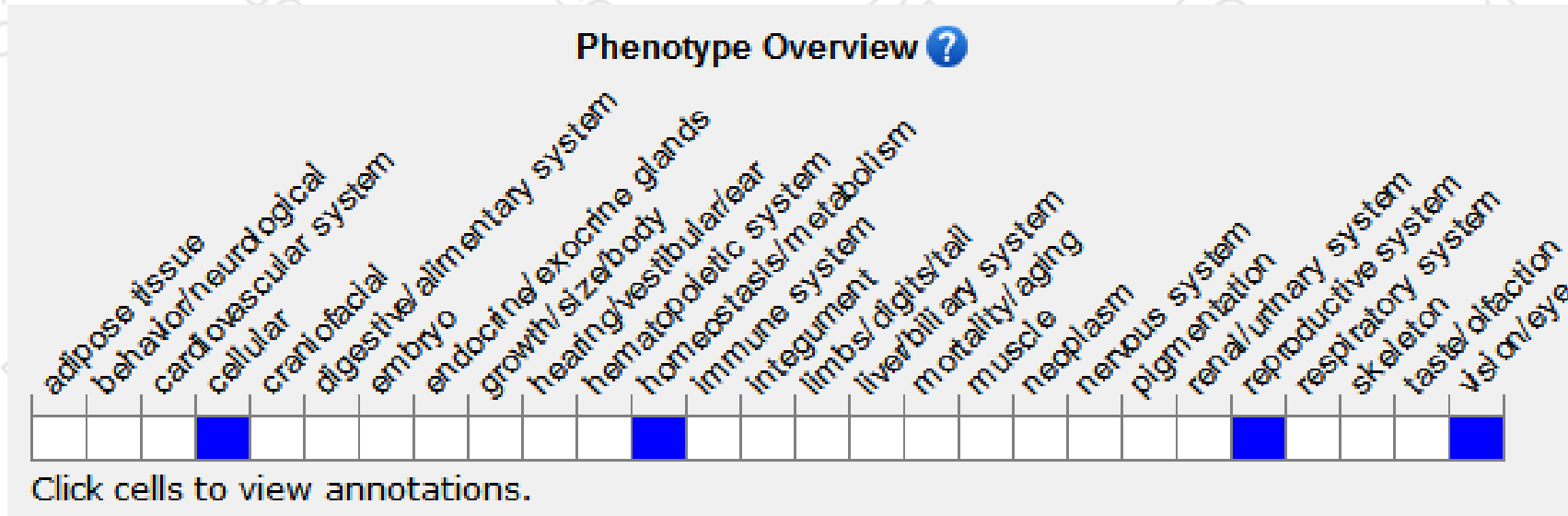




# Protein domain



# 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 disruptions in this gene have lower levels of circulating HDL and exhibit symptoms of dry eye syndrome such as corneal epithelial damage.

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