

Amfr Cas9-KO Strategy

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Design Date: 2019-11-20
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Project Overview

Project Name

Amfr

Project type

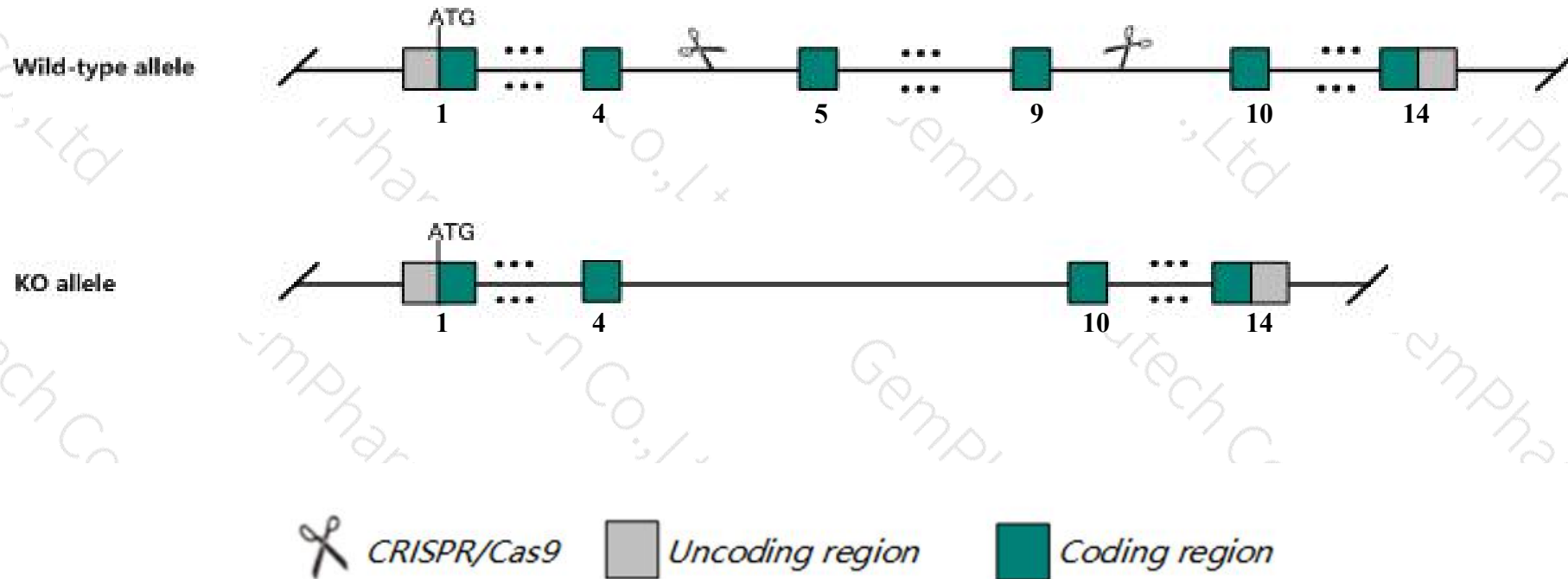
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Amfr* gene has 4 transcripts. According to the structure of *Amfr* gene, exon5-exon9 of *Amfr-201* (ENSMUST00000053766.13) transcript is recommended as the knockout region. The region contains 610bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Amfr* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice for a gene-trapped null allele are obese and develop liver steatosis and/or hepatic inflammation resembling nonalcoholic steatohepatitis. Some mice develop liver tumors. Mice homozygous for another knock-out allele exhibit normal HMGCR turnover in mouse embryonic fibroblasts.
- The *Amfr* gene is located on the Chr8. 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)

Amfr autocrine motility factor receptor [*Mus musculus* (house mouse)]

Gene ID: 23802, updated on 10-Oct-2019

Summary

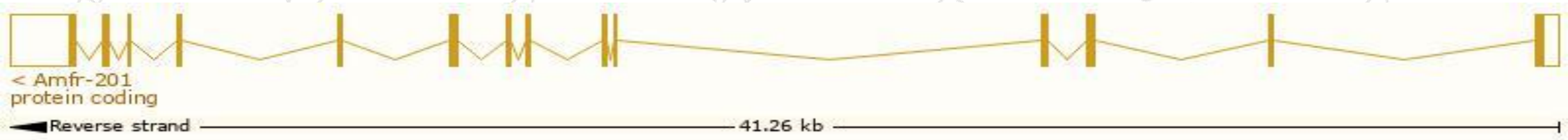
Official Symbol	Amfr provided by MGI
Official Full Name	autocrine motility factor receptor provided by MGI
Primary source	MGI:MGI:1345634
See related	Ensembl:ENSMUSG00000031751
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	gp78
Expression	Ubiquitous expression in adrenal adult (RPKM 95.7), liver adult (RPKM 63.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

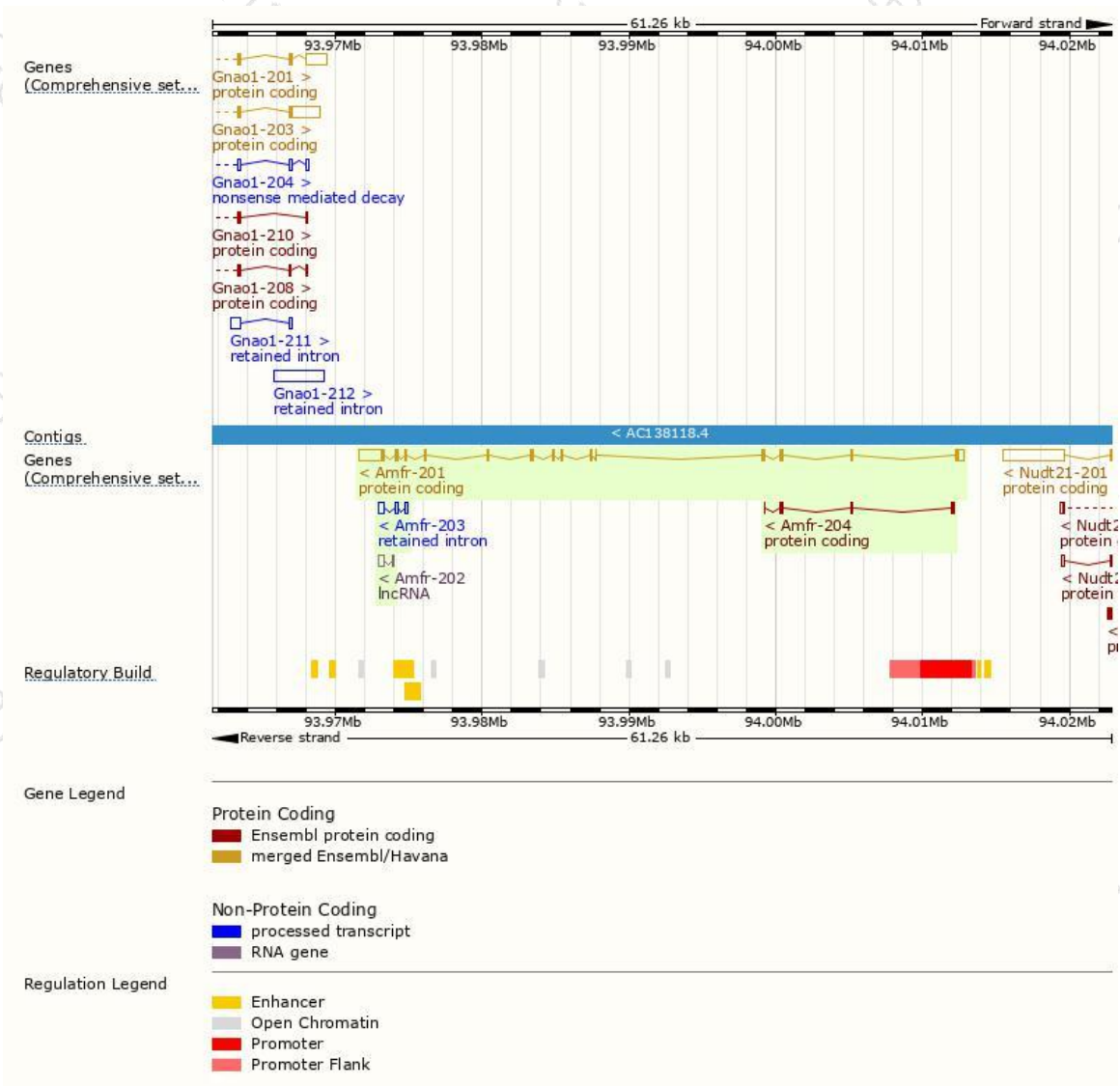
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Amfr-201	ENSMUST00000053766.13	3880	639aa	Protein coding	CCDS22533	Q3TCI2 Q9R049	TSL:1 GENCODE basic APPRIS P1
Amfr-204	ENSMUST00000143265.1	414	105aa	Protein coding	-	H3BJC0	CDS 3' incomplete TSL:5
Amfr-203	ENSMUST00000139702.1	779	No protein	Retained intron	-	-	TSL:2
Amfr-202	ENSMUST00000137475.1	392	No protein	lncRNA	-	-	TSL:5

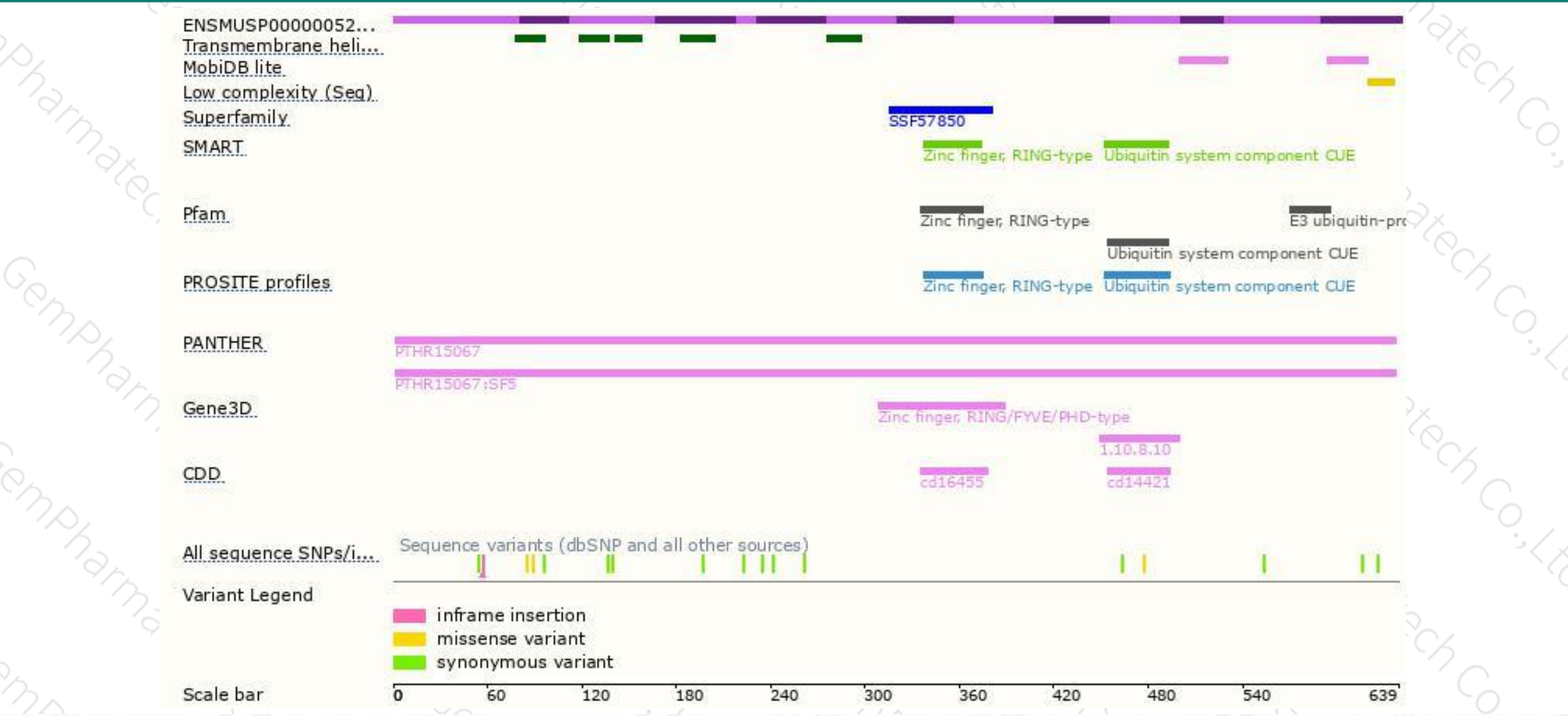
The strategy is based on the design of *Amfr-201* transcript,The transcription is shown below



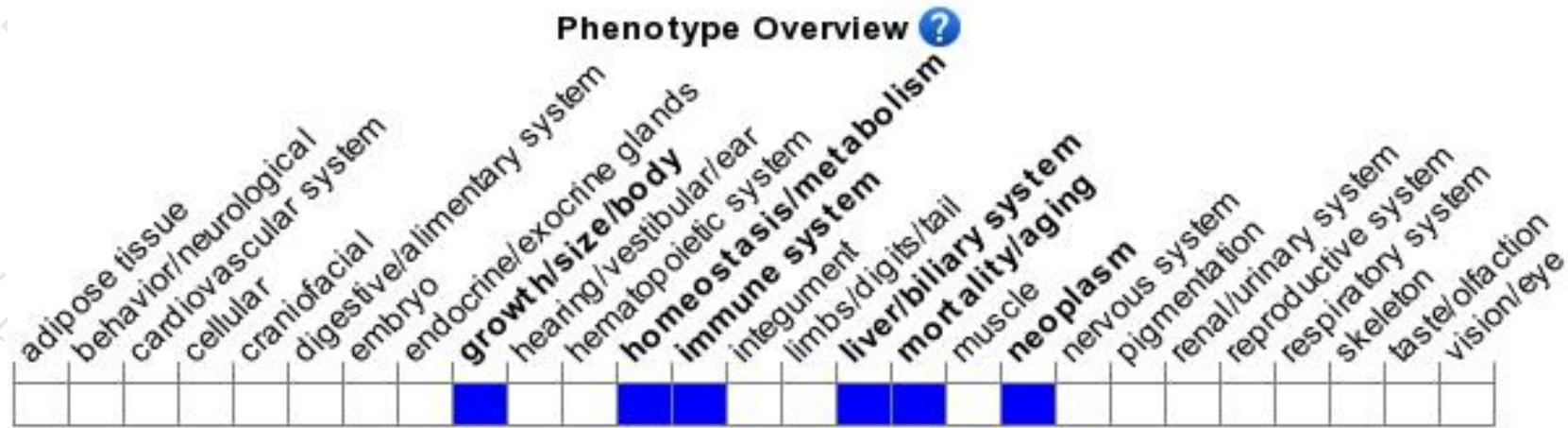
Genomic location distribution



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 for a gene-trapped null allele are obese and develop liver steatosis and/or hepatic inflammation resembling nonalcoholic steatohepatitis. Some mice develop liver tumors. Mice homozygous for another knock-out allele exhibit normal HMGCR turnover in mouse embryonic fibroblasts.

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

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