Rad21 Cas9-KO Strategy

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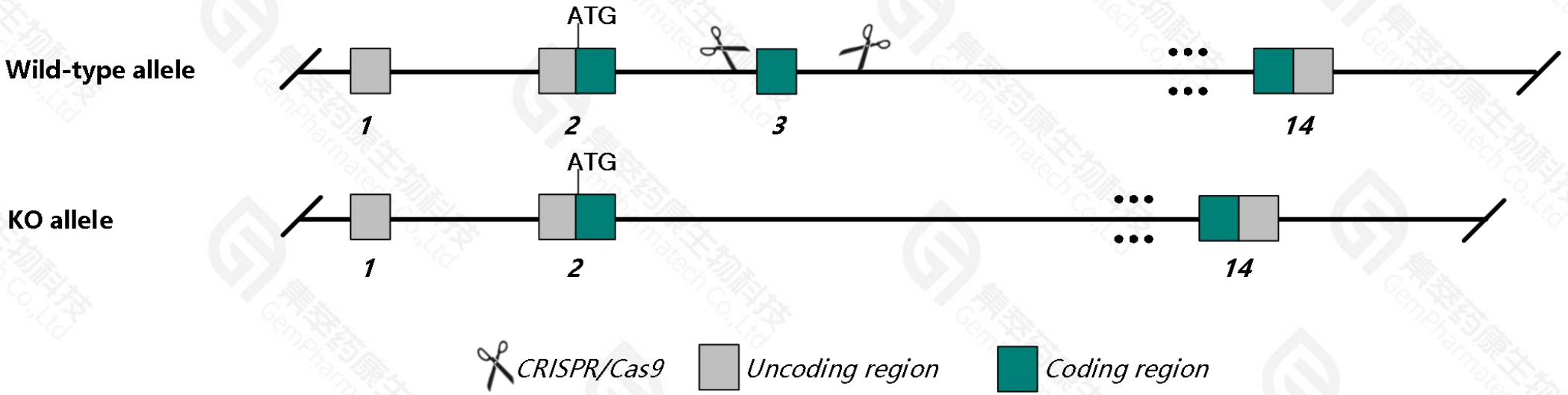
Project Overview

Project Name	***Rad21***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rad21* gene. The schematic diagram is as follows:



Technical routes

➢ The *Rad21* gene has 2 transcripts. According to the structure of *Rad21* gene, exon3 of *Rad21-201*(ENSMUST00000022927.11) transcript is recommended as the knockout region.The region contains 130bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rad21* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,mice homozygous for a targeted allele exhibit prenatal lethality, reduced male fertility, and produce oocytes that fail to maintain sister chromatids in the first mitosis following fertilization.

➢ The *Rad21* gene is located on the Chr15. 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）

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Rad21 RAD21 cohesin complex component [Mus musculus (house mouse)]

Gene ID: 19357, updated on 13-Mar-2020

Summary

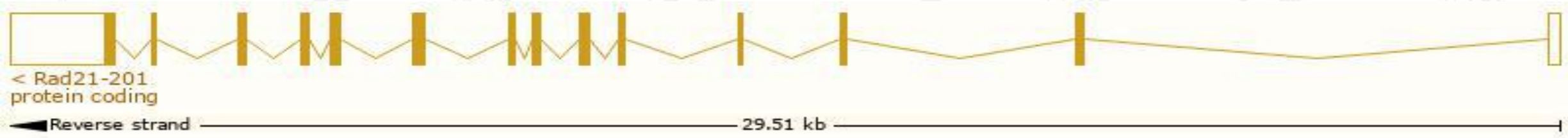
Official Symbol	Rad21 provided by MGI
Official Full Name	RAD21 cohesin complex component provided by MGI
Primary source	MGI:MGI:108016
See related	Ensembl:ENSMUSG00000022314
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	SCC1, mHR21, mKIAA0078
Expression	Ubiquitous expression in CNS E11.5 (RPKM 53.2), liver E14 (RPKM 45.0) and 24 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

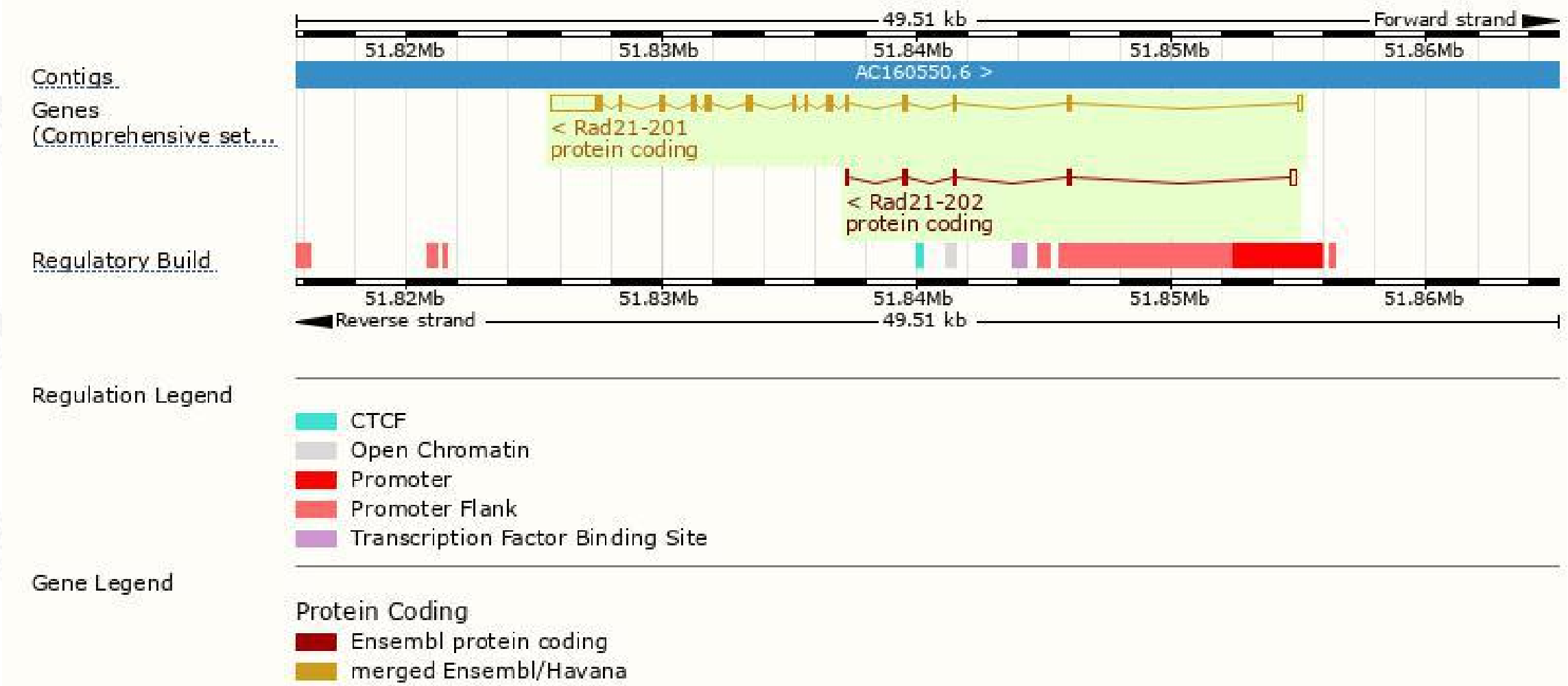
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rad21-201	ENSMUST00000022927.10	3956	635aa	Protein coding	CCDS27463	Q61550	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Rad21-202	ENSMUST00000226529.1	788	160aa	Protein coding	-	A0A2I3BS25	CDS 3' incomplete

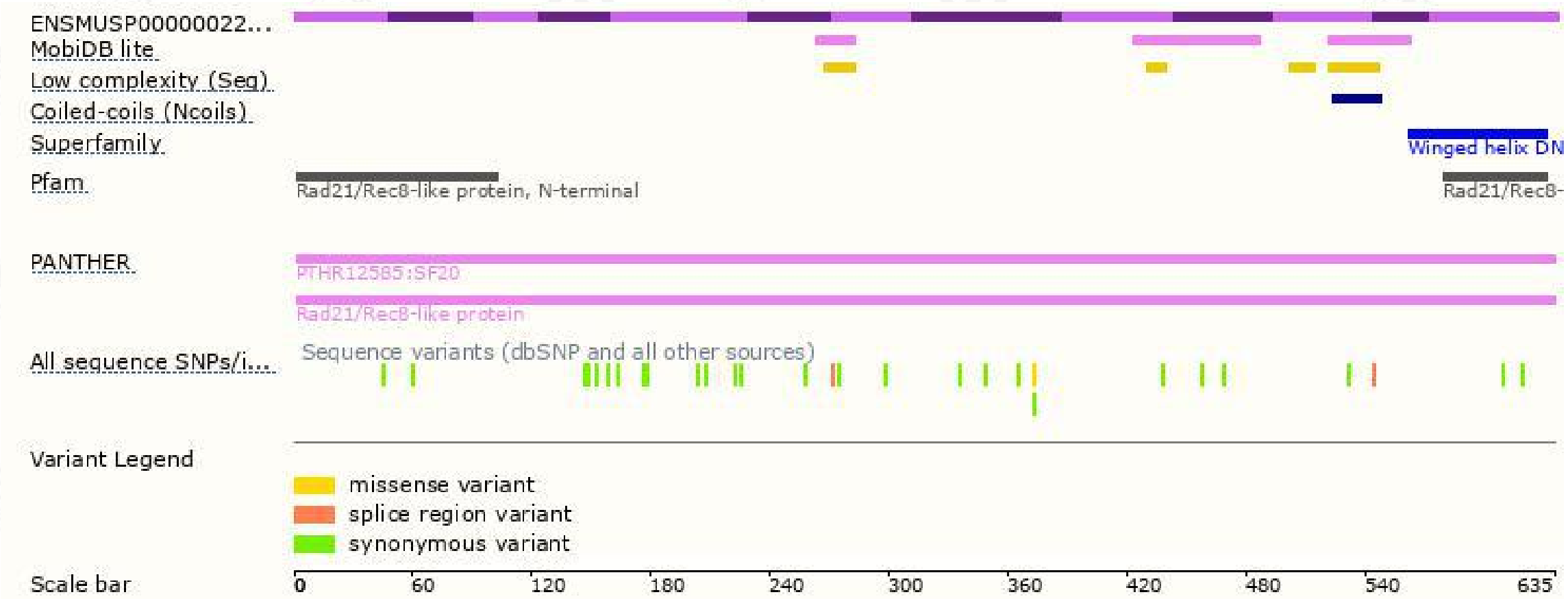
The strategy is based on the design of *Rad21-201* transcript,the transcription is shown below:



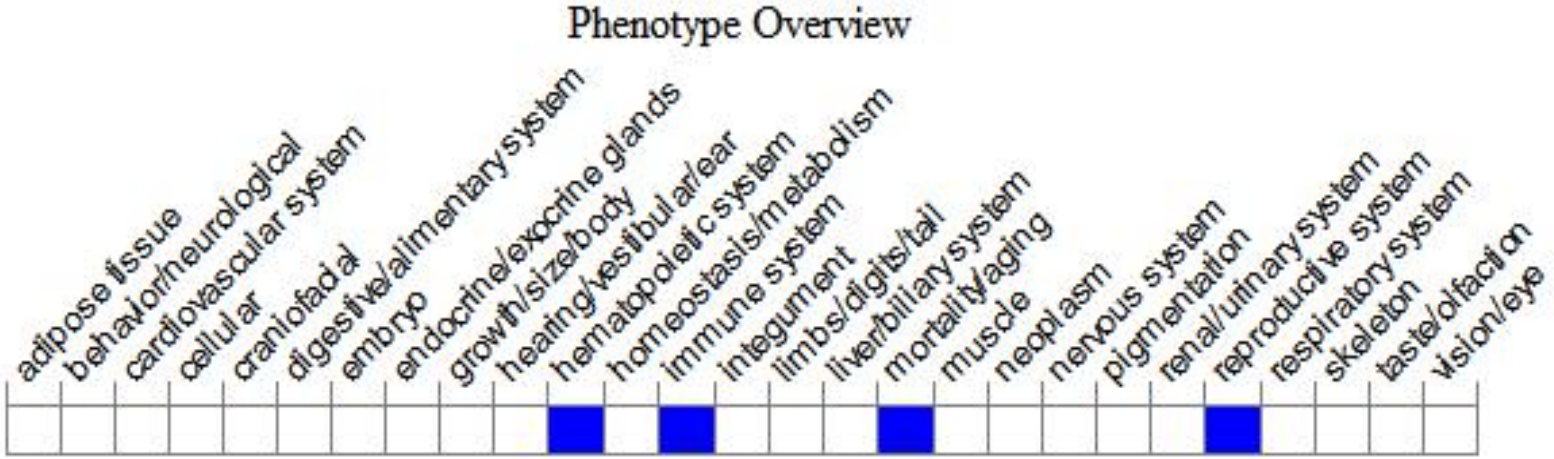
Genomic location distribution



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 targeted allele exhibit prenatal lethality, reduced male fertility, and produce oocytes that fail to maintain sister chromatids in the first mitosis following fertilization.

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