

Epor Cas9-CKO Strategy

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Project Overview

Project Name

Epor

Project type

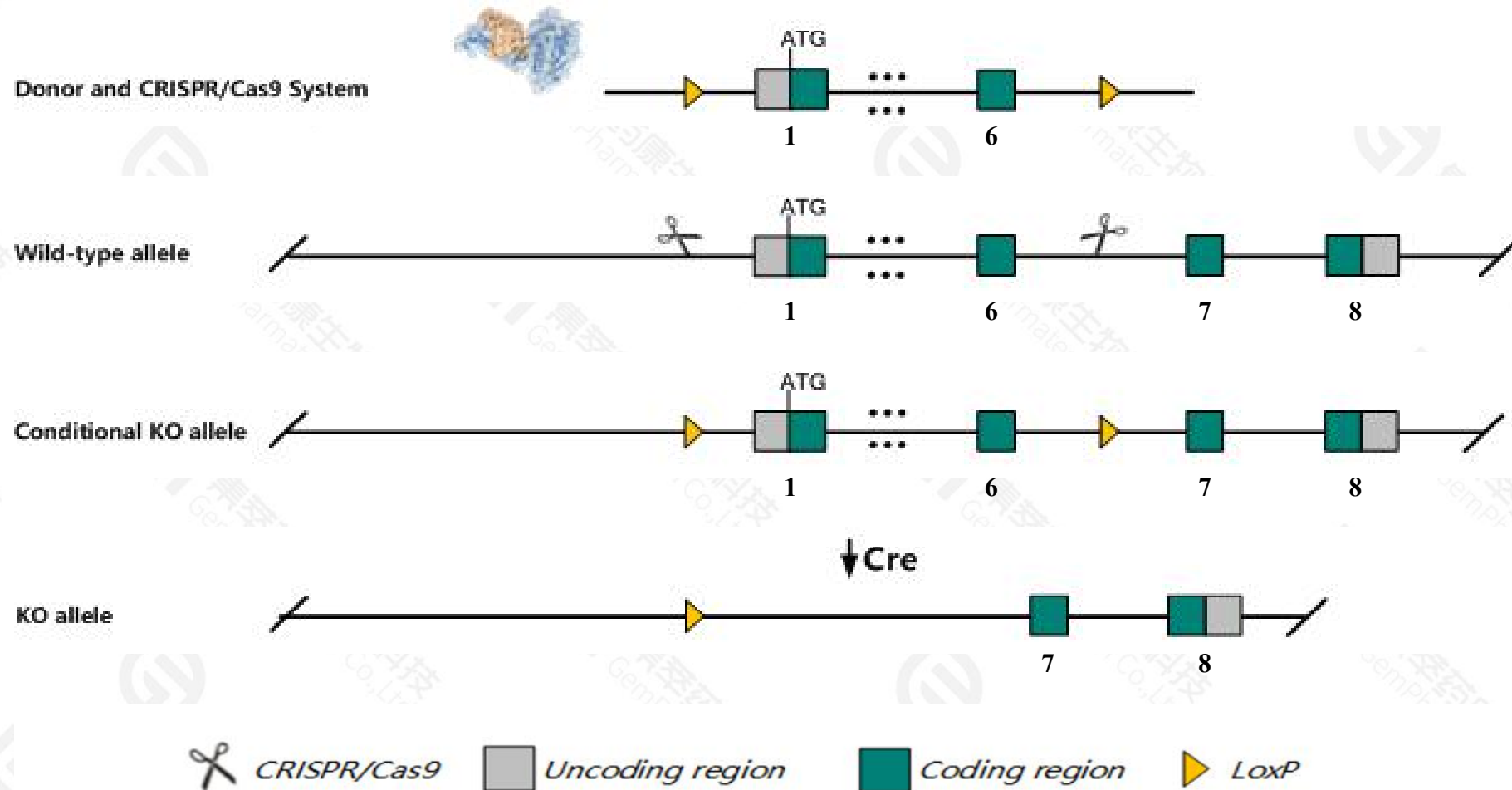
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Epor* gene has 2 transcripts. According to the structure of *Epor* gene, exon1-exon6 of *Epor-201*(ENSMUST00000006397.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Epor* 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.

- According to the existing MGI data, mutations in this locus affect erythropoiesis. Targeted null mutants die at embryonic day 11-12.5 with severe anemia. Mutants with truncated alleles are viable with mild changes in erythropoiesis. A human mutation replacement allele produces polycythemia.
- The *Epor* gene is located on the Chr9. 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)

Epor erythropoietin receptor [Mus musculus (house mouse)]

Gene ID: 13857, updated on 13-Mar-2020

Summary



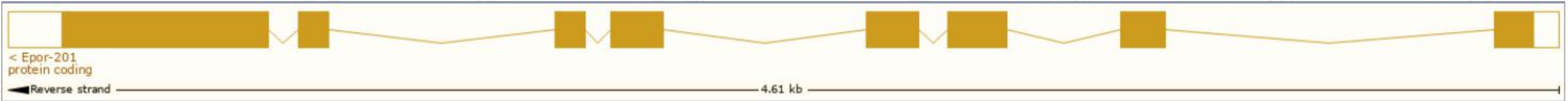
Official Symbol	Epor provided by MGI
Official Full Name	erythropoietin receptor provided by MGI
Primary source	MGI:MGI:95408
See related	Ensembl:ENSMUSG000000006235
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Biased expression in liver E14.5 (RPKM 73.4), liver E14 (RPKM 57.8) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

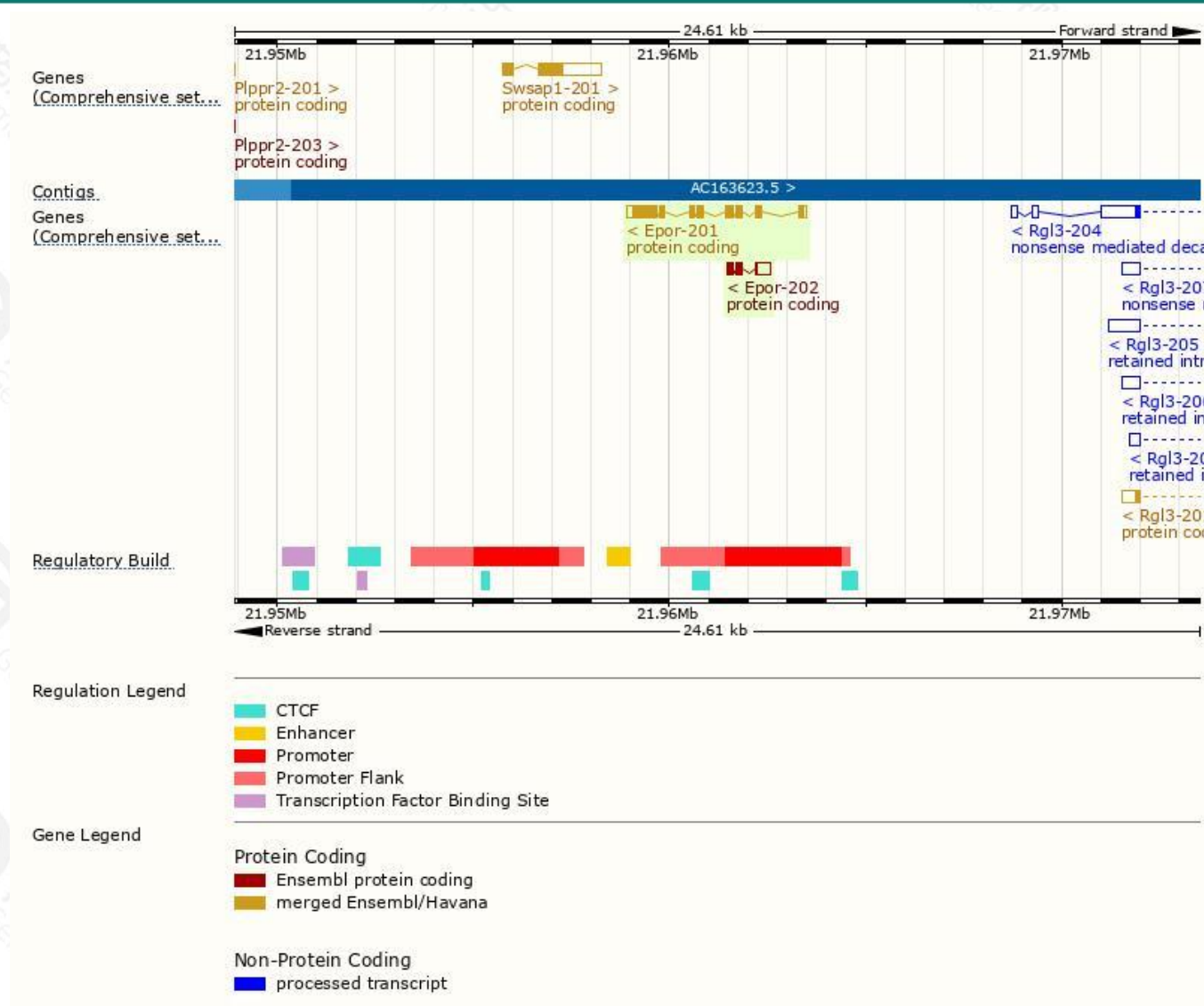
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epor-201	ENSMUST00000006397.6	1761	507aa	Protein coding	CCDS22915	P14753 Q3UTV9	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
Epor-202	ENSMUST00000213181.1	659	111aa	Protein coding	-	A0A1L1SRC0	CDS 3' incomplete TSL:2

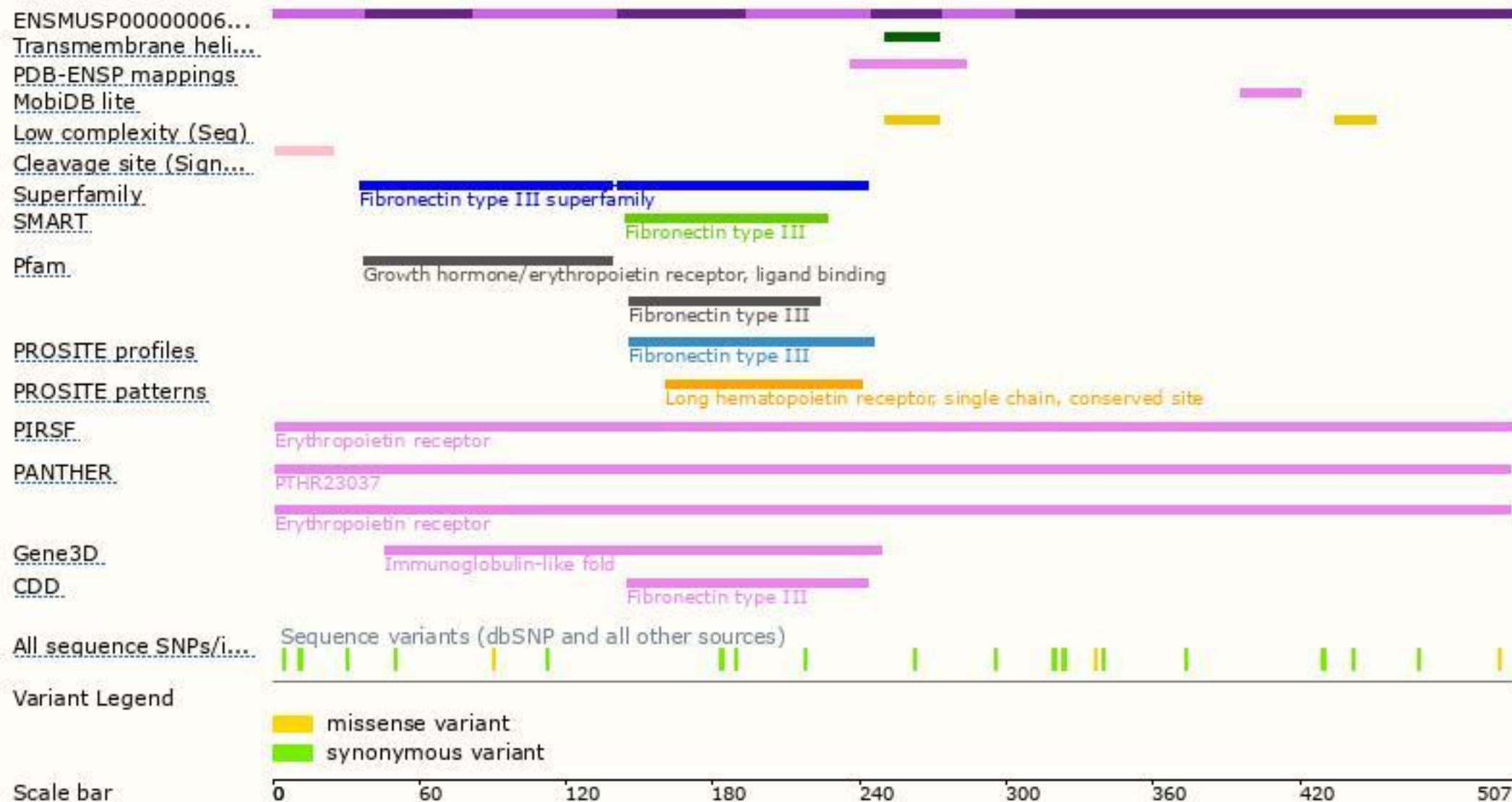
The strategy is based on the design of *Epor-201* transcript,the transcription is shown below:



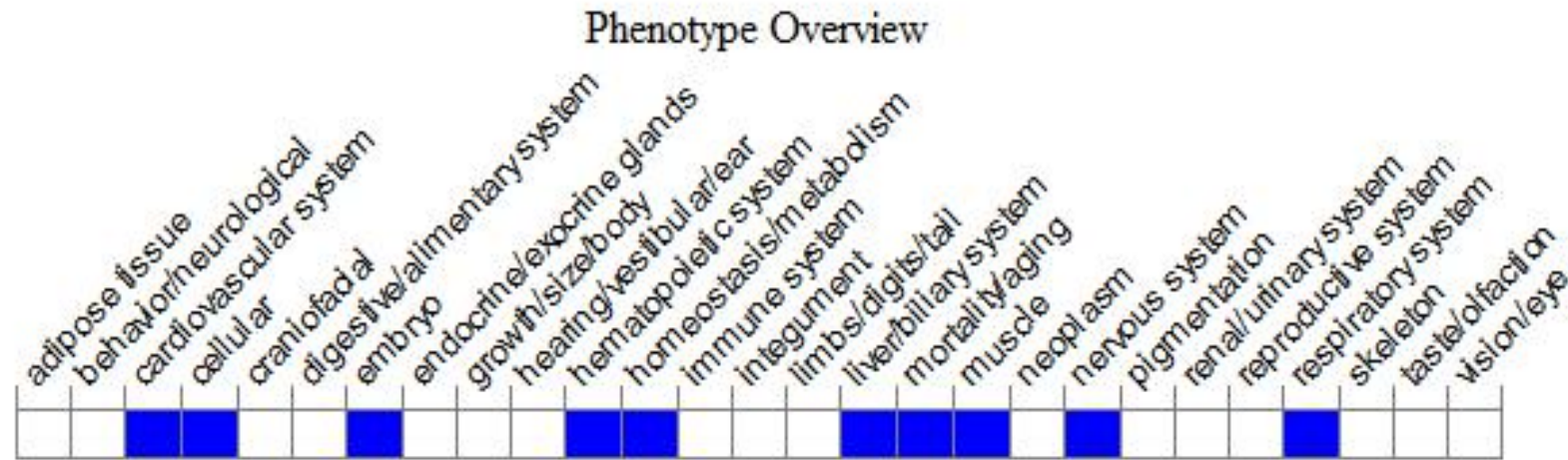
Genomic location distribution



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/>).

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