Adamts18 Cas9-CKO Strategy

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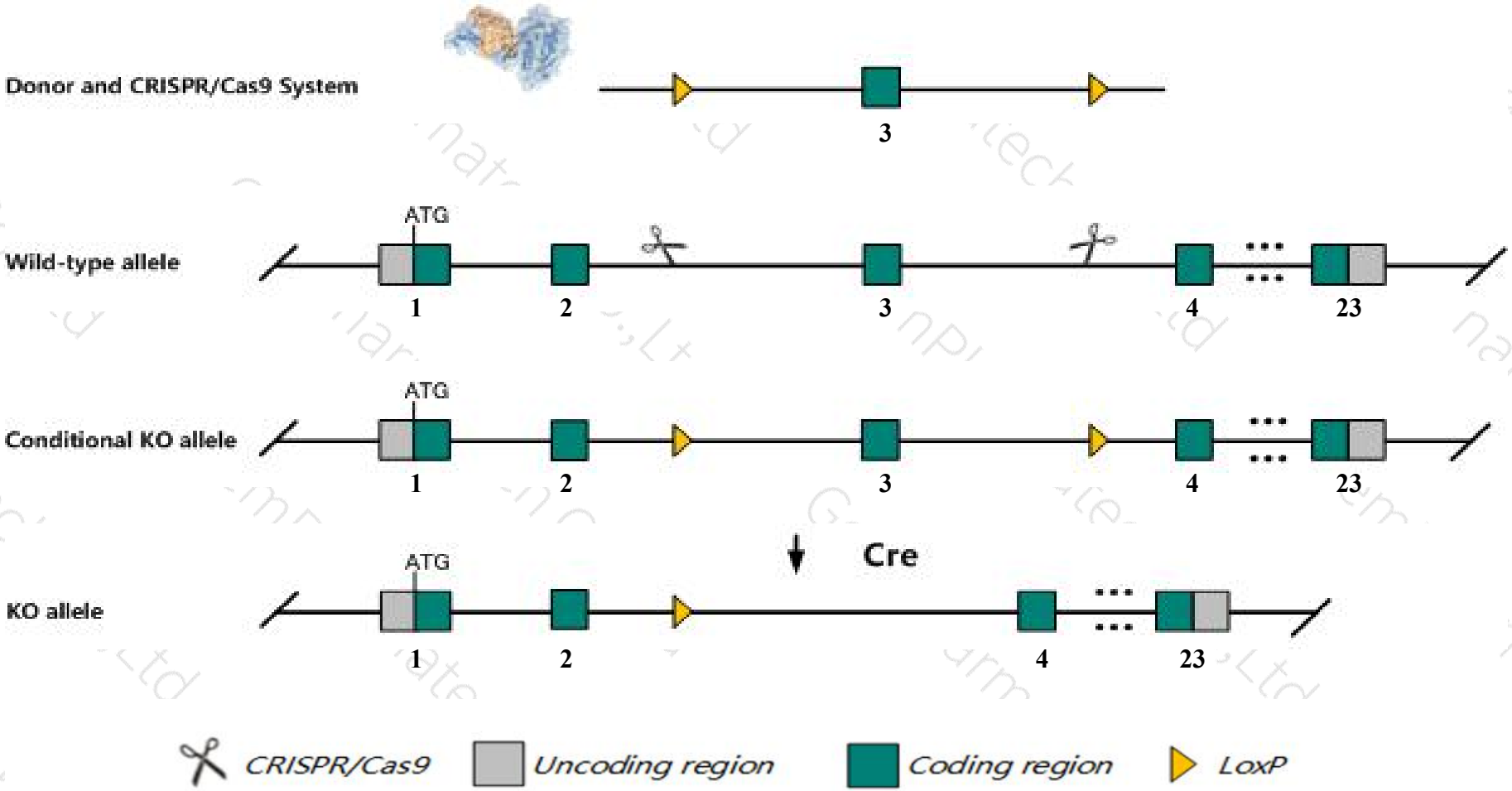
Project Overview

Project Name	***Adamts18***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adamts18* gene. The schematic diagram is as follows:



Technical routes

- The *Adamts18* gene has 7 transcripts. According to the structure of *Adamts18* gene, exon3 of *Adamts18-201* (ENSMUST00000093113.4) transcript is recommended as the knockout region.The region contains 314bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Adamts18* 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.

Notice

➢ According to the existing MGI data,Mice homozygous for a floxed allele exhibit some fertility defects. Mice homozygous for a null allele exhibit growth and eye defects and increased susceptibility to chemically induced tumors.

➢ The *Adamts18* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Adamts18 a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 18 [*Mus musculus* (house mouse)]

Gene ID: 208936, updated on 24-Dec-2019

Summary

Official Symbol	Adamts18 provided by MGI
Official Full Name	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 18 provided by MGI
Primary source	MGI:MGI:2442600
See related	Ensembl:ENSMUSG00000053399
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	ADAMTS21; 9630038L21; E130314N14Rik
Expression	Biased expression in CNS E14 (RPKM 1.9), CNS E18 (RPKM 1.8) and 12 other tissues See more
Orthologs	human all

Genomic context

Location: 8; 8 E1

See Adamts18 in Genome Data Viewer

Exon count: 24

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	8	NC_000074.6 (113697123..113849343, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	8	NC_000074.5 (116222037..116372739, complement)

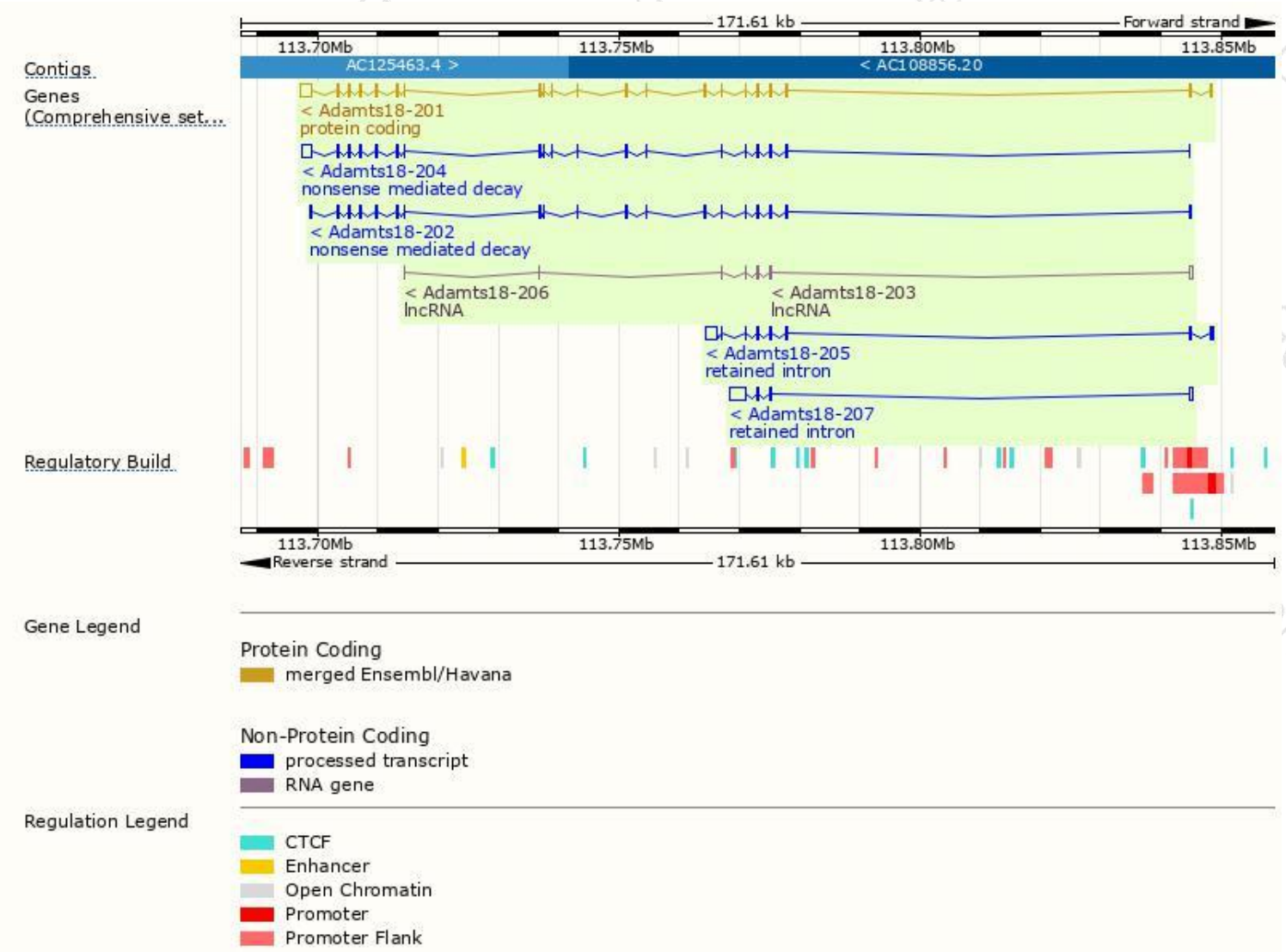
Transcript information（Ensembl）

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

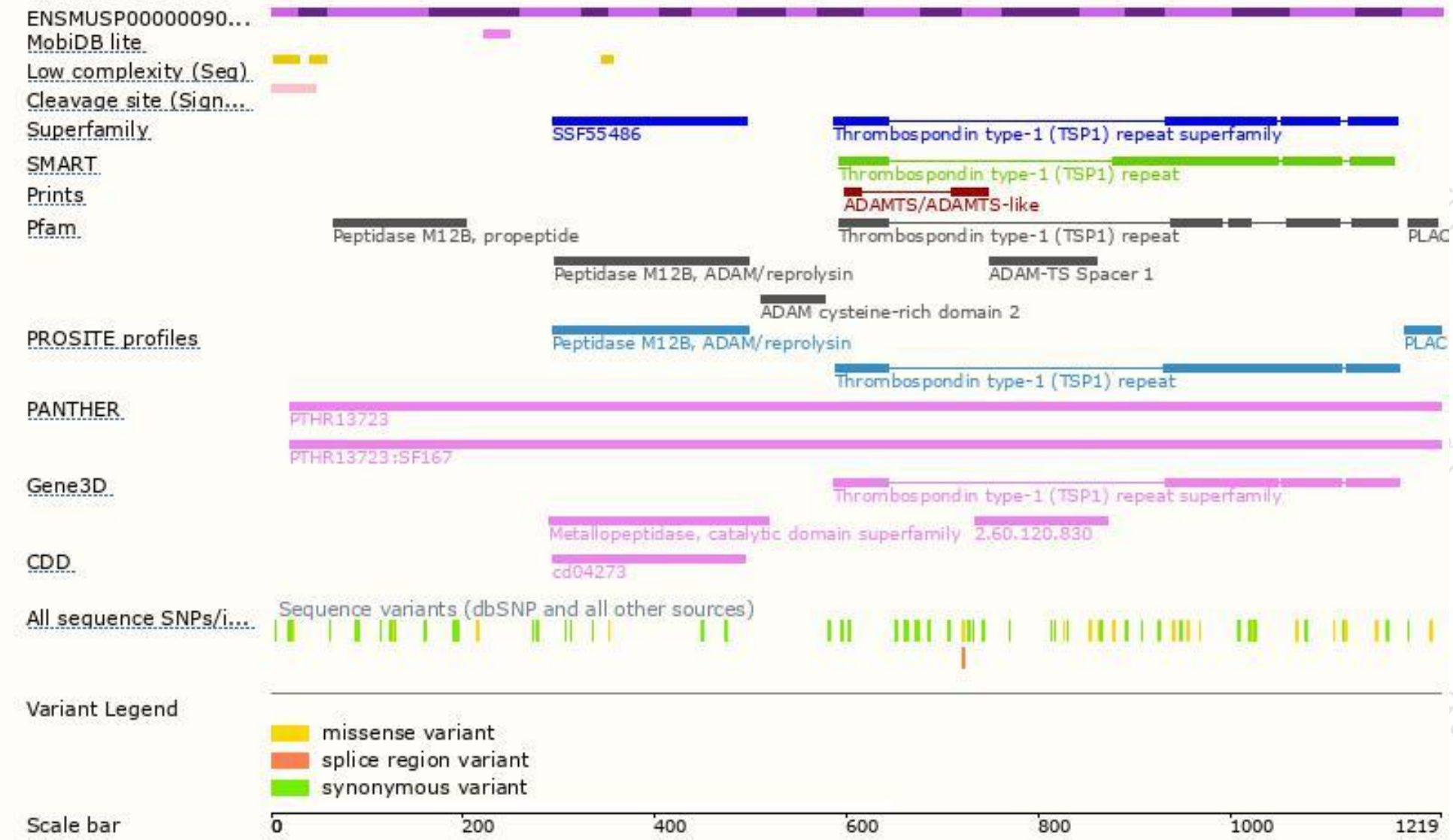
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adamts18-201	ENSMUST00000093113.4	5642	1219aa	Protein coding	CCDS40485	Q4VC17	TSL:1 GENCODE basic APPRIS P1
Adamts18-204	ENSMUST00000212665.1	4591	117aa	Nonsense mediated decay	-	A0A1D5RLE1	CDS 5' incomplete TSL:1
Adamts18-202	ENSMUST00000212437.1	3307	148aa	Nonsense mediated decay	-	A0A1D5RLA5	CDS 5' incomplete TSL:1
Adamts18-207	ENSMUST00000213078.1	3524	No protein	Retained intron	-	-	TSL:1
Adamts18-205	ENSMUST00000213061.1	3397	No protein	Retained intron	-	-	TSL:1
Adamts18-206	ENSMUST00000213076.1	693	No protein	lncRNA	-	-	TSL:3
Adamts18-203	ENSMUST00000212527.1	637	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Adamts18-201* transcript,The transcription is shown below

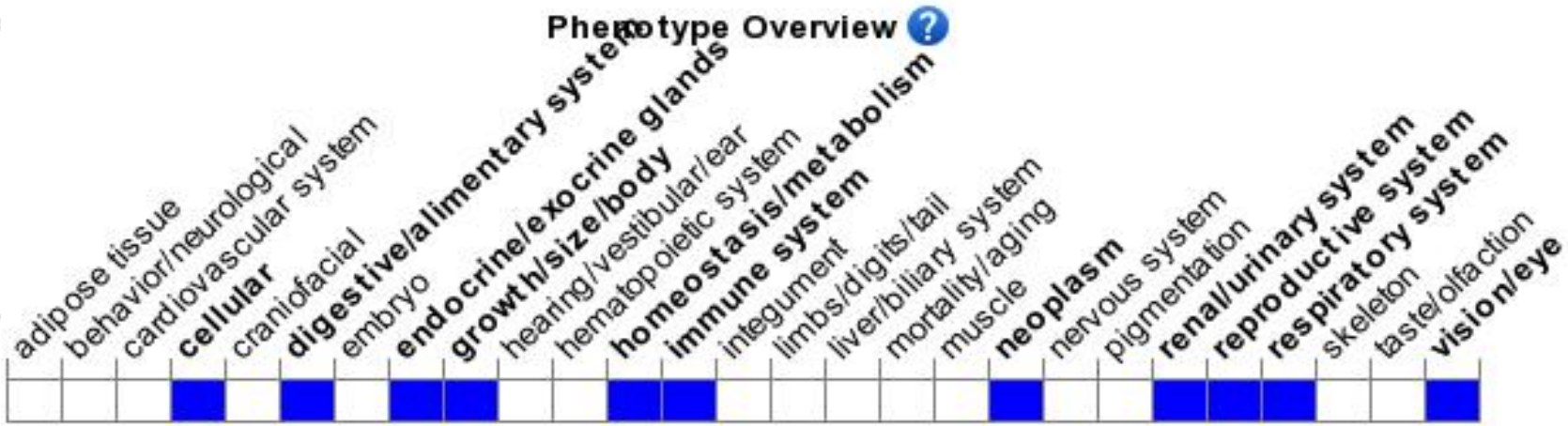
Genomic location distribution



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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