Smap1 Cas9-KO Strategy

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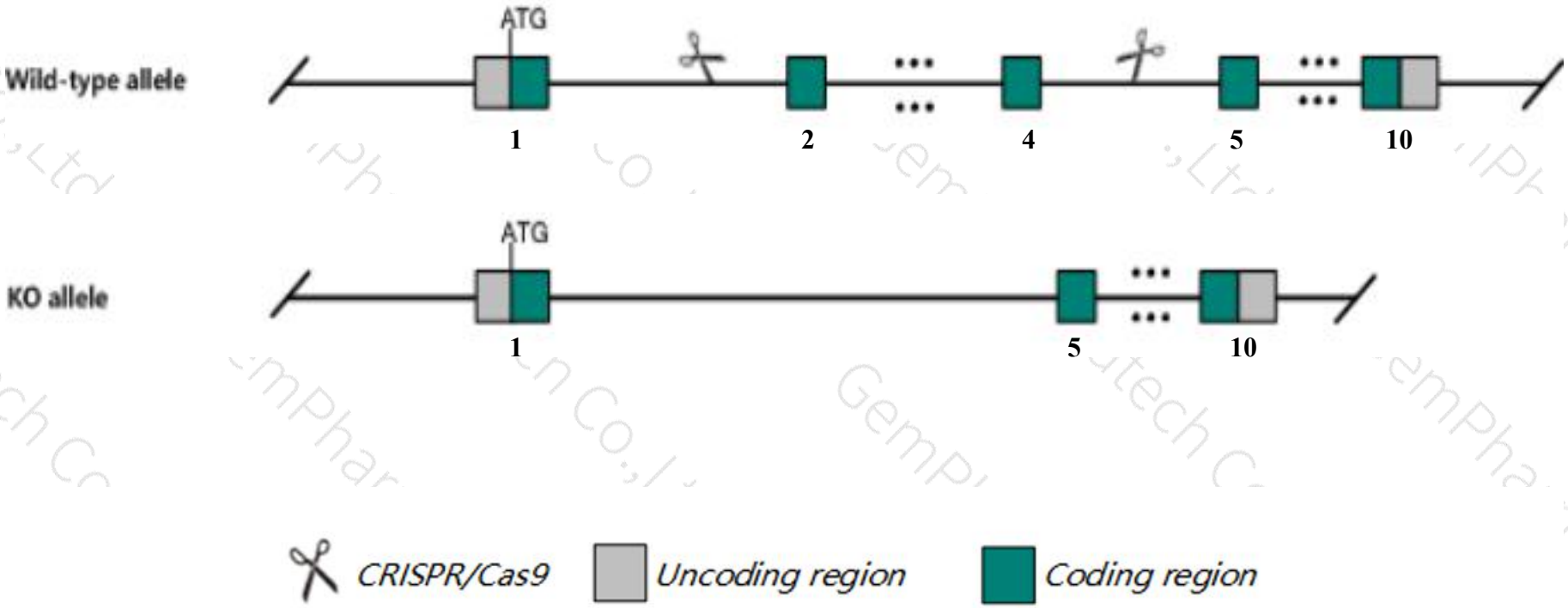
Project Overview

Project Name	***Smap1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Smap1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Smap1* gene has 7 transcripts. According to the structure of *Smap1* gene, exon2-exon4 of *Smap1-201* (ENSMUST00000027339.13) transcript is recommended as the knockout region.The region contains 296bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Smap1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit perturbed receptor trafficking and myelodysplasia.

- The *Smap1* gene is located on the Chr1. 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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Smap1 small ArfGAP 1 [Mus musculus (house mouse)]

Gene ID: 98366, updated on 13-Mar-2020

Summary

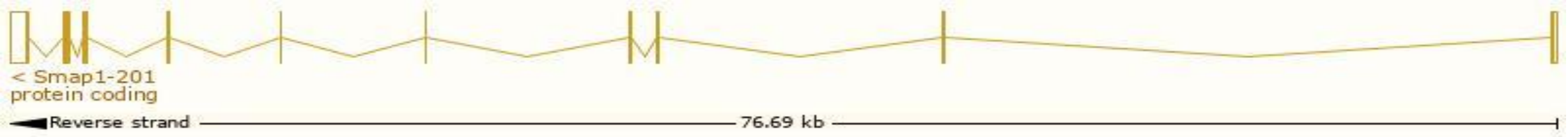
Official Symbol	Smap1 provided by MGI
Official Full Name	small ArfGAP 1 provided by MGI
Primary source	MGI:MGI:2138261
See related	Ensembl:ENSMUSG00000026155
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700056O10Rik, 4921514B13Rik, 4921525H11Rik, AI462175
Expression	Ubiquitous expression in testis adult (RPKM 50.0), CNS E18 (RPKM 24.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

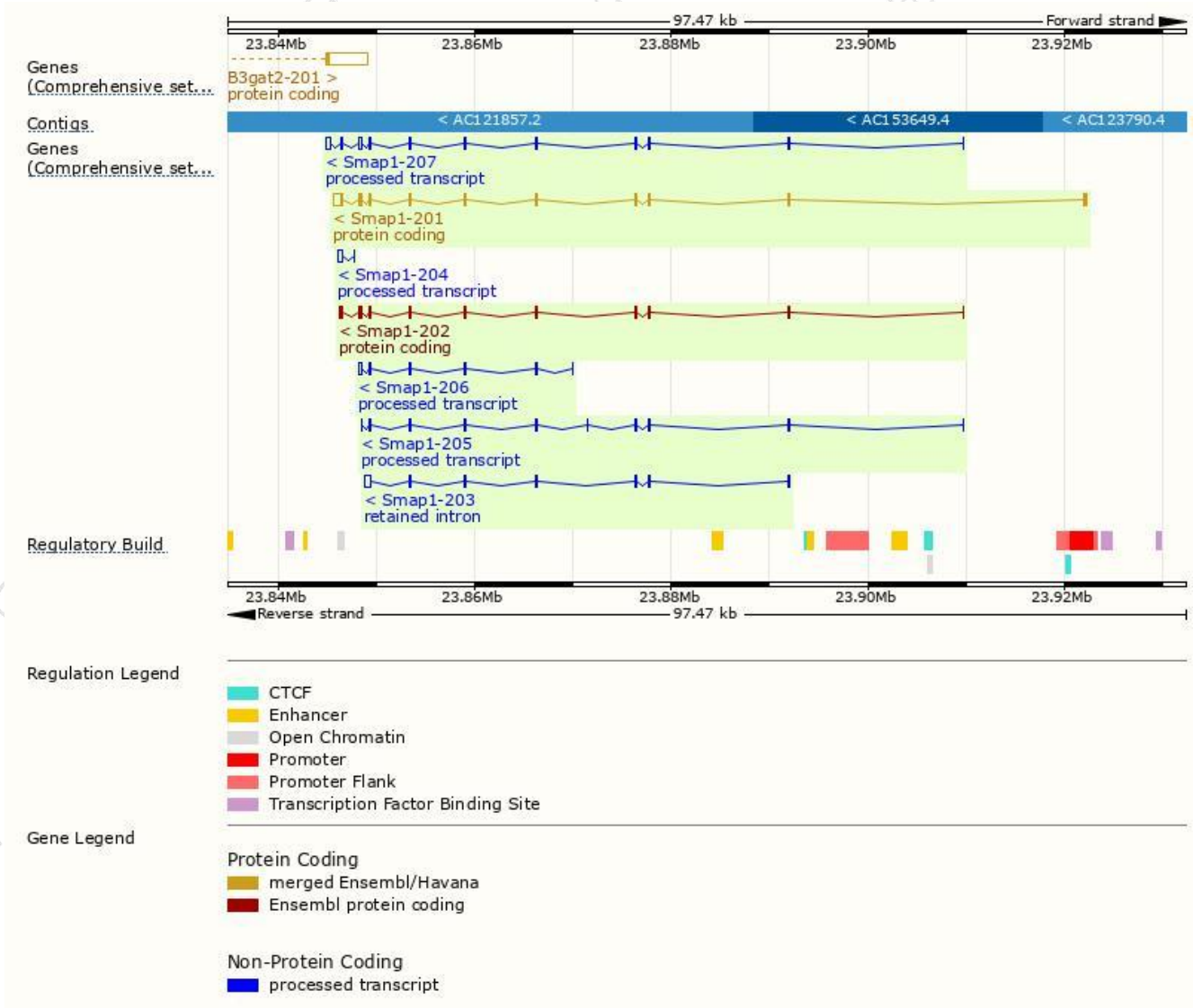
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Smap1-201	ENSMUST00000027339.13	2289	440aa	Protein coding	CCDS14851	Q91VZ6	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
Smap1-202	ENSMUST00000129254.7	1365	355aa	Protein coding	CCDS69870	D3YVX4	TSL:1 GENCODE basic
Smap1-207	ENSMUST00000149737.7	1864	No protein	Processed transcript	-	-	TSL:1
Smap1-205	ENSMUST00000141330.7	923	No protein	Processed transcript	-	-	TSL:5
Smap1-206	ENSMUST00000148710.7	809	No protein	Processed transcript	-	-	TSL:3
Smap1-204	ENSMUST00000136506.1	445	No protein	Processed transcript	-	-	TSL:3
Smap1-203	ENSMUST00000133398.1	1271	No protein	Retained intron	-	-	TSL:2

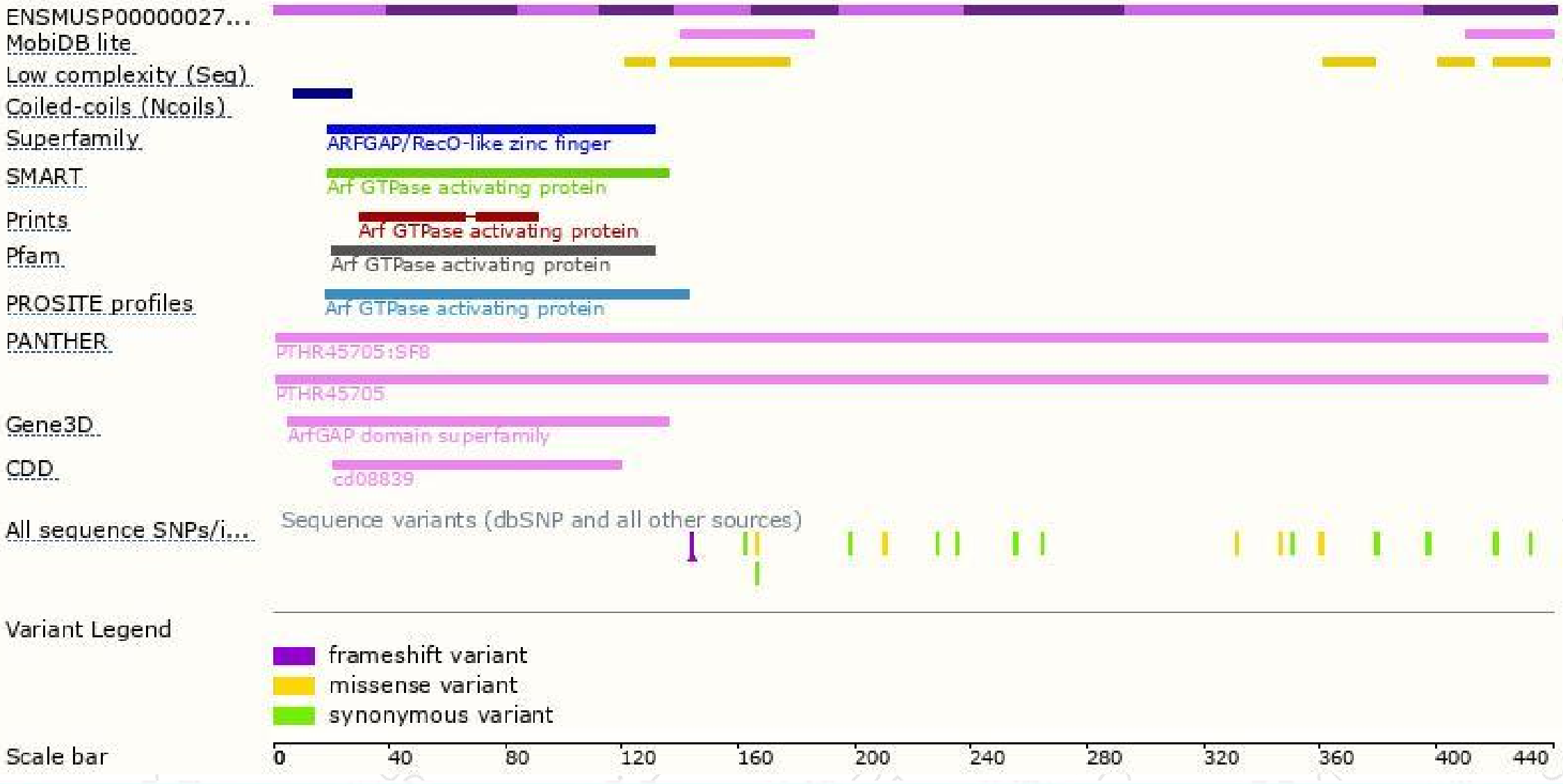
The strategy is based on the design of *Smap1-201* transcript,The transcription is shown below



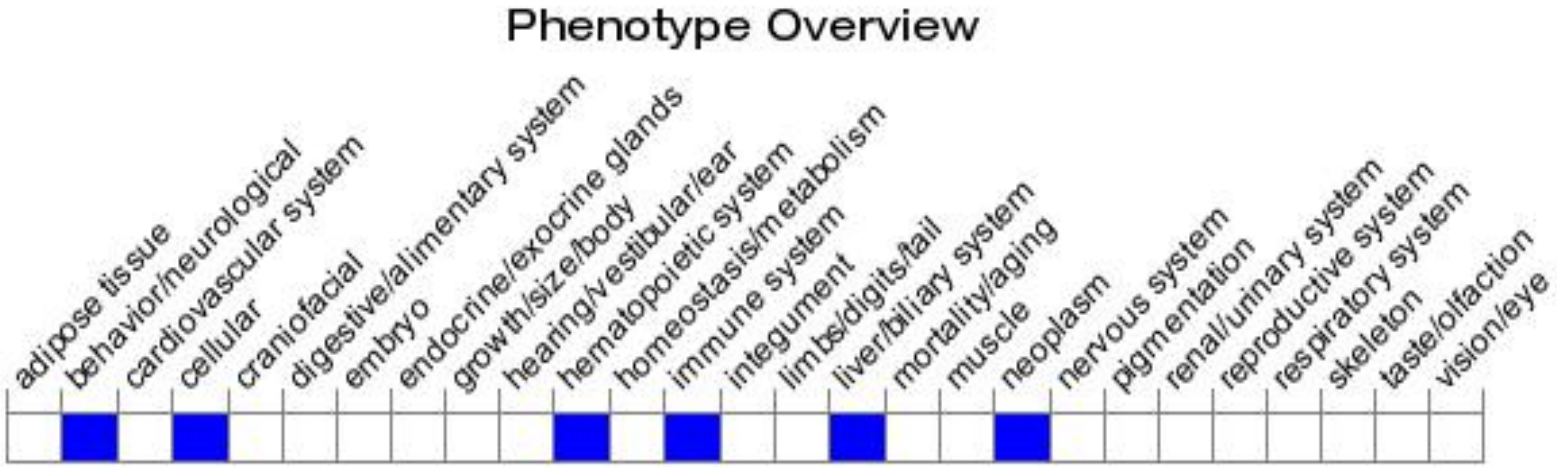
Genomic location distribution



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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