Cplane1 Cas9-KO Strategy

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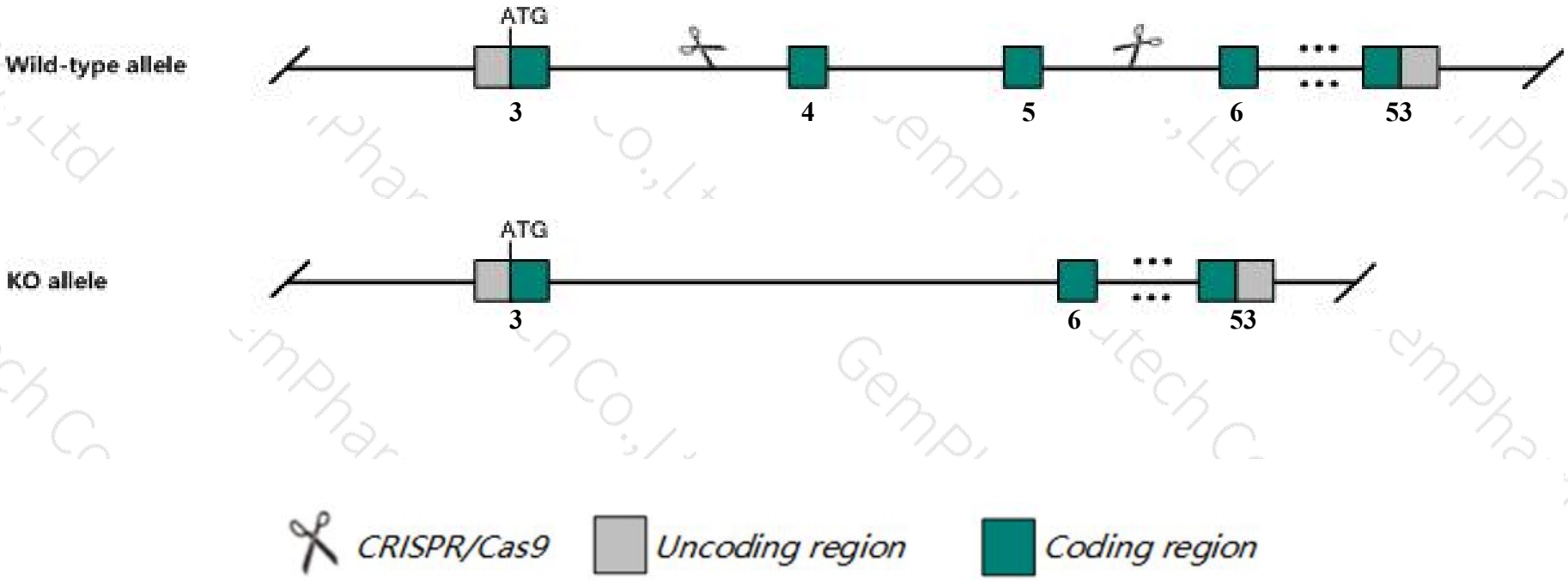
Project Overview

Project Name	***Cplane1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cplane1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Cplane1* gene has 6 transcripts. According to the structure of *Cplane1* gene, exon4-exon5 of *Cplane1-201* (ENSMUST00000110617.1) transcript is recommended as the knockout region.The region contains 256bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cplane1* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Homozygotes exhibit double outlet right ventricle {SDD}, pulmonary atresia/hypolastic pulmonary artery, atrioventricular septal defect, and right aortic arch. Non-cardiovascular defects include cleft palate, polydactyly, transparent chest wall (sternal bone hypoplasia) and hypoplastic lungs.

- The *Cplane1* 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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Cplane1 ciliogenesis and planar polarity effector 1 [Mus musculus (house mouse)]

Gene ID: 73692, updated on 31-Jan-2019

Summary

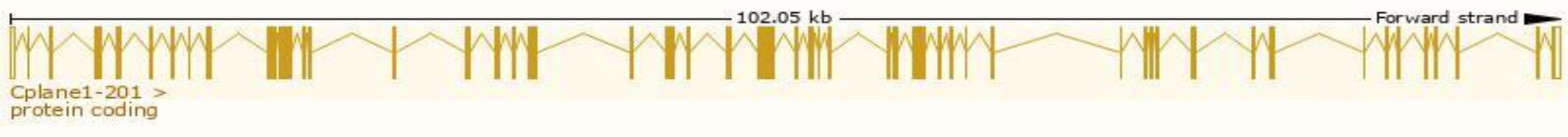
Official Symbol	Cplane1 provided by MGI
Official Full Name	ciliogenesis and planar polarity effector 1 provided by MGI
Primary source	MGI:MGI:1920942
See related	Ensembl:ENSMUSG00000039801
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410089E03Rik, 4732468D17Rik, Hug, Jbts17, b2b012Clo
Expression	Broad expression in CNS E18 (RPKM 7.5), testis adult (RPKM 7.0) and 21 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

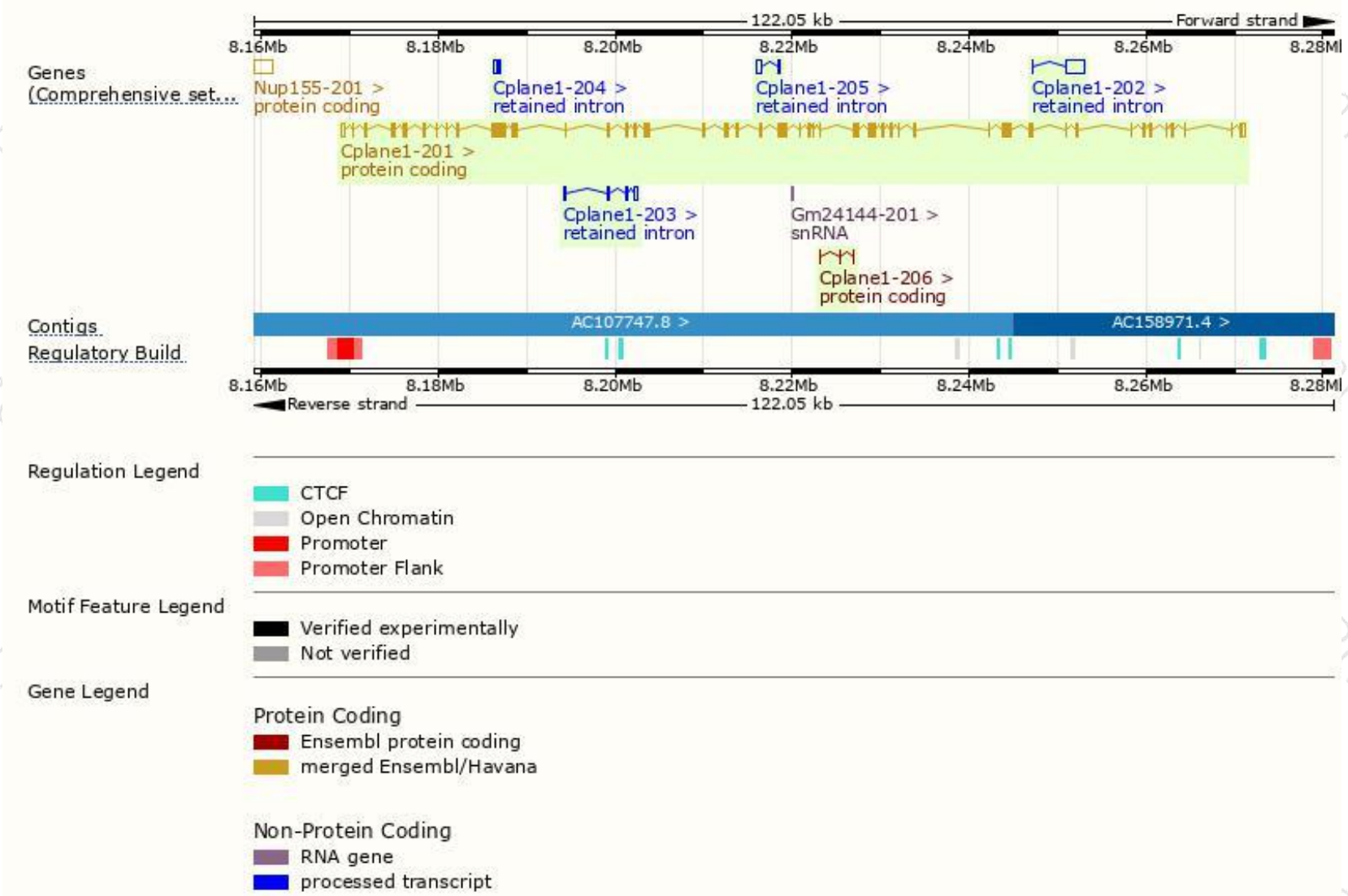
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cplane1-201	ENSMUST00000110617.1	10469	3214aa	Protein coding	CCDS49578	Q8CE72	TSL:5 GENCODE basic APPRIS P1
Cplane1-206	ENSMUST00000228039.1	93	31aa	Protein coding	-	A0A2I3BRY0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Cplane1-202	ENSMUST00000128772.1	2153	No protein	Retained intron	-	-	TSL:1
Cplane1-203	ENSMUST00000130748.1	989	No protein	Retained intron	-	-	TSL:1
Cplane1-205	ENSMUST00000154291.1	840	No protein	Retained intron	-	-	TSL:2
Cplane1-204	ENSMUST00000150869.1	683	No protein	Retained intron	-	-	TSL:3

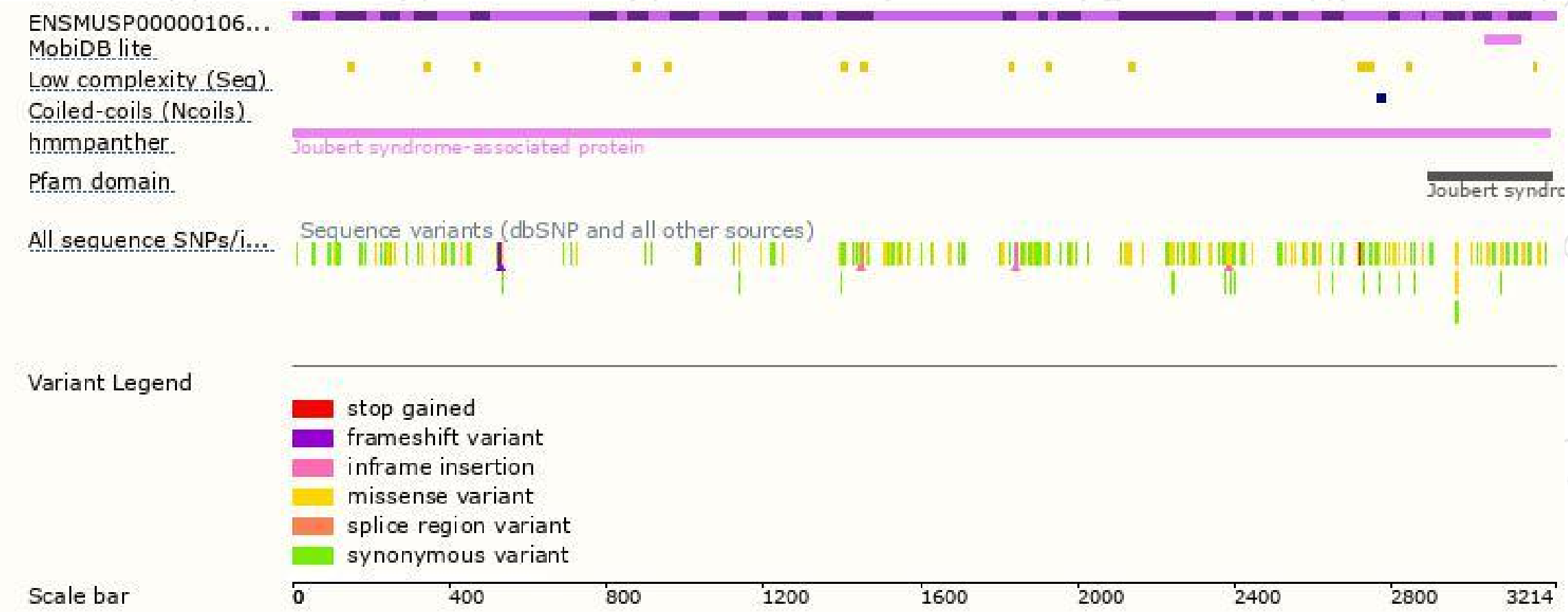
The strategy is based on the design of *Cplane1-201* transcript,The transcription is shown below



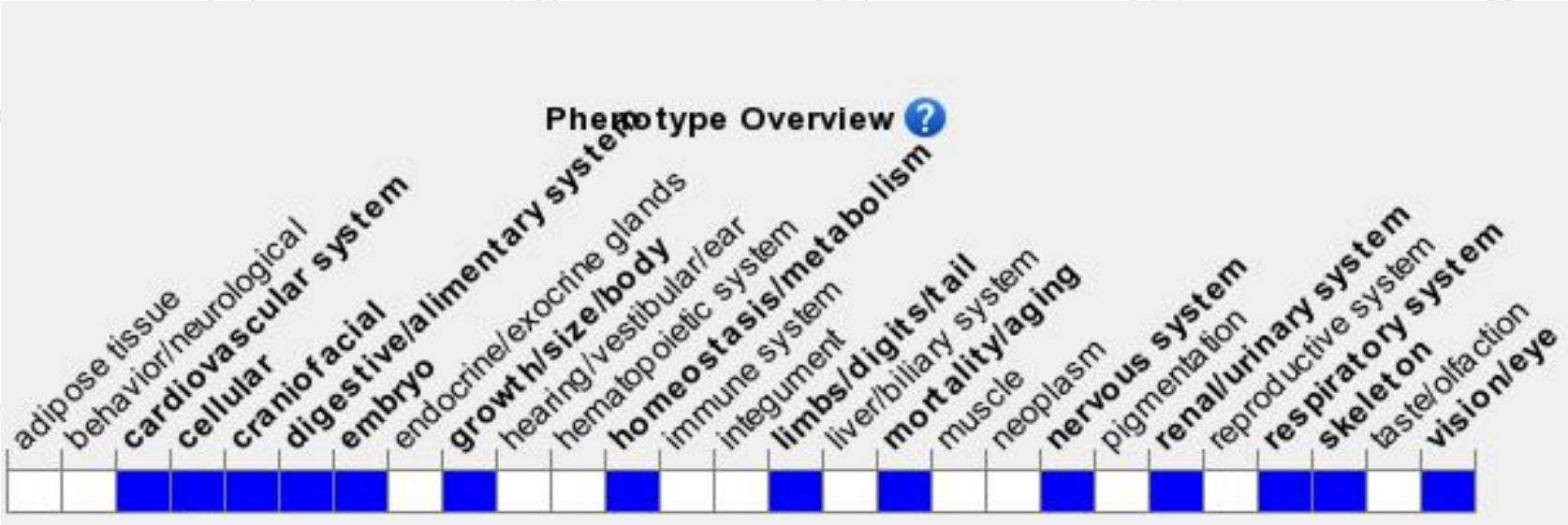
Genomic location distribution



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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