Ivns1abp Cas9-KO Strategy

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Reviewer: Xiaojing Li

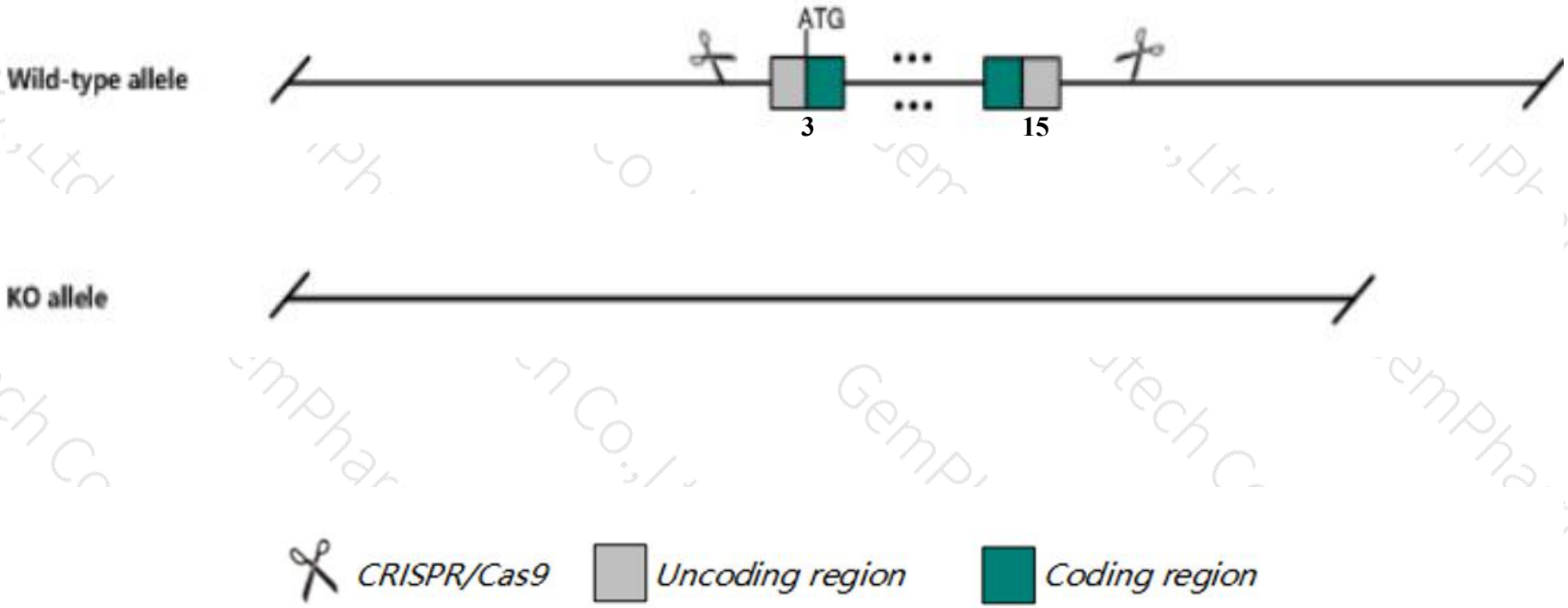
Design Date: 2020-7-21

Project Overview

Project Name	***Ivns1abp***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ivns1abp* gene. The schematic diagram is as follows:



Technical routes

➢ The *Ivns1abp* gene has 5 transcripts. According to the structure of *Ivns1abp* gene, exon3-exon15 of *Ivns1abp-201*(ENSMUST00000023918.12) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ivns1abp* 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 knock-out allele exhibit some early lethality, increased cellular sensitivity to cytochalasin and doxorubicin, and doxorubicin-induced cardiotoxicity.

➢ The *Ivns1abp* 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）

Ivns1abp influenza virus NS1A binding protein [Mus musculus (house mouse)]

Gene ID: 117198, updated on 13-Mar-2020

Summary

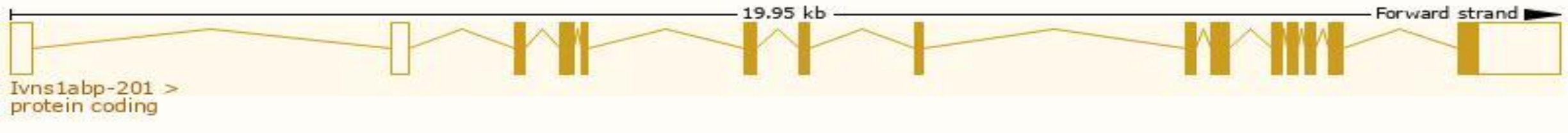
Official Symbol	Ivns1abp provided by MGI
Official Full Name	influenza virus NS1A binding protein provided byMGI
Primary source	MGI:MGI:2152389
See related	Ensembl:ENSMUSG00000023150
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1190004M08Rik, 1700126I16Rik, AA960440, HSPC068, ND1, NS-1, NS1-BP, Nd1-L, Nd1-S, mKIAA0850
Expression	Ubiquitous expression in heart adult (RPKM 79.1), CNS E11.5 (RPKM 71.2) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

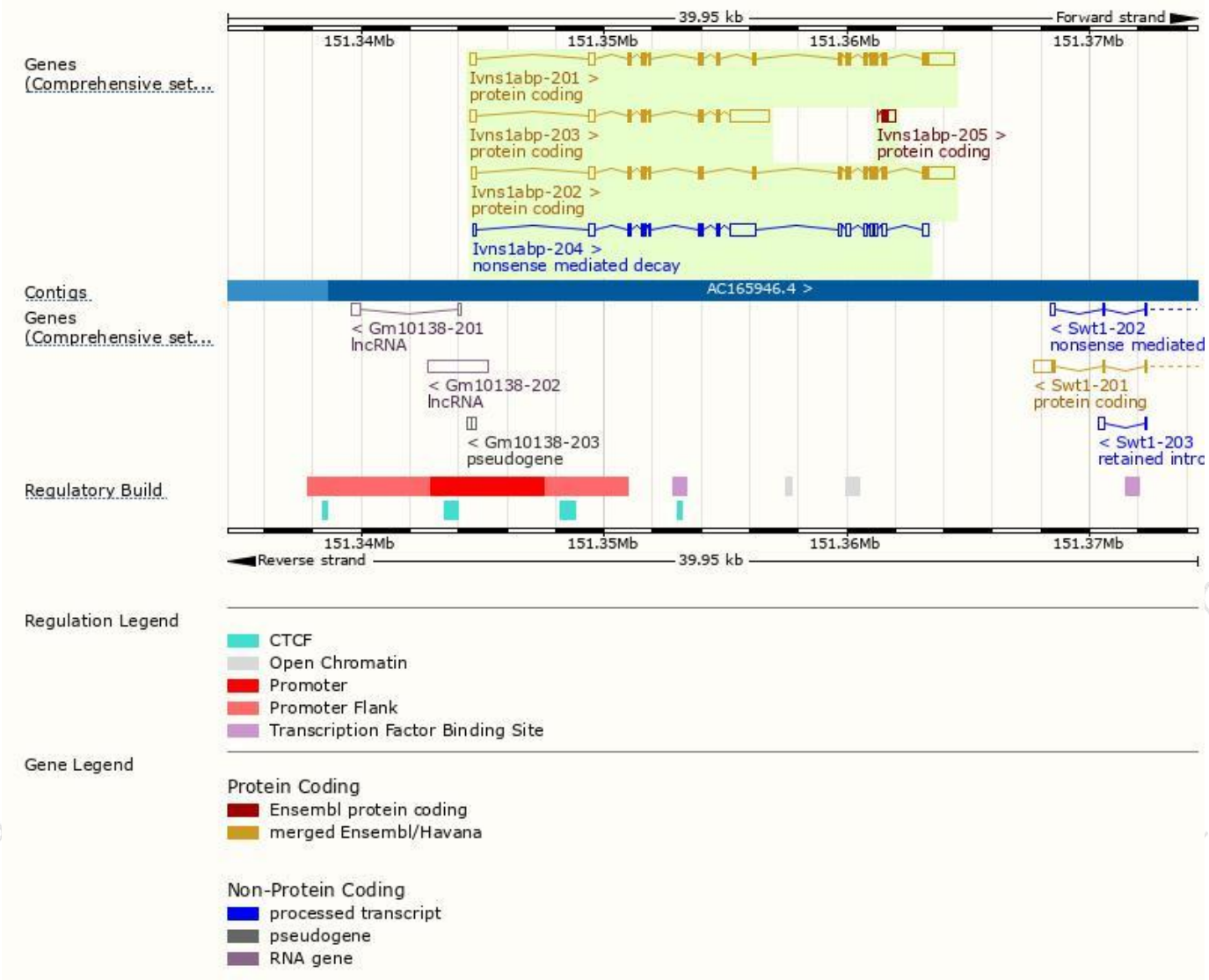
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ivns1abp-201	ENSMUST00000023918.12	3511	642aa	Protein coding	CCDS15359	Q920Q8	TSL:1 GENCODE basic APPRIS P1
Ivns1abp-202	ENSMUST00000097543.7	3337	600aa	Protein coding	CCDS15358	Q920Q8	TSL:1 GENCODE basic
Ivns1abp-203	ENSMUST00000111887.9	2783	221aa	Protein coding	CCDS35735	Q920Q8	TSL:1 GENCODE basic
Ivns1abp-205	ENSMUST00000190872.1	601	77aa	Protein coding	-	A0A087WQT3	CDS 5' incomplete TSL:3
Ivns1abp-204	ENSMUST00000186745.1	3315	221aa	Nonsense mediated decay	-	Q920Q8	TSL:1

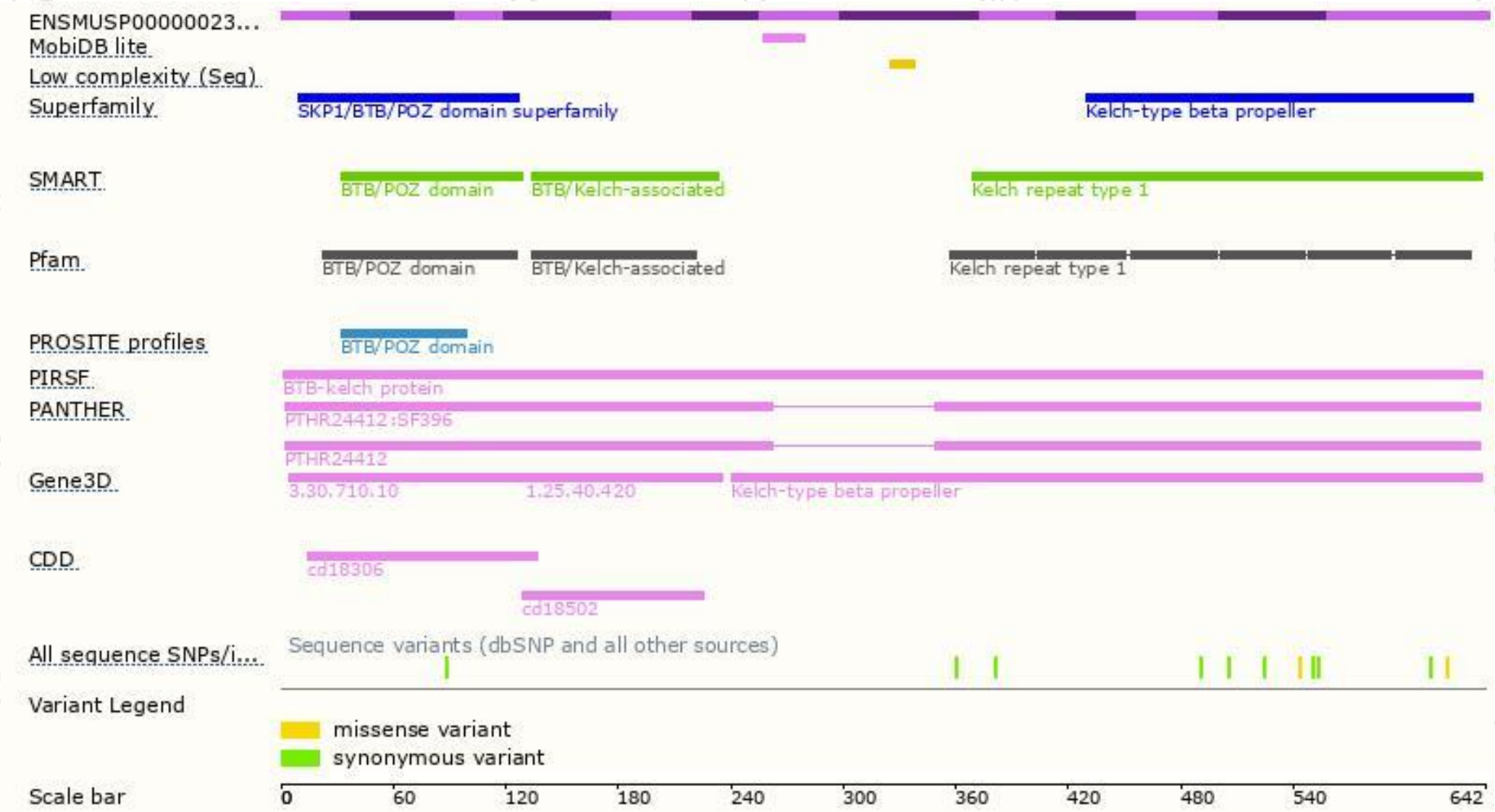
The strategy is based on the design of *Ivns1abp-201* transcript,the transcription is shown below:



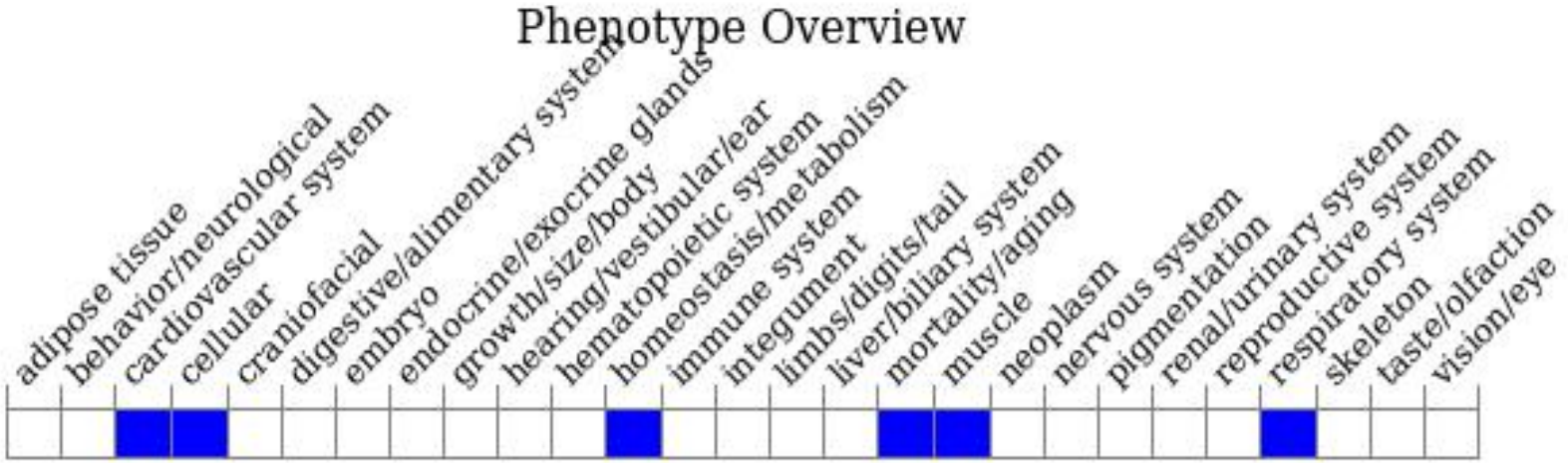
Genomic location distribution



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 knock-out allele exhibit some early lethality, increased cellular sensitivity to cytochalasin and doxorubicin, and doxorubicin-induced cardiotoxicity.

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

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