

# *Cd93* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Cd93***

**Project type**

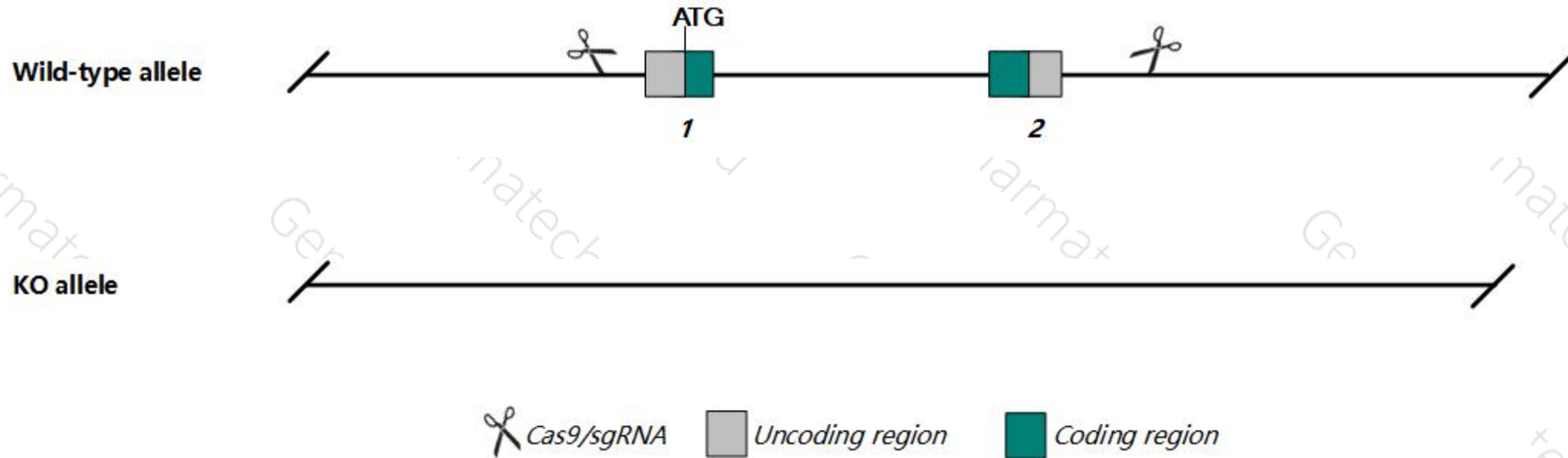
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cd93* gene. The schematic diagram is as follows:



- The *Cd93* gene has 1 transcript. According to the structure of *Cd93* gene, exon1-exon2 of *Cd93-201* (ENSMUST00000099269.3) 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 *Cd93* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygous null mutants have a defect in clearance of apoptotic cells.
- The *Cd93* gene is located on the Chr2. 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)

## Cd93 CD93 antigen [Mus musculus (house mouse)]

Gene ID: 17064, updated on 13-Mar-2020

### Summary



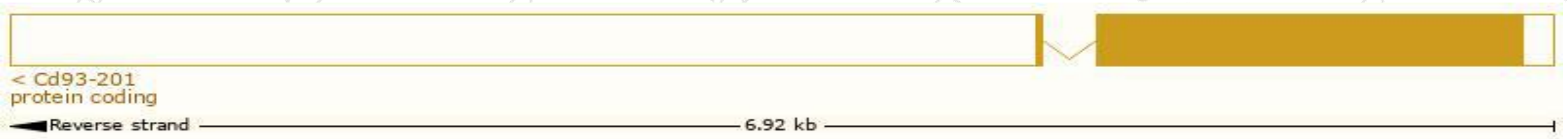
<b>Official Symbol</b>	Cd93 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	CD93 antigen provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:106664</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000027435</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	PROVISIONAL
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	6030404G09Rik, AA145088, AA4.1, AW555904, C1qr1, C1qrp, Ly68
<b>Expression</b>	Broad expression in lung adult (RPKM 38.3), subcutaneous fat pad adult (RPKM 17.9) and 15 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

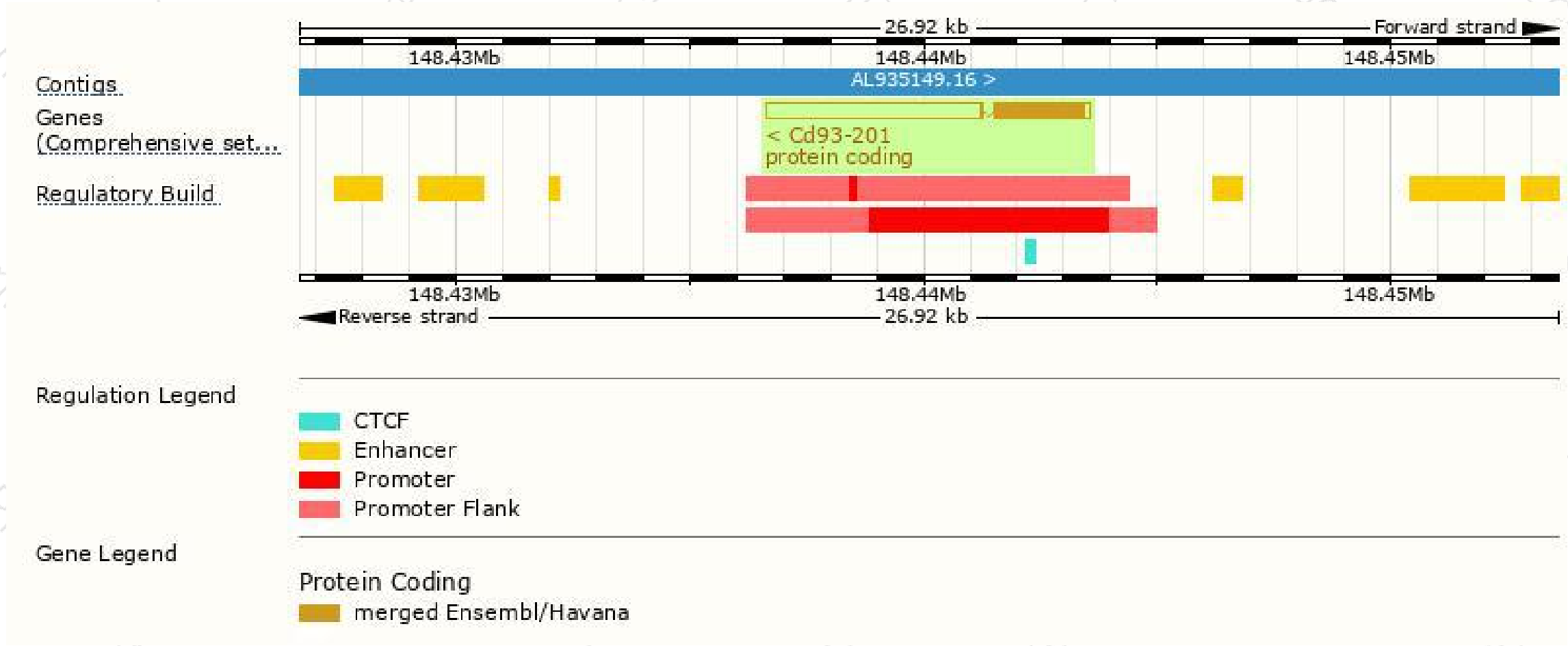
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cd93-201	<a href="#">ENSMUST00000099269.3</a>	6677	<a href="#">644aa</a>	Protein coding	<a href="#">CCDS16839</a>	<a href="#">O89103</a>	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Cd93-201* transcript, the transcription is shown below:

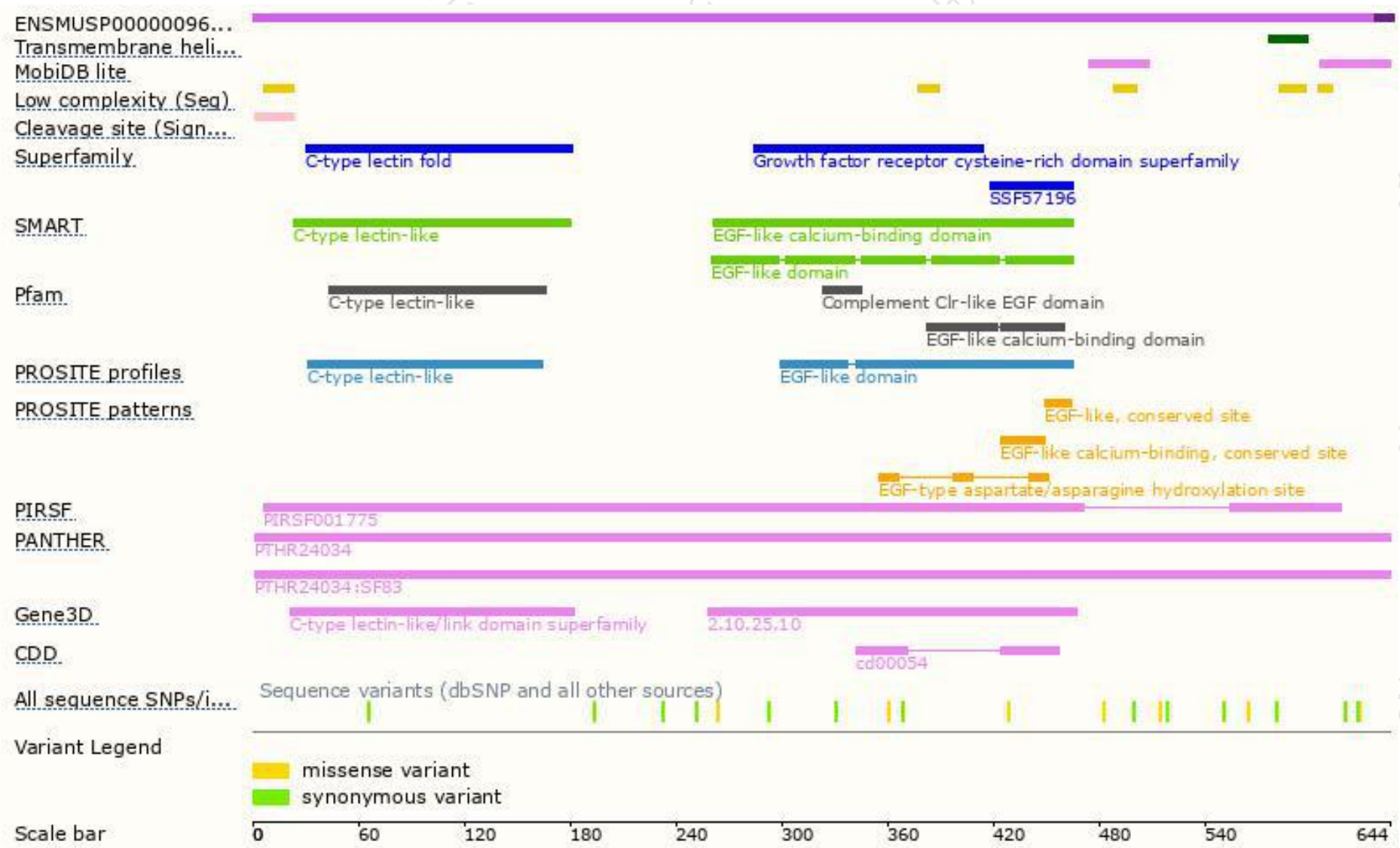


# Genomic location distribution

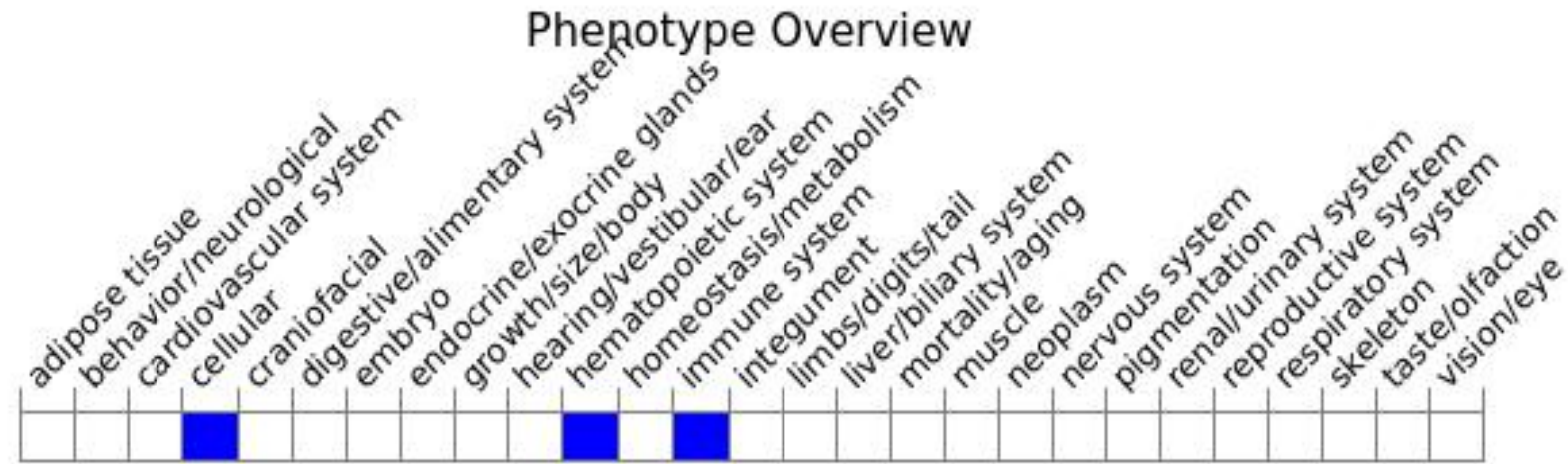




# Protein domain



# 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, homozygous null mutants have a defect in clearance of apoptotic cells.

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

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