

Efna1 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Efnal

Project type

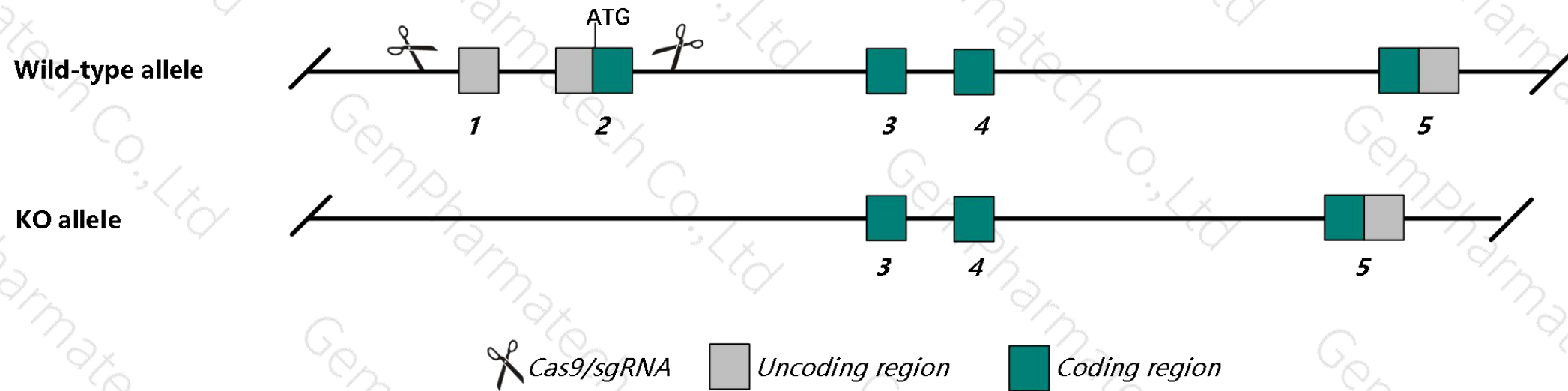
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Efnal* gene has 3 transcripts. According to the structure of *Efnal* gene, exon1-exon2 of *Efnal*-202 (ENSMUST00000118587.7) transcript is recommended as the knockout region. The region contains 199bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Efnal* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased cardiac muscle contractility associated with increased mitral and aortic valve thickness and increased epithelial to mesenchyme transition in outflow tract endocardial cushions.
- The *Efnal* gene is located on the Chr3. 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.

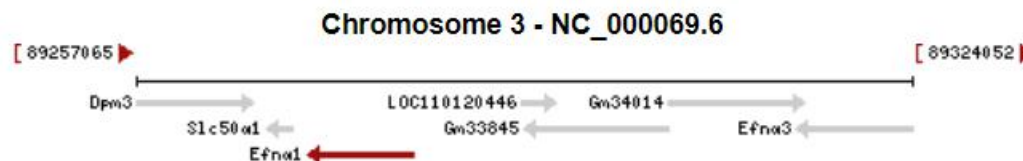
Gene information (NCBI)

Efna1 ephrin A1 [*Mus musculus* (house mouse)]

Gene ID: 13636, updated on 21-Aug-2019

Summary

Official Symbol	Efna1 provided by MGI
Official Full Name	ephrin A1 provided by MGI
Primary source	MGI:MGI:103236
See related	Ensembl:ENSMUSG000000027954
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	B61; Ef11; Epl1; Eplg1; Lerk1; AI325262
Expression	Broad expression in colon adult (RPKM 52.5), lung adult (RPKM 50.2) and 20 other tissues See more
Orthologs	human all

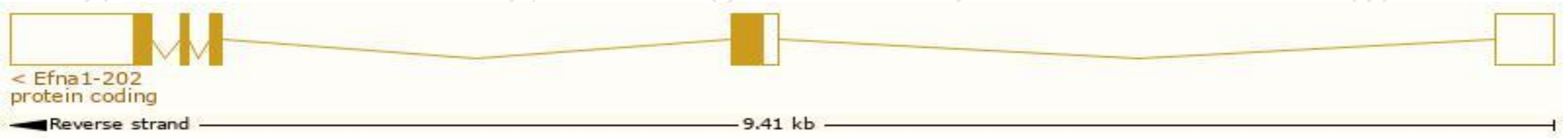


Transcript information (Ensembl)

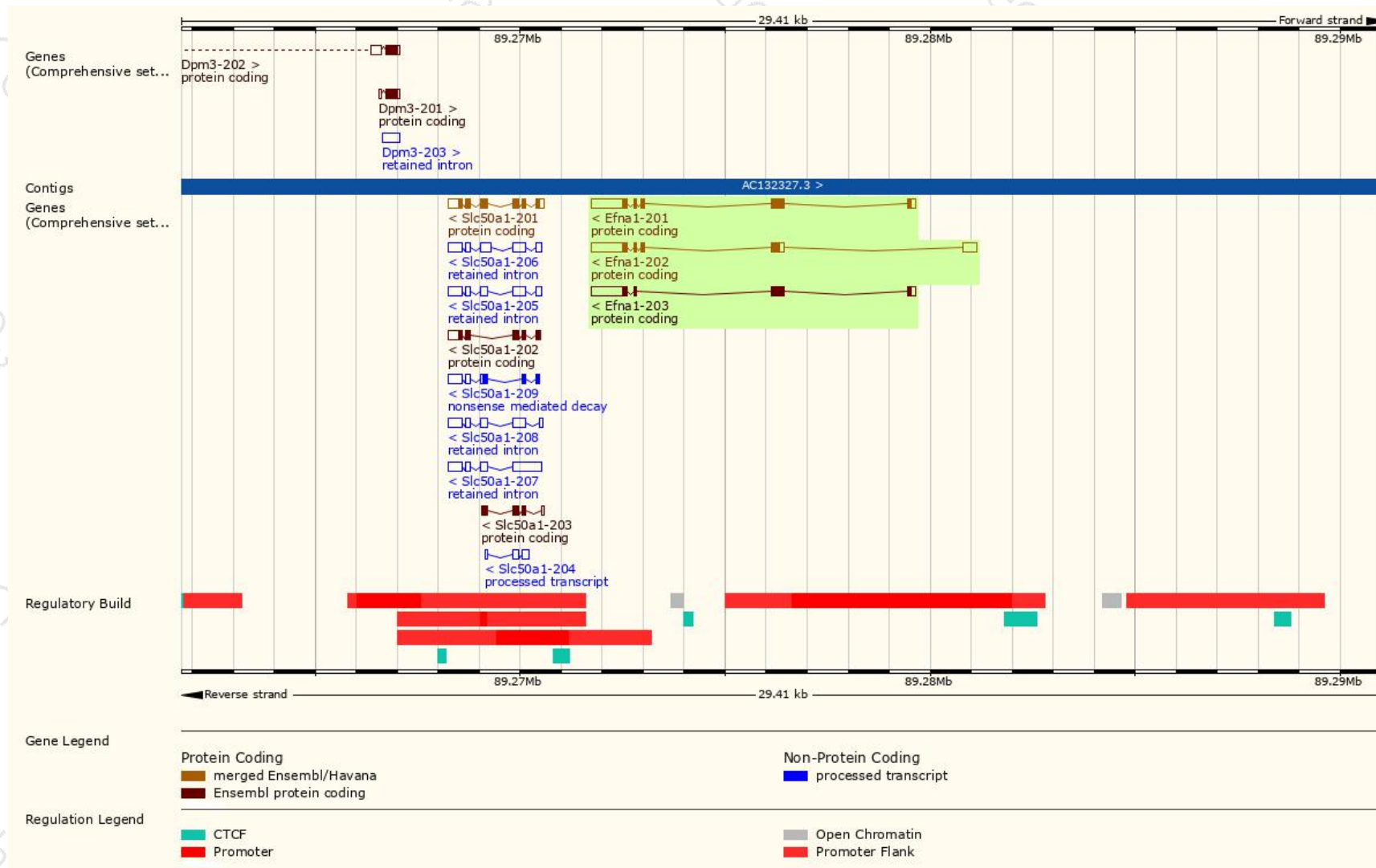
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Efna1-202	ENSMUST00000118587.7	1632	142aa	Protein coding	CCDS50961	D3YTT5	TSL:1 GENCODE basic
Efna1-201	ENSMUST00000029566.8	1480	205aa	Protein coding	CCDS17501	P52793	TSL:1 GENCODE basic APPRIS P1
Efna1-203	ENSMUST00000118860.1	1403	183aa	Protein coding	-	D3Z7A6	TSL:5 GENCODE basic

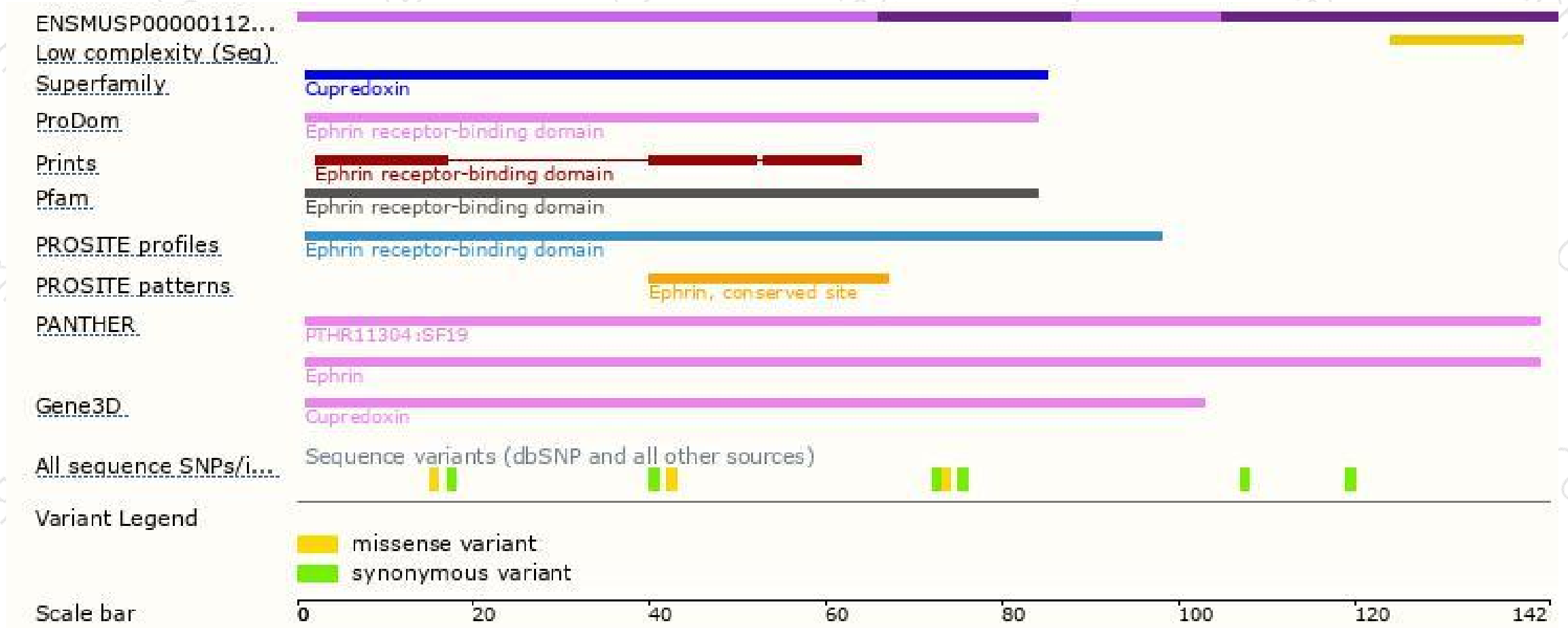
The strategy is based on the design of *Efna1-202* transcript,The transcription is shown below



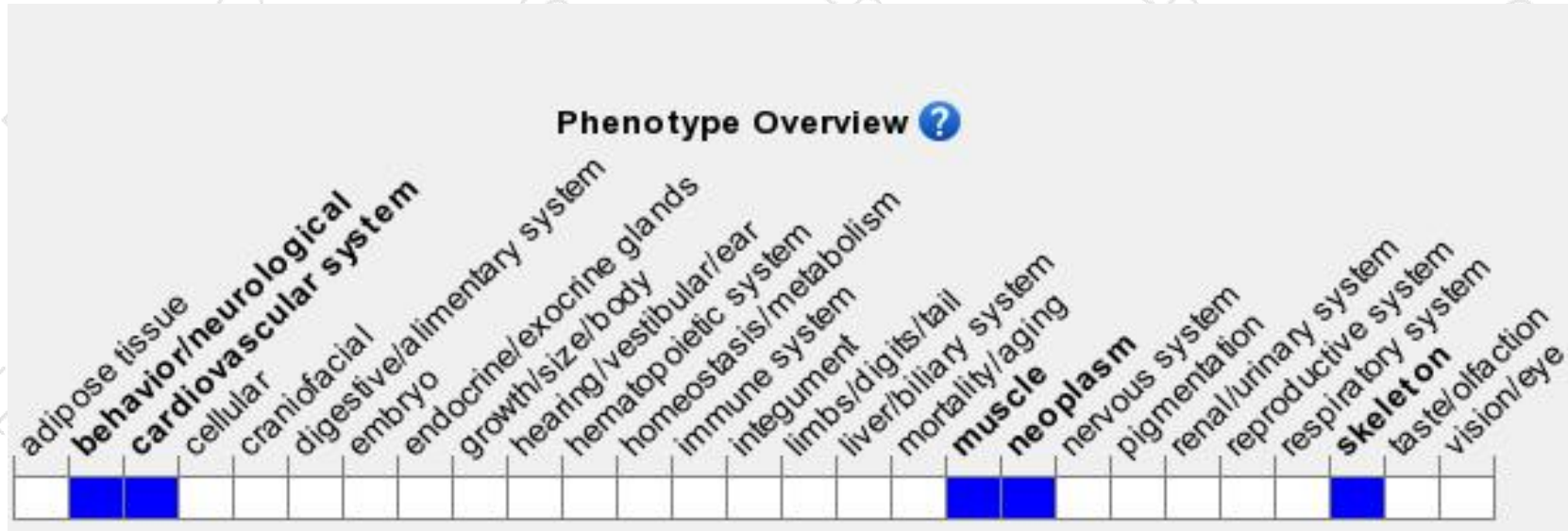
Genomic location distribution



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 decreased cardiac muscle contractility associated with increased mitral and aortic valve thickness and increased epithelial to mesenchyme transition in outflow tract endocardial cushions.

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

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