Jade1 Cas9-KO Strategy

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Project Overview

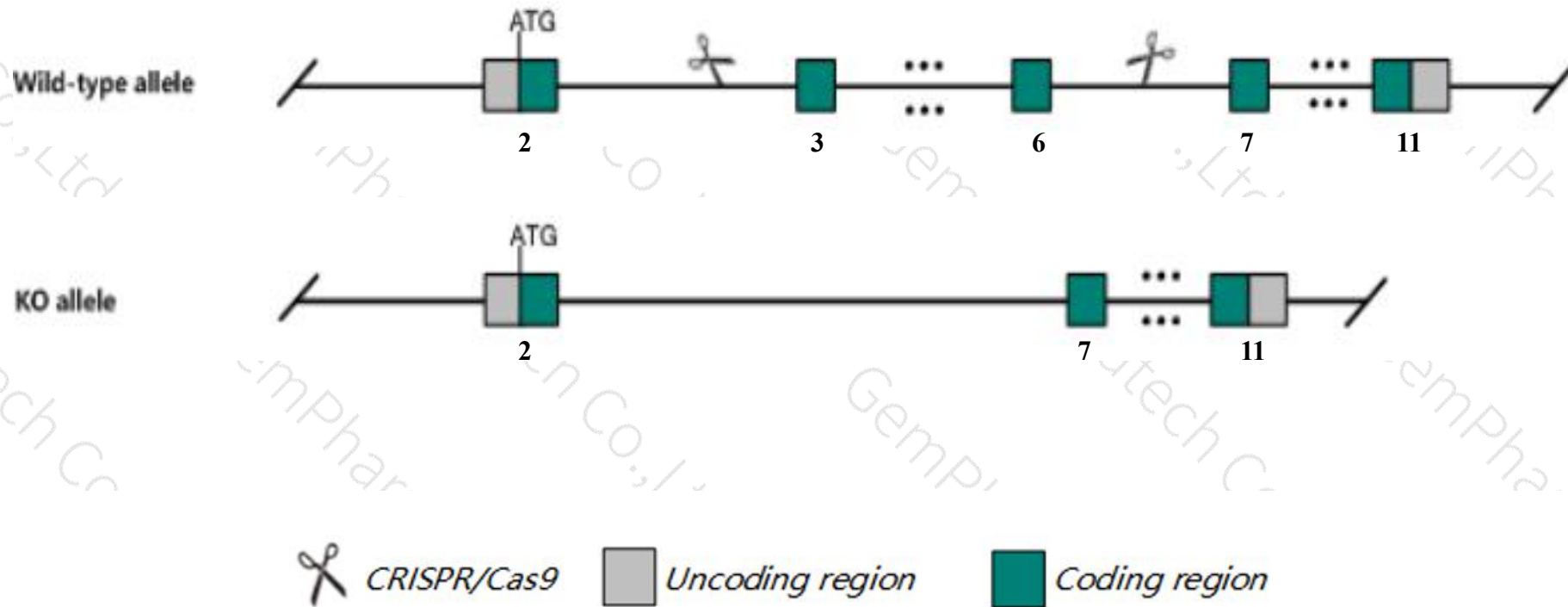|	
Project Name	*Jade1*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Jade1* gene. The schematic diagram is as follows:

Technical routes

➢ The *Jade1* gene has 14 transcripts. According to the structure of *Jade1* gene, exon3-exon6 of *Jade1-202*(ENSMUST00000163764.7) transcript is recommended as the knockout region.The region contains 647bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Jade1* 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,though mice homozygous for mutations of this locus show no overt phenotype at birth, fewer survive to weaning than expected by Mendelian ratios.

➢ The *Jade1* 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）

Jade1 jade family PHD finger 1 [Mus musculus (house mouse)]

Gene ID: 269424, updated on 13-Mar-2020

▲ Summary

Official Symbol	Jade1 provided by MGI
Official Full Name	jade family PHD finger 1 provided by MGI
Primary source	MGI:MGI:1925835
See related	Ensembl:ENSMUSG00000025764
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	AU041499, D530048A03Rik, Phf17, mKIAA1807
Expression	Ubiquitous expression in placenta adult (RPKM 17.9), bladder adult (RPKM 5.1) and 27 other tissuesSee more
Orthologs	human all

The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Jade1-202	ENSMUST00000163764.7	5584	834aa	Protein coding	CCDS17331	Q6ZPI0	TSL:1 GENCODE basic APPRIS P2
Jade1-201	ENSMUST00000026865.14	5481	834aa	Protein coding	CCDS17331	Q6ZPI0	TSL:1 GENCODE basic APPRIS P2
Jade1-203	ENSMUST00000168086.6	4790	834aa	Protein coding	CCDS17331	Q6ZPI0	TSL:1 GENCODE basic APPRIS P2
Jade1-204	ENSMUST00000170711.7	2896	834aa	Protein coding	CCDS17331	Q6ZPI0	TSL:5 GENCODE basic APPRIS P2
Jade1-206	ENSMUST00000191952.1	3327	510aa	Protein coding	-	Q6ZPI0	TSL:5 GENCODE basic APPRIS ALT2
Jade1-214	ENSMUST00000195846.5	543	152aa	Protein coding	-	A0A0A6YWV0	CDS 3' incomplete TSL:5
Jade1-210	ENSMUST00000194181.5	542	104aa	Protein coding	-	A0A0A6YWS2	CDS 3' incomplete TSL:5
Jade1-208	ENSMUST00000192451.1	491	164aa	Protein coding	-	A0A0A6YXU2	CDS 5' and 3' incomplete TSL:3
Jade1-207	ENSMUST00000192300.1	449	No protein	Processed transcript	-	-	TSL:3
Jade1-209	ENSMUST00000193080.5	434	No protein	Processed transcript	-	-	TSL:5
Jade1-211	ENSMUST00000194348.1	382	No protein	Processed transcript	-	-	TSL:3
Jade1-205	ENSMUST00000191921.1	774	No protein	Retained intron	-	-	TSL:2
Jade1-213	ENSMUST00000195322.5	718	No protein	Retained intron	-	-	TSL:2
Jade1-212	ENSMUST00000195200.1	487	No protein	Retained intron	-	-	TSL:1

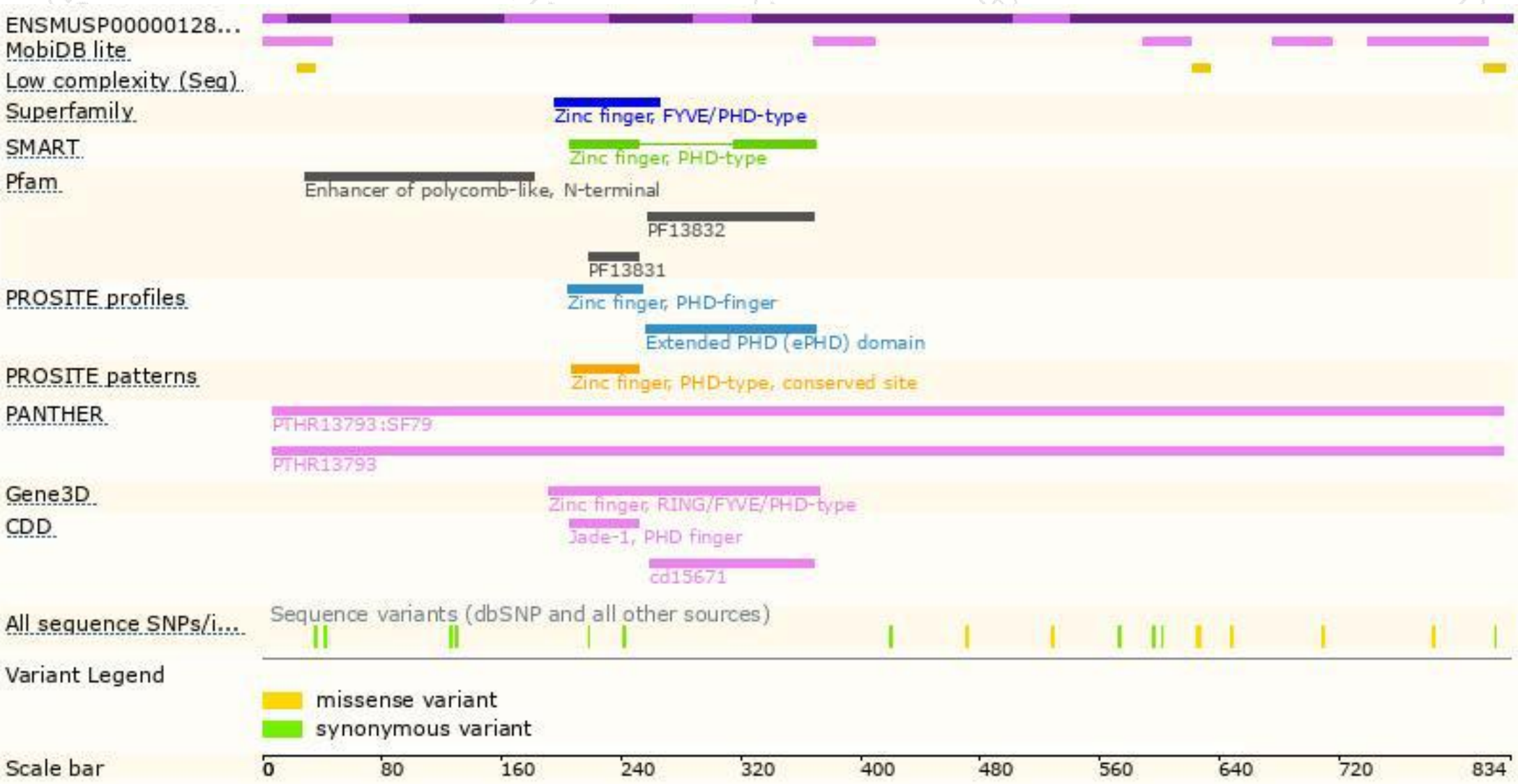The strategy is based on the design of *Jade1-202* transcript,the transcription is shown below:
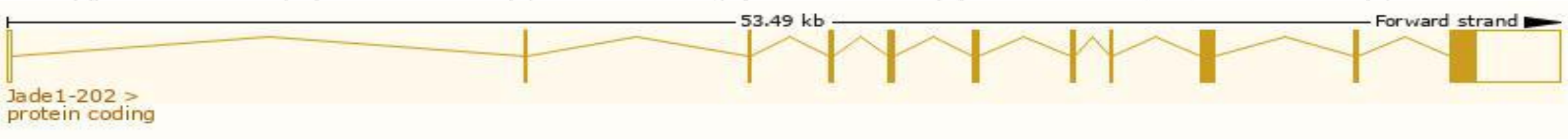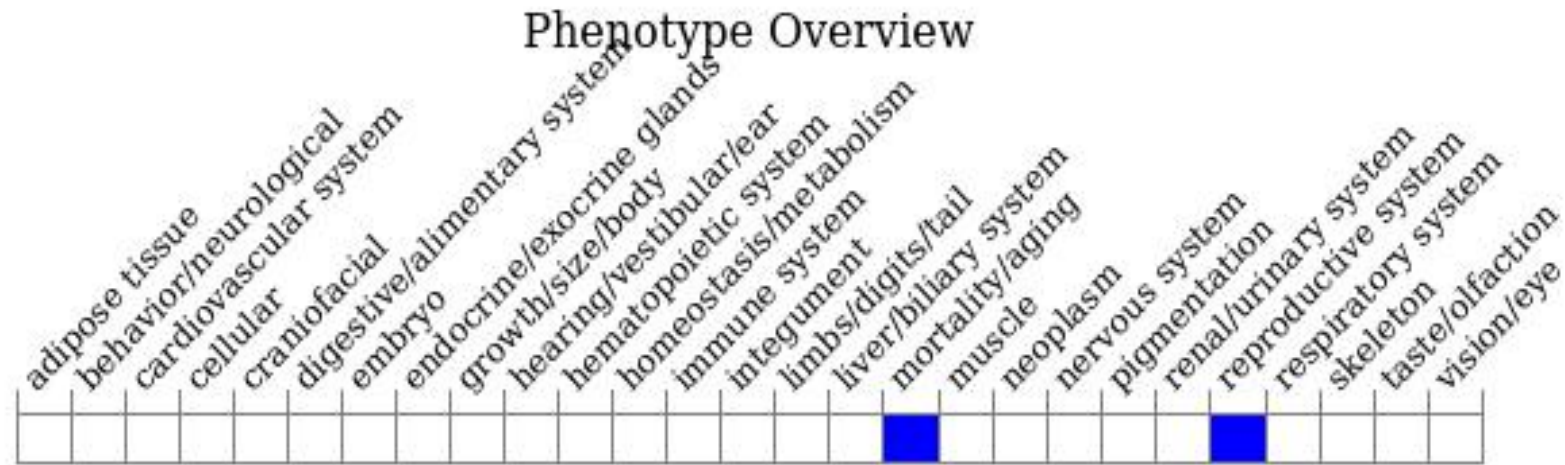
Genomic location distribution
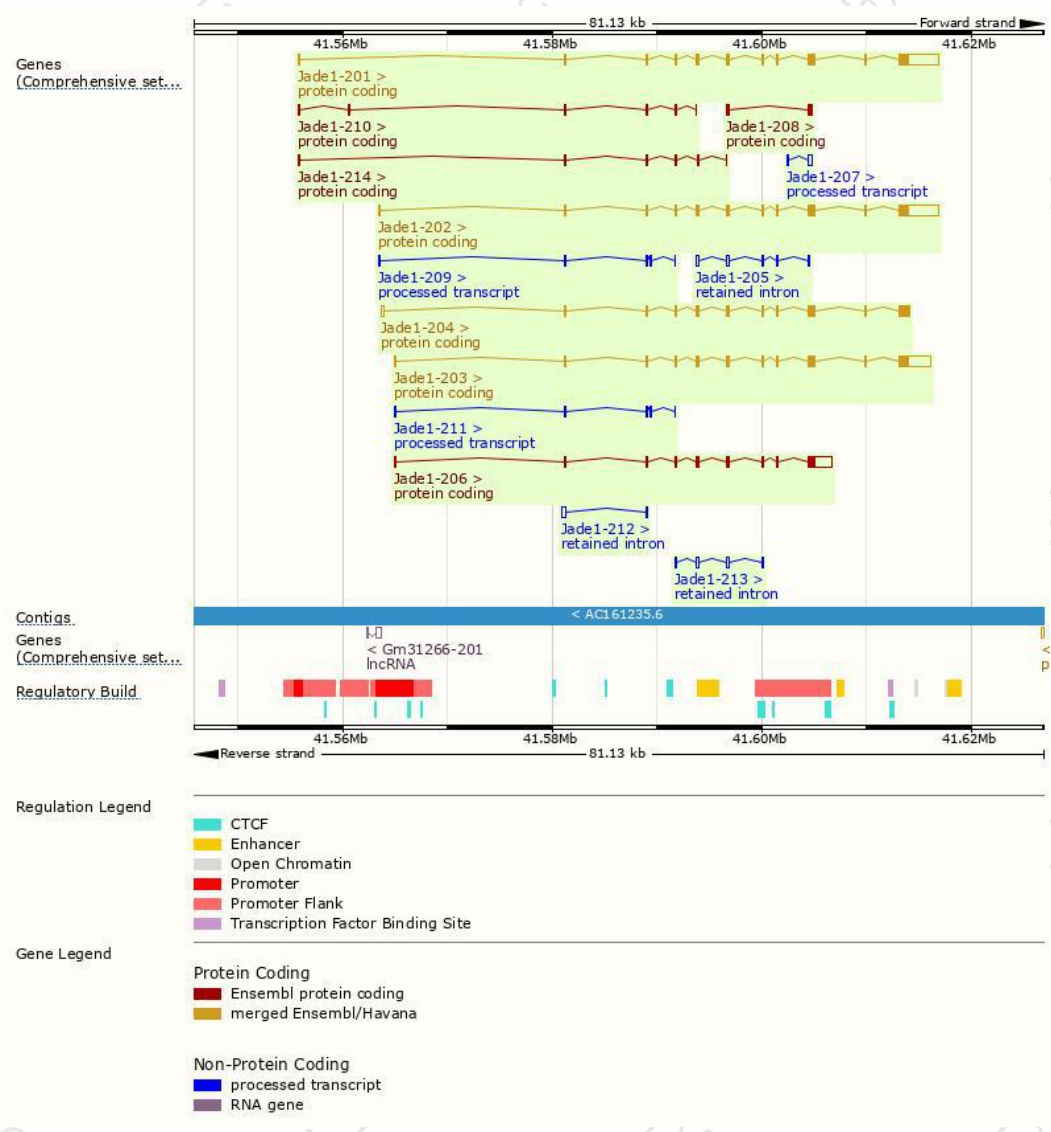
Protein domain

Mouse phenotype description(MGI)

Phenotype Overview

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,though mice homozygous for mutations of this locus show no overt phenotype at birth, fewer survive to weaning than expected by Mendelian ratios.

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