

Mllt6 Cas9-CKO Strategy

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Project Overview

Project Name

Mllt6

Project type

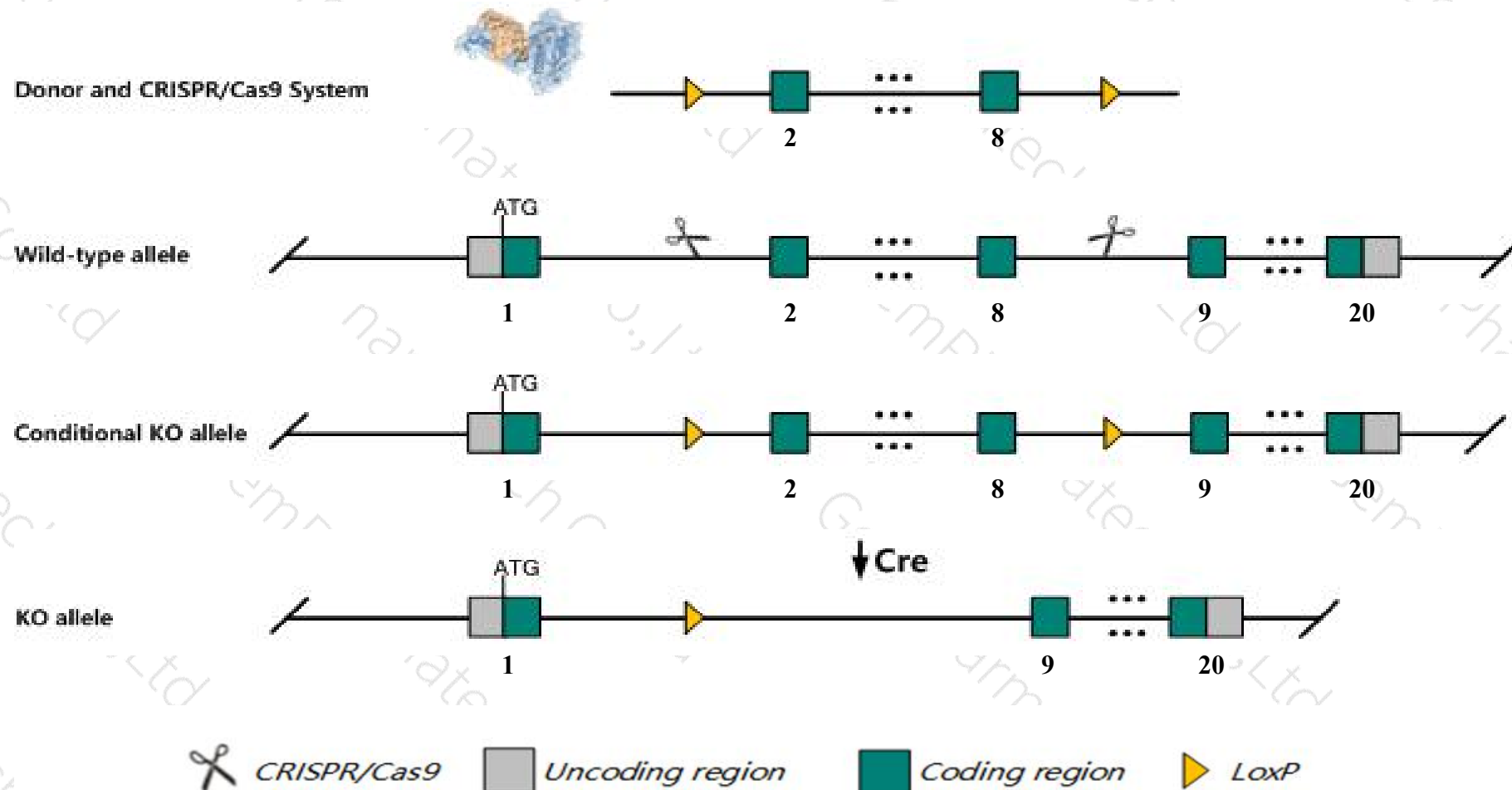
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mllt6* gene. The schematic diagram is as follows:



- The *Mllt6* gene has 6 transcripts. According to the structure of *Mllt6* gene, exon2-exon8 of *Mllt6-201* (ENSMUST00000044730.11) transcript is recommended as the knockout region. The region contains 755bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mllt6* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, mice homozygous for a gene trap allele exhibit no abnormal phenotype.
- The *Mllt6* gene is located on the Chr11. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Mllt6 myeloid/lymphoid or mixed-lineage leukemia; translocated to, 6 [Mus musculus (house mouse)]

Gene ID: 246198, updated on 13-Mar-2020

Summary



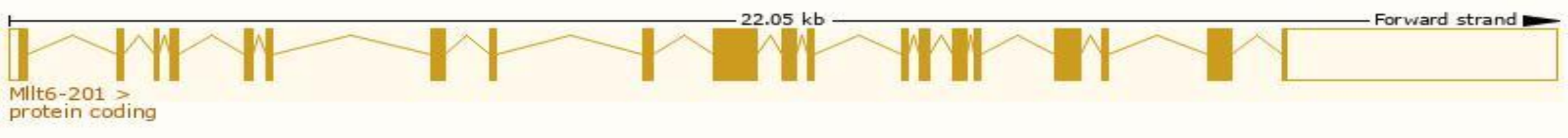
Official Symbol	Mllt6 provided by MGI
Official Full Name	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 6 provided by MGI
Primary source	MGI:MGI:1935145
See related	Ensembl:ENSMUSG00000038437
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI315037, Af17
Expression	Ubiquitous expression in spleen adult (RPKM 32.0), lung adult (RPKM 28.2) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

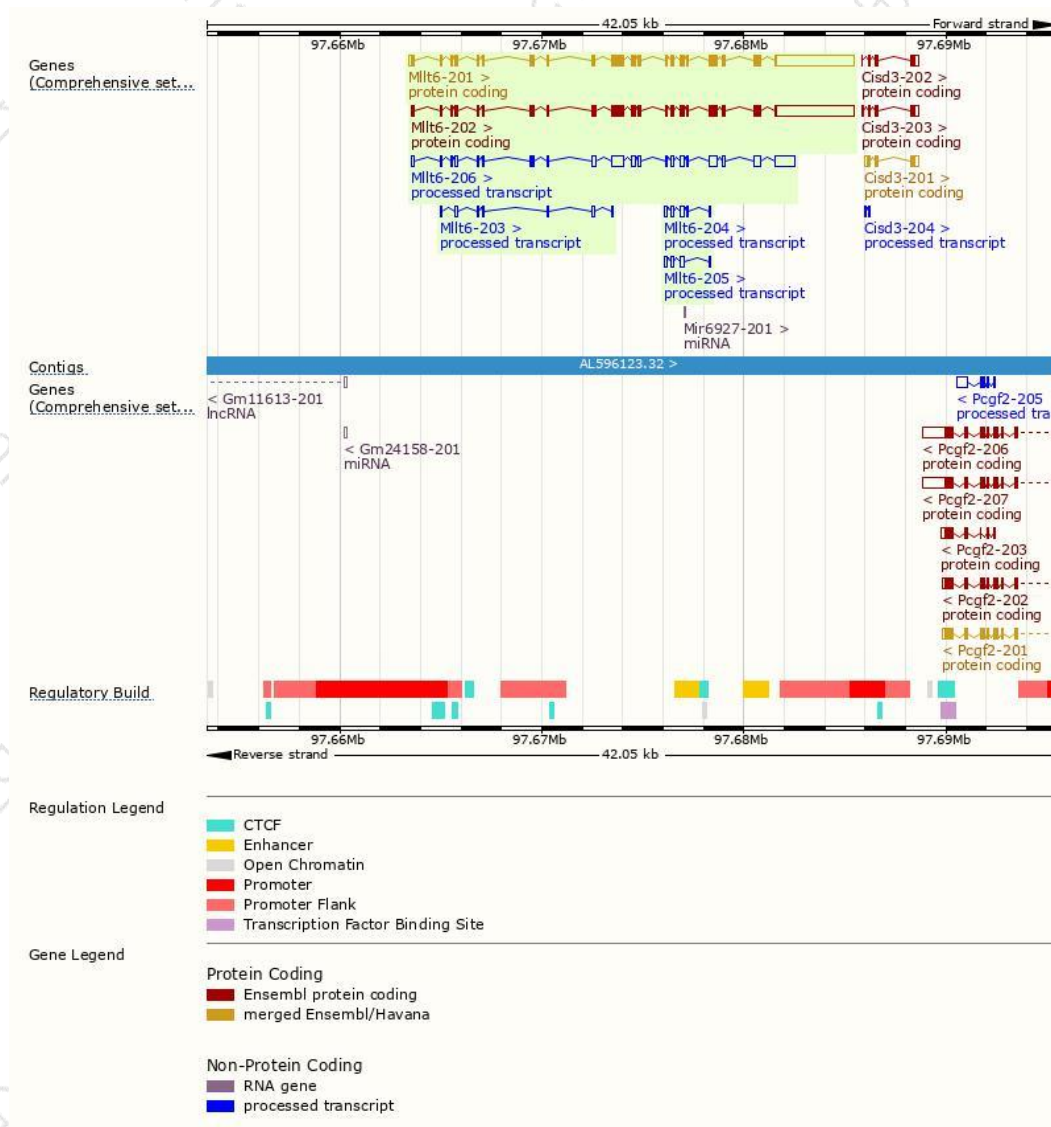
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mllt6-201	ENSMUST00000044730.11	7274	1079aa	Protein coding	CCDS25323	B1AR09	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Mllt6-202	ENSMUST00000107586.2	7206	1109aa	Protein coding	-	B1AR10	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Mllt6-206	ENSMUST00000155835.7	4225	No protein	Processed transcript	-	-	TSL:5
Mllt6-203	ENSMUST00000134158.1	666	No protein	Processed transcript	-	-	TSL:5
Mllt6-204	ENSMUST00000143220.1	641	No protein	Processed transcript	-	-	TSL:3
Mllt6-205	ENSMUST00000151729.7	552	No protein	Processed transcript	-	-	TSL:5

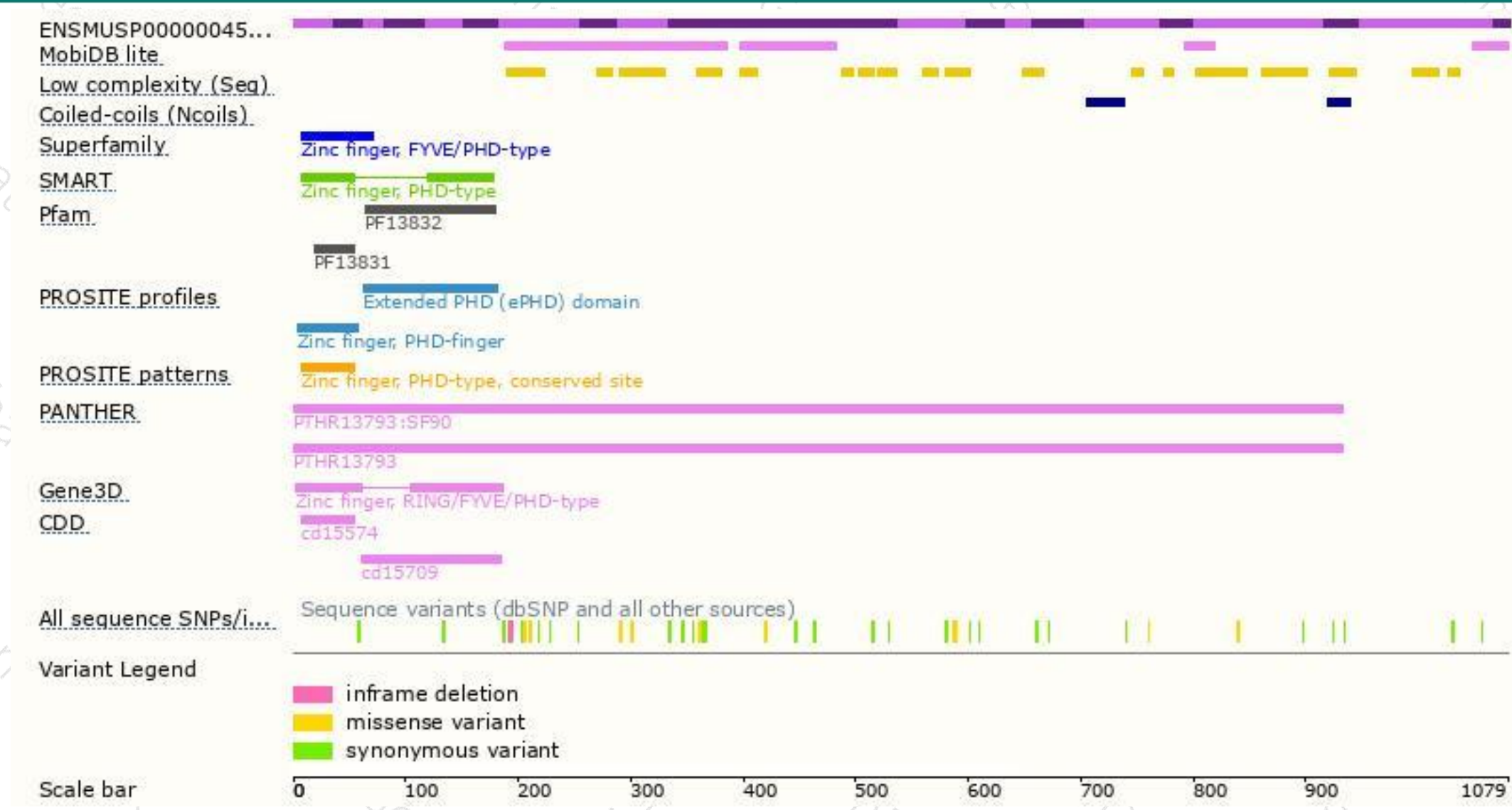
The strategy is based on the design of *Mllt6-201* transcript,the transcription is shown below:



Genomic location distribution

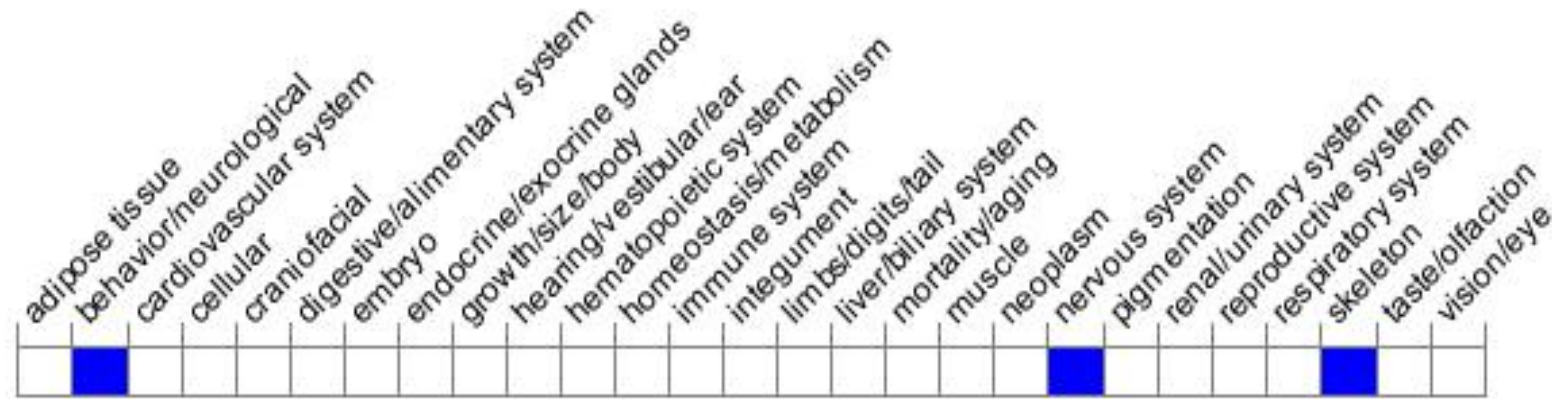


Protein domain



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, mice homozygous for a gene trap allele exhibit no abnormal phenotype.

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

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