Samd8 Cas9-CKO Strategy

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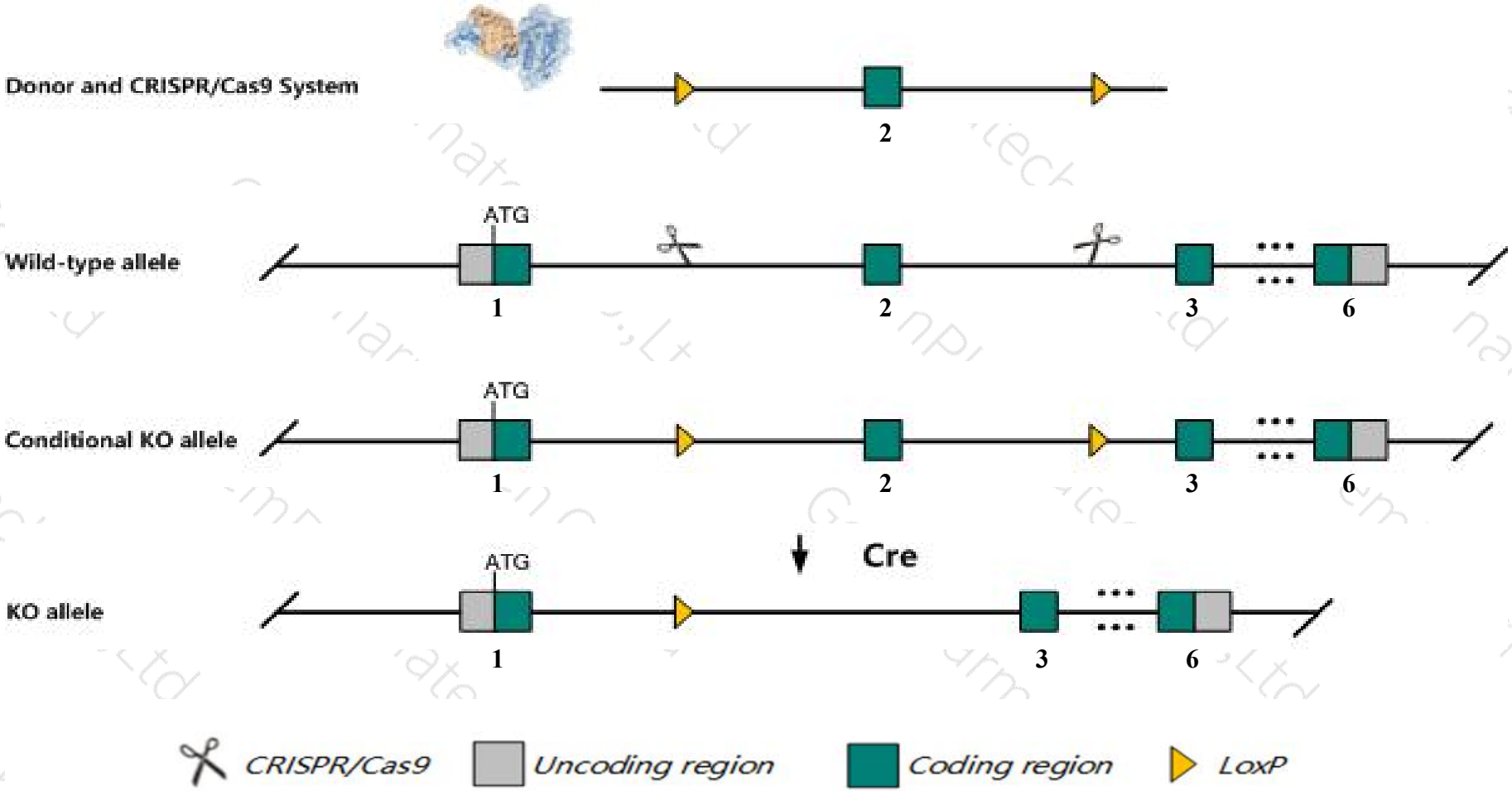
Project Overview

Project Name	***Samd8***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Samd8* gene. The schematic diagram is as follows:



Technical routes

- The *Samd8* gene has 4 transcripts. According to the structure of *Samd8* gene, exon2 of *Samd8-201* (ENSMUST00000022292.9) transcript is recommended as the knockout region.The region contains 593bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Samd8* 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.

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit decreased ceramide phosphoethanolamine synthase activity but normal liver, kidney and spleen histology.

- The *Samd8* gene is located on the Chr14. 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）

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Samd8 sterile alpha motif domain containing 8 [Mus musculus (house mouse)]

Gene ID: 67630, updated on 31-Jan-2019

Summary

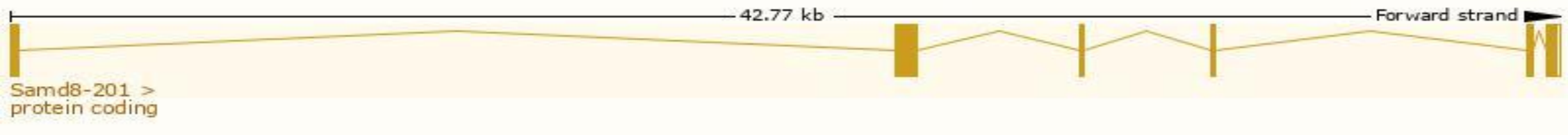
Official Symbol	Samd8 provided by MGI
Official Full Name	sterile alpha motif domain containing 8 provided by MGI
Primary source	MGI:MGI:1914880
See related	Ensembl:ENSMUSG00000021770
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110053F04Rik, 1700010P07Rik, SMSr
Expression	Ubiquitous expression in testis adult (RPKM 10.0), CNS E18 (RPKM 6.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

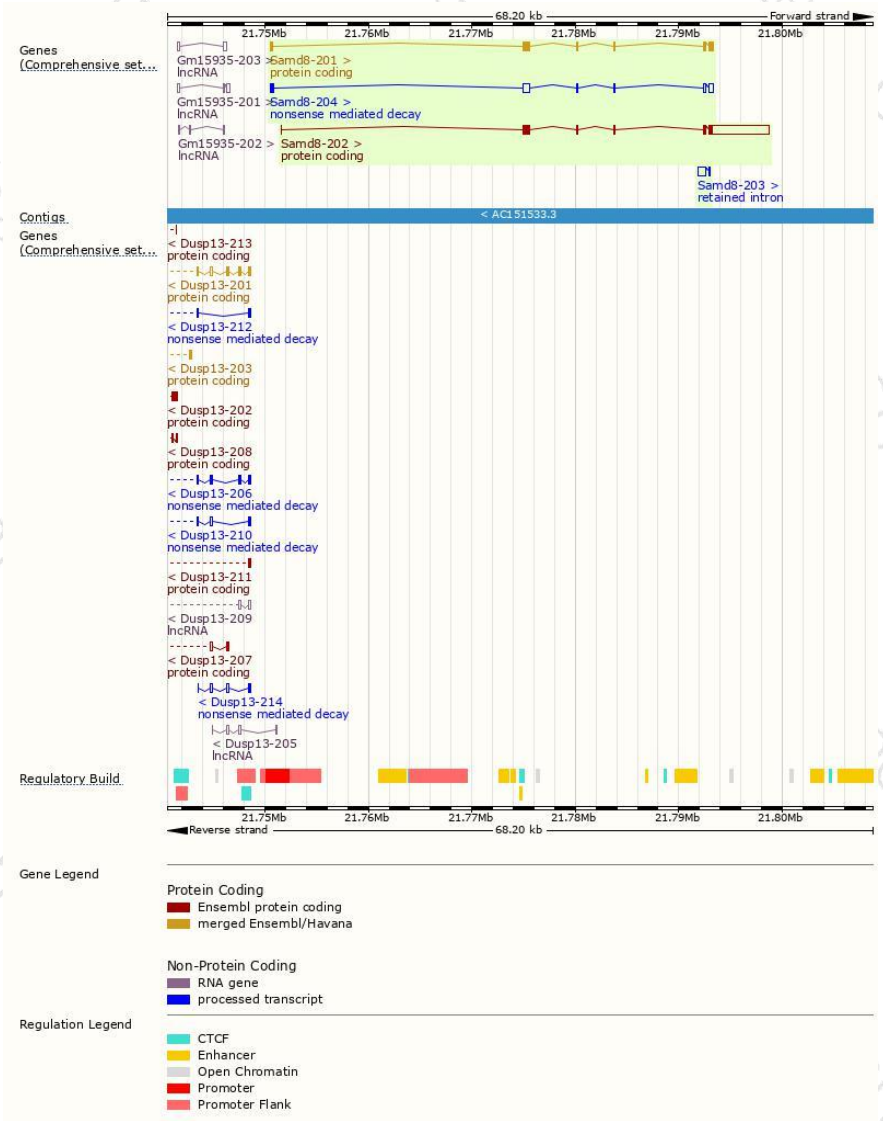
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Samd8-201	ENSMUST00000022292.9	1574	478aa	Protein coding	CCDS26866	Q14AQ4 Q9DA37	TSL:1 GENCODE basic
Samd8-202	ENSMUST00000119430.2	6801	415aa	Protein coding	-	Q3UH82	TSL:1 GENCODE basic APPRIS P1
Samd8-204	ENSMUST00000144061.1	1613	64aa	Nonsense mediated decay	-	D6REI9	TSL:1
Samd8-203	ENSMUST00000142023.1	722	No protein	Retained intron	-	-	TSL:2

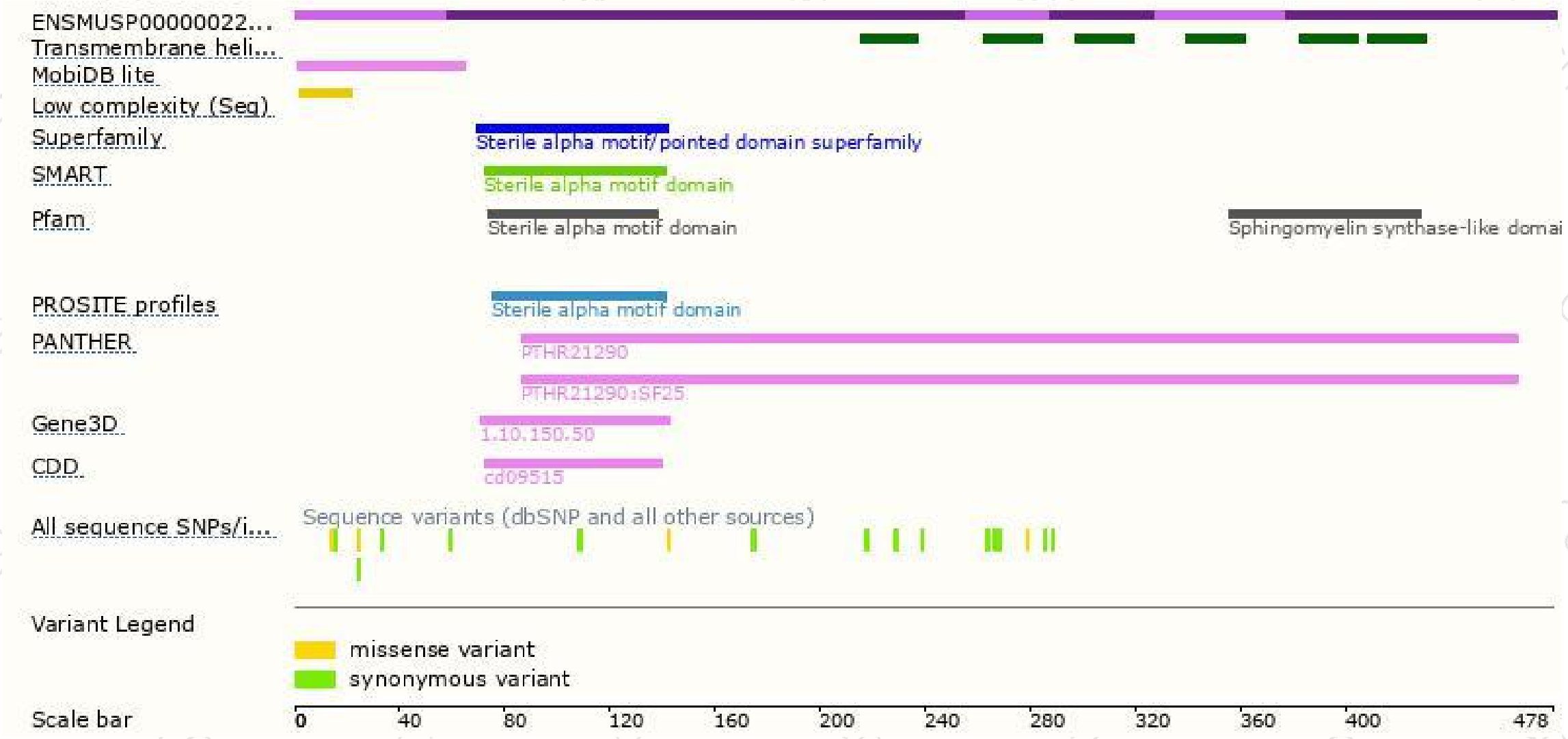
The strategy is based on the design of *Samd8-201* transcript,The transcription is shown below



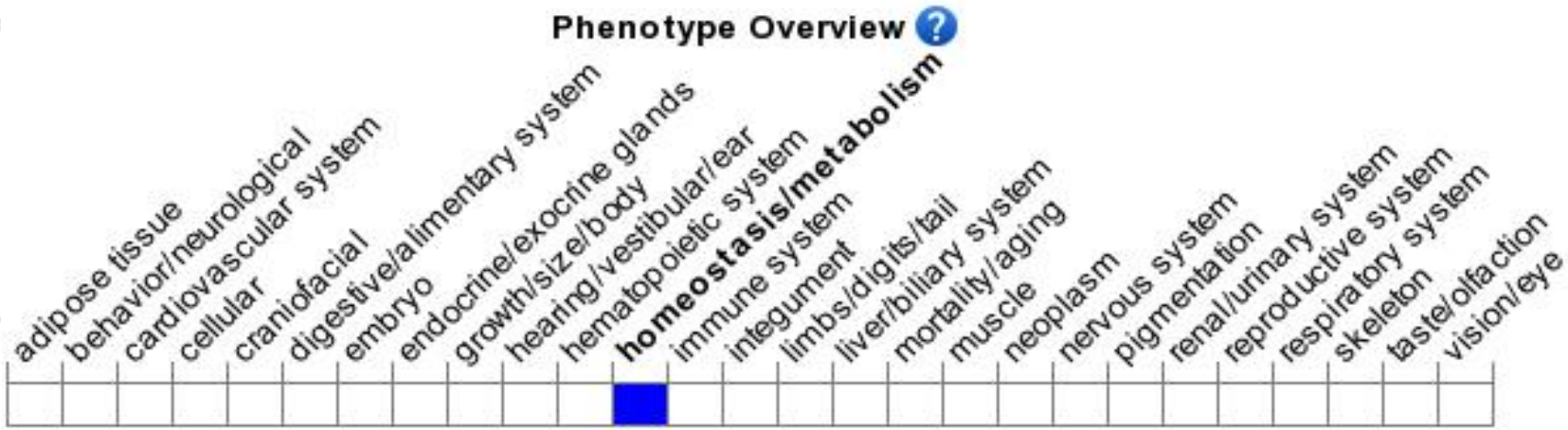
Genomic location distribution



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 decreased ceramide phosphoethanolamine synthase activity but normal liver, kidney and spleen histology.

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

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