

Nhlrc1 Cas9-KO Strategy

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Design Date:	2020-5-12

Project Overview

Project Name

Nhlrc1

Project type

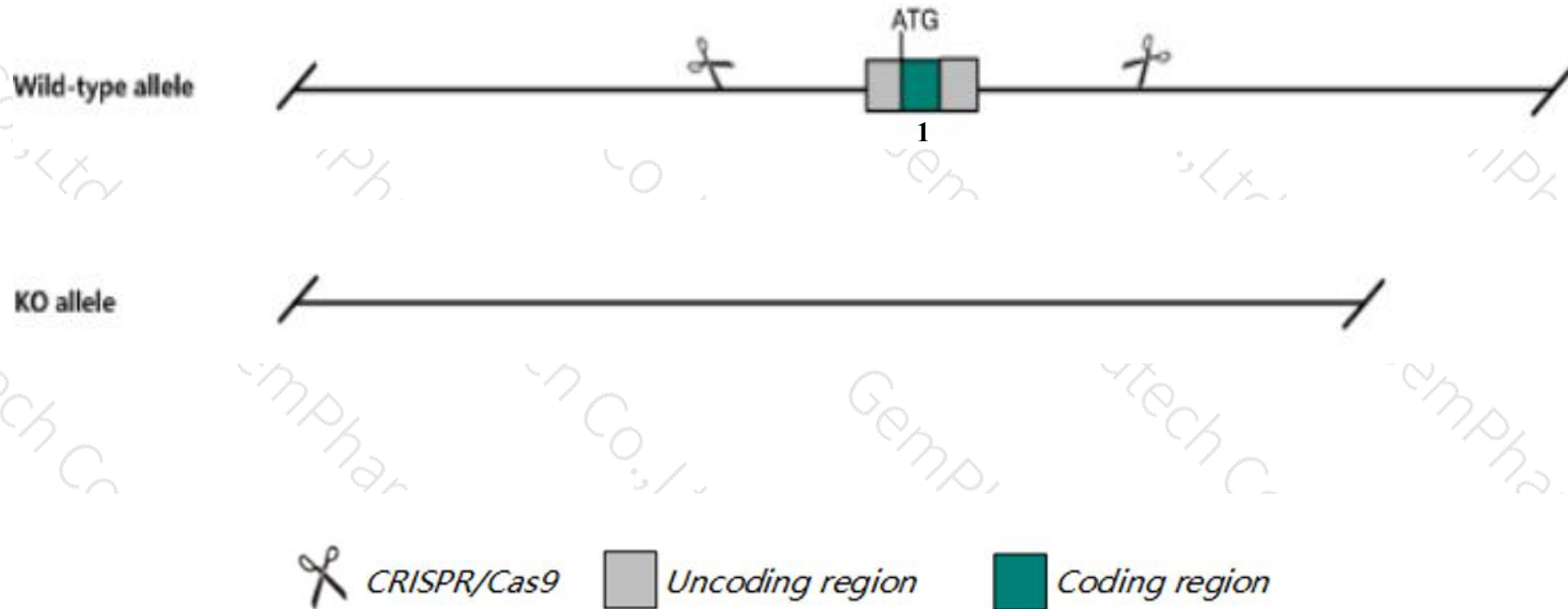
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nhlrc1* gene. The schematic diagram is as follows:



- The *Nhlrc1* gene has 1 transcript. According to the structure of *Nhlrc1* gene, exon1 of *Nhlrc1-201* (ENSMUST00000052747.3) 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 *Nhlrc1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit accumulation of lafora bodies and total glycogen levels in the heart muscle, skeletal muscle, and brain.
- The *Nhlrc1* gene is located on the Chr13. 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)

Nhlrc1 NHL repeat containing 1 [Mus musculus (house mouse)]

Gene ID: 105193, updated on 13-Mar-2020

Summary



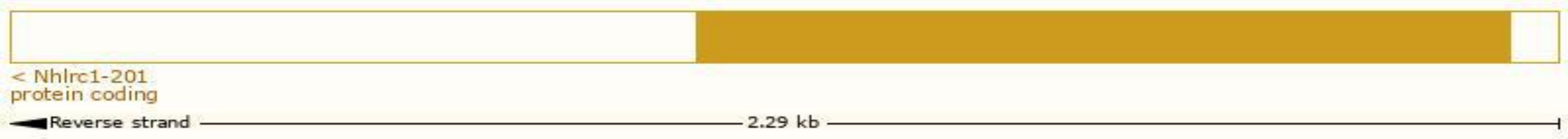
Official Symbol	Nhlrc1 provided by MGI
Official Full Name	NHL repeat containing 1 provided by MGI
Primary source	MGI:MGI:2145264
See related	Ensembl:ENSMUSG00000044231
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI505271, B230309E09Rik, EPM2B
Orthologs	human all

Transcript information (Ensembl)

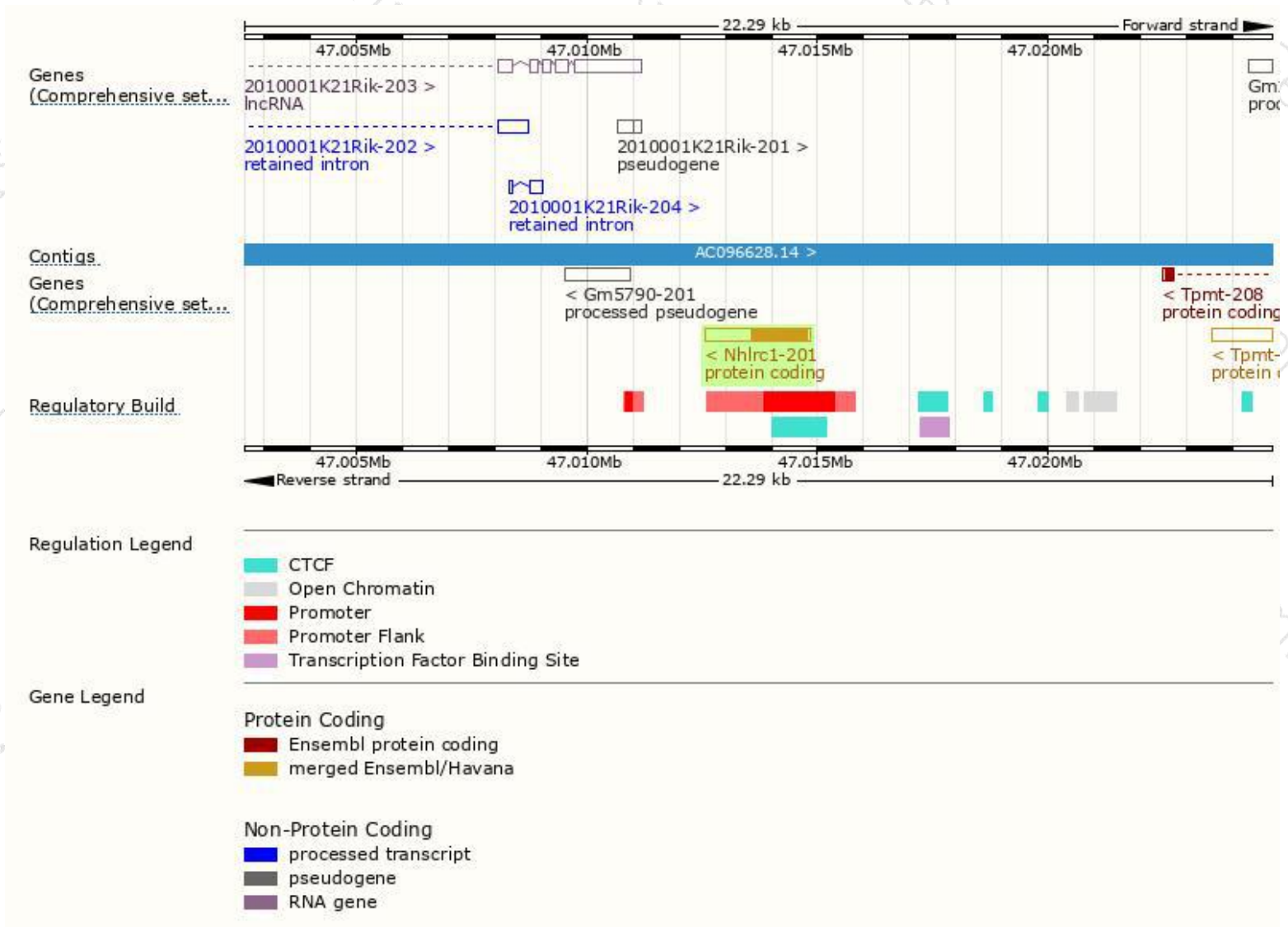
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nhlrc1-201	ENSMUST00000052747.3	2294	401aa	Protein coding	CCDS26487	Q0VF71 Q8BR37	TSL:NA 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 P1

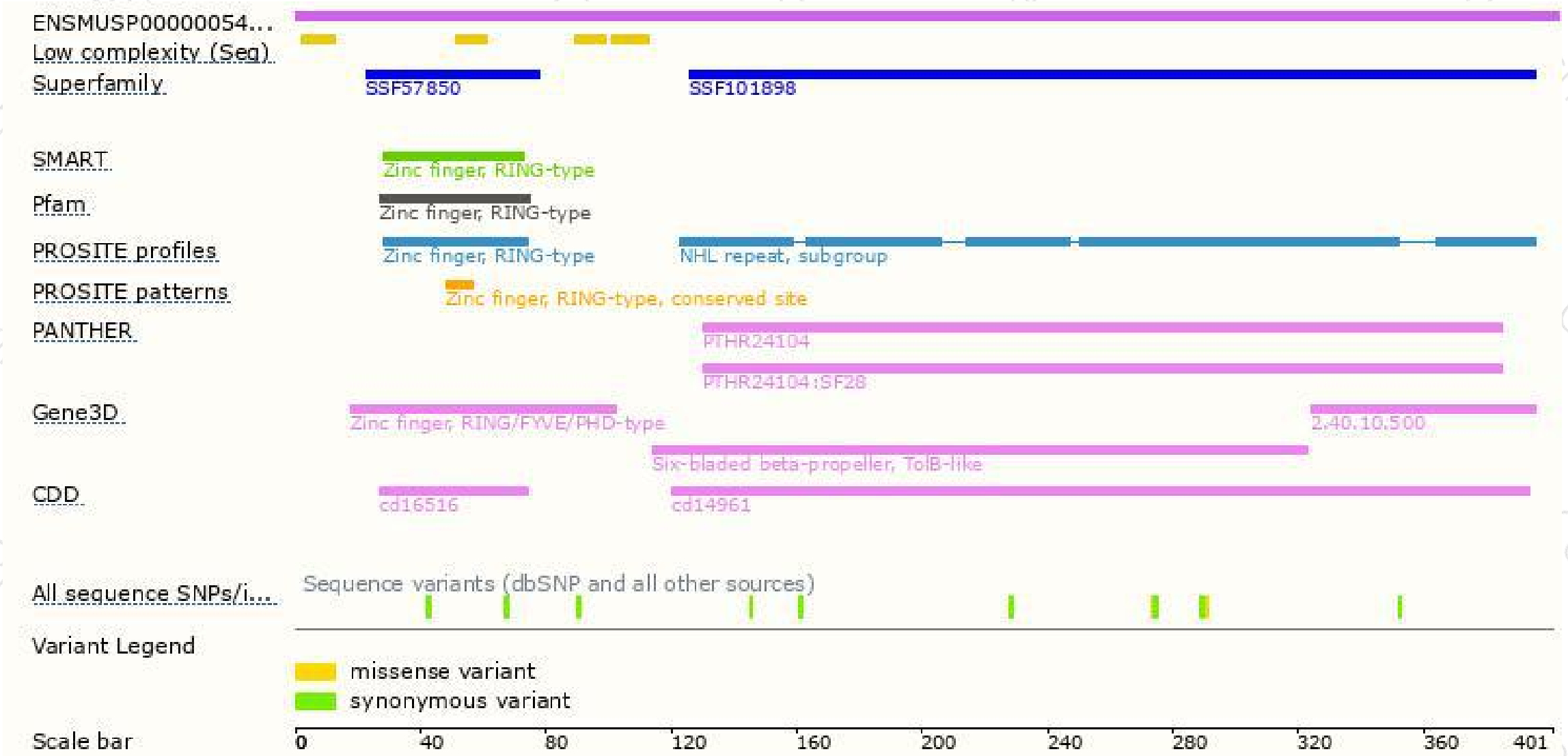
The strategy is based on the design of *Nhlrc1-201* transcript, the transcription is shown below



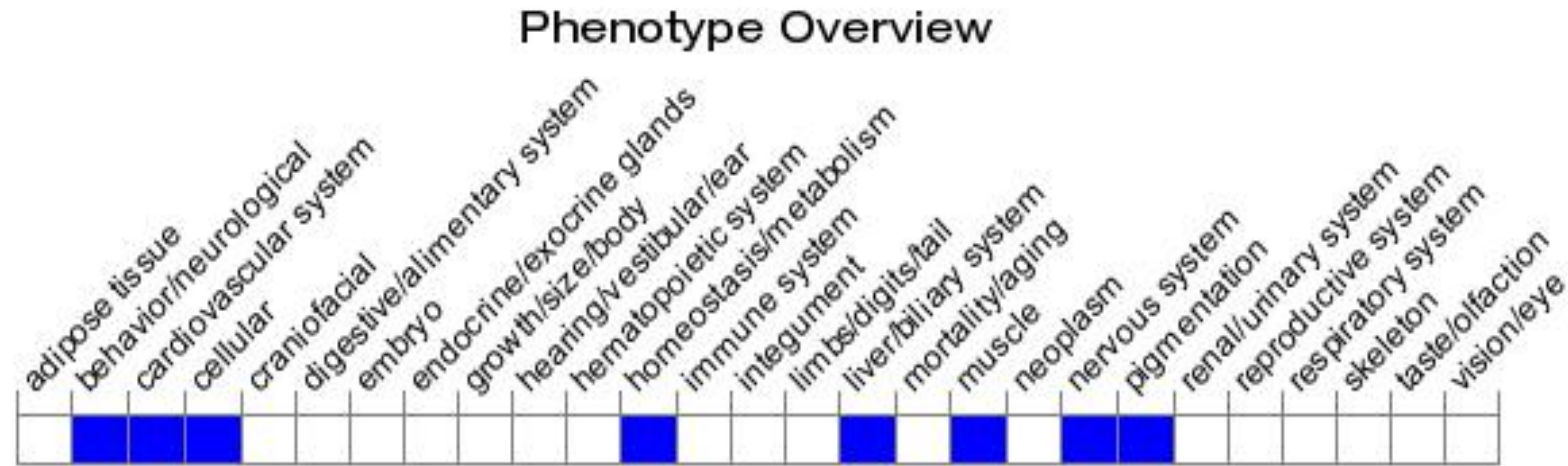
Genomic location distribution



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 accumulation of Lafora bodies and total glycogen levels in the heart muscle, skeletal muscle, and brain.

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

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