

Cdk1 Cas9-KO Strategy

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Project Overview

Project Name

Cdk1

Project type

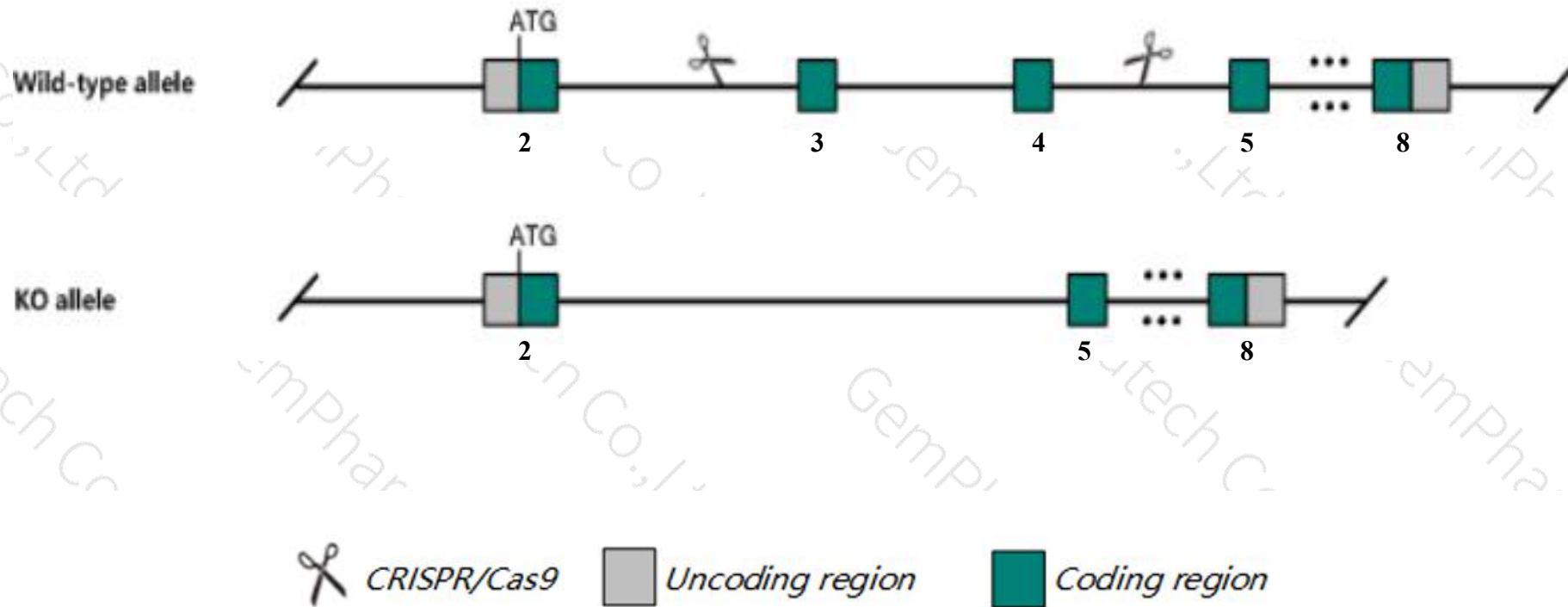
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cdk1* gene. The schematic diagram is as follows:



- The *Cdk1* gene has 7 transcripts. According to the structure of *Cdk1* gene, exon3-exon4 of *Cdk1-201* (ENSMUST00000020099.12) transcript is recommended as the knockout region. The region contains 281bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cdk1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, mice homozygous for a null allele die prior to e1.5.
- The *Cdk1* gene is located on the Chr10. 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)

Cdk1 cyclin-dependent kinase 1 [Mus musculus (house mouse)]

Gene ID: 12534, updated on 13-Mar-2020

Summary



Official Symbol Cdk1 provided by [MGI](#)

Official Full Name cyclin-dependent kinase 1 provided by [MGI](#)

Primary source [MGI:MGI:88351](#)

See related [Ensembl:ENSMUSG00000019942](#)

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 Cdc2, Cdc2a, p34

Expression Biased expression in liver E14 (RPKM 47.0), placenta adult (RPKM 44.1) and 11 other tissues [See more](#)

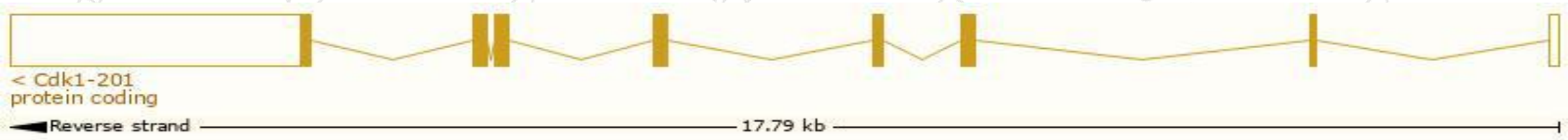
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

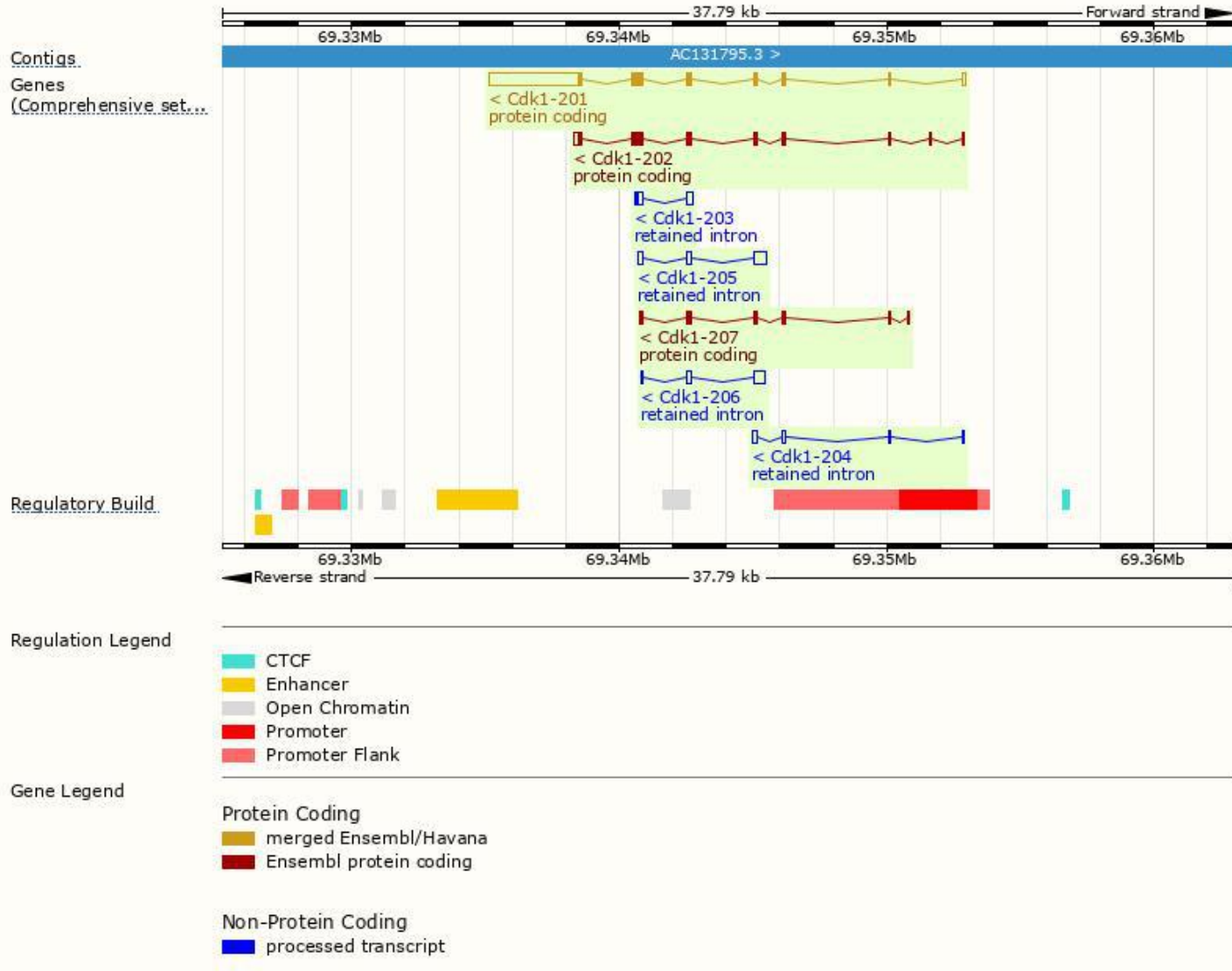
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cdk1-201	ENSMUST0000020099.12	4375	297aa	Protein coding	CCDS23908	P11440	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 P1
Cdk1-202	ENSMUST00000119827.7	1253	297aa	Protein coding	CCDS23908	P11440	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 P1
Cdk1-207	ENSMUST00000152448.1	695	200aa	Protein coding	-	D3Z2T9	CDS 3' incomplete TSL:3
Cdk1-205	ENSMUST00000129444.7	770	No protein	Retained intron	-	-	TSL:3
Cdk1-206	ENSMUST00000149474.1	616	No protein	Retained intron	-	-	TSL:5
Cdk1-204	ENSMUST00000124054.1	475	No protein	Retained intron	-	-	TSL:2
Cdk1-203	ENSMUST00000123458.1	378	No protein	Retained intron	-	-	TSL:2

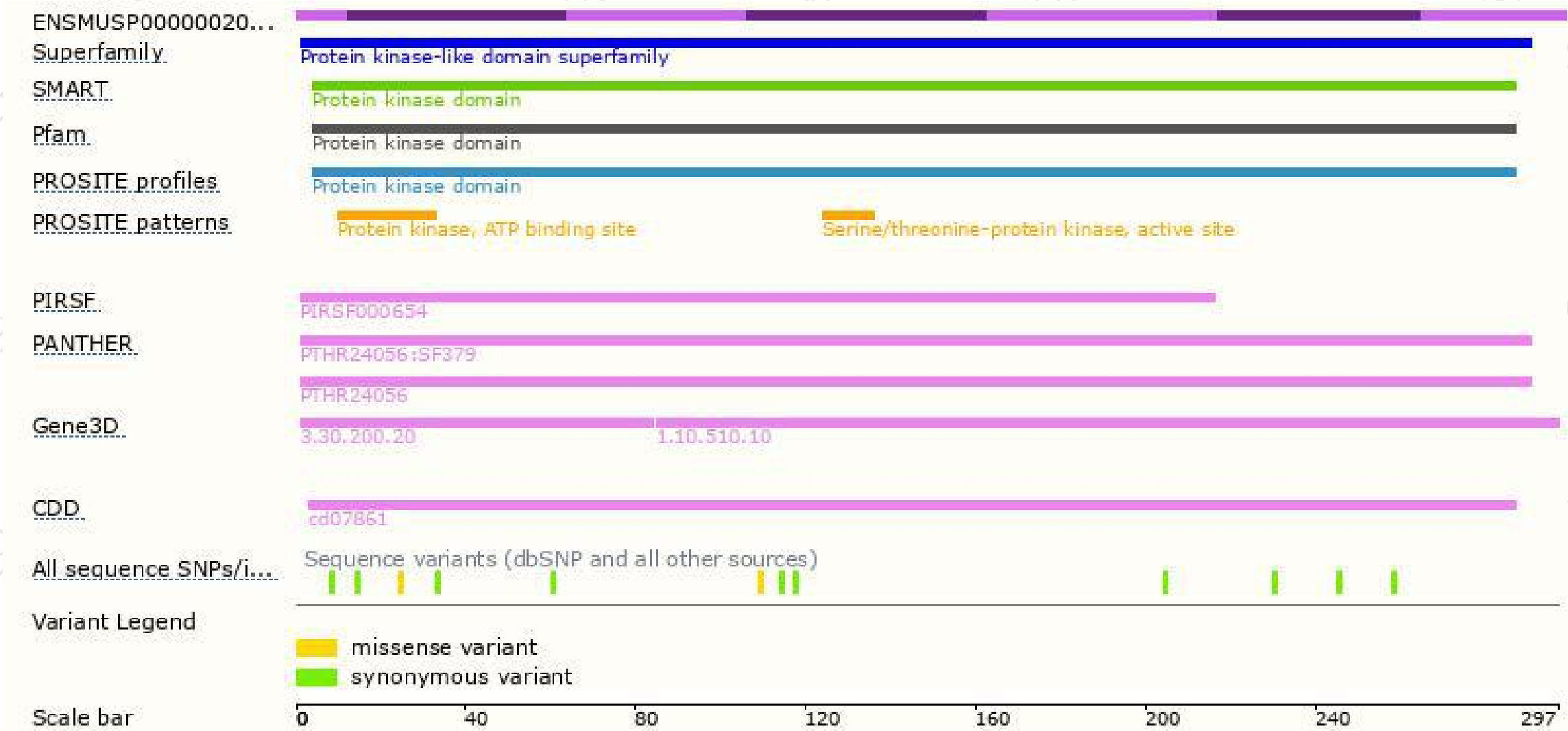
The strategy is based on the design of *Cdk1-201* transcript,the transcription is shown below:



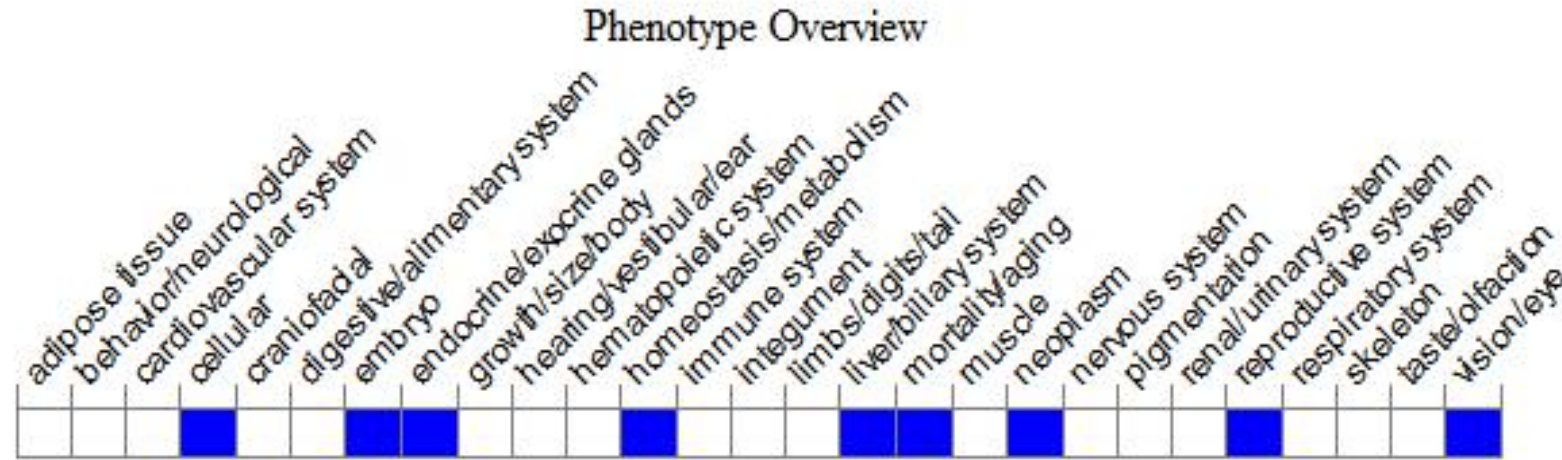
Genomic location distribution



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 null allele die prior to E1.5.

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

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