

Kcne3 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Kcne3

Project type

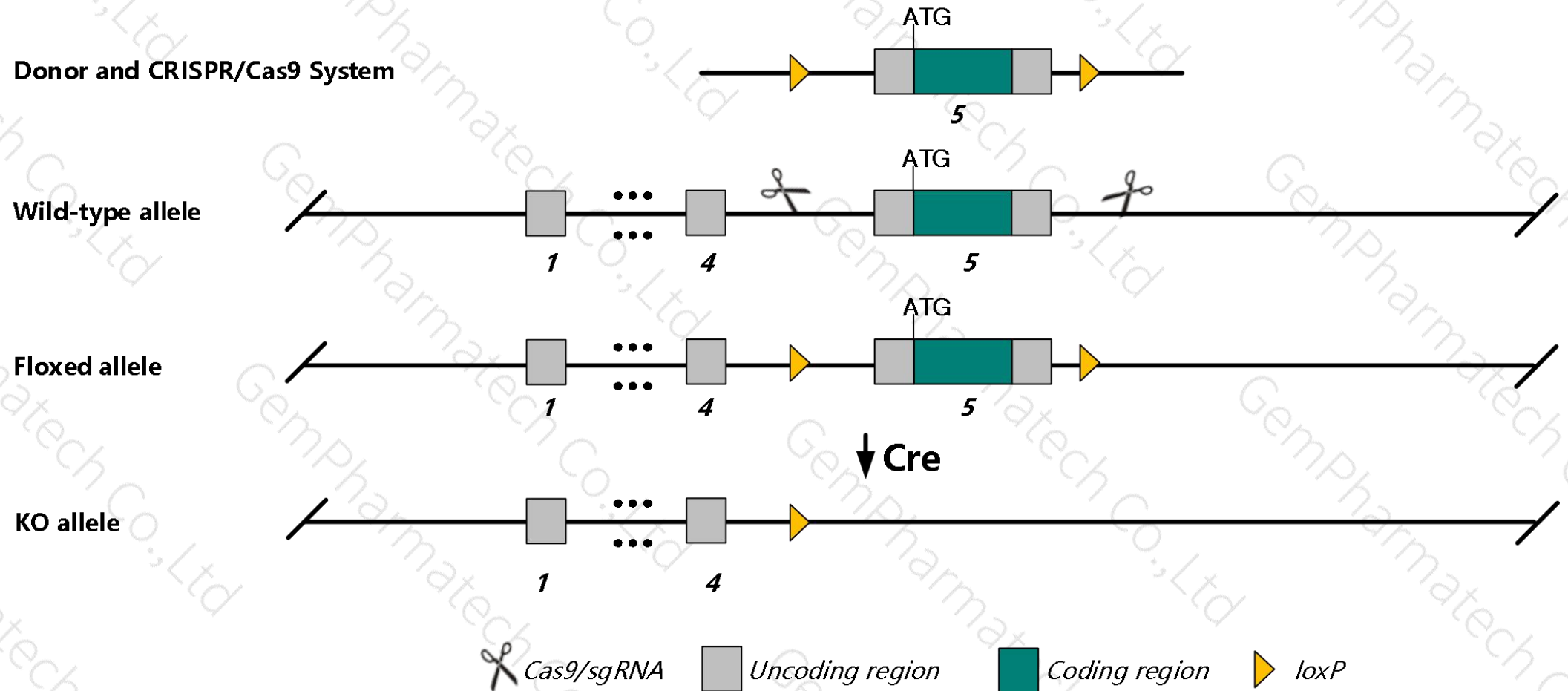
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcne3* gene. The schematic diagram is as follows:



- The *Kcne3* gene has 8 transcripts. According to the structure of *Kcne3* gene, exon5 of *Kcne3-203* (ENSMUST00000178946.8) 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 *Kcne3* 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 knock-out allele exhibit decreased cAMP-stimulated electrogenic Cl⁻ secretion across tracheal and intestinal epithelia. Another knock-out allele shows age-dependent alterations in action potential and firing properties of spiral ganglion neurons in the cochlea.
- The flox region is in the intron of the Gm34821 gene, which may affect the regulation of this gene.
- The *Kcne3* gene is located on the Chr7. 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)

Kcne3 potassium voltage-gated channel, Isk-related subfamily, gene 3 [*Mus musculus* (house mouse)]

Gene ID: 57442, updated on 24-Oct-2019

Summary

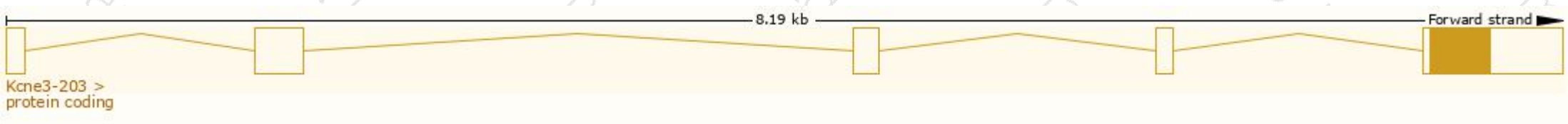
Official Symbol	Kcne3 provided by MGI
Official Full Name	potassium voltage-gated channel, Isk-related subfamily, gene 3 provided by MGI
Primary source	MGI:MGI:1891124
See related	Ensembl:ENSMUSG00000035165
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MiRP2; 2210017H05Rik
Expression	Biased expression in colon adult (RPKM 22.2), testis adult (RPKM 22.1) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

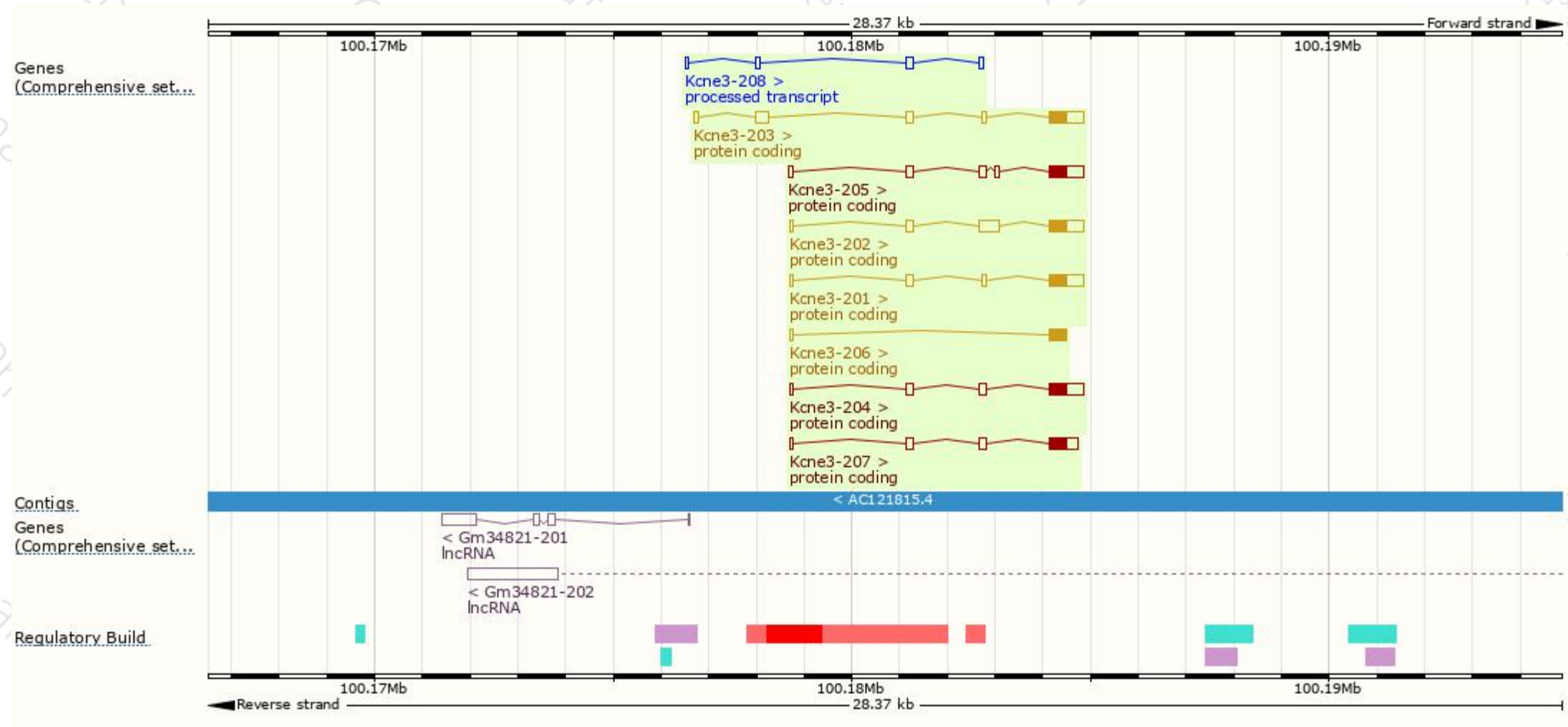
The gene has 8 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcne3-203	ENSMUST00000178946.8	1323	103aa	Protein coding	CCDS21495	Q545H9 Q9WTW2	TSL:1 GENCODE basic APPRIS P1
Kcne3-202	ENSMUST00000170954.9	1315	103aa	Protein coding	CCDS21495	Q545H9 Q9WTW2	TSL:1 GENCODE basic APPRIS P1
Kcne3-205	ENSMUST00000207358.1	1154	103aa	Protein coding	CCDS21495	Q545H9 Q9WTW2	TSL:5 GENCODE basic APPRIS P1
Kcne3-204	ENSMUST00000179842.2	1059	103aa	Protein coding	CCDS21495	Q545H9 Q9WTW2	TSL:1 GENCODE basic APPRIS P1
Kcne3-201	ENSMUST00000049333.12	1012	103aa	Protein coding	CCDS21495	Q545H9 Q9WTW2	TSL:1 GENCODE basic APPRIS P1
Kcne3-207	ENSMUST00000208260.1	929	103aa	Protein coding	CCDS21495	Q545H9 Q9WTW2	TSL:3 GENCODE basic APPRIS P1
Kcne3-206	ENSMUST00000207995.1	439	103aa	Protein coding	CCDS21495	Q545H9 Q9WTW2	TSL:2 GENCODE basic APPRIS P1
Kcne3-208	ENSMUST00000208555.1	374	No protein	Processed transcript	-	-	TSL:3

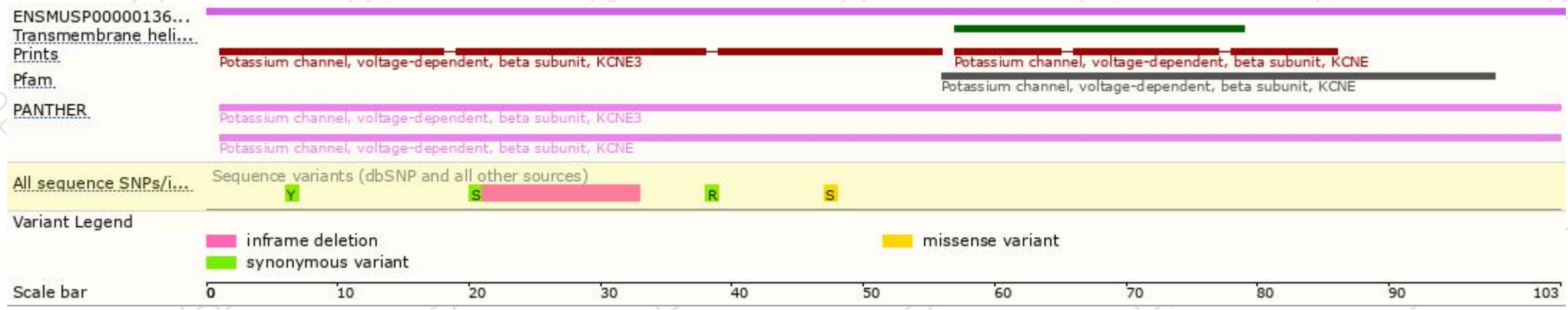
The strategy is based on the design of *Kcne3-203* transcript,The transcription is shown below



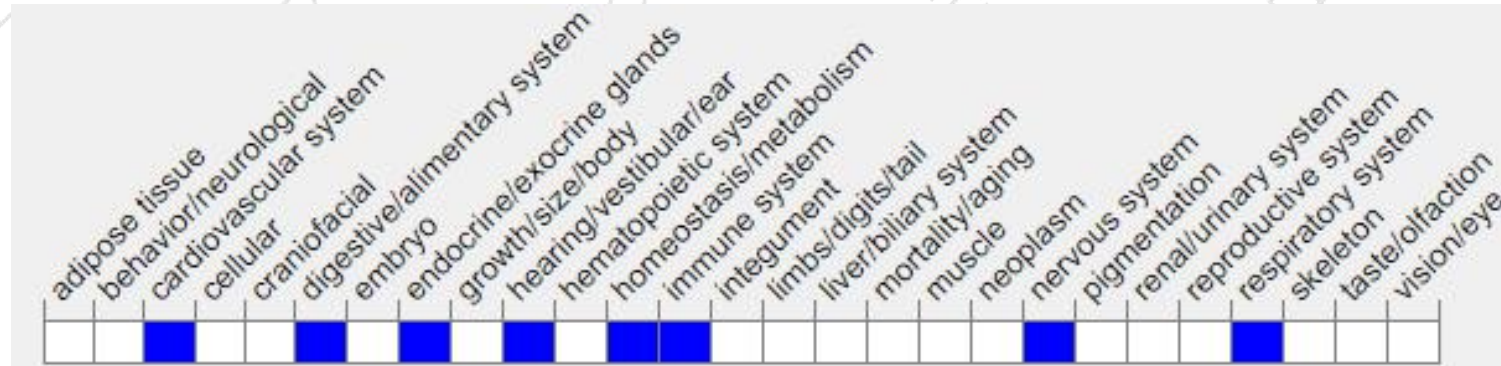
Genomic location distribution



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 cAMP-stimulated electrogenic Cl⁻ secretion across tracheal and intestinal epithelia. Another knock-out allele shows age-dependent alterations in action potential and firing properties of spiral ganglion neurons in the cochlea.

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

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