Scaf11 Cas9-KO Strategy

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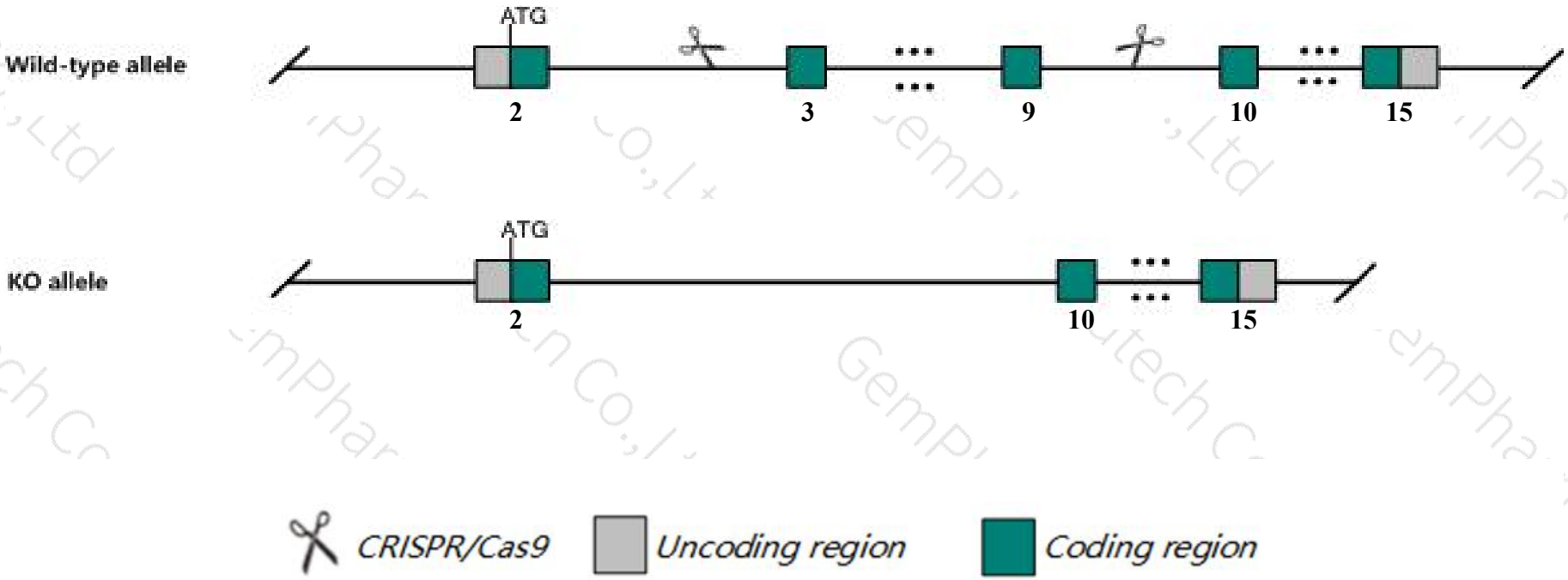
Project Overview

Project Name	***Scaf11***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Scaf11* gene. The schematic diagram is as follows:



Technical routes

➢ The *Scaf11* gene has 6 transcripts. According to the structure of *Scaf11* gene, exon3-exon9 of *Scaf11-201* (ENSMUST00000047835.7) transcript is recommended as the knockout region.The region contains 667bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Scaf11* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- Transcript *Scaf11*-203 may not be affected . And the effect on transcript *Scaf11*-204&205&206 is unknown.
- The *Scaf11* gene is located on the Chr15. 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）

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Scaf11 SR-related CTD-associated factor 11 [*Mus musculus* (house mouse)]

Gene ID: 72193, updated on 12-Aug-2019

Summary

Official Symbol	Scaf11 provided by MGI
Official Full Name	SR-related CTD-associated factor 11 provided by MGI
Primary source	MGI:MGI:1919443
See related	Ensembl:ENSMUSG00000033228
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	SIP1; CASP11; SRRP129; Sfrs2ip; Srsf2ip; AI462454; mKIAA3013; 1110061H03Rik; 2610510E10Rik
Expression	Ubiquitous expression in placenta adult (RPKM 13.7), CNS E11.5 (RPKM 12.4) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 15; 15 F1

See Scaf11 in Genome Data Viewer

Exon count: 16

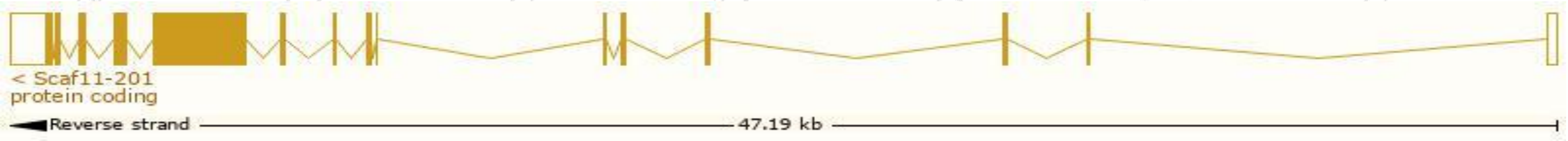
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	15	NC_000081.6 (96411698..96460988, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	15	NC_000081.5 (96242129..96291274, complement)

Transcript information（Ensembl）

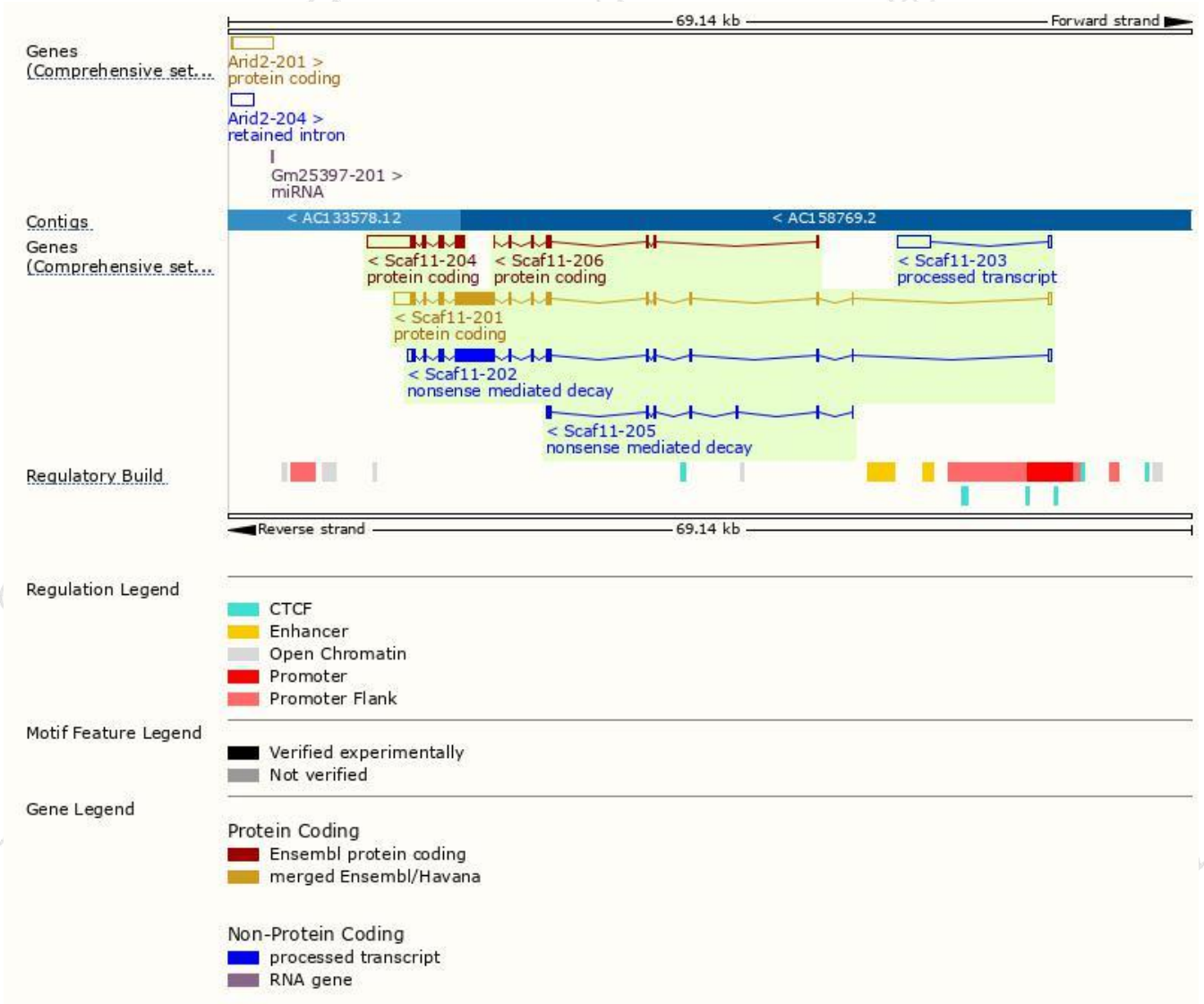
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Scaf11-201	ENSMUST00000047835.7	5766	1456aa	Protein coding	CCDS37186	E9PZM7	TSL:5 GENCODE basic APPRIS P1
Scaf11-204	ENSMUST00000228072.1	4519	476aa	Protein coding	-	A0A2I3BRQ7	CDS 5' incomplete
Scaf11-206	ENSMUST00000228535.1	696	232aa	Protein coding	-	A0A2I3BQX1	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Scaf11-202	ENSMUST00000227069.1	4829	1389aa	Nonsense mediated decay	-	A0A2I3BQU5	
Scaf11-205	ENSMUST00000228260.1	796	84aa	Nonsense mediated decay	-	A0A2I3BQ68	CDS 5' incomplete
Scaf11-203	ENSMUST00000227133.1	2599	No protein	Processed transcript	-	-	

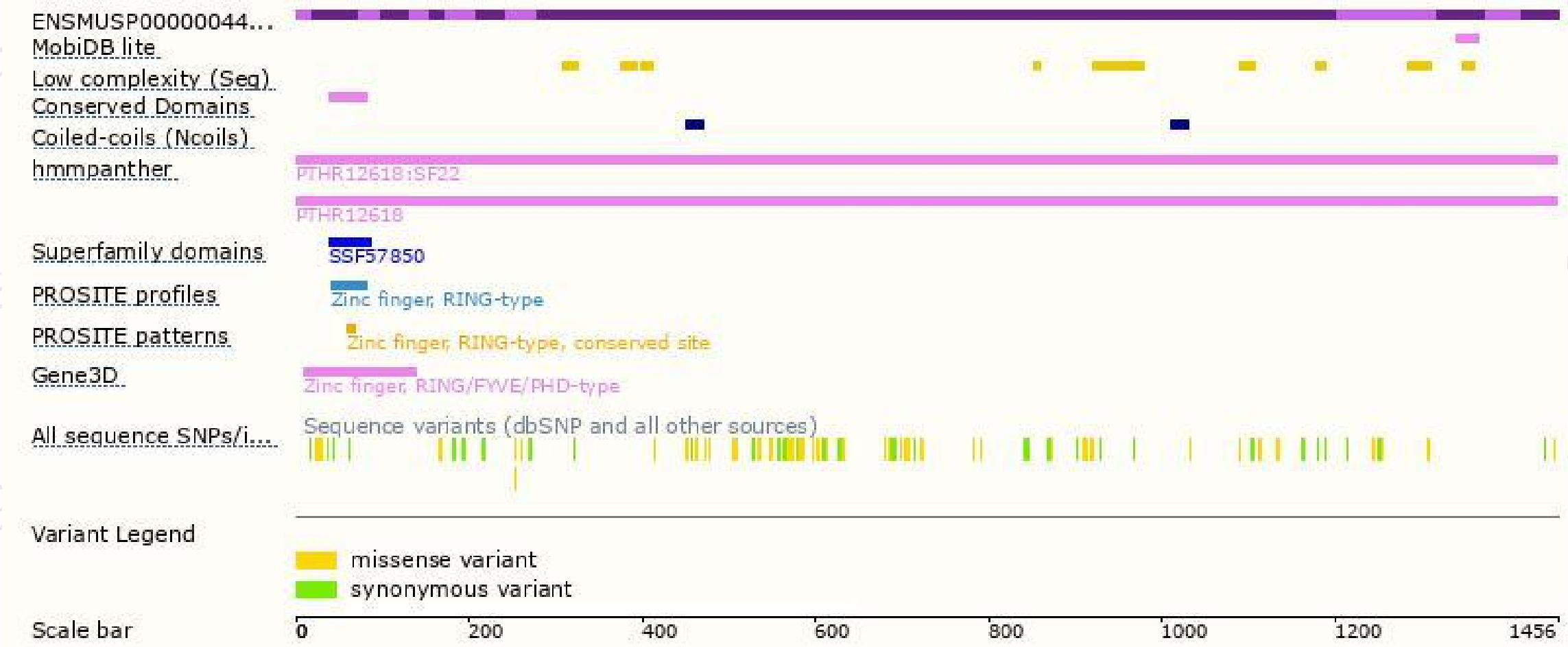
The strategy is based on the design of *Scaf11-201* transcript,The transcription is shown below



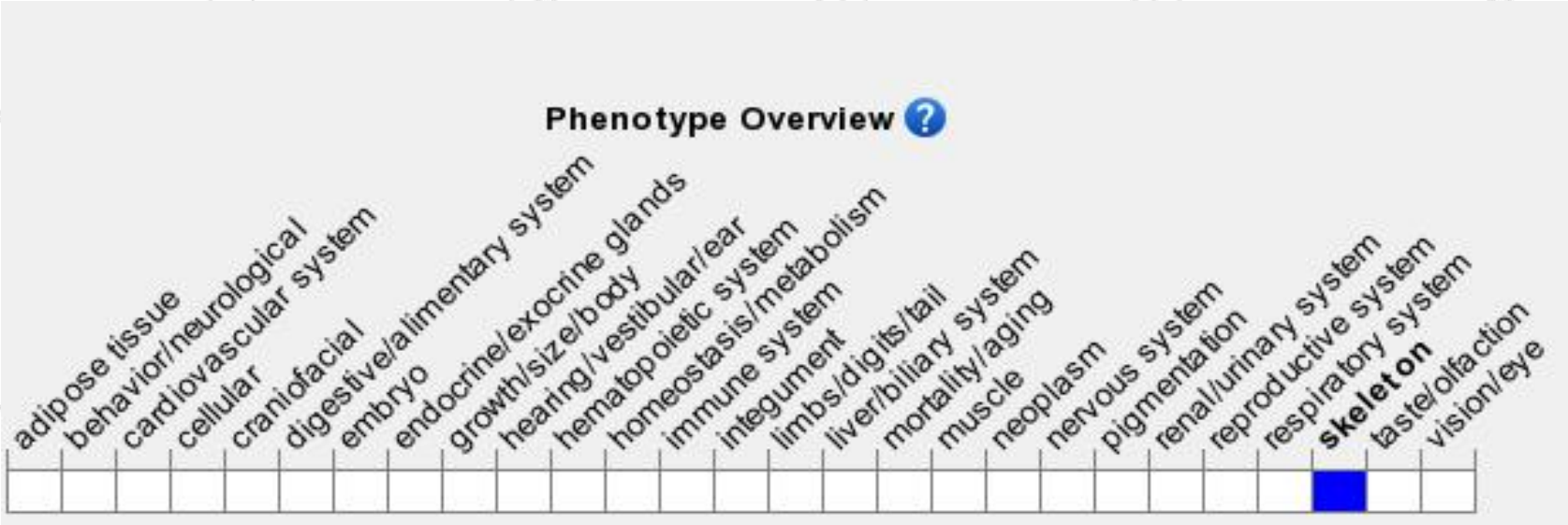
Genomic location distribution



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/).

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

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