

Atp6v0d2 Cas9-KO Strategy

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Project Overview

Project Name

Atp6v0d2

Project type

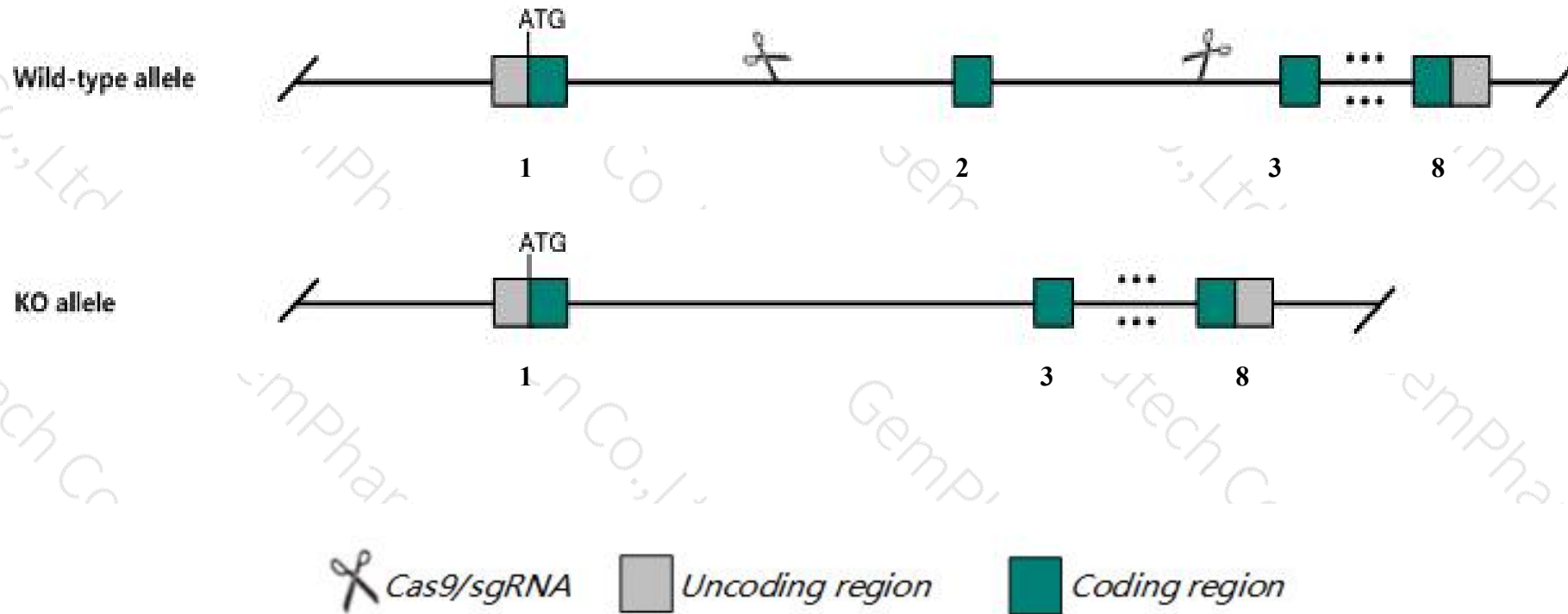
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp6v0d2* gene. The schematic diagram is as follows:



- The *Atp6v0d2* gene has 2 transcripts. According to the structure of *Atp6v0d2* gene, exon2 of *Atp6v0d2-201* (ENSMUST00000029900.5) transcript is recommended as the knockout region. The region contains 172bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp6v0d2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Mice homozygous for a null mutation display osteopetrosis and impaired osteoclast maturation.
- The *Atp6v0d2* gene is located on the Chr4. 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)

Atp6v0d2 ATPase, H⁺ transporting, lysosomal V0 subunit D2 [Mus musculus (house mouse)]

Gene ID: 242341, updated on 31-Jan-2019

Summary



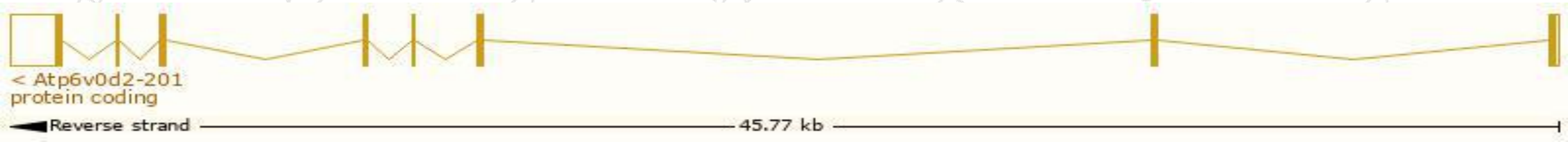
Official Symbol	Atp6v0d2 provided by MGI
Official Full Name	ATPase, H ⁺ transporting, lysosomal V0 subunit D2 provided by MGI
Primary source	MGI:MGI:1924415
See related	Ensembl:ENSMUSG00000028238
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1620401A02Rik, A1324824, V-ATPase
Expression	Biased expression in kidney adult (RPKM 4.2), genital fat pad adult (RPKM 2.8) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

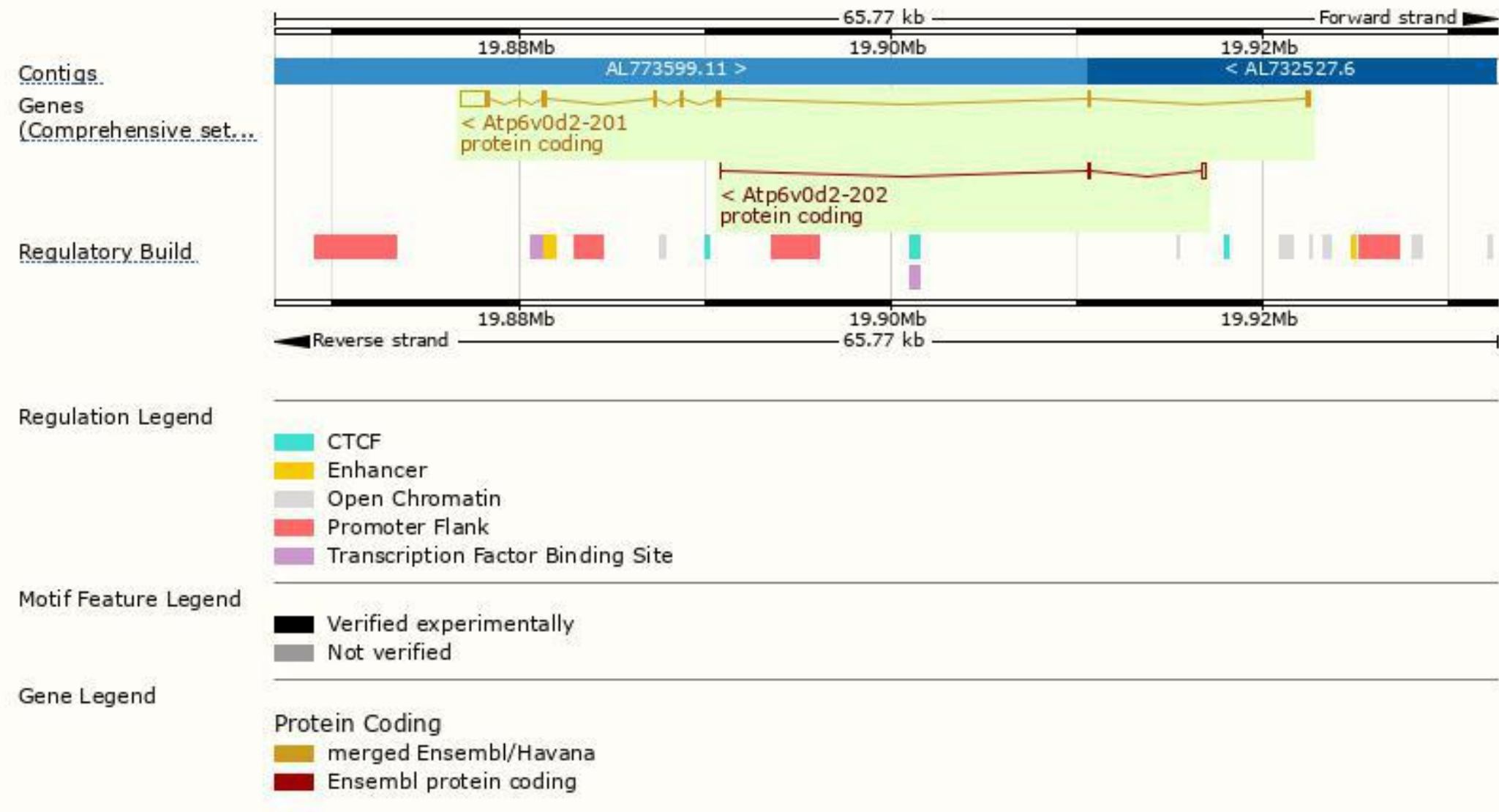
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp6v0d2-201	ENSMUST00000029900.5	2539	350aa	Protein coding	CCDS17994	Q80SY3	TSL:1 GENCODE basic APPRIS P1
Atp6v0d2-202	ENSMUST00000128605.1	374	36aa	Protein coding	-	B1AWC2	CDS 3' incomplete TSL:5

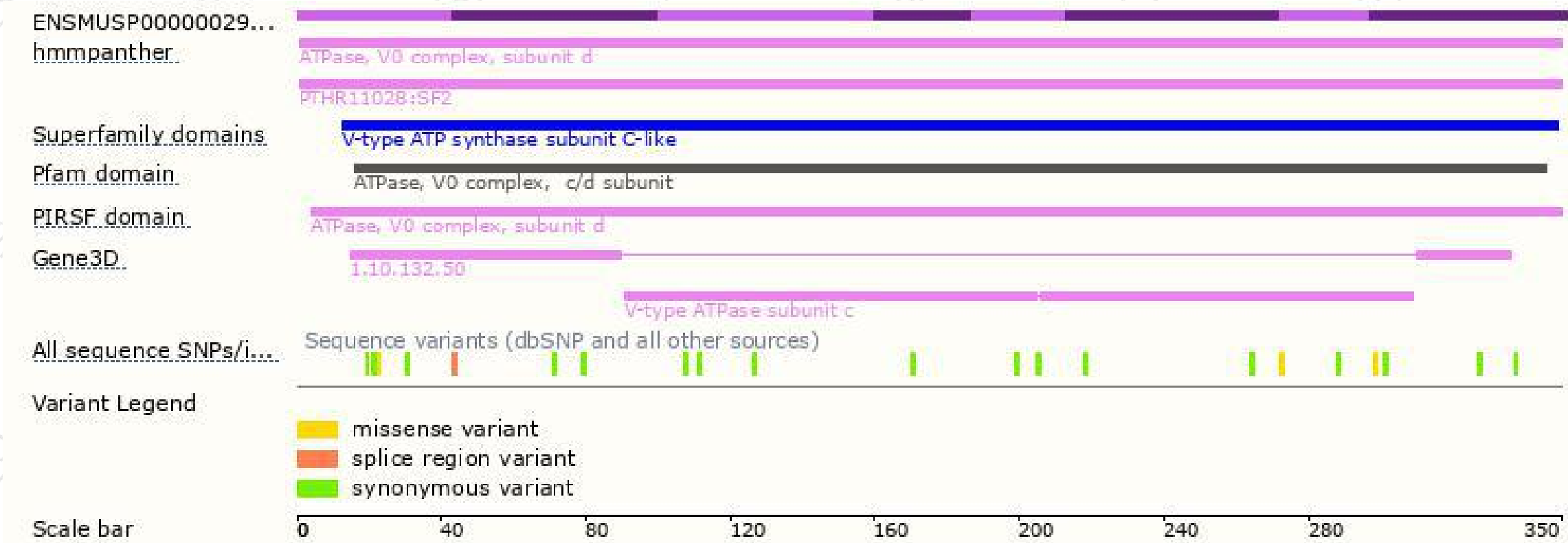
The strategy is based on the design of *Atp6v0d2-201* transcript,The transcription is shown below



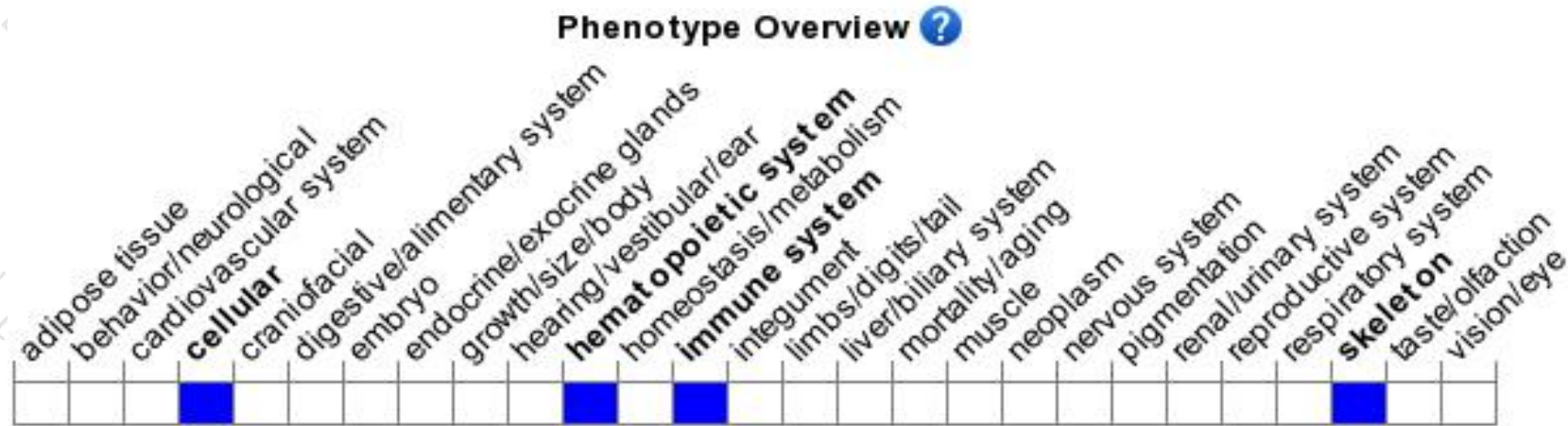
Genomic location distribution



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 mutation display osteopetrosis and impaired osteoclast maturation.

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

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