Mcfd2 Cas9-KO Strategy

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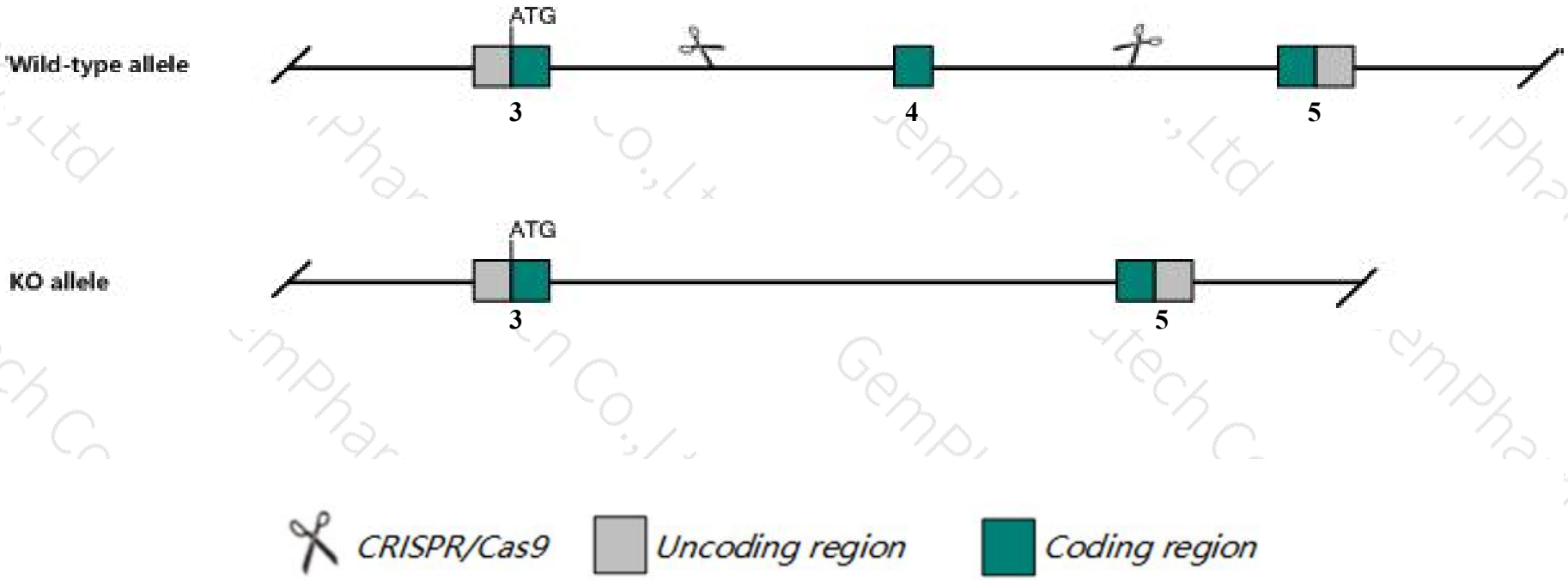
Project Overview

Project Name	***Mcfd2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mcfd2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mcfd2* gene has 7 transcripts. According to the structure of *Mcfd2* gene, exon4 of *Mcfd2-204* (ENSMUST00000144236.8) transcript is recommended as the knockout region.The region contains 160bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mcfd2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a null allele exhibit decreased serum factor V and VIII and aspartate transaminase serum levels with accumulation of the proteins in the ER of hepatocytes.

- Transcript *Mcfd2*-203 may not be affected.

- The *Mcfd2* gene is located on the Chr17. 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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Mcfd2 multiple coagulation factor deficiency 2 [Mus musculus (house mouse)]

Gene ID: 193813, updated on 23-Feb-2019

Summary

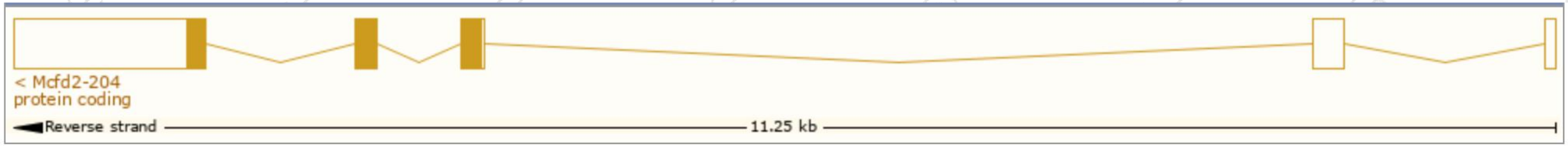
Official Symbol	Mcfd2 provided by MGI
Official Full Name	multiple coagulation factor deficiency 2 provided by MGI
Primary source	MGI:MGI:2183439
See related	Ensembl:ENSMUSG00000024150
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810021C21Rik, F5f8d, Lman1ip, Sdnsf
Expression	Ubiquitous expression in liver E18 (RPKM 52.3), liver adult (RPKM 47.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

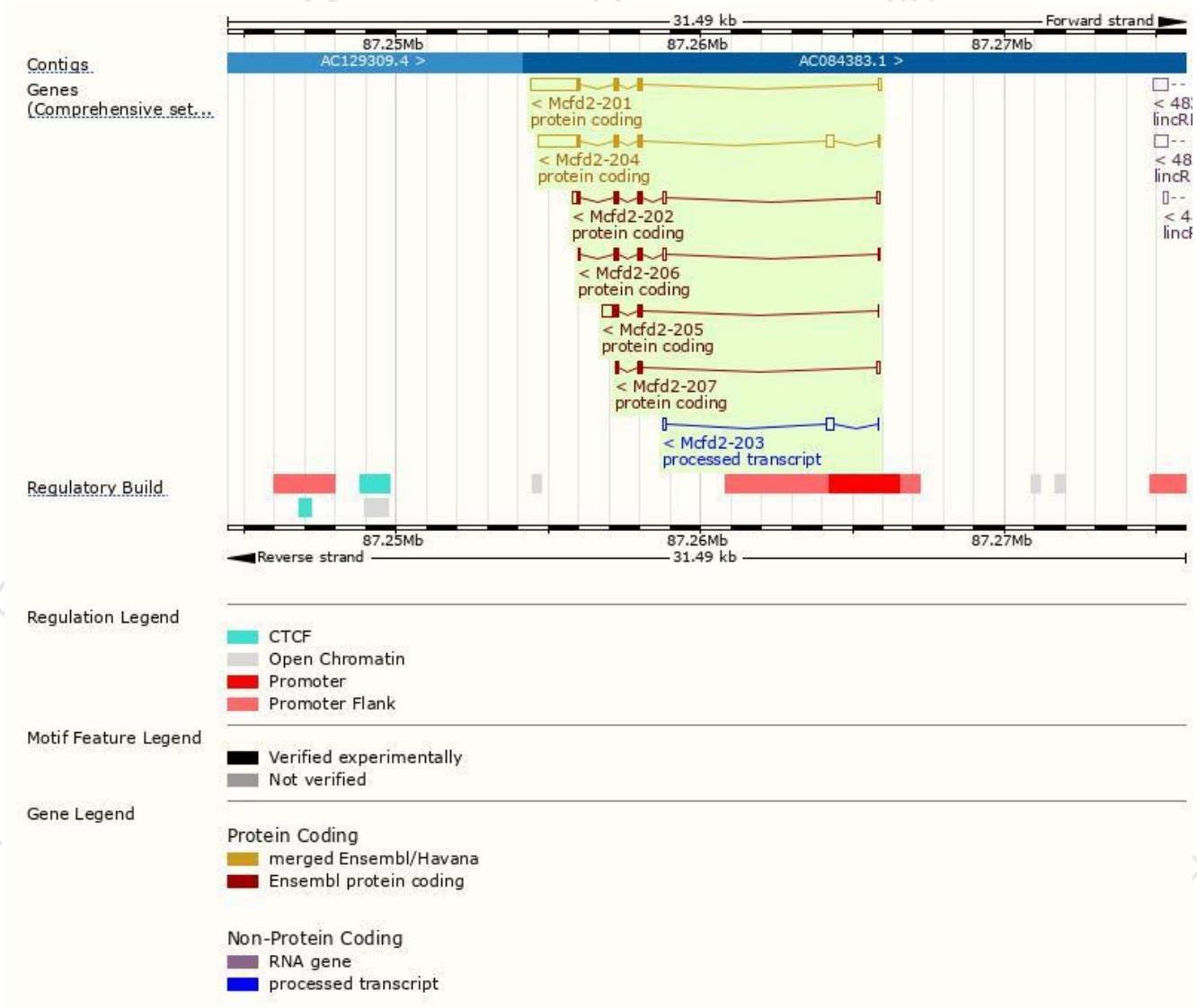
The gene has 7 transcripts,all transcripts are shown below:

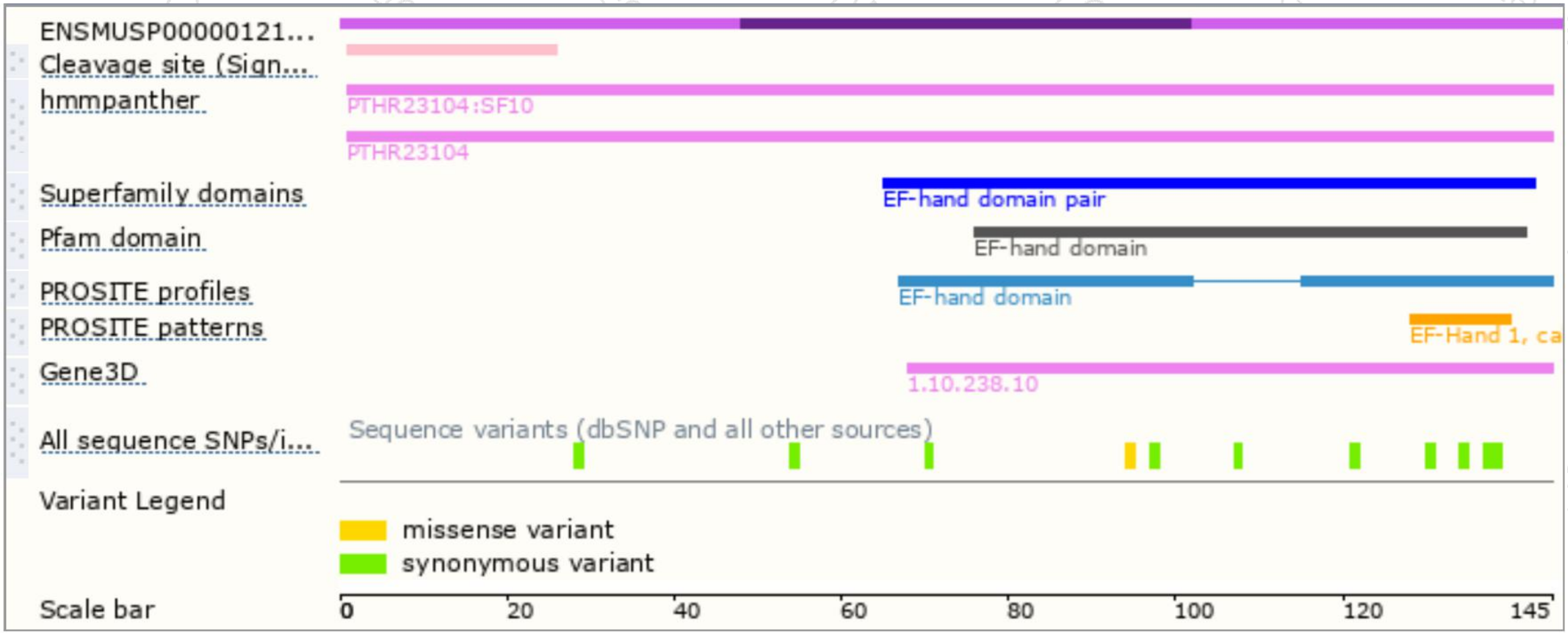
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mcfd2-201	ENSMUST00000024963.10	2038	145aa	Protein coding	CCDS29015	D0EW11 Q8K5B2	TSL:1 GENCODE basic APPRIS P1
Mcfd2-204	ENSMUST00000144236.8	2017	145aa	Protein coding	CCDS29015	D0EW11 Q8K5B2	TSL:1 GENCODE basic APPRIS P1
Mcfd2-202	ENSMUST00000129616.7	813	145aa	Protein coding	CCDS29015	D0EW11 Q8K5B2	TSL:3 GENCODE basic APPRIS P1
Mcfd2-205	ENSMUST00000145895.7	751	120aa	Protein coding	-	D3Z6A4	TSL:2 GENCODE basic
Mcfd2-206	ENSMUST00000151155.7	603	131aa	Protein coding	-	D3Z1G3	CDS 3' incomplete TSL:5
Mcfd2-207	ENSMUST00000155904.1	327	74aa	Protein coding	-	D3YVL4	CDS 3' incomplete TSL:2
Mcfd2-203	ENSMUST00000139258.1	353	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Mcfd2-204* transcript,The transcription is shown below

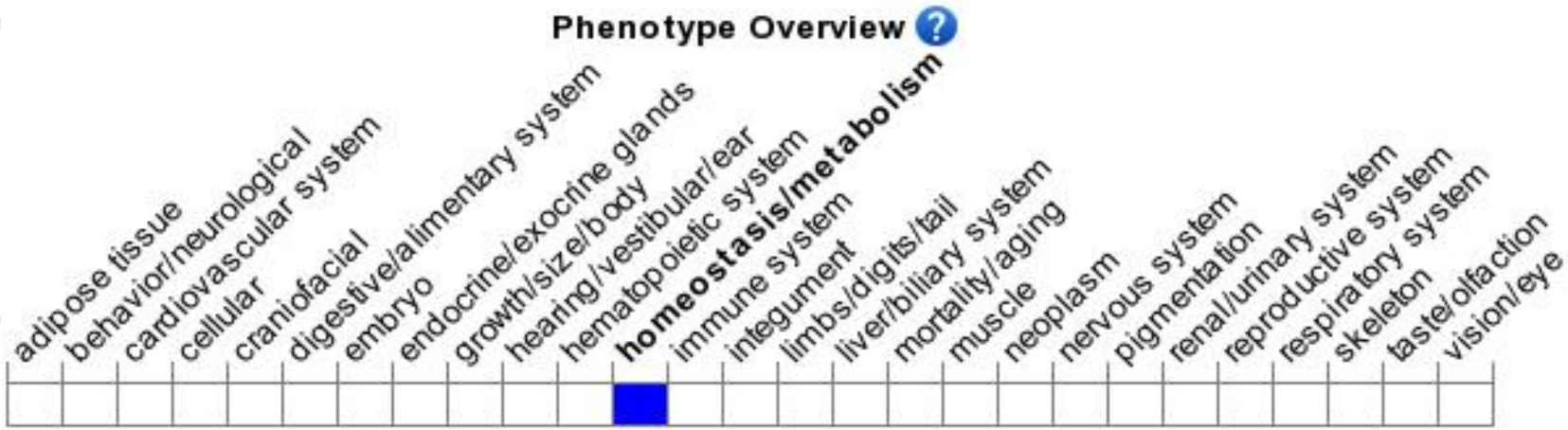


Genomic location distribution




ENSMUSP00000121...
Cleavage site (Sign...
hmmpanther
PTHR23104:SF10
PTHR23104
Superfamily domains
EF-hand domain pair
Pfam domain
EF-hand domain
PROSITE profiles
EF-hand domain
PROSITE patterns
EF-Hand 1, ca
Gene3D
1.10.238.10
All sequence SNPs/i...
Sequence variants (dbSNP and all other sources)
Variant Legend
missense variant
synonymous variant
Scale bar
0
20
40
60
80
100
120
145

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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