

Lrp8 Cas9-KO Strategy

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Project Overview

Project Name

Lrp8

Project type

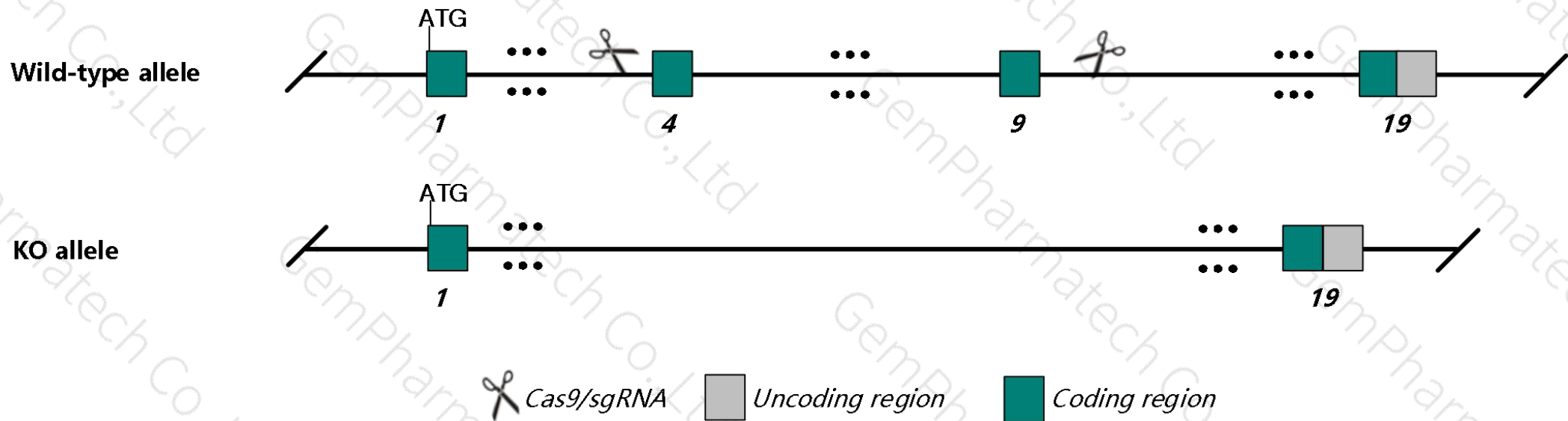
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lrp8* gene. The schematic diagram is as follows:



Technical routes

- The *Lrp8* gene has 23 transcripts. According to the structure of *Lrp8* gene, exon4-exon9 of *Lrp8-203* transcript is recommended as the knockout region. The region contains 799bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lrp8* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, Homozygotes for a targeted null mutation exhibit impaired granule cell migration, radial glial scaffold formation, contextual fear conditioning, and long-term potentiation. Mutant males have abnormal sperm and are sterile.
- The *Lrp8* 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 gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Lrp8 low density lipoprotein receptor-related protein 8, apolipoprotein e receptor [Mus musculus (house mouse)]

Gene ID: 16975, updated on 16-Mar-2019

Summary



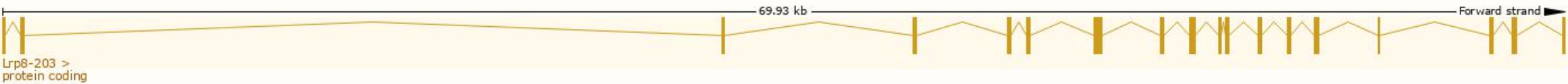
Official Symbol	Lrp8 provided by MGI
Official Full Name	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor provided by MGI
Primary source	MGI:MGI:1340044
See related	Ensembl:ENSMUSG00000028613
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4932703M08Rik, AA921429, AI848122, ApoER2, Lr8b
Expression	Biased expression in CNS E18 (RPKM 24.6), whole brain E14.5 (RPKM 23.2) and 14 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

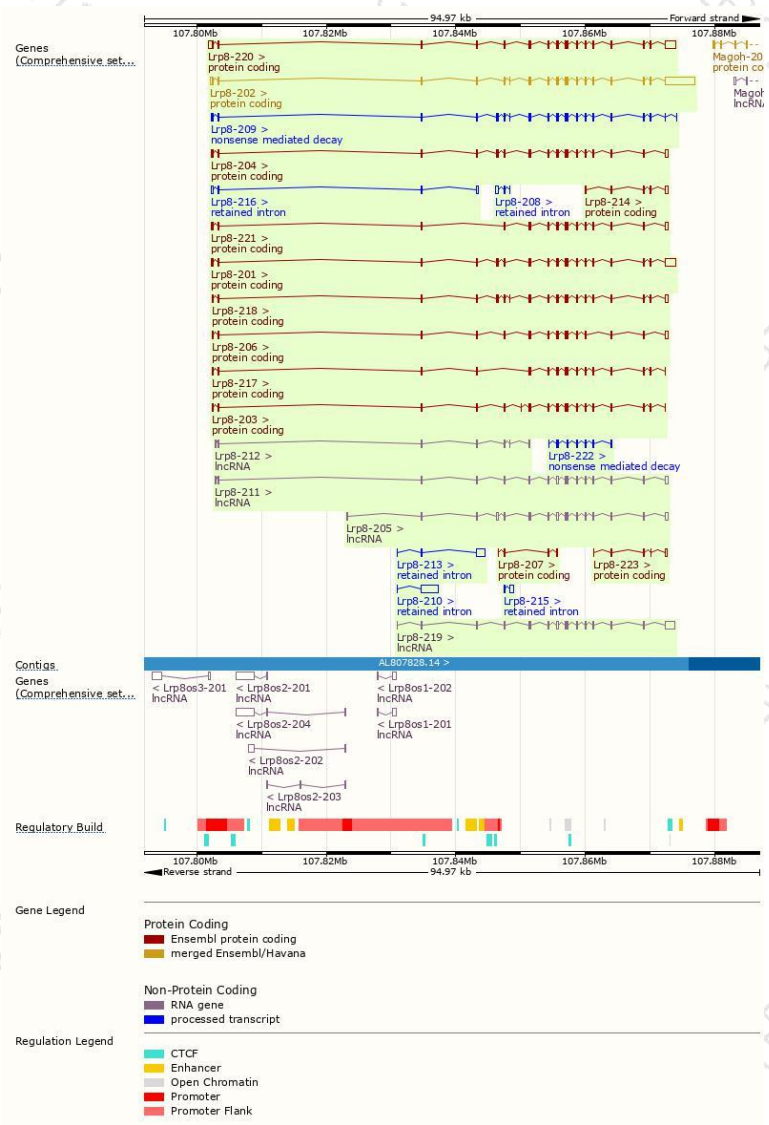
The gene has 23 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lrp8-202	ENSMUST00000106731.3	7391	870aa	Protein coding	CCDS51255	F6YZZ8	TSL:1 GENCODE basic
Lrp8-220	ENSMUST00000238584.1	4618	828aa	Protein coding	-	-	GENCODE basic
Lrp8-201	ENSMUST00000030356.9	4555	955aa	Protein coding	-	B1AXJ4	TSL:5 GENCODE basic
Lrp8-218	ENSMUST00000238569.1	3497	996aa	Protein coding	-	-	GENCODE basic APPRIS P1
Lrp8-204	ENSMUST00000106733.9	3333	896aa	Protein coding	-	B1AXJ5	TSL:5 GENCODE basic
Lrp8-221	ENSMUST00000238651.1	2799	726aa	Protein coding	-	-	GENCODE basic
Lrp8-206	ENSMUST00000126573.7	2590	694aa	Protein coding	-	B1AXJ6	TSL:5 GENCODE basic
Lrp8-203	ENSMUST00000106732.9	2531	832aa	Protein coding	-	B1AXJ3	CDS 5' incomplete TSL:1
Lrp8-217	ENSMUST00000238421.1	2364	787aa	Protein coding	-	-	GENCODE basic
Lrp8-214	ENSMUST00000238255.1	1105	189aa	Protein coding	-	-	CDS 5' incomplete
Lrp8-223	ENSMUST00000238693.1	764	124aa	Protein coding	-	-	CDS 5' incomplete
Lrp8-207	ENSMUST00000135022.2	471	157aa	Protein coding	-	-	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Lrp8-209	ENSMUST00000143601.7	3291	996aa	Nonsense mediated decay	-	Q924X6	TSL:1
Lrp8-222	ENSMUST00000238658.1	1074	135aa	Nonsense mediated decay	-	-	CDS 5' incomplete
Lrp8-210	ENSMUST00000145832.1	2629	No protein	Retained intron	-	-	TSL:1
Lrp8-213	ENSMUST00000238207.1	1434	No protein	Retained intron	-	-	
Lrp8-215	ENSMUST00000238304.1	822	No protein	Retained intron	-	-	
Lrp8-216	ENSMUST00000238405.1	737	No protein	Retained intron	-	-	
Lrp8-208	ENSMUST00000135591.1	557	No protein	Retained intron	-	-	TSL:5
Lrp8-219	ENSMUST00000238570.1	3532	No protein	lncRNA	-	-	
Lrp8-205	ENSMUST00000123140.7	3129	No protein	lncRNA	-	-	TSL:1
Lrp8-211	ENSMUST00000146552.8	2713	No protein	lncRNA	-	-	TSL:5
Lrp8-212	ENSMUST00000147319.7	797	No protein	lncRNA	-	-	TSL:5

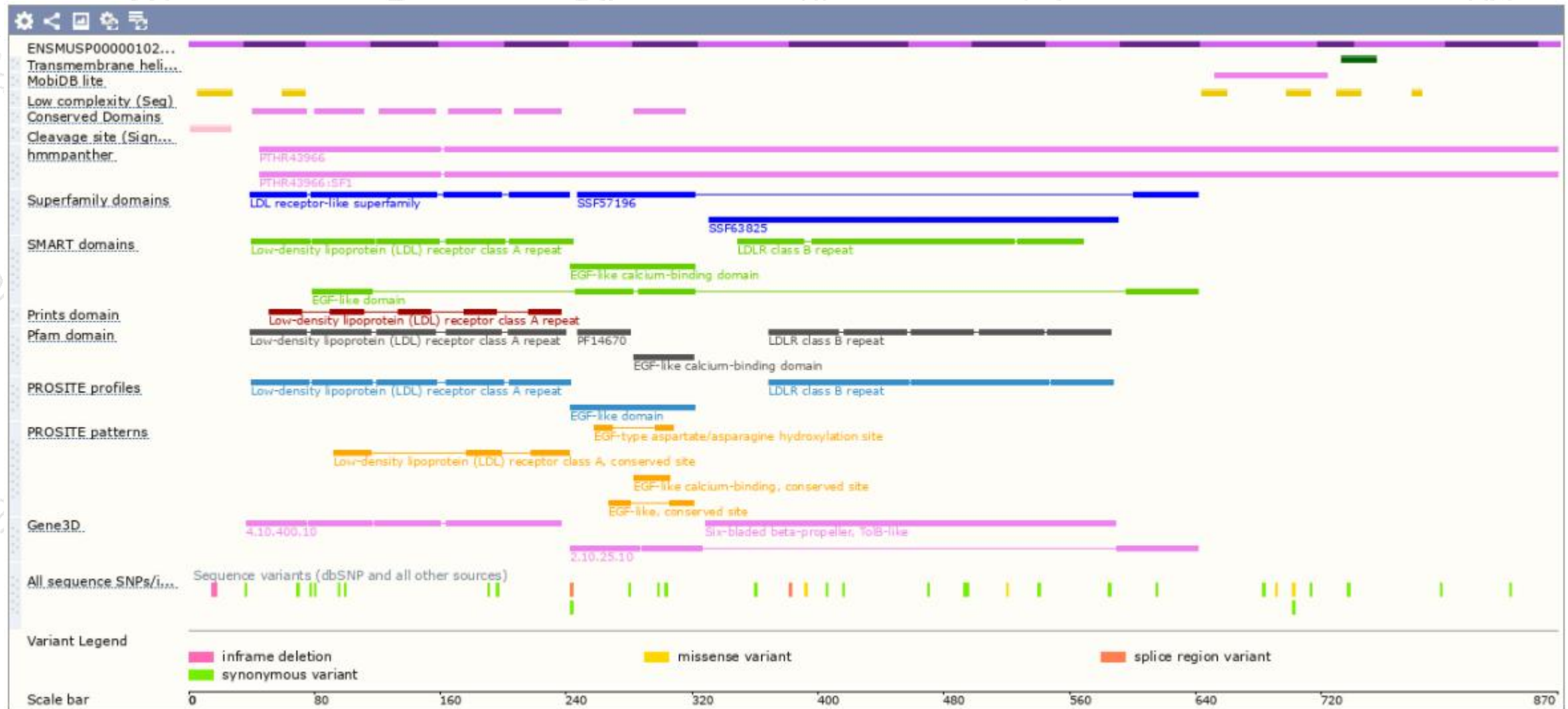
The strategy is based on the design of *Lrp8-203* transcript,The transcription is shown below



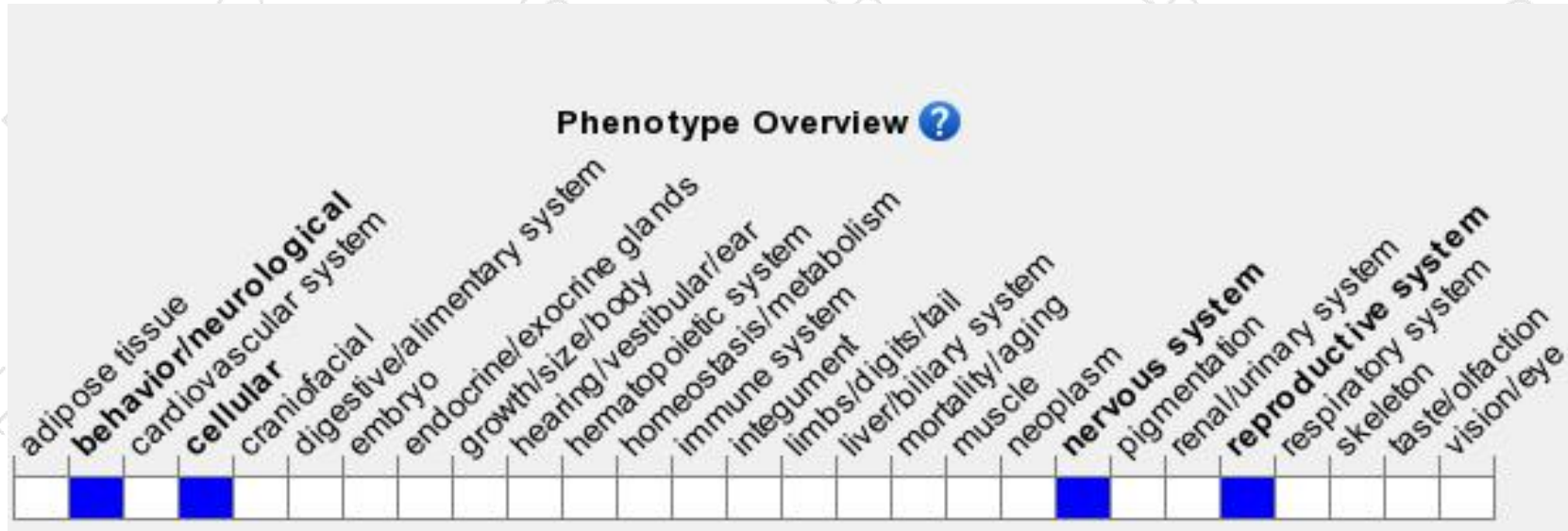
Genomic location distribution



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, Homozygotes for a targeted null mutation exhibit impaired granule cell migration, radial glial scaffold formation, contextual fear conditioning, and long-term potentiation. Mutant males have abnormal sperm and are sterile.

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

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