

Abcb6 Cas9-CKO Strategy

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Project Overview

Project Name

Abcb6

Project type

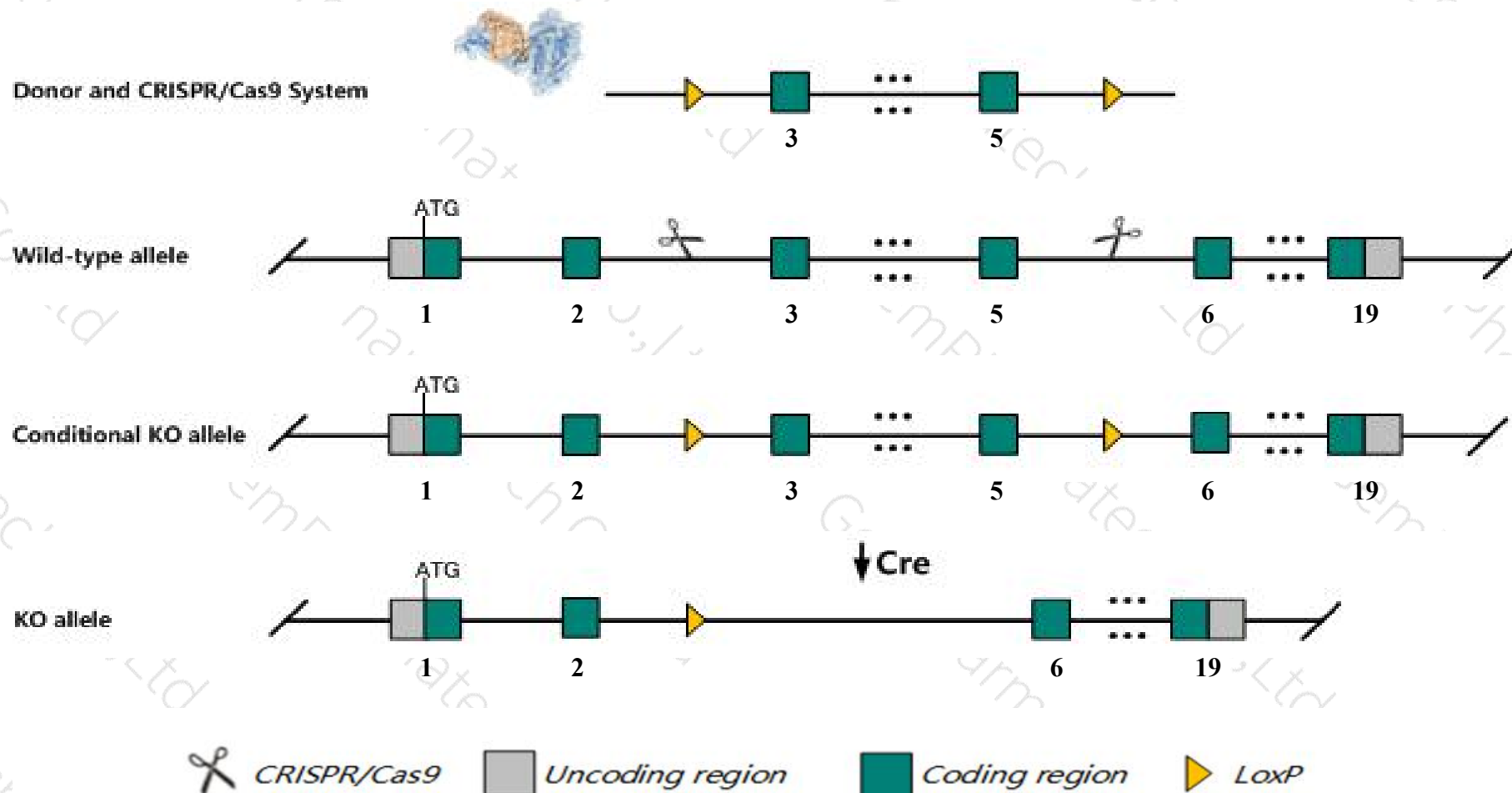
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abcb6* gene. The schematic diagram is as follows:



- The *Abcb6* gene has 6 transcripts. According to the structure of *Abcb6* gene, exon3-exon5 of *Abcb6*-201 (ENSMUST00000027396.14) transcript is recommended as the knockout region. The region contains 467bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Abcb6* 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 null mutation display partial lethality, impaired stress erythropoiesis, and absence of ATP-dependent transport of Coproporphyrin III in mitochondria.
- The N-terminal of *Abcb6* gene will remain several amino acids, it may remain the partial function of *Abcb6* gene.
- The effect on transcript *Abcb6*-206 is unknown.
- Transcript *Abcb6*-205 may be destroyed directly.
- The *Abcb6* gene is located on the Chr1. 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)

Abcb6 ATP-binding cassette, sub-family B (MDR/TAP), member 6 [*Mus musculus* (house mouse)]

Gene ID: 74104, updated on 27-Feb-2020

Summary

- Official Symbol** Abcb6 provided by MGI
- Official Full Name** ATP-binding cassette, sub-family B (MDR/TAP), member 6 provided by MGI
- Primary source** [MGI:MGI:1921354](#)
- See related** [Ensembl:ENSMUSG00000026196](#)
- 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** 1200005B17Rik
- Expression** Ubiquitous expression in liver adult (RPKM 38.1), colon adult (RPKM 25.7) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 1; 1 C4

See Abcb6 in [Genome Data Viewer](#)

Exon count: 19

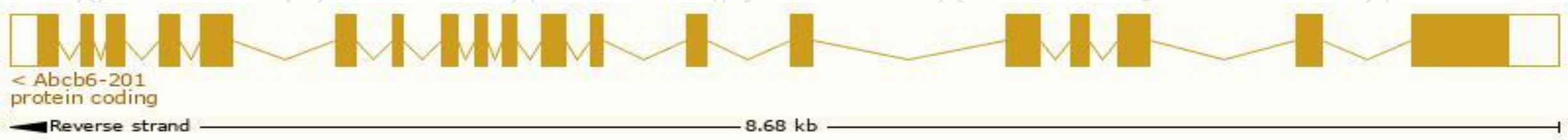
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (75171640..75180392, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (75168214..75176857, complement)

Transcript information (Ensembl)

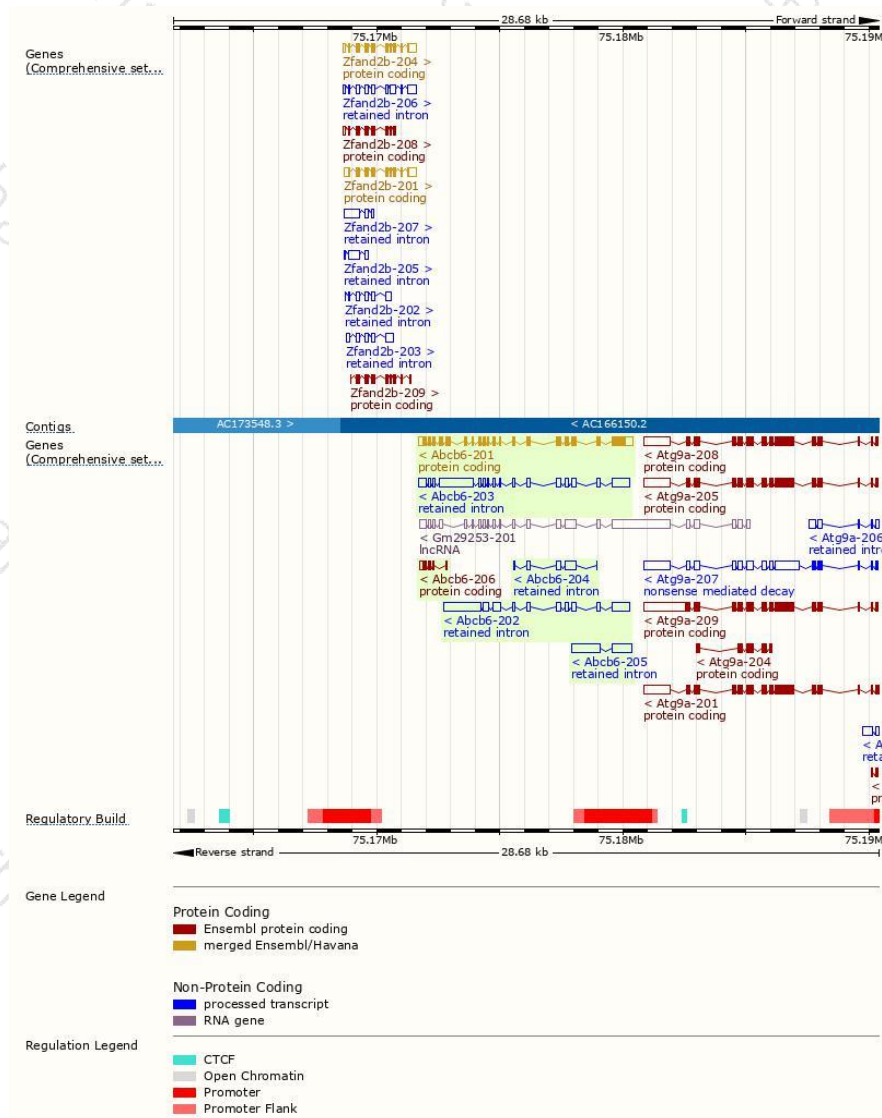
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abcb6-201	ENSMUST00000027396.14	2966	842aa	Protein coding	CCDS15065	Q9DC29	TSL:1 GENCODE basic APPRIS P1
Abcb6-206	ENSMUST00000161215.1	416	97aa	Protein coding	-	F6SGP4	CDS 5' incomplete TSL:5
Abcb6-203	ENSMUST00000160081.7	3772	No protein	Retained intron	-	-	TSL:2
Abcb6-202	ENSMUST00000159219.7	3625	No protein	Retained intron	-	-	TSL:2
Abcb6-205	ENSMUST00000161103.1	1966	No protein	Retained intron	-	-	TSL:1
Abcb6-204	ENSMUST00000160757.1	829	No protein	Retained intron	-	-	TSL:5

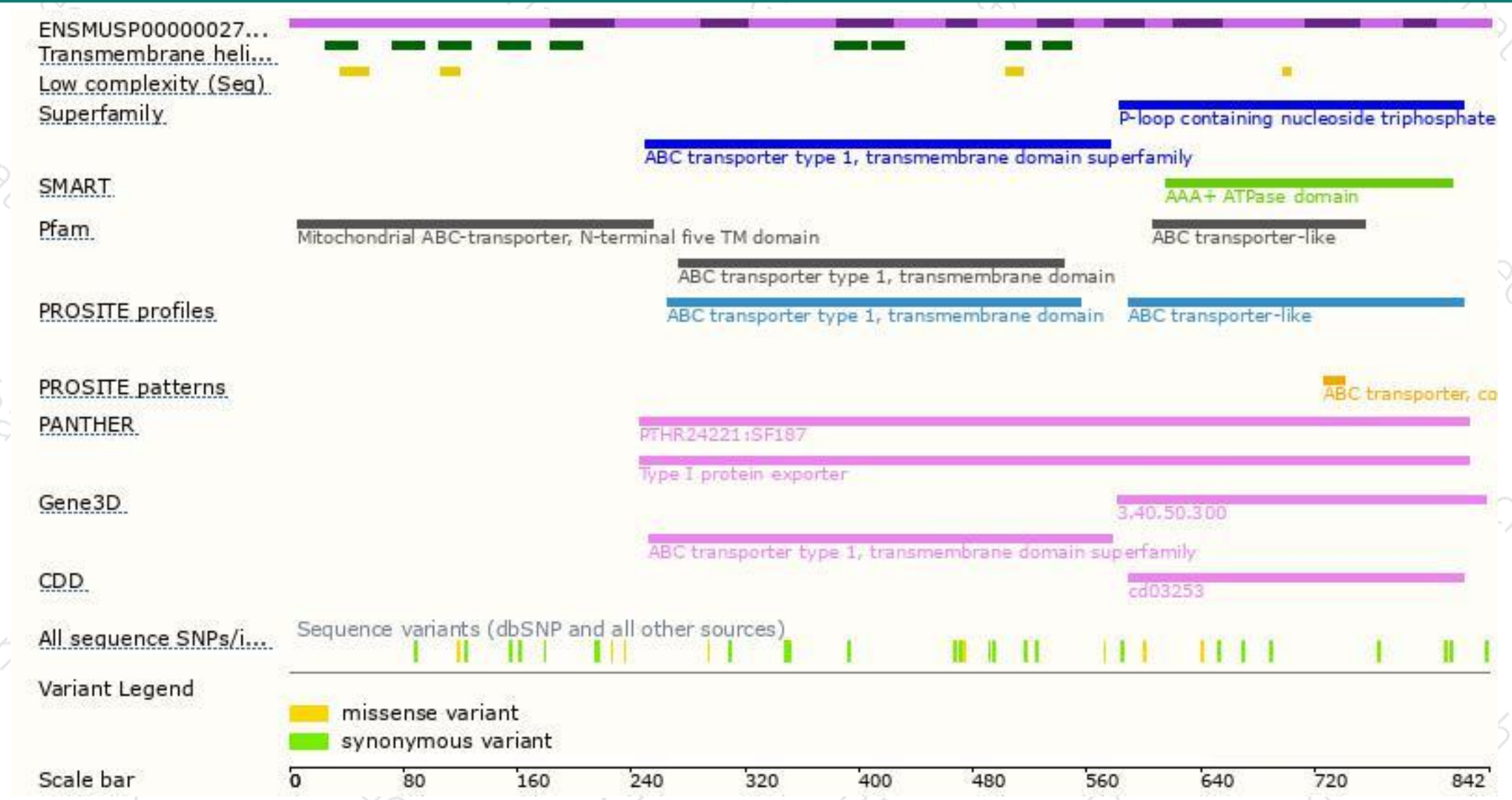
The strategy is based on the design of *Abcb6-201* transcript,The transcription is shown below



Genomic location distribution

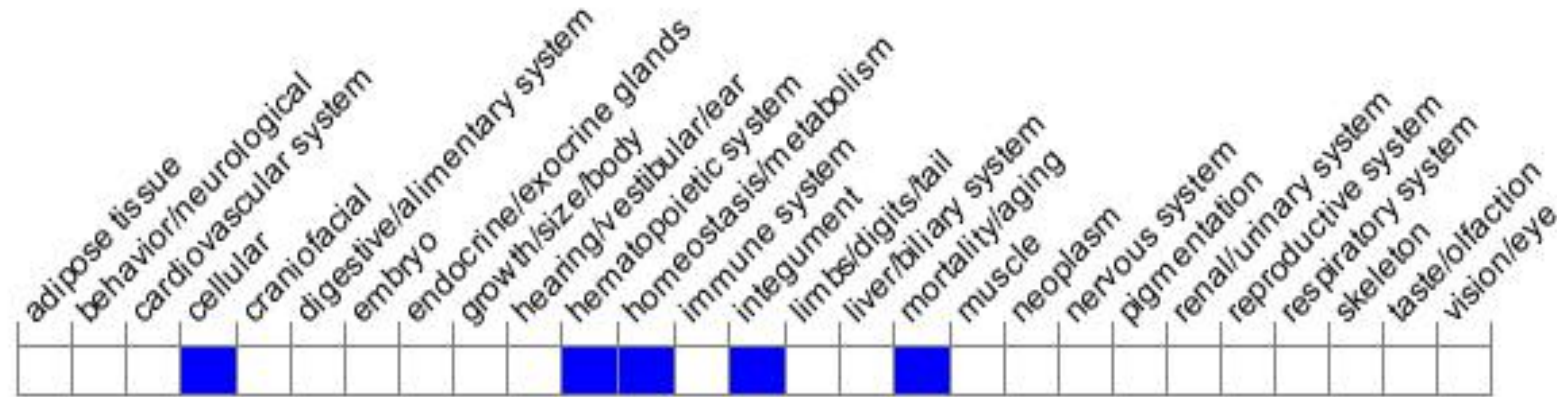


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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 partial lethality, impaired stress erythropoiesis, and absence of ATP-dependent transport of Coproporphyrin III in mitochondria.

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

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