

Magoh Cas9-KO Strategy

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Project Overview

Project Name

Magoh

Project type

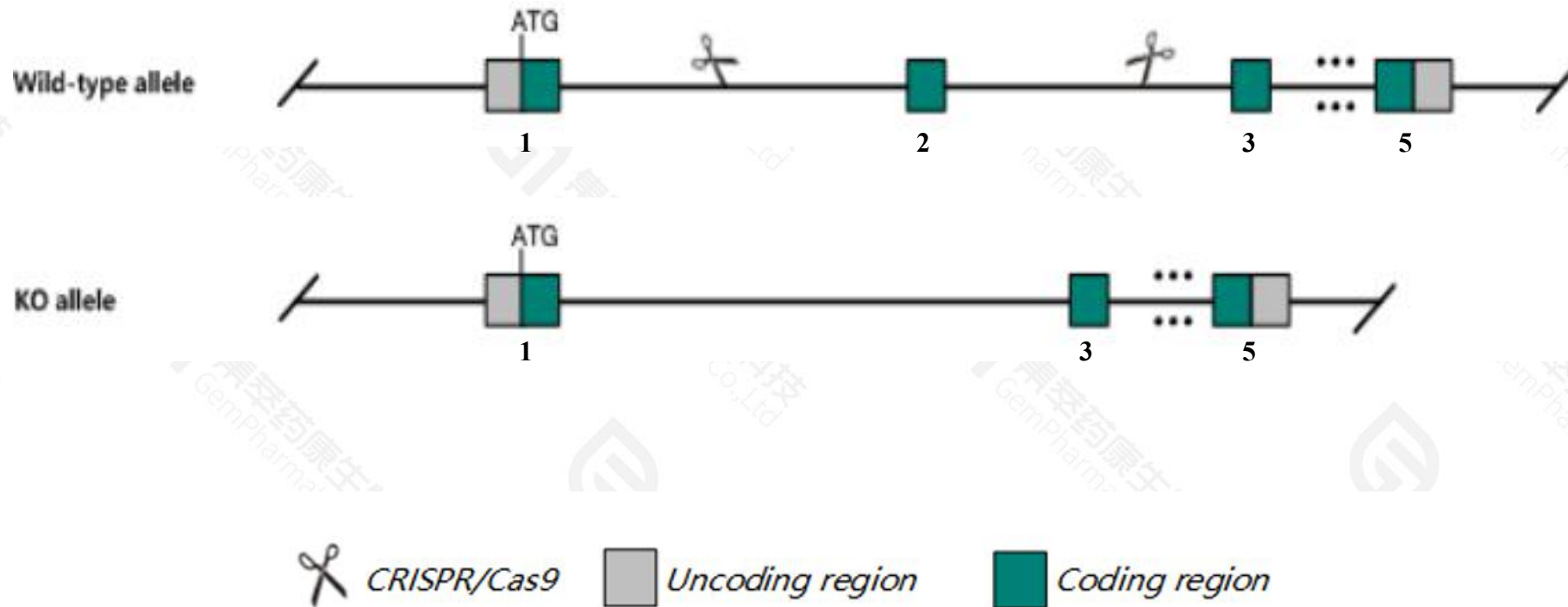
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Magoh* gene has 2 transcripts. According to the structure of *Magoh* gene, exon2 of *Magoh-201*(ENSMUST00000030348.6) transcript is recommended as the knockout region. The region contains 59bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Magoh* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, homozygous null mutation in this gene is embryonic lethal and heterozygous mice are postnatal lethal with incomplete penetrance with reduced body size and microcephaly.
- The *Magoh* 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)

Magoh mago homolog, exon junction complex core component [Mus musculus (house mouse)]

Gene ID: 17149, updated on 13-Mar-2020

Summary



Official Symbol Magoh provided by [MGI](#)

Official Full Name mago homolog, exon junction complex core component provided by [MGI](#)

Primary source [MGI:MGI:1330312](#)

See related [Ensembl:ENSMUSG00000028609](#)

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 Mago-m, Mos2

Expression Broad expression in CNS E11.5 (RPKM 75.7), placenta adult (RPKM 62.8) and 27 other tissues [See more](#)

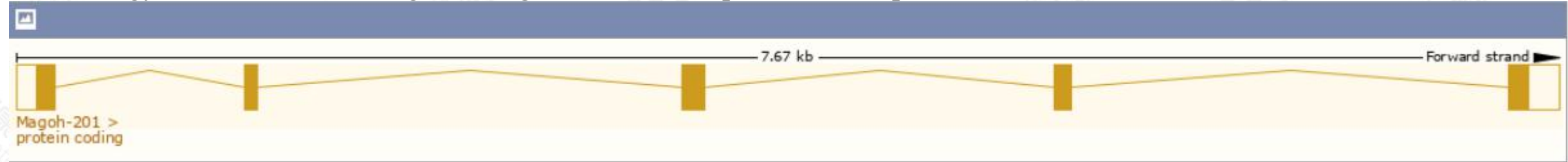
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

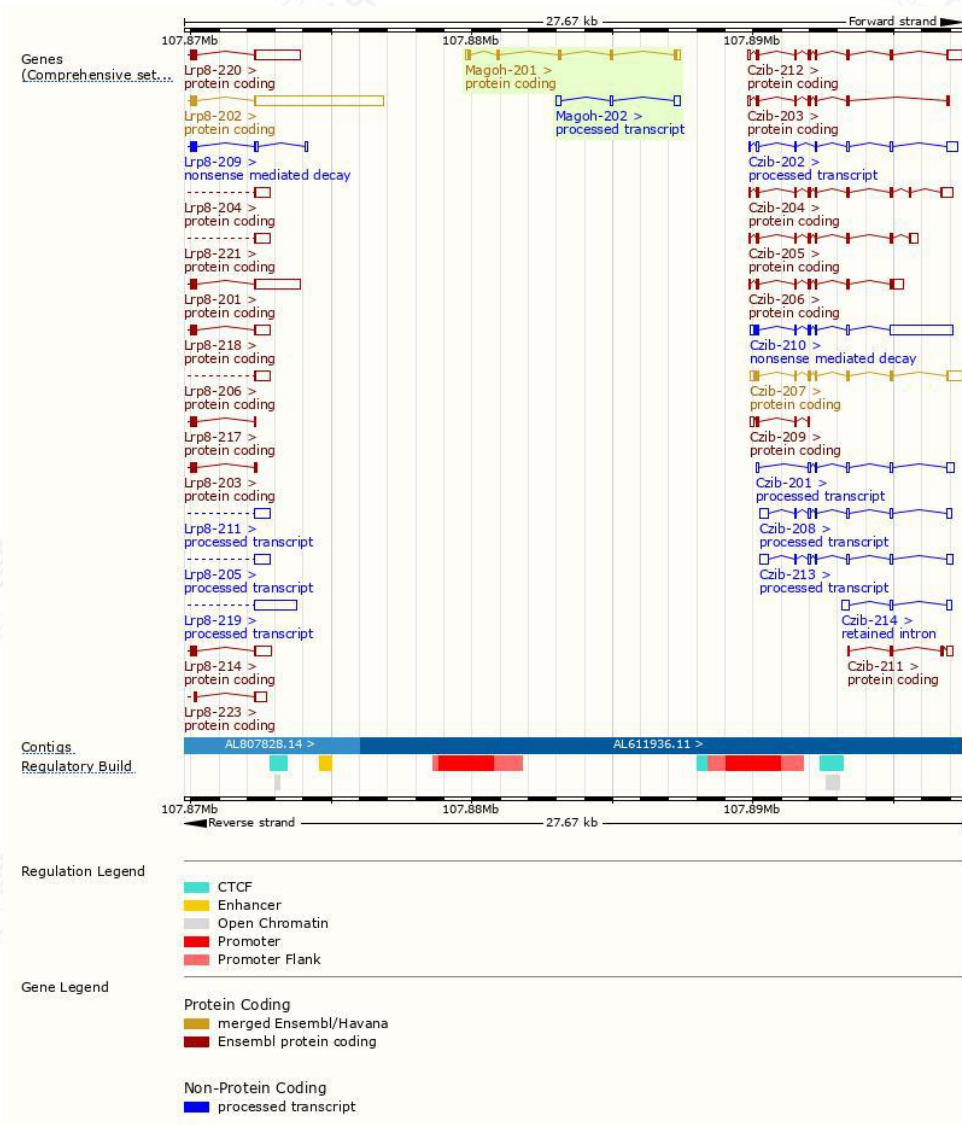
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Magoh-201	ENSMUST00000030348.5	692	146aa	Protein coding	CCDS18441	P61327	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Magoh-202	ENSMUST000000141376.1	483	No protein	Processed transcript	-	-	TSL:2

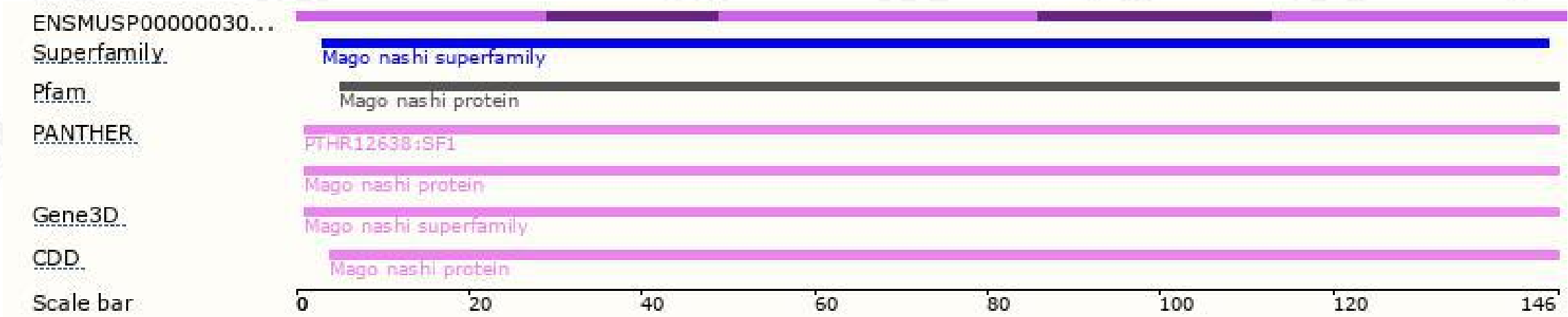
The strategy is based on the design of *Magoh-201* transcript,the transcription is shown below:



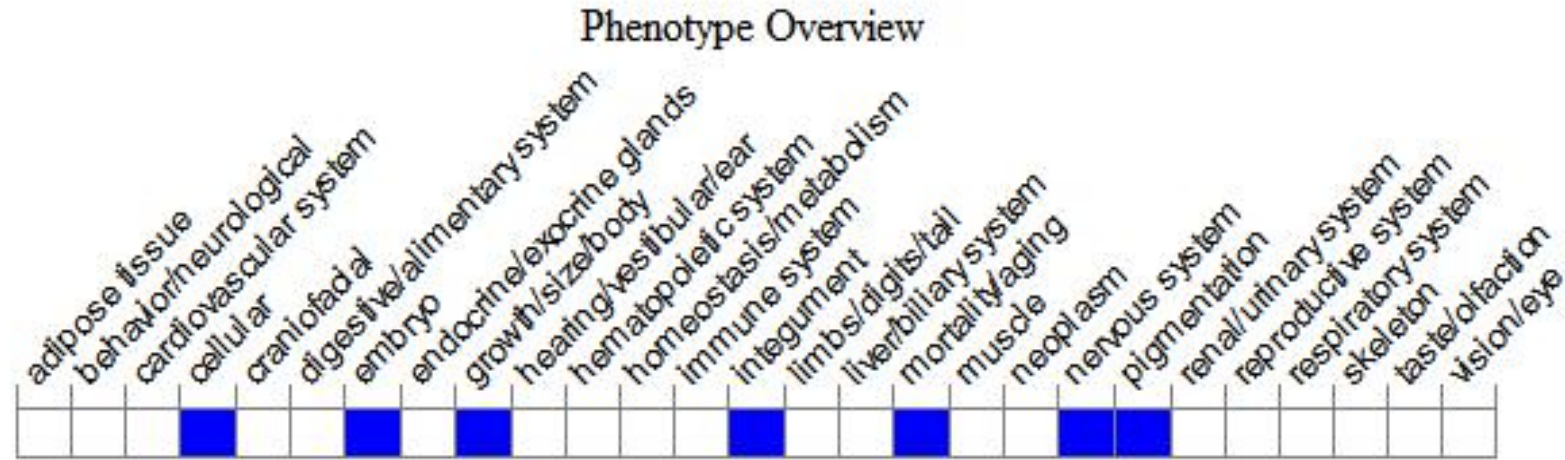
Genomic location distribution



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, homozygous null mutation in this gene is embryonic lethal and heterozygous mice are postnatal lethal with incomplete penetrance with reduced body size and microcephaly.

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