

# Megf10 Cas9-CKO Strategy

Designer: Xueting Zhang

# **Project Overview**



**Project Name** 

Megf10

**Project type** 

Cas9-CKO

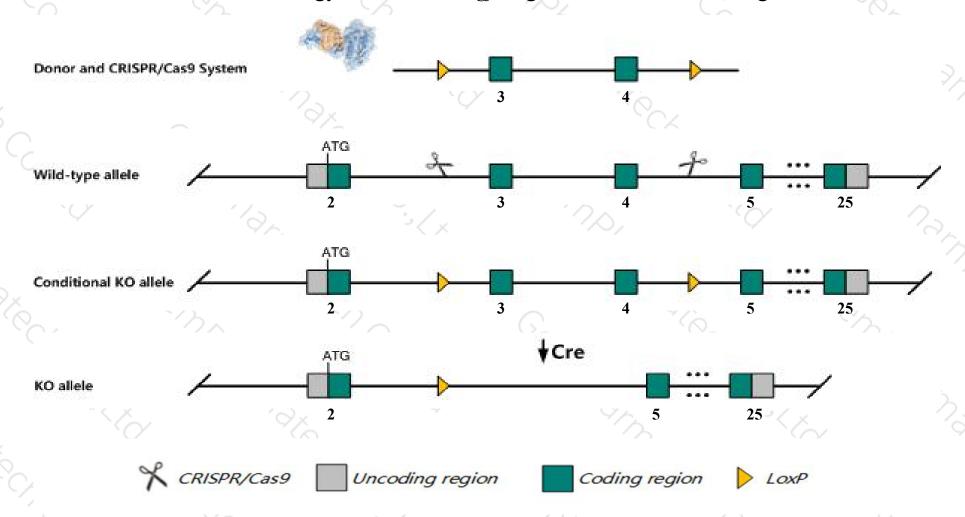
Strain background

C57BL/6JGpt

## Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Megf10 gene. The schematic diagram is as follows:



### Technical routes



- The *Megf10* gene has 2 transcripts. According to the structure of *Megf10* gene, exon3-exon4 of *Megf10-201* (ENSMUST00000075770.12) transcript is recommended as the knockout region. The region contains 203bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Megf10* 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.

### **Notice**



- ➤ According to the existing MGI data, Mice homozygous for a targeted allele exhibit abnormal spacing of starburst amacrine cells and horizontal cells. Homozygotes for another targeted allele exhibit impaired phagocytosis of apoptotic cells by astrocytes. Mice heterozygous for this same allele exhibit mild disorganization of starburts amacrine cells.
- The *Megf10* gene is located on the Chr18. 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)



#### Megf10 multiple EGF-like-domains 10 [Mus musculus (house mouse)]

Gene ID: 70417, updated on 31-Jan-2019

#### Summary

☆ ?

Official Symbol Megf10 provided by MGI

Official Full Name multiple EGF-like-domains 10 provided by MGI

Primary source MGI:MGI:2685177

See related Ensembl: ENSMUSG00000024593

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 3000002B06Rik, Gm331

Expression Biased expression in cerebellum adult (RPKM 5.1), CNS E11.5 (RPKM 3.5) and 7 other tissuesSee more

Orthologs <u>human</u> all

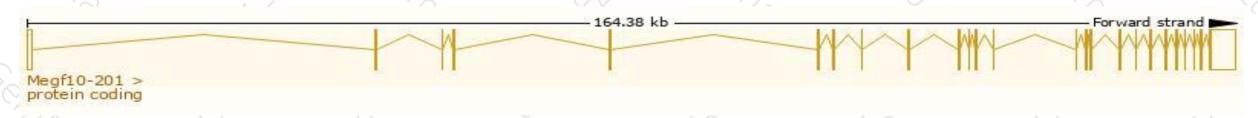
# Transcript information (Ensembl)



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

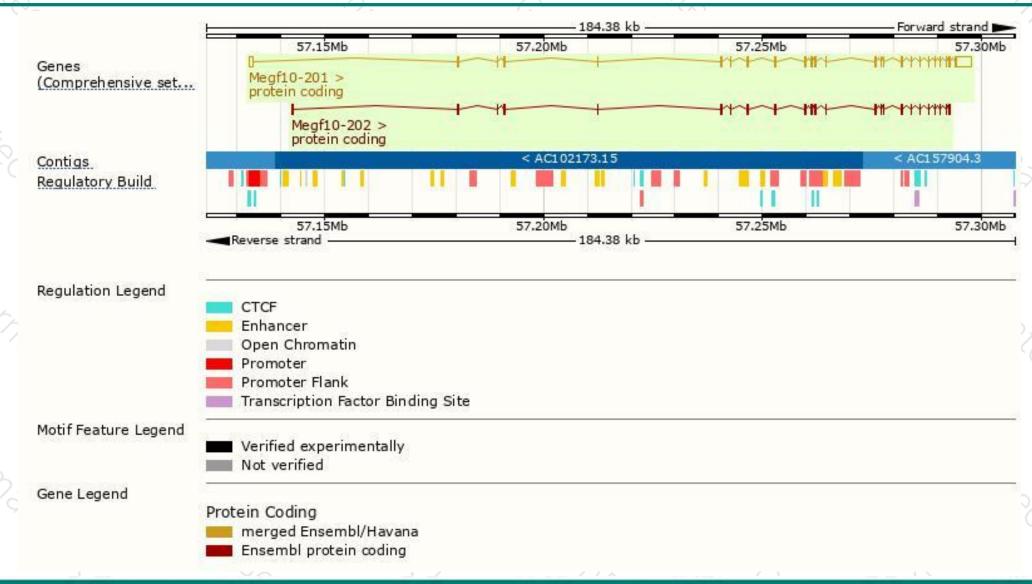
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Megf10-201	ENSMUST00000075770.12	7514	<u>1147aa</u>	Protein coding	CCDS29264	Q6DIB5	TSL:1 GENCODE basic APPRIS P1
Megf10-202	ENSMUST00000139892.1	3406	1061aa	Protein coding		A0A140T8S0	CDS 3' incomplete TSL:1

The strategy is based on the design of Megf10-201 transcript, The transcription is shown below



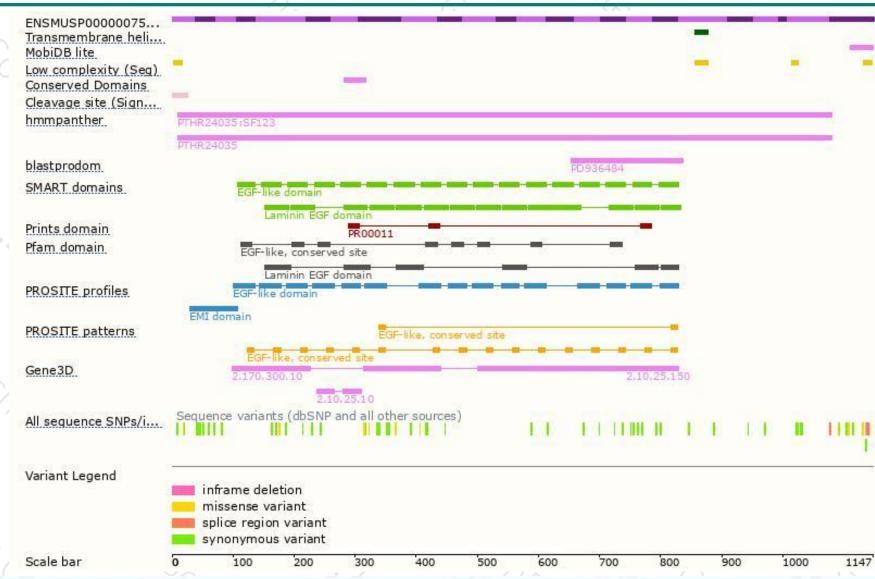
### Genomic location distribution





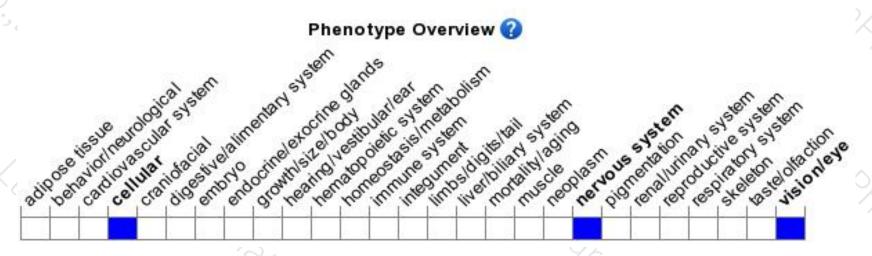
### Protein domain





# 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 targeted allele exhibit abnormal spacing of starburst amacrine cells and horizontal cells. Homozygotes for another targeted allele exhibit impaired phagocytosis of apoptotic cells by astrocytes. Mice heterozygous for this same allele exhibit mild disorganization of starburts amacrine cells.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





