

Mefv Cas9-CKO Strategy

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Project Overview

Project Name

Mefv

Project type

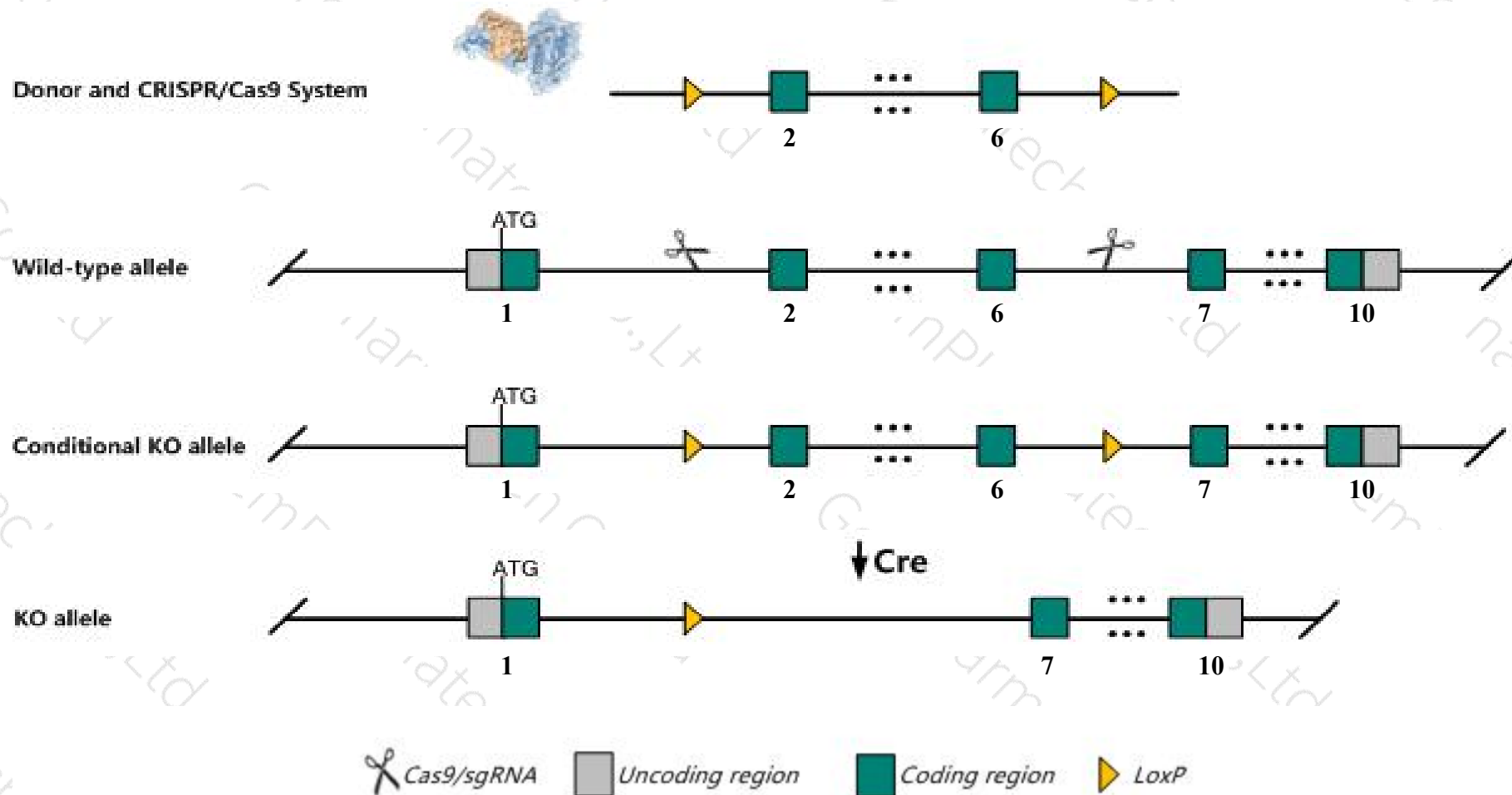
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Mefv* gene has 3 transcripts. According to the structure of *Mefv* gene, exon2-exon6 of *Mefv*-202 (ENSMUST00000100222.3) transcript is recommended as the knockout region. The region contains 1528bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mefv* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was 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, Homozygous null mice develop normally but show increased susceptibility to infection. Mice homozygous for another knock-out allele exhibit increased macrophage secretion of IL1b and Il18 following stimulation.
- The N-terminal of *Mefv* gene will remain 92aa, it may remain the partial function of *Mefv* gene.
- The *Mefv* gene is located on the Chr16. 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)

Mefv Mediterranean fever [Mus musculus (house mouse)]

Gene ID: 54483, updated on 19-Mar-2019

Summary



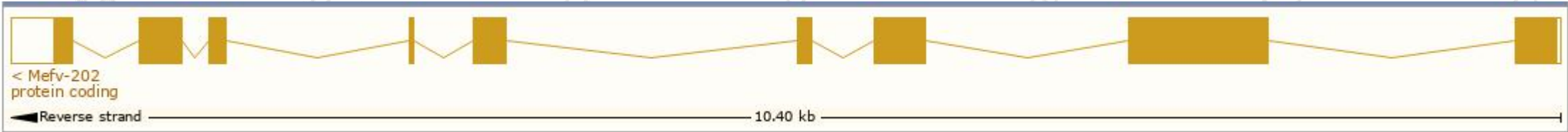
Official Symbol	Mefv provided by MGI
Official Full Name	Mediterranean fever provided by MGI
Primary source	MGI:MGI:1859396
See related	Ensembl:ENSMUSG00000022534
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	FMF, TRIM20, pyrin
Expression	Biased expression in spleen adult (RPKM 1.2), liver E18 (RPKM 0.4) and 11 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

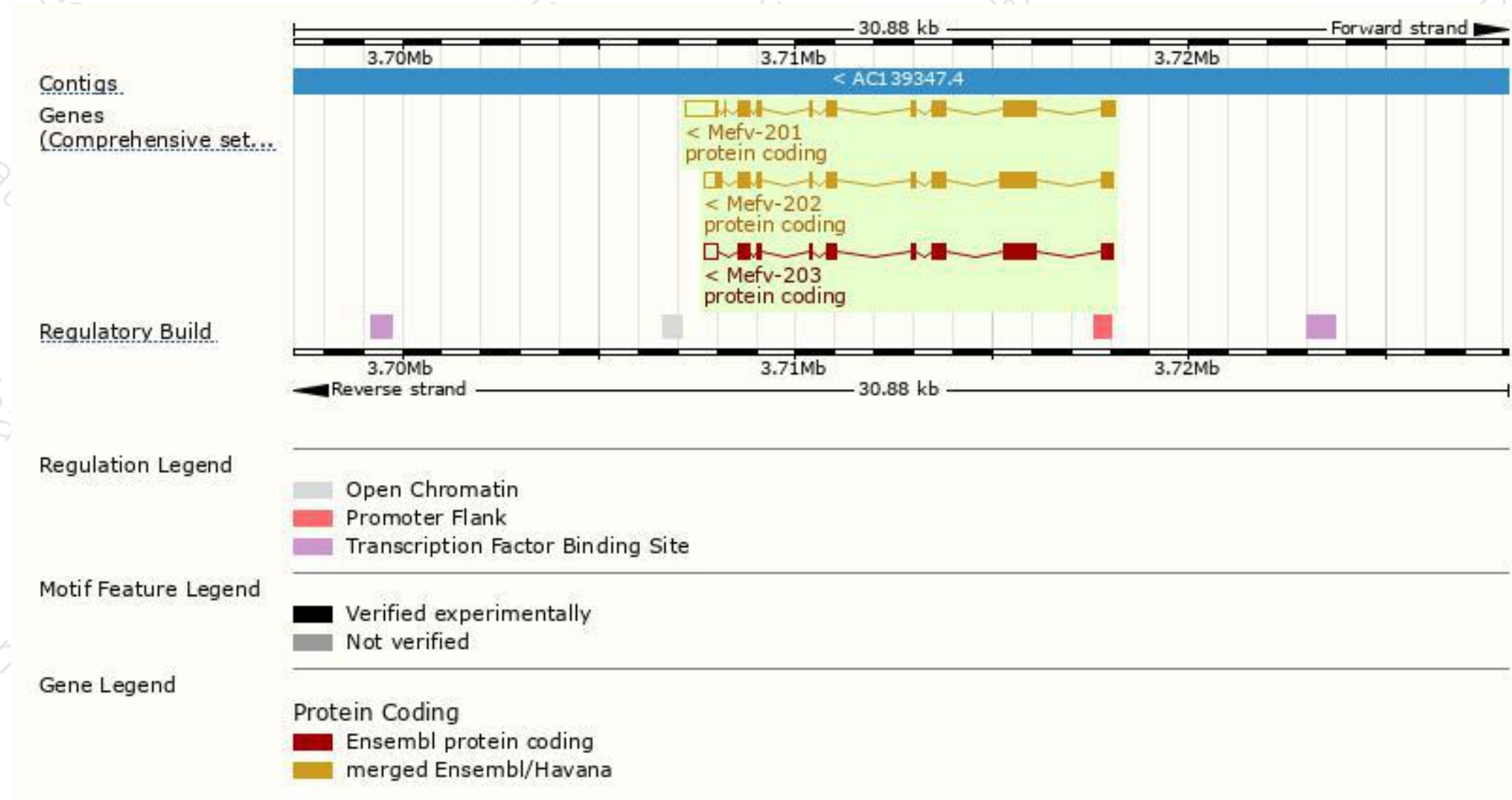
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mefv-201	ENSMUST00000023180.14	3096	767aa	Protein coding	CCDS27907	Q9JJ26	TSL:1 GENCODE basic APPRIS P3
Mefv-202	ENSMUST00000100222.3	2739	808aa	Protein coding	CCDS49745	Q32MT0	TSL:1 GENCODE basic APPRIS ALT2
Mefv-203	ENSMUST00000229725.1	2584	740aa	Protein coding	-	Q32MT1	GENCODE basic APPRIS ALT2

The strategy is based on the design of *Mefv-202* transcript,The transcription is shown below



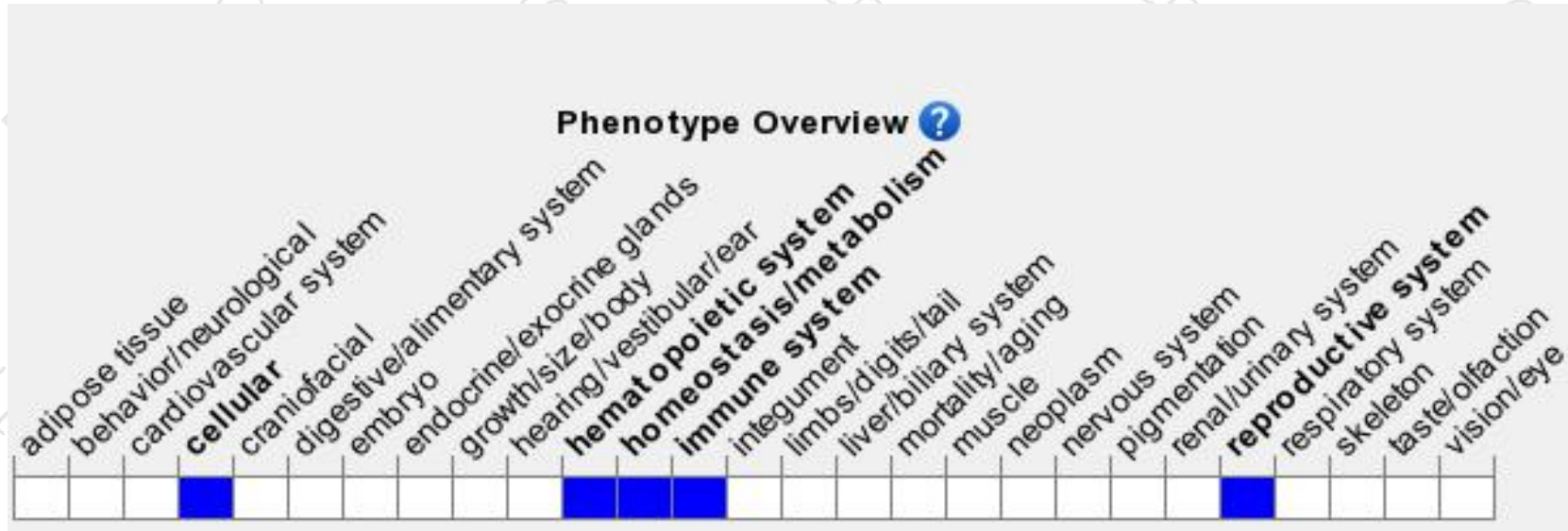
Genomic location distribution



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 mice develop normally but show increased susceptibility to infection.

Mice homozygous for another knock-out allele exhibit increased macrophage secretion of IL1b and Il18 following stimulation.

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

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