

Fmnl1 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Fmnl1

Project type

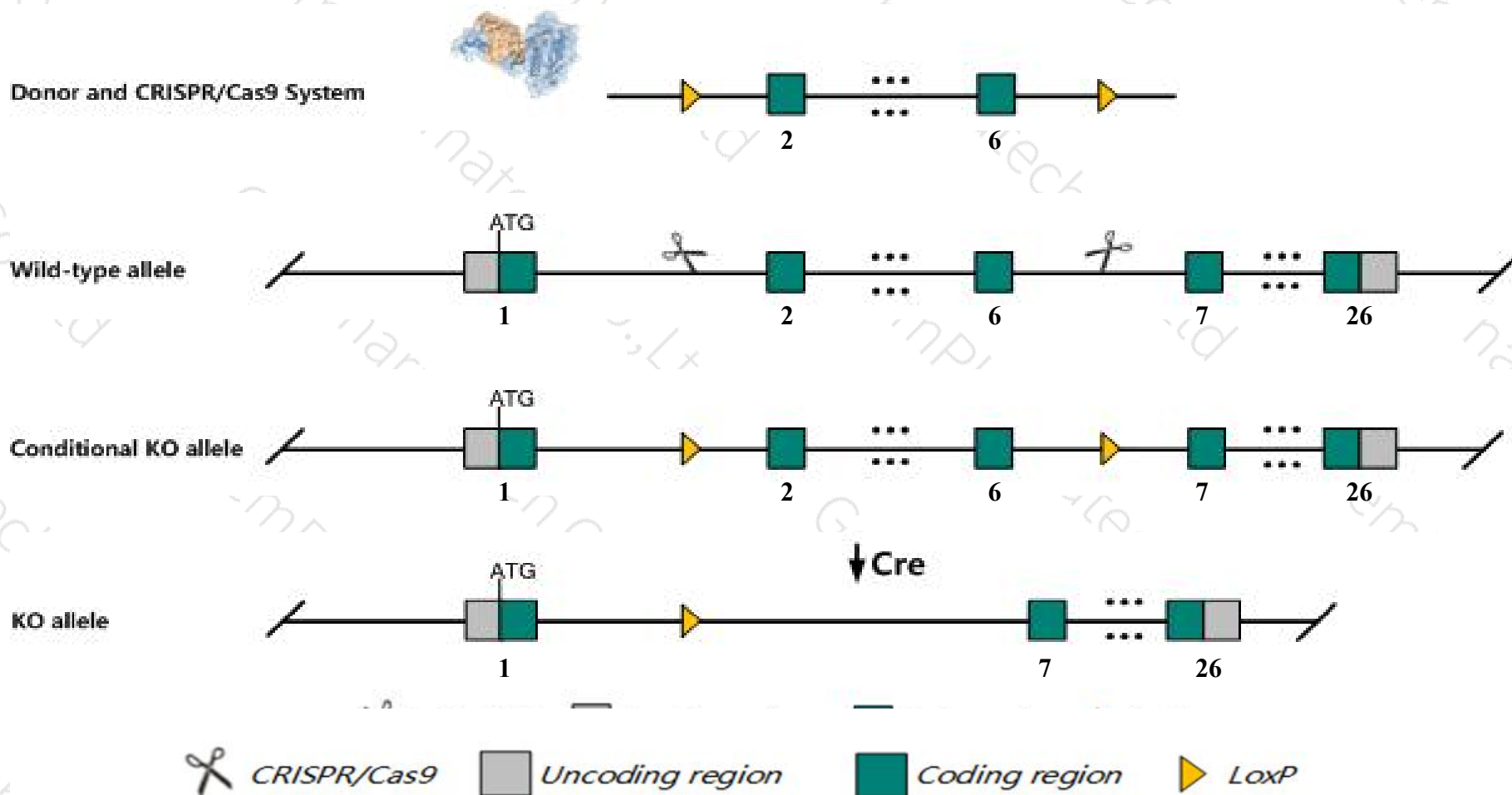
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fmn11* gene. The schematic diagram is as follows:



- The *Fmn11* gene has 7 transcripts. According to the structure of *Fmn11* gene, exon2-exon6 of *Fmn11*-202 (ENSMUST00000042286.11) transcript is recommended as the knockout region. The region contains 482bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fmn11* 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, Constitutive homozygous KO is embryonic lethal. Conditional homozygous KO in myeloid cells leads to reduced macrophage migration and podosome formation.
- The *Fmn11* gene is located on the Chr11. 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)

Fmn1 formin-like 1 [*Mus musculus* (house mouse)]

Gene ID: 57778, updated on 10-Oct-2019

Summary

Official Symbol

Fmn1 provided by MGI

Official Full Name

formin-like 1 provided by MGI

Primary source

MGI:MGI:1888994

See related

Ensembl:ENSMUSG00000055805

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

Fmnl; Fnrl; Frls; AI553564; 8030453N10Rik

Expression

Biased expression in thymus adult (RPKM 65.2), spleen adult (RPKM 49.0) and 11 other tissues [See more](#)

Orthologs

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

Genomic context

Location: 11; 11 E1

Exon count: 28

[See Fmn1 in Genome Data Viewer](#)

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (103171004..103198902)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (103032452..103060214)

Chromosome 11 - NC_000077.6

[103123260]

Hexim2

Gw51919

Fmn1

Efcab15

Spat32

Gw51920

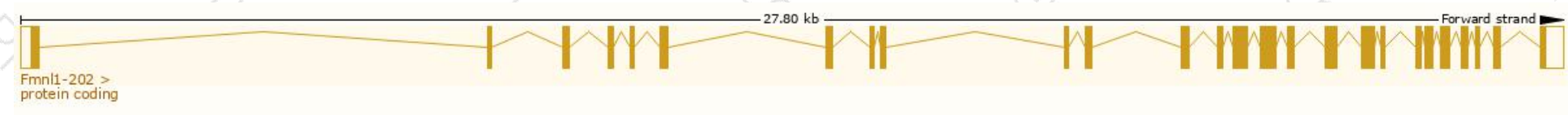
[103218432]

Transcript information (Ensembl)

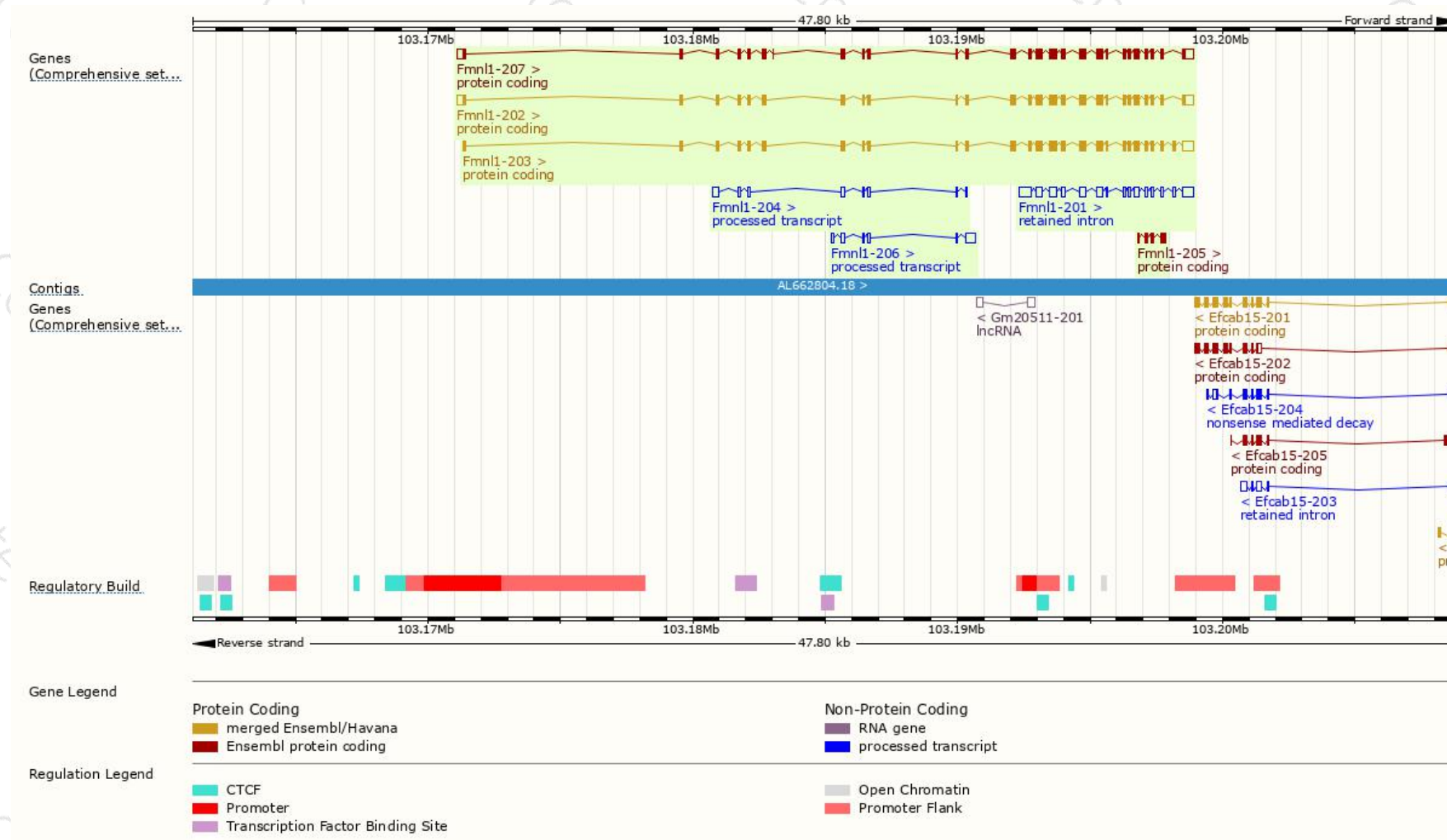
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fmn11-202	ENSMUST00000042286.11	3806	1094aa	Protein coding	CCDS36348	Q9JL26	TSL:1 GENCODE basic APPRIS P4
Fmn11-203	ENSMUST00000107027.8	3693	1090aa	Protein coding	CCDS36349	A2AB60	TSL:5 GENCODE basic APPRIS ALT2
Fmn11-207	ENSMUST00000218163.1	3824	1100aa	Protein coding	-	A0A1W2P6X3	TSL:5 GENCODE basic APPRIS ALT2
Fmn11-205	ENSMUST00000129726.2	450	150aa	Protein coding	-	G3UWI1	CDS 5' and 3' incomplete TSL:3
Fmn11-206	ENSMUST00000154871.1	829	No protein	Processed transcript	-	-	TSL:1
Fmn11-204	ENSMUST00000126425.7	805	No protein	Processed transcript	-	-	TSL:5
Fmn11-201	ENSMUST00000021322.6	2830	No protein	Retained intron	-	-	TSL:1

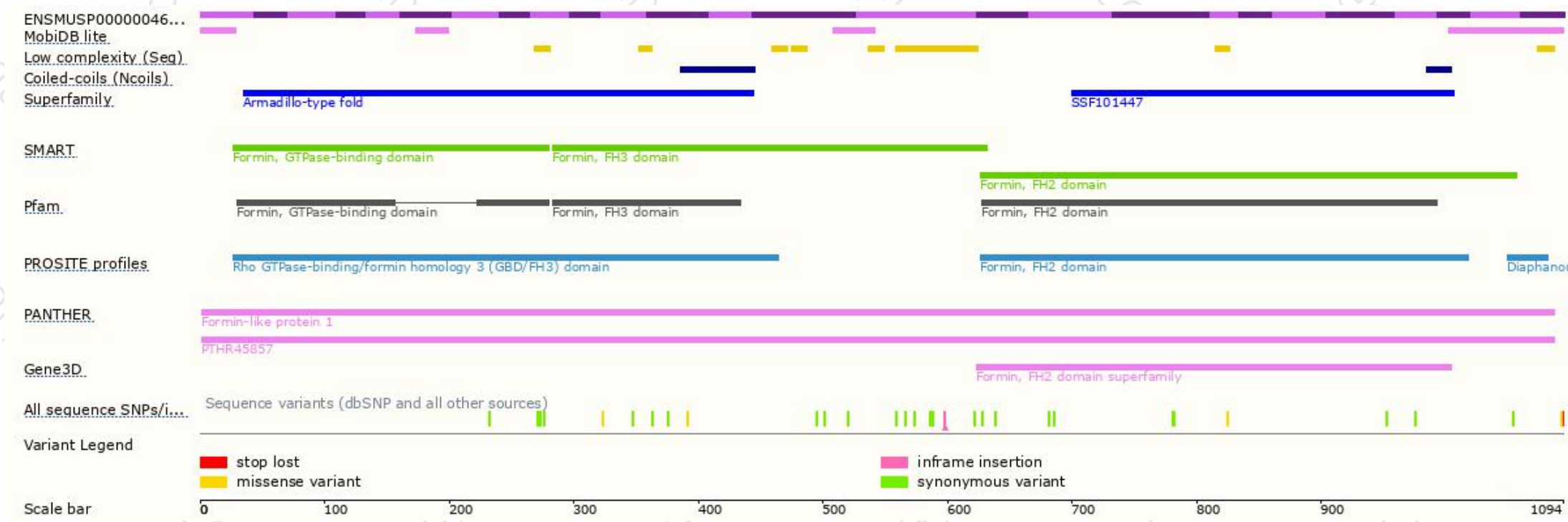
The strategy is based on the design of *Fmn11-202* transcript,The transcription is shown below



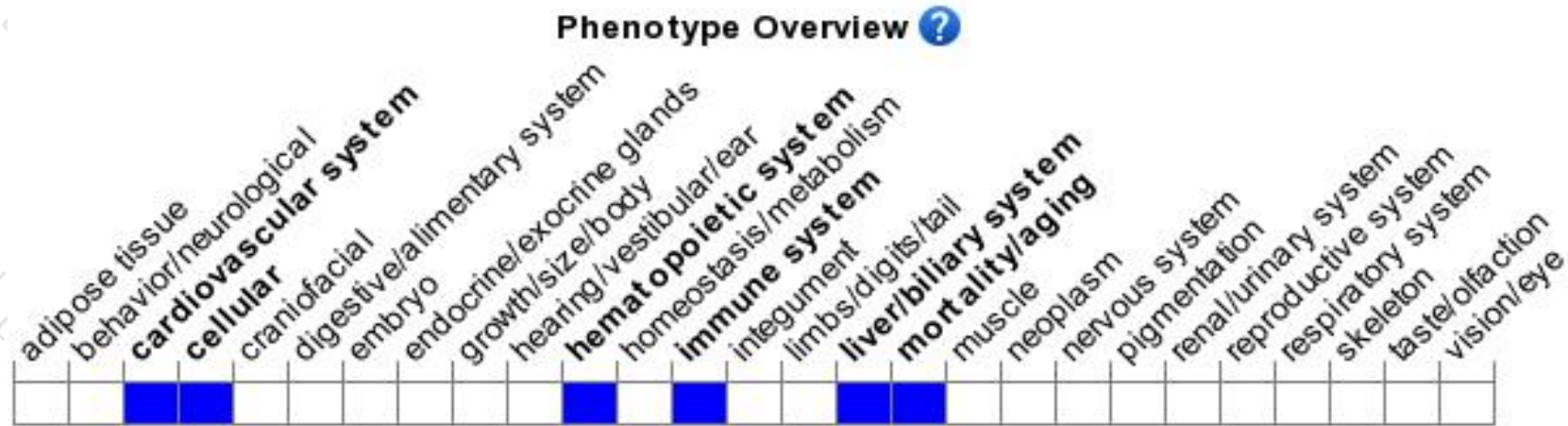
Genomic location distribution



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, Constitutive homozygous KO is embryonic lethal. Conditional homozygous KO in myeloid cells leads to reduced macrophage migration and podosome formation.

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

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