

# ***Fmnl1* Cas9-KO Strategy**

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**Design Date:**

**2020-2-18**

# Project Overview

**Project Name**

***Fmnl1***

**Project type**

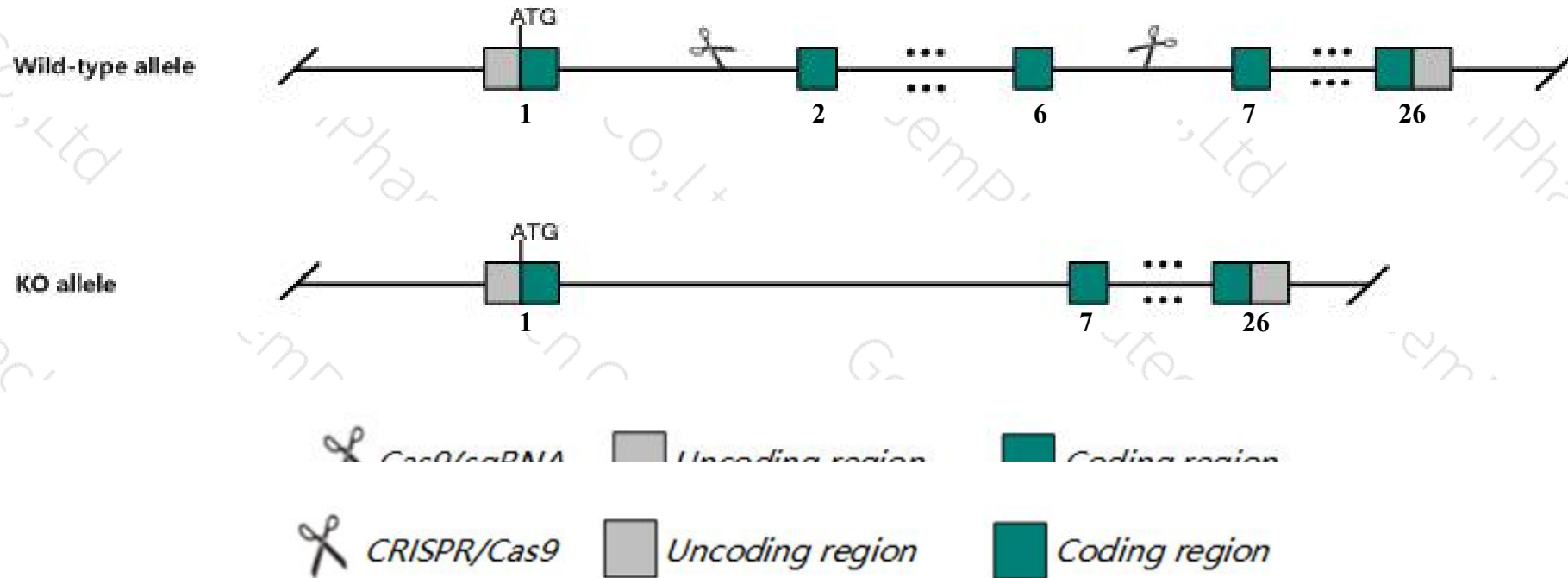
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# 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 w

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Fmn11 formin-like 1 [ *Mus musculus* (house mouse) ]

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

Summary

Official Symbol

Fmn11 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 Fmn11 in [Genome Data Viewer](#)

Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	11	NC_000077.6 (103171004..103198902)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	11	NC_000077.5 (103032452..103060214)

Chromosome 11 - NC\_000077.6

[ 103123260 ]

[ 103218432 ]

Hexim2

Gw51919

Fmn11

Efcab15

Spata32

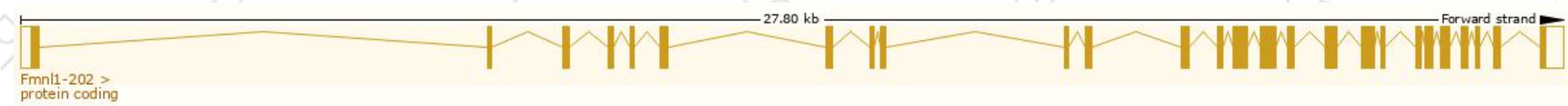
Gw51920

# Transcript information (Ensembl)

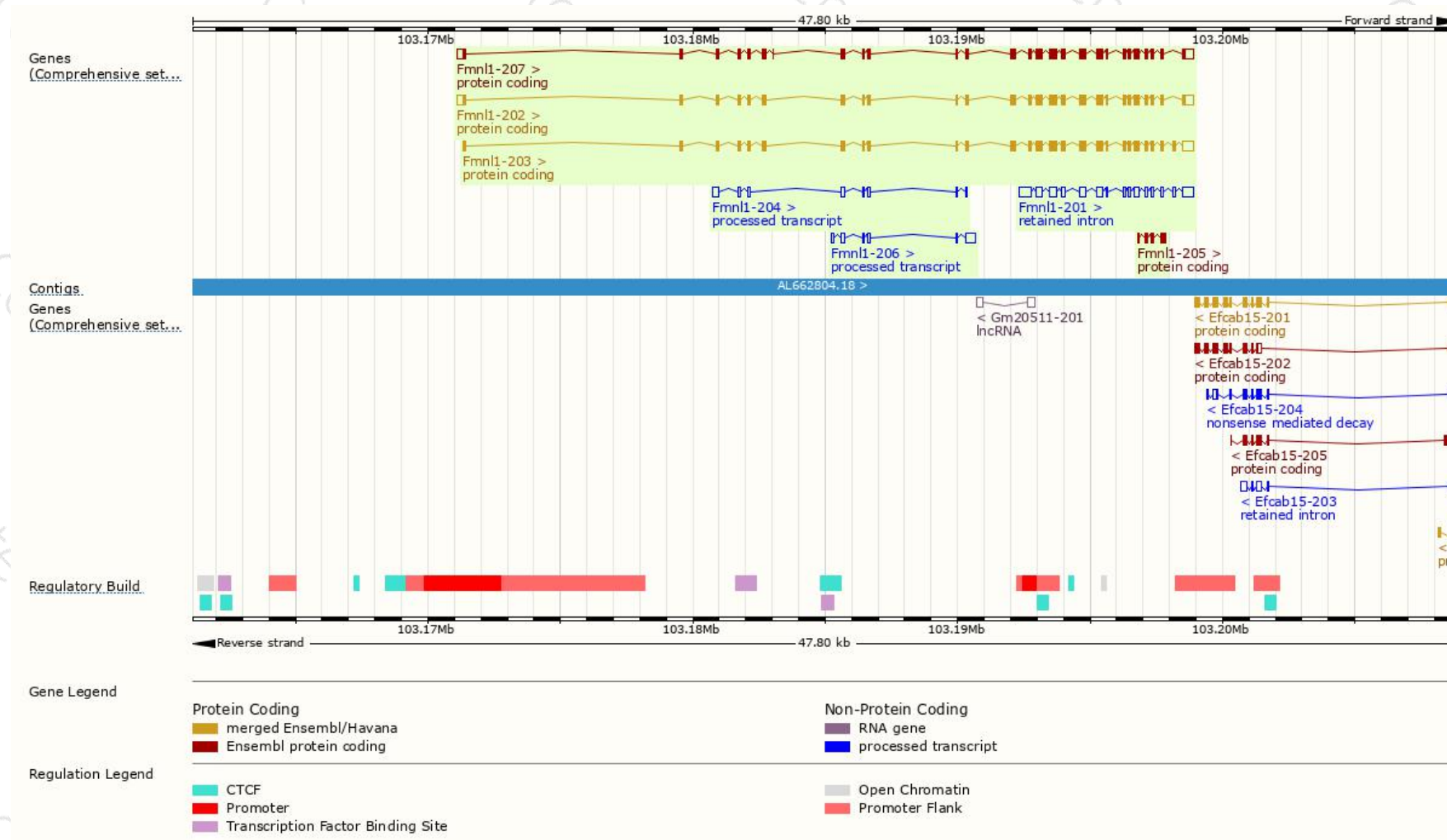
The gene has 7 transcripts,all transcripts are shown below:

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

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

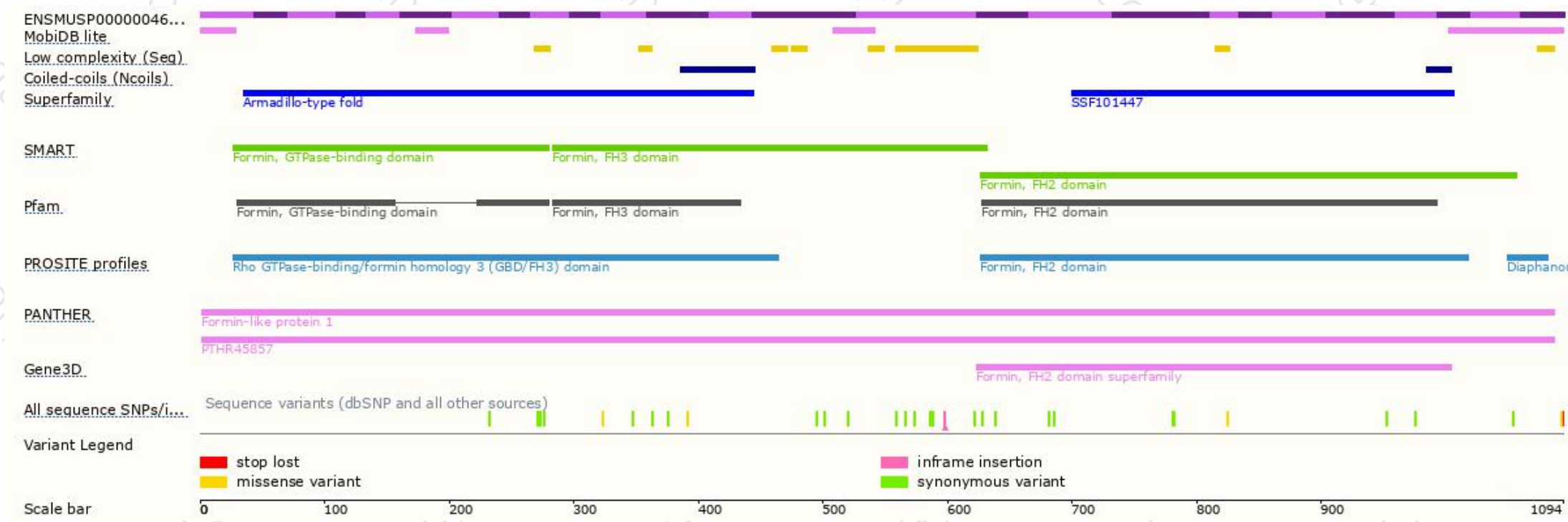


# Genomic location distribution

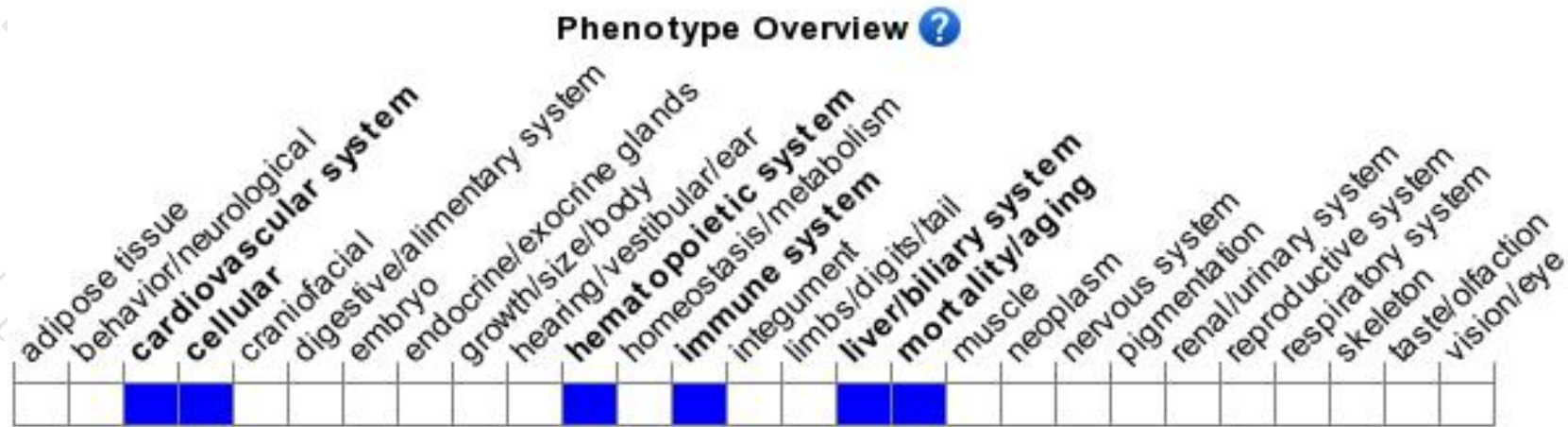




# Protein domain



# 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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