

# ***Fmn1* Cas9-KO Strategy**

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**Reviewer:**

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# Project Overview

**Project Name**

***Fmn1***

**Project type**

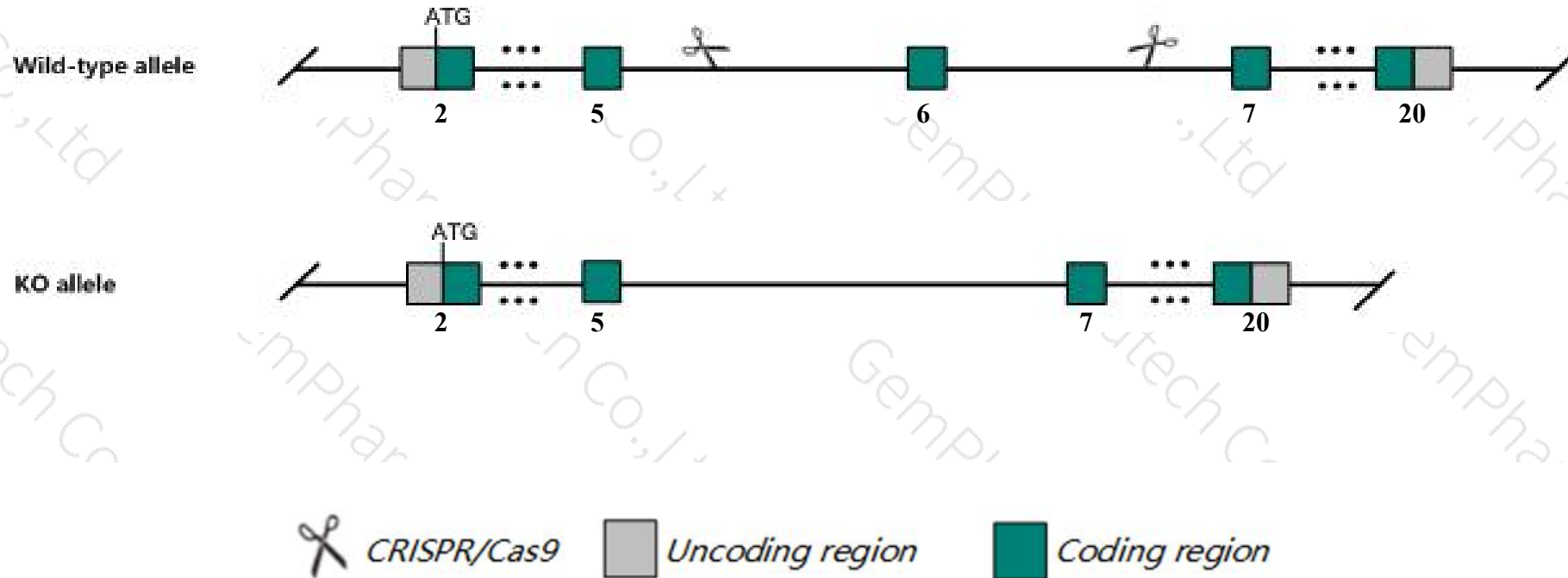
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fmn1* gene. The schematic diagram is as follows:



- The *Fmn1* gene has 9 transcripts. According to the structure of *Fmn1* gene, exon6 of *Fmn1-203* (ENSMUST00000102547.9) transcript is recommended as the knockout region. The region contains 791bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fmn1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for spontaneous, irradiation-induced, and transgene-insertional mutations show severe syndactyly and oligodactyly of the feet, abnormal long bones (including radius-ulna fusions), and reduced or absent kidneys. Many mutants survive and breed.
- Transcript *Fmn1*-204/205/206/207/208/209 lncRNA may not be affected.
- The *Fmn1* gene is located on the Chr2. 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.



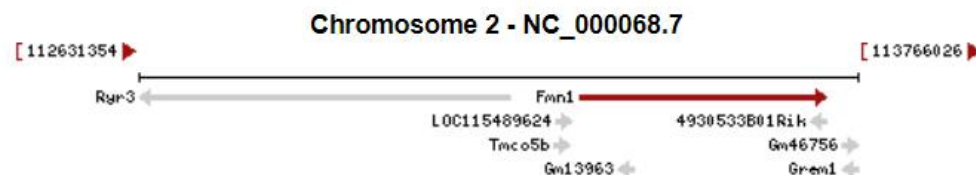
# Gene information (NCBI)

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

Gene ID: 14260, updated on 10-Oct-2019

### Summary

<b>Official Symbol</b>	Fmn1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	formin 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:101815</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000044042</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	Id; Fmn; formin-1
<b>Expression</b>	Broad expression in testis adult (RPKM 2.9), kidney adult (RPKM 1.9) and 19 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

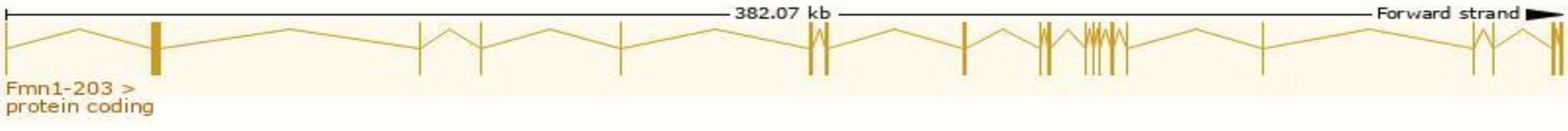


# Transcript information (Ensembl)

The gene has 9 transcripts,all transcripts are shown below:

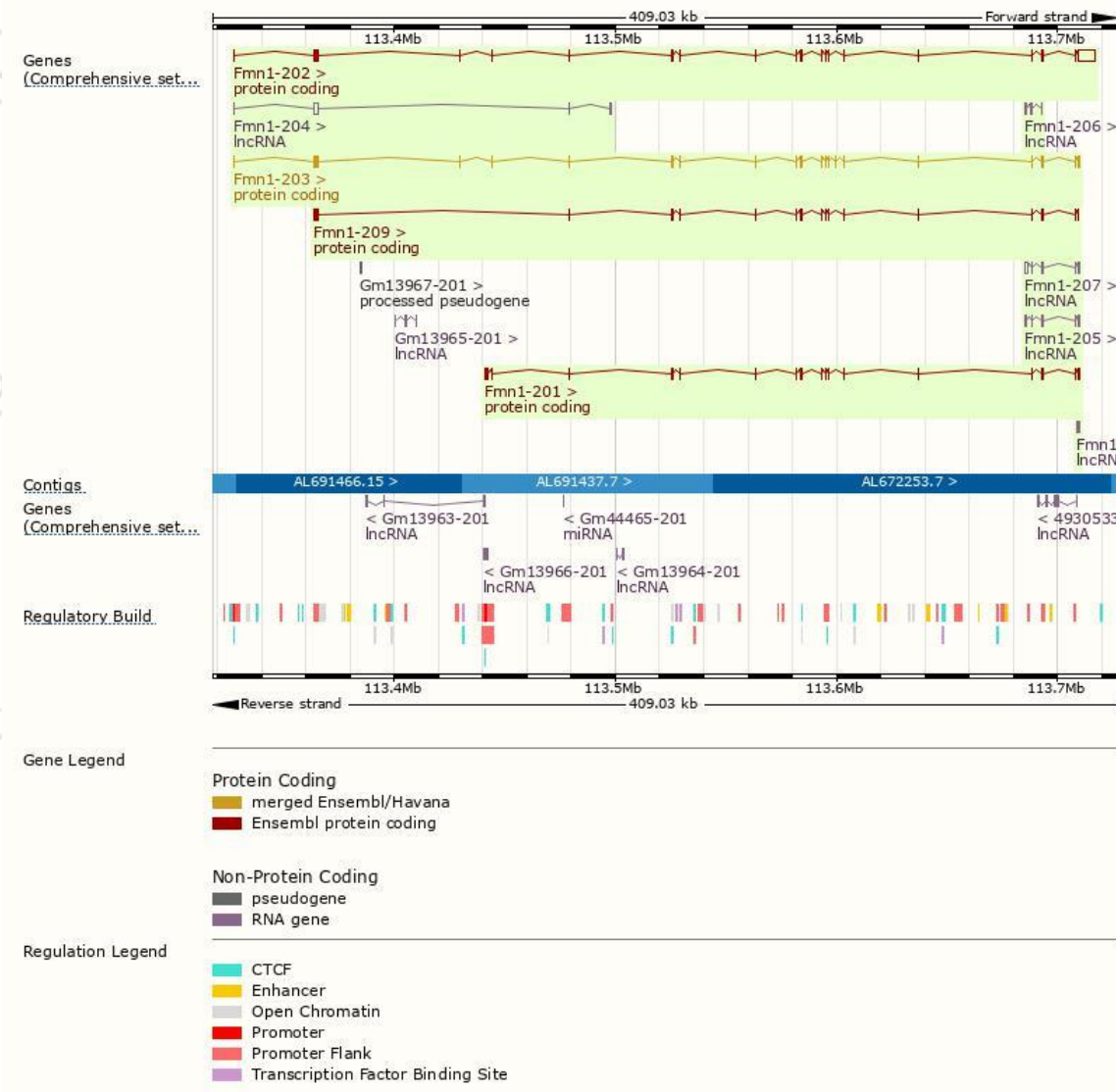
Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Fmn1-203	<a href="#">ENSMUST00000102547.9</a>	4967	<a href="#">1466aa</a>	<a href="#">ENSMUSP00000099606.3</a>	Protein coding	<a href="#">CCDS16559</a>	<a href="#">Q05860</a>	TSL:1 GENCODE basic
Fmn1-210	<a href="#">ENSMUST00000161731.4</a>	4262	<a href="#">1332aa</a>	<a href="#">ENSMUSP00000125052.1</a>	Protein coding	<a href="#">CCDS71112</a>	<a href="#">E9Q7P6</a>	TSL:1 GENCODE basic APPRIS P4
Fmn1-201	<a href="#">ENSMUST00000081349.8</a>	4235	<a href="#">1204aa</a>	<a href="#">ENSMUSP00000080093.6</a>	Protein coding	<a href="#">CCDS71113</a>	<a href="#">Q05860</a>	TSL:1 GENCODE basic APPRIS ALT2
Fmn1-202	<a href="#">ENSMUST00000099576.8</a>	11817	<a href="#">1430aa</a>	<a href="#">ENSMUSP00000097171.2</a>	Protein coding	-	<a href="#">Q05860</a>	TSL:5 GENCODE basic APPRIS ALT2
Fmn1-211	<a href="#">ENSMUST00000238883.1</a>	2644	<a href="#">850aa</a>	<a href="#">ENSMUSP00000159010.1</a>	Protein coding	-	-	GENCODE basic APPRIS ALT2
Fmn1-204	<a href="#">ENSMUST00000110954.6</a>	2384	No protein	-	lncRNA	-	-	TSL:1
Fmn1-207	<a href="#">ENSMUST00000152255.1</a>	2097	No protein	-	lncRNA	-	-	TSL:1
Fmn1-205	<a href="#">ENSMUST00000145891.7</a>	719	No protein	-	lncRNA	-	-	TSL:2
Fmn1-209	<a href="#">ENSMUST00000154834.1</a>	576	No protein	-	lncRNA	-	-	TSL:3
Fmn1-208	<a href="#">ENSMUST00000153151.1</a>	474	No protein	-	lncRNA	-	-	TSL:1
Fmn1-206	<a href="#">ENSMUST00000150510.7</a>	385	No protein	-	lncRNA	-	-	TSL:5

The strategy is based on the design of *Fmn1-203* transcript,The transcription is shown below





# Genomic location distribution



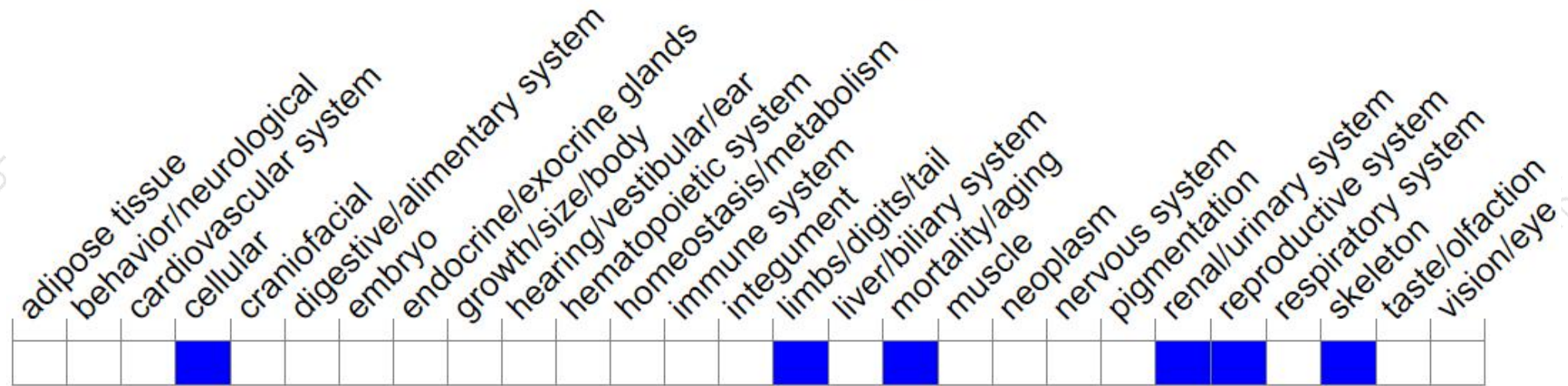


# Protein domain



# Mouse phenotype description(MGI)

## Phenotype Overview ?



*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, Homozygotes for spontaneous, irradiation-induced, and transgene-insertional mutations show severe syndactyly and oligodactyly of the feet, abnormal long bones (including radius-ulna fusions), and reduced or absent kidneys. Many mutants survive and breed.

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

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