

Fbln2 **Cas9-KO Strategy**

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Reviewer:	
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Project Overview

Project Name

Fbln2

Project type

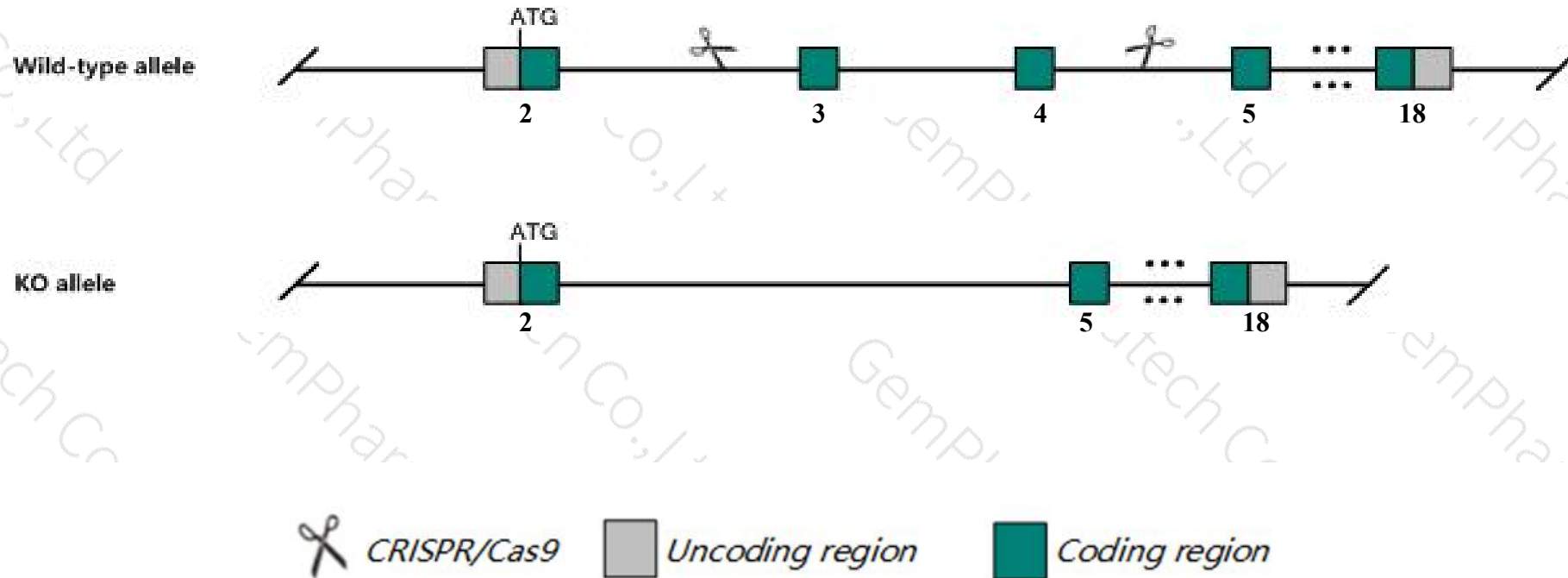
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fbln2* gene. The schematic diagram is as follows:



- The *Fbln2* gene has 9 transcripts. According to the structure of *Fbln2* gene, exon3-exon4 of *Fbln2-201* (ENSMUST00000041544.7) transcript is recommended as the knockout region. The region contains 242bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fbln2* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for a knock-out allele are viable, fertile and grossly normal with no apparent defects in elastic fiber formation in the aorta and skin.
- Transcripts *Fbln2*-203/205/208 CDS are incomplete, whether they will be affected is unknown.
- The *Fbln2* gene is located on the Chr6. 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.

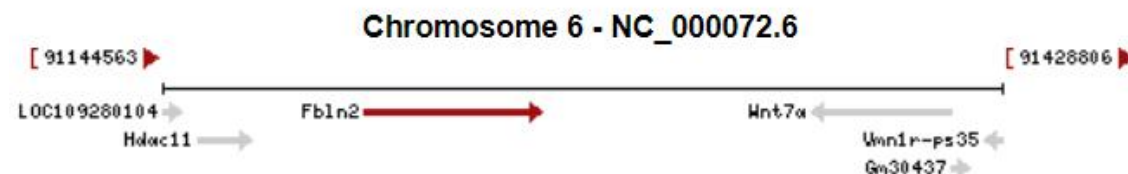
Gene information (NCBI)

Fbln2 fibulin 2 [*Mus musculus* (house mouse)]

Gene ID: 14115, updated on 12-Aug-2019

Summary

Official Symbol	Fbln2 provided by MGI
Official Full Name	fibulin 2 provided by MGI
Primary source	MGI:MGI:95488
See related	Ensembl:ENSMUSG00000064080
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	FIBL-2; 5730577E14Rik
Expression	Broad expression in limb E14.5 (RPKM 77.0), subcutaneous fat pad adult (RPKM 55.8) and 20 other tissues See more
Orthologs	human all

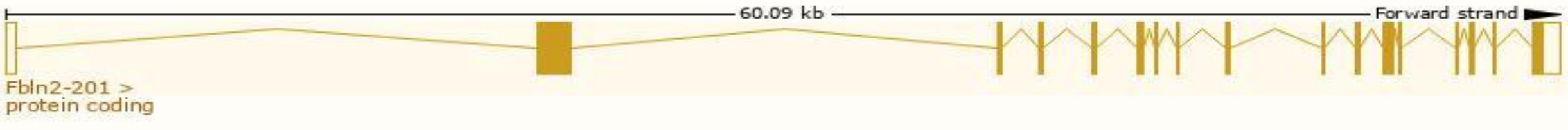


Transcript information (Ensembl)

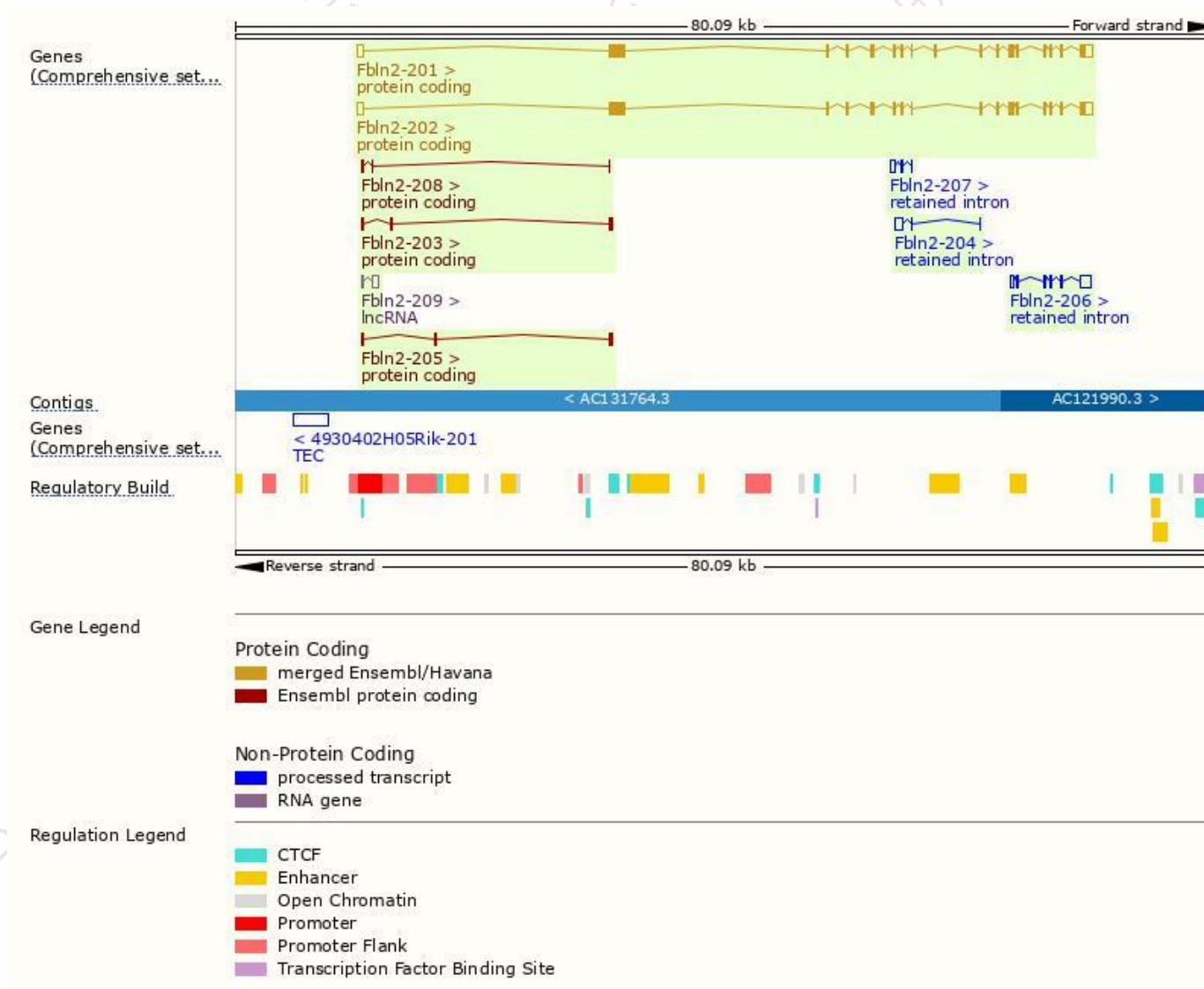
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Fbln2-201	ENSMUST00000041544.7	4786	1221aa	ENSMUSP00000048334.7	Protein coding	CCDS39566	P37889	TSL:1 GENCODE basic APPRIS P1
Fbln2-202	ENSMUST00000113498.8	4644	1174aa	ENSMUSP00000109126.2	Protein coding	CCDS39567	P37889 Q3TGL4	TSL:1 GENCODE basic
Fbln2-203	ENSMUST00000132021.1	477	69aa	ENSMUSP00000116456.1	Protein coding	-	D3Z5B0	CDS 3' incomplete TSL:5
Fbln2-205	ENSMUST00000134974.1	377	76aa	ENSMUSP00000116302.1	Protein coding	-	D3Z5S2	CDS 3' incomplete TSL:2
Fbln2-208	ENSMUST00000153364.1	223	10aa	ENSMUSP00000120101.1	Protein coding	-	A0A1C7ZMZ9	CDS 3' incomplete TSL:5
Fbln2-206	ENSMUST00000137029.1	1612	No protein	-	Retained intron	-	-	TSL:1
Fbln2-204	ENSMUST00000134286.1	752	No protein	-	Retained intron	-	-	TSL:5
Fbln2-207	ENSMUST00000147371.7	660	No protein	-	Retained intron	-	-	TSL:2
Fbln2-209	ENSMUST00000203406.1	669	No protein	-	lncRNA	-	-	TSL:1

The strategy is based on the design of *Fbln2-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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