

Flnc Cas9-KO Strategy

Designer:Xiaojing Li

Reviewer:JiaYu

Design Date:2020-3-9

Project Overview



Project Name

Flnc

Project type

Cas9-KO

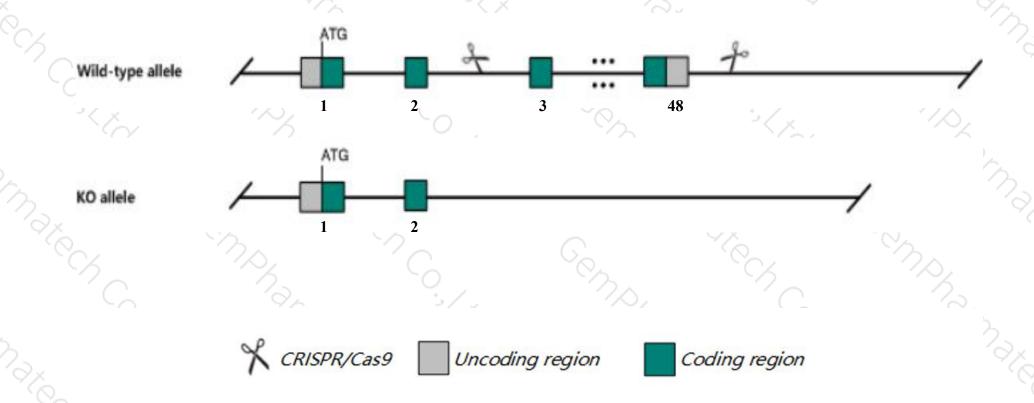
Strain background

C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Flnc* gene has 3 transcripts. According to the structure of *Flnc* gene, exon3-exon48 of *Flnc-201* (ENSMUST00000065090.7) transcript is recommended as the knockout region. The region contains 7577bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Flnc* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice



- > According to the existing MGI data, Mice homozygous for a hypomorphic allele display neonatal lethality, respiratory failure, reduced skeletal muscle mass, and abnormal skeletal muscle fiber morphology.
- The *Flnc* 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)



Finc filamin C, gamma [Mus musculus (house mouse)]

Gene ID: 68794, updated on 12-Aug-2019

Summary

Official Symbol Finc provided by MGI

Official Full Name filamin C, gamma provided by MGI

Primary source MGI:MGI:95557

See related Ensembl: ENSMUSG00000068699

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 ABPL; Fln2; ABP-280; 1110055E19Rik

Expression Broad expression in bladder adult (RPKM 22.4), heart adult (RPKM 22.2) and 16 other tissues See more

Orthologs human all

Transcript information (Ensembl)



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

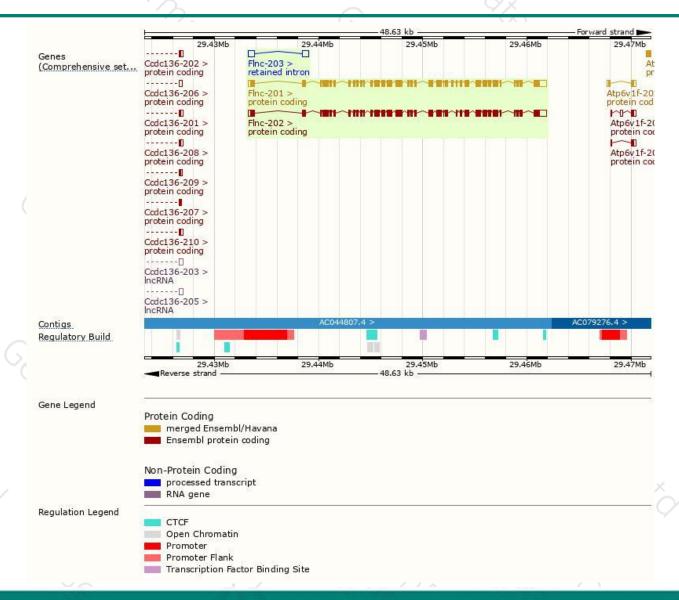
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Finc-201	ENSMUST00000065090.7	9038	2726aa	Protein coding	CCDS39452	Q8VHX6	TSL:1 GENCODE basic
Finc-202	ENSMUST00000101617.8	8939	<u>2693aa</u>	Protein coding	CCDS80503	Q8VHX6	TSL:1 GENCODE basic APPRIS P1
Finc-203	ENSMUST00000148404.1	1151	No protein	Retained intron	4-	-	TSL:1

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



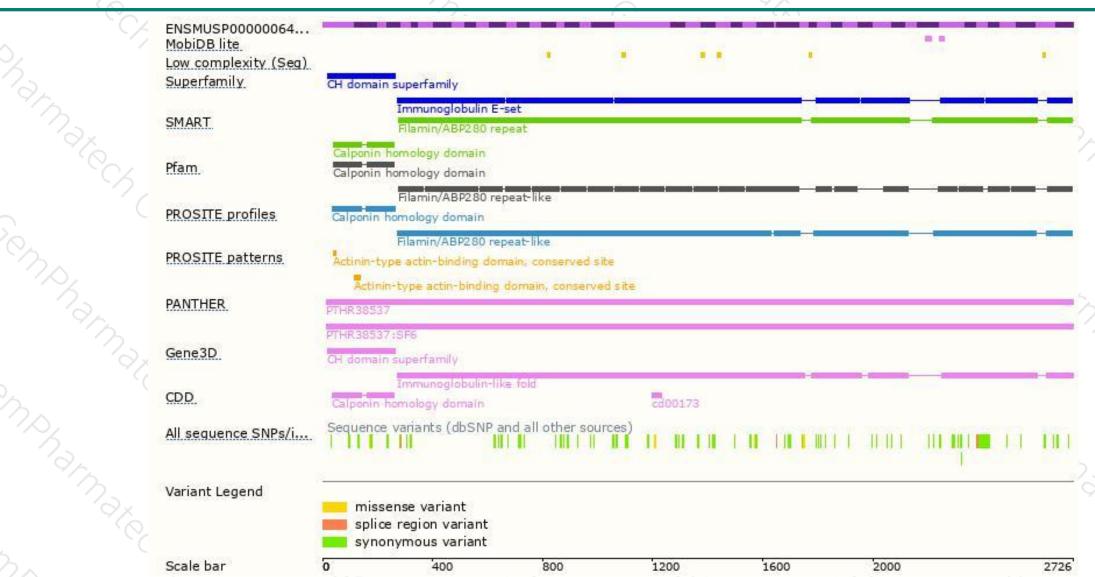
Genomic location distribution





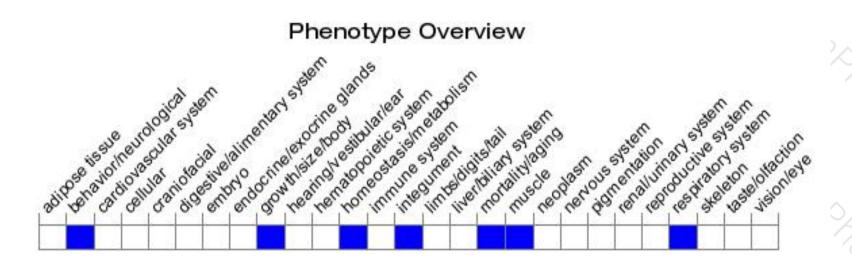
Protein domain





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, Mice homozygous for a hypomorphic allele display neonatal lethality, respiratory failure, reduced skeletal muscle mass, and abnormal skeletal muscle fiber morphology.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





