

Fgf18 Cas9-KO Strategy

Designer:

Yanhua Shen

Reviewer:

Xueting Zhang

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Project Overview

Project Name

Fgf18

Project type

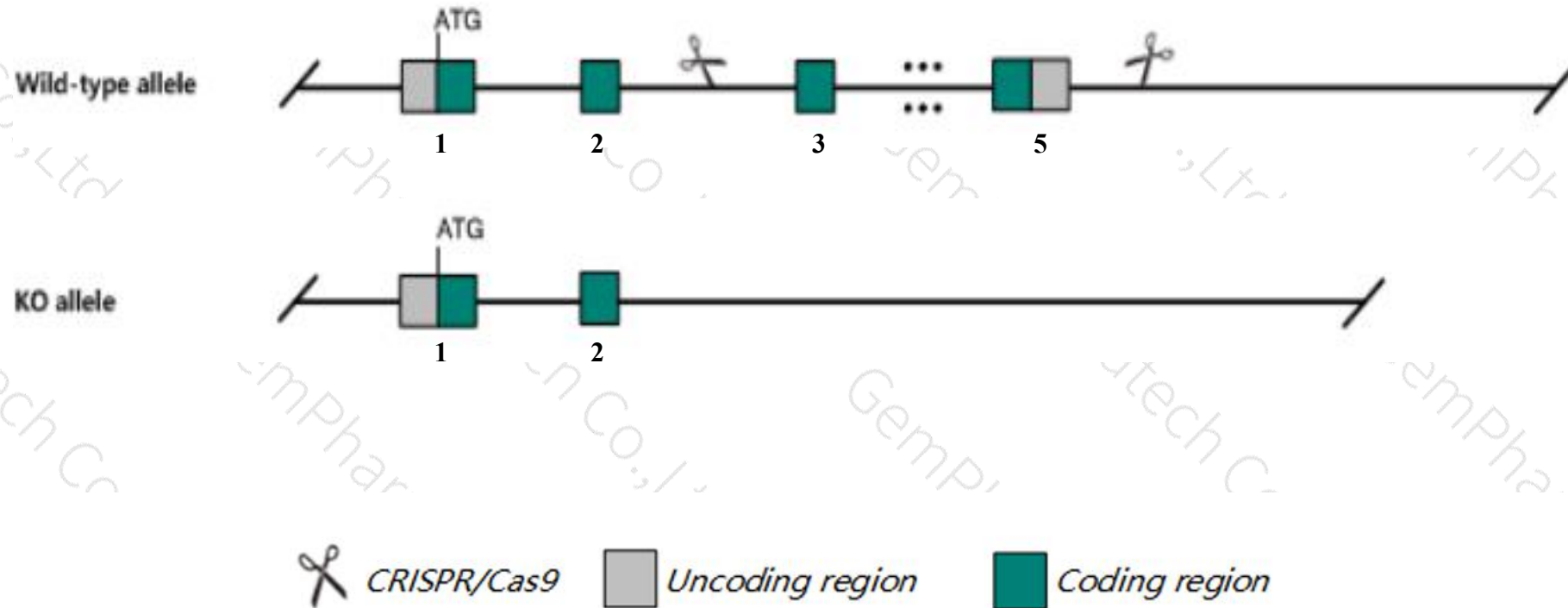
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fgf18* gene. The schematic diagram is as follows:



- The *Fgf18* gene has 2 transcripts. According to the structure of *Fgf18* gene, exon3-exon5 of *Fgf18-201* (ENSMUST00000020507.7) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fgf18* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, homozygotes for targeted null mutations die perinatally and exhibit impaired proliferation and differentiation of osteoblasts, shortened and thickened long bones, and delayed ossification of the calvarium and long bones.
- The *Fgf18* 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)

Fgf18 fibroblast growth factor 18 [Mus musculus (house mouse)]

Gene ID: 14172, updated on 13-Mar-2020

Summary

Official Symbol Fgf18 provided by [MGI](#)

Official Full Name fibroblast growth factor 18 provided by [MGI](#)

Primary source [MGI:MGI:1277980](#)

See related [Ensembl:ENSMUSG00000057967](#)

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 D130055P09Rik, FGF-18

Expression Broad expression in limb E14.5 (RPKM 4.9), lung adult (RPKM 2.9) and 17 other tissues [See more](#)

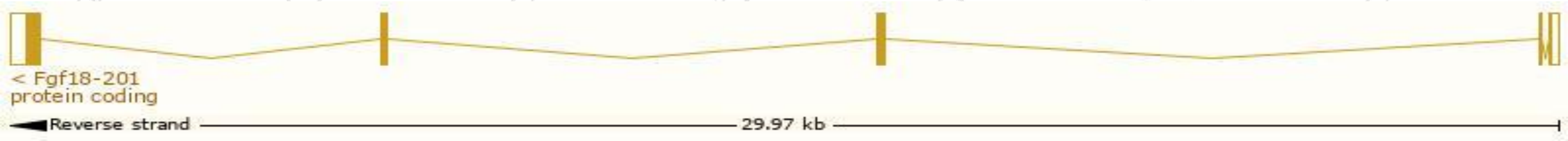
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

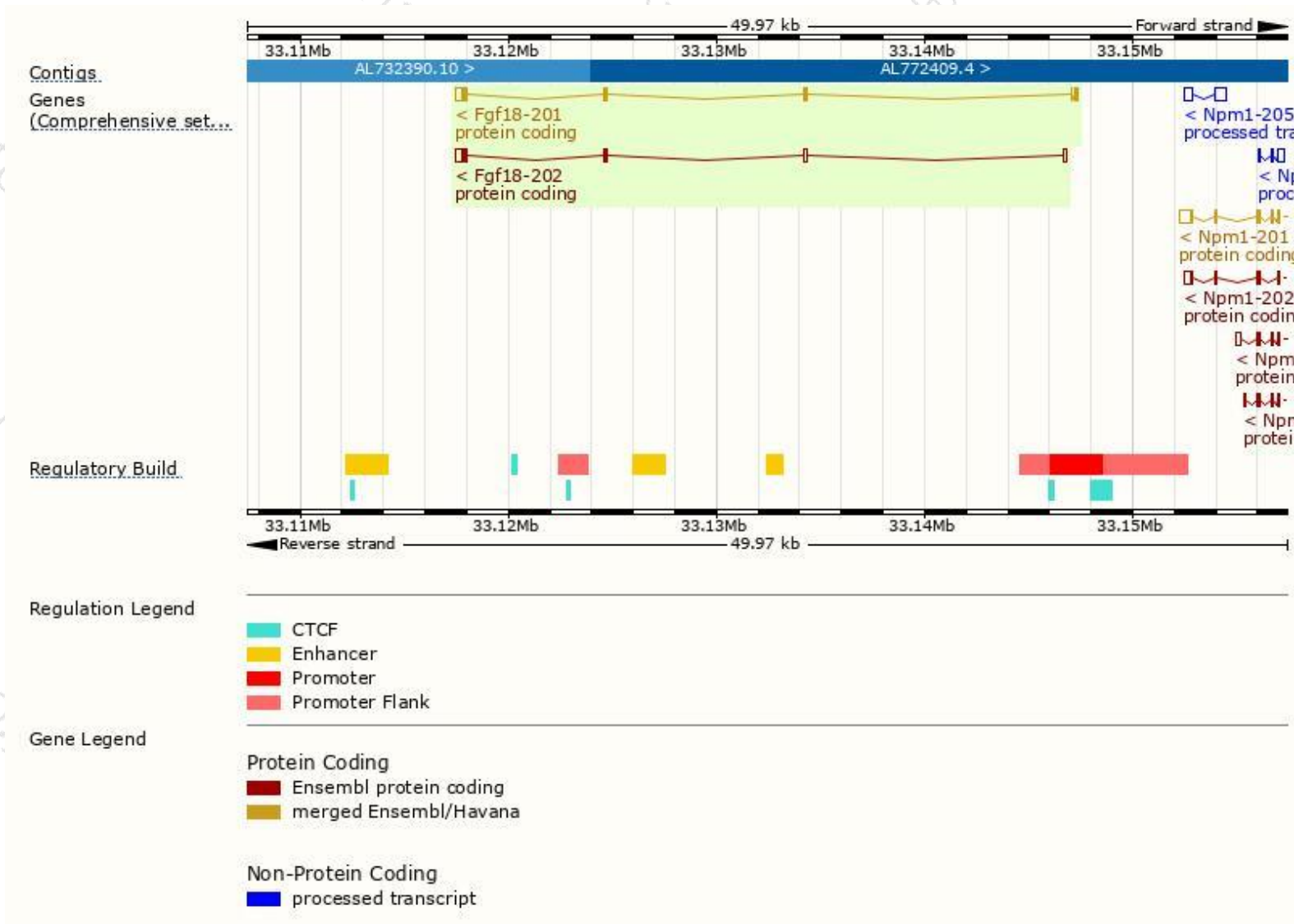
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fgf18-201	ENSMUST00000020507.7	1086	207aa	Protein coding	CCDS24531	O89101	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Fgf18-202	ENSMUST00000109363.7	991	98aa	Protein coding	-	Q5SQB3	TSL:3 GENCODE basic

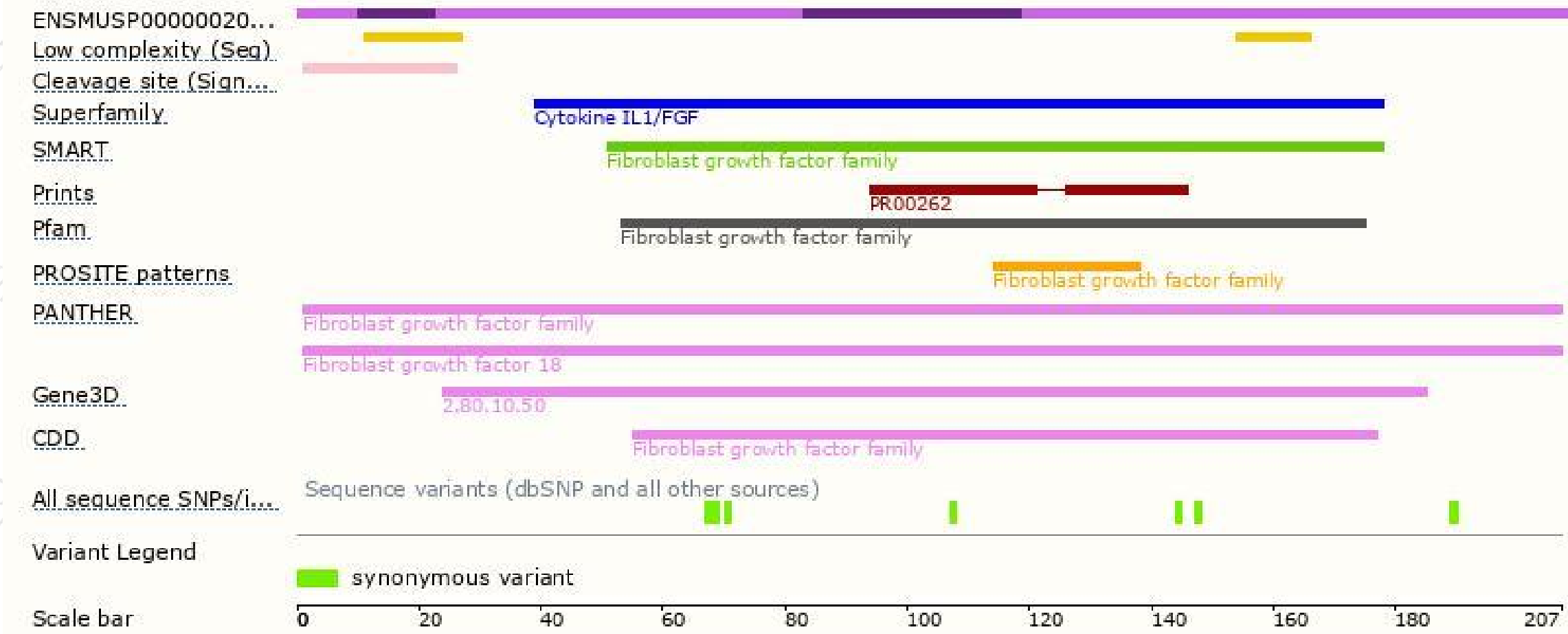
The strategy is based on the design of *Fgf18-201* transcript,The transcription is shown below



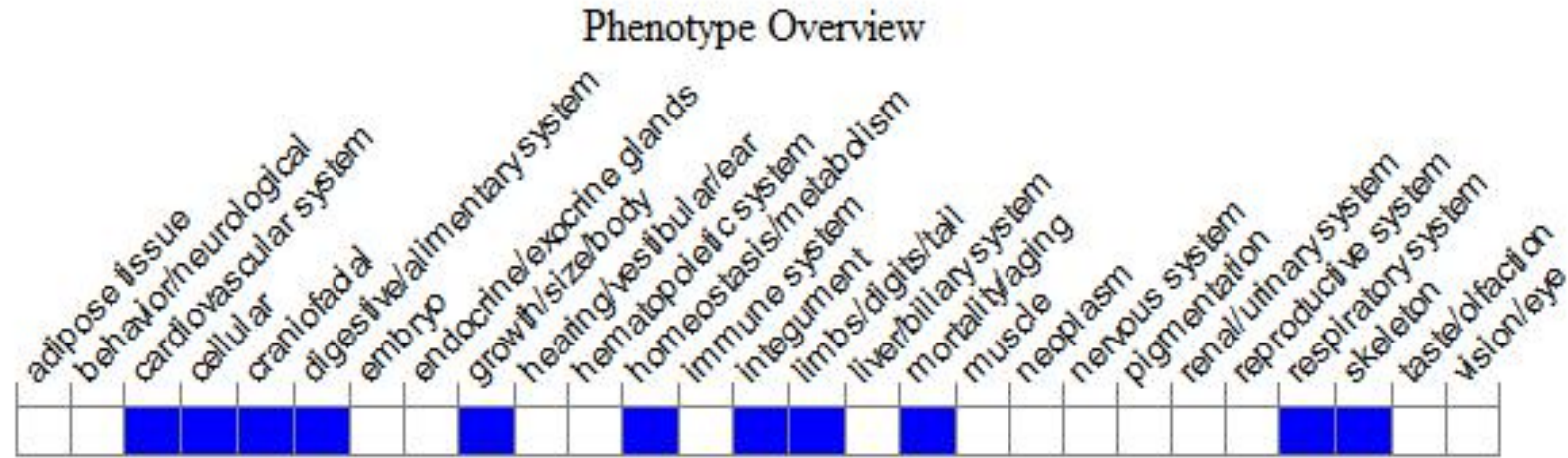
Genomic location distribution



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, homozygotes for targeted null mutations die perinatally and exhibit impaired proliferation and differentiation of osteoblasts, shortened and thickened long bones, and delayed ossification of the calvarium and long bones.

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

Tel: 400-9660890

