Fgfrl1 Cas9-KO Strategy

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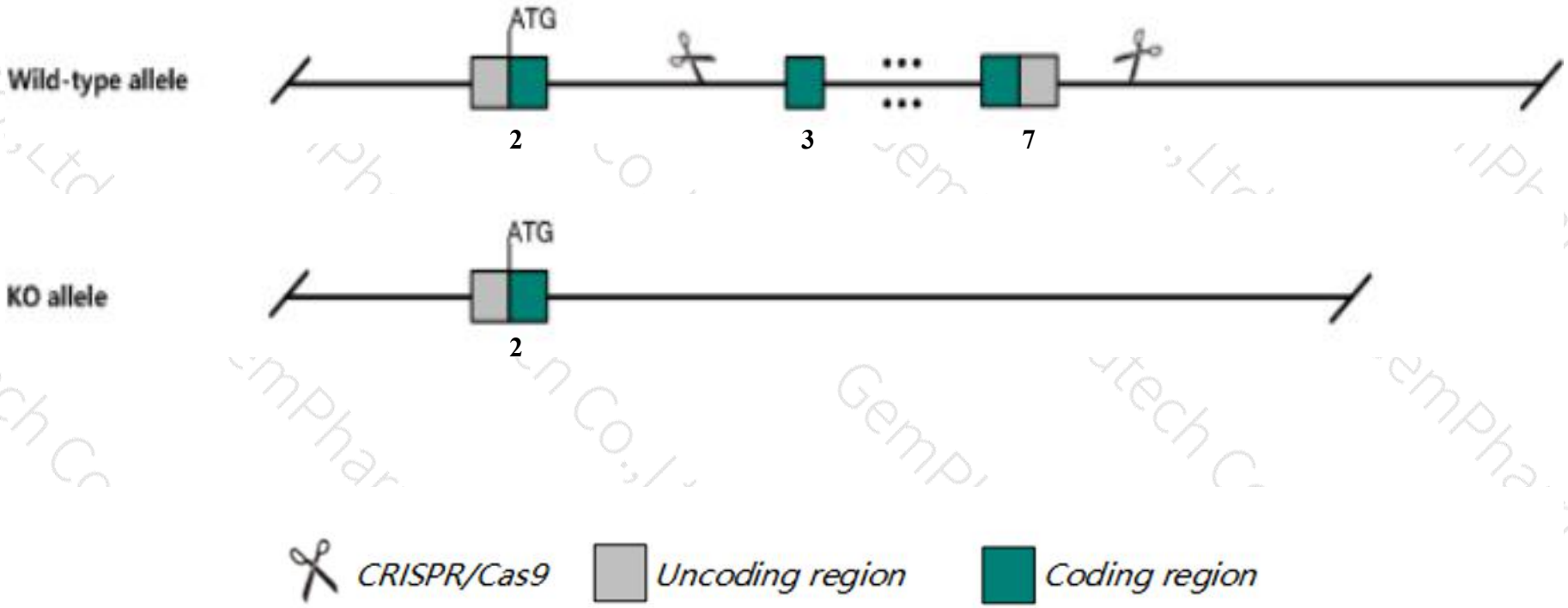
Project Overview

Project Name	***Fgfrl1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fgfrl1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Fgfrl1* gene has 5 transcripts. According to the structure of *Fgfrl1* gene, exon3-exon7 of *Fgfrl1-201*(ENSMUST00000013633.11) transcript is recommended as the knockout region.The region contains most of coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Fgfrl1* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

Notice

➢ According to the existing MGI data,homozygotes for a null allele show neonatal death due to respiratory distress, a malformed diaphragm, and lack of metanephric kidneys. Homozygotes for a different null allele show both fetal and neonatal death, a similar diaphragm defect, as well as cardiac and skeletal defects, and fetal anemia.

➢ The *Fgfrl1* gene is located on the Chr5. 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）

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Fgfrl1 fibroblast growth factor receptor-like 1 [*Mus musculus* (house mouse)]

Gene ID: 116701, updated on 27-Jun-2020

Summary

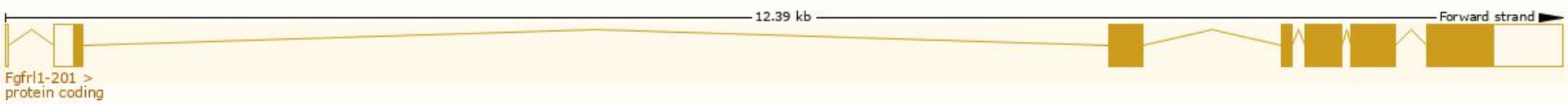
Official Symbol	Fgfrl1 provided by MGI
Official Full Name	fibroblast growth factor receptor-like 1 provided by MGI
Primary source	MGI:MGI:2150920
See related	Ensembl:ENSMUSG00000008090
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	FGFR5; FGFR5beta; FGFR5gamma
Expression	Broad expression in subcutaneous fat pad adult (RPKM 80.9), genital fat pad adult (RPKM 60.2) and 26 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

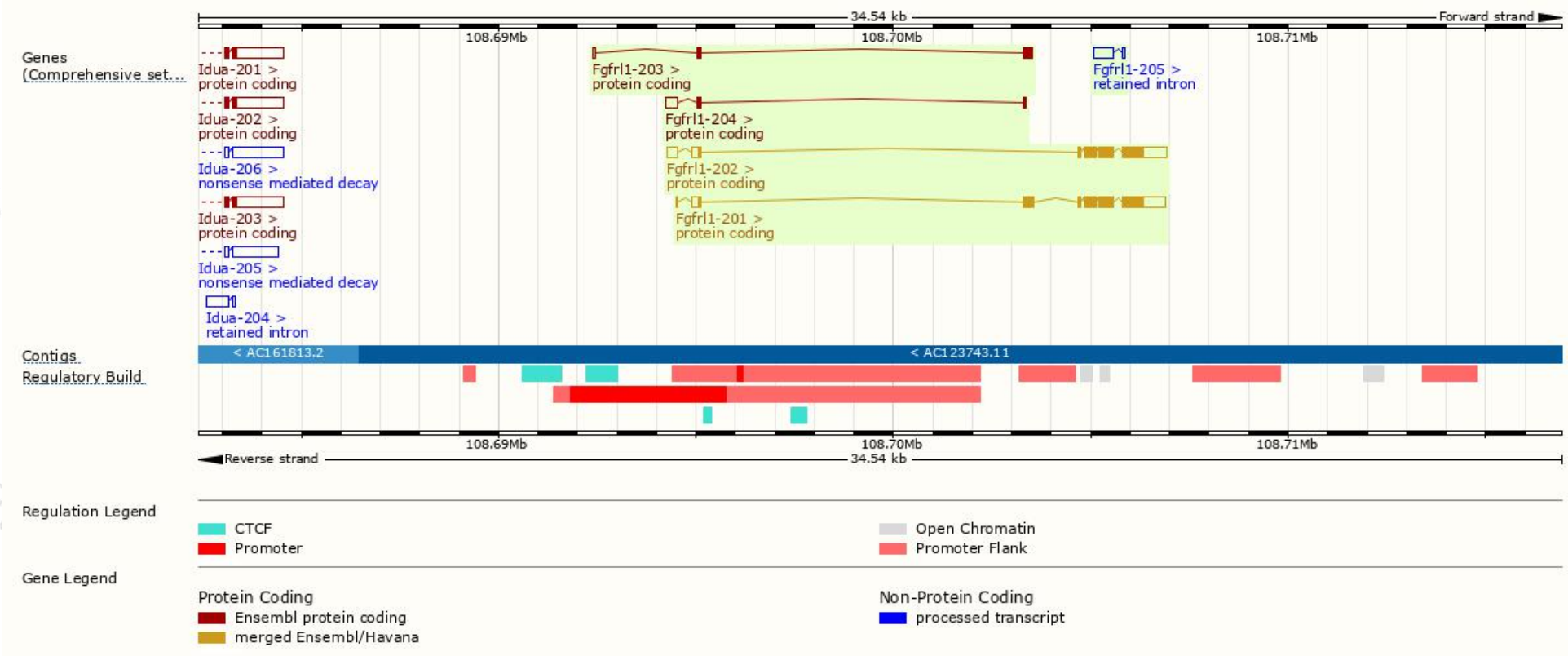
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein ▲	Biotype	CCDS	UniProt	Flags
Fgfrl1-204	ENSMUST00000197255.1	438	40aa	Protein coding	-	A0A0G2JDM8	CDS 3' incomplete TSL:2
Fgfrl1-203	ENSMUST00000196222.4	406	106aa	Protein coding	-	A0A0G2JF62	CDS 3' incomplete TSL:3
Fgfrl1-202	ENSMUST00000112560.7	2318	438aa	Protein coding	CCDS51592	Q91V87	TSL:1 GENCODE basic
Fgfrl1-201	ENSMUST00000013633.11	2329	529aa	Protein coding	CCDS19518	Q91V87	TSL:1 GENCODE basic APPRIS P1
Fgfrl1-205	ENSMUST00000199802.1	556	No protein	Retained intron	-	-	TSL:2

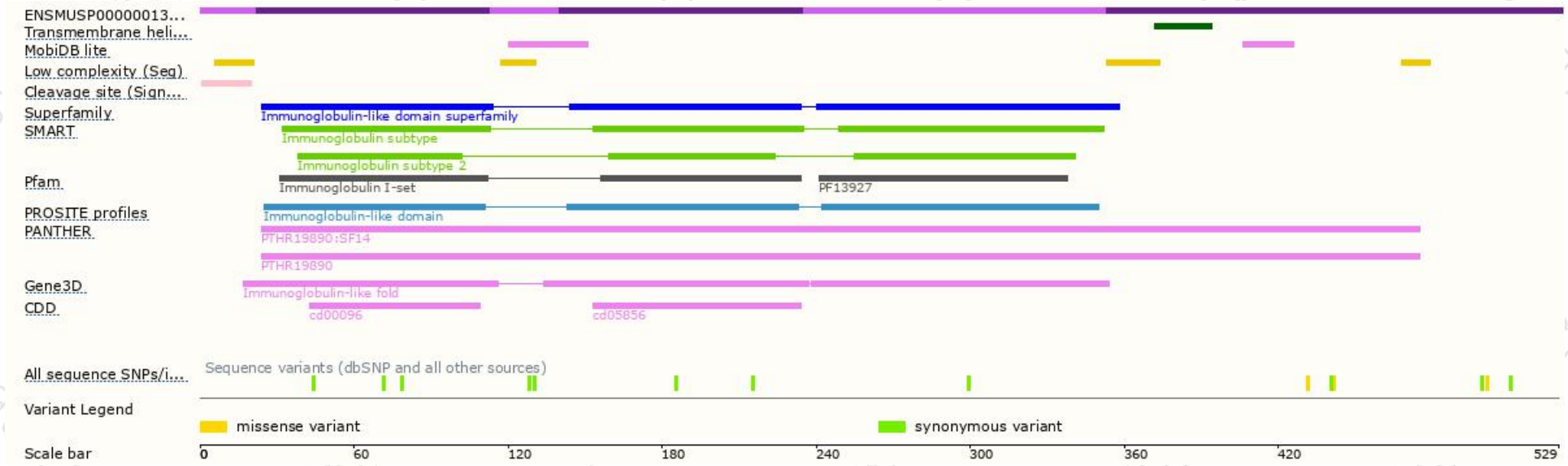
The strategy is based on the design of *Fgfrl1-201* transcript,the transcription is shown below:



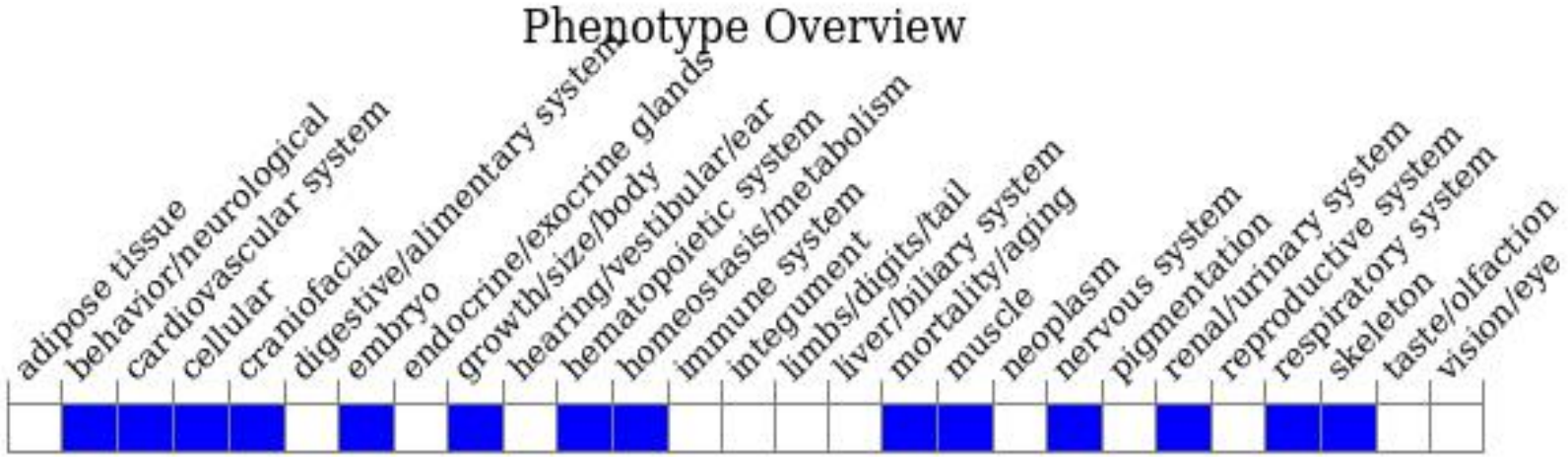
Genomic location distribution



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 a null allele show neonatal death due to respiratory distress, a malformed diaphragm, and lack of metanephric kidneys. Homozygotes for a different null allele show both fetal and neonatal death, a similar diaphragm defect, as well as cardiac and skeletal defects, and fetal anemia.

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

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