

Ifrd1 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Ifrd1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ifrd1* gene. The schematic diagram is as follows:



- The *Ifrd1* gene has 10 transcripts. According to the structure of *Ifrd1* gene, exon2-exon8 of *Ifrd1-201* (ENSMUST00000001672.11) transcript is recommended as the knockout region. The region contains 812bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ifrd1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous null mice display impaired muscle regeneration and myogenic differentiation and decreased body weight in older mice.
- The KO region contains functional region of the *Gm17024* gene. Knockout the region may affect the function of *Gm17024* gene.
- The *Ifrd1* gene is located on the Chr12. 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)

lfrd1 interferon-related developmental regulator 1 [Mus musculus (house mouse)]

Gene ID: 15982, updated on 19-Mar-2019

Summary



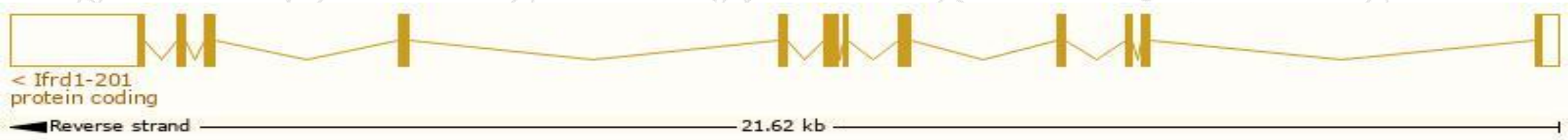
Official Symbol	lfrd1 provided by MGI
Official Full Name	interferon-related developmental regulator 1 provided by MGI
Primary source	MGI:MGI:1316717
See related	Ensembl:ENSMUSG000000001627
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	lfrl, PC4, Tis7
Expression	Ubiquitous expression in small intestine adult (RPKM 45.7), duodenum adult (RPKM 33.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

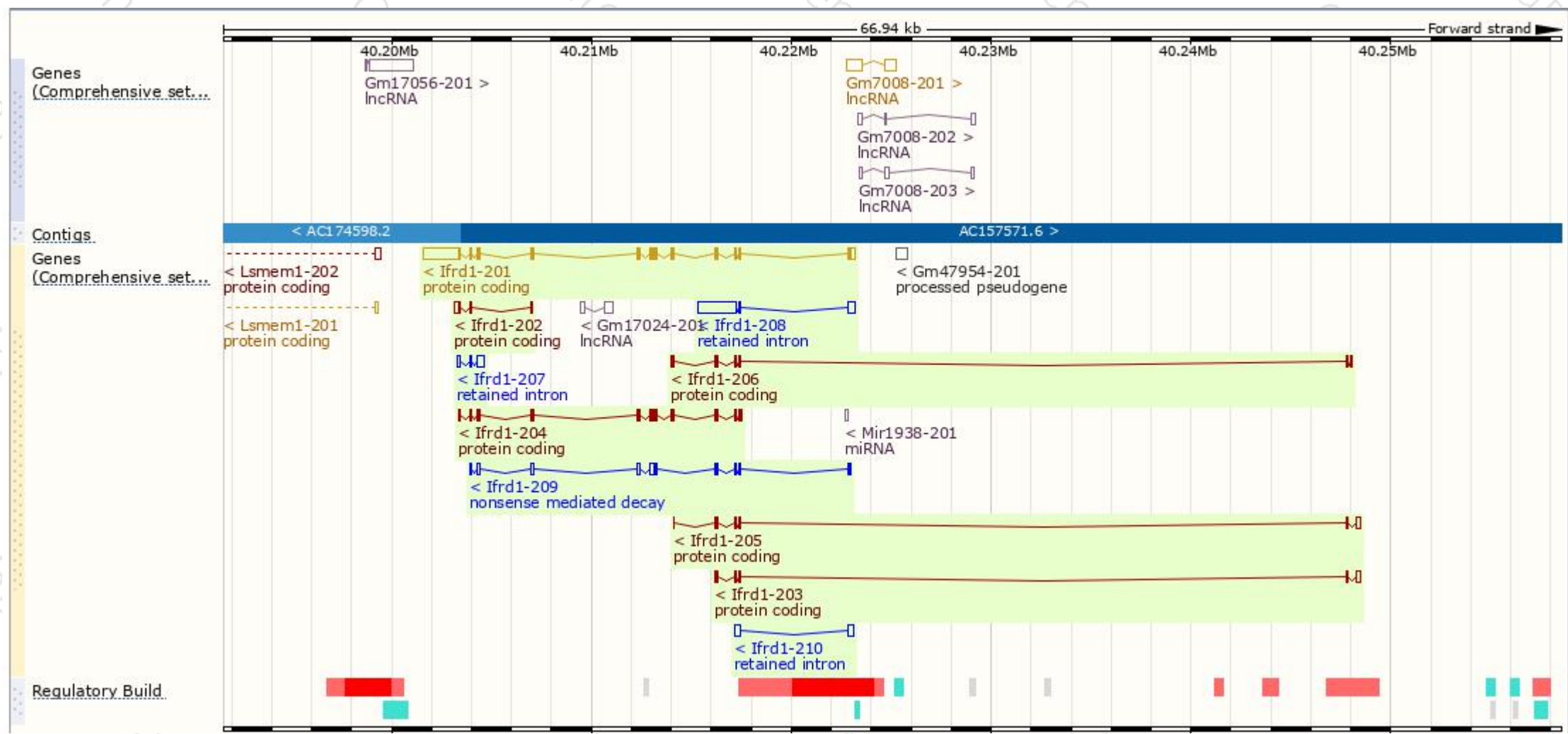
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ifrd1-201	ENSMUST00000001672.11	3378	449aa	Protein coding	CCDS25893	P19182	TSL:1 GENCODE basic APPRIS P2
Ifrd1-204	ENSMUST00000165027.8	1293	401aa	Protein coding	-	E9PVS0	TSL:5 GENCODE basic APPRIS ALT1
Ifrd1-206	ENSMUST00000169926.7	660	138aa	Protein coding	-	E9Q1E6	CDS 3' incomplete TSL:5
Ifrd1-203	ENSMUST00000164354.1	617	86aa	Protein coding	-	E9QA38	CDS 3' incomplete TSL:3
Ifrd1-205	ENSMUST00000169319.7	607	100aa	Protein coding	-	E9QA50	CDS 3' incomplete TSL:3
Ifrd1-202	ENSMUST00000164047.1	491	86aa	Protein coding	-	F6TBT6	CDS 5' incomplete TSL:3
Ifrd1-209	ENSMUST00000171530.7	1108	148aa	Nonsense mediated decay	-	E9Q949	TSL:5
Ifrd1-208	ENSMUST00000170752.1	2303	No protein	Retained intron	-	-	TSL:1
Ifrd1-210	ENSMUST00000171553.1	606	No protein	Retained intron	-	-	TSL:2
Ifrd1-207	ENSMUST00000170119.7	574	No protein	Retained intron	-	-	TSL:1

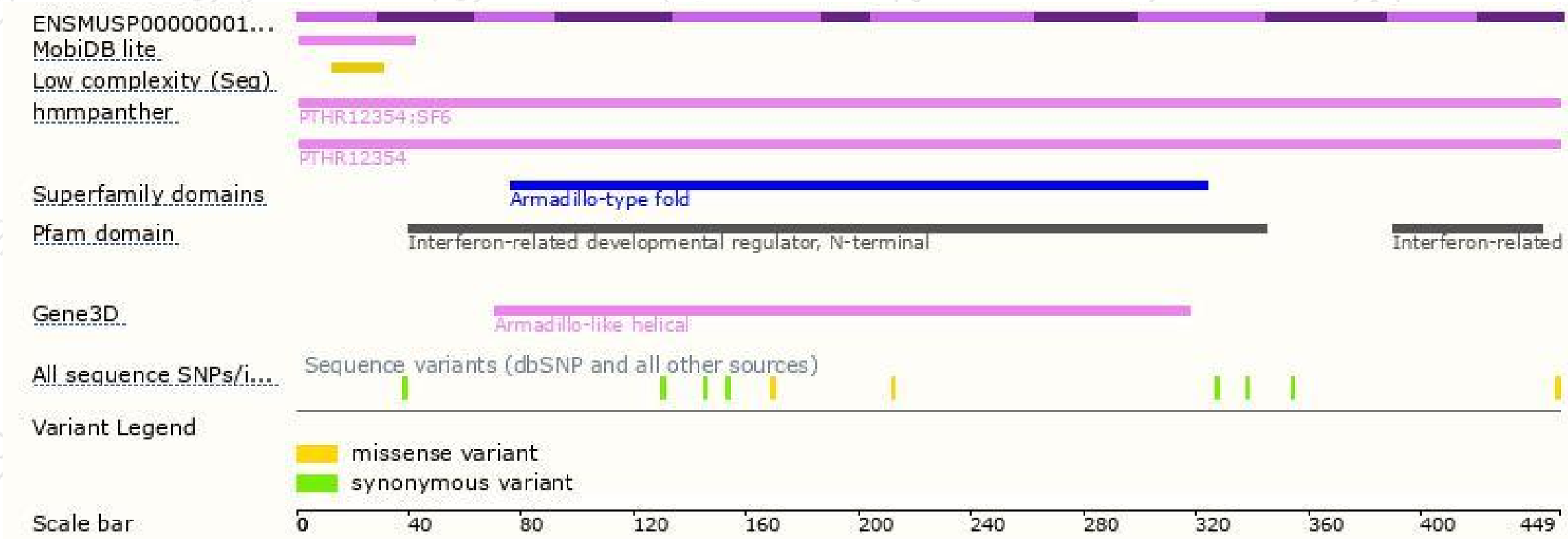
The strategy is based on the design of *Ifrd1-201* transcript,The transcription is shown below



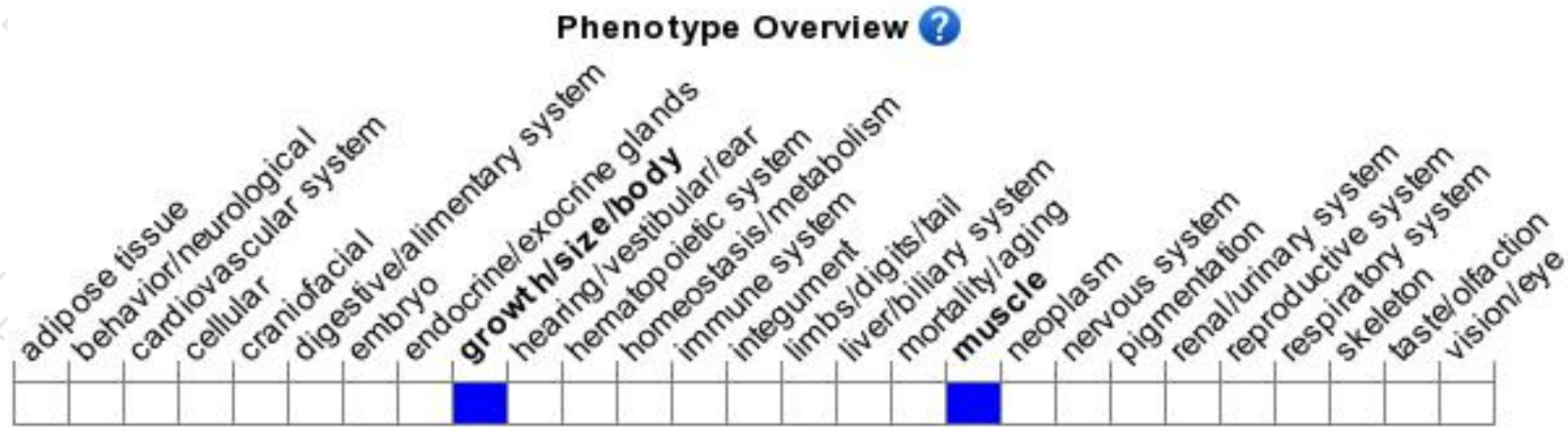
Genomic location distribution



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, Homozygous null mice display impaired muscle regeneration and myogenic differentiation and decreased body weight in older mice.

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

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