

Ifngr2 Cas9-CKO Strategy

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Project Overview

Project Name

Ifngr2

Project type

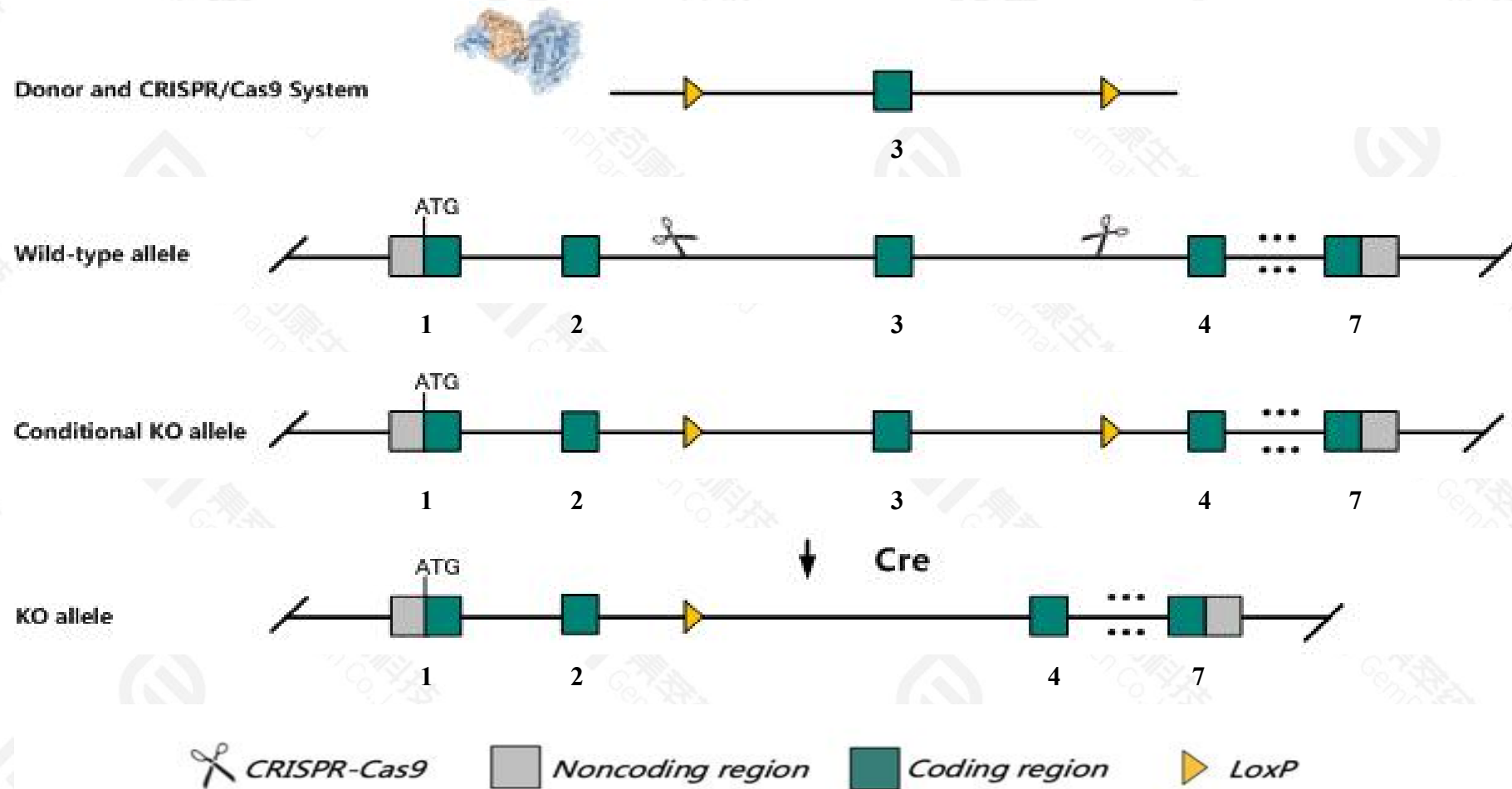
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Ifngr2* gene. The schematic diagram is as follows:



Technical routes

- The *Ifngr2* gene has 3 transcripts. According to the structure of *Ifngr2* gene, exon3 of *Ifngr2*-201(ENSMUST00000023687.9) transcript is recommended as the knockout region. The region contains 194bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Ifngr2* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, mice homozygous for disruptions in this gene develop normally.
- The *Ifngr2* gene is located on the Chr16. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Ifngr2 interferon gamma receptor 2 [Mus musculus (house mouse)]

Gene ID: 15980, updated on 13-Mar-2020

Summary

Official Symbol Ifngr2 provided by [MGI](#)

Official Full Name interferon gamma receptor 2 provided by [MGI](#)

Primary source [MGI:MGI:107654](#)

See related [Ensembl:ENSMUSG00000022965](#)

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 Ifgr2, Ifgt

Expression Broad expression in duodenum adult (RPKM 148.1), small intestine adult (RPKM 81.1) and 22 other tissues [See more](#)

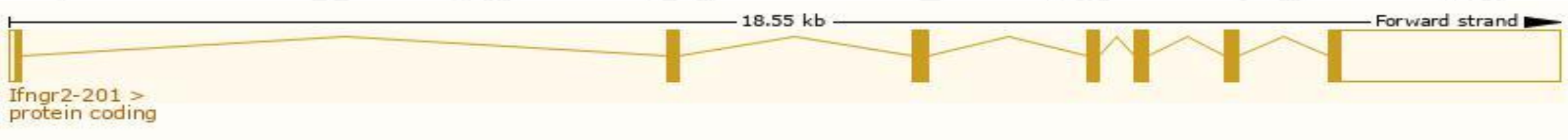
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

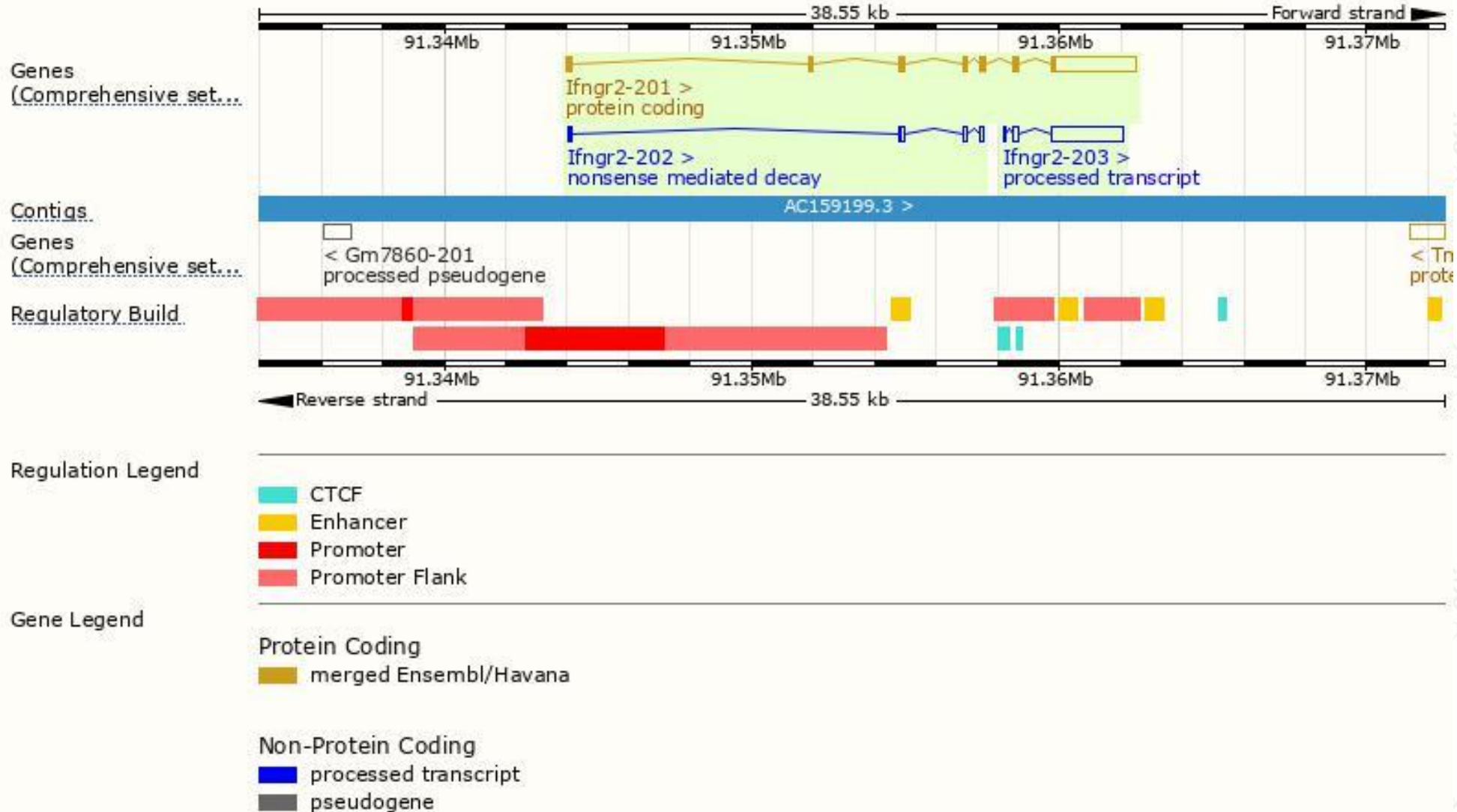
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ifngr2-201	ENSMUST0000023687.8	3708	332aa	Protein coding	CCDS28327	Q63953	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
Ifngr2-202	ENSMUST00000127644.1	534	46aa	Nonsense mediated decay	-	D6RIP6	TSL:5
Ifngr2-203	ENSMUST00000130404.1	2516	No protein	Processed transcript	-	-	TSL:3

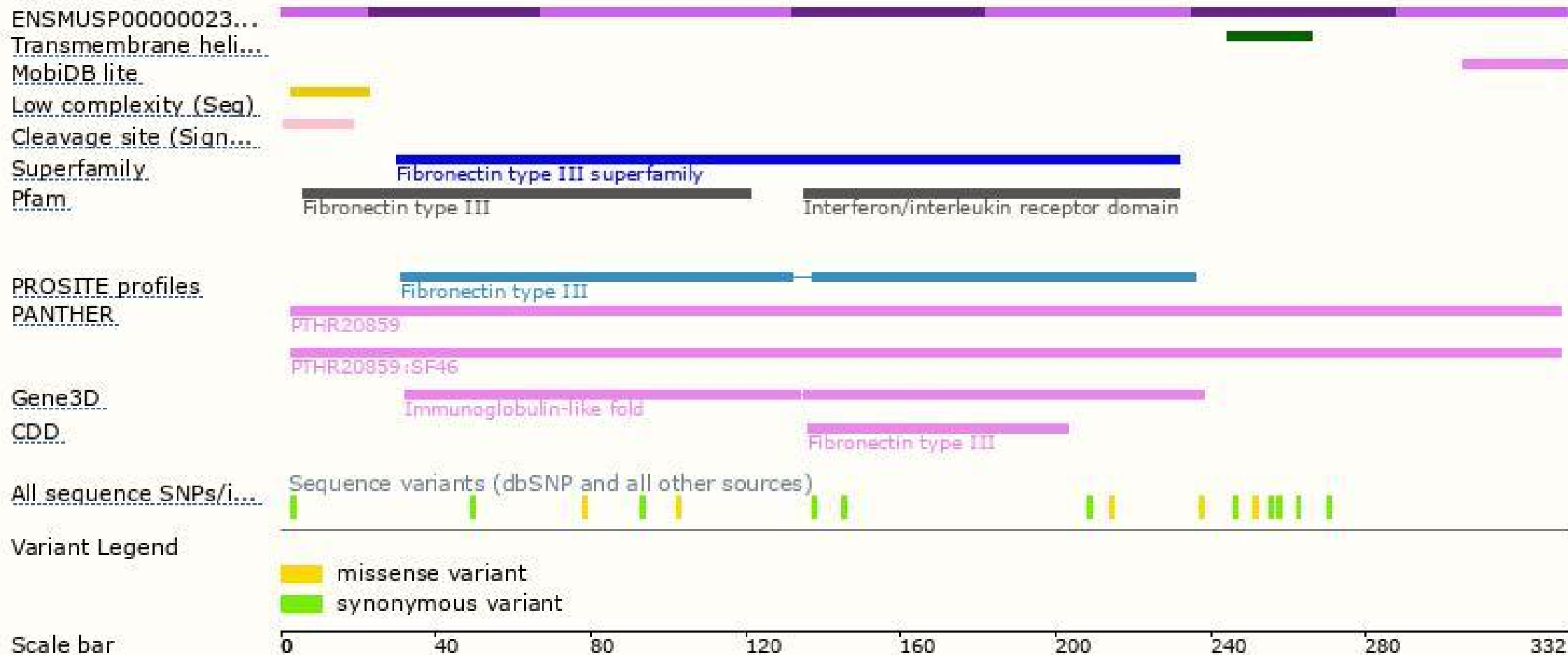
The strategy is based on the design of *Ifngr2-201* transcript,the transcription is shown below:



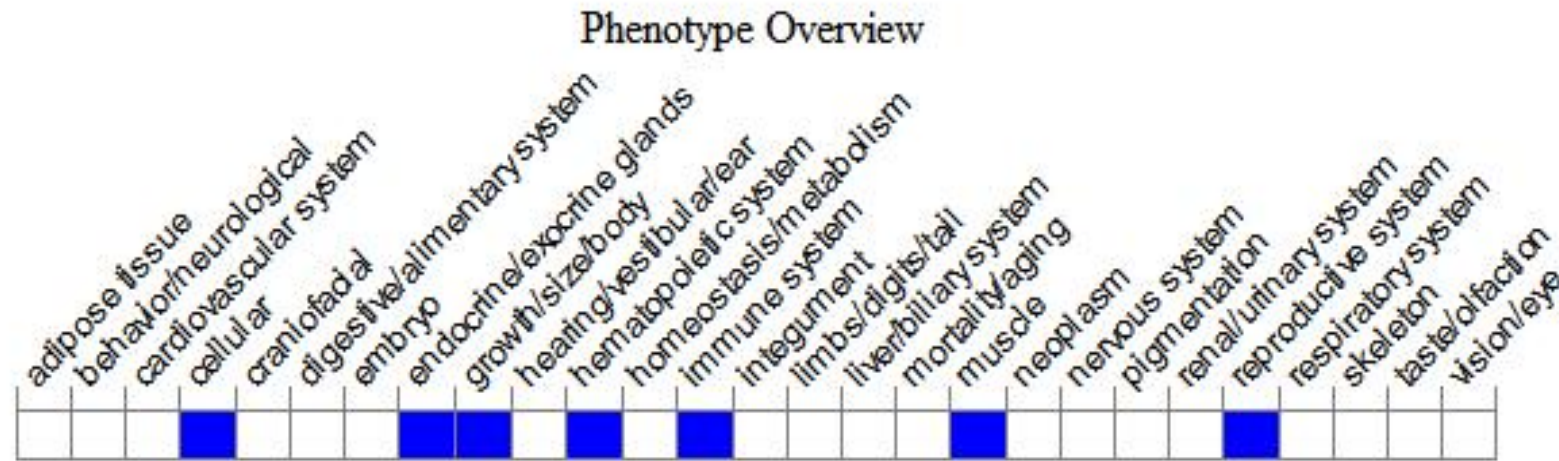
Genomic location distribution



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 disruptions in this gene develop normally.

[1] Ingram J P , Tursi S , Zhang T , et al. A Nonpyroptotic IFN- γ -Triggered Cell Death Mechanism in Nonphagocytic Cells Promotes Salmonella Clearance In Vivo[J]. Journal of Immunology, 2018:ji1701386.

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

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