

Ifnar1 Cas9-KO Strategy

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Project Overview



Project Name

Ifnar1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ifnar1* gene. The schematic diagram is as follows:



- The *Ifnar1* gene has 8 transcripts. According to the structure of *Ifnar1* gene, exon2-exon6 of *Ifnar1-201* (ENSMUST00000023689.10) transcript is recommended as the knockout region. The region contains 718bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ifnar1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit increased susceptibility to viral infection, elevated levels of myeloid lineage cells in the peripheral blood and bone marrow, and reduced immune response to immunostimulatory DNA.
- The *Ifnar1* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Ifnar1 interferon (alpha and beta) receptor 1 [Mus musculus (house mouse)]

Gene ID: 15975, updated on 9-Apr-2019

Summary



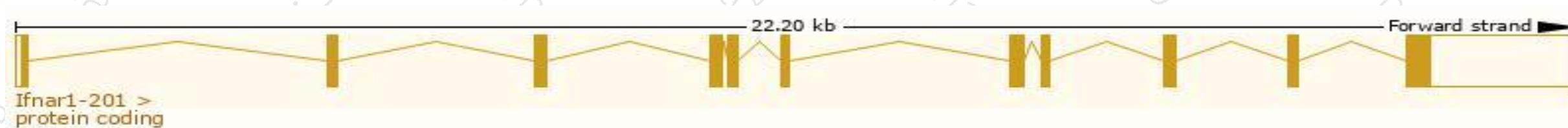
Official Symbol	Ifnar1 provided by MGI
Official Full Name	interferon (alpha and beta) receptor 1 provided by MGI
Primary source	MGI:MGI:107658
See related	Ensembl:ENSMUSG00000022967
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ifar, Ifnar, Ifrc, Infar
Expression	Ubiquitous expression in limb E14.5 (RPKM 8.7), CNS E18 (RPKM 8.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

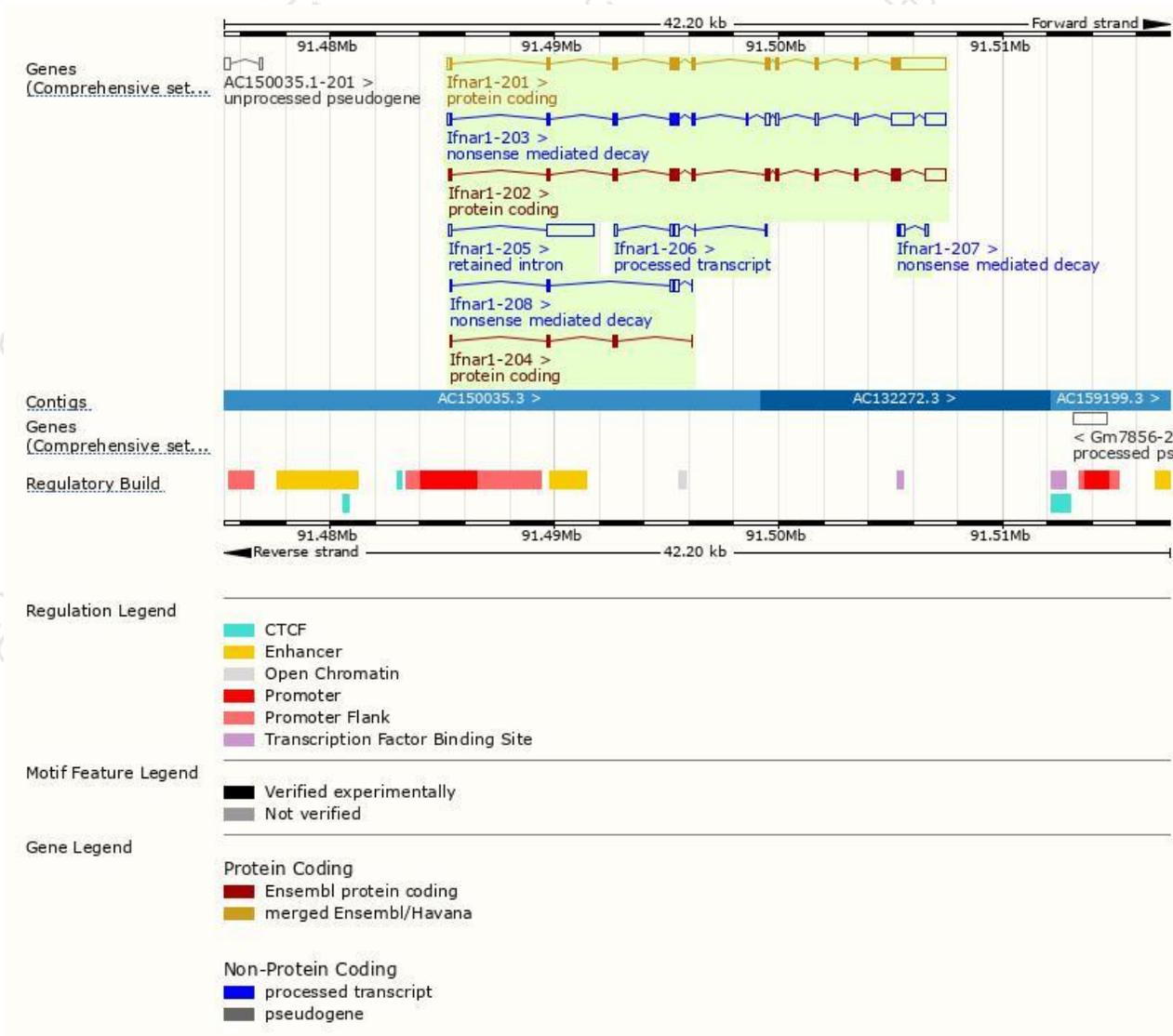
The gene has 8 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ifnar1-201	ENSMUST00000023689.10	3909	590aa	Protein coding	CCDS28326	P33896	TSL:1 GENCODE basic APPRIS P1
Ifnar1-202	ENSMUST000000117748.7	2771	590aa	Protein coding	CCDS28326	P33896	TSL:1 GENCODE basic APPRIS P1
Ifnar1-204	ENSMUST000000129878.1	415	135aa	Protein coding	-	E9PWM1	CDS 3' incomplete TSL:5
Ifnar1-203	ENSMUST000000123196.8	3433	283aa	Nonsense mediated decay	-	A0A384DVB8	TSL:5
Ifnar1-208	ENSMUST000000232509.1	552	77aa	Nonsense mediated decay	-	A0A338P6T9	-
Ifnar1-207	ENSMUST000000232453.1	468	35aa	Nonsense mediated decay	-	A0A338P6X7	CDS 5' incomplete
Ifnar1-205	ENSMUST000000145008.1	2234	No protein	Retained intron	-	-	TSL:2
Ifnar1-206	ENSMUST000000231604.1	543	No protein	lncRNA	-	-	-

The strategy is based on the design of *Ifnar1-201* transcript, The transcription is shown below



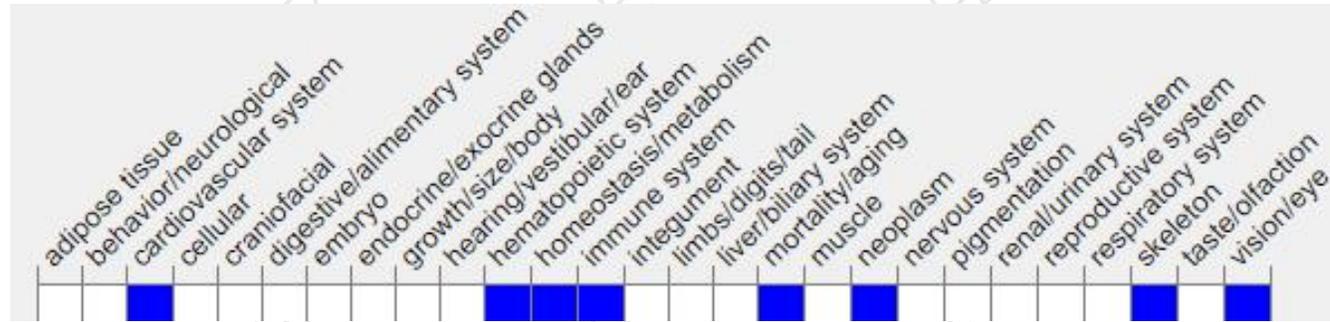
Genomic location distribution



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 exhibit increased susceptibility to viral infection, elevated levels of myeloid lineage cells in the peripheral blood and bone marrow, and reduced immune response to immunostimulatory DNA.

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

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