

Irf7 Cas9-CKO Strategy

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Project Overview

Project Name

Irf7

Project type

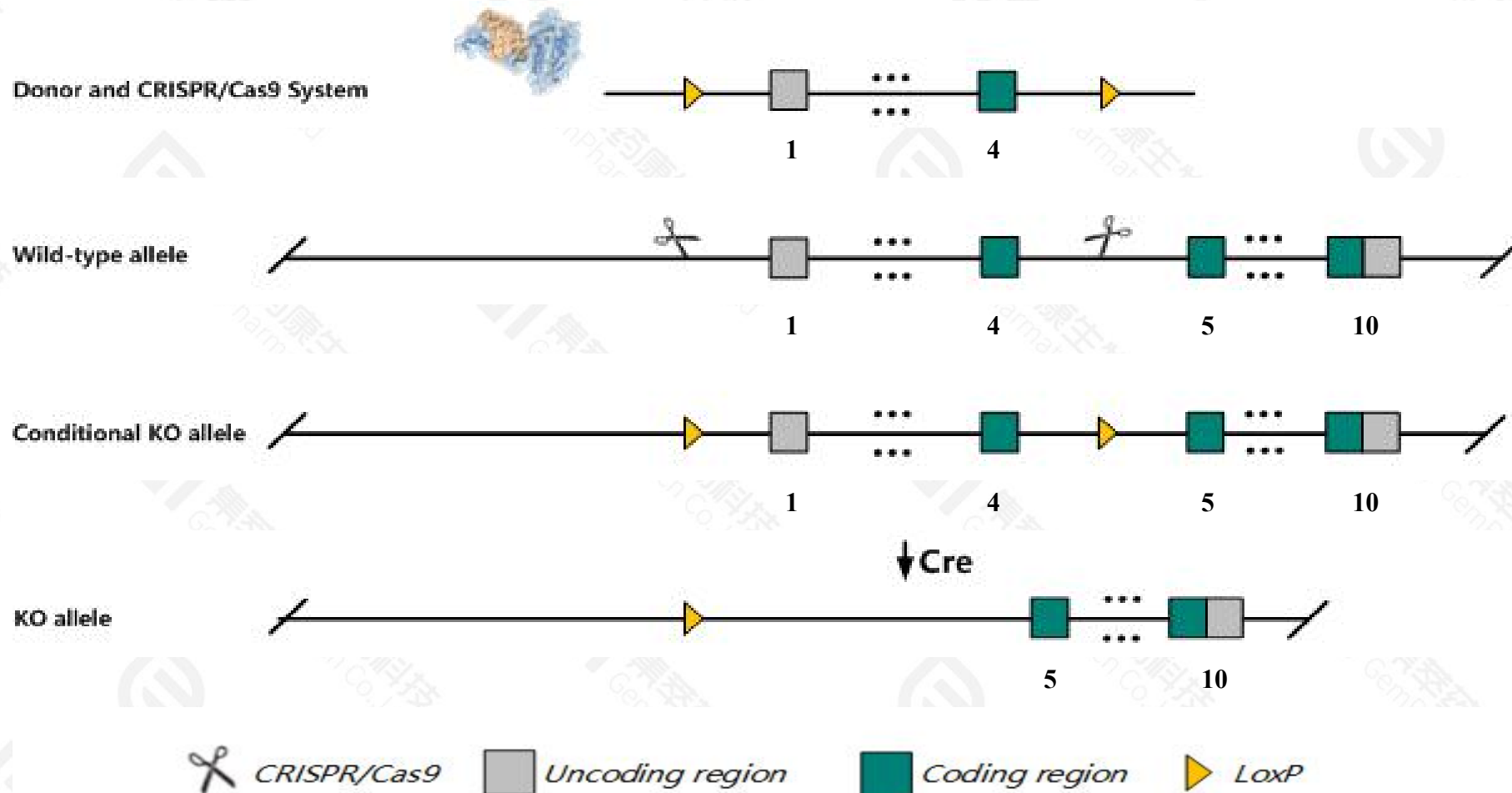
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Irf7* gene. The schematic diagram is as follows:



- The *Irf7* gene has 13 transcripts. According to the structure of *Irf7* gene, exon1-exon4 of *Irf7*-203(ENSMUST00000106023.8) transcript is recommended as the knockout region. The region contains 394bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Irf7* 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, homozygous null mice are more vulnerable to viral infection and exhibit decreased serum interferon levels in response to viral infection.
- The Intron4 is only 291bp, loxp insertion may affect mRNA splicing, The target gene overlaps with Phrf1.
- The *Irf7* gene is located on the Chr7. 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)

Irf7 interferon regulatory factor 7 [Mus musculus (house mouse)]

Gene ID: 54123, updated on 13-Mar-2020

Summary



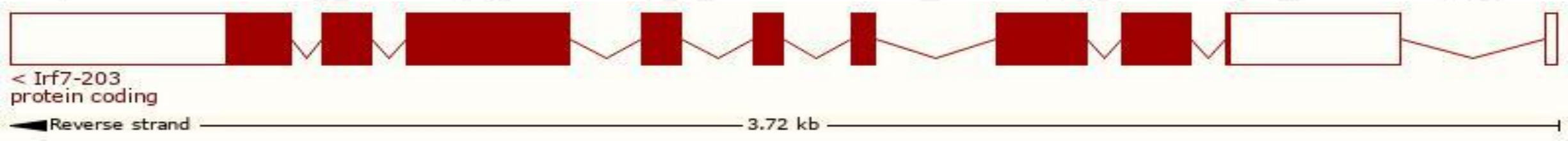
Official Symbol	Irf7 provided by MGI
Official Full Name	interferon regulatory factor 7 provided by MGI
Primary source	MGI:MGI:1859212
See related	Ensembl:ENSMUSG00000025498
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Broad expression in duodenum adult (RPKM 108.3), small intestine adult (RPKM 93.2) and 18 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

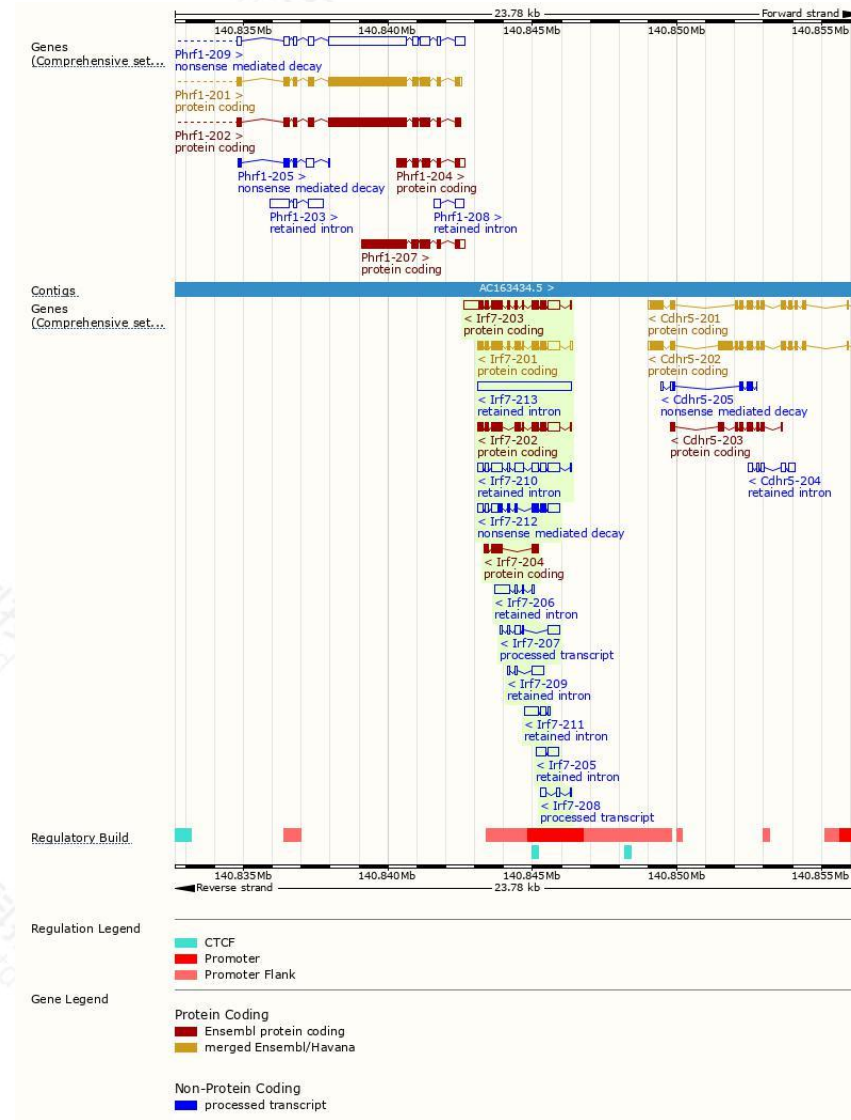
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Irf7-203	ENSMUST00000106023.7	2237	425aa	Protein coding	CCDS57594	D3Z4U9	TSL:1 GENCODE basic APPRIS ALT2
Irf7-201	ENSMUST00000026571.10	1916	457aa	Protein coding	CCDS22005	P70434 Q542T3	TSL:1 GENCODE basic APPRIS P3
Irf7-202	ENSMUST00000097952.8	1764	426aa	Protein coding	CCDS57595	Q3TW14	TSL:1 GENCODE basic APPRIS ALT2
Irf7-204	ENSMUST00000123525.1	751	251aa	Protein coding	-	F6TQ89	CDS 5' and 3' incomplete TSL:5
Irf7-212	ENSMUST00000209899.1	1622	237aa	Nonsense mediated decay	-	A0A1B0GRH7	TSL:1
Irf7-207	ENSMUST00000131399.7	813	No protein	Processed transcript	-	-	TSL:5
Irf7-208	ENSMUST00000146373.1	332	No protein	Processed transcript	-	-	TSL:3
Irf7-213	ENSMUST00000210506.1	3240	No protein	Retained intron	-	-	TSL:NA
Irf7-210	ENSMUST00000155744.7	1922	No protein	Retained intron	-	-	TSL:2
Irf7-211	ENSMUST00000156938.1	740	No protein	Retained intron	-	-	TSL:2
Irf7-206	ENSMUST00000127223.7	708	No protein	Retained intron	-	-	TSL:3
Irf7-205	ENSMUST00000127161.1	687	No protein	Retained intron	-	-	TSL:2
Irf7-209	ENSMUST00000148414.1	559	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Irf7-203* transcript,the transcription is shown below:



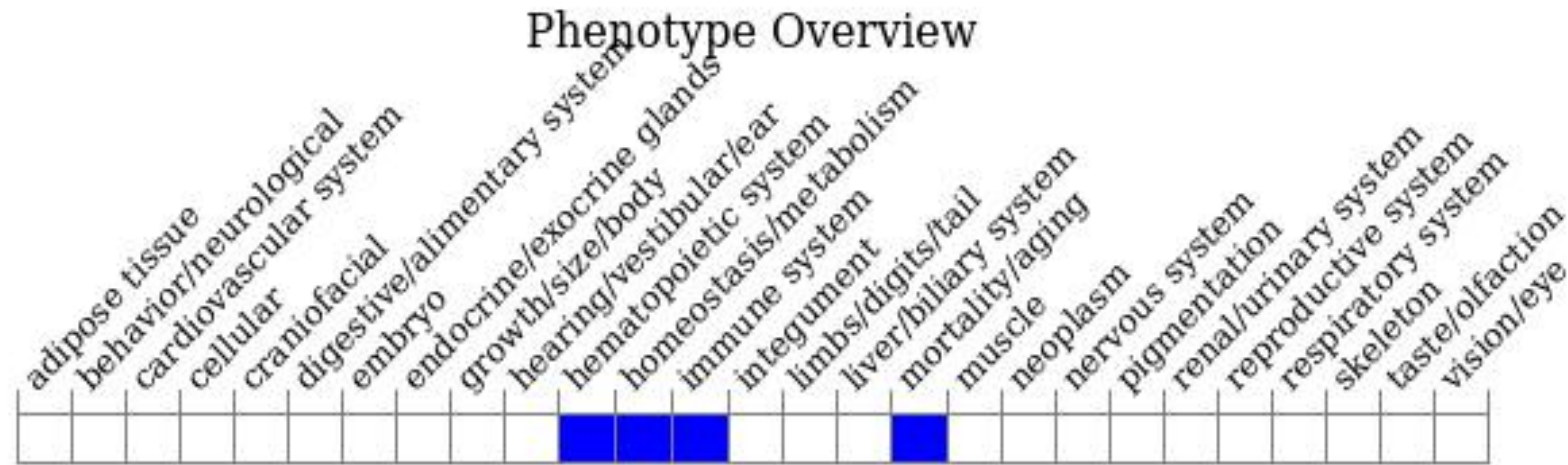
Genomic location distribution



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 are more vulnerable to viral infection and exhibit decreased serum interferon levels in response to viral infection.

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