

Irf4 Cas9-KO Strategy

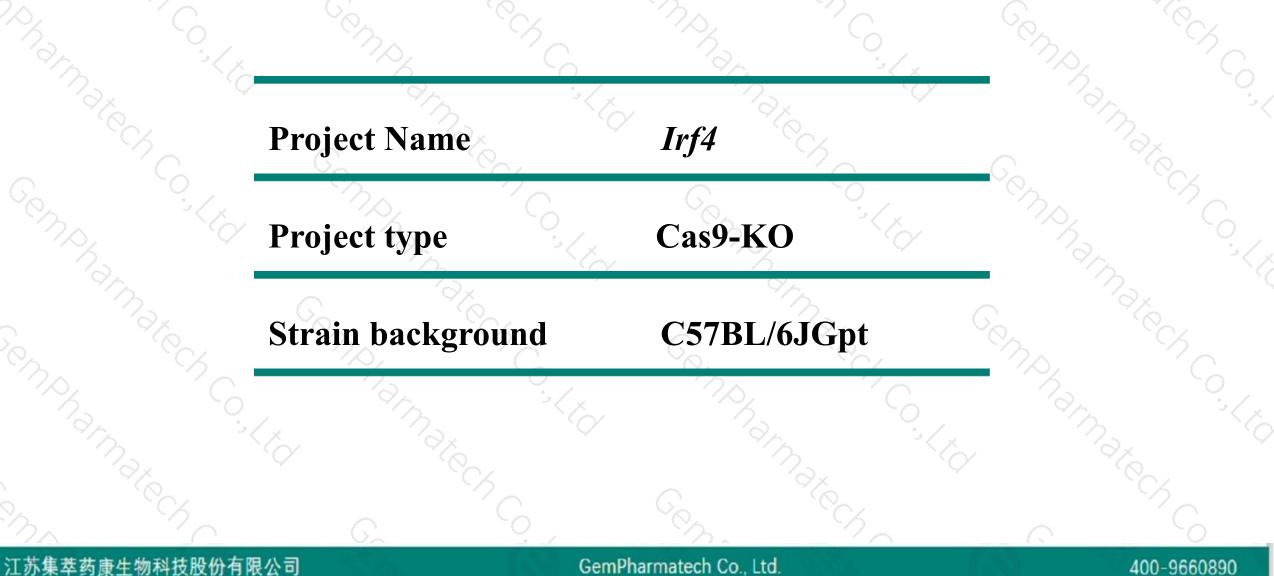
Designer: Design Date:

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Daohua Xu 2019-7-18

Project Overview



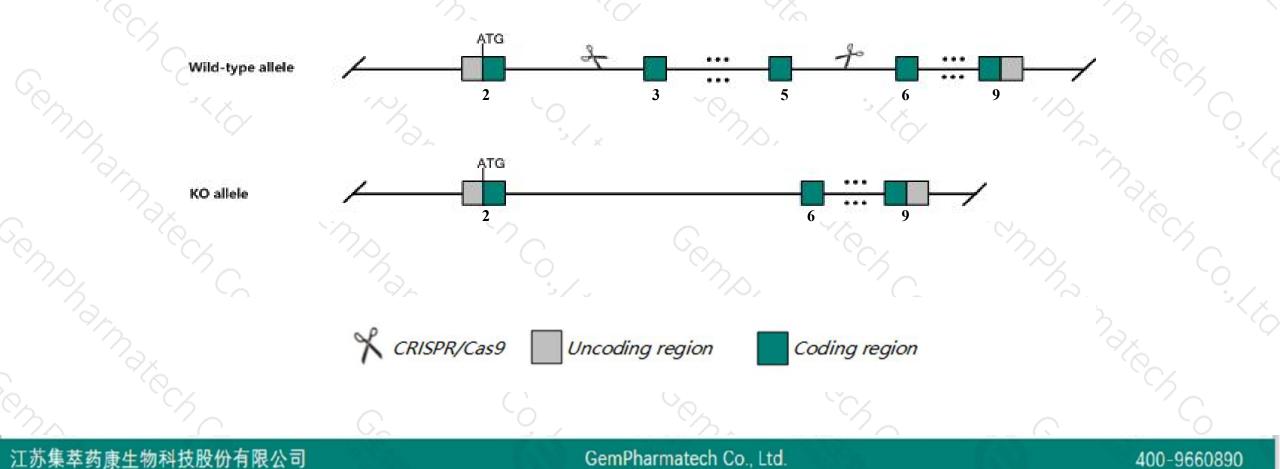


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Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Irf4* gene. The schematic diagram is as follows:





- The Irf4 gene has 3 transcripts. According to the structure of Irf4 gene, exon3-exon5 of Irf4-201 (ENSMUST0000021784.9) transcript is recommended as the knockout region. The region contains 421bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Irf4 gene. The brief process is as follows: CRISPR/Cas9 system w



- According to the existing MGI data, Mice homozygous for disruptions in this gene display immune system abnormalities involving development of both T and B cells and affecting susceptibility to both bacterial and viral infections as well as impaired thermogenic gene expression and energy expenditure.
- The Irf4 gene is located on the Chr13. 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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Irf4 interferon regulatory factor 4 [Mus musculus (house mouse)]

Gene ID: 16364, updated on 24-Feb-2019

Summary

Official Symbol	Irf4 provided by MGI
Official Full Name	interferon regulatory factor 4 provided by MGI
Primary source	MGI:MGI:1096873
See related	Ensembl:ENSMUSG0000021356
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	AI385587, IRF-4, LSIRF, NF-EM5, Spip
Expression	Biased expression in spleen adult (RPKM 8.0), mammary gland adult (RPKM 5.2) and 12 other tissues See more
Orthologs	human all

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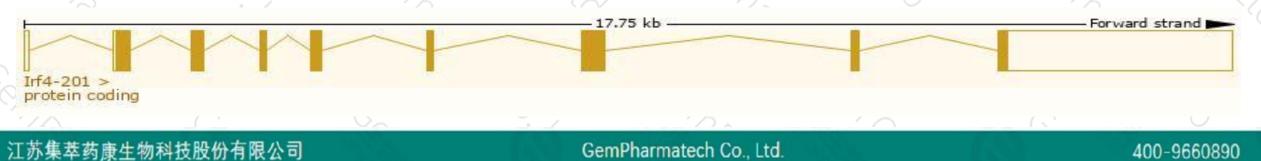
Transcript information (Ensembl)



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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
lrf4-201	ENSMUST00000021784.9	4764	<u>450aa</u>	Protein coding	CCDS26419	Q5SUZ4 Q64287	TSL:1 GENCODE basic APPRIS P3
lrf4-202	ENSMUST00000110307.2	4761	<u>449aa</u>	Protein coding	CCDS84017	Q5SUZ5 Q64287	TSL:1 GENCODE basic APPRIS ALT1
lrf4-203	ENSMUST00000222125.1	360	<u>63aa</u>	Protein coding	(12)	A0A1Y7VIT1	CDS 3' incomplete TSL:2

The strategy is based on the design of *Irf4-201* transcript, The transcription is shown below



Genomic location distribution



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Protein domain

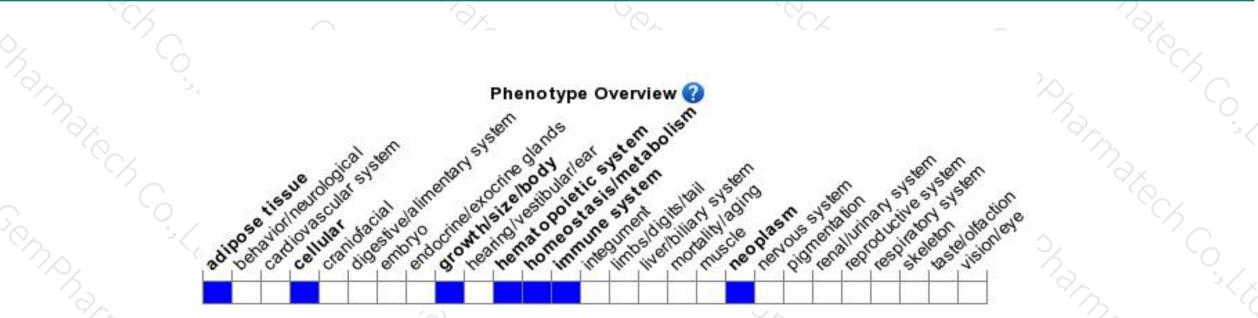
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Mouse phenotype description(MGI)





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 display immune system abnormalities involving development of both T and B cells and affecting susceptibility to both bacterial and viral infections as well as impaired thermogenic gene expression and energy expenditure.

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If you have any questions, you are welcome to inquire. Tel: 400-9660890



