

Nfatc2 Cas9-KO Strategy

Designer:	Daohua Xu
Reviewer:	Huimin Su
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Project Overview

Project Name

Nfatc2

Project type

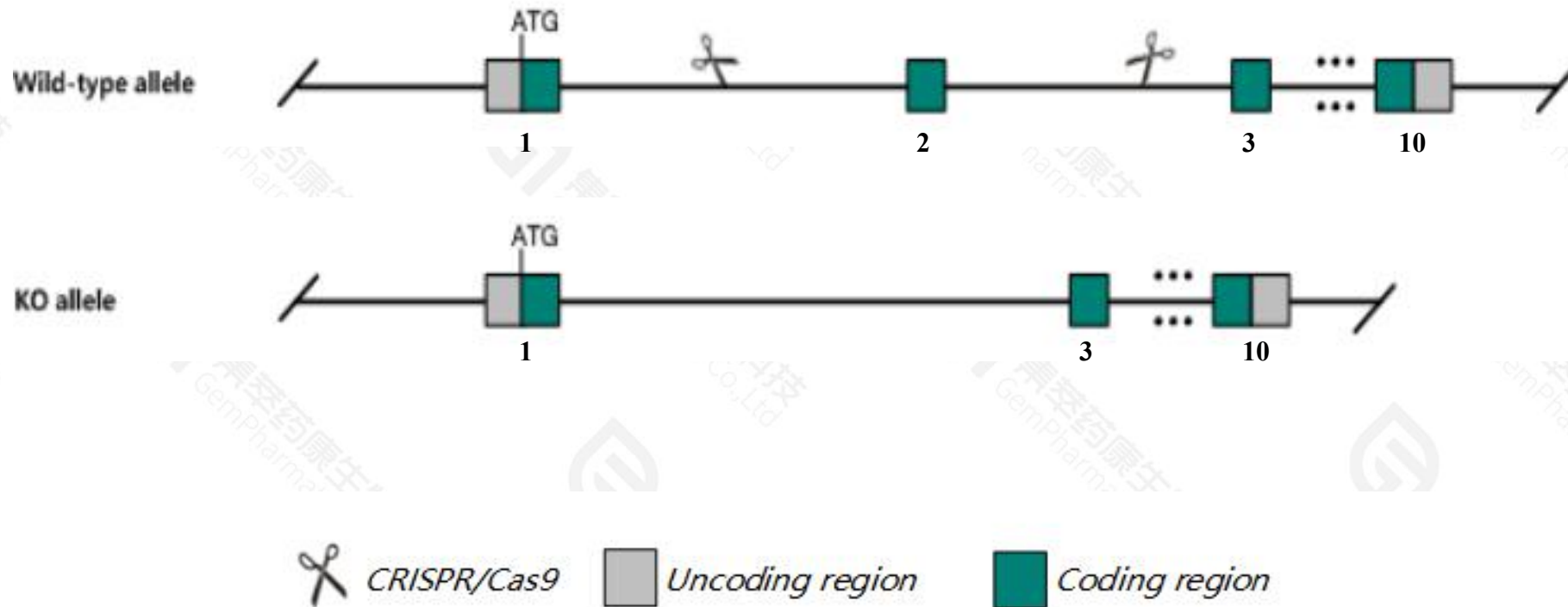
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nfatc2* gene. The schematic diagram is as follows:



- The *Nfatc2* gene has 9 transcripts. According to the structure of *Nfatc2* gene, exon2 of *Nfatc2*-202(ENSMUST00000074618.10) transcript is recommended as the knockout region. The region contains 1036bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nfatc2* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mutations in this locus cause altered immune system function such as decreased cytokine production by mast cells, increased Th2 responses after infection with a parasite but decreased Th1 responses after myobacterial infection, retarded thymic involution and massive germinal center formation.
- The *Nfatc2* gene is located on the Chr2. 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)

Nfatc2 nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 [Mus musculus (house mouse)]

Gene ID: 18019, updated on 20-Mar-2020

Summary

Official Symbol Nfatc2 provided by [MGI](#)

Official Full Name nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 2 provided by [MGI](#)

Primary source [MGI:MGI:102463](#)

See related [Ensembl:ENSMUSG000000027544](#)

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 AI607462, NF-ATc2, NF-ATp, NFAT1, NFAT1-D, Nfatp

Expression Broad expression in spleen adult (RPKM 4.4), thymus adult (RPKM 3.6) and 24 other tissues [See more](#)

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

Transcript information (Ensembl)

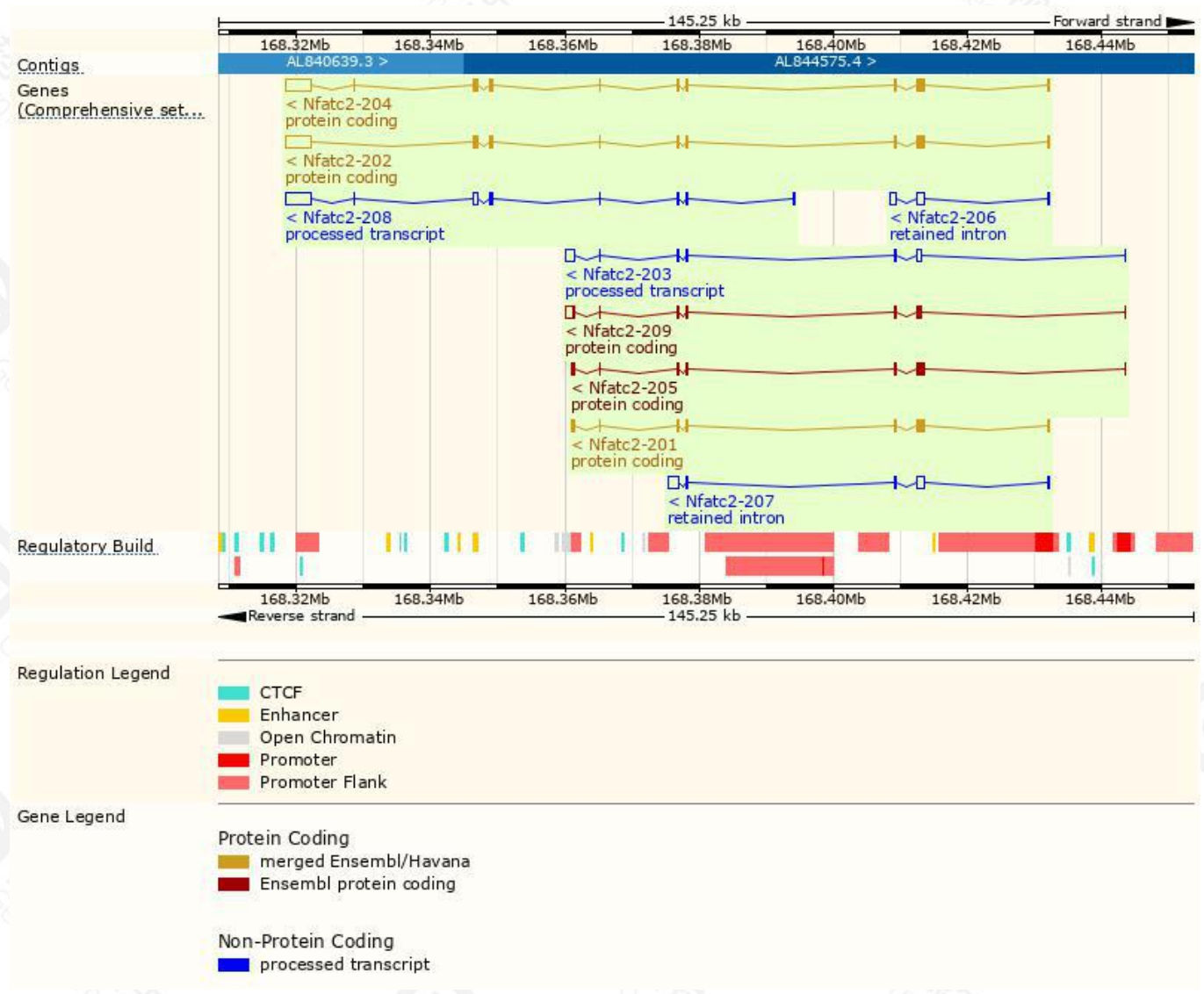
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nfatc2-204	ENSMUST00000109184.7	6828	923aa	Protein coding	CCDS50803	B5B2P7 Q60591	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 ALT2
Nfatc2-202	ENSMUST00000074618.9	6637	927aa	Protein coding	CCDS17112	Q60591	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 P3
Nfatc2-209	ENSMUST00000171689.7	2742	452aa	Protein coding	CCDS17114	Q8C443	TSL:1 GENCODE basic
Nfatc2-205	ENSMUST00000137451.1	2369	653aa	Protein coding	CCDS71201	A2AQC8	TSL:1 GENCODE basic
Nfatc2-201	ENSMUST00000029057.12	2310	673aa	Protein coding	CCDS17113	B5B2R5	TSL:1 GENCODE basic
Nfatc2-208	ENSMUST00000151292.7	5399	No protein	Processed transcript	-	-	TSL:1
Nfatc2-203	ENSMUST00000099067.9	2727	No protein	Processed transcript	-	-	TSL:1
Nfatc2-207	ENSMUST00000140137.7	3309	No protein	Retained intron	-	-	TSL:1
Nfatc2-206	ENSMUST00000138546.1	2174	No protein	Retained intron	-	-	TSL:1

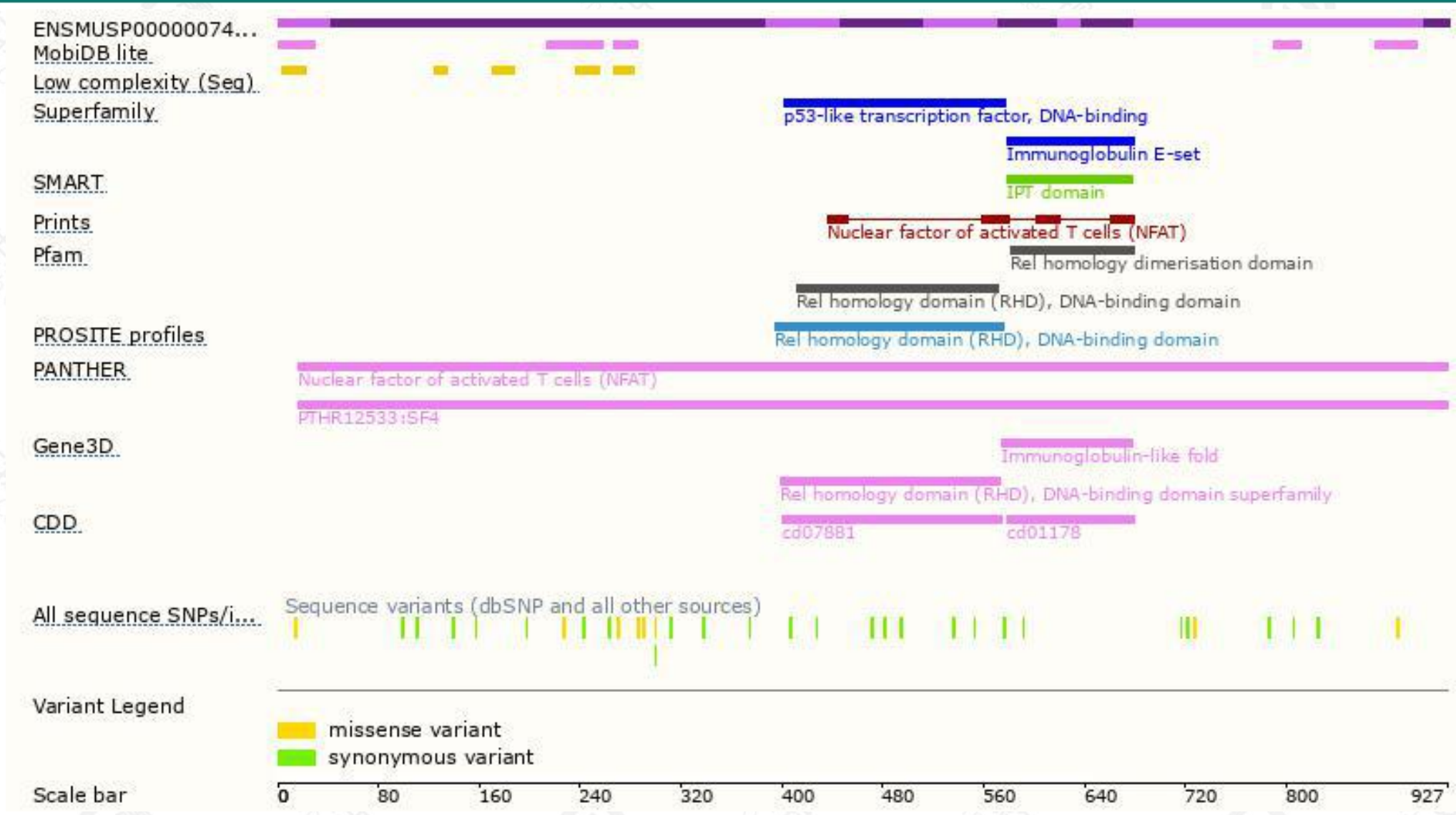
The strategy is based on the design of *Nfatc2-202* transcript,the transcription is shown below:



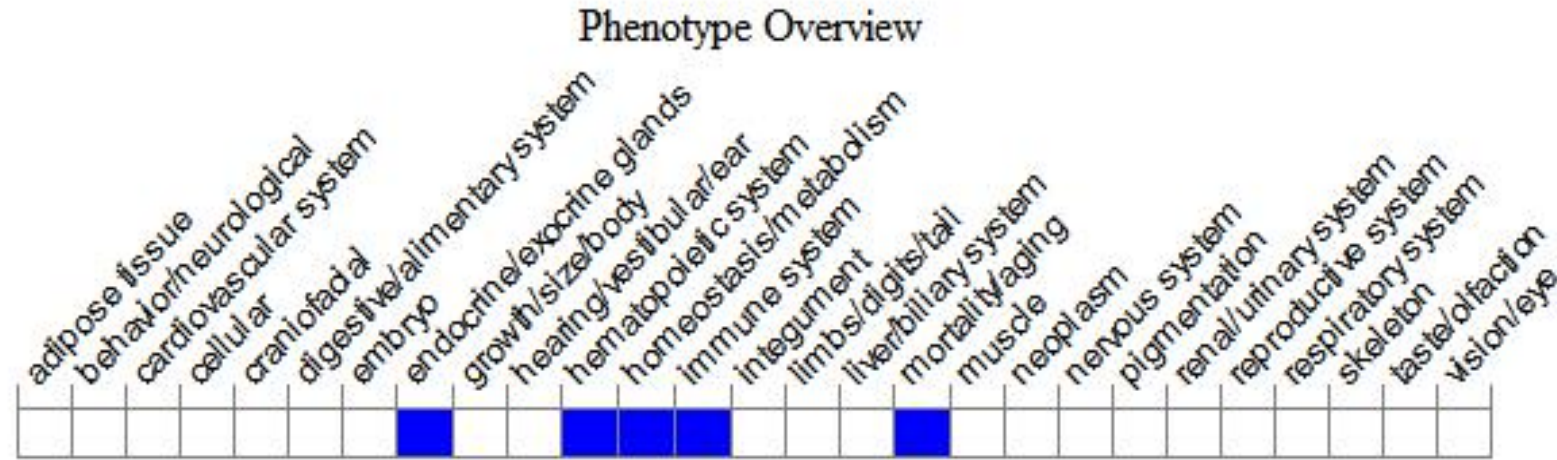
Genomic location distribution



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, mutations in this locus cause altered immune system function such as decreased cytokine production by mast cells, increased Th2 responses after infection with a parasite but decreased Th1 responses after myobacterial infection, retarded thymic involution and massive germinal center formation.

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

