Nfatc1 Cas9-KO Strategy

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Project Overview

Project Name	***Nfatc1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nfatc1* gene. The schematic diagram is as follows:

Technical routes

➢ The *Nfatc1* gene has 7 transcripts. According to the structure of *Nfatc1* gene, exon3 of *Nfatc1-203* (ENSMUST00000167977.7) transcript is recommended as the knockout region.The region contains 160bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Nfatc1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Homozygous mutation of this gene results in lethality throughout fetal growth and development due to cardiac failure. Mutants exhibit blood circulation, cardiac valve and ventricular septal abnormalities, edema, abdominal hemorrhage, and semilunar valveregurgitation.

- The *Nfatc1* gene is located on the Chr18. 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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Nfatc1 nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 1 [Mus musculus (house mouse)]

Gene ID: 18018, updated on 19-Mar-2019

Summary

Official Symbol	Nfatc1 provided by MGI
Official Full Name	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 1 provided by MGI
Primary source	MGI:MGI:102469
See related	Ensembl:ENSMUSG00000033016
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	2210017P03Rik, AI449492, AV076380, NF-ATc, NFAT2, NFATc, Nfatcb
Expression	Broad expression in spleen adult (RPKM 23.0), thymus adult (RPKM 14.6) and 15 other tissues See more
Orthologs	human all

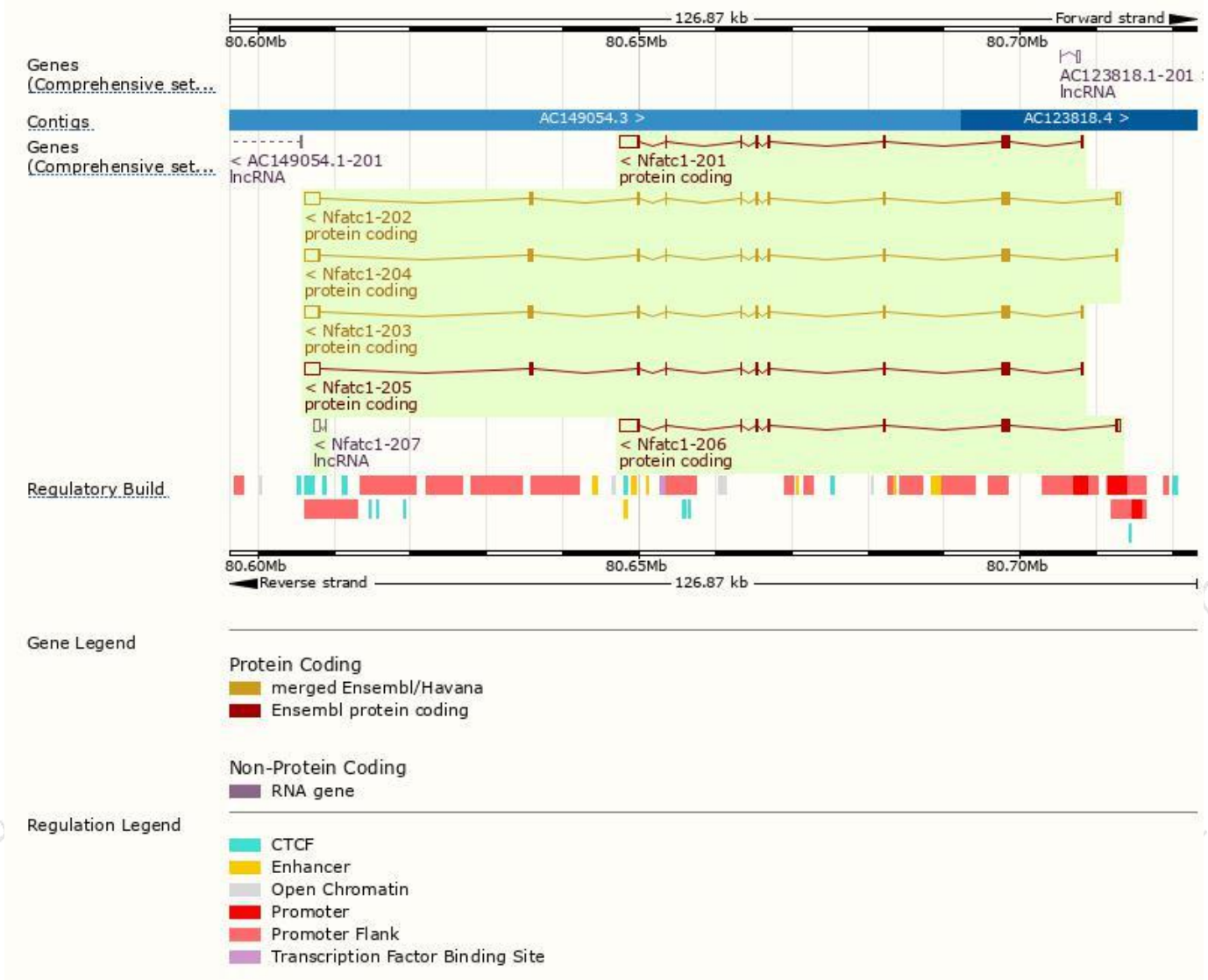
Transcript information（Ensembl）

The gene has 7 transcripts,all transcripts are shown below:

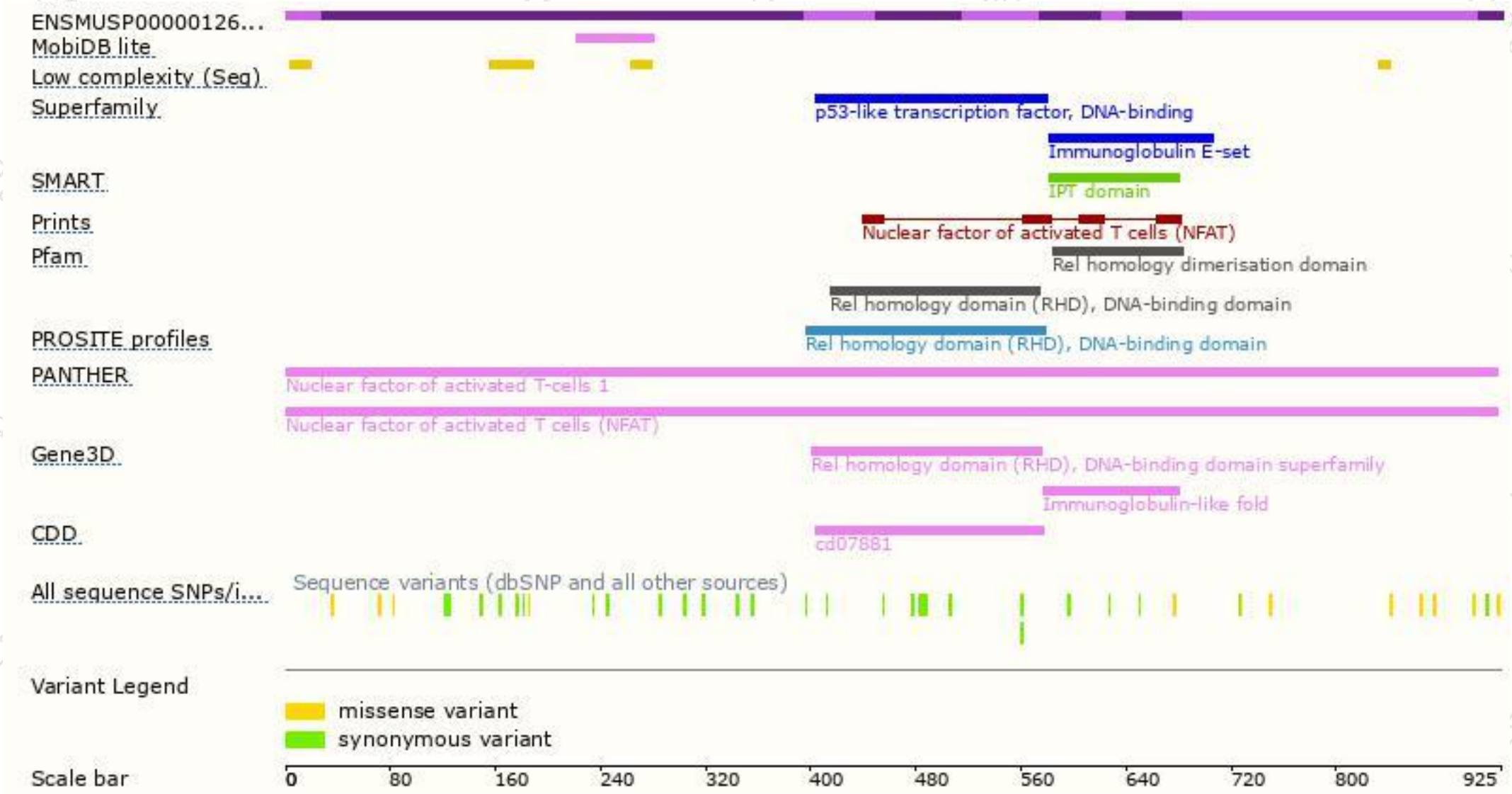
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nfatc1-203	ENSMUST00000167977.7	4604	925aa	Protein coding	CCDS50335	B5B2N7	TSL:1 GENCODE basic APPRIS ALT2
Nfatc1-202	ENSMUST00000078049.11	4594	827aa	Protein coding	CCDS37873	Q6P7T9	TSL:1 GENCODE basic APPRIS ALT2
Nfatc1-204	ENSMUST00000170905.8	4591	939aa	Protein coding	CCDS50336	B5B2N2	TSL:1 GENCODE basic APPRIS ALT2
Nfatc1-201	ENSMUST00000035800.7	4505	703aa	Protein coding	CCDS29369	Q9DBQ6	TSL:1 GENCODE basic APPRIS P3
Nfatc1-206	ENSMUST00000236711.1	4797	717aa	Protein coding	-	B5B2N5	GENCODE basic APPRIS ALT2
Nfatc1-205	ENSMUST00000236310.1	4315	813aa	Protein coding	-	B5B2N4	GENCODE basic APPRIS ALT2
Nfatc1-207	ENSMUST00000237776.1	672	No protein	lncRNA	-	-	

The strategy is based on the design of *Nfatc1-203* transcript,The transcription is shown below

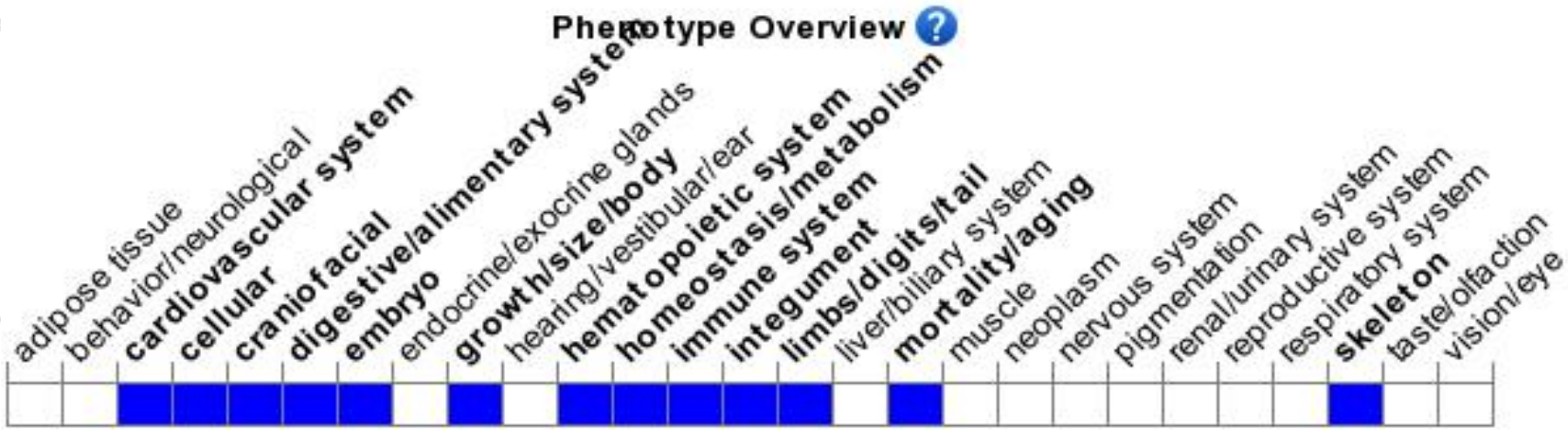
Genomic location distribution



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/).

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

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