

Nfatc4 Cas9-KO Strategy

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Design Date:

2019/10/12

Project Overview

Project Name

Nfatc4

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nfatc4* gene. The schematic diagram is as follows:



- The *Nfatc4* gene has 11 transcripts. According to the structure of *Nfatc4* gene, exon1-exon6 of *Nfatc4-201* (ENSMUST00000024179.5) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nfatc4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele are viable and overtly normal and exhibit normal embryonic heart morphology as well as normal pathophysiologic cardiac hypertrophy in response to angiotensin II infusion or aortic banding.
- The *Nfatc4* gene is located on the Chr14. 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)

Nfatc4 nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 4 [*Mus musculus* (house mouse)]

Gene ID: 73181, updated on 12-Aug-2019

Summary

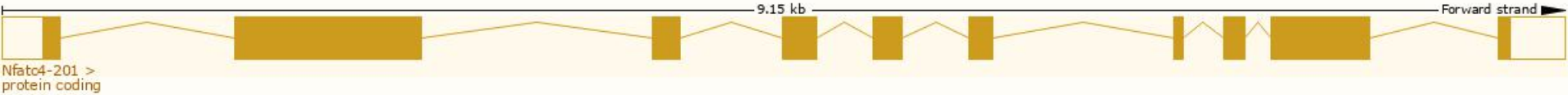
Official Symbol	Nfatc4 provided by MGI
Official Full Name	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 4 provided by MGI
Primary source	MGI:MGI:1920431
See related	Ensembl:ENSMUSG00000023411
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Nfat3; AW107667; AW546455; 3110041H08Rik
Expression	Biased expression in limb E14.5 (RPKM 41.5), CNS E11.5 (RPKM 14.6) and 14 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

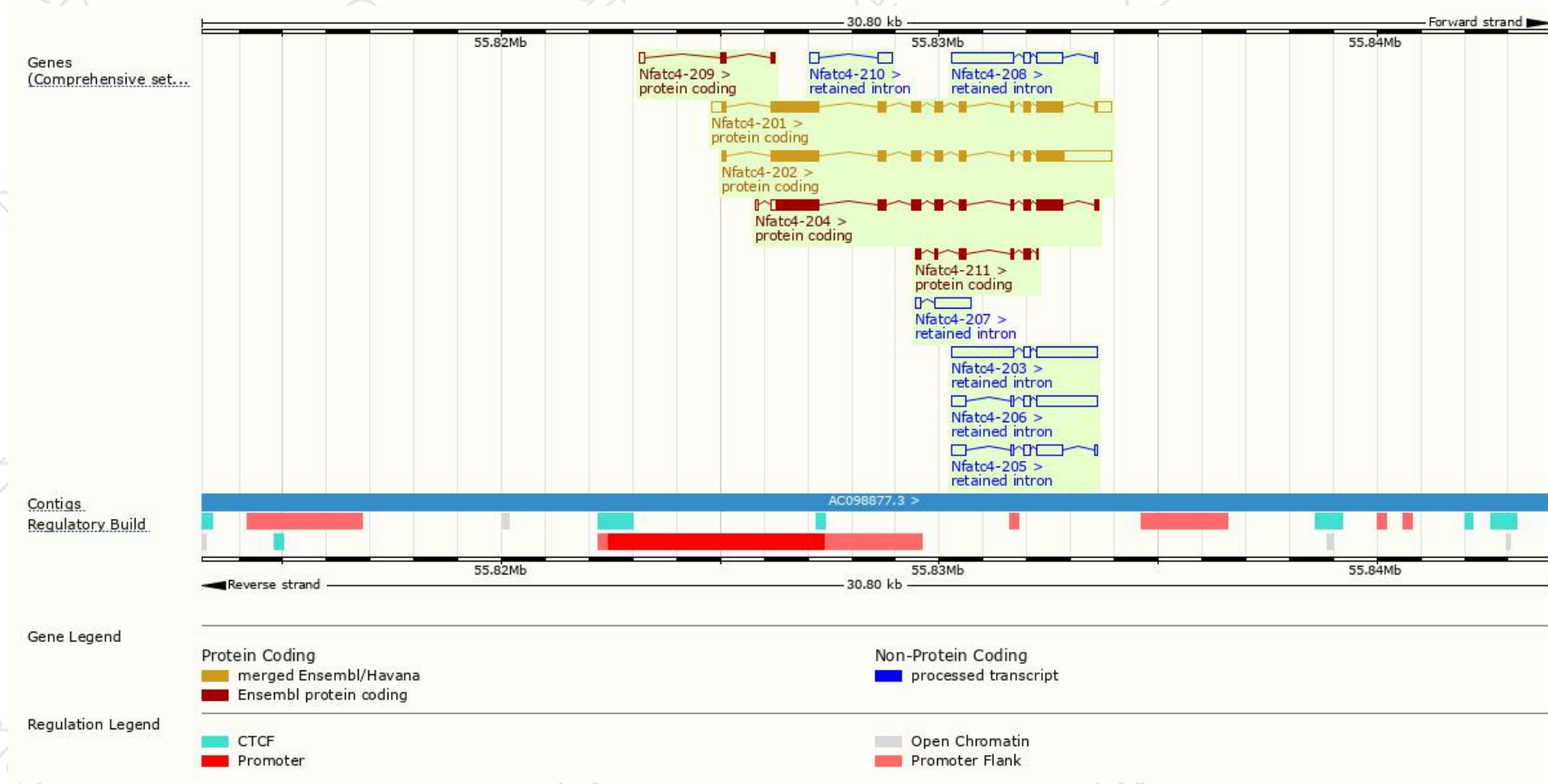
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nfatc4-202	ENSMUST00000172271.8	3775	890aa	Protein coding	CCDS49500	Q8K120	TSL:1 GENCODE basic APPRIS ALT2
Nfatc4-201	ENSMUST00000024179.5	3267	901aa	Protein coding	CCDS27132	Q8K120	TSL:1 GENCODE basic APPRIS P3
Nfatc4-204	ENSMUST00000226357.1	2680	831aa	Protein coding	-	A0A2I3BRR0	GENCODE basic APPRIS ALT2
Nfatc4-211	ENSMUST00000228308.1	509	170aa	Protein coding	-	A0A2I3BRX2	CDS 5' and 3' incomplete
Nfatc4-209	ENSMUST00000226979.1	325	58aa	Protein coding	-	A0A2I3BS51	CDS 3' incomplete
Nfatc4-203	ENSMUST00000226293.1	2969	No protein	Retained intron	-	-	-
Nfatc4-208	ENSMUST00000226869.1	2217	No protein	Retained intron	-	-	-
Nfatc4-206	ENSMUST00000226716.1	1913	No protein	Retained intron	-	-	-
Nfatc4-205	ENSMUST00000226536.1	1161	No protein	Retained intron	-	-	-
Nfatc4-207	ENSMUST00000226834.1	916	No protein	Retained intron	-	-	-
Nfatc4-210	ENSMUST00000227746.1	540	No protein	Retained intron	-	-	-

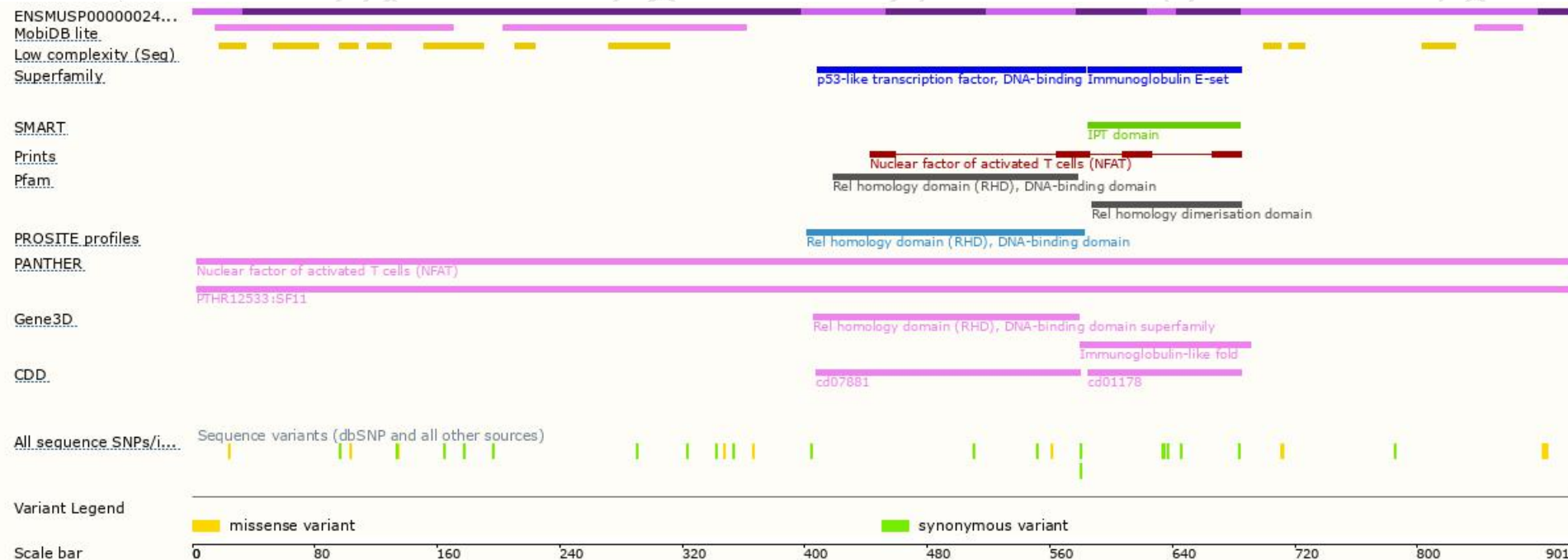
The strategy is based on the design of *Nfatc4-201* transcript,The transcription is shown below



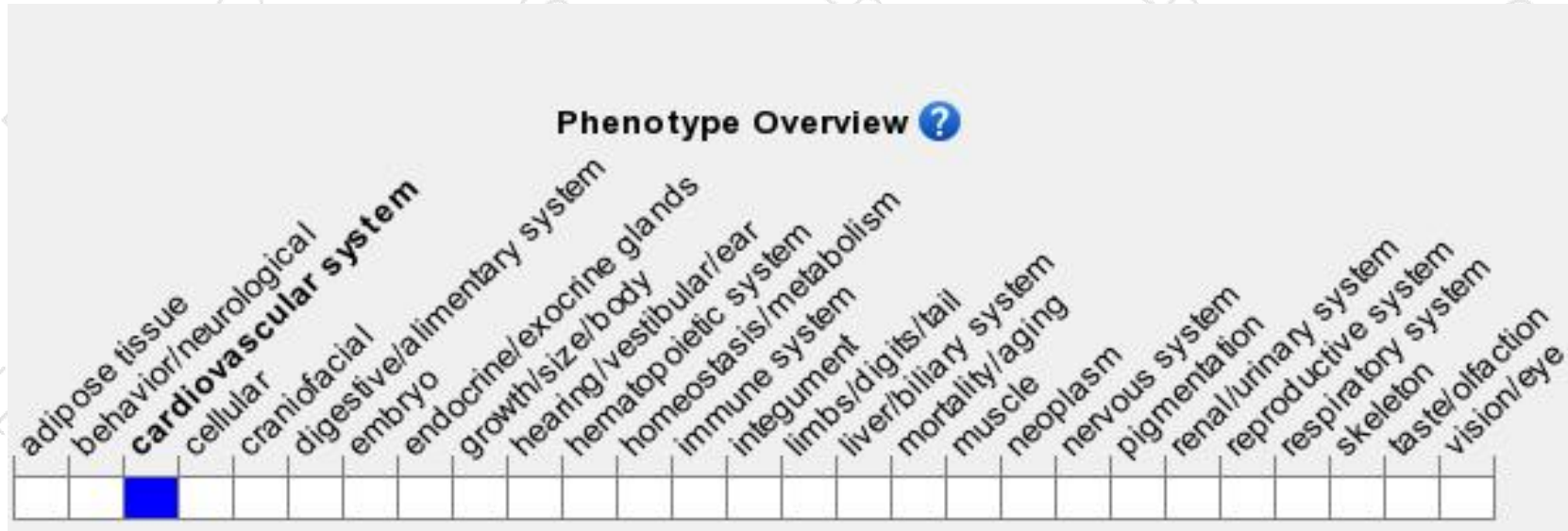
Genomic location distribution



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, Mice homozygous for a knock-out allele are viable and overtly normal and exhibit normal embryonic heart morphology as well as normal pathophysiologic cardiac hypertrophy in response to angiotensin II infusion or aortic banding.

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

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