

Nfkbie Cas9-KO Strategy

Designer:

JiaYu

Reviewer:

Xiaojing Li

Design Date:

2020-1-17

Project Overview

Project Name

Nfkbie

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Nfkbie* gene has 3 transcripts. According to the structure of *Nfkbie* gene, exon2-exon3 of *Nfkbie-201* (ENSMUST00000024742.8) transcript is recommended as the knockout region. The region contains 326bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nfkbie* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions of this gene display an essentially normal phenotype.
- The *Nfkbie* gene is located on the Chr17. 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)

Nfkbie nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon [Mus musculus (house mouse)]

Gene ID: 18037, updated on 31-Jan-2019

Summary

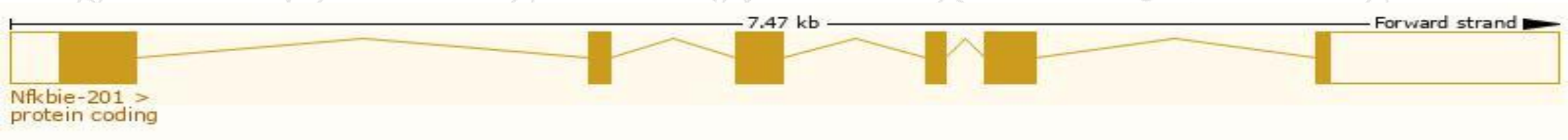
Official Symbol	Nfkbie provided by MGI
Official Full Name	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon provided by MGI
Primary source	MGI:MGI:1194908
See related	Ensembl:ENSMUSG00000023947
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	I-kappa-B-epsilon, IKB-E, NF-kappa-BIE, ikB-epsilon
Expression	Biased expression in spleen adult (RPKM 27.7), thymus adult (RPKM 23.0) and 13 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

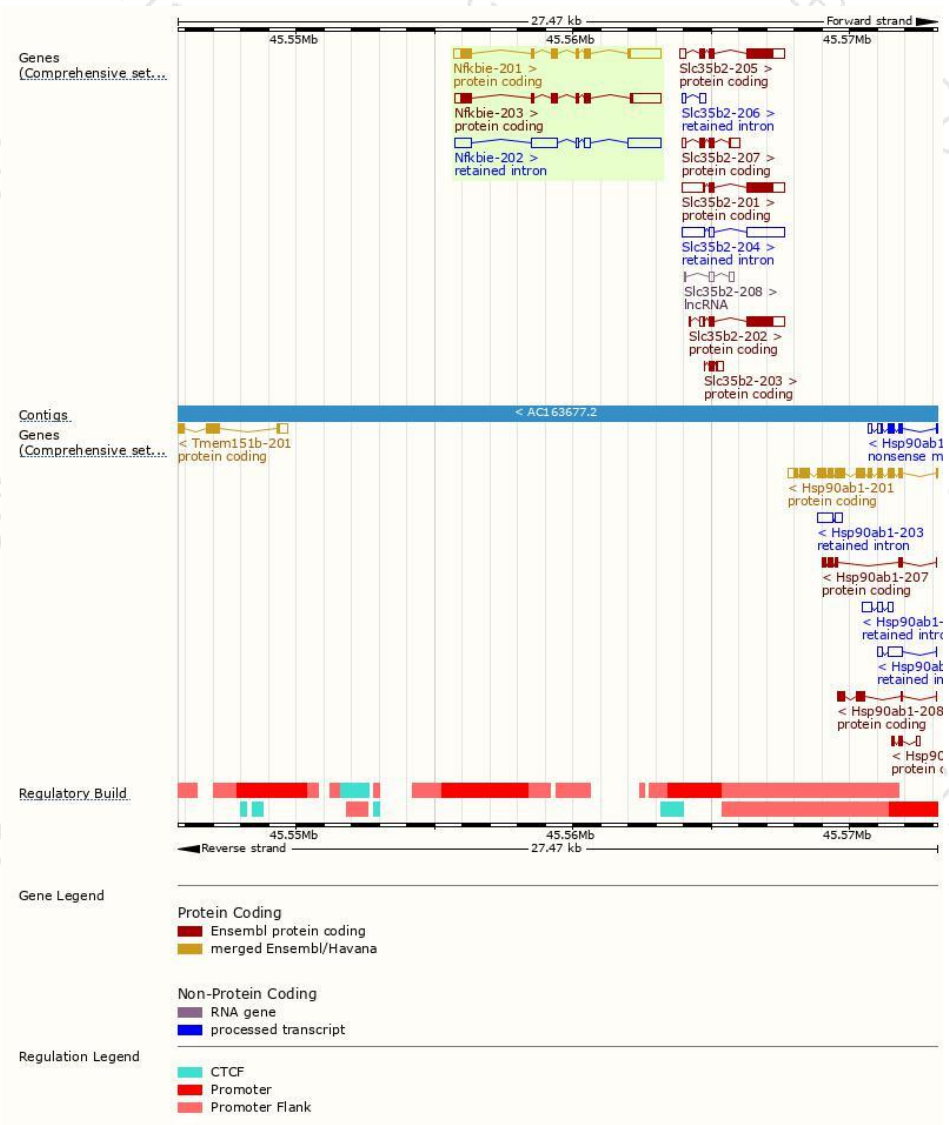
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nfkbie-201	ENSMUST00000024742.8	2435	364aa	Protein coding	CCDS28811	O54910	TSL:1 GENCODE basic APPRIS P2
Nfkbie-203	ENSMUST00000233929.1	2356	371aa	Protein coding	-	A0A3B2WAY2	GENCODE basic APPRIS ALT2
Nfkbie-202	ENSMUST00000233379.1	3006	No protein	Retained intron	-	-	

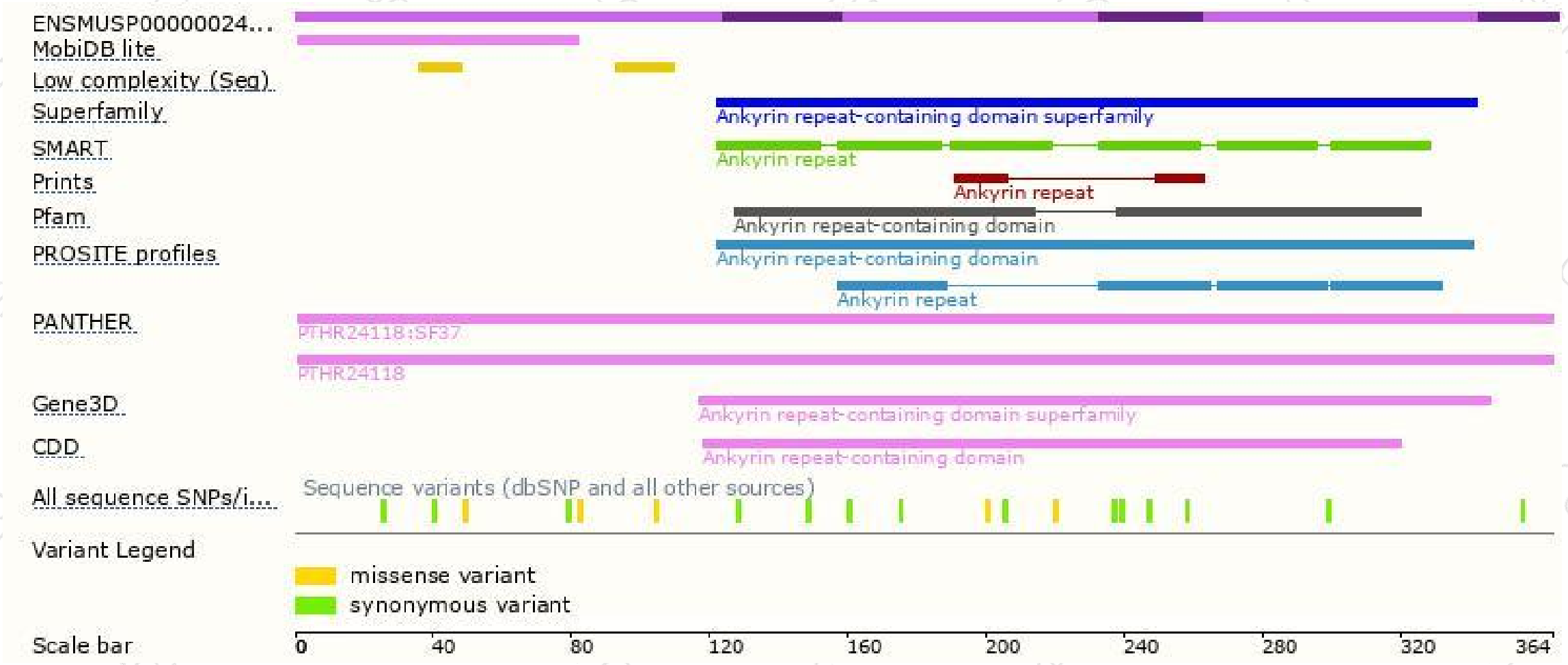
The strategy is based on the design of *Nfkbie-201* transcript,The transcription is shown below



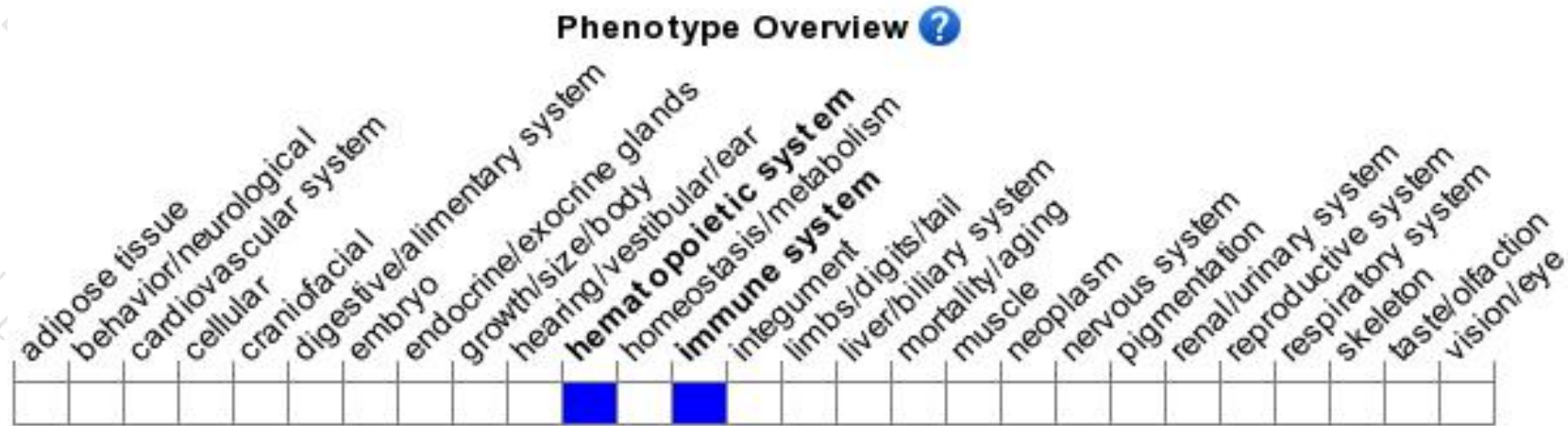
Genomic location distribution



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 disruptions of this gene display an essentially normal phenotype.

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

Tel: 400-9660890

