

# Nfil3 Cas9-KO Strategy

**Designer:** 

Huan Fan

**Design Date:** 

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# **Project Overview**



**Project Name** 

Nfil3

**Project type** 

Cas9-KO

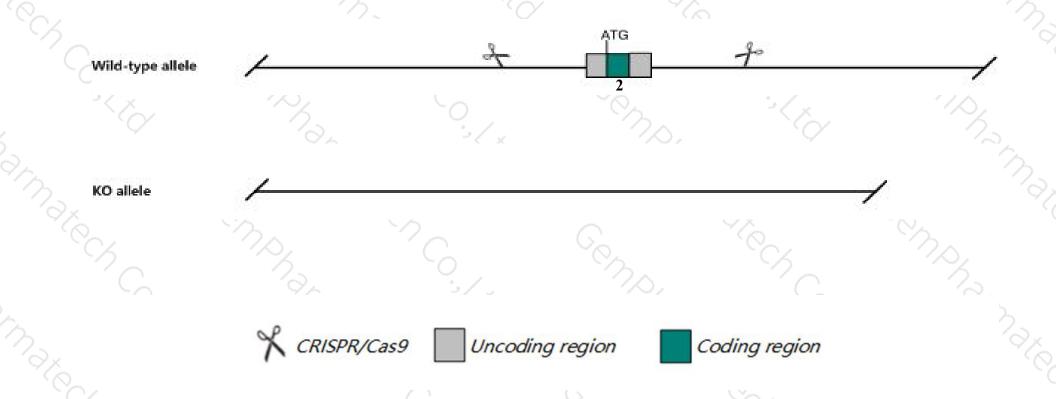
Strain background

C57BL/6JGpt

# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the Nfil3 gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *Nfil3* gene has 1 transcript. According to the structure of *Nfil3* gene, exon2 of *Nfil3-201* (ENSMUST00000071065.7) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Nfil3* gene. The brief process is as follows: CRISPR/Cas9 system v

### **Notice**



- ➤ According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased NK cell differentiation, numbers, and activity. Mice homozygous for a different knock-out allele exhibit reduced class switching and IgE production.
- > The *Nfil3* 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)



#### Nfil3 nuclear factor, interleukin 3, regulated [Mus musculus (house mouse)]

Gene ID: 18030, updated on 20-Mar-2019

#### Summary

↑ ?

Official Symbol Nfil3 provided by MGI

Official Full Name nuclear factor, interleukin 3, regulated provided by MGI

Primary source MGI:MGI:109495

See related Ensembl:ENSMUSG00000056749

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 AV225605, E4BP4

Summary The protein encoded by this gene is a transcriptional regulator that binds as a homodimer to activating transcription factor (ATF) sites in

many cellular and viral promoters. The encoded protein represses Per1 and Per2 expression and therefore plays a role in the regulation of

circadian rhythm. [provided by RefSeq, Feb 2014]

Expression Ubiquitous expression in large intestine adult (RPKM 2.7), CNS E14 (RPKM 2.5) and 28 other tissuesSee more

Orthologs <u>human all</u>

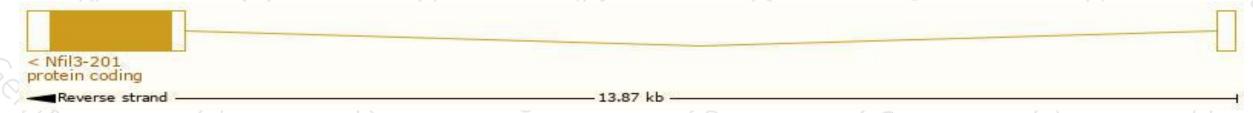
# Transcript information (Ensembl)



The gene has 1 transcript, and the transcript is shown below:

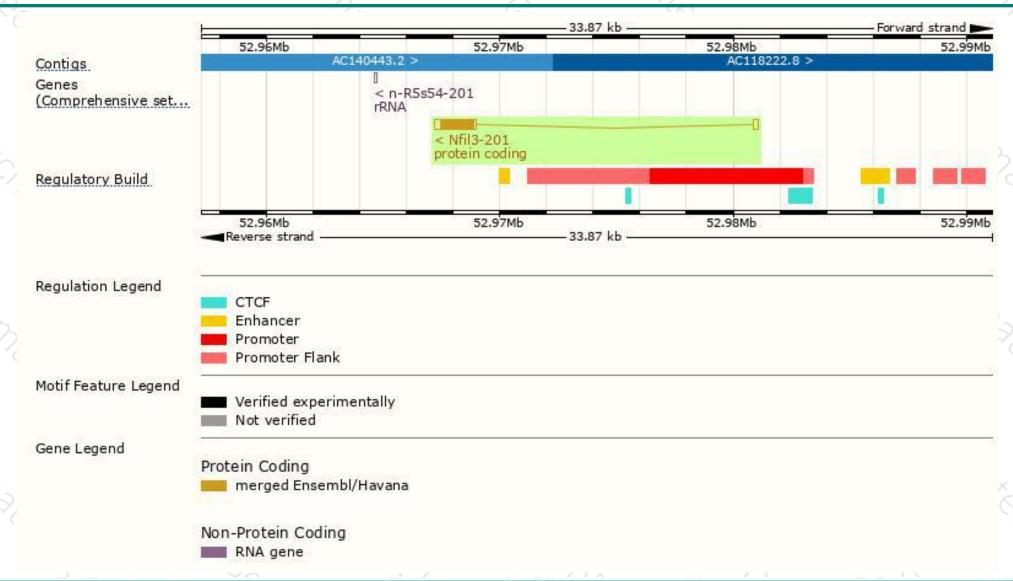
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nfil3-201	ENSMUST00000071065.7	2026	462aa	Protein coding	CCDS26519	008750	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Nfil3-201* transcript, The transcription is shown below



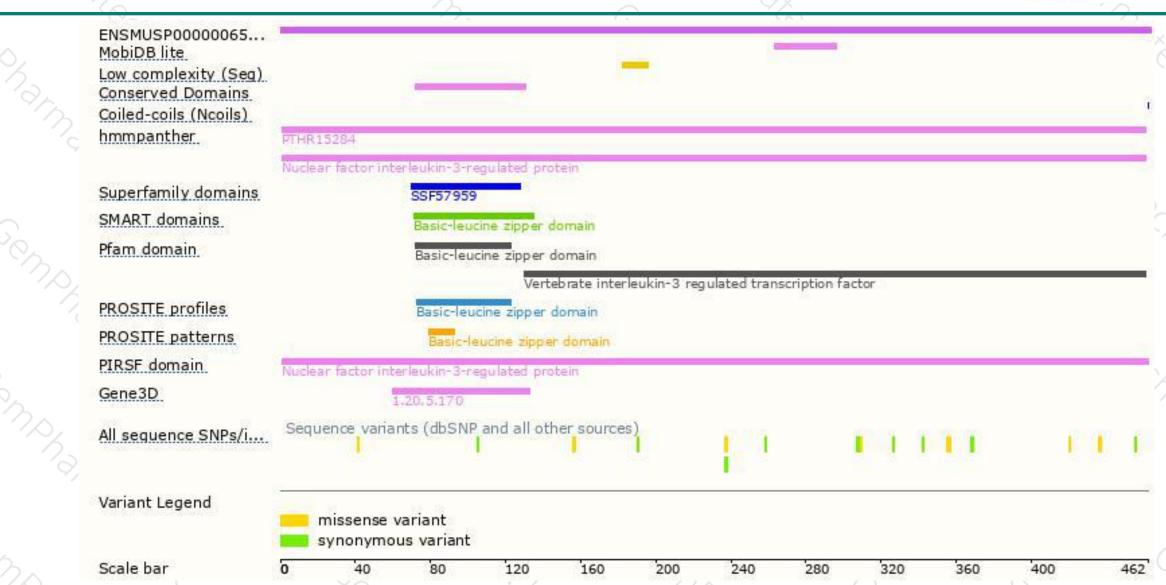
### Genomic location distribution





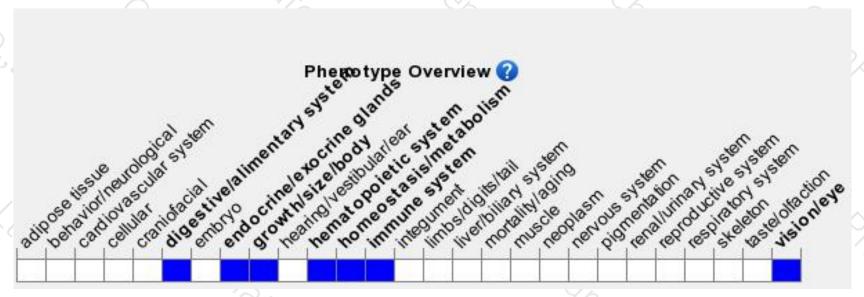
### Protein domain





## 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 exhibit decreased NK cell differentiation, numbers, and activity. Mice homozygous for a different knock-out allele exhibit reduced class switching and IgE production.



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





