

Nfkb1 Cas9-KO Strategy

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Project Overview



Project Name Nfkb1

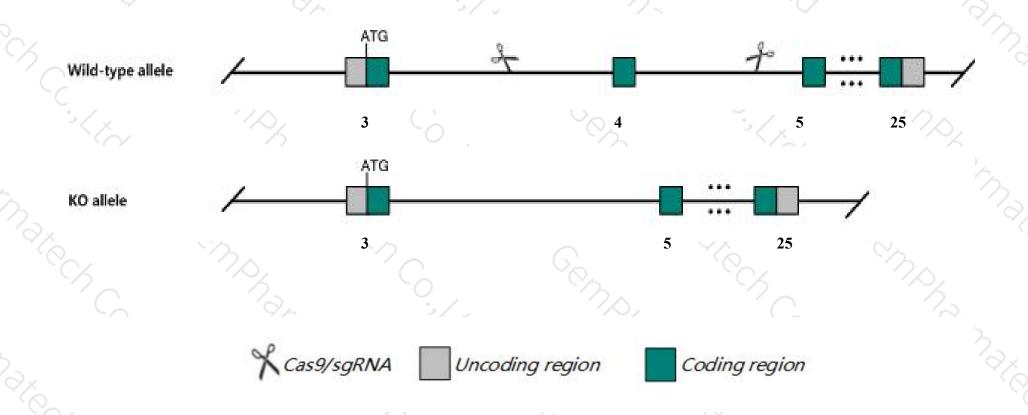
Project type Cas9-KO

Strain background C57BL/6J

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Nfkb1* gene. The schematic diagram is as follows:



Technical routes



> The Nfkb1 gene has 10 transcripts. According to the structure of Nfkb1 gene, exon4 of Nfkb1-201 (

ENSMUST00000029812.13) transcript is recommended as the knockout region. The region contains 79 bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Nfkb1* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

Notice



- ➤ According to the existing MGI data, Homozygous null mice have a decreased survivor rate, abnormal T cell development and decreased number of peripheral T cells, abnormal humoral responses with decreased immunoglobulin class switching, exhibit mild organ inflammation, and are susceptible toboth bacterial infections and hearing loss.
- ➤ The *Nfkb1* gene is located on the Chr3. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)



Nfkb1 nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105 [Mus musculus (house mouse)]

Gene ID: 18033, updated on 2-Apr-2019

Summary



Official Symbol Nfkb1 provided by MGI

Official Full Name nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105 provided by MGI

Primary source MGI:MGI:97312

See related Ensembl:ENSMUSG00000028163

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 NF-KB1, NF-kappaB, NF-kappaB1, p105, p50, p50/p105

Expression Ubiquitous expression in spleen adult (RPKM 34.6), lung adult (RPKM 23.6) and 28 other tissuesSee more

Orthologs <u>human</u> all

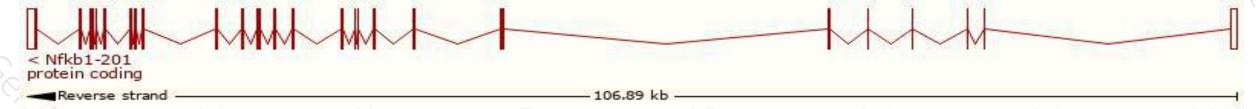
Transcript information (Ensembl)



The gene has 10 transcripts, all transcripts are shown below:

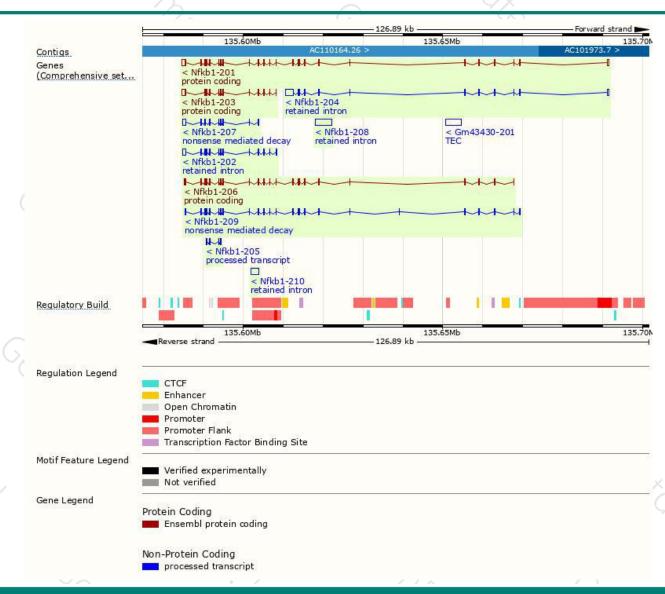
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000029812.13	4117	971aa	Protein coding	CCDS17858	P25799	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000164430.6	3007	<u>971aa</u>	Protein coding	CCDS17858	P25799	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000132668.7	2354	<u>534aa</u>	Protein coding	-	F6Z9G5	CDS 5' incomplete TSL:5
ENSMUST00000196469.4	3084	<u>128aa</u>	Nonsense mediated decay	20	A0A0G2JGK6	TSL:1
ENSMUST00000184550.7	1924	<u>270aa</u>	Nonsense mediated decay	9	V9GX90	CDS 5' incomplete TSL:1
ENSMUST00000150007.1	528	No protein	Processed transcript		, = = = = = = = = = = = = = = = = = = =	TSL:2
ENSMUST00000196246.1	4149	No protein	Retained intron	-	49	TSL:NA
ENSMUST00000138602.2	3383	No protein	Retained intron	20	20	TSL:1
ENSMUST00000129428.7	2520	No protein	Retained intron	9	54	TSL:1
ENSMUST00000199588.1	2001	No protein	Retained intron	-		TSL:NA
	ENSMUST00000029812.13 ENSMUST00000164430.6 ENSMUST00000132668.7 ENSMUST00000196469.4 ENSMUST00000184550.7 ENSMUST00000150007.1 ENSMUST00000196246.1 ENSMUST00000138602.2 ENSMUST00000129428.7	ENSMUST00000164430.6 3007 ENSMUST00000132668.7 2354 ENSMUST00000196469.4 3084 ENSMUST00000184550.7 1924 ENSMUST00000150007.1 528 ENSMUST00000196246.1 4149 ENSMUST00000138602.2 3383 ENSMUST00000129428.7 2520	ENSMUST00000164430.6 3007 971aa ENSMUST00000132668.7 2354 534aa ENSMUST00000196469.4 3084 128aa ENSMUST00000184550.7 1924 270aa ENSMUST00000150007.1 528 No protein ENSMUST00000196246.1 4149 No protein ENSMUST00000138602.2 3383 No protein ENSMUST00000129428.7 2520 No protein	ENSMUST00000029812.13 4117 971aa Protein coding ENSMUST00000164430.6 3007 971aa Protein coding ENSMUST00000132668.7 2354 534aa Protein coding ENSMUST00000196469.4 3084 128aa Nonsense mediated decay ENSMUST00000184550.7 1924 270aa Nonsense mediated decay ENSMUST00000150007.1 528 No protein Processed transcript ENSMUST00000196246.1 4149 No protein Retained intron ENSMUST00000138602.2 3383 No protein Retained intron ENSMUST00000129428.7 2520 No protein Retained intron	ENSMUST00000029812.13 4117 971aa Protein coding CCDS17858 ENSMUST00000164430.6 3007 971aa Protein coding CCDS17858 ENSMUST00000132668.7 2354 534aa Protein coding - ENSMUST00000196469.4 3084 128aa Nonsense mediated decay - ENSMUST00000184550.7 1924 270aa Nonsense mediated decay - ENSMUST00000150007.1 528 No protein Processed transcript - ENSMUST00000196246.1 4149 No protein Retained intron - ENSMUST00000138602.2 3383 No protein Retained intron - ENSMUST00000129428.7 2520 No protein Retained intron -	ENSMUST00000029812.13 4117 971aa Protein coding CCDS17858 P25799 ENSMUST00000164430.6 3007 971aa Protein coding CCDS17858 P25799 ENSMUST00000132668.7 2354 534aa Protein coding - F6Z9G5 ENSMUST00000196469.4 3084 128aa Nonsense mediated decay - A0A0G2JGK6 ENSMUST00000184550.7 1924 270aa Nonsense mediated decay - V9GX90 ENSMUST00000150007.1 528 No protein Processed transcript - - ENSMUST00000196246.1 4149 No protein Retained intron - - ENSMUST00000129428.7 2520 No protein Retained intron - -

The strategy is based on the design of Nfkb1-201 transcript, The transcription is shown below



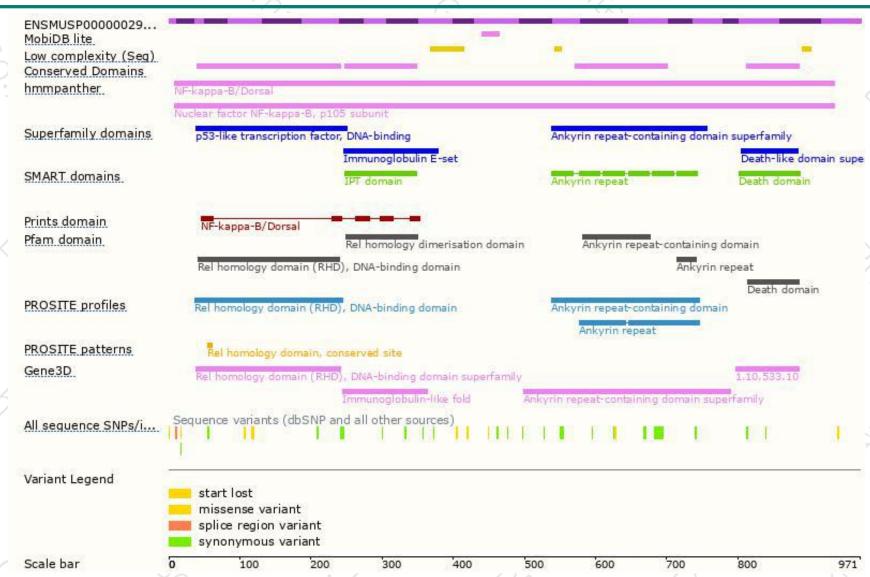
Genomic location distribution





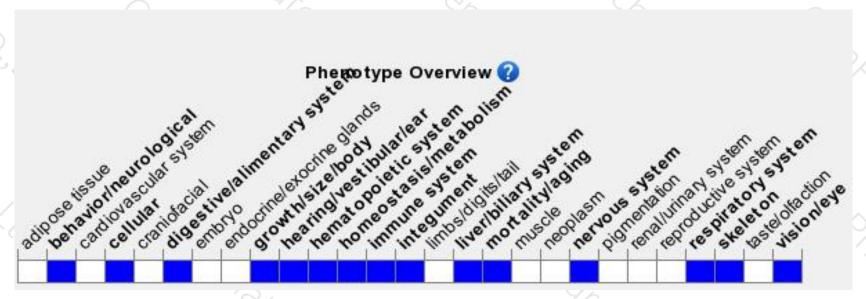
Protein domain





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, Homozygous null mice have a decreased survivor rate, abnormal T cell development and decreased number of peripheral T cells, abnormal humoral responses with decreased immunoglobulin class switching, exhibit mild organ inflammation, and are susceptible toboth bacterial infections and hearing loss.



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

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