

# Nfkb2 Cas9-CKO Strategy

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Design Date: 2019-08-08

## **Project Overview**



Project Name Nfkb2

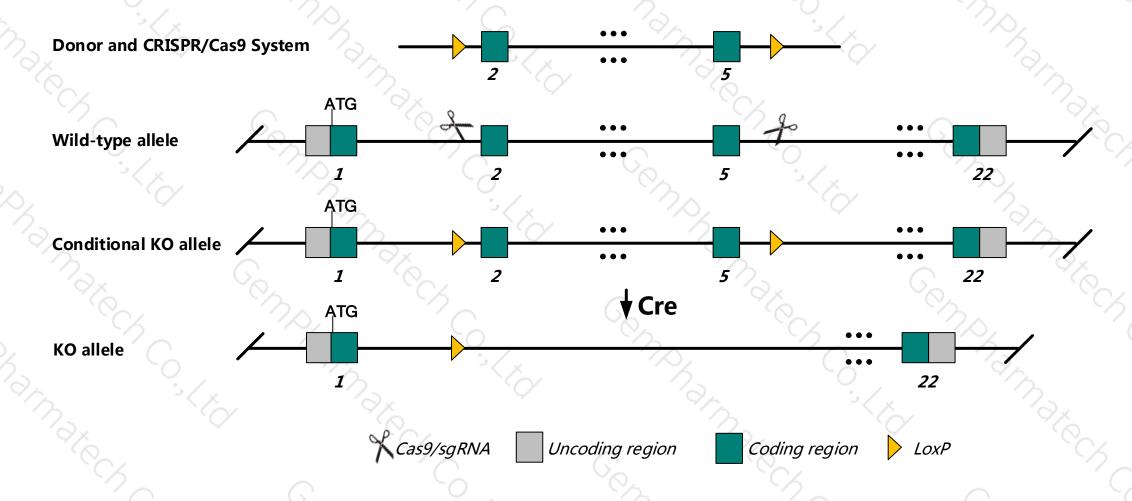
Project type Cas9-CKO

Strain background C57BL/6JGpt

## **Conditional Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Nfkb2* gene. The schematic diagram is as follows:



#### **Technical routes**



- ➤ The *Nfkb2* gene has 8 transcripts. According to the structure of *Nfkb2* gene, exon2-exon5 of *Nfkb2-202* (ENSMUST00000111881.3) transcript is recommended as the knockout region. The region contains 374bp of coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Nfkb2* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.
- ➤ The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

#### **Notice**



- ➤ According to the existing MGI data, Homozygotes for targeted null mutations exhibit gastric hyperplasia, enlarged lymph nodes, enhanced cytokine production by activated T cells, absence of Peyer's patches, increased susceptibility to Leishmania major, and early postnatal mortality.
- ➤ Intron 1-2 (258 bp) & Intron 5-6 (270 bp) are small, and insertion of loxp at both ends may affect normal splicing of the gene.
- ➤ The *Nfkb2* gene is located on the Chr19. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

### Gene information (NCBI)



Nfkb2 nuclear factor of kappa light polypeptide gene enhancer in B cells 2, p49/p100 [ *Mus musculus* (house mouse) ]

Gene ID: 18034, updated on 30-Jul-2019

Summary

☆ ?

Official Symbol Nfkb2 provided by MGI

Official Full Name nuclear factor of kappa light polypeptide gene enhancer in B cells 2, p49/p100 provided by MGI

Primary source MGI:MGI:1099800

See related Ensembl: ENSMUSG00000025225

Gene type protein coding
RefSeq status VALIDATED
Organism <u>Mus musculus</u>

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as lyt; p49; p52; p50B; p49/p100; NF-kappaB2

Expression Broad expression in spleen adult (RPKM 67.0), mammary gland adult (RPKM 33.7) and 15 other tissues See more

Orthologs human all

## Transcript information (Ensembl)



The gene has 8 transcripts, all transcripts are shown below:

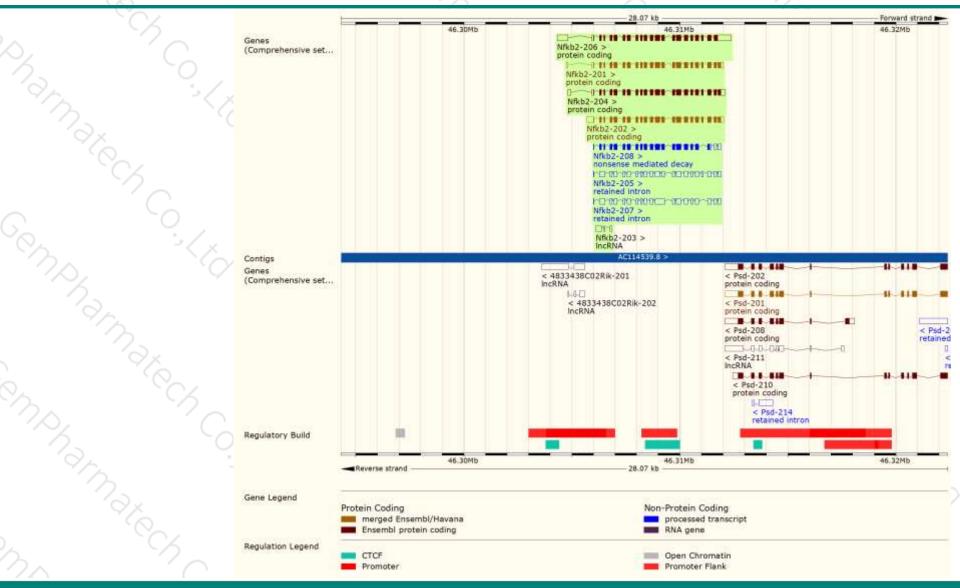
Name 🍦	Transcript ID 🖕	bp 🌲	Protein 🍦	Biotype	CCDS 🍦	UniProt	Flags -
Nfkb2-202	ENSMUST00000111881.3	3141	<u>899aa</u>	Protein coding	CCDS29874 ₽	Q3UG25 & Q9WTK5 &	TSL:1 GENCODE basic APPRIS P2
Nfkb2-204	ENSMUST00000236591.1	3132	<u>899aa</u>	Protein coding	CCDS29874 ₽	Q3UG25₽	GENCODE basic   APPRIS P2
Nfkb2-201	ENSMUST00000073116.12	2979	<u>899aa</u>	Protein coding	CCDS29874 ₽	Q3UG25 & Q9WTK5 &	TSL:1 GENCODE basic APPRIS P2
Nfkb2-206	ENSMUST00000237330.1	3846	<u>878aa</u>	Protein coding	-	-	GENCODE basic APPRIS ALT2
Nfkb2-208	ENSMUST00000237791.1	2636	<u>776aa</u>	Nonsense mediated decay	-	-	-
Nfkb2-207	ENSMUST00000237761.1	2837	No protein	Retained intron	-	-	-
Nfkb2-205	ENSMUST00000236820.1	2827	No protein	Retained intron	-	-	-
Nfkb2-203	ENSMUST00000235868.1	384	No protein	IncRNA	-	-	-

The strategy is based on the design of Nfkb2-202 transcript, The transcription is shown below



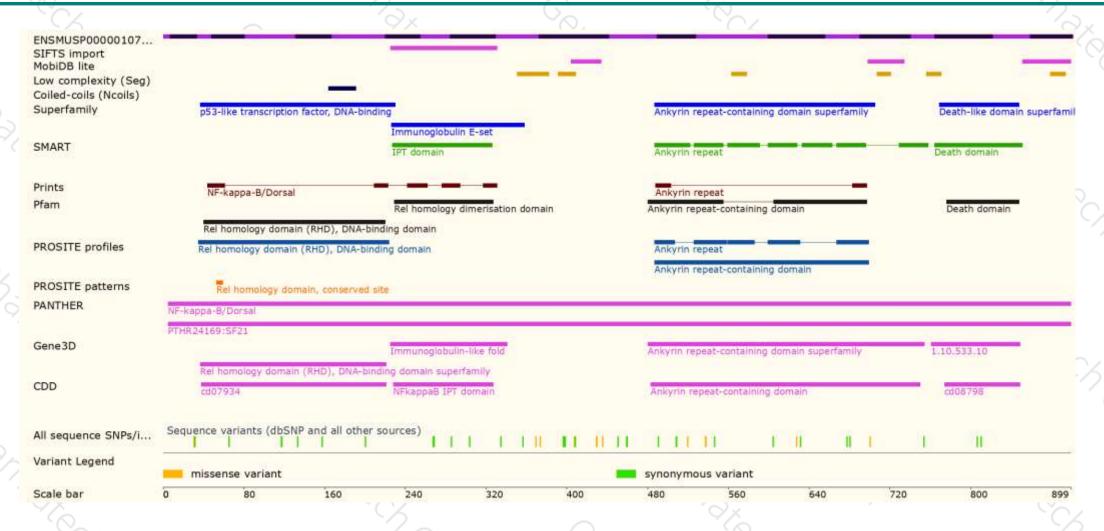
### Genomic location distribution





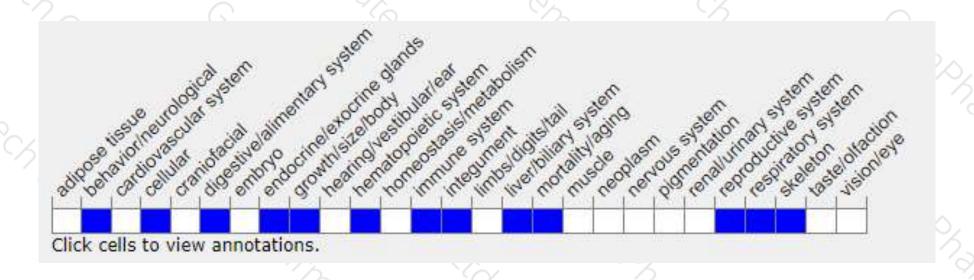
#### Protein domain





## 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, Homozygotes for targeted null mutations exhibit gastric hyperplasia, enlarged lymph nodes, enhanced cytokine production by activated T cells, absence of Peyer's patches, increased susceptibility to Leishmania major, and early postnatal mortality.



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

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