

# *Nfkb2* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Nfkb2*

**Project type**

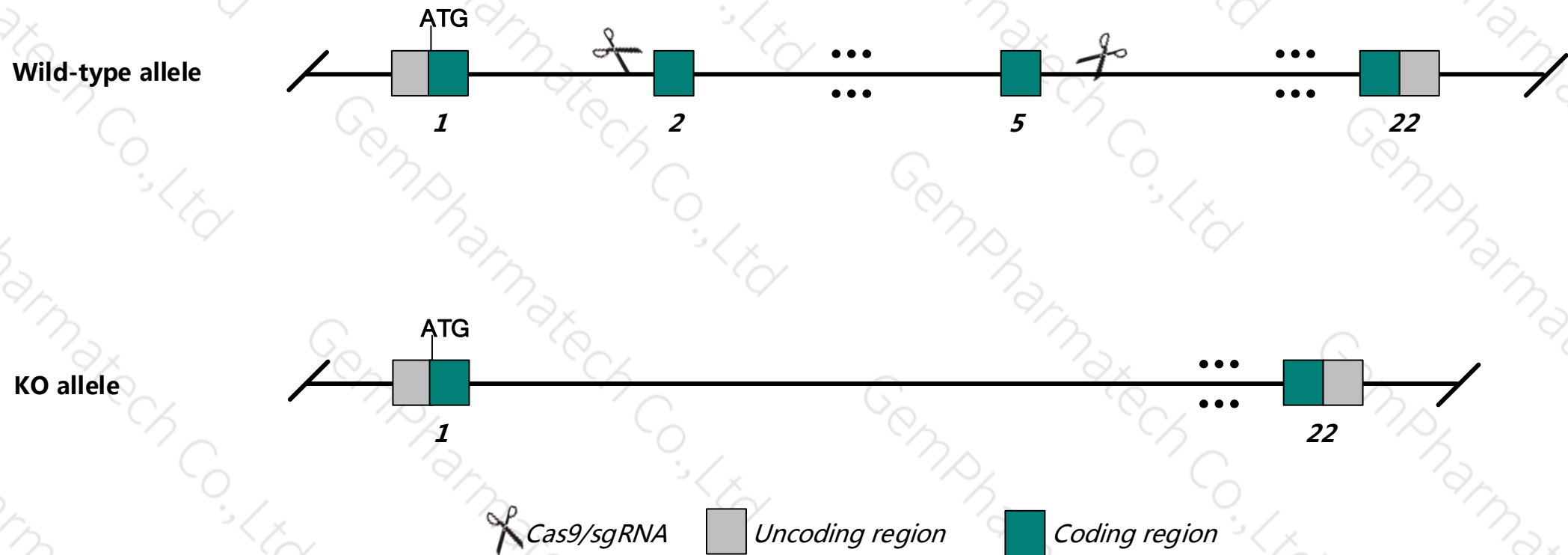
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- 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. Cas9 and sgRNA 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.

- 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.
- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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 <a href="#">MGI</a>
Official Full Name	nuclear factor of kappa light polypeptide gene enhancer in B cells 2, p49/p100 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1099800</a>
See related	<a href="#">Ensembl:ENSMUSG00000025225</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
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 <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

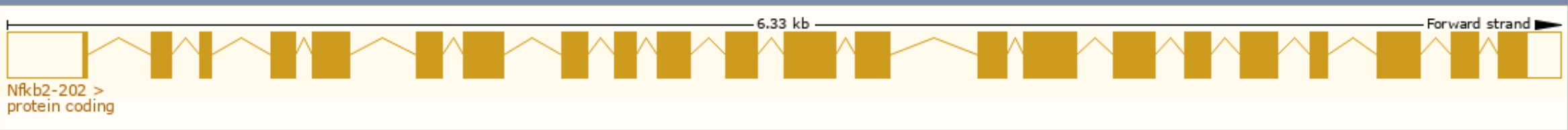


# Transcript information (Ensembl)

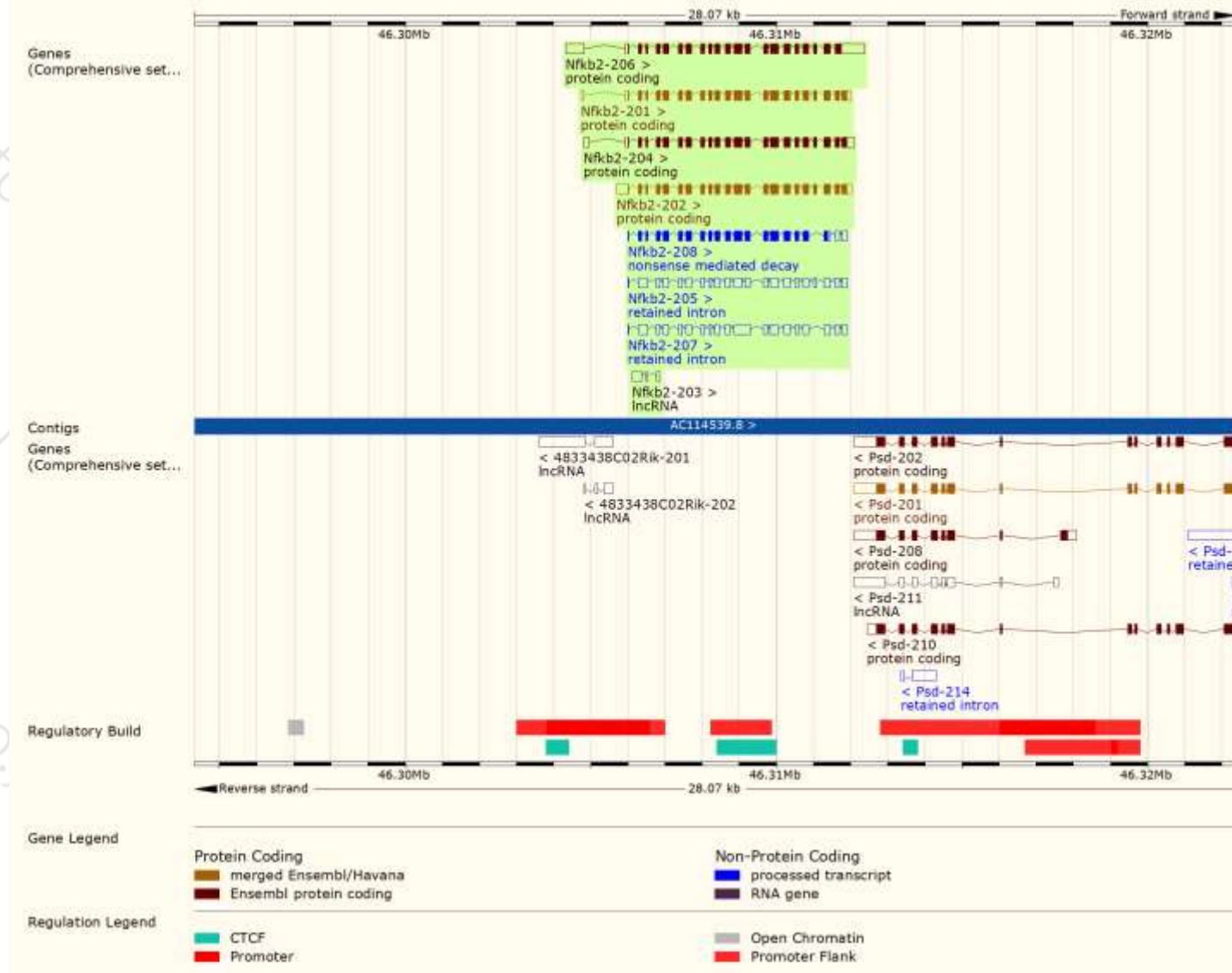
The gene has 8 transcripts,all transcripts are shown below:

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

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

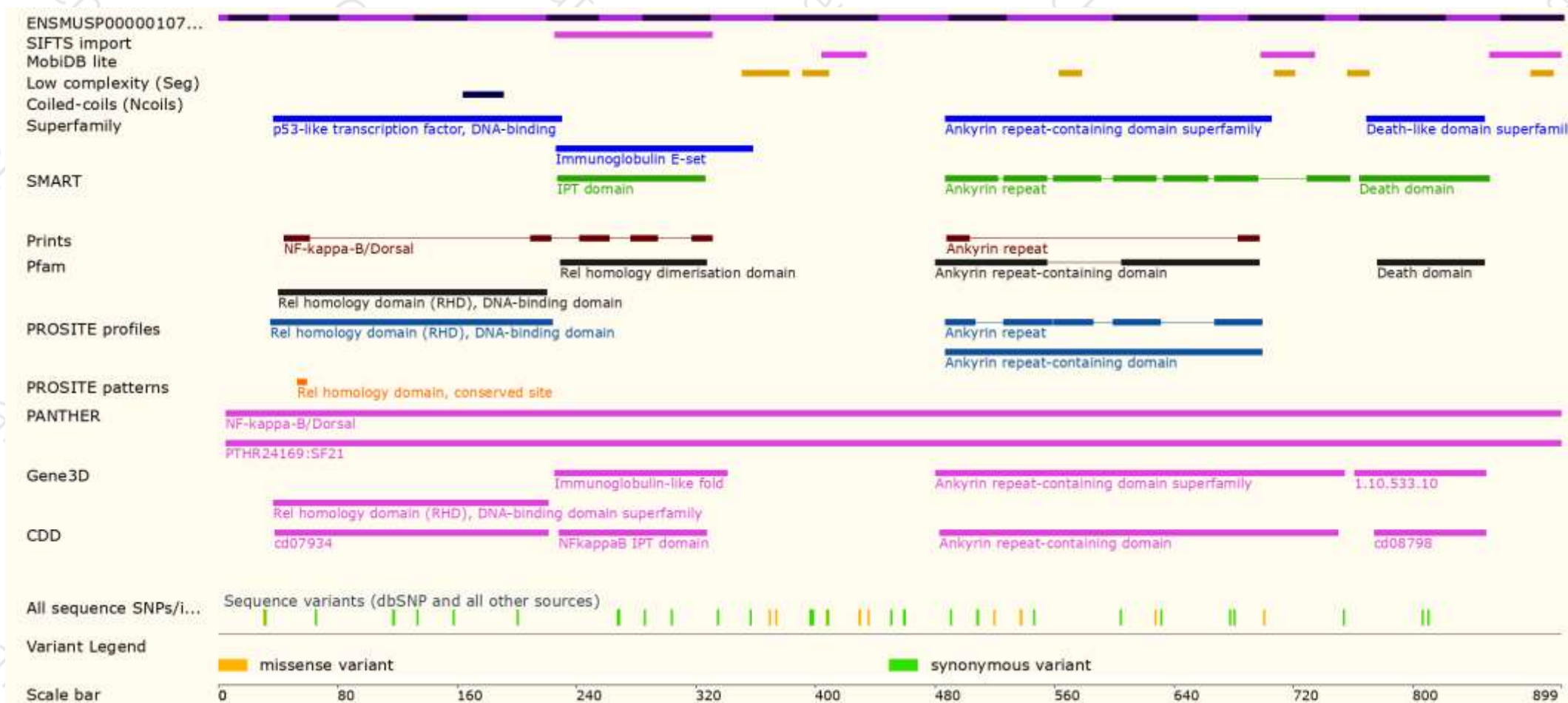


# Genomic location distribution

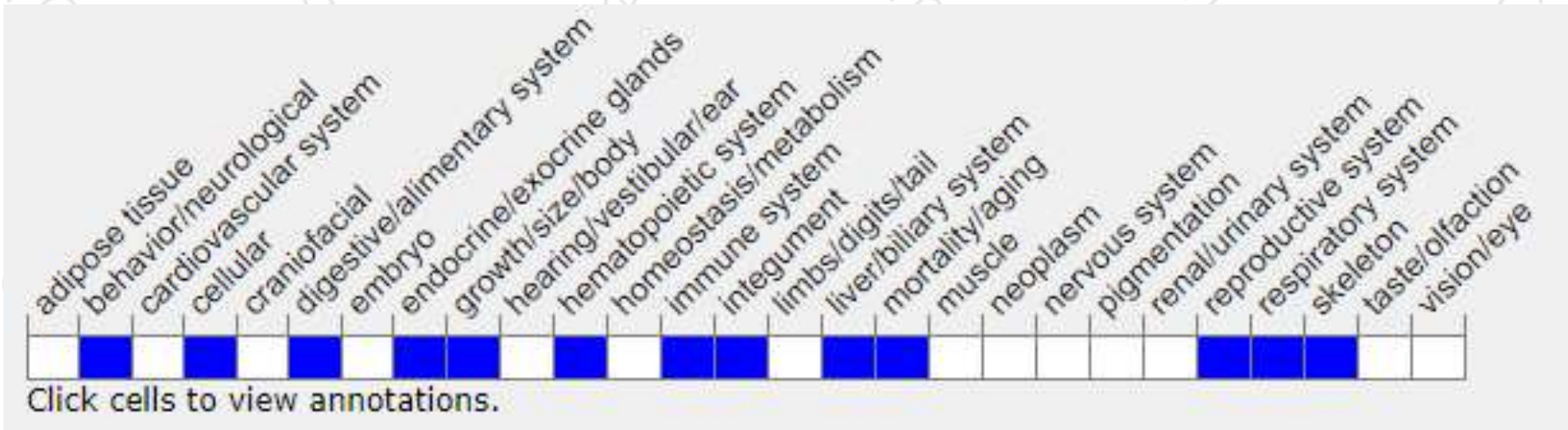




# Protein domain



# 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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