

# *Nfkb1* Cas9-CKO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Nfkb1*

**Project type**

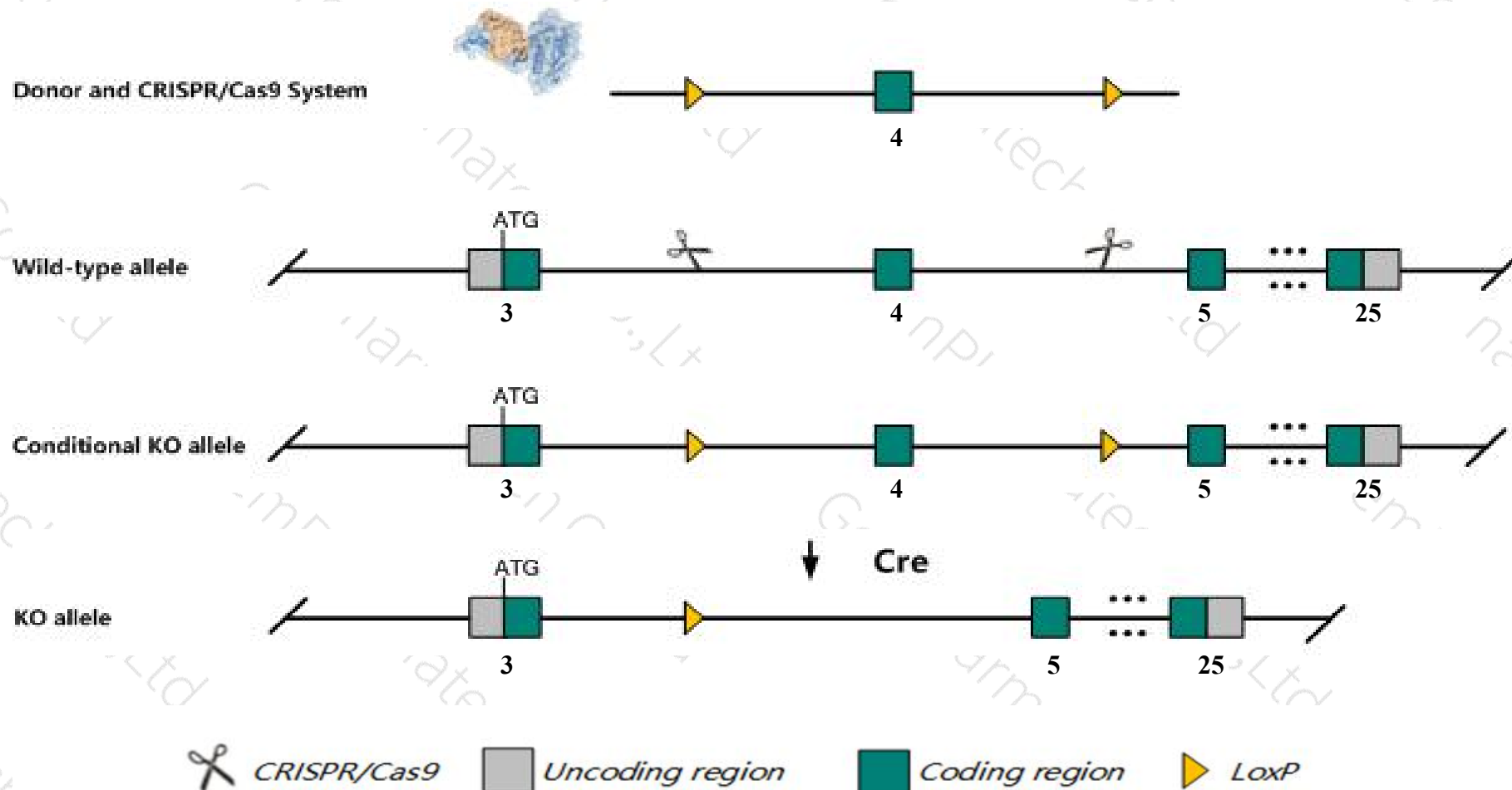
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



- 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 79bp 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: CRISPR/Cas9 system 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 will be 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.

- 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 to both 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 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)

## 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



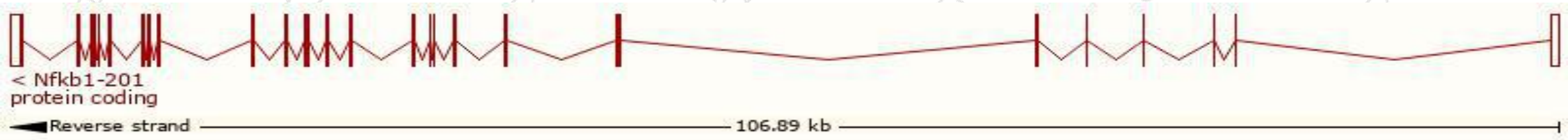
<b>Official Symbol</b>	Nfkb1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	nuclear factor of kappa light polypeptide gene enhancer in B cells 1, p105 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:97312</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000028163</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	NF-KB1, NF-kappaB, NF-kappaB1, p105, p50, p50/p105
<b>Expression</b>	Ubiquitous expression in spleen adult (RPKM 34.6), lung adult (RPKM 23.6) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

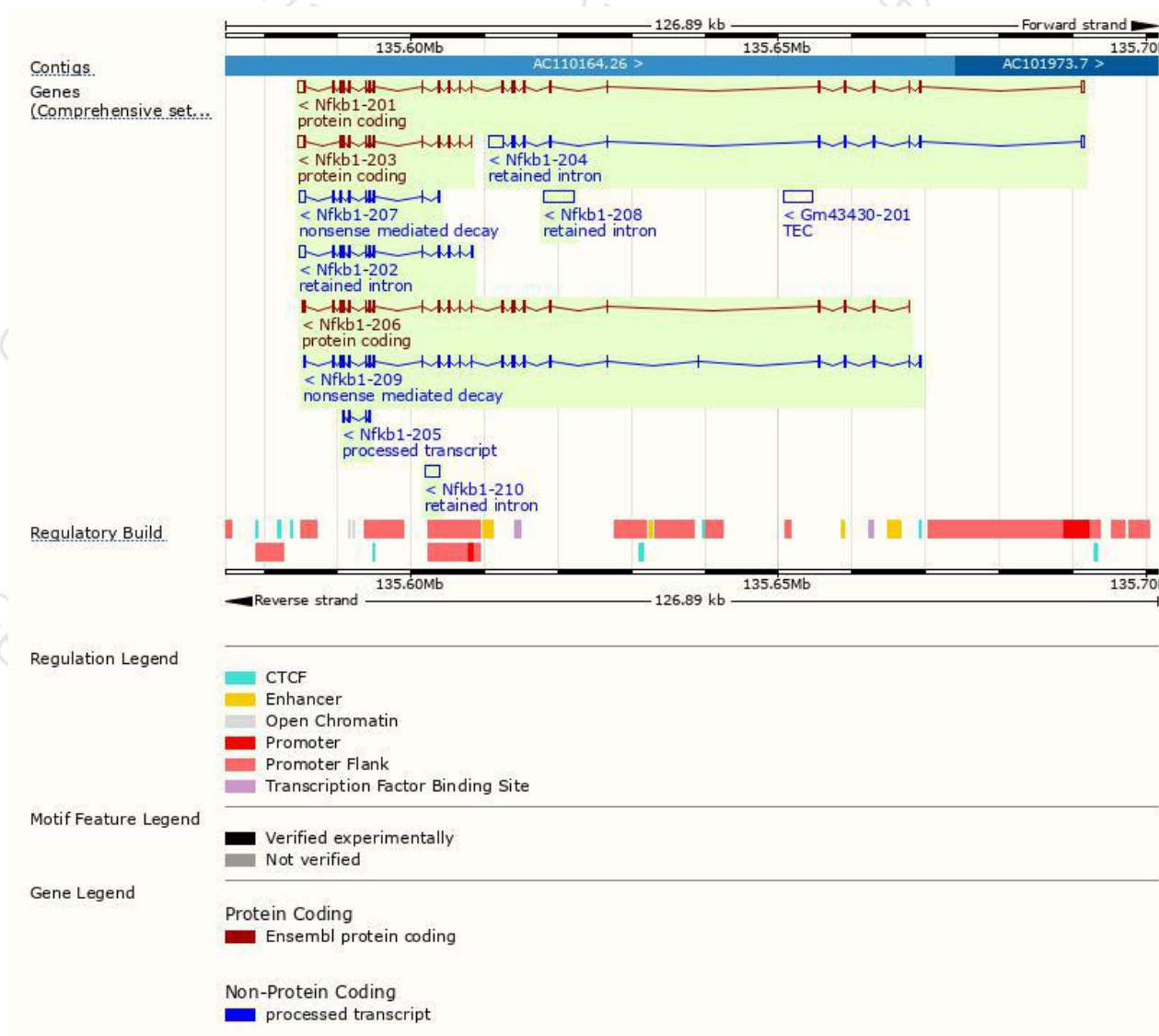
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nfkb1-201	<a href="#">ENSMUST00000029812.13</a>	4117	<a href="#">971aa</a>	Protein coding	<a href="#">CCDS17858</a>	<a href="#">P25799</a>	TSL:1 GENCODE basic APPRIS P1
Nfkb1-206	<a href="#">ENSMUST00000164430.6</a>	3007	<a href="#">971aa</a>	Protein coding	<a href="#">CCDS17858</a>	<a href="#">P25799</a>	TSL:1 GENCODE basic APPRIS P1
Nfkb1-203	<a href="#">ENSMUST00000132668.7</a>	2354	<a href="#">534aa</a>	Protein coding	-	<a href="#">F6Z9G5</a>	CDS 5' incomplete TSL:5
Nfkb1-209	<a href="#">ENSMUST00000196469.4</a>	3084	<a href="#">128aa</a>	Nonsense mediated decay	-	<a href="#">A0A0G2JGK6</a>	TSL:1
Nfkb1-207	<a href="#">ENSMUST00000184550.7</a>	1924	<a href="#">270aa</a>	Nonsense mediated decay	-	<a href="#">V9GX90</a>	CDS 5' incomplete TSL:1
Nfkb1-205	<a href="#">ENSMUST00000150007.1</a>	528	No protein	Processed transcript	-	-	TSL:2
Nfkb1-208	<a href="#">ENSMUST00000196246.1</a>	4149	No protein	Retained intron	-	-	TSL:NA
Nfkb1-204	<a href="#">ENSMUST00000138602.2</a>	3383	No protein	Retained intron	-	-	TSL:1
Nfkb1-202	<a href="#">ENSMUST00000129428.7</a>	2520	No protein	Retained intron	-	-	TSL:1
Nfkb1-210	<a href="#">ENSMUST00000199588.1</a>	2001	No protein	Retained intron	-	-	TSL:NA

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

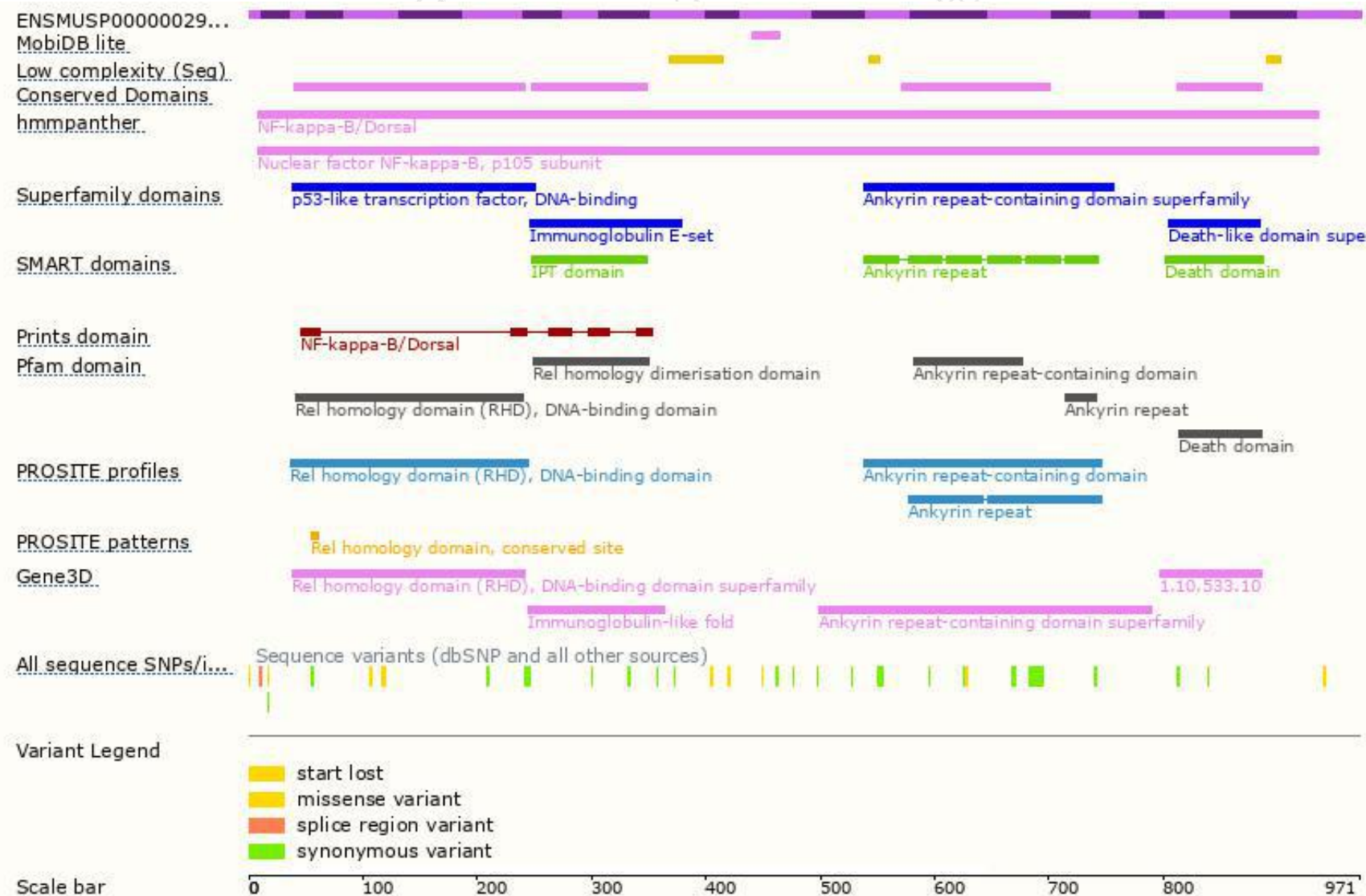


# Genomic location distribution

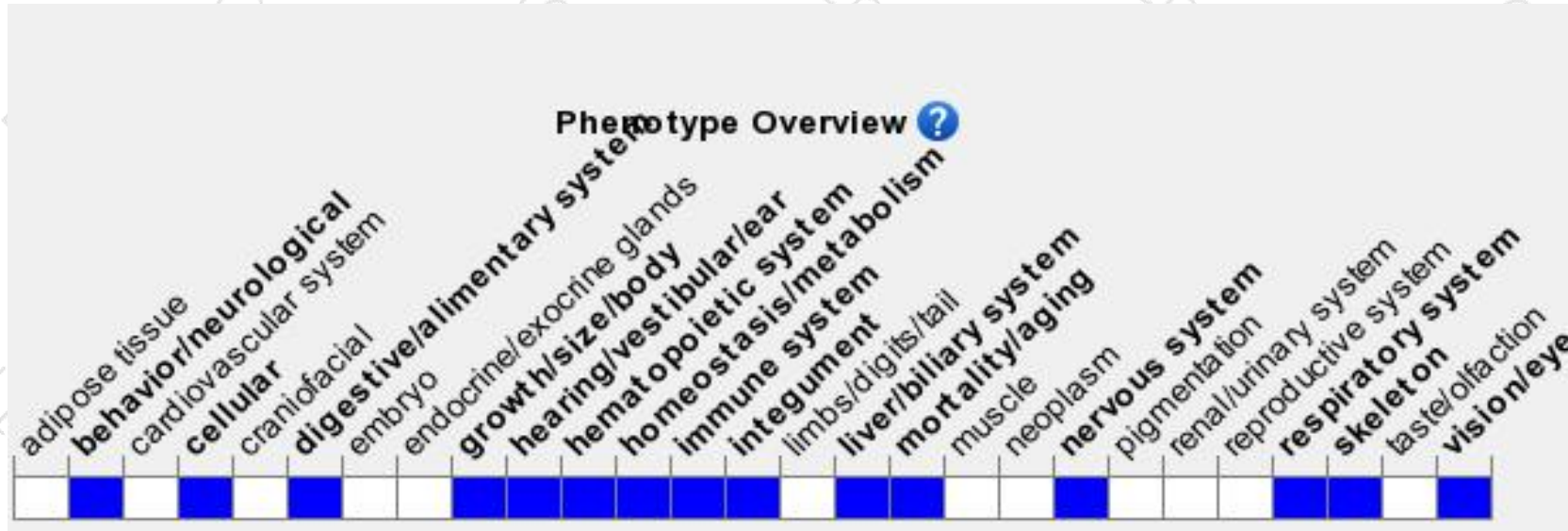




# Protein domain



# 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 to both bacterial infections and hearing loss.

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

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