

# ***Ncr1-P2A-iCre* Cas9-KI Strategy**

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**Reviewer:**

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**Design Date:**

**2018-07-25**

# Project Overview

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<b>Project Name</b>	<b><i>Ncr1-P2A-iCre</i></b>
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<b>Project type</b>	<b>Cas9-KI</b>
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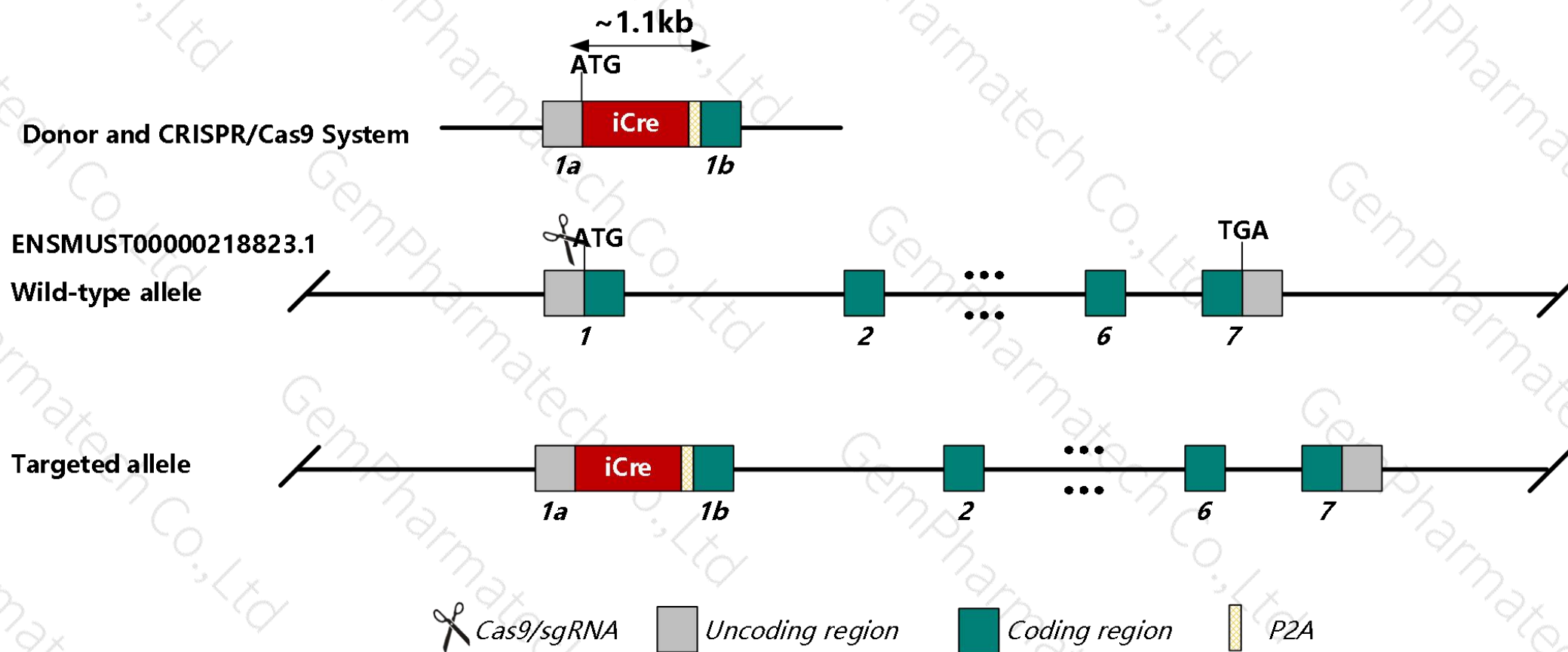
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<b>Strain background</b>	<b>C57BL/6J</b>
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# Knockin strategy

This model will use CRISPR/Cas9 technology to edit the *Ncr1* gene. The schematic diagram is as follows:



- The *Ncr1* gene has 2 transcripts. According to the structure of *Ncr1* gene, *Ncr1-201*(ENSMUST00000006792.5) is selected for presentation of the recommended strategy.
- *Ncr1-201* gene has 7 exons, with the ATG start codon in exon1 and TGA stop codon in exon7.
- We make *Ncr1-P2A-iCre* knockin mice via CRISPR/Cas9 system. Cas9 mRNA, sgRNA and donor will be co-injected into zygotes. sgRNA direct Cas9 endonuclease cleavage near start coding(ATG) of *Ncr1* gene, and create a DSB(double-strand break). Such breaks will be repaired, and result in *P2A-iCre* after start coding(ATG) of *Ncr1* gene by homologous recombination. The pups will be genotyped by PCR, followed by sequence analysis.

- According to the existing MGI data, mutations in this gene lead to alterations in susceptibility to viral infection induced morbidity/mortality, NK cell number, NK cell cytotoxicity, and T cell responses.
- Insertion of iCre may affect the regulation of the 5' end of the *Ncr1* gene.
- *Ncr1* gene specific expression site: natural killer (NK) cells.
- There will be 1 to 2 amino acid synonymous mutation in exon1 of *Ncr1* gene in this strategy.
- The P2A-linked gene drives expression in the same promoter and is cleaved at the translational level. The gene expression levels are consistent, and the before of P2A expressing gene carries the P2A-translated polypeptide.
- The *Ncr1* gene is located on the Chr7. If the knockin 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)

## Ncr1 natural cytotoxicity triggering receptor 1 [ *Mus musculus* (house mouse) ]



Gene ID: 17086, updated on 12-Aug-2019

### Summary

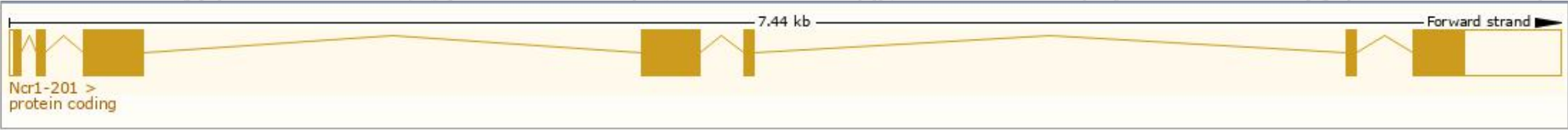
Official Symbol	Ncr1 provided by <a href="#">MGI</a>
Official Full Name	natural cytotoxicity triggering receptor 1 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1336212</a>
See related	<a href="#">Ensembl:ENSMUSG00000062524</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<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	Ly94; NKp46
Expression	Biased expression in spleen adult (RPKM 2.2), lung adult (RPKM 0.8) and 7 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

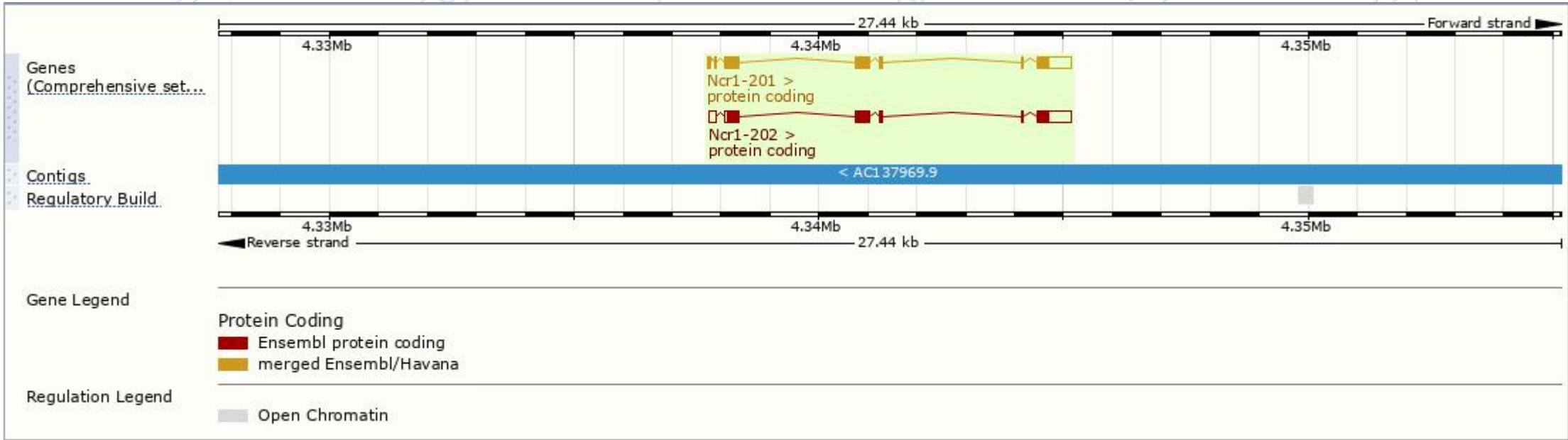
The gene has 2 transcripts, and the transcript is shown below :

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ncr1-201	<a href="#">ENSMUST00000006792.5</a>	1463	<a href="#">325aa</a>	 Protein coding	<a href="#">CCDS20734</a>	<a href="#">A0A0R4IZY7</a>	TSL:1 GENCODE basic APPRIS P2
Ncr1-202	<a href="#">ENSMUST00000126417.2</a>	1495	<a href="#">288aa</a>	 Protein coding	-	<a href="#">A0A0U1RP63</a>	TSL:1 GENCODE basic APPRIS ALT2

The strategy is based on the design of *Ncr1-201* transcript. The transcription is shown below

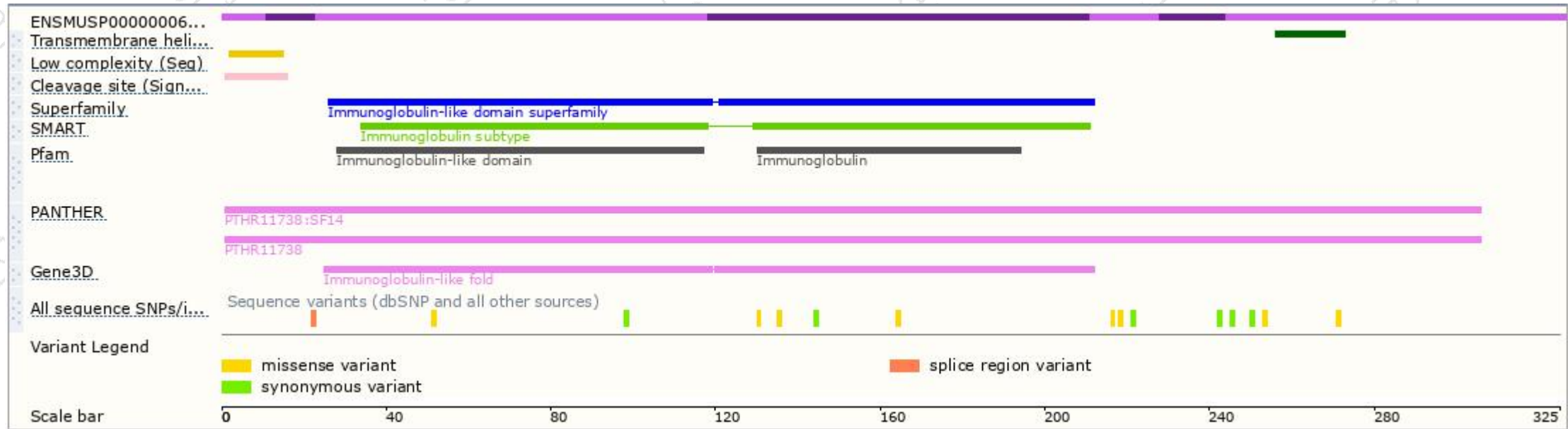


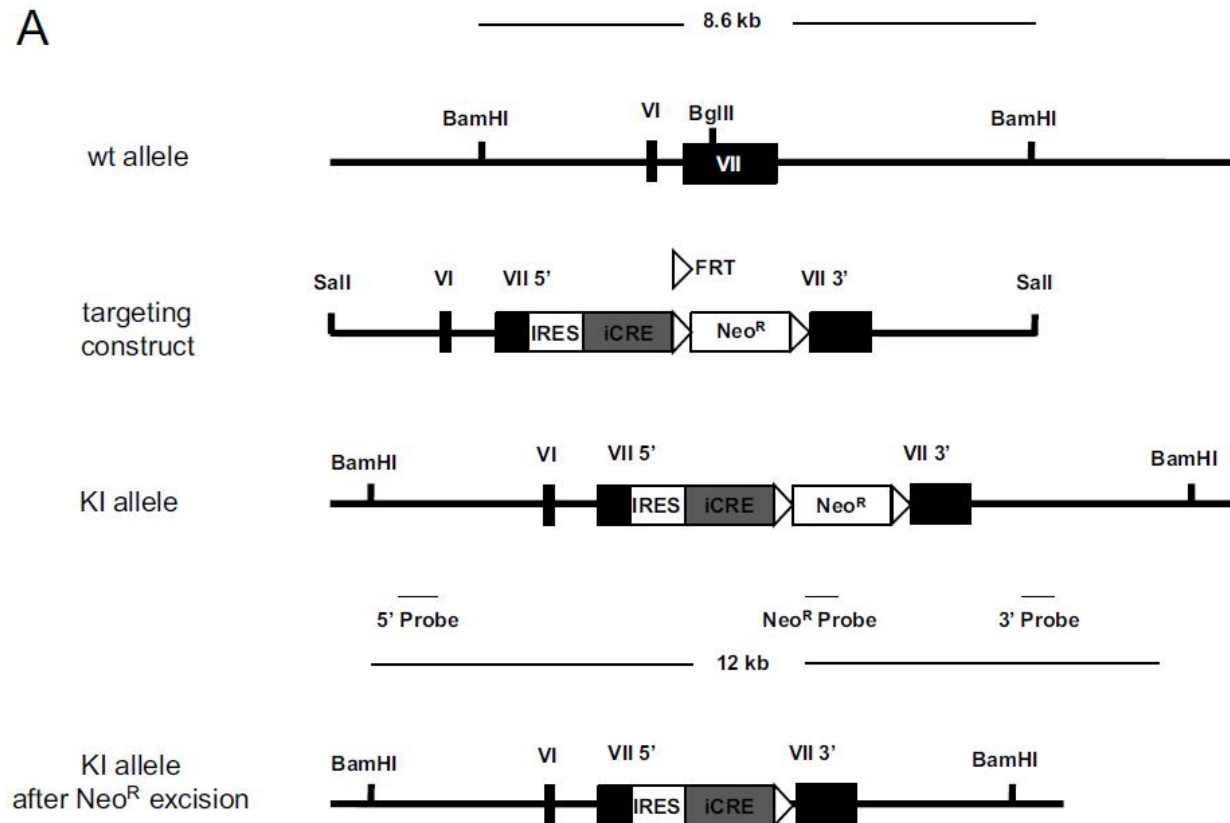
# Genomic location distribution





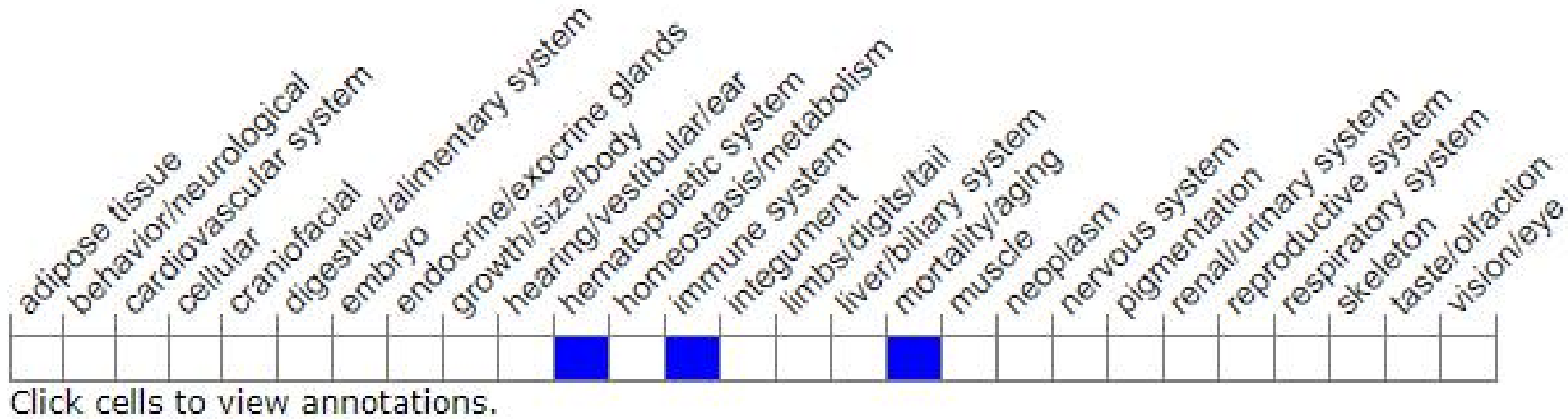
# Protein domain





1. Narni-Mancinelli E, Chaix J, Fenis A, et al. Fate mapping analysis of lymphoid cells expressing the NKp46 cell surface receptor[J]. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108(45):18324-18329.

# Mouse phenotype description(MGI)



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>) .*

Mutations in this gene lead to alterations in susceptibility to viral infection induced morbidity/mortality, NK cell number, NK cell cytolysis, and T cell responses.

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