

# *Fcamr* Cas9-KO Strategy

**Designer: Xiaojing Li**

**Reviewer: JiaYu**

**Design Date: 2022-9-20**

# Project Overview

---

**Project Name**

*Fcamr*

---

**Project type**

**Cas9-KO**

---

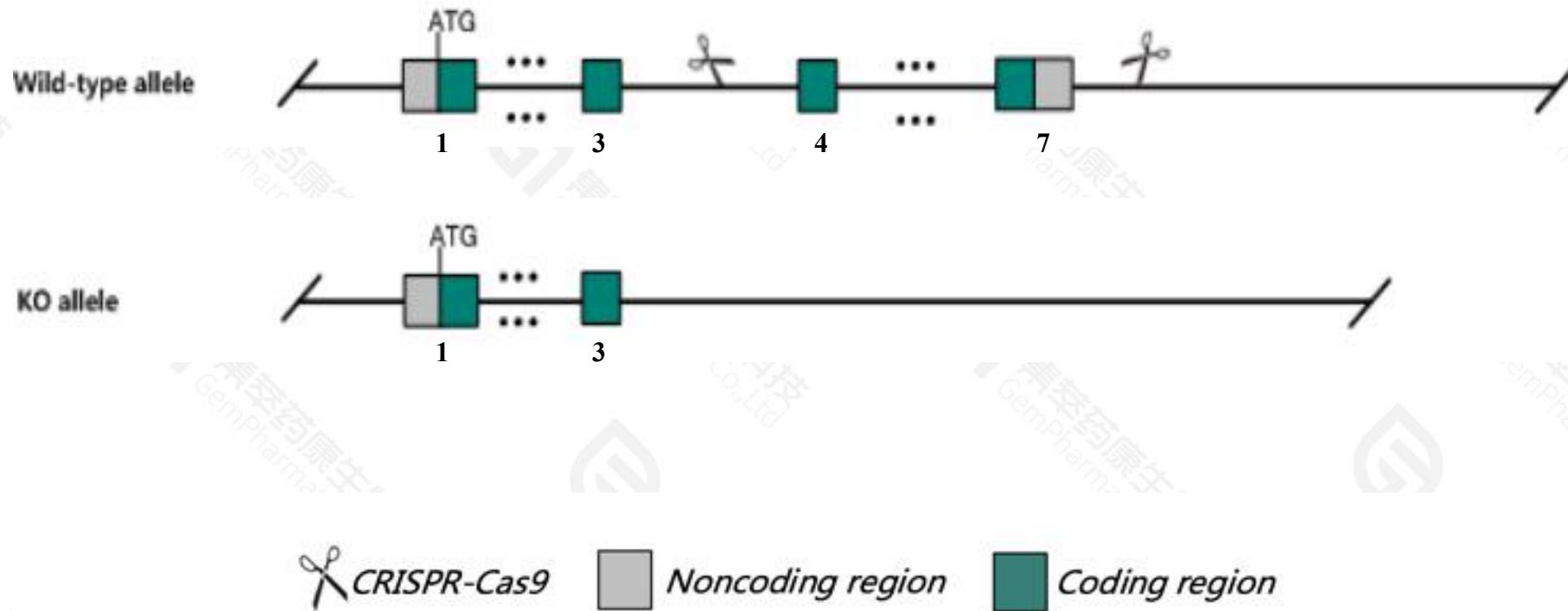
**Strain background**

**C57BL/6JGpt**

---

# Knockout strategy

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



- The *Fcamr* gene has 2 transcripts. According to the structure of *Fcamr* gene, exon4-exon7 of *Fcamr*-202(ENSMUST00000112477.9) transcript is recommended as the knockout region. The region contains 1370bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Fcamr* gene. The brief process is as follows: CRISPR-Cas9 system 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, homozygous null mice have enhanced germinal center formation, affinity maturation and memory induction of IgG3 producing B cells after immunization with T cell-independent antigens.
- Knockout region is located in the intron of *Gm15848* gene, which may affect its splicing regulation function.
- The *Fcamr* gene is located on the Chr1. 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)

## Fcamr Fc receptor, IgA, IgM, high affinity [Mus musculus (house mouse)]

Gene ID: 64435, updated on 31-Jan-2019

### Summary



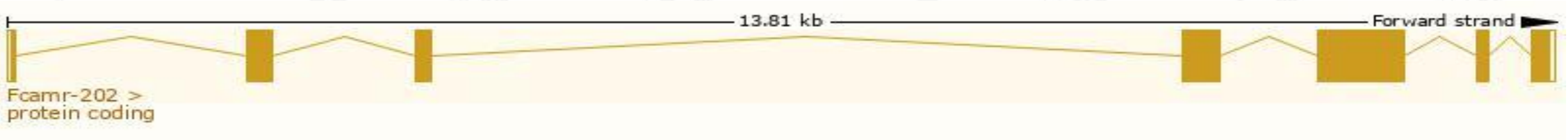
<b>Official Symbol</b>	Fcamr provided by <a href="#">MGI</a>
<b>Official Full Name</b>	Fc receptor, IgA, IgM, high affinity provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1927803</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000026415</a>
<b>Gene type</b>	protein coding
<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>Expression</b>	Biased expression in spleen adult (RPKM 2.6), kidney adult (RPKM 1.8) and 10 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

The gene has 2 transcripts,all transcripts are shown below:

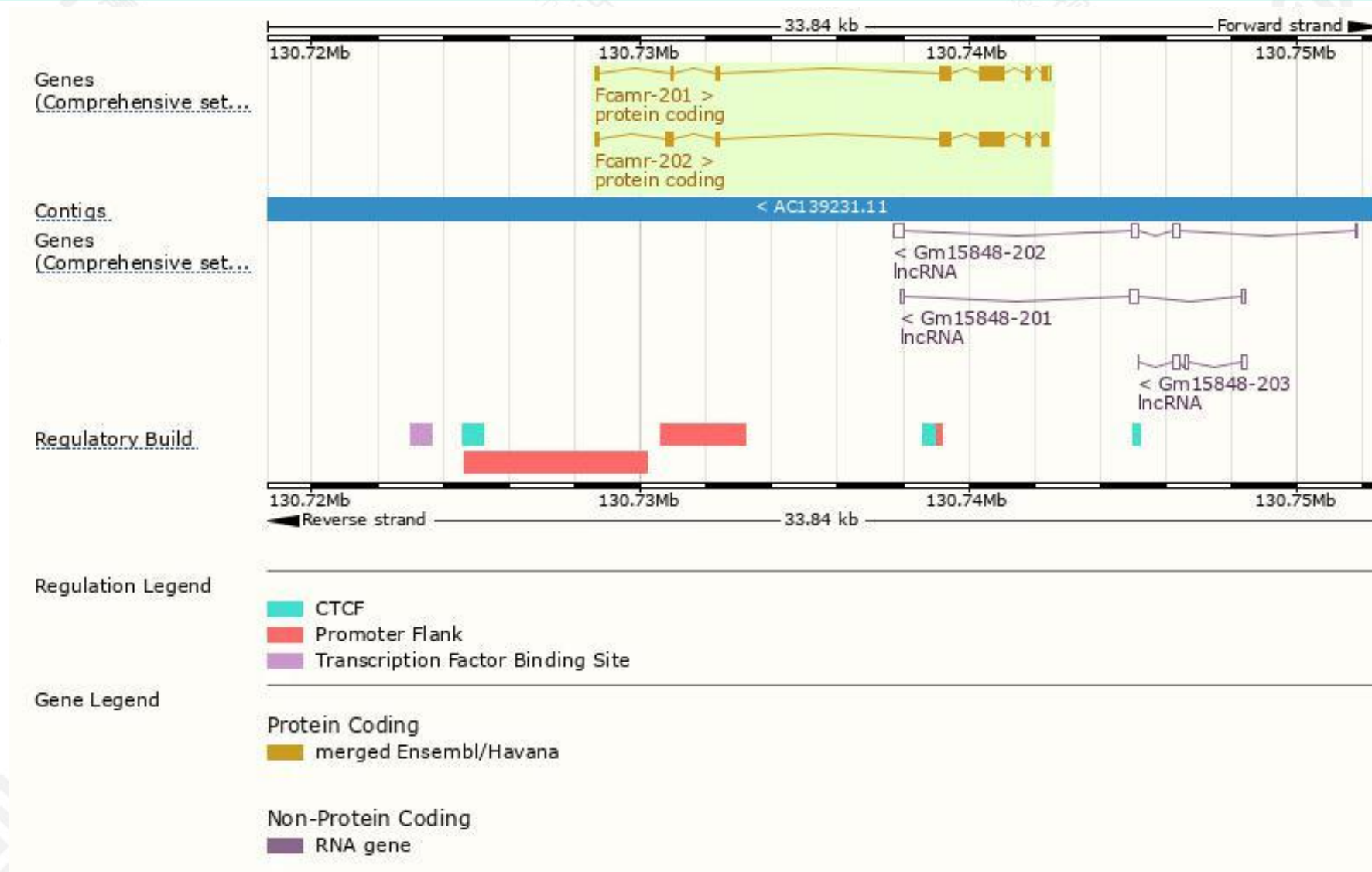
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fcamr-202	<a href="#">ENSMUST00000112477.8</a>	1879	<a href="#">591aa</a>	Protein coding	<a href="#">CCDS48353</a>	<a href="#">Q2TB54</a>	TSL:1 GENCODE basic APPRIS ALT2
Fcamr-201	<a href="#">ENSMUST00000027670.3</a>	1743	<a href="#">535aa</a>	Protein coding	<a href="#">CCDS15259</a>	<a href="#">Q2TB54</a>	TSL:1 GENCODE basic APPRIS P3

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



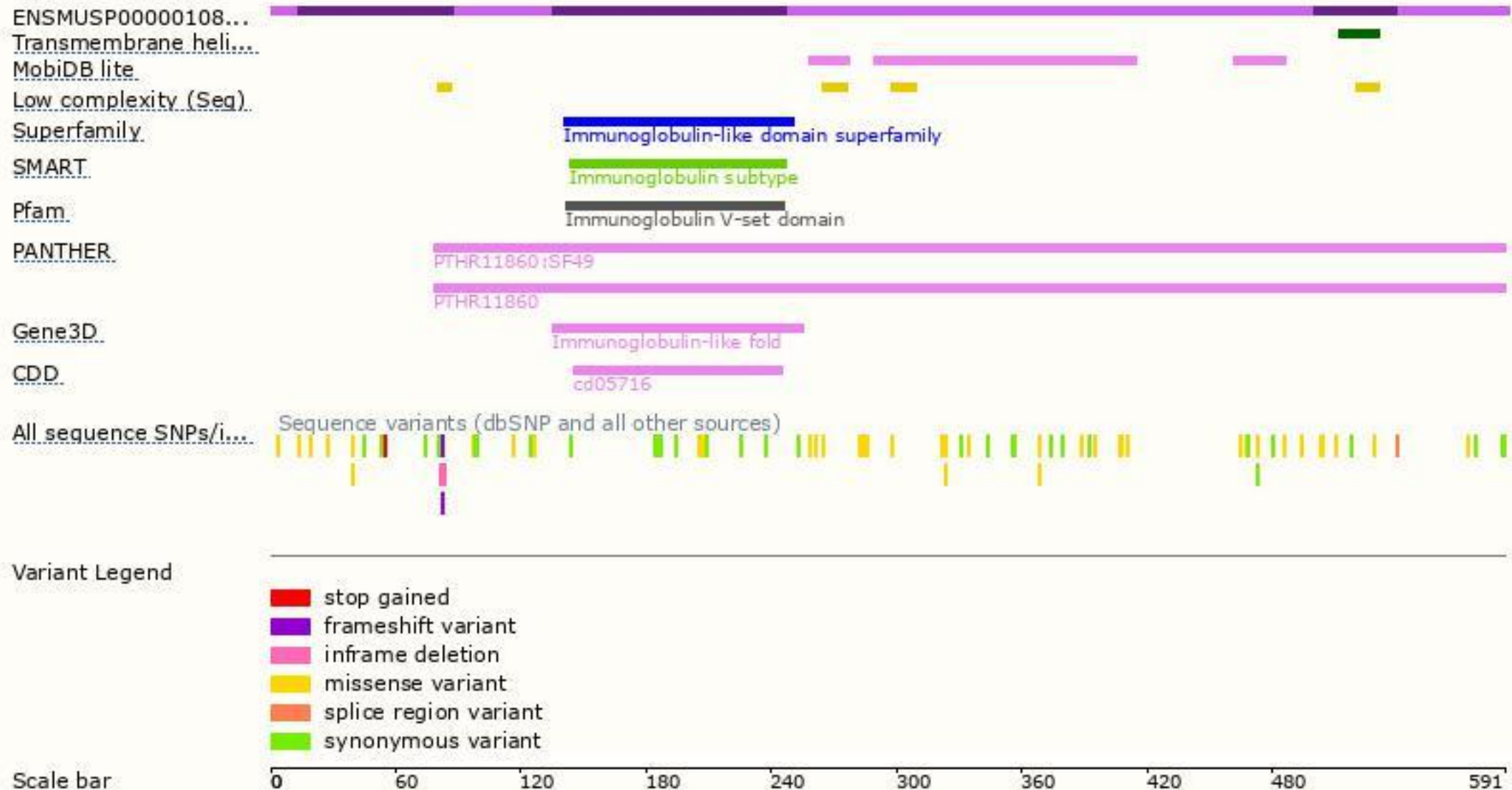


# Genomic location distribution

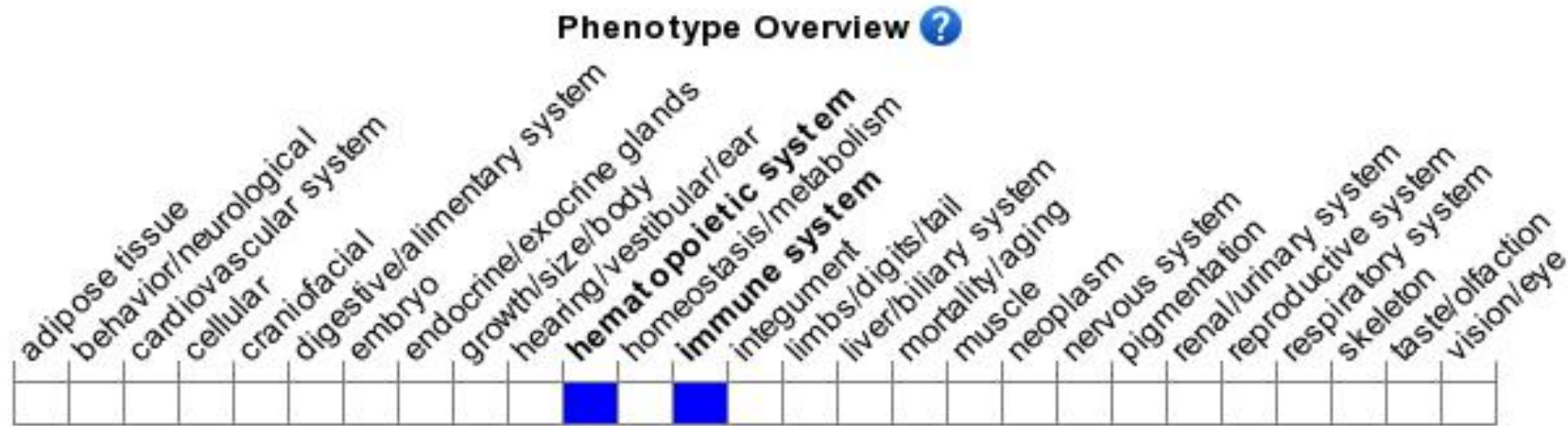




# Protein domain



# 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, homozygous null mice have enhanced germinal center formation, affinity maturation and memory induction of IgG3 producing B cells after immunization with T cell-independent antigens.

If you have any questions, you are welcome to inquire.  
Tel: 400-9660890

