

# ***Ffar2(Gpr43)*** Cas9-KO Strategy

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# Project Overview

**Project Name**

*Ffar2*

**Project type**

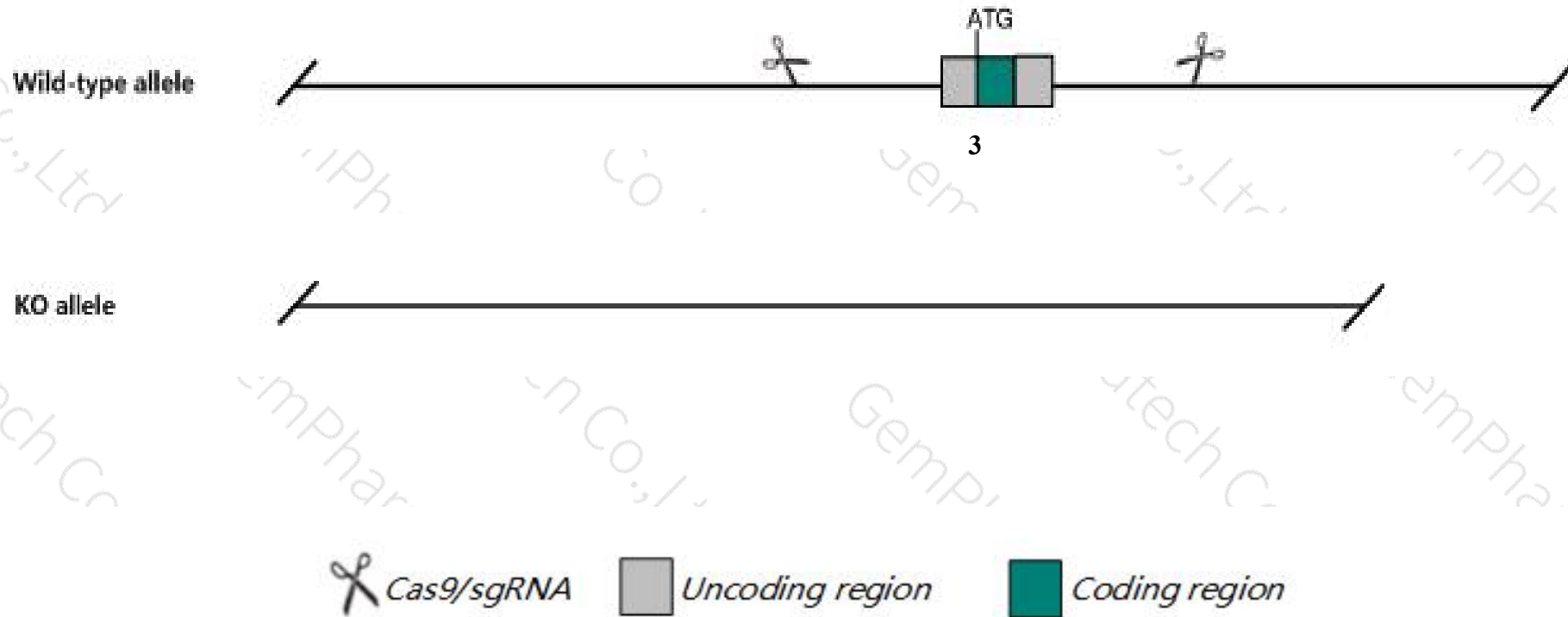
**Cas9-KO**

**Strain background**

**C57BL/6J**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ffar2* gene. The schematic diagram is as follows:



- The *Ffar2* gene has 6 transcripts. According to the structure of *Ffar2* gene, exon3 of *Ffar2-201* (ENSMUST00000053156.9) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ffar2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Mice homozygous for a null allele show altered granulocyte and neutrophil physiology and increased inflammation in models of induced colitis, arthritis and asthma, whereas homozygotes for a different null allele show reduced neutrophil recruitment and decreased susceptibility to induced colitis.
- The *Ffar2* gene is located on the Chr7. 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)

## Ffar2 free fatty acid receptor 2 [Mus musculus (house mouse)]

Gene ID: 233079, updated on 12-Mar-2019

### Summary



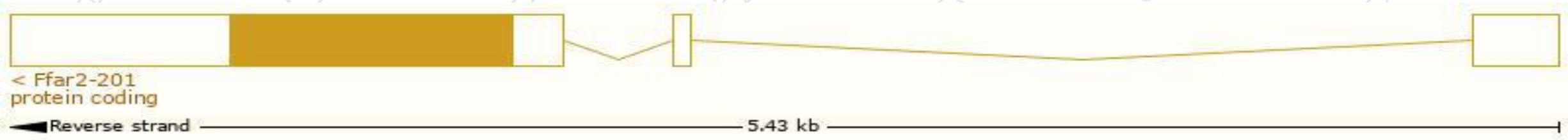
<b>Official Symbol</b>	Ffar2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	free fatty acid receptor 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2441731</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000051314</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	GPCR43, Gpr43
<b>Expression</b>	Biased expression in colon adult (RPKM 10.2), subcutaneous fat pad adult (RPKM 8.2) and 10 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

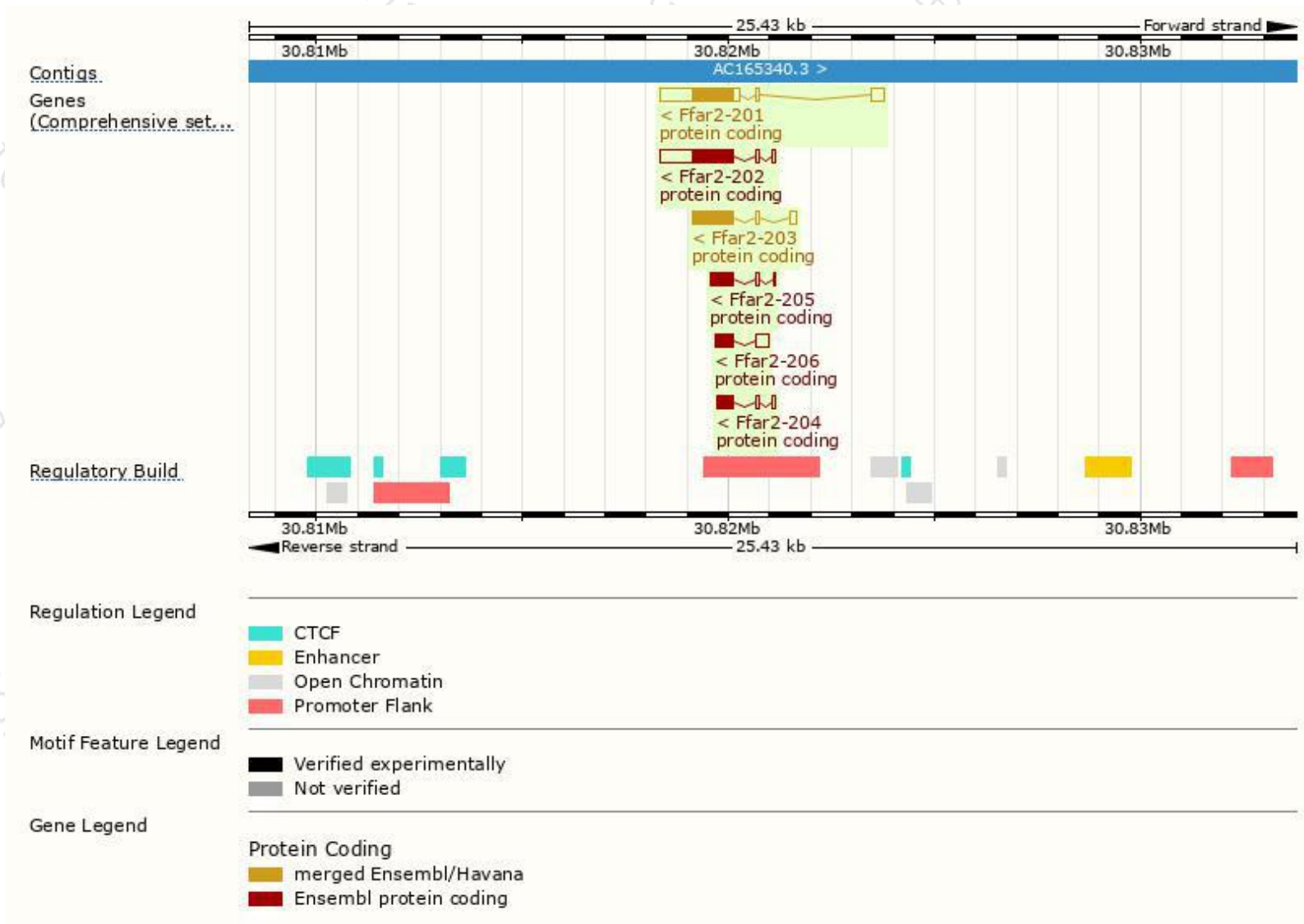
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ffar2-201	<a href="#">ENSMUST00000053156.9</a>	2301	<a href="#">330aa</a>	Protein coding	<a href="#">CCDS21111</a>	<a href="#">Q8VCK6</a>	TSL:1 GENCODE basic APPRIS P1
Ffar2-202	<a href="#">ENSMUST00000163504.7</a>	1913	<a href="#">330aa</a>	Protein coding	<a href="#">CCDS21111</a>	<a href="#">Q8VCK6</a>	TSL:2 GENCODE basic APPRIS P1
Ffar2-203	<a href="#">ENSMUST00000168528.7</a>	1210	<a href="#">330aa</a>	Protein coding	<a href="#">CCDS21111</a>	<a href="#">Q8VCK6</a>	TSL:1 GENCODE basic APPRIS P1
Ffar2-204	<a href="#">ENSMUST00000186059.1</a>	565	<a href="#">133aa</a>	Protein coding	-	<a href="#">A0A087WR60</a>	CDS 3' incomplete TSL:2
Ffar2-205	<a href="#">ENSMUST00000186339.6</a>	641	<a href="#">182aa</a>	Protein coding	-	<a href="#">A0A087WR67</a>	CDS 3' incomplete TSL:2
Ffar2-206	<a href="#">ENSMUST00000186534.1</a>	730	<a href="#">142aa</a>	Protein coding	-	<a href="#">A0A087WQJ1</a>	CDS 3' incomplete TSL:2

The strategy is based on the design of *Ffar2-201* transcript,The transcription is shown below

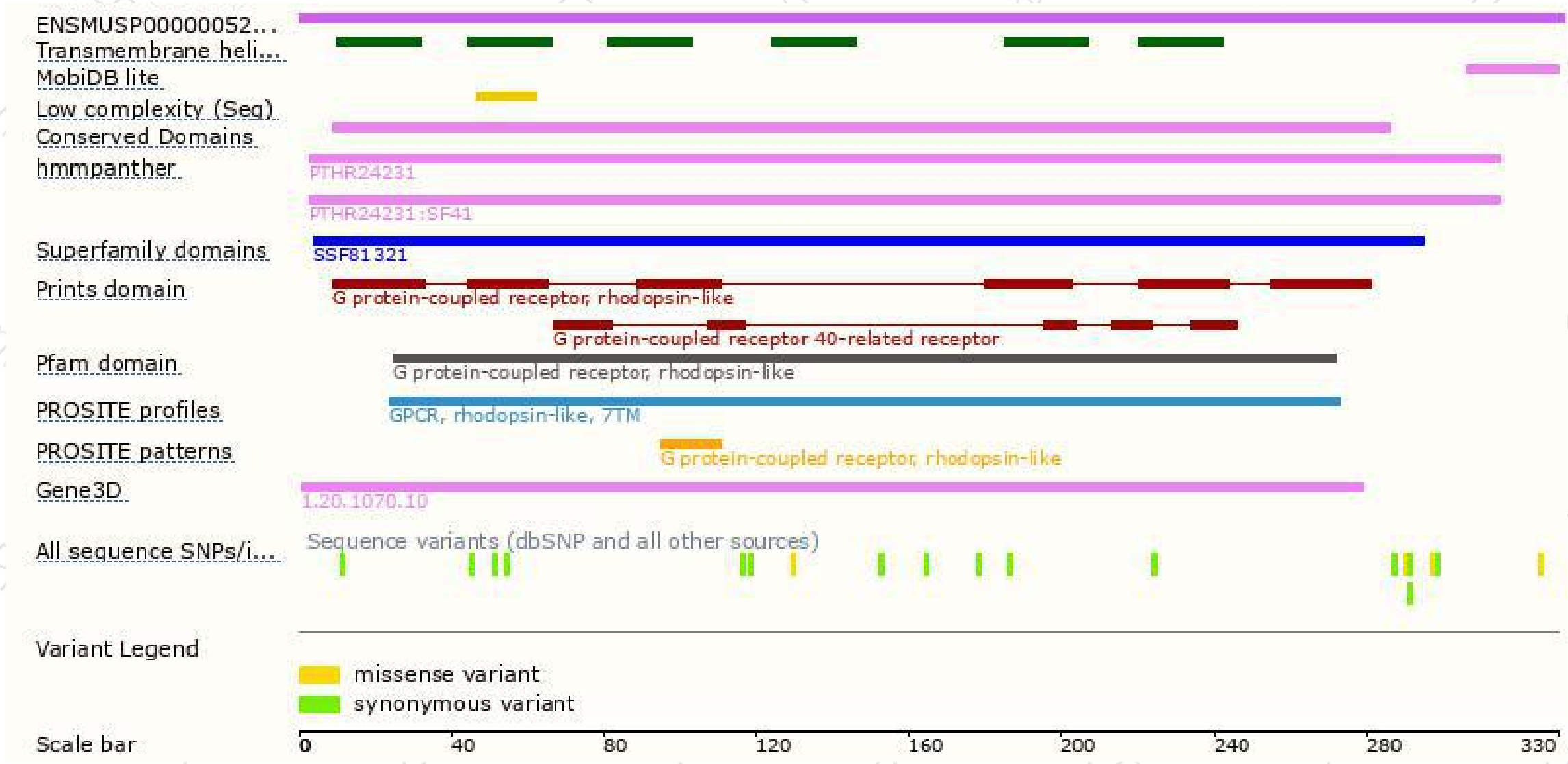


# Genomic location distribution

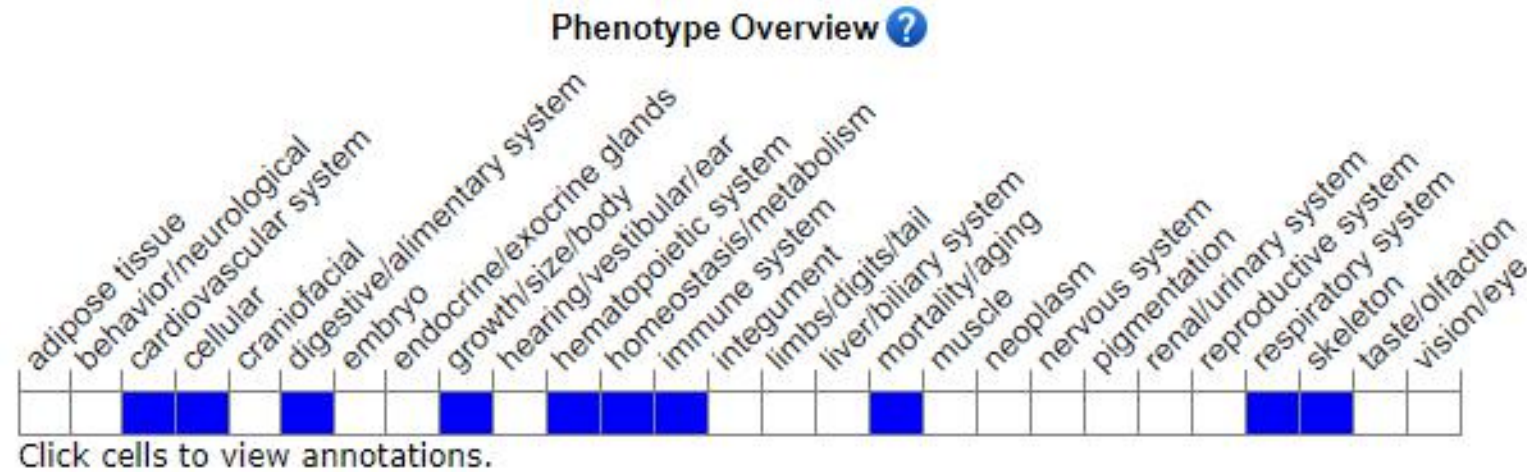




# Protein domain



# 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, Mice homozygous for a null allele show altered granulocyte and neutrophil physiology and increased inflammation in models of induced colitis, arthritis and asthma, whereas homozygotes for a different null allele show reduced neutrophil recruitment and decreased susceptibility to induced colitis.

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

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