

Arhgap15 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Arhgap15

Project type

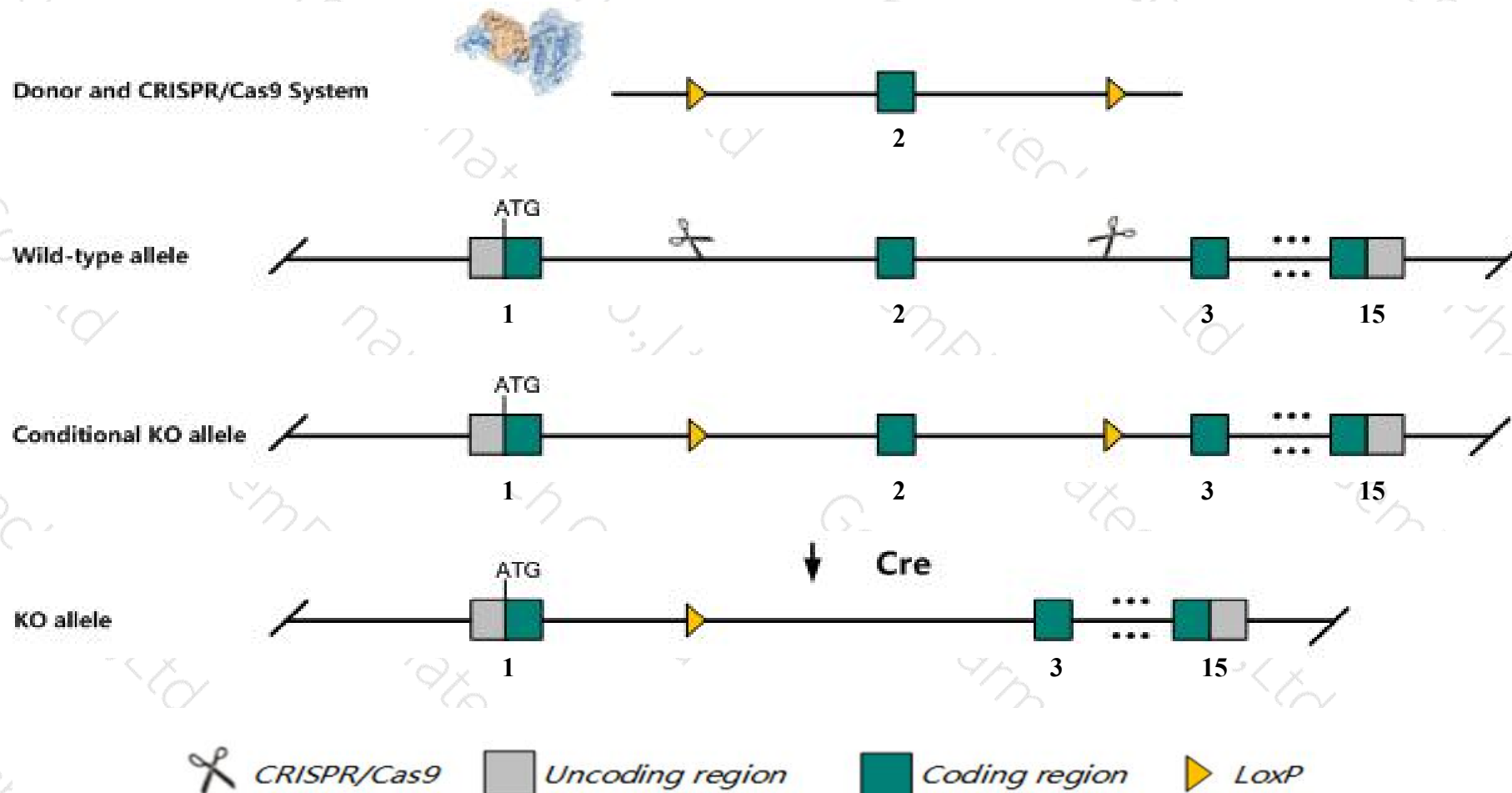
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgap15* gene. The schematic diagram is as follows:



- The *Arhgap15* gene has 5 transcripts. According to the structure of *Arhgap15* gene, exon2 of *Arhgap15*-203 (ENSMUST00000112824.7) transcript is recommended as the knockout region. The region contains 178bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arhgap15* 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, Mice homozygous for disruption of this gene display reduced leukocyte numbers and abnormally shaped macrophage. Chemotactic responses of macrophage are normal while neutrophil chemoattraction and bacterial phagocytosis are increased.
- The *Arhgap15* gene is located on the Chr2. 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)

Arhgap15 Rho GTPase activating protein 15 [*Mus musculus* (house mouse)]

Gene ID: 76117, updated on 13-Mar-2020

Summary

Official Symbol	Arhgap15 provided by MGI
Official Full Name	Rho GTPase activating protein 15 provided by MGI
Primary source	MGI:MGI:1923367
See related	Ensembl:ENSMUSG00000049744
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5830480G12Rik
Summary	The protein encoded by this gene is a RAC GTPase-activating protein that is regulated through its PH domain and by recruitment to the membrane. The protein accelerates hydrolysis of guanosine triphosphate to guanosine diphosphate to repress Rac activity. Knock-out of Arhgap15 function demonstrates that this gene is required to regulate multiple functions in macrophages and neutrophils. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Sep 2014]
Expression	Broad expression in thymus adult (RPKM 1.0), cortex adult (RPKM 0.9) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

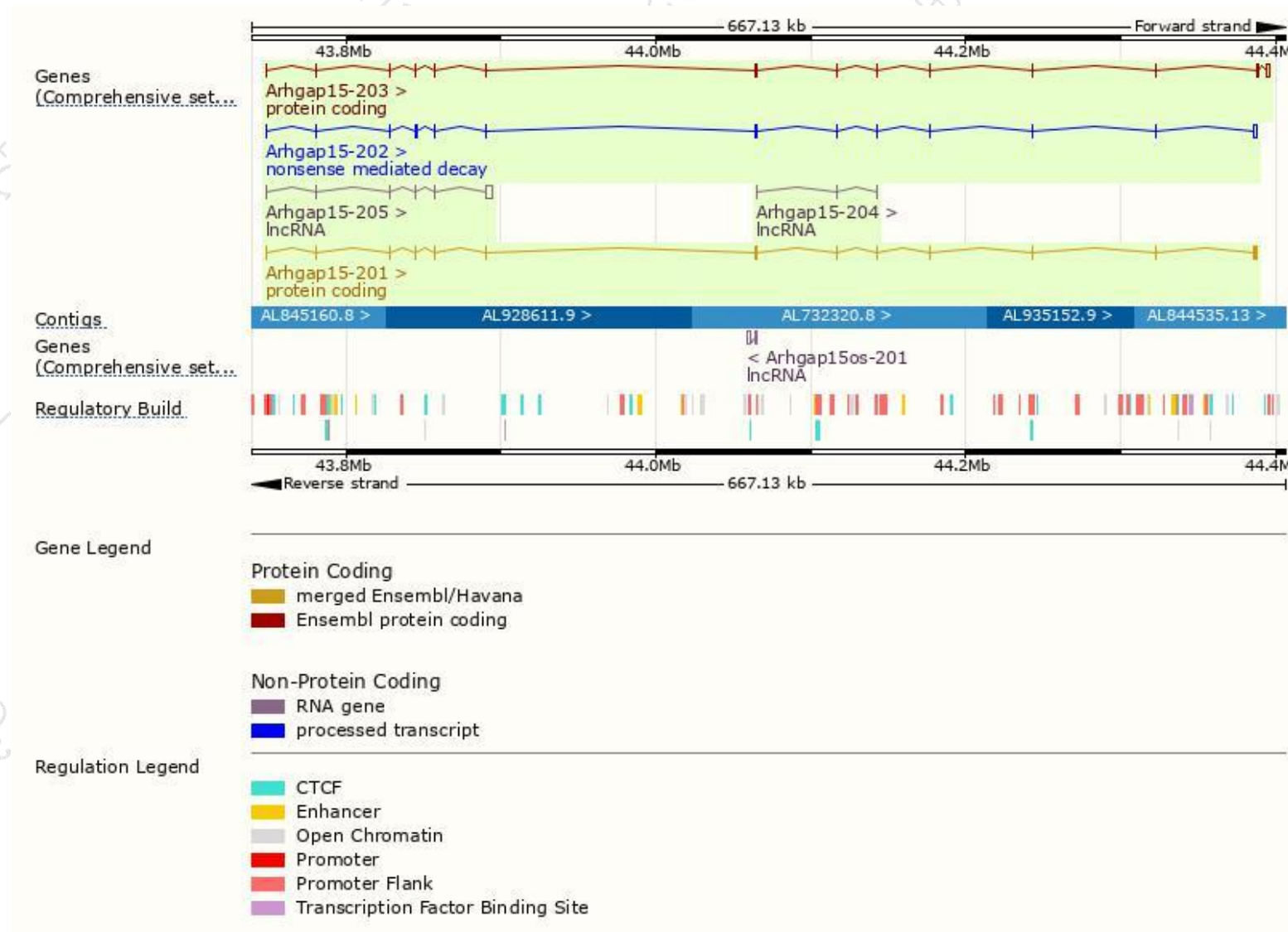
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arhgap15-203	ENSMUST00000112824.7	3118	477aa	Protein coding	CCDS79793	B1AW40	TSL:1 GENCODE basic
Arhgap15-201	ENSMUST00000055776.7	2604	481aa	Protein coding	CCDS16019	Q811M1	TSL:1 GENCODE basic APPRIS P1
Arhgap15-202	ENSMUST00000112822.7	2714	108aa	Nonsense mediated decay	-	Q811M1	TSL:1
Arhgap15-205	ENSMUST00000140528.1	4709	No protein	Processed transcript	-	-	TSL:2
Arhgap15-204	ENSMUST00000128630.1	397	No protein	Processed transcript	-	-	TSL:3

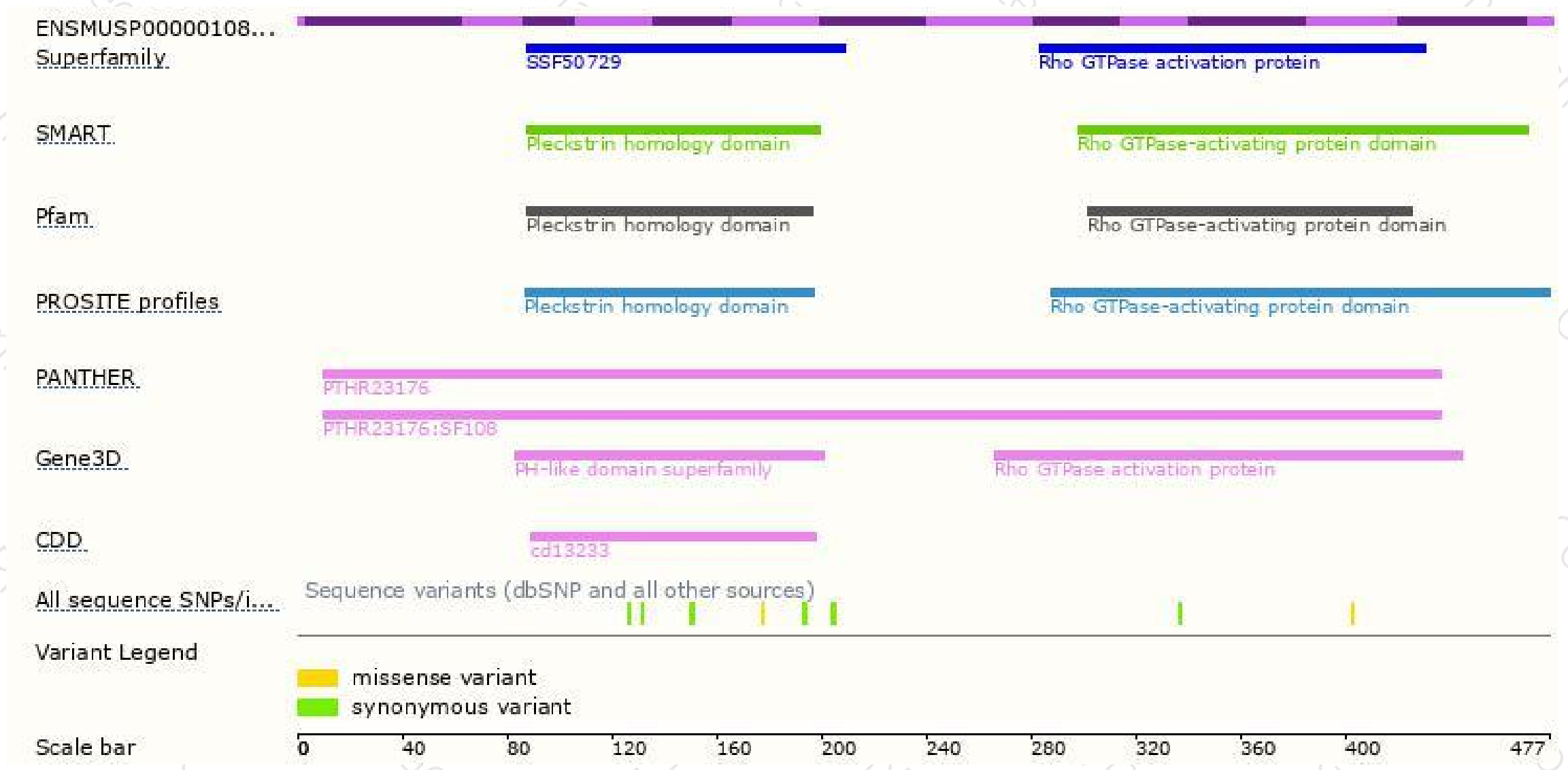
The strategy is based on the design of *Arhgap15-203* transcript,The transcription is shown below



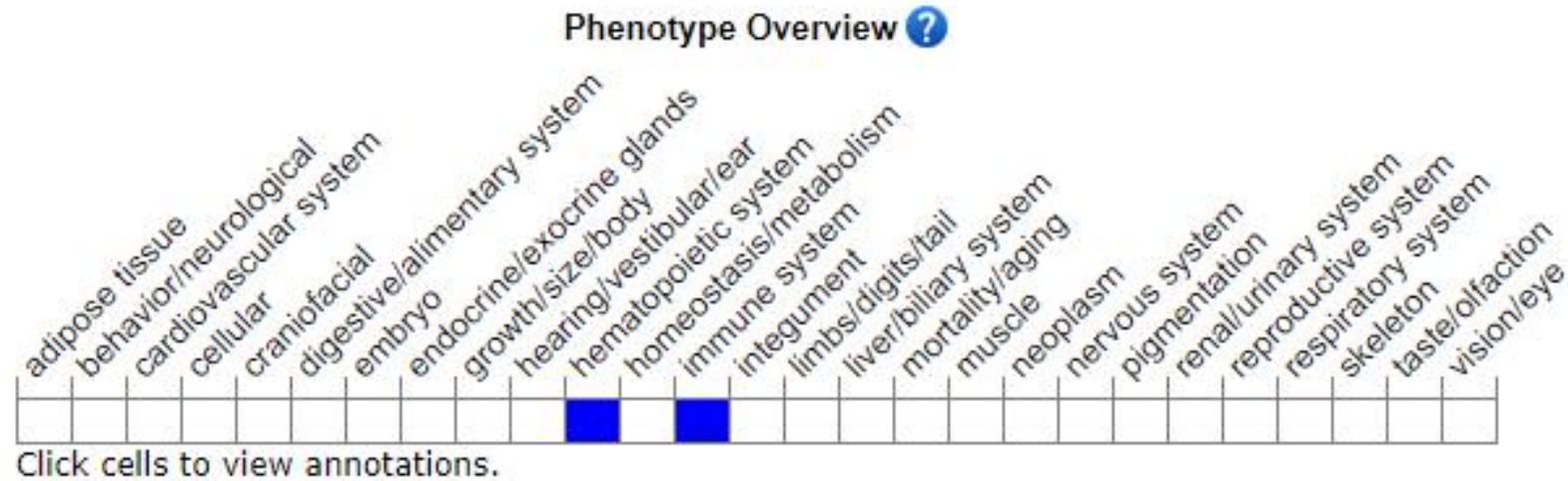
Genomic location distribution



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 disruption of this gene display reduced leukocyte numbers and abnormally shaped macrophage. Chemotactic responses of macrophage are normal while neutrophil chemoattraction and bacterial phagocytosis are increased.

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

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