Irf2 Cas9-CKO Strategy

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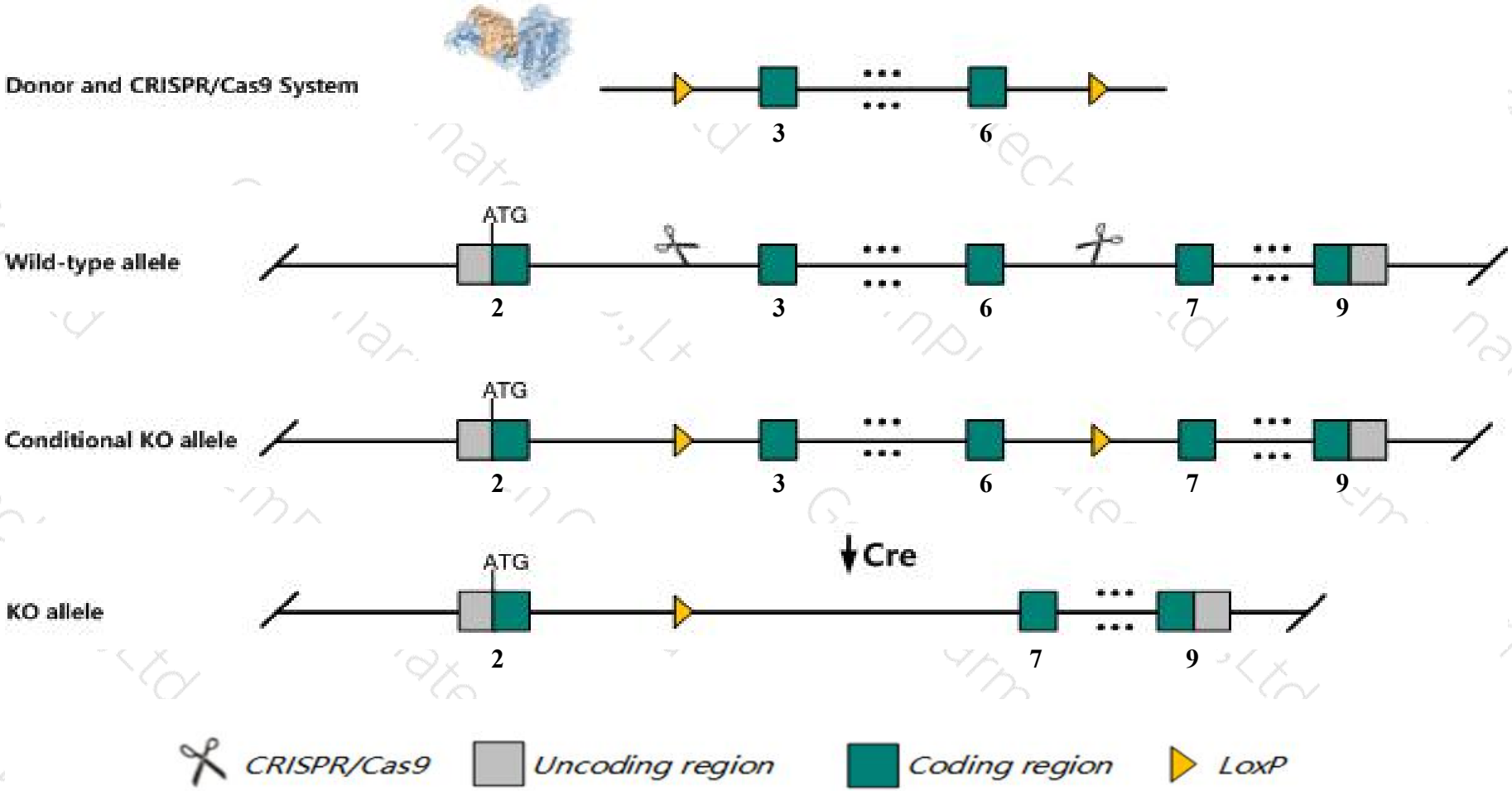
Project Overview

Project Name	***Irf2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Irf2* gene. The schematic diagram is as follows:



Technical routes

- The *Irf2* gene has 11 transcripts. According to the structure of *Irf2* gene, exon3-exon6 of *Irf2-201* (ENSMUST00000034041.8) transcript is recommended as the knockout region.The region contains 442bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Irf2* 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.

Notice

➢ According to the existing MGI data,Mice homozygous for a knock-out allele exhibit abnormalities in B lymphopoiesis and hematopoiesis, often die prematurely, show increased mortality following lymphocytic choriomeningitis virus infection, and develop an inflammatory skin disease involving CD8+ Tcells.

➢The effect of transcript 209 is unknown.

➢ The *Irf2* gene is located on the Chr8. 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）

集萃药康 GemPharmatech

Irf2 interferon regulatory factor 2 [*Mus musculus* (house mouse)]

Gene ID: 16363, updated on 12-Aug-2019

Summary

Official Symbol	Irf2 provided by MGI
Official Full Name	interferon regulatory factor 2 provided by MGI
Primary source	MGI:MGI:96591
See related	Ensembl:ENSMUSG00000031627
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Irf-2; AI646973; 9830146E22Rik
Expression	Ubiquitous expression in spleen adult (RPKM 5.7), colon adult (RPKM 4.6) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 8; 8 B1.1

See Irf2 in Genome Data Viewer

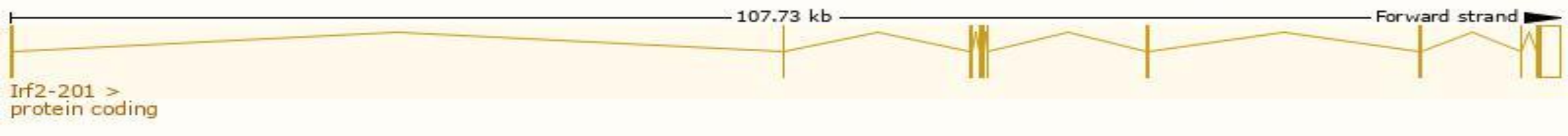
Exon count: 13

Transcript information（Ensembl）

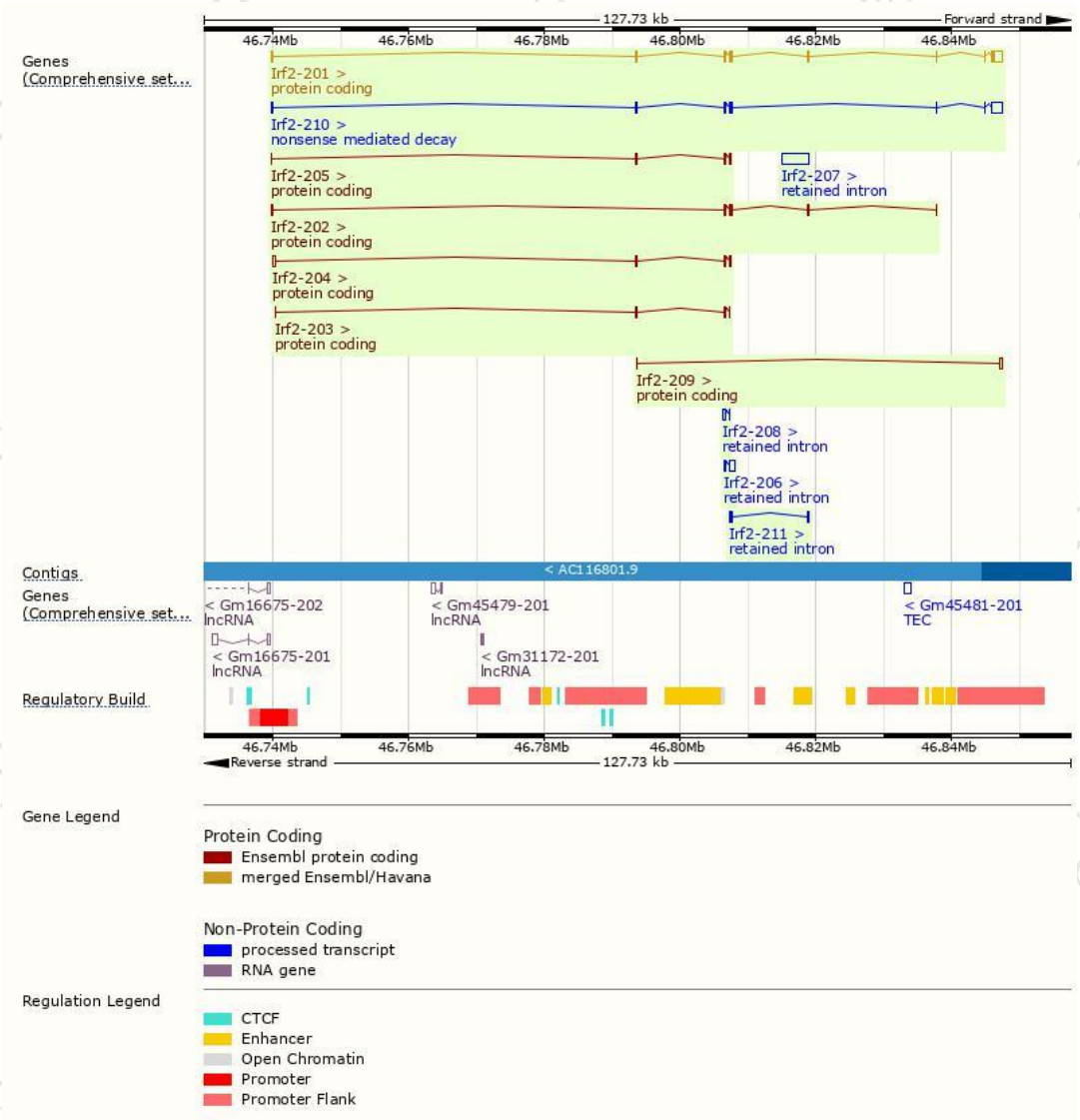
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Irf2-201	ENSMUST00000034041.8	2497	349aa	Protein coding	CCDS22295	P23906 Q3U2Z2	TSL:1 GENCODE basic APPRIS P1
Irf2-202	ENSMUST00000207105.1	720	180aa	Protein coding	-	A0A140LI82	CDS 3' incomplete TSL:5
Irf2-204	ENSMUST00000208433.1	566	118aa	Protein coding	-	A0A140LIX2	CDS 3' incomplete TSL:2
Irf2-209	ENSMUST00000210218.1	535	41aa	Protein coding	-	A0A1B0GQZ7	TSL:3 GENCODE basic
Irf2-205	ENSMUST00000208507.1	383	113aa	Protein coding	-	A0A140LJA4	CDS 3' incomplete TSL:5
Irf2-203	ENSMUST00000207571.2	352	88aa	Protein coding	-	A0A140LHP8	CDS 3' incomplete TSL:5
Irf2-210	ENSMUST00000210284.1	2338	138aa	Nonsense mediated decay	-	A0A1B0GQW5	TSL:1
Irf2-207	ENSMUST00000209820.1	3965	No protein	Retained intron	-	-	TSL:NA
Irf2-206	ENSMUST00000208976.1	944	No protein	Retained intron	-	-	TSL:1
Irf2-211	ENSMUST00000210334.1	397	No protein	Retained intron	-	-	TSL:3
Irf2-208	ENSMUST00000210095.1	324	No protein	Retained intron	-	-	TSL:1

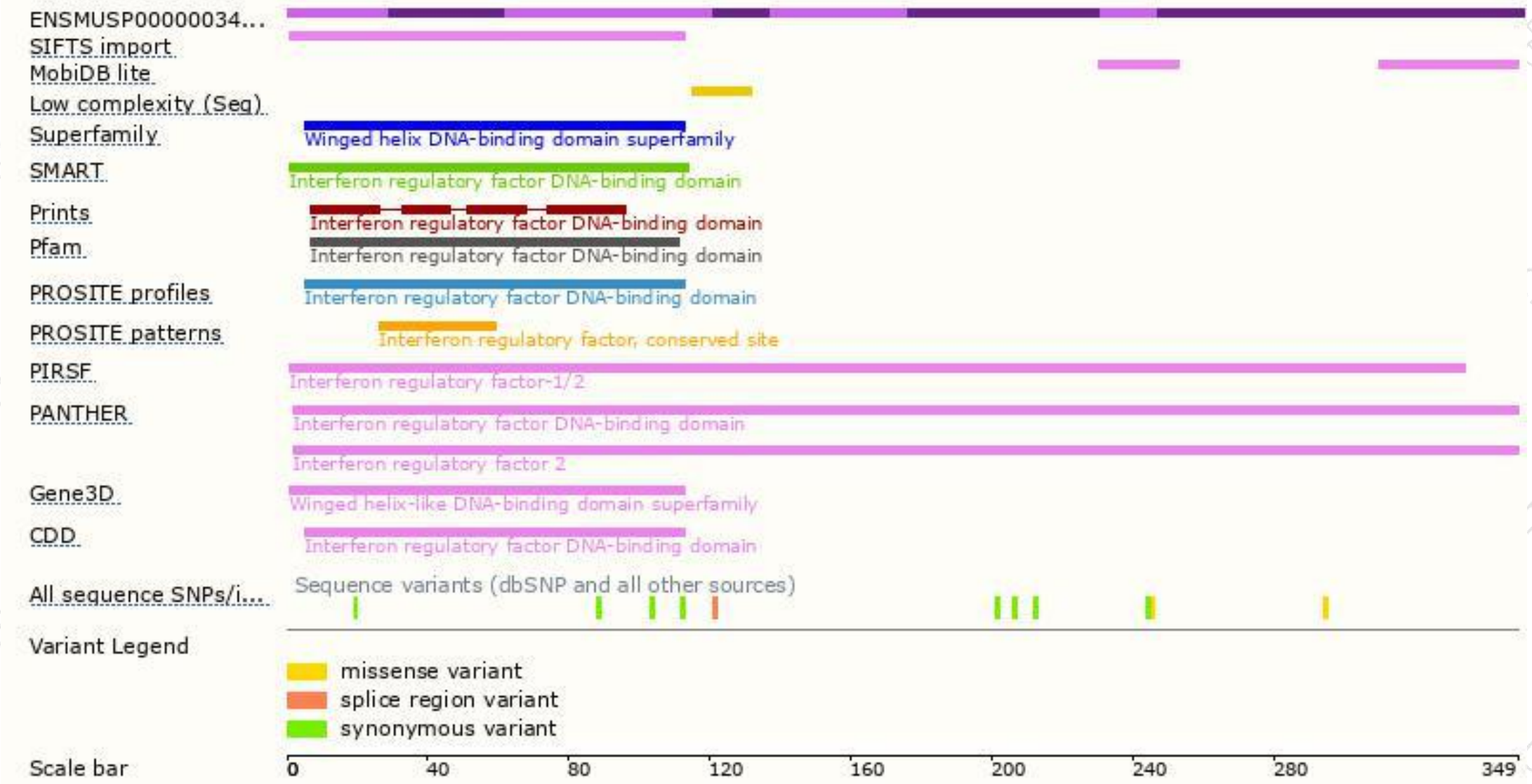
The strategy is based on the design of *Irf2-201* transcript,The transcription is shown below



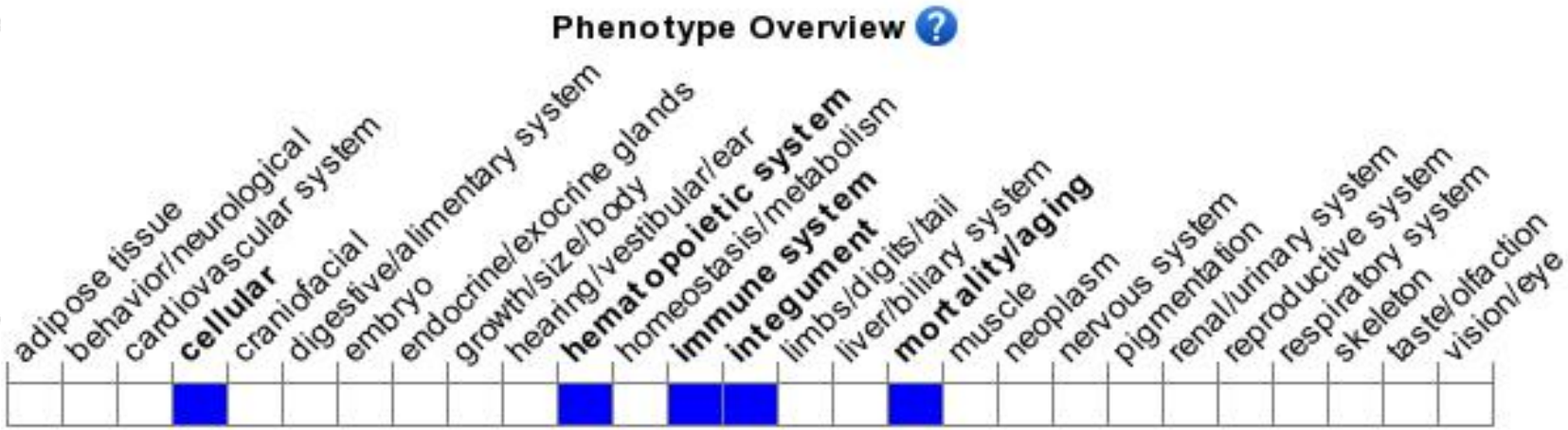
Genomic location distribution



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 knock-out allele exhibit abnormalities in B lymphopoiesis and hematopoiesis, often die prematurely, show increased mortality following lymphocytic choriomeningitis virus infection, and develop an inflammatory skin disease involving CD8+ Tcells.

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

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