Irf8 Cas9-CKO Strategy

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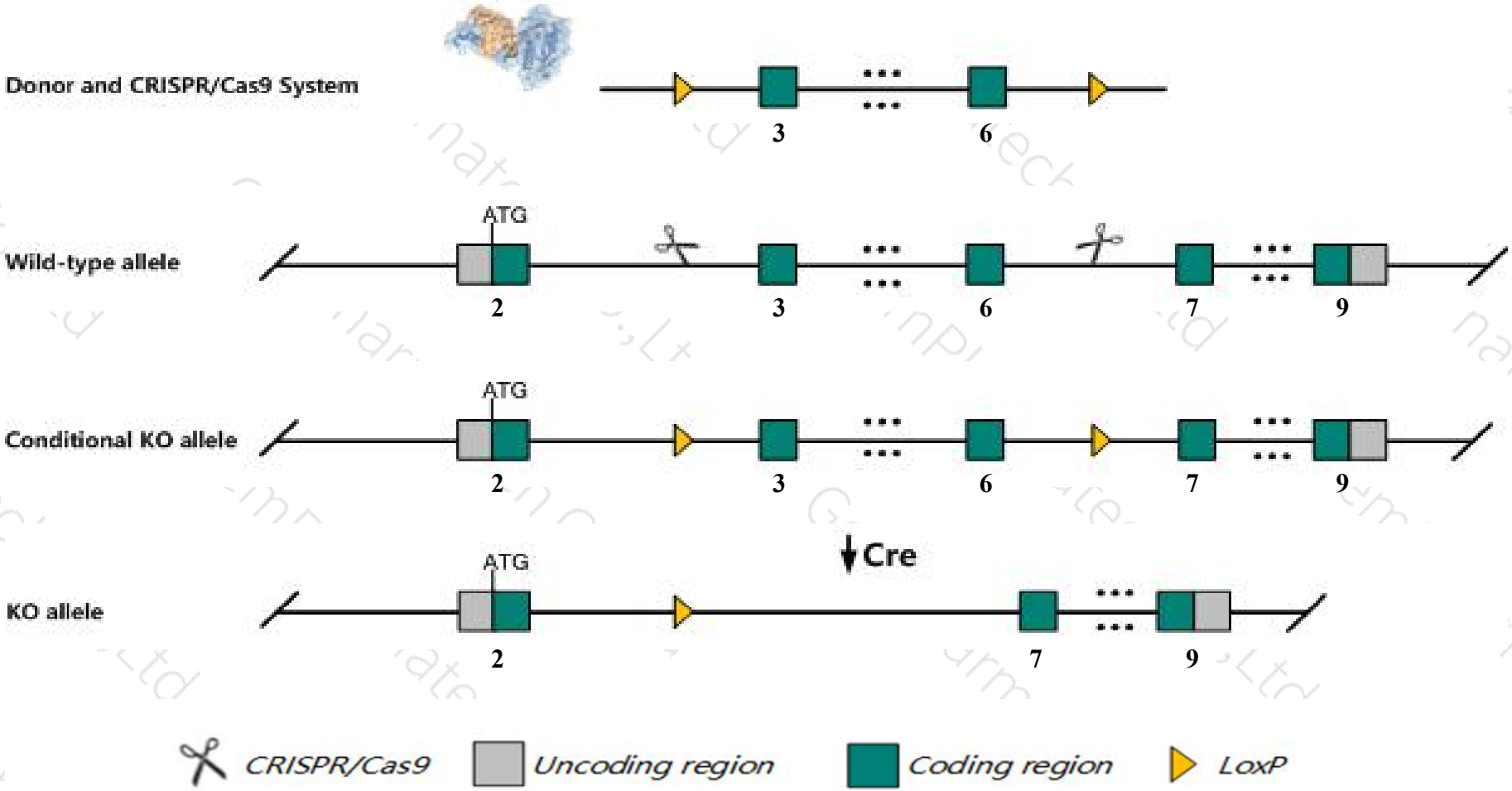
Project Overview

Project Name	***Irf8***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Irf8* gene. The schematic diagram is as follows:



Technical routes

- The *Irf8* gene has 7 transcripts. According to the structure of *Irf8* gene, exon3-exon6 of *Irf8-201* (ENSMUST00000047737.9) transcript is recommended as the knockout region.The region contains 427bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Irf8* 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,Homozygotes for a targeted null mutation exhibit increased incidence of viral infections, shortened life span, deregulated hematopoiesis, and hematological neoplasias. Heterozygotes show similar, but milder, phenotypes.

➢ The KO region contains functional region of the *Gm20388* gene. Knockout the region may affect the function of *Gm20388* gene .

➢ The *Irf8* 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）

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Irf8 interferon regulatory factor 8 [Mus musculus (house mouse)]

Gene ID: 15900, updated on 9-Apr-2019

Summary

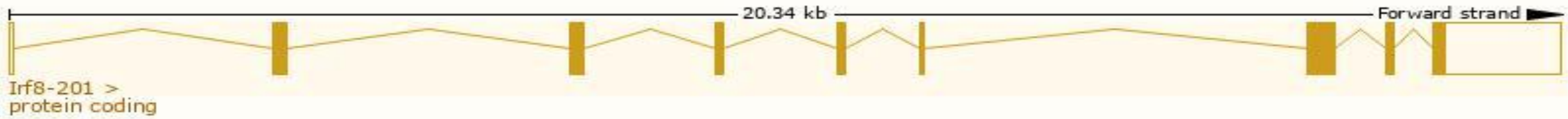
Official Symbol	Irf8 provided by MGI
Official Full Name	interferon regulatory factor 8 provided byMGI
Primary source	MGI:MGI:96395
See related	Ensembl:ENSMUSG00000041515
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI893568, ICSBP, IRF-8, Icsbp1, Myls
Summary	The protein encoded by this gene is a transcription factor that belongs to the interferon regulatory factor family. Proteins belonging to this family have a DNA binding domain at the amino terminus that contains five well-conserved tryptophan-rich repeats. This domain recognizes DNA sequences similar to the interferon-stimulated response element. The protein encoded by this gene promotes or suppresses lineage-specific genes to regulate the differentation of lymphoid and myeloid lineage cells. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2014]
Expression	Biased expression in spleen adult (RPKM 59.4), large intestine adult (RPKM 27.2) and 12 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

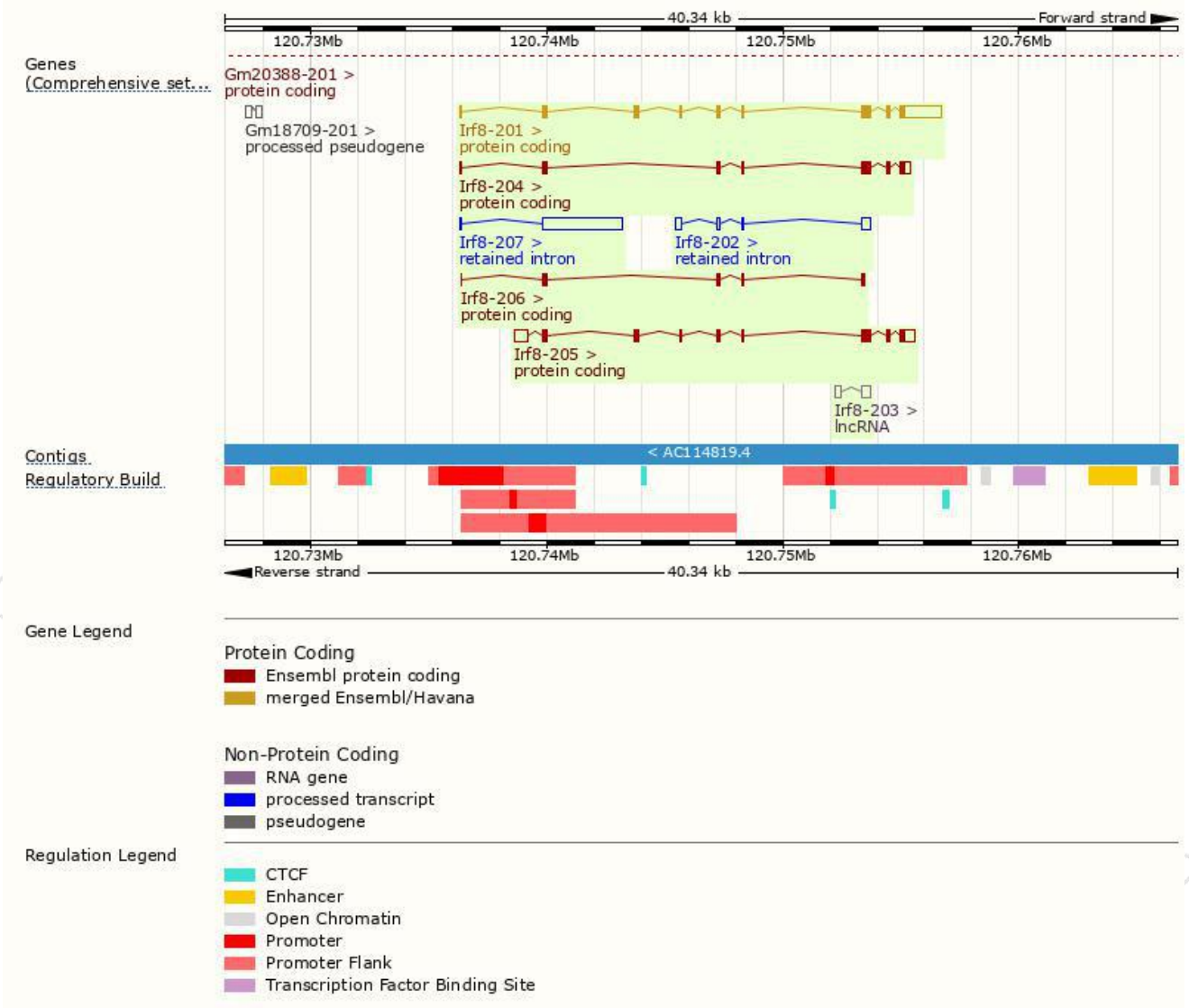
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Irf8-201	ENSMUST00000047737.9	2847	424aa	Protein coding	CCDS22721	P23611 Q544J7	TSL:1 GENCODE basic APPRIS P1
Irf8-205	ENSMUST00000162001.7	2270	424aa	Protein coding	CCDS22721	P23611 Q544J7	TSL:1 GENCODE basic APPRIS P1
Irf8-204	ENSMUST00000160943.2	1284	333aa	Protein coding	-	F7C1A3	TSL:5 GENCODE basic
Irf8-206	ENSMUST00000162658.7	480	151aa	Protein coding	-	E0CZE4	CDS 3' incomplete TSL:3
Irf8-207	ENSMUST00000162775.1	3469	No protein	Retained intron	-	-	TSL:1
Irf8-202	ENSMUST00000160388.1	764	No protein	Retained intron	-	-	TSL:2
Irf8-203	ENSMUST00000160594.1	596	No protein	lncRNA	-	-	TSL:2

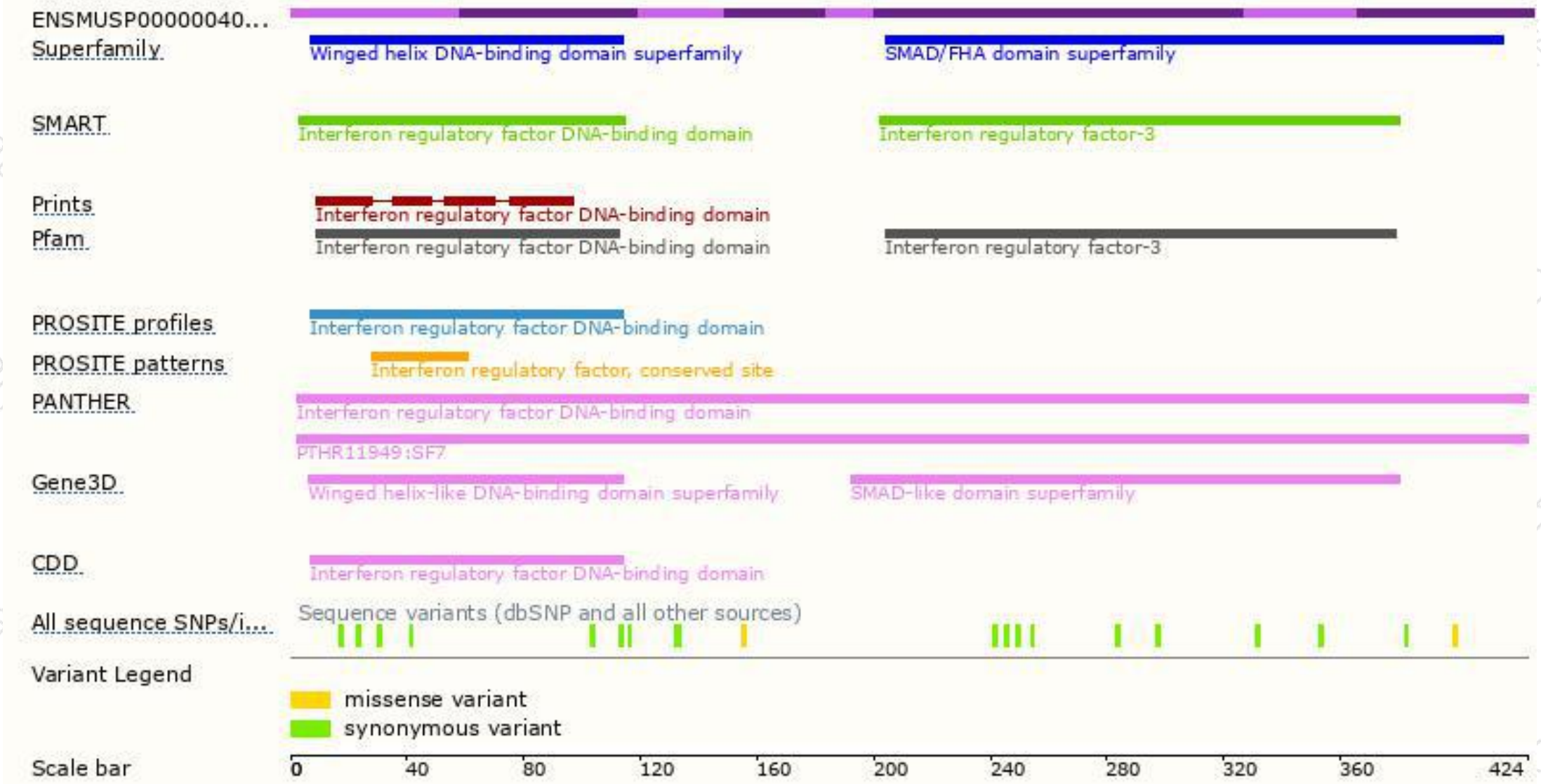
The strategy is based on the design of *Irf8-201* transcript,The transcription is shown below



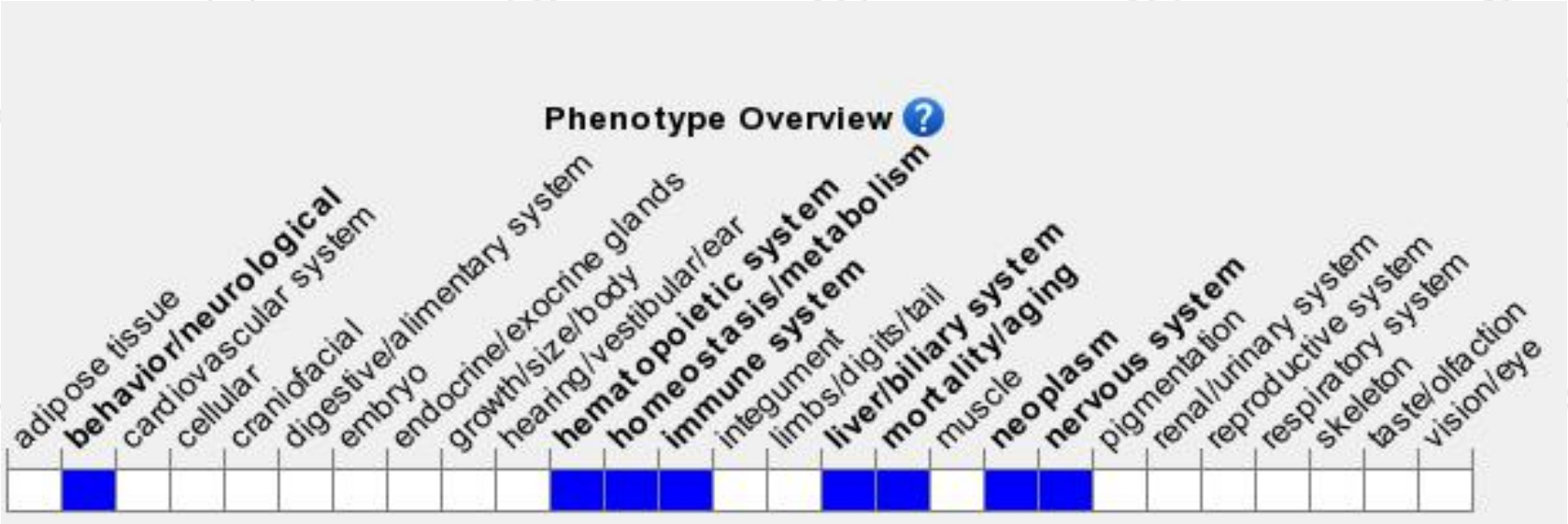
Genomic location distribution



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/).

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

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