Irf1 Cas9-CKO Strategy

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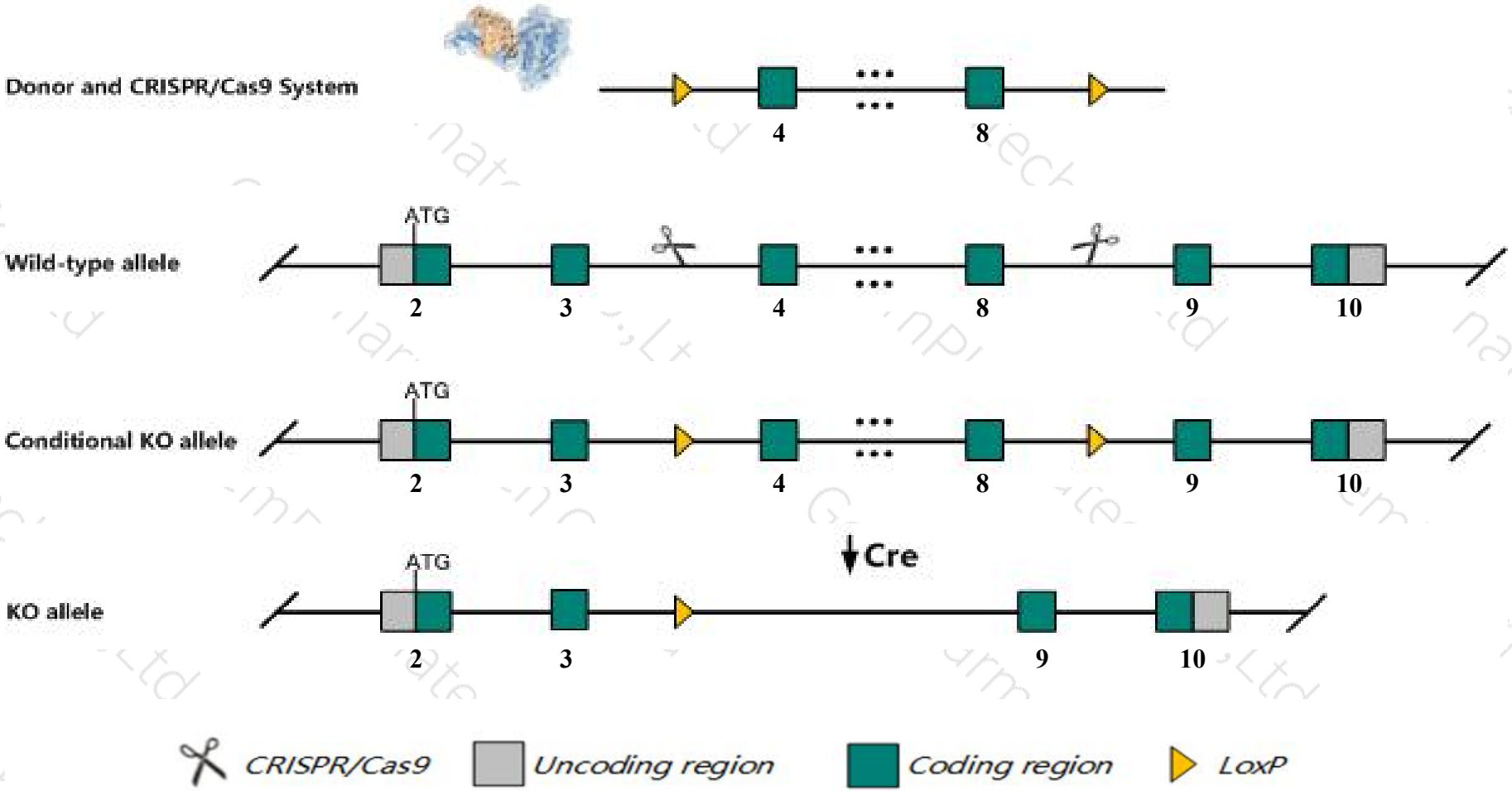
Design Date: 2019-7-25

Project Overview

Project Name	***Irf1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Irf1* gene. The schematic diagram is as follows:



Technical routes

- The *Irf1* gene has 10 transcripts. According to the structure of *Irf1* gene, exon4-exon8 of *Irf1-202* (ENSMUST00000108920.8) transcript is recommended as the knockout region.The region contains 533bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Irf1* 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,Homozygous disruption of this gene leads to reduced CD8+ T cell number and altered response to viral infection and may cause alterations in cytokine levels, CD4+ cell subset homeostasis, blood vessel healing, DNA repair, and susceptibility to induced lymphomas, arthritis and autoimmune encephalitis.

➢Transcript *Irf1-207* may not be affected.

➢ The *Irf1* gene is located on the Chr11. 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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Irf1 interferon regulatory factor 1 [Mus musculus (house mouse)]

Gene ID: 16362, updated on 9-Apr-2019

Summary

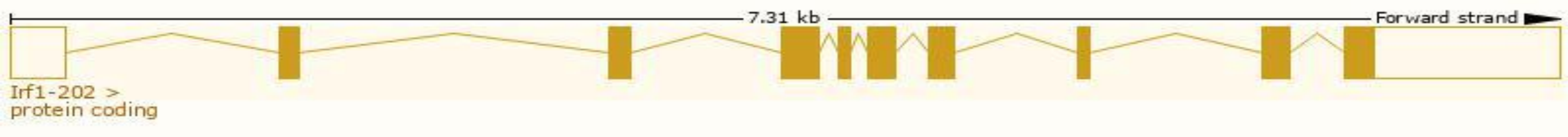
Official Symbol	Irf1 provided by MGI
Official Full Name	interferon regulatory factor 1 provided by MGI
Primary source	MGI:MGI:96590
See related	Ensembl:ENSMUSG00000018899
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU020929, Irf-1
Expression	Broad expression in large intestine adult (RPKM 53.2), colon adult (RPKM 41.6) and 20 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

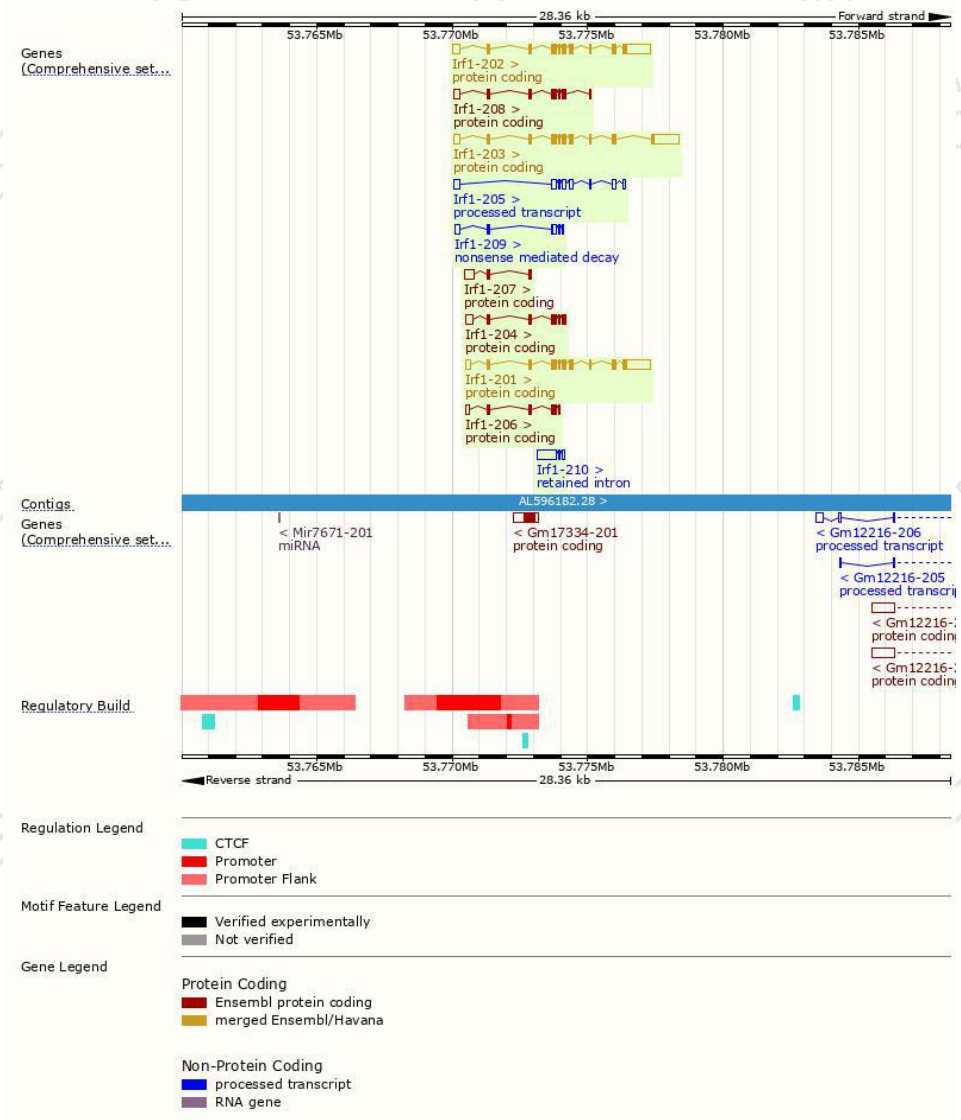
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Irf1-202	ENSMUST00000108920.8	2137	329aa	Protein coding	CCDS24686	P15314 Q5SX13	TSL:1 GENCODE basic APPRIS P3
Irf1-203	ENSMUST00000108922.7	2092	304aa	Protein coding	CCDS48796	Q3U5M1	TSL:1 GENCODE basic APPRIS ALT2
Irf1-201	ENSMUST00000019043.12	2069	329aa	Protein coding	CCDS24686	P15314 Q5SX13	TSL:1 GENCODE basic APPRIS P3
Irf1-208	ENSMUST00000140866.7	833	199aa	Protein coding	-	A8Y5B9	CDS 3' incomplete TSL:5
Irf1-204	ENSMUST00000123376.7	823	182aa	Protein coding	-	Q5SX14	CDS 3' incomplete TSL:5
Irf1-207	ENSMUST00000138913.7	525	62aa	Protein coding	-	Q5SX16	CDS 3' incomplete TSL:5
Irf1-206	ENSMUST00000133291.2	515	132aa	Protein coding	-	Q5SX15	CDS 3' incomplete TSL:3
Irf1-209	ENSMUST00000142221.7	517	51aa	Nonsense mediated decay	-	D6RH71	TSL:2
Irf1-205	ENSMUST00000128336.7	943	No protein	Processed transcript	-	-	TSL:5
Irf1-210	ENSMUST00000153054.1	799	No protein	Retained intron	-	-	TSL:3

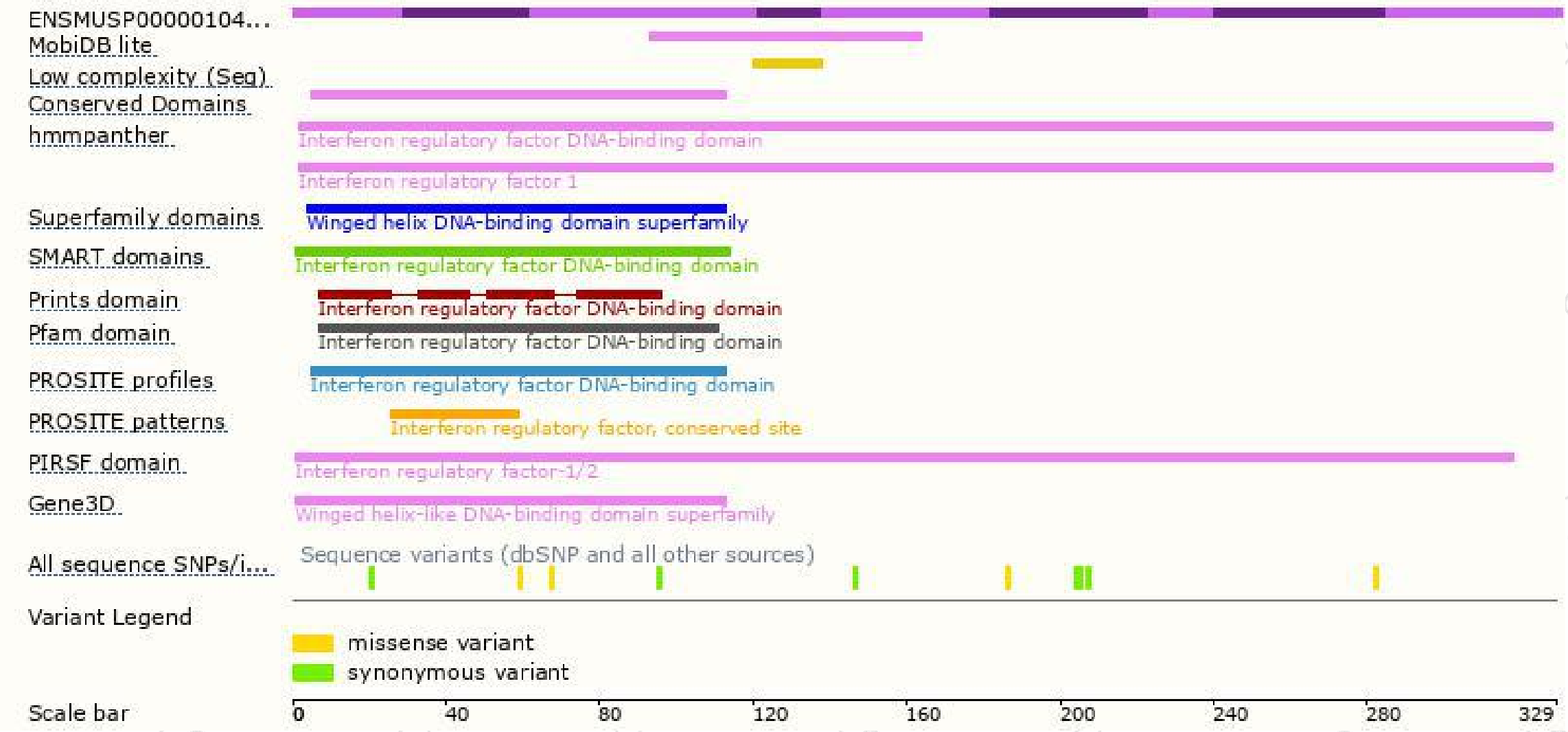
The strategy is based on the design of *Irf1-202* transcript,The transcription is shown below



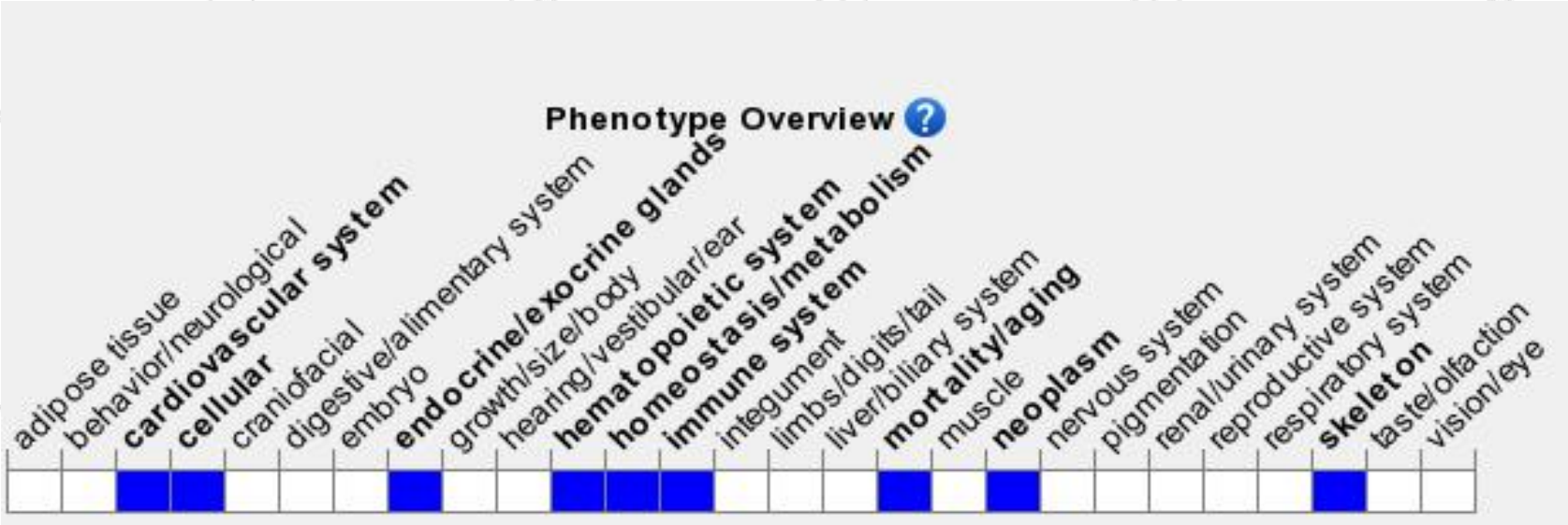
Genomic location distribution



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/).

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

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