Hnrnpl Cas9-CKO Strategy

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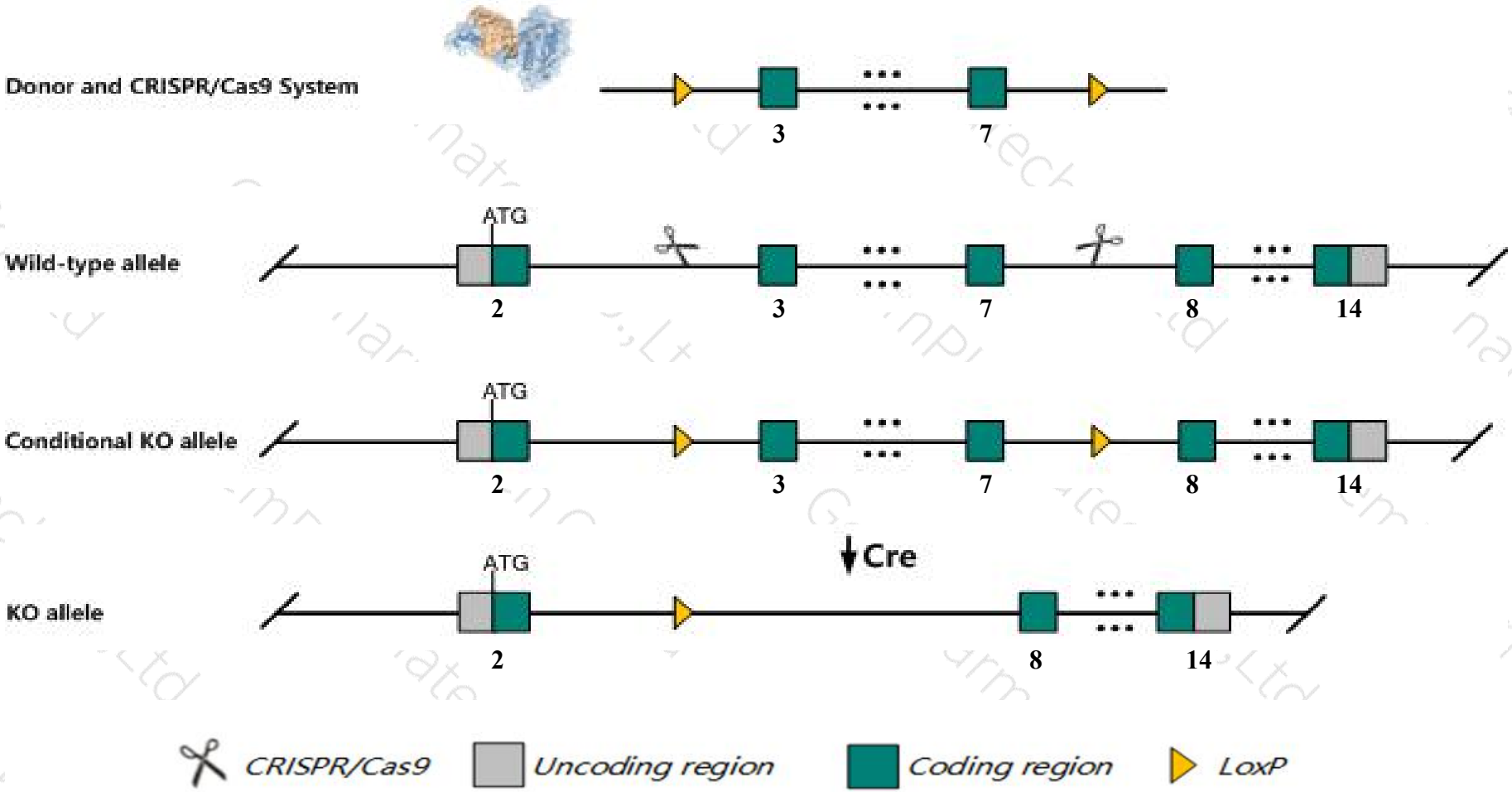
Design Date: 2020-1-19

Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Hnrnpl* gene has 13 transcripts. According to the structure of *Hnrnpl* gene, exon3-exon7 of *Hnrnpl-211* (ENSMUST00000174548.7) transcript is recommended as the knockout region.The region contains 613bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Hnrnpl* 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 targeted allele exhibit embryonic letahlity after E3.5. Mice homozygous for a conditional allele activated in thymocytes exhibit decreased T cells in the periphery associated with impaired thymocyte chemotaxis.

➢The flox region is about 3 kb away from the 5th end of the Gm44702 gene, which may affect the regulation of this gene.

➢ The *Hnrnpl* 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 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

Hnrnpl heterogeneous nuclear ribonucleoprotein L [Mus musculus (house mouse)]

Gene ID: 15388, updated on 31-Jan-2019

Summary

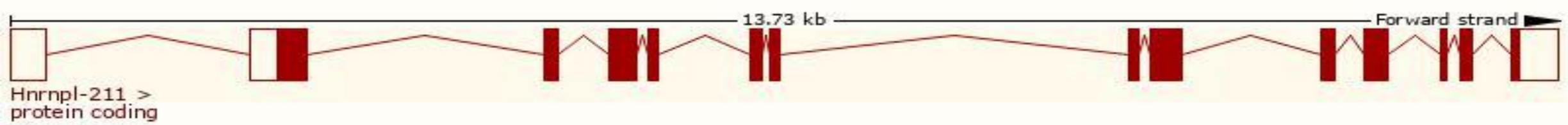
Official Symbol	Hnrnpl provided by MGI
Official Full Name	heterogeneous nuclear ribonucleoprotein L provided by MGI
Primary source	MGI:MGI:104816
See related	Ensembl:ENSMUSG00000015165
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C79783, D830027H13Rik, Hnrpl
Expression	Ubiquitous expression in CNS E11.5 (RPKM 136.9), limb E14.5 (RPKM 90.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

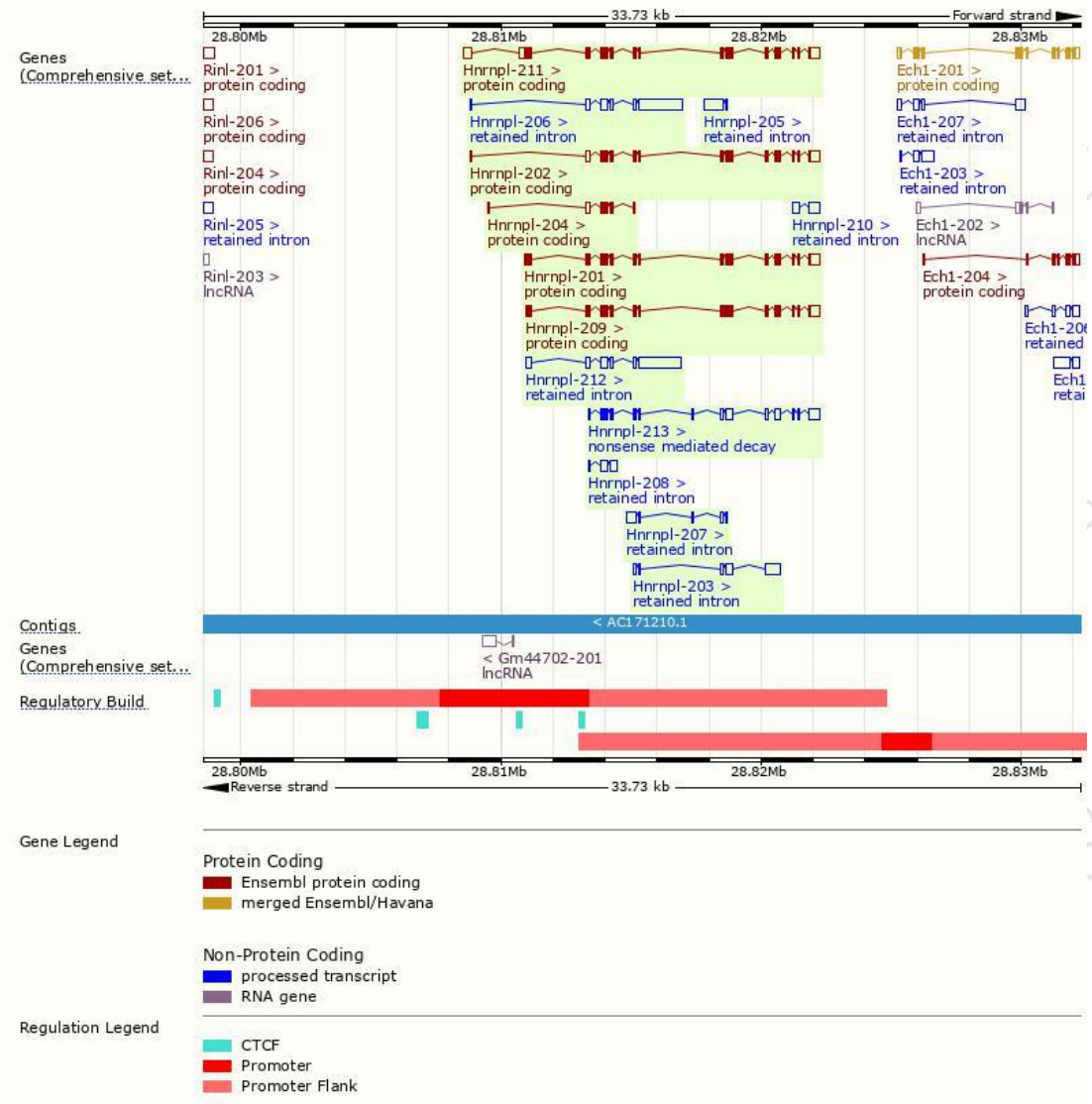
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hnrnpl-211	ENSMUST00000174548.7	2679	586aa	Protein coding	CCDS39864	Q8R081	TSL:5 GENCODE basic APPRIS P1
Hnrnpl-201	ENSMUST00000038572.14	2142	586aa	Protein coding	CCDS39864	Q8R081	TSL:1 GENCODE basic APPRIS P1
Hnrnpl-209	ENSMUST00000174477.7	2180	615aa	Protein coding	-	G5E924	CDS 5' incomplete TSL:1
Hnrnpl-202	ENSMUST00000172529.7	1898	456aa	Protein coding	-	G3UY38	TSL:5 GENCODE basic
Hnrnpl-204	ENSMUST00000172884.7	502	112aa	Protein coding	-	G3UYY3	CDS 3' incomplete TSL:5
Hnrnpl-213	ENSMUST00000174882.7	1850	201aa	Nonsense mediated decay	-	G3UY56	CDS 5' incomplete TSL:5
Hnrnpl-212	ENSMUST00000174755.7	2426	No protein	Retained intron	-	-	TSL:1
Hnrnpl-206	ENSMUST00000173750.7	2275	No protein	Retained intron	-	-	TSL:1
Hnrnpl-203	ENSMUST00000172841.1	1087	No protein	Retained intron	-	-	TSL:3
Hnrnpl-205	ENSMUST00000173578.1	768	No protein	Retained intron	-	-	TSL:2
Hnrnpl-210	ENSMUST00000174526.1	672	No protein	Retained intron	-	-	TSL:2
Hnrnpl-207	ENSMUST00000173818.7	644	No protein	Retained intron	-	-	TSL:3
Hnrnpl-208	ENSMUST00000174396.1	504	No protein	Retained intron	-	-	TSL:2

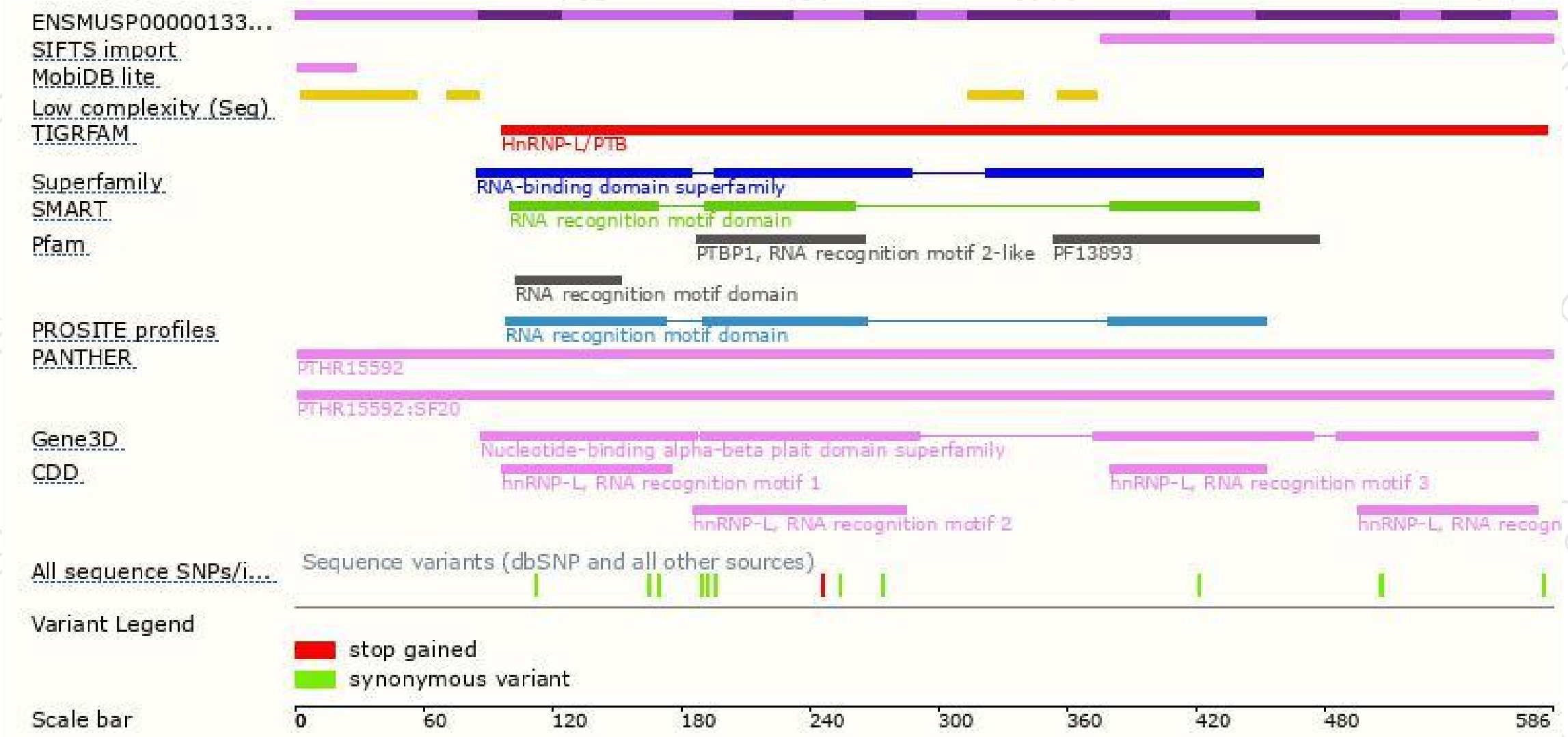
The strategy is based on the design of *Hnrnpl-211* transcript,The transcription is shown below



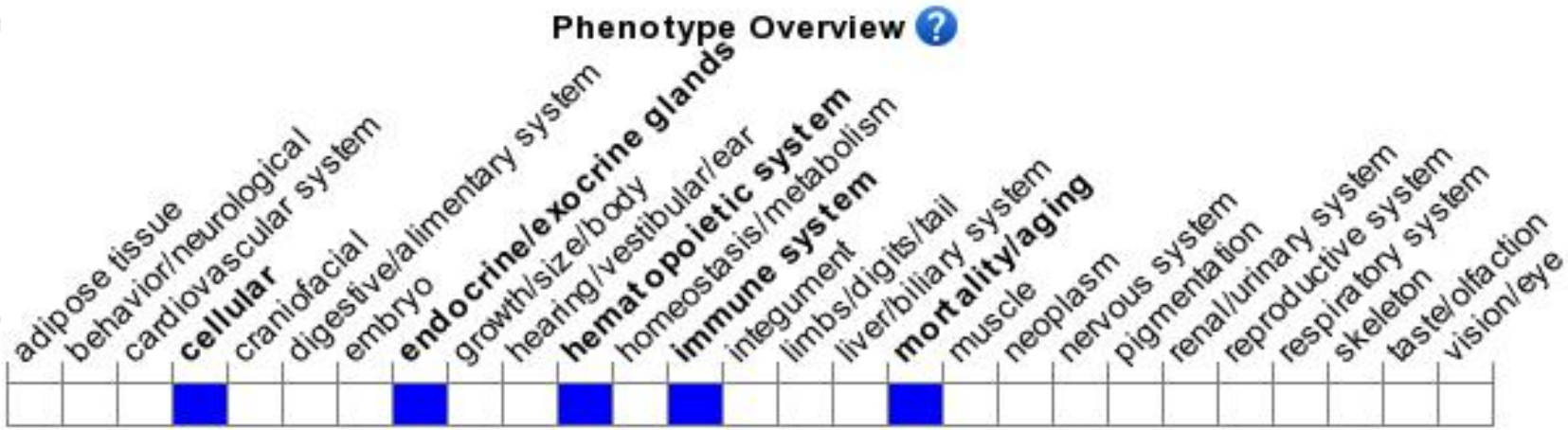
Genomic location distribution



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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