Hnrnpll Cas9-CKO Strategy

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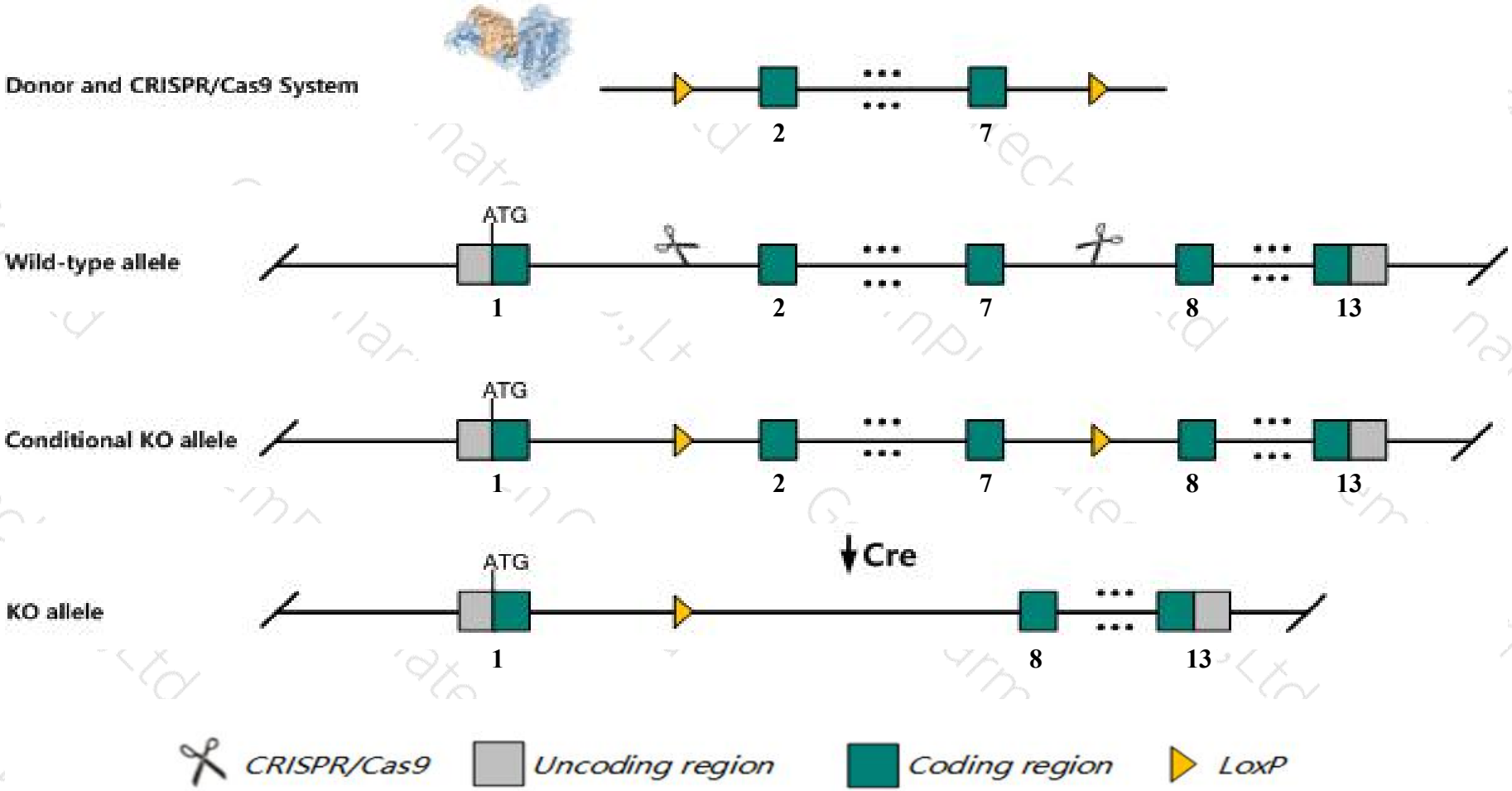
Project Overview

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

Conditional Knockout strategy

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



Technical routes

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- The *Hnrnpll* gene has 7 transcripts. According to the structure of *Hnrnpll* gene, exon2-exon7 of *Hnrnpll-205* (ENSMUST00000184635.7) transcript is recommended as the knockout region.The region contains 685bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Hnrnpll* 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 point mutation in a RNA recognition motif of the gene product have defects in the generation of alternative transcripts normally found in memory T cells. Total CD4 .
- Transcript *Hnrnpll*-202 may not be affected.
- *Gpx4-ps1* gene may be destroyed directly.
- The *Hnrnpll* gene is located on the Chr17. 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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Hnrnpll heterogeneous nuclear ribonucleoprotein L-like [*Mus musculus* (house mouse)]

Gene ID: 72692, updated on 5-Jan-2020

Summary

Official Symbol	Hnrnpll provided by MGI
Official Full Name	heterogeneous nuclear ribonucleoprotein L-like provided by MGI
Primary source	MGI:MGI:1919942
See related	Ensembl:ENSMUSG00000024095
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	Hnrpll; AI256697; AI852082; 2510028H02Rik; 2810036L13Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 34.1), CNS E14 (RPKM 22.4) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 17; 17 E3

See Hnrnpll in Genome Data Viewer

Exon count: 14

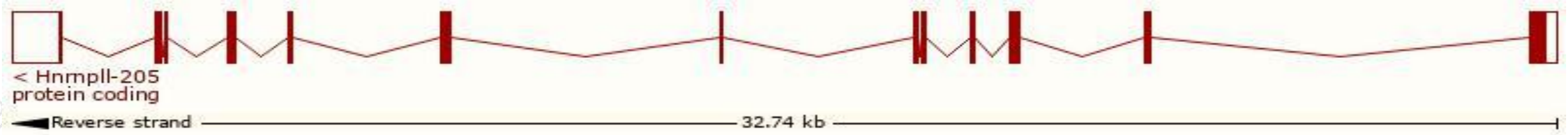
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	17	NC_000083.6 (80029487..80062268, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	17	NC_000083.5 (80428827..80461674, complement)

Transcript information（Ensembl）

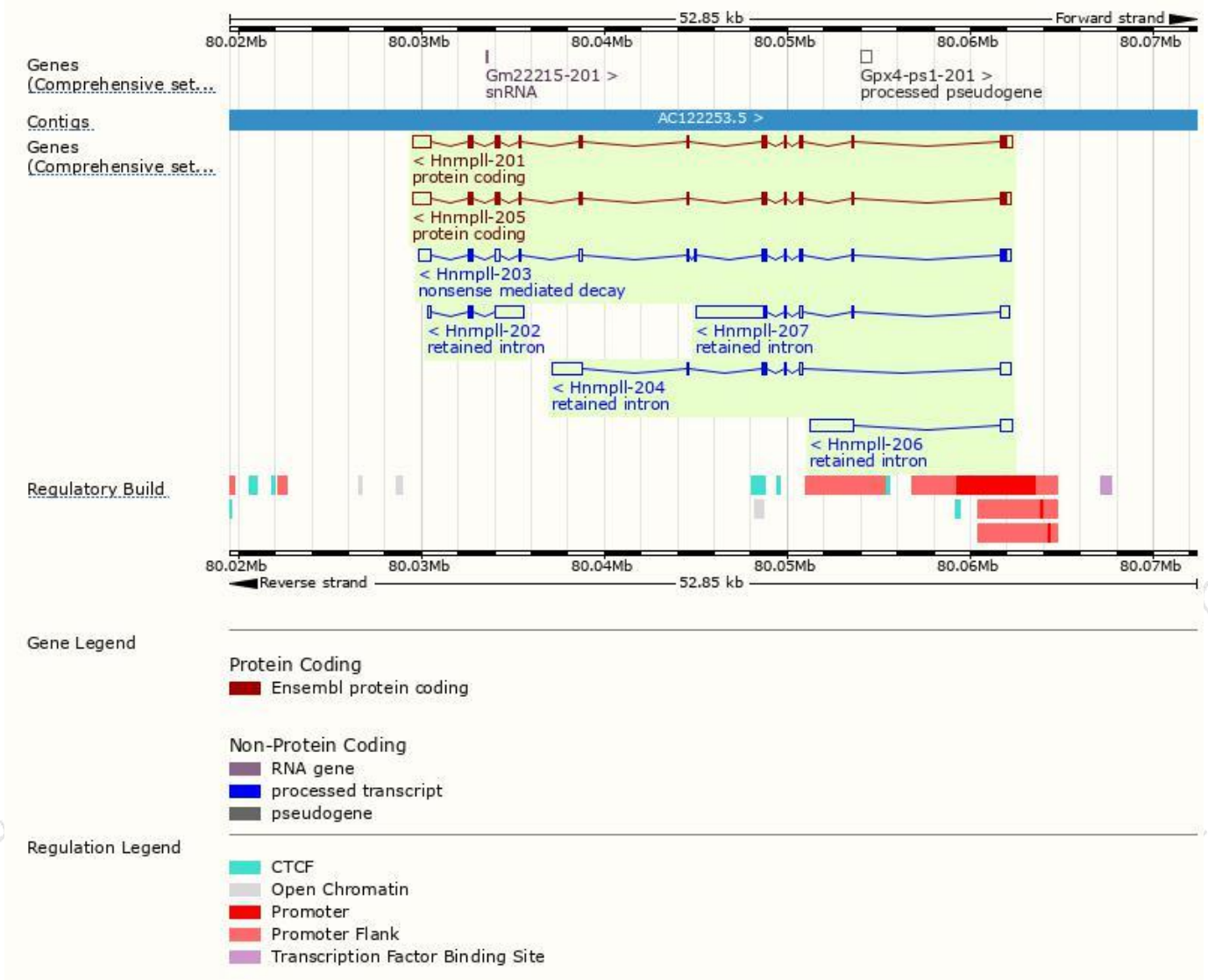
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hnrnpll-205	ENSMUST00000184635.7	3009	591aa	Protein coding	CCDS70845	Q921F4	TSL:1 GENCODE basic APPRIS P1
Hnrnpll-201	ENSMUST00000061331.13	3116	591aa	Protein coding	-	Q921F4	TSL:5 GENCODE basic APPRIS P1
Hnrnpll-203	ENSMUST00000184297.7	2742	331aa	Nonsense mediated decay	-	V9GXB6	TSL:5
Hnrnpll-207	ENSMUST00000184889.1	4651	No protein	Retained intron	-	-	TSL:1
Hnrnpll-206	ENSMUST00000184726.1	3019	No protein	Retained intron	-	-	TSL:1
Hnrnpll-204	ENSMUST00000184578.7	2765	No protein	Retained intron	-	-	TSL:1
Hnrnpll-202	ENSMUST00000183516.1	1868	No protein	Retained intron	-	-	TSL:1

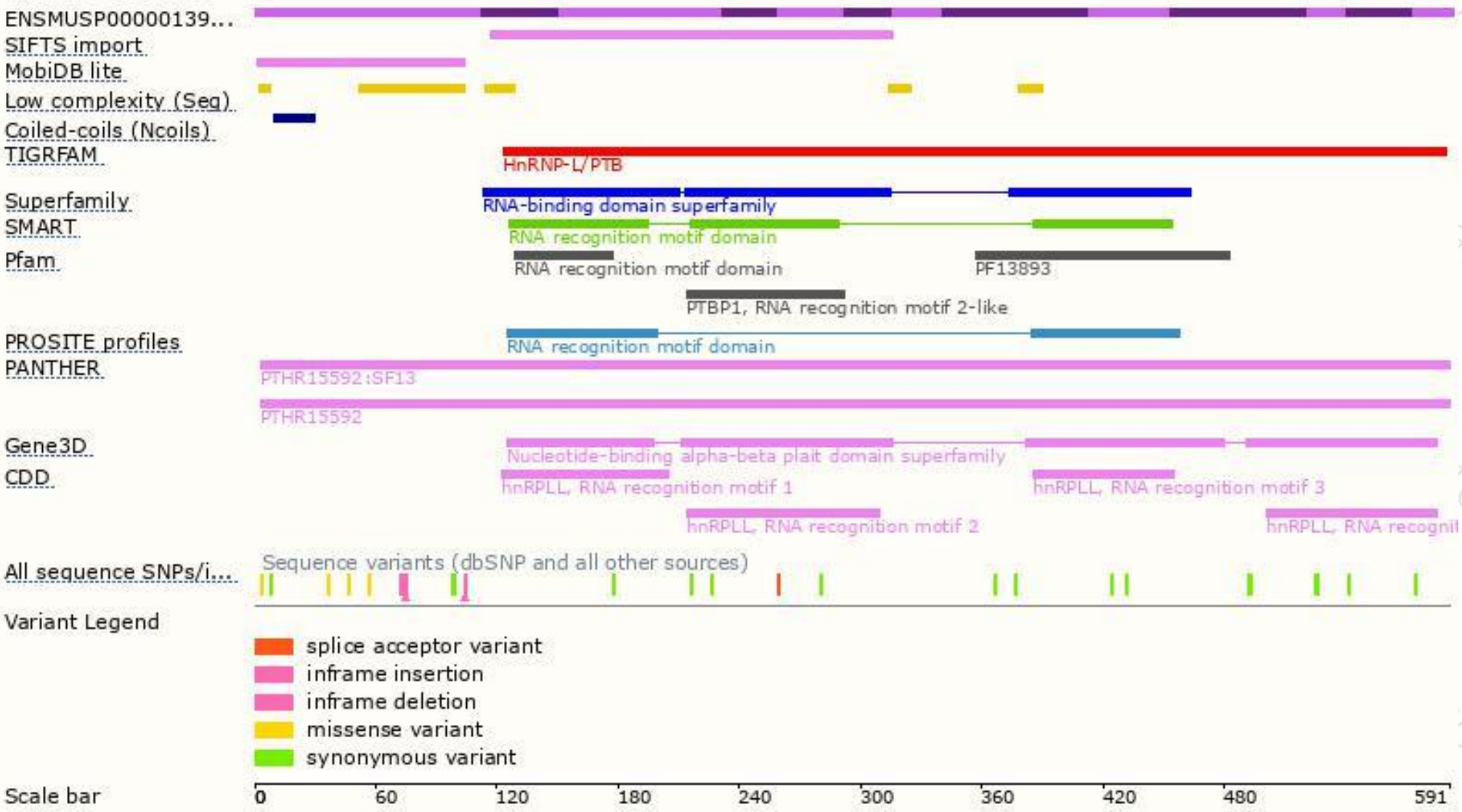
The strategy is based on the design of *Hnrnpll-205* transcript,The transcription is shown below



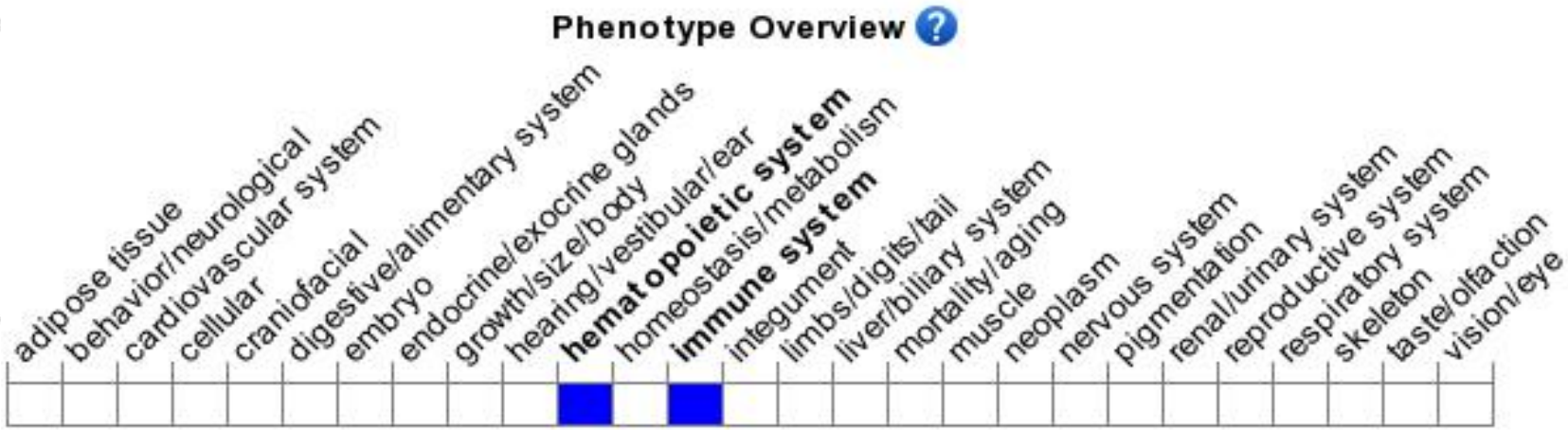
Genomic location distribution



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 point mutation in a RNA recognition motif of the gene product have defects in the generation of alternative transcripts normally found in memory T cells. Total CD4

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

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