

Mras Cas9-CKO Strategy

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Project Overview

Project Name

Mras

Project type

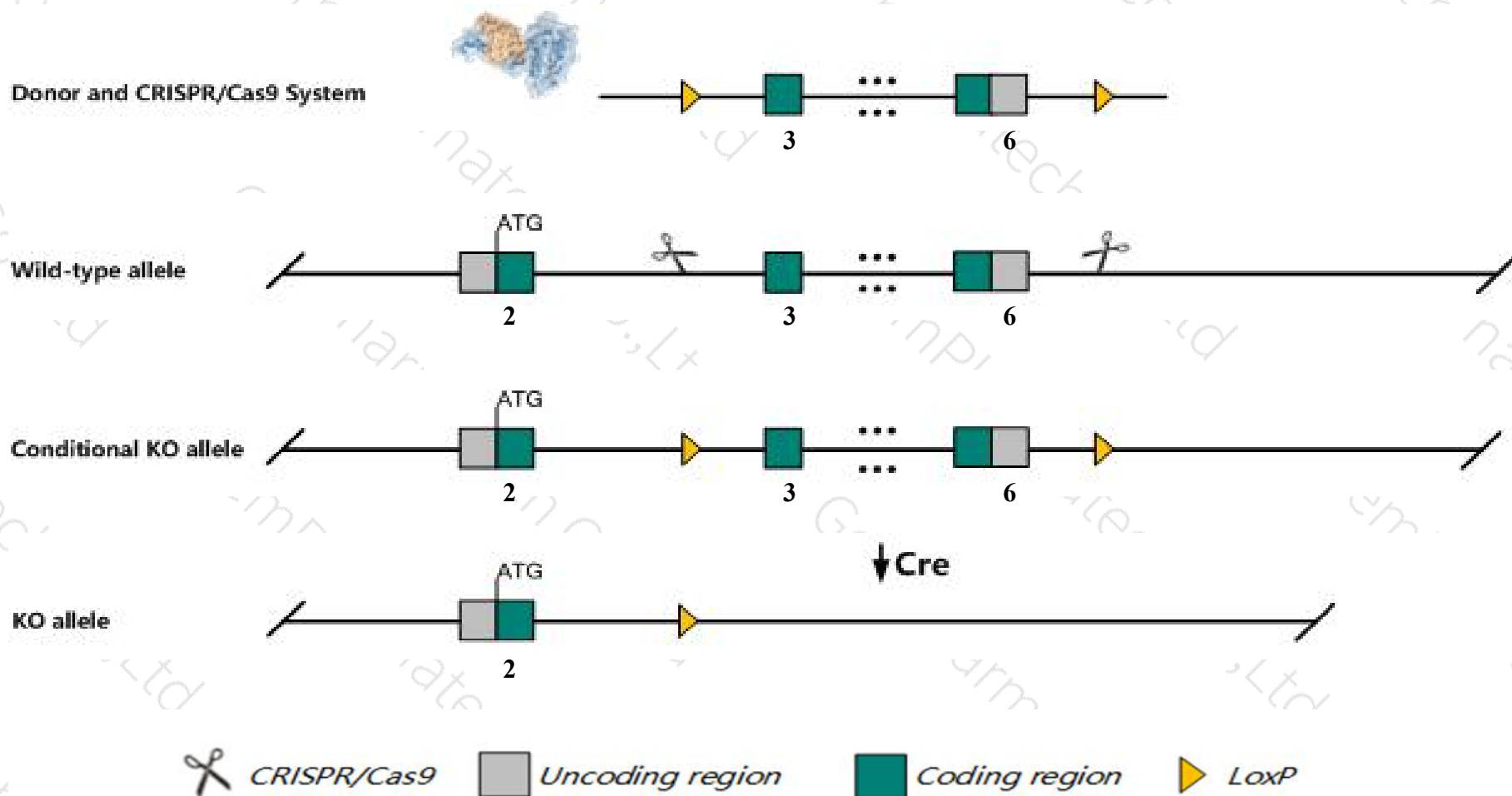
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Mras* gene has 6 transcripts. According to the structure of *Mras* gene, exon3-exon6 of *Mras*-201 (ENSMUST00000035045.14) transcript is recommended as the knockout region. The region contains 434bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mras* 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.

- According to the existing MGI data, Mice homozygous for an insertional mutation that inactivates the gene exhibit a decreased mean percentage of peripheral blood B cells but no other evidence of morphological or neurological defects; mutant astrocytes display normal responsiveness to different trophic factors.
- The *Mras* gene is located on the Chr9. 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)

Mras muscle and microspikes RAS [Mus musculus (house mouse)]

Gene ID: 17532, updated on 31-Jan-2019

Summary



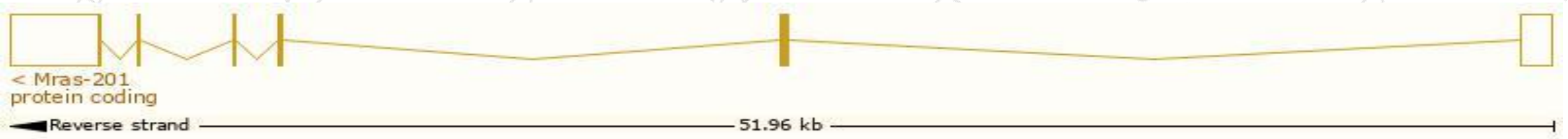
Official Symbol	Mras provided by MGI
Official Full Name	muscle and microspikes RAS provided by MGI
Primary source	MGI:MGI:1100856
See related	Ensembl:ENSMUSG00000032470
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2900078C09Rik, AI326250
Expression	Broad expression in cortex adult (RPKM 34.0), ovary adult (RPKM 30.7) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

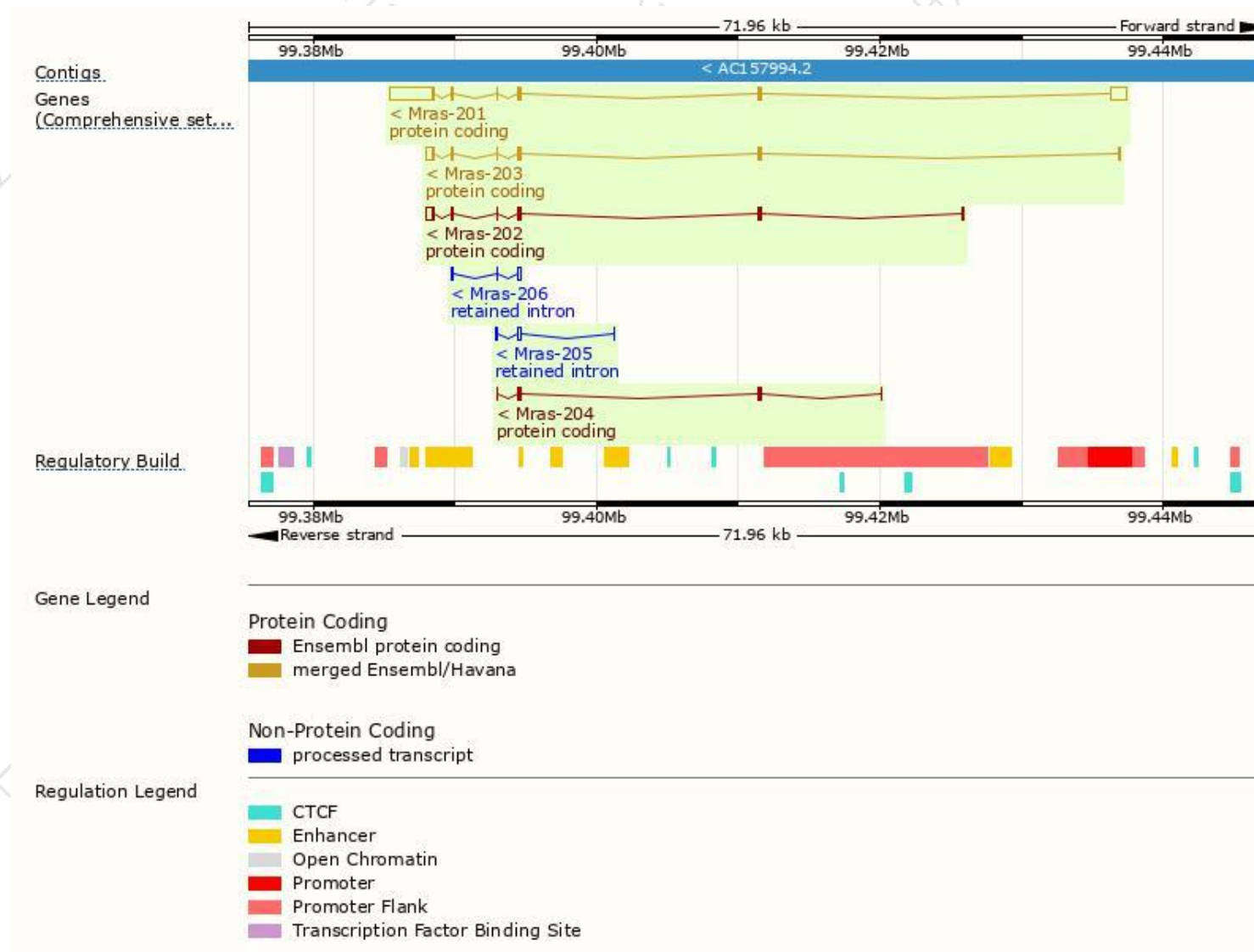
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mras-201	ENSMUST00000035045.14	4701	208aa	Protein coding	CCDS23433	O08989 Q3TPX5	TSL:1 GENCODE basic APPRIS P1
Mras-202	ENSMUST00000119472.7	1190	208aa	Protein coding	CCDS23433	O08989 Q3TPX5	TSL:1 GENCODE basic APPRIS P1
Mras-203	ENSMUST00000122384.8	1167	208aa	Protein coding	CCDS23433	O08989 Q3TPX5	TSL:1 GENCODE basic APPRIS P1
Mras-204	ENSMUST00000123771.1	482	130aa	Protein coding	-	D3Z2V6	CDS 3' incomplete TSL:5
Mras-205	ENSMUST00000131047.1	421	No protein	Retained intron	-	-	TSL:3
Mras-206	ENSMUST00000147078.1	407	No protein	Retained intron	-	-	TSL:2

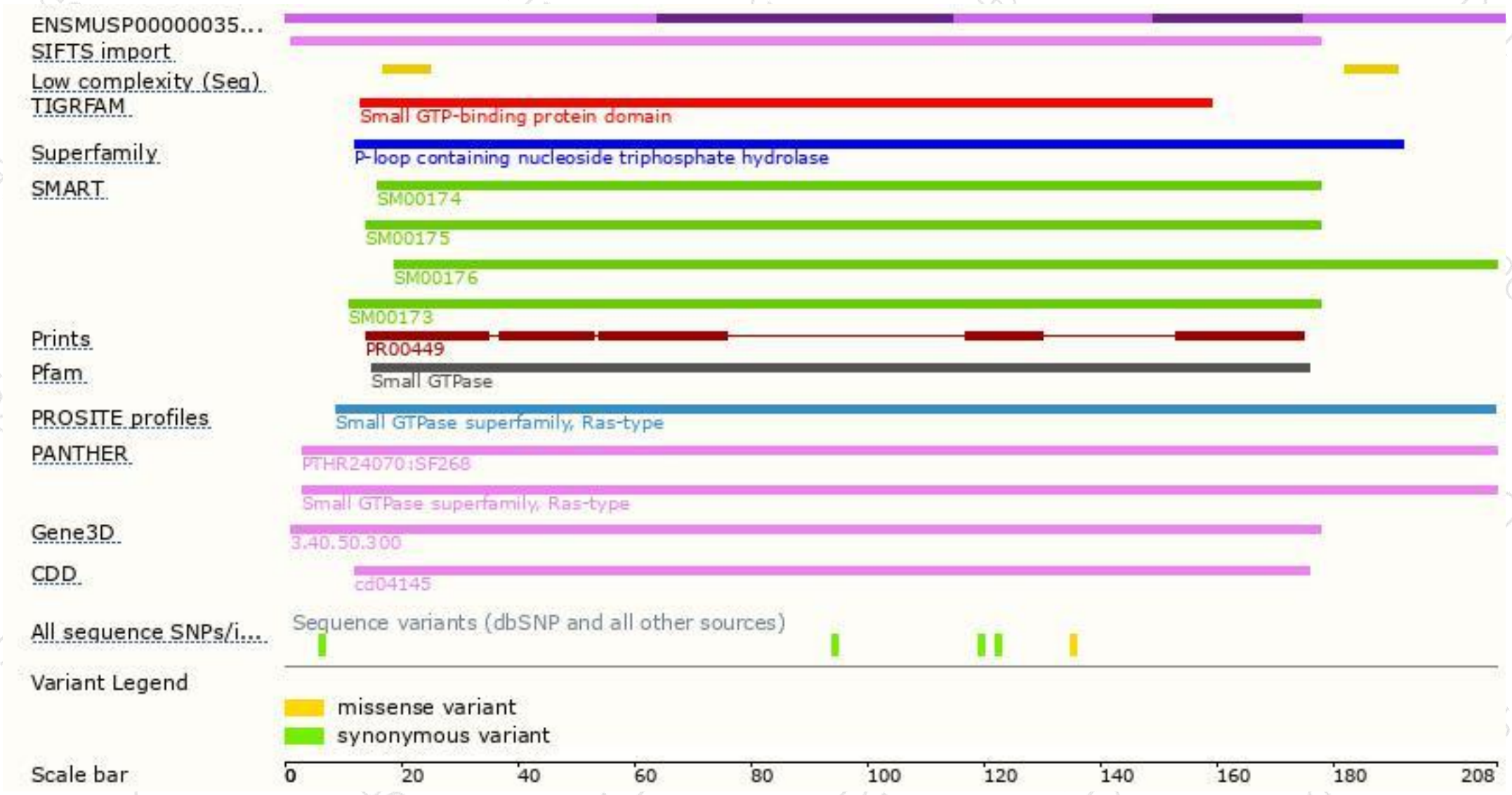
The strategy is based on the design of *Mras-201* transcript,The transcription is shown below



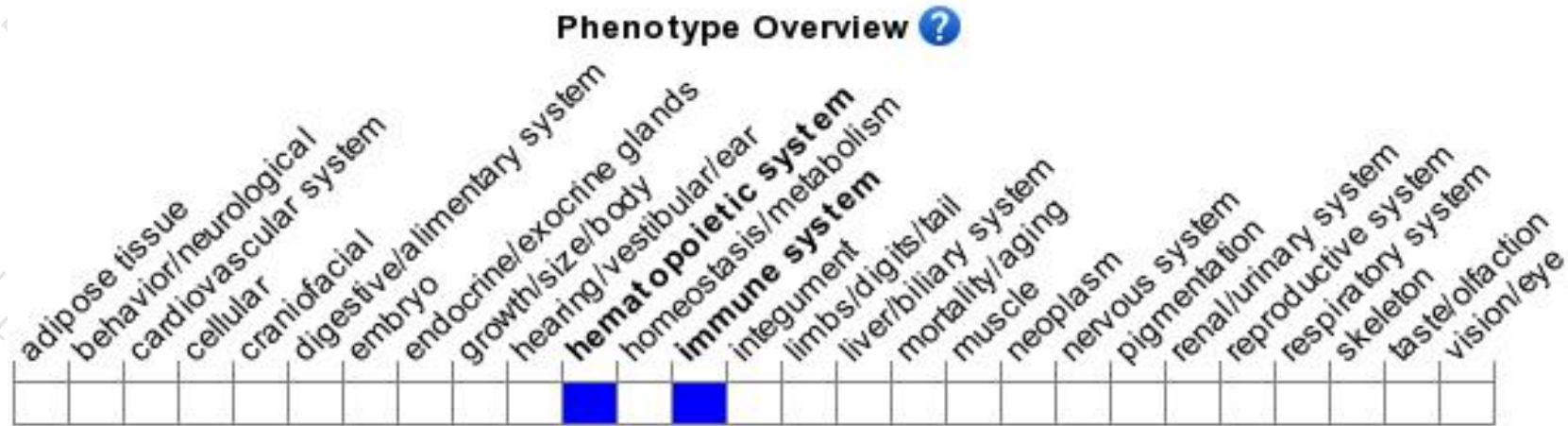
Genomic location distribution



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 an insertional mutation that inactivates the gene exhibit a decreased mean percentage of peripheral blood B cells but no other evidence of morphological or neurological defects; mutant astrocytes display normal responsiveness to different trophic factors.

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

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