

Msh2 Cas9-CKO Strategy

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Design Date: 2019-9-20

Project Overview

Project Name

Msh2

Project type

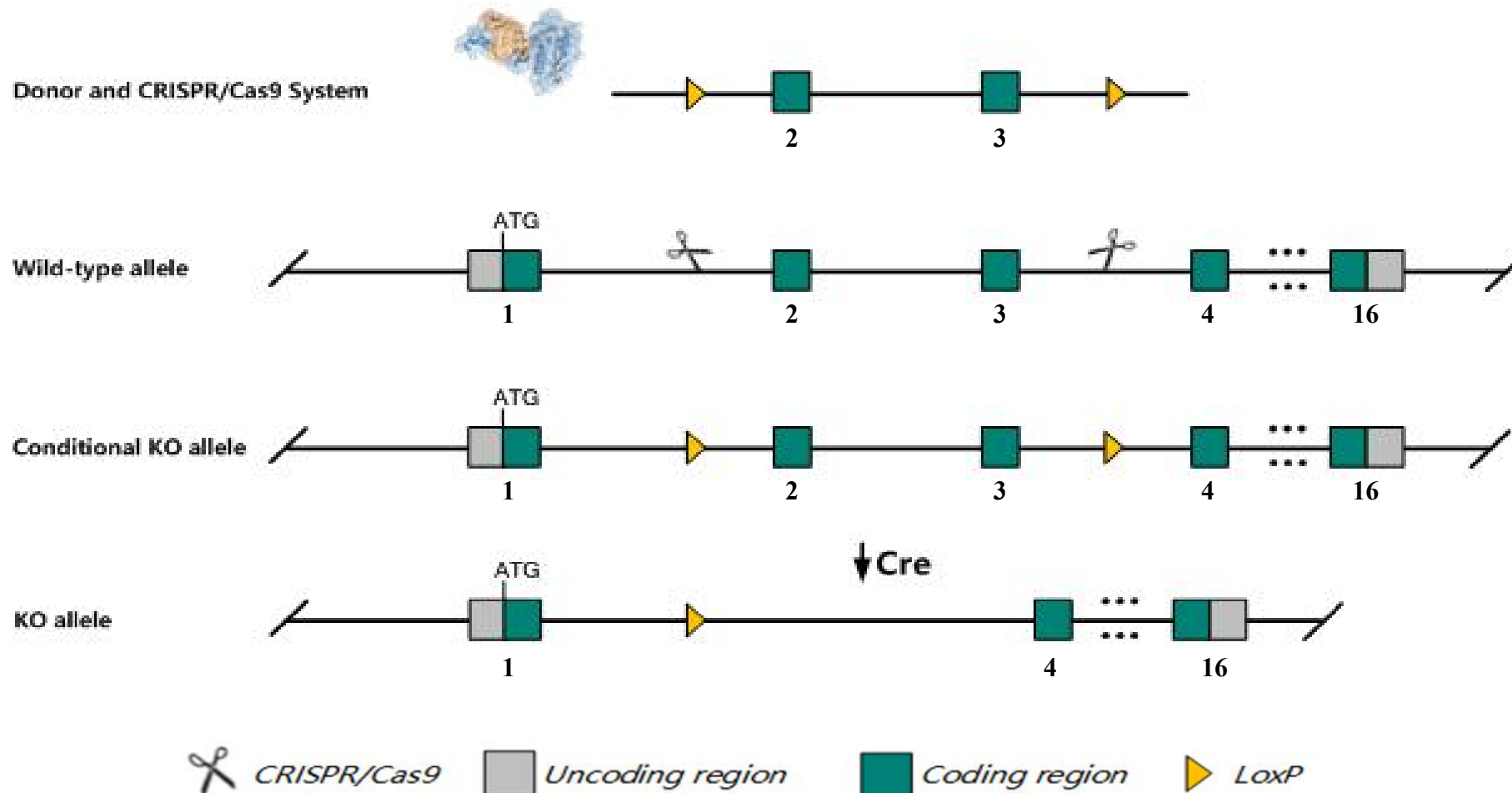
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Msh2* gene. The schematic diagram is as follows:



The *Msh2* gene has 6 transcripts. According to the structure of *Msh2* gene, exon2-exon3 of *Msh2-201* (ENSMUST00000024967.13) 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 *Msh2* 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 a number of different targeted mutations develop lymphomas. In addition, depending on the allele, mutants may show intestinal adenocarcinomas and reduced class switch recombination or adenocarcinomas and abnormal mismatch repair or squamous cell carcinomas and skin tumors.

The *Msh2* 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.

Msh2 mutS homolog 2 [Mus musculus (house mouse)]

Gene ID: 17685, updated on 3-Mar-2019

Summary



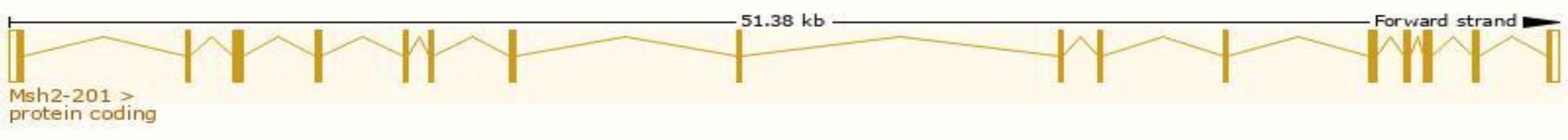
Official Symbol	Msh2 provided by MGI
Official Full Name	mutS homolog 2 provided by MGI
Primary source	MGI:MGI:101816
See related	Ensembl:ENSMUSG00000024151
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI788990
Expression	Broad expression in CNS E11.5 (RPKM 24.0), CNS E14 (RPKM 14.5) and 24 other tissues See more
Orthologs	human all

Transcript information Ensembl

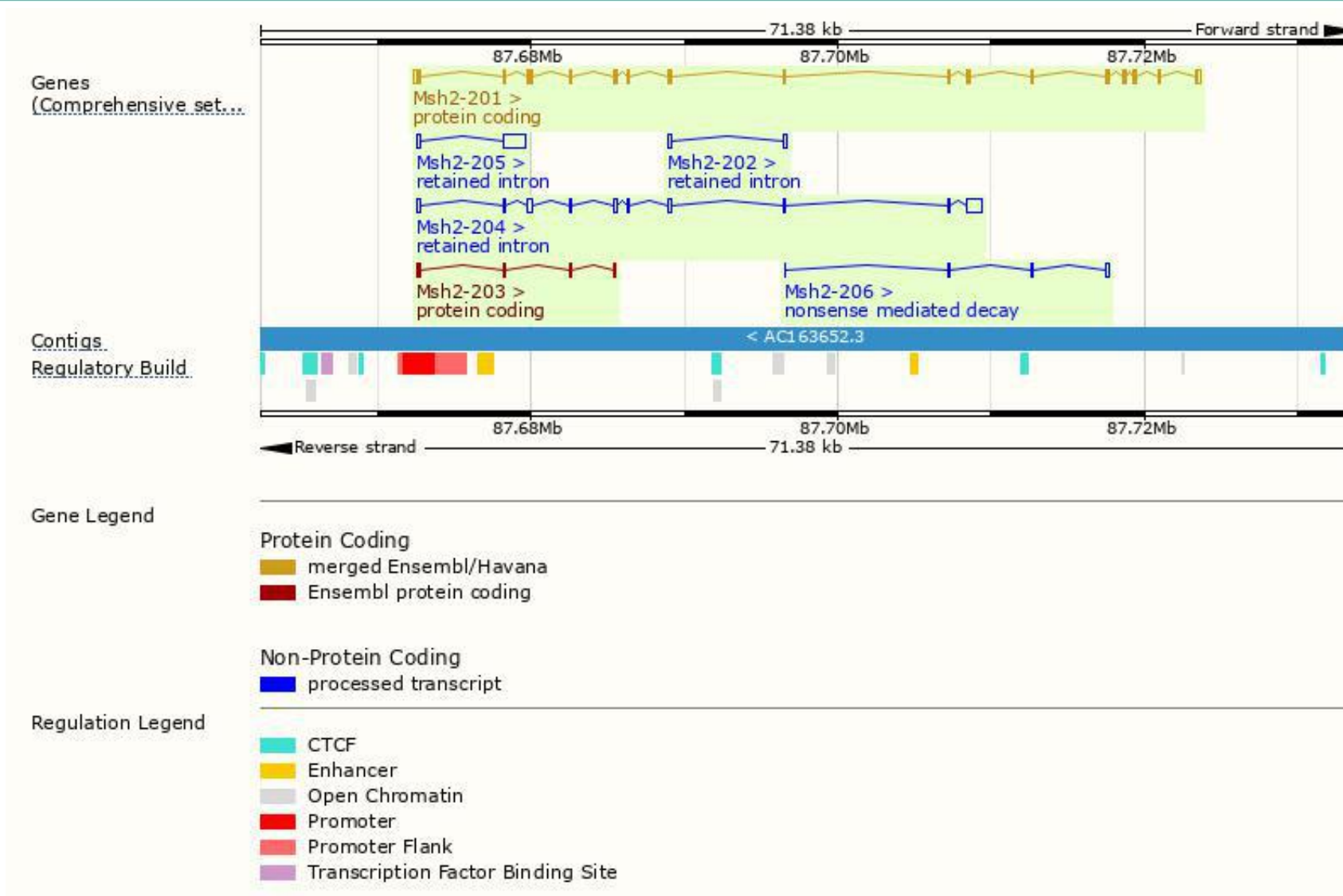
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Msh2-201	ENSMUST00000024967.13	3283	935aa	Protein coding	CCDS29019	P43247 Q3TZI5	TSL:1 GENCODE basic APPRIS P1
Msh2-203	ENSMUST00000172855.1	630	210aa	Protein coding	-	G3UXD8	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Msh2-206	ENSMUST00000174703.1	510	68aa	Nonsense mediated decay	-	G3UWZ8	CDS 5' incomplete TSL:5
Msh2-204	ENSMUST00000173097.7	2502	No protein	Retained intron	-	-	TSL:1
Msh2-205	ENSMUST00000174240.1	1752	No protein	Retained intron	-	-	TSL:1
Msh2-202	ENSMUST00000172596.1	409	No protein	Retained intron	-	-	TSL:2

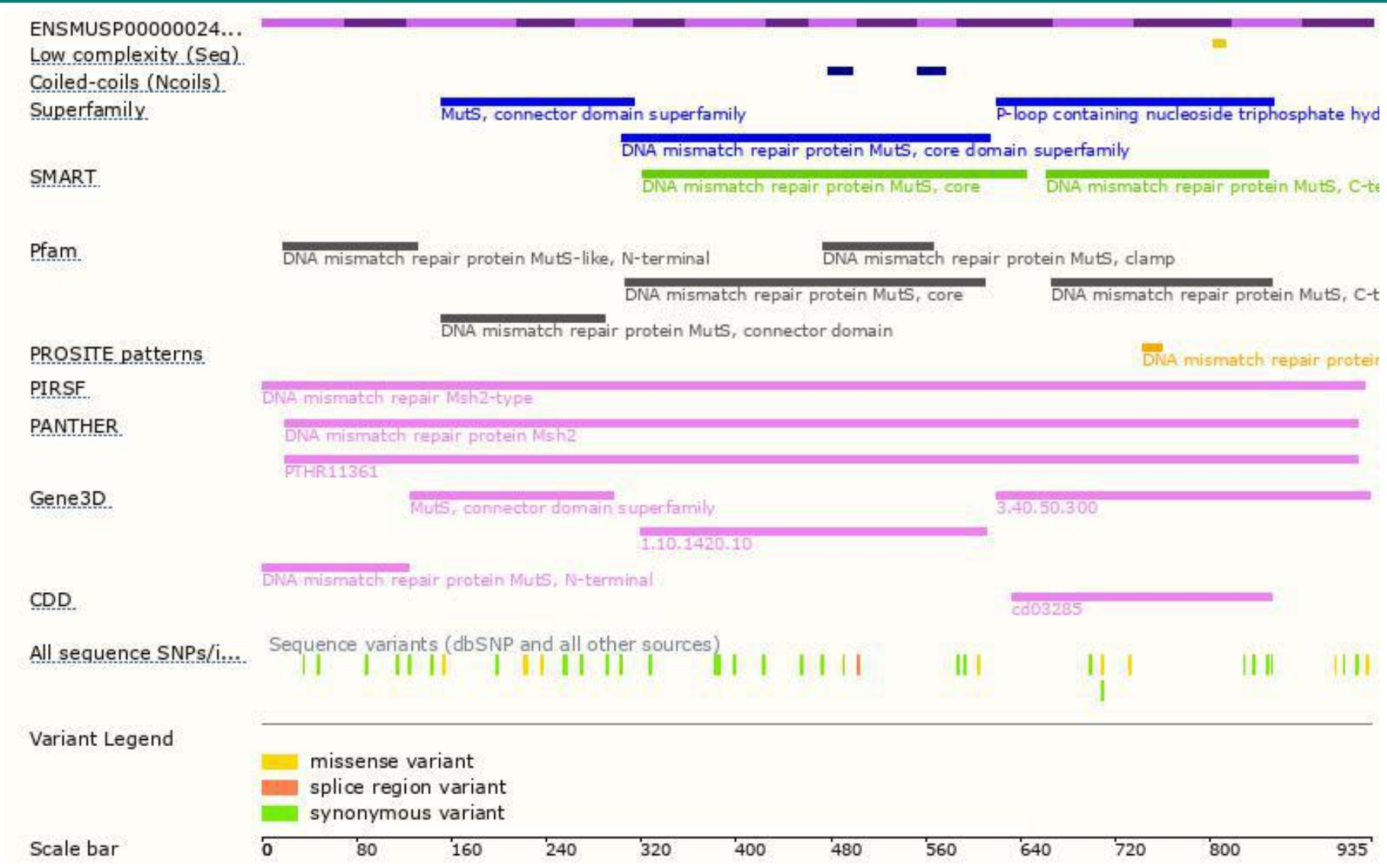
The strategy is based on the design of *Msh2-201* transcript,The transcription is shown below



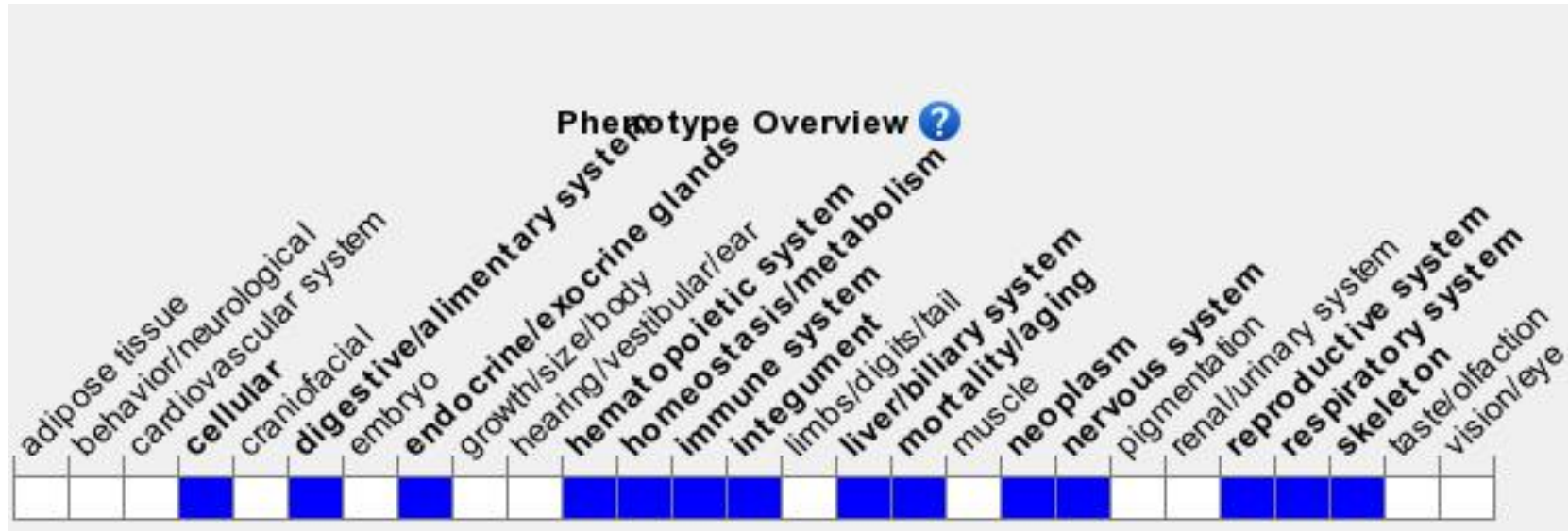
Genomic location distribution



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 a number of different targeted mutations develop lymphomas. In addition, depending on the allele, mutants may show intestinal adenocarcinomas and reduced class switch recombination or adenocarcinomas and abnormal mismatch repair or squamous cell carcinomas and skin tumors.

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