

Endou Cas9-KO Strategy

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Project Overview

Project Name

Endou

Project type

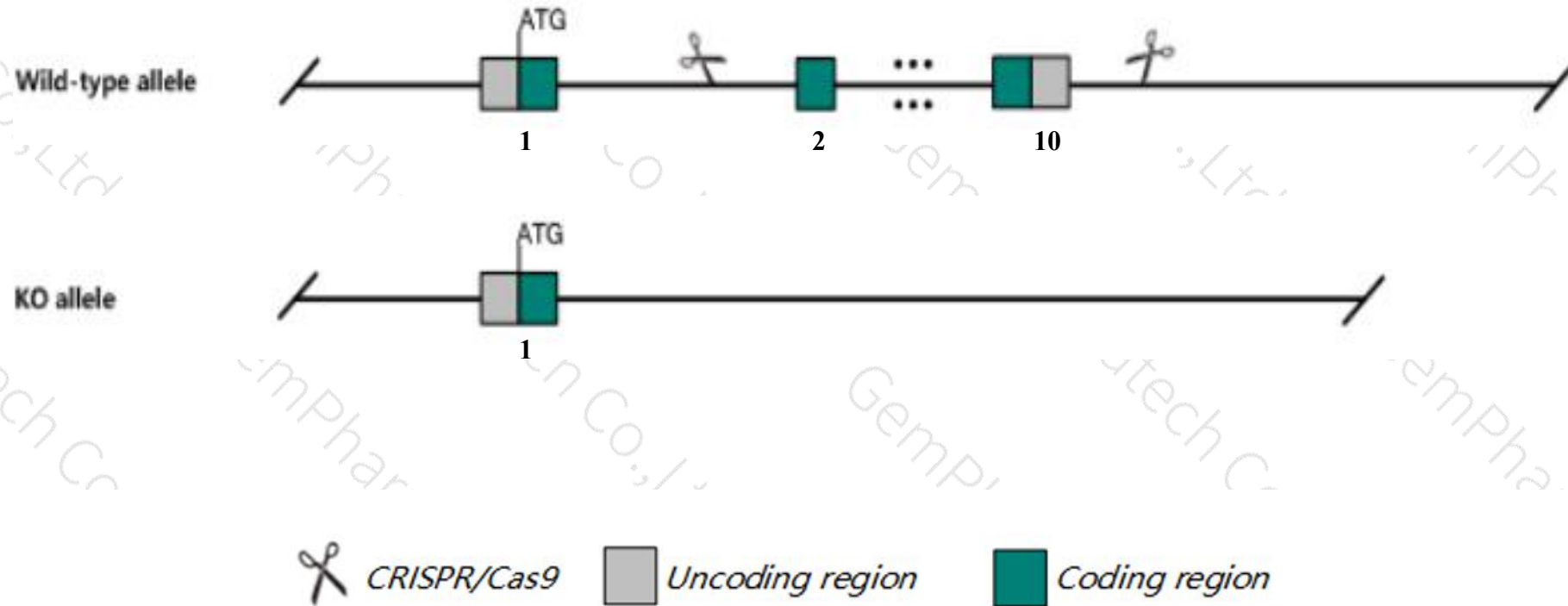
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Endou* gene has 3 transcripts. According to the structure of *Endou* gene, exon2-exon10 of *Endou-202* (ENSMUST00000100249.9) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Endou* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit normal splenic b cell numbers and activation-induced b cell apoptosis.
- The knockout region is near to the N-terminal of *Rpap3* gene, this strategy may influence the regulatory function of the N-terminal of *Rpap3* gene.
- The *Endou* gene is located on the Chr15. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Endou endonuclease, polyU-specific [Mus musculus (house mouse)]

Gene ID: 19011, updated on 13-Mar-2020

Summary



Official Symbol Endou provided by [MGI](#)

Official Full Name endonuclease, polyU-specific provided by [MGI](#)

Primary source [MGI:MGI:97746](#)

See related [Ensembl:ENSMUSG00000022468](#)

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 Pp11r, Tcl-30

Expression Biased expression in thymus adult (RPKM 54.3) and lung adult (RPKM 2.5)[See more](#)

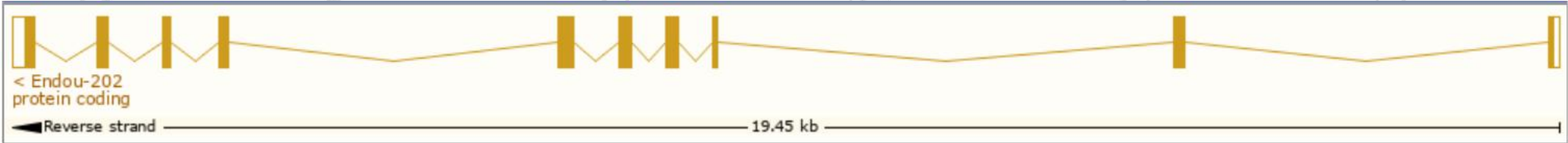
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

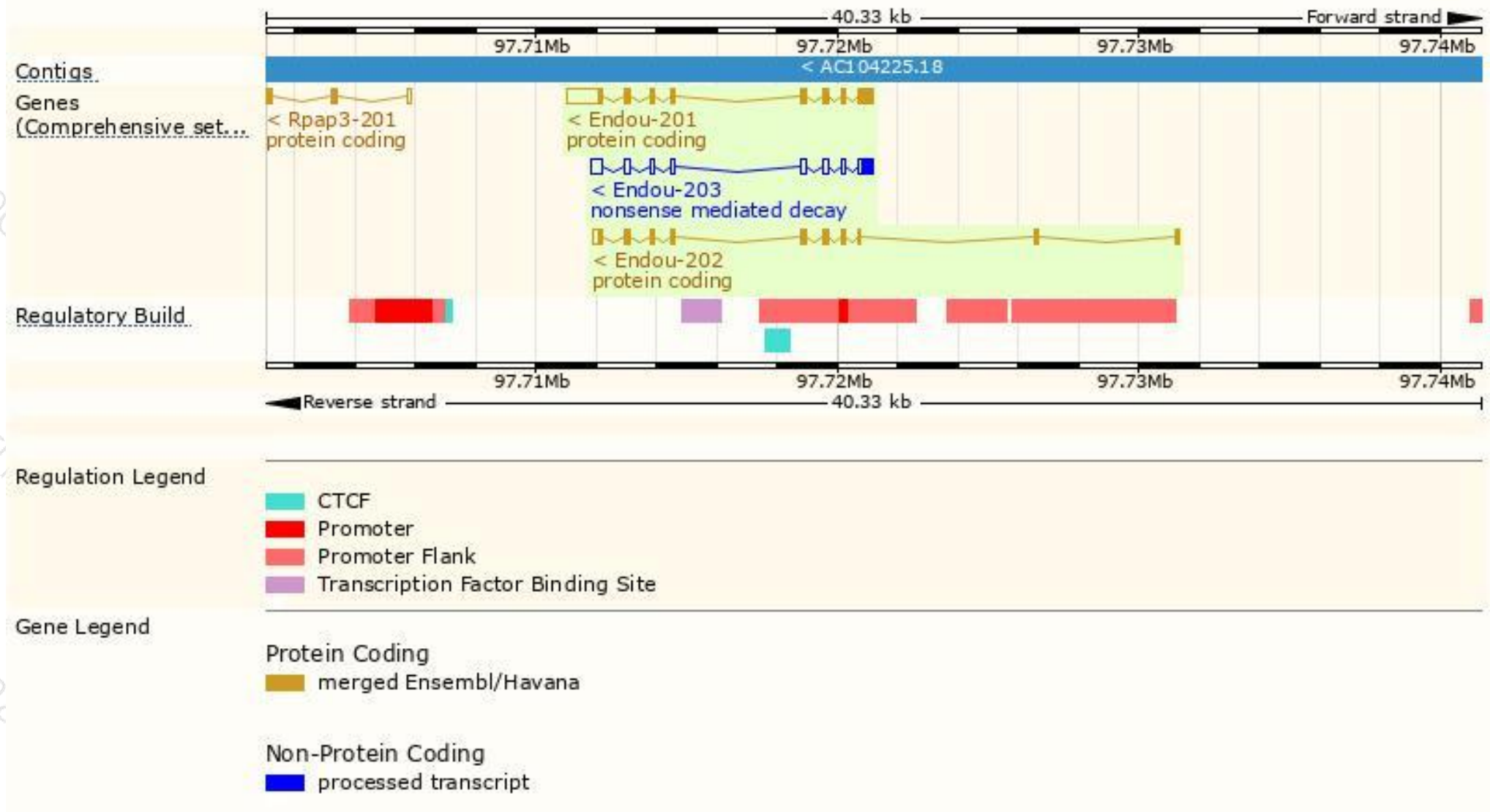
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Endou-201	ENSMUST00000023105.4	2408	454aa	Protein coding	CCDS27783	Q3V188	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Endou-202	ENSMUST00000100249.9	1467	412aa	Protein coding	CCDS49712	Q3V188	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Endou-203	ENSMUST00000230430.1	1668	119aa	Nonsense mediated decay	-	A0A2R8VHM5	

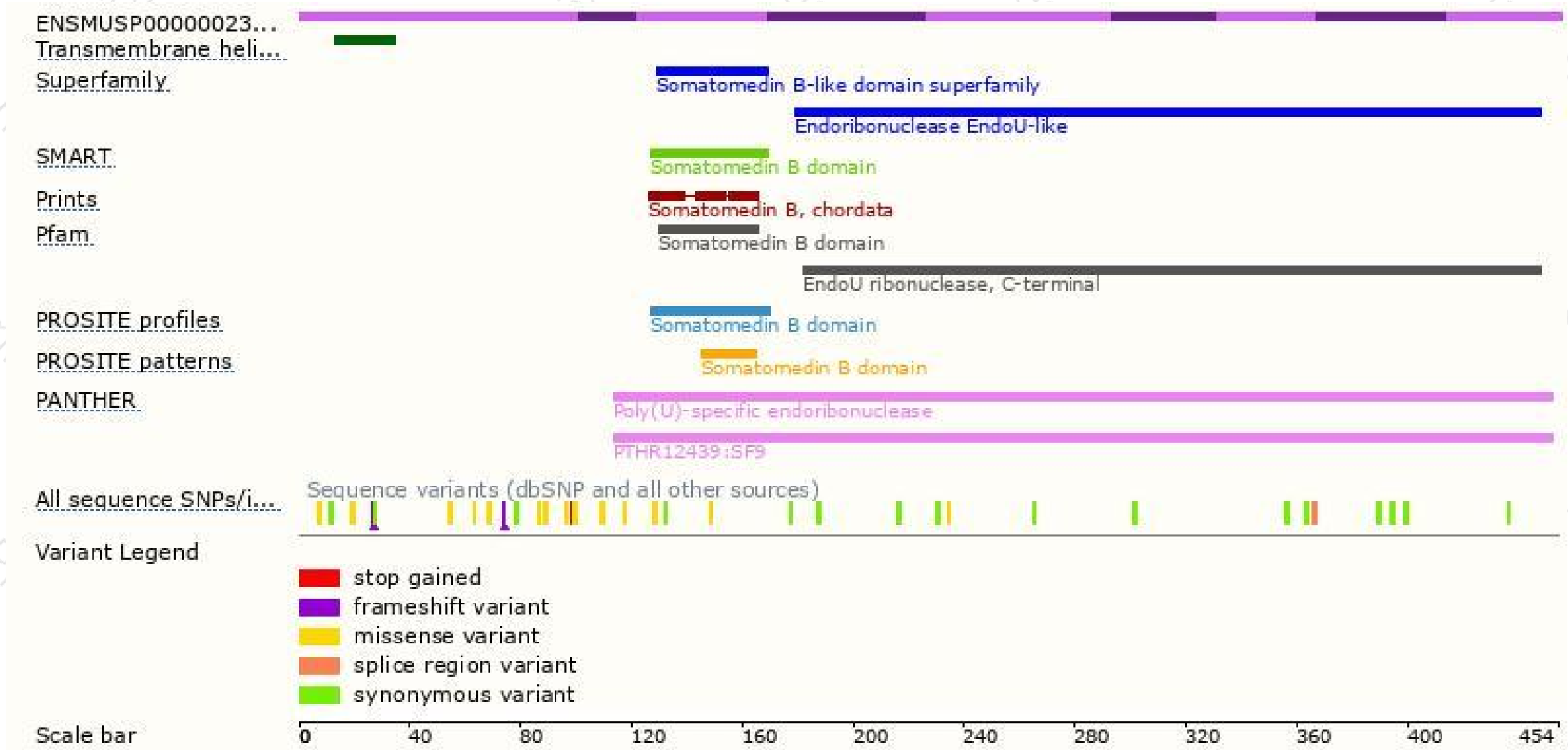
The strategy is based on the design of *Endou-202* transcript,the transcription is shown below:



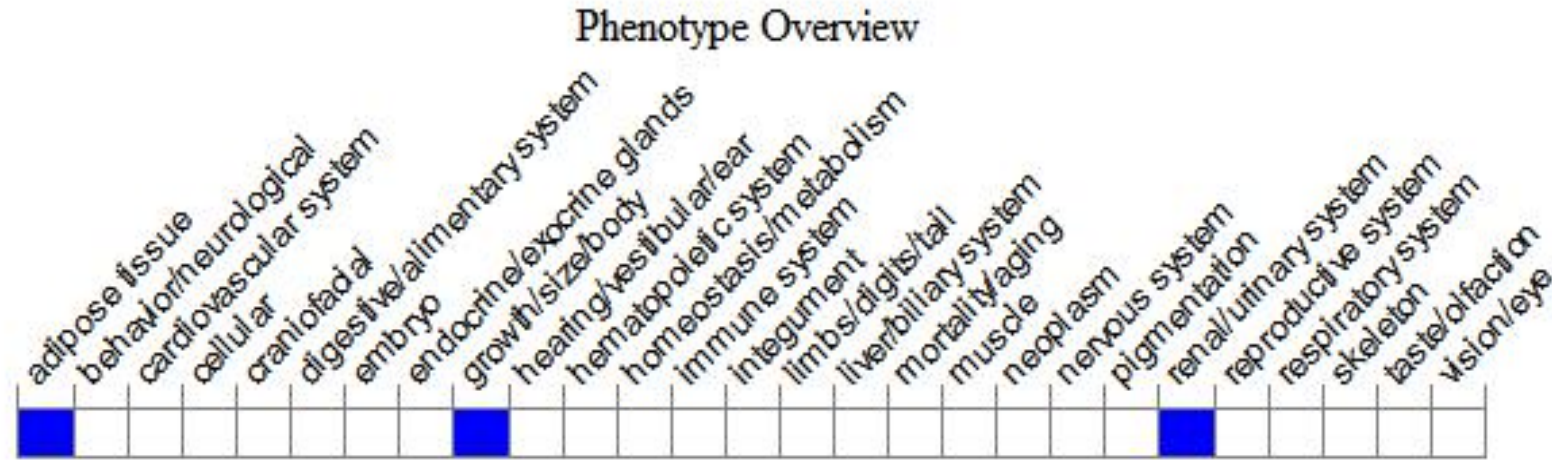
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a knock-out allele exhibit normal splenic B cell numbers and activation-induced B cell apoptosis.

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

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