

Cyp1b1 Cas9-CKO Strategy

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Project Overview

Project Name

Cyp1b1

Project type

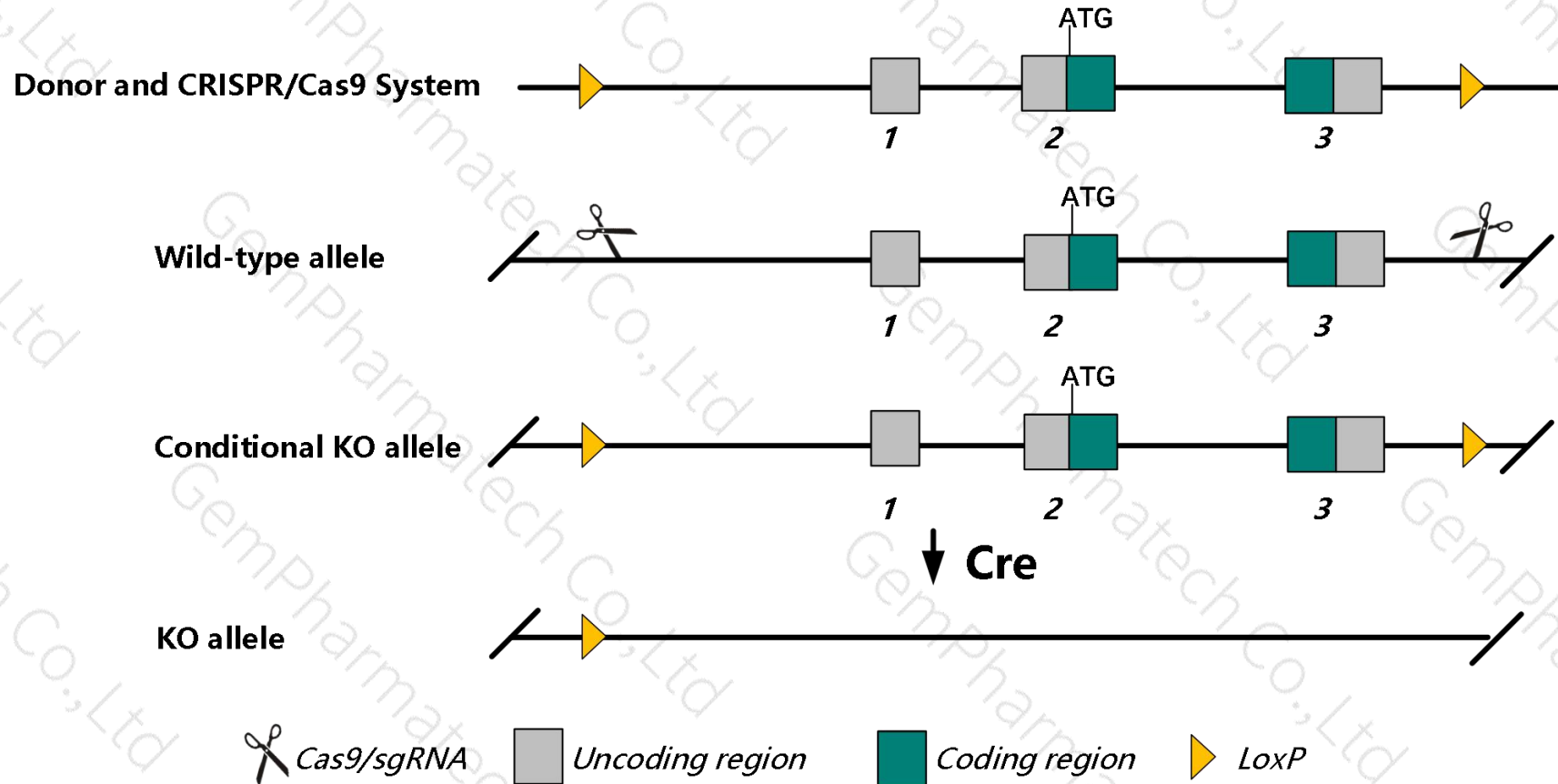
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cyp1b1* gene. The schematic diagram is as follows:



- The *Cyp1b1* gene has 3 transcripts. According to the structure of *Cyp1b1* gene, exon1-exon3 of *Cyp1b1-201*(ENSMUST00000024894.1) transcript is recommended as the knockout region. The region contains all 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 *Cyp1b1* 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 knock-out allele are protected from the acute bone marrow cytotoxic and preleukemic effects of DMBA, show a decreased incidence of DMBA-induced lymphomas, and display background-sensitive ocular abnormalities.
- The *Cyp1b1* 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)

Cyp1b1 cytochrome P450, family 1, subfamily b, polypeptide 1 [Mus musculus (house mouse)]

Gene ID: 13078, updated on 13-Mar-2020

Summary



Official Symbol Cyp1b1 provided by [MGI](#)

Official Full Name cytochrome P450, family 1, subfamily b, polypeptide 1 provided by [MGI](#)

Primary source [MGI:MGI:88590](#)

See related [Ensembl:ENSMUSG00000024087](#)

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 CP1B, CYP1B1, P4501b1

Expression Biased expression in ovary adult (RPKM 41.8), spleen adult (RPKM 11.1) and 7 other tissues [See more](#)

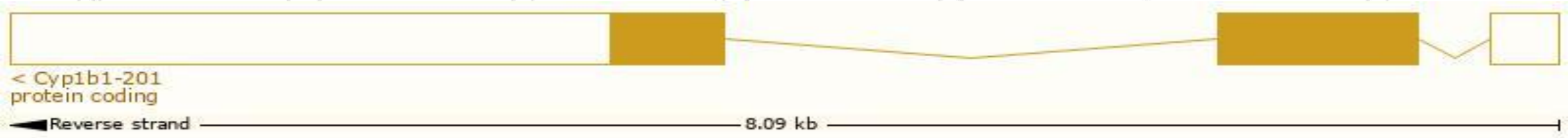
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

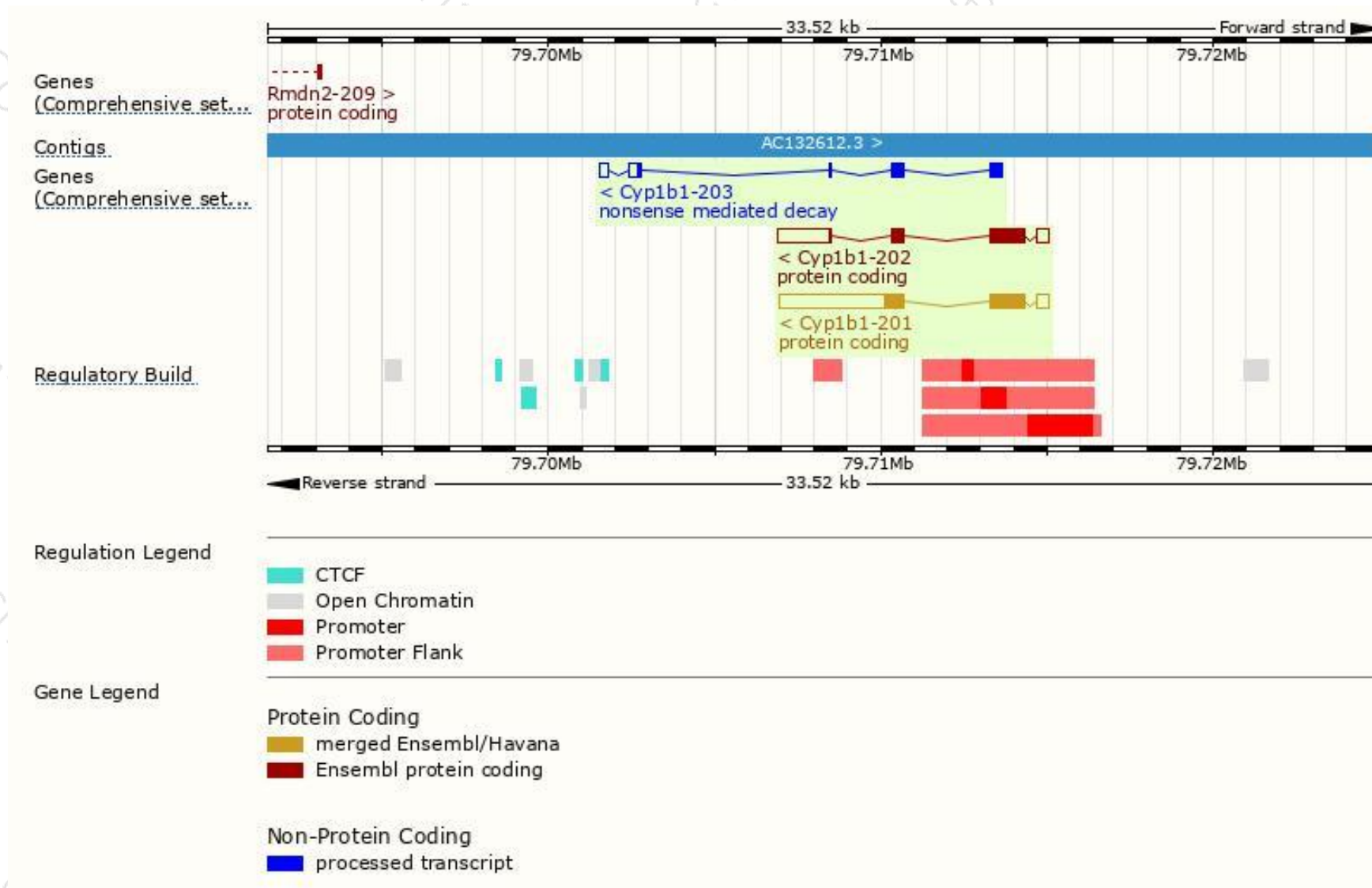
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cyp1b1-201	ENSMUST00000024894.1	5128	543aa	Protein coding	CCDS28986	Q64429	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 P1
Cyp1b1-202	ENSMUST000000234361.1	3398	487aa	Protein coding	-	Q3UTK2	GENCODE basic
Cyp1b1-203	ENSMUST000000234927.1	1436	289aa	Nonsense mediated decay	-	A0A3Q4L2V1	CDS 5' incomplete

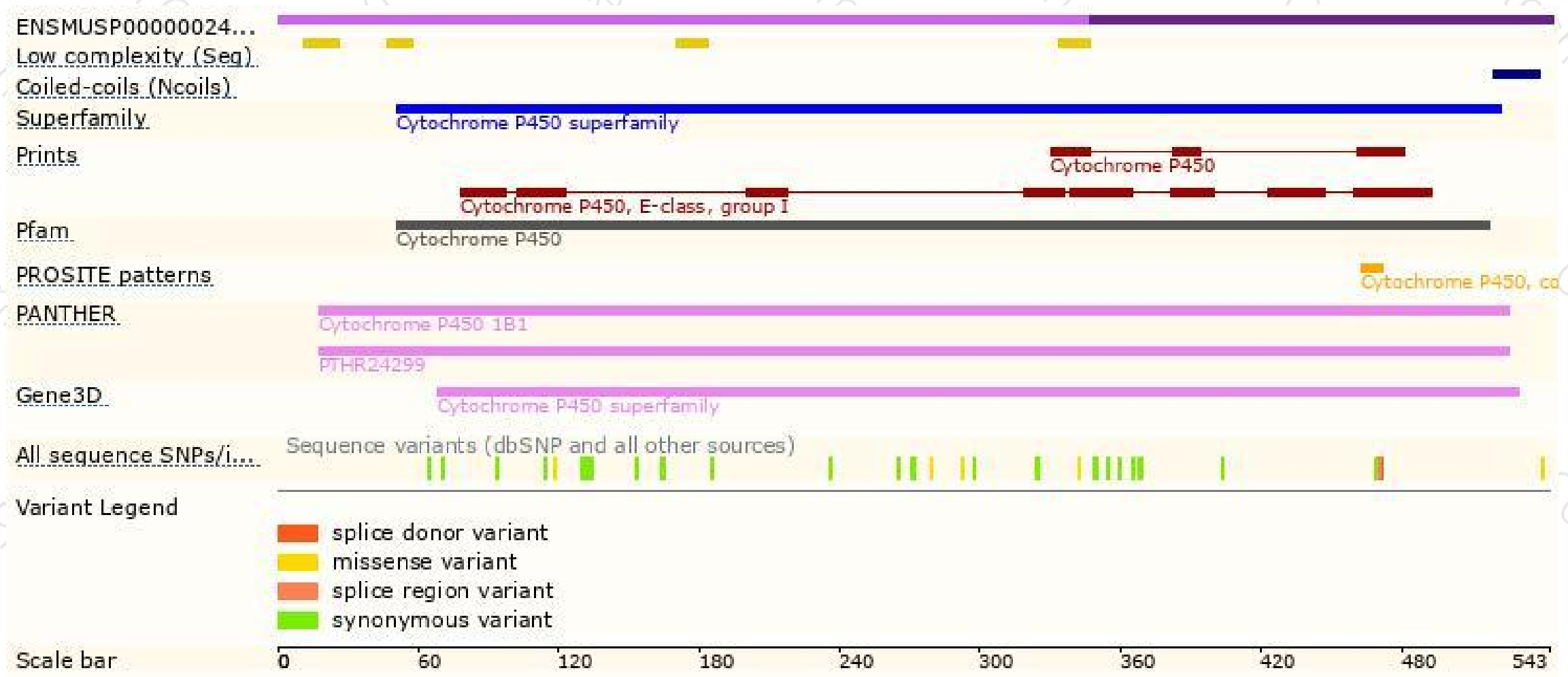
The strategy is based on the design of *Cyp1b1-201* transcript,the transcription is shown below:



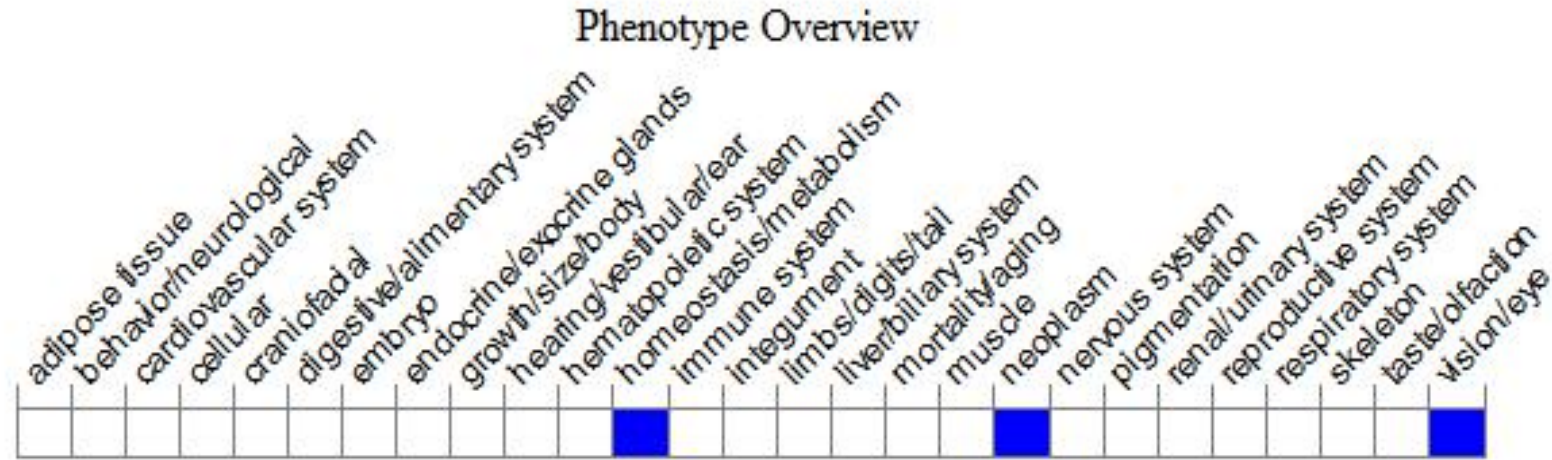
Genomic location distribution



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 knock-out allele are protected from the acute bone marrow cytotoxic and preleukemic effects of DMBA, show a decreased incidence of DMBA-induced lymphomas, and display background-sensitive ocular abnormalities.

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

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