

***Bhlhe41* Cas9-KO Strategy**

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Project Overview

Project Name

Bhlhe41

Project type

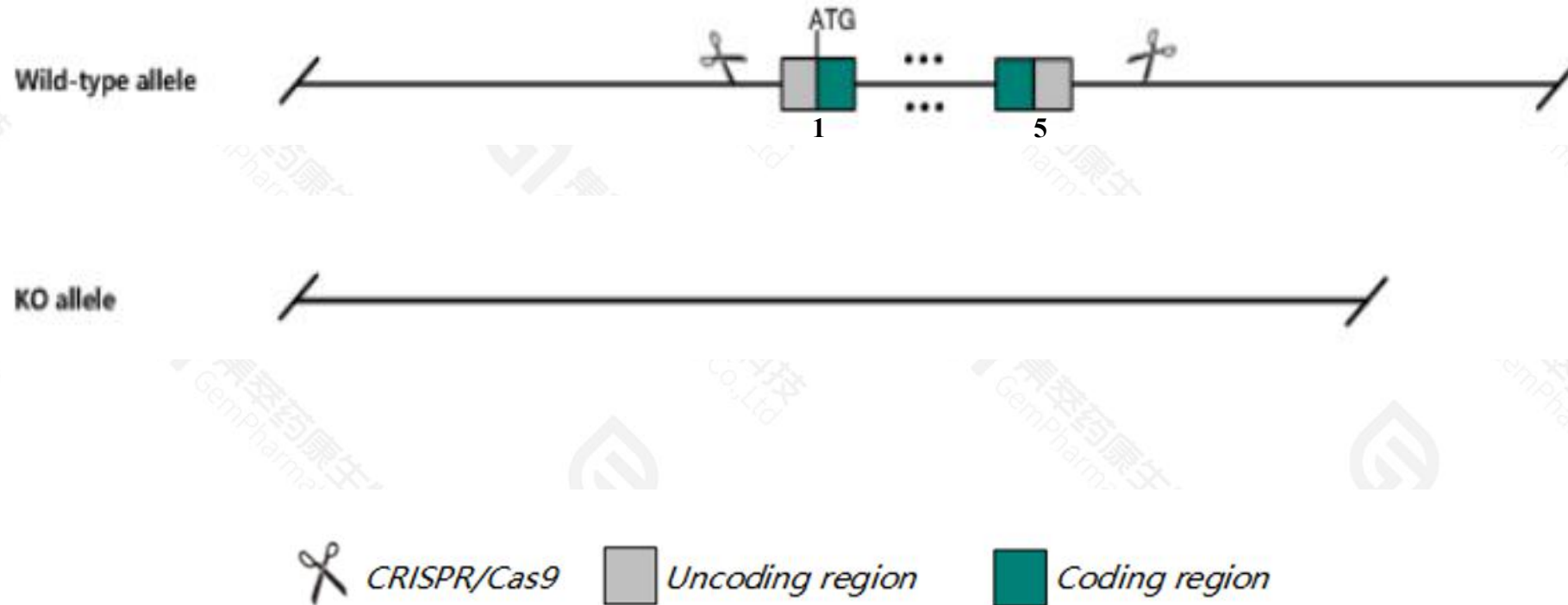
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bhlhe41* gene. The schematic diagram is as follows:



- The *Bhlhe41* gene has 3 transcripts. According to the structure of *Bhlhe41* gene, exon1-exon5 of *Bhlhe41*-201(ENSMUST00000032386.10) 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 *Bhlhe41* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for one knock-out allele exhibit delayed circadian phase. Mice homozygous for another knock-out allele exhibit impaired TH2 differentiation in response to numerous stimuli.
- The *Bhlhe41* gene is located on the Chr6. 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.

Bhlhe41 basic helix-loop-helix family, member e41 [Mus musculus (house mouse)]

Gene ID: 79362, updated on 13-Mar-2020

Summary



Official Symbol Bhlhe41 provided by [MGI](#)

Official Full Name basic helix-loop-helix family, member e41 provided by [MGI](#)

Primary source [MGI:MGI:1930704](#)

See related [Ensembl:ENSMUSG00000030256](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 6430520M22Rik, Bhlhb2l, Bhlhb3, DEC2, Sharp1

Summary This gene encodes a basic helix-loop-helix protein expressed in various tissues. The encoded protein can interact with Arntl or compete for E-box binding sites in the promoter of Per1 and repress Clock/Arntl's transactivation of Per1. This gene is believed to be involved in the control of circadian rhythm and cell differentiation. Defects in this gene are associated with the short sleep phenotype. Alternatively spliced transcript variants encoding multiple isoforms have been observed for this gene. [provided by RefSeq, Feb 2014]

Expression Broad expression in mammary gland adult (RPKM 17.6), adrenal adult (RPKM 12.4) and 16 other tissues [See more](#)

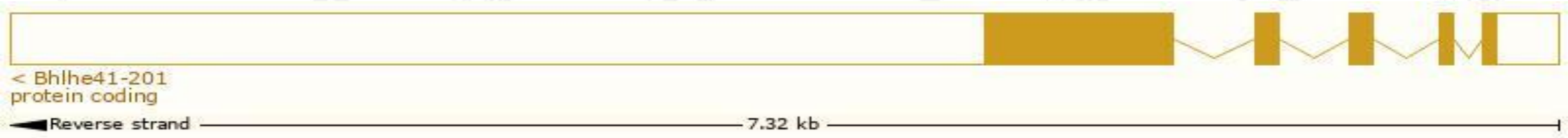
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

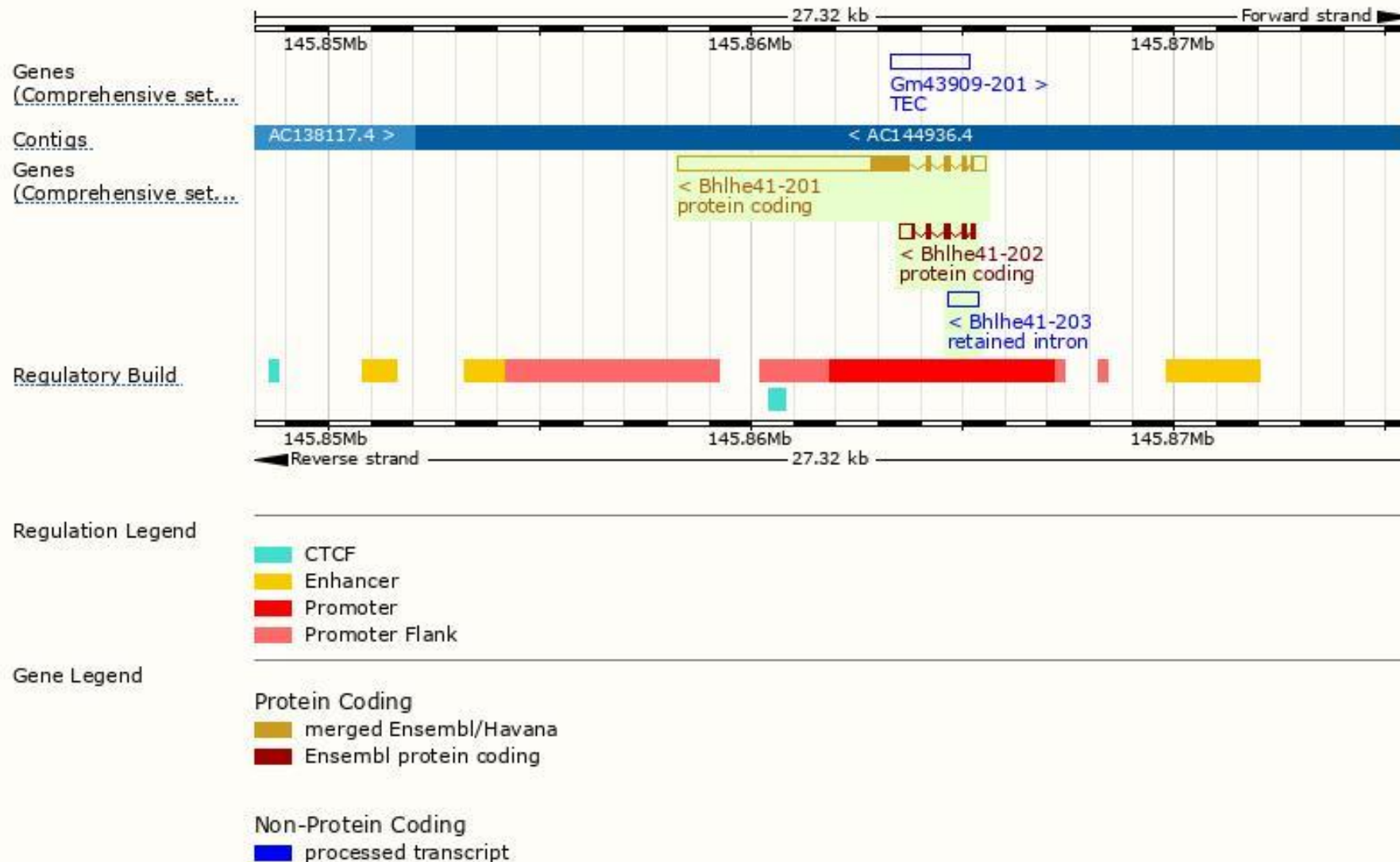
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bhlhe41-201	ENSMUST00000032386.10	6133	410aa	Protein coding	CCDS20697	Q6L8F5 Q99PV5	TSL:1 GENCODE basic APPRIS P1
Bhlhe41-202	ENSMUST00000111703.1	744	131aa	Protein coding	CCDS71860	D3Z2G6	TSL:3 GENCODE basic
Bhlhe41-203	ENSMUST00000203949.1	690	No protein	Retained intron	-	-	TSL:NA

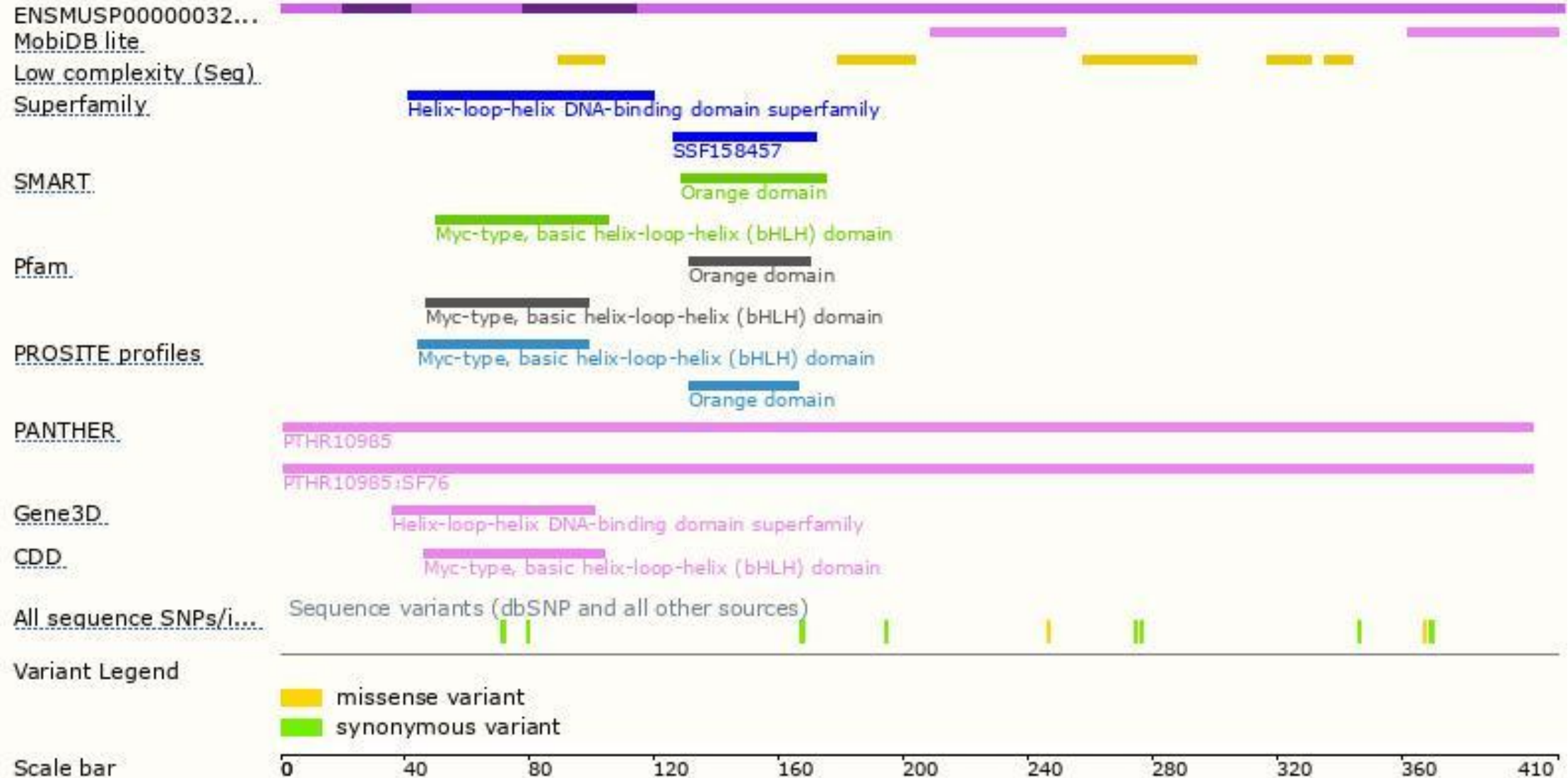
The strategy is based on the design of *Bhlhe41-201* transcript,the transcription is shown below:



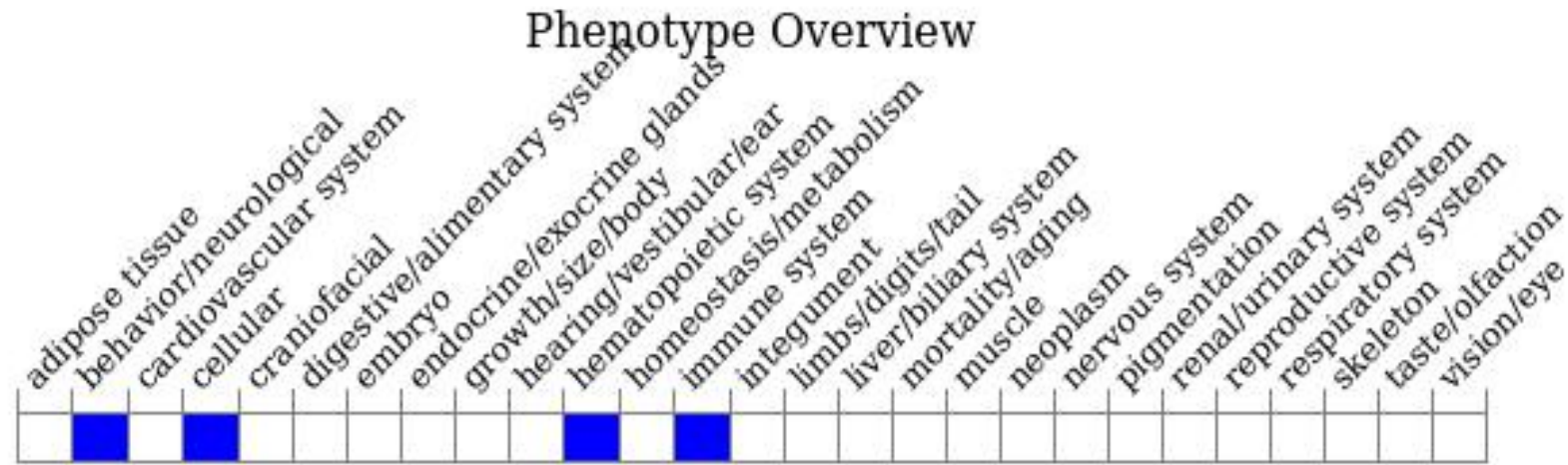
Genomic location distribution



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 one knock-out allele exhibit delayed circadian phase. Mice homozygous for another knock-out allele exhibit impaired TH2 differentiation in response to numerous stimuli.

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