

Mcm5 Cas9-CKO Strategy

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Design Date: 2021-5-26

Project Overview

Project Name

Mcm5

Project type

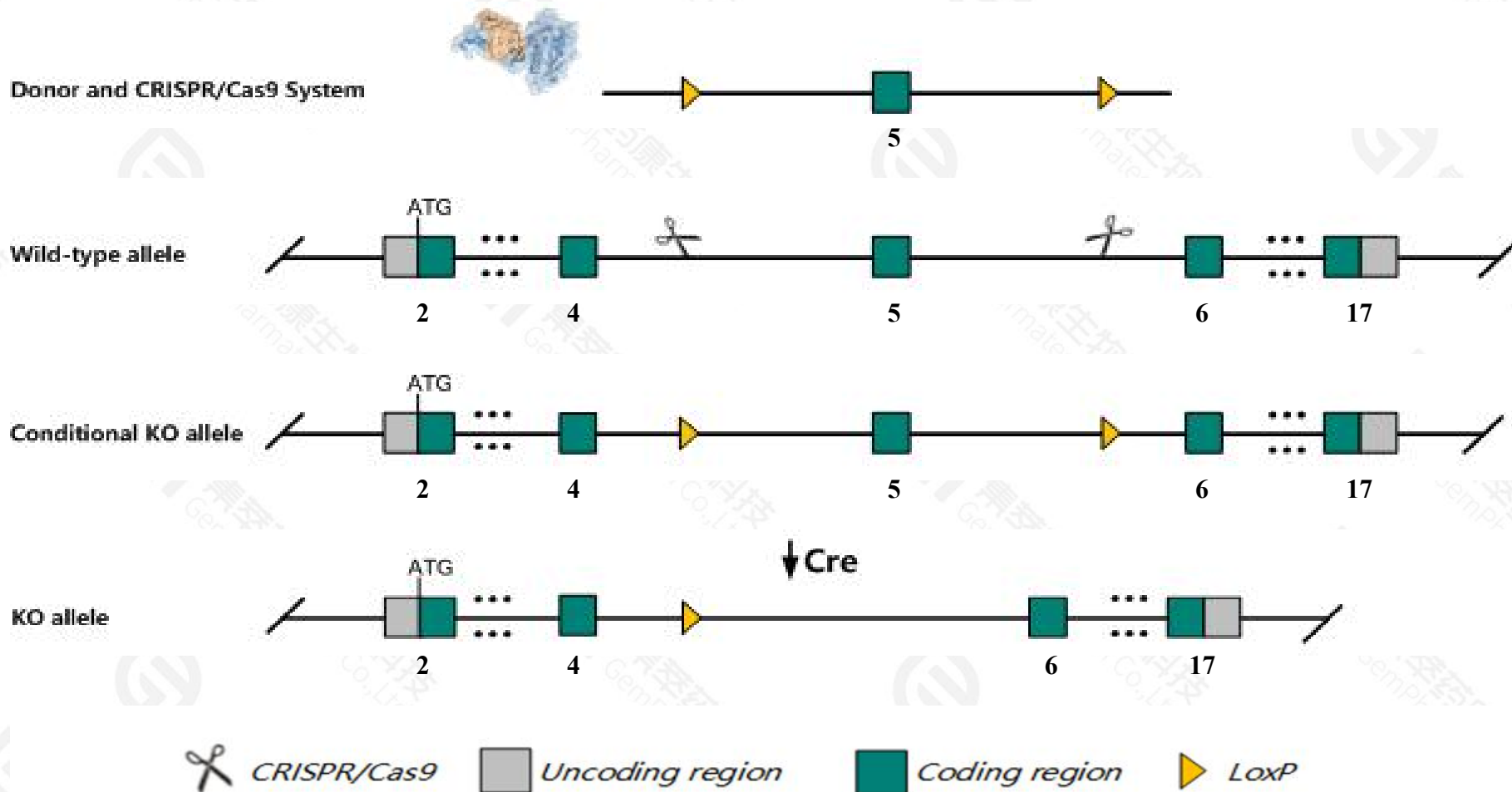
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mcm5* gene. The schematic diagram is as follows:



Technical routes

- The *Mcm5* gene has 5 transcripts. According to the structure of *Mcm5* gene, exon5 of *Mcm5*-201(ENSMUST00000164309.3) transcript is recommended as the knockout region. The region contains 173bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mcm5* 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 ENU-induced allele exhibit embryonic lethality.
- The *Mcm5* gene is located on the Chr8. 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)

Mcm5 minichromosome maintenance complex component 5 [Mus musculus (house mouse)]

Gene ID: 17218, updated on 13-Mar-2020

Summary

Official Symbol Mcm5 provided by [MGI](#)

Official Full Name minichromosome maintenance complex component 5 provided by [MGI](#)

Primary source [MGI:MGI:103197](#)

See related [Ensembl:ENSMUSG00000005410](#)

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 AA617332, AI324988, AL033333, Cdc46, Mcmd5, P1-CDC46

Summary The protein encoded by this gene is a member of the oligameric minichromosome maintenance protein complex. During DNA replication, the complex loads onto chromatin in early G1 and is converted into an active replicative helicase during S phase. It functions to limit DNA synthesis to once per cell cycle. During embryogenesis, the encoded protein is negatively regulated through expression of paired box protein Pax 3. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Oct 2014]

Expression Broad expression in liver E14.5 (RPKM 77.8), liver E14 (RPKM 74.7) and 18 other tissues [See more](#)

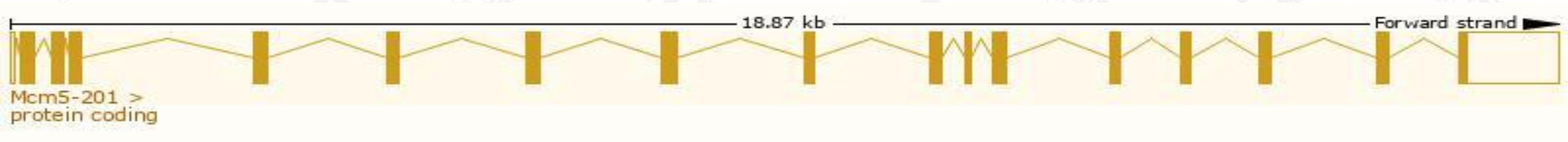
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

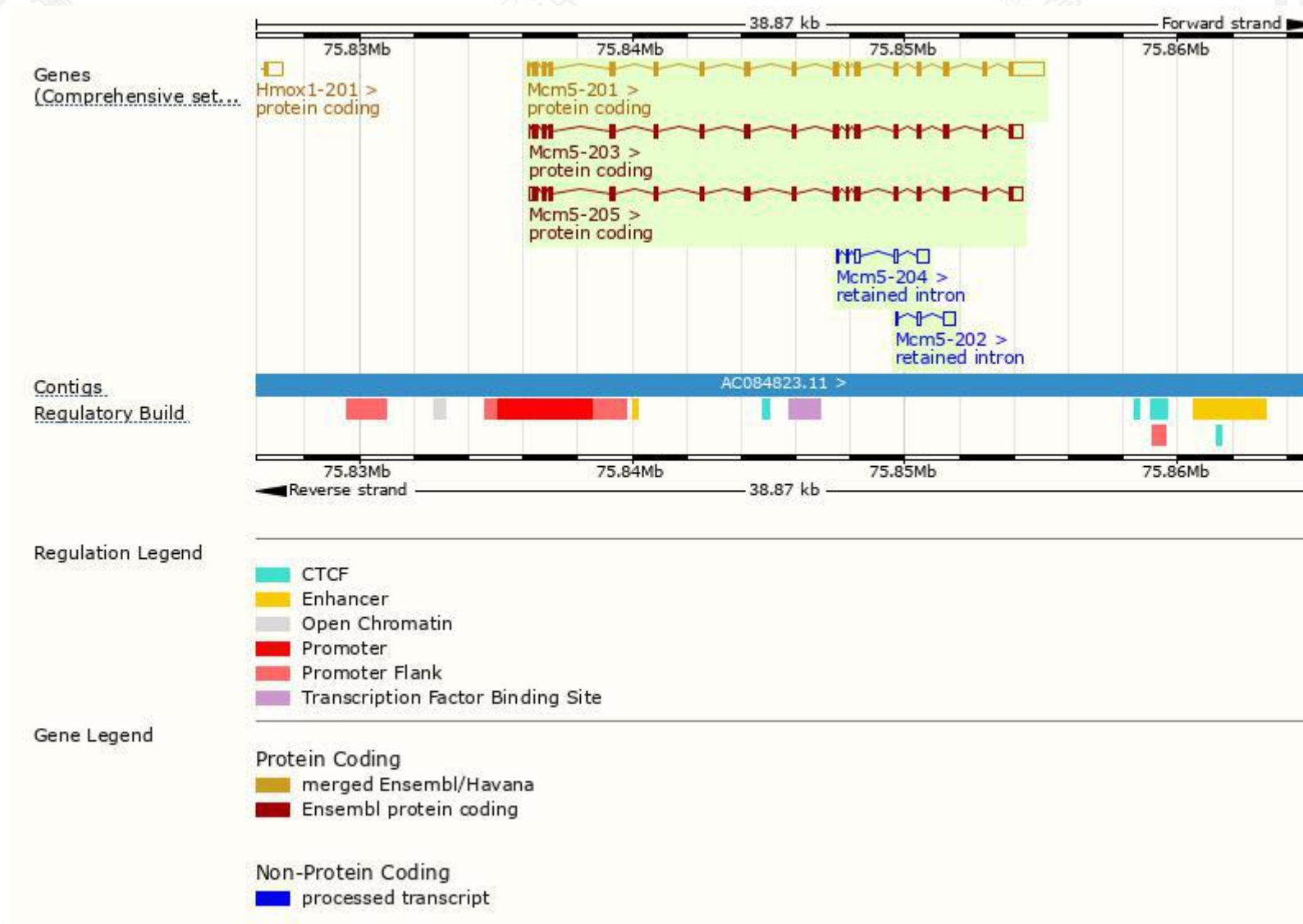
The gene has 5 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|--------------------------------------|------|-----------------------|-----------------|---------------------------|------------------------|---|
| Mcm5-201 | ENSMUST00000164309.2 | 3381 | 734aa | Protein coding | CCDS22424 | P49718 | 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 |
| Mcm5-205 | ENSMUST00000212811.1 | 2653 | 734aa | Protein coding | CCDS22424 | P49718 | 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 |
| Mcm5-203 | ENSMUST00000212426.1 | 2604 | 734aa | Protein coding | CCDS22424 | P49718 | 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 |
| Mcm5-204 | ENSMUST00000212648.1 | 760 | No protein | Retained intron | - | - | TSL:2 |
| Mcm5-202 | ENSMUST00000211912.1 | 595 | No protein | Retained intron | - | - | TSL:3 |

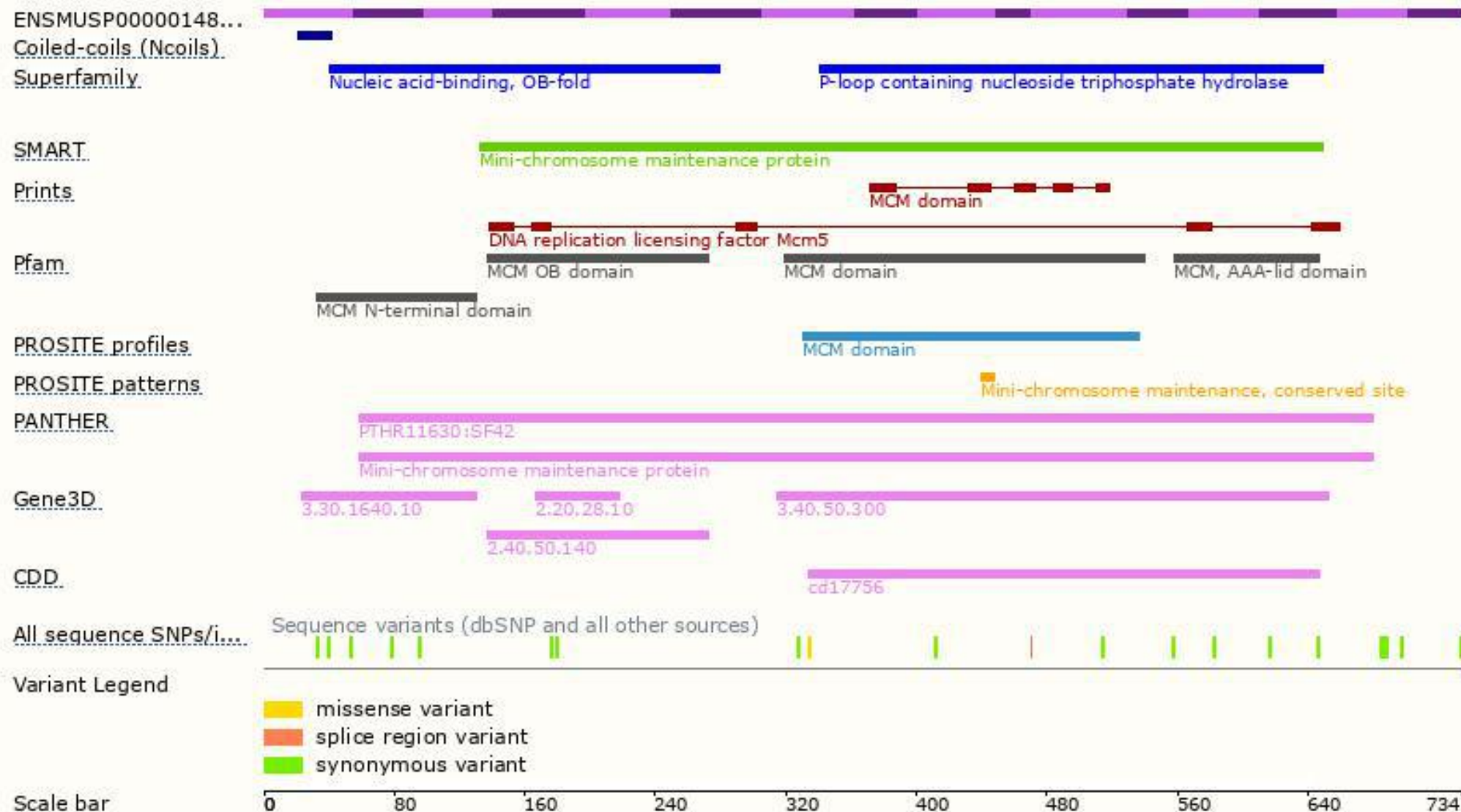
The strategy is based on the design of *Mcm5-201* transcript,the transcription is shown below:



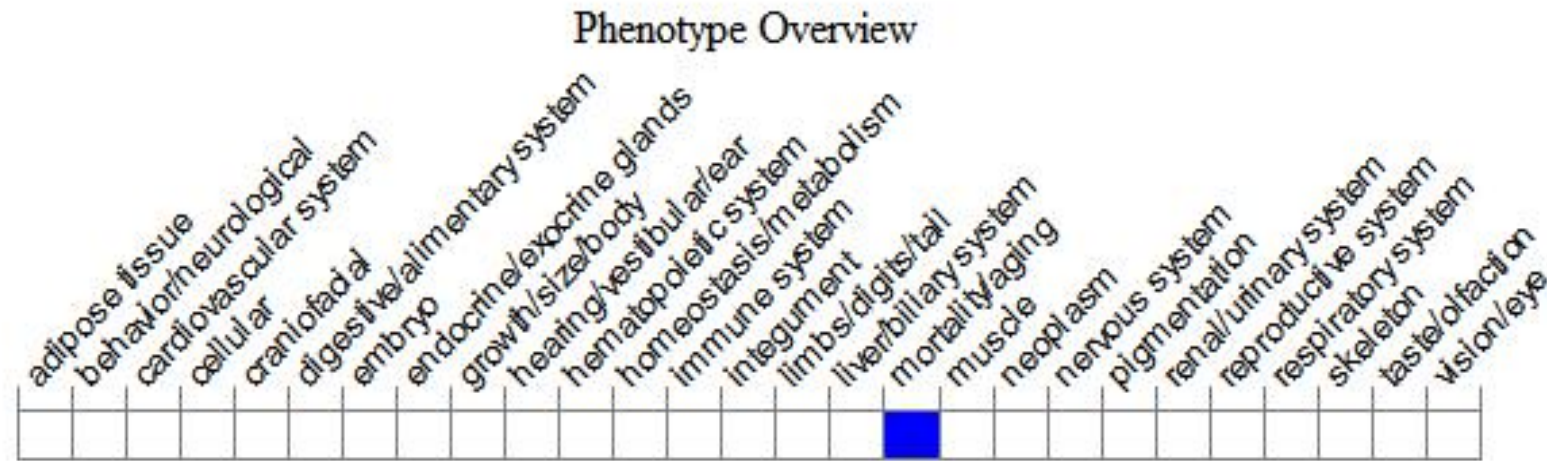
Genomic location distribution



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 ENU-induced allele exhibit embryonic lethality.

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