

Hhex Cas9-KO Strategy

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| Reviewer: | Huan Fan |
| Design Date: | 2020-5-6 |

Project Overview

Project Name

Hhex

Project type

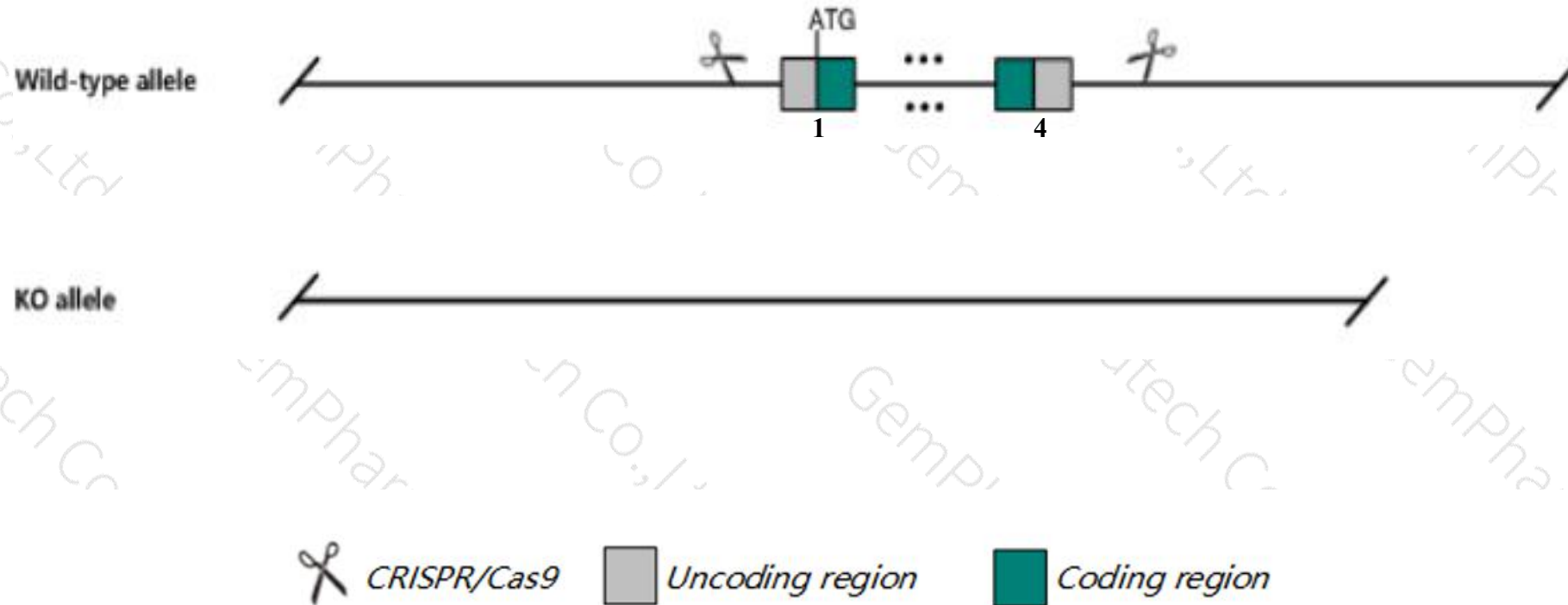
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Hhex* gene has 3 transcripts. According to the structure of *Hhex* gene, exon1-exon4 of *Hhex-201* (ENSMUST00000025944.8) 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 *Hhex* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit embryonic lethality associated with abnormal embryogenesis and cardiac development. mice homozygous for another knock-out allele exhibit embryonic lethality, fetal lethality and abnormal nervous system development.
- The KO region contains the *Gm38345* gene. Knockout the region may affect the function of *Gm38345* gene.
- The *Hhex* gene is located on the Chr19. 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)

Hhex hematopoietically expressed homeobox [Mus musculus (house mouse)]

Gene ID: 15242, updated on 13-Mar-2020

Summary



Official Symbol Hhex provided by [MGI](#)

Official Full Name hematopoietically expressed homeobox provided by [MGI](#)

Primary source [MGI:MGI:96086](#)

See related [Ensembl:ENSMUSG00000024986](#)

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 Hex, Hex1, Hhex-rs2, Prh, Prhx

Expression Biased expression in adrenal adult (RPKM 160.1), liver adult (RPKM 39.6) and 5 other tissues [See more](#)

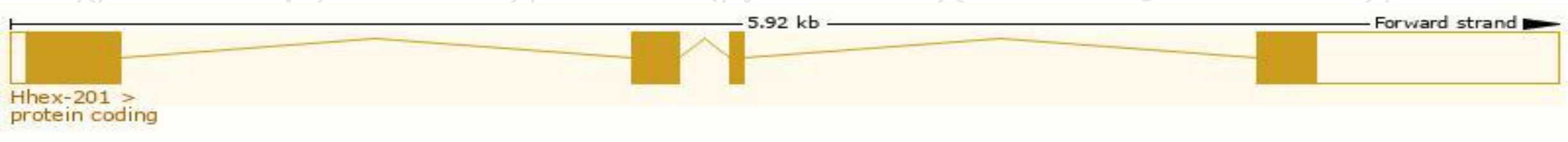
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

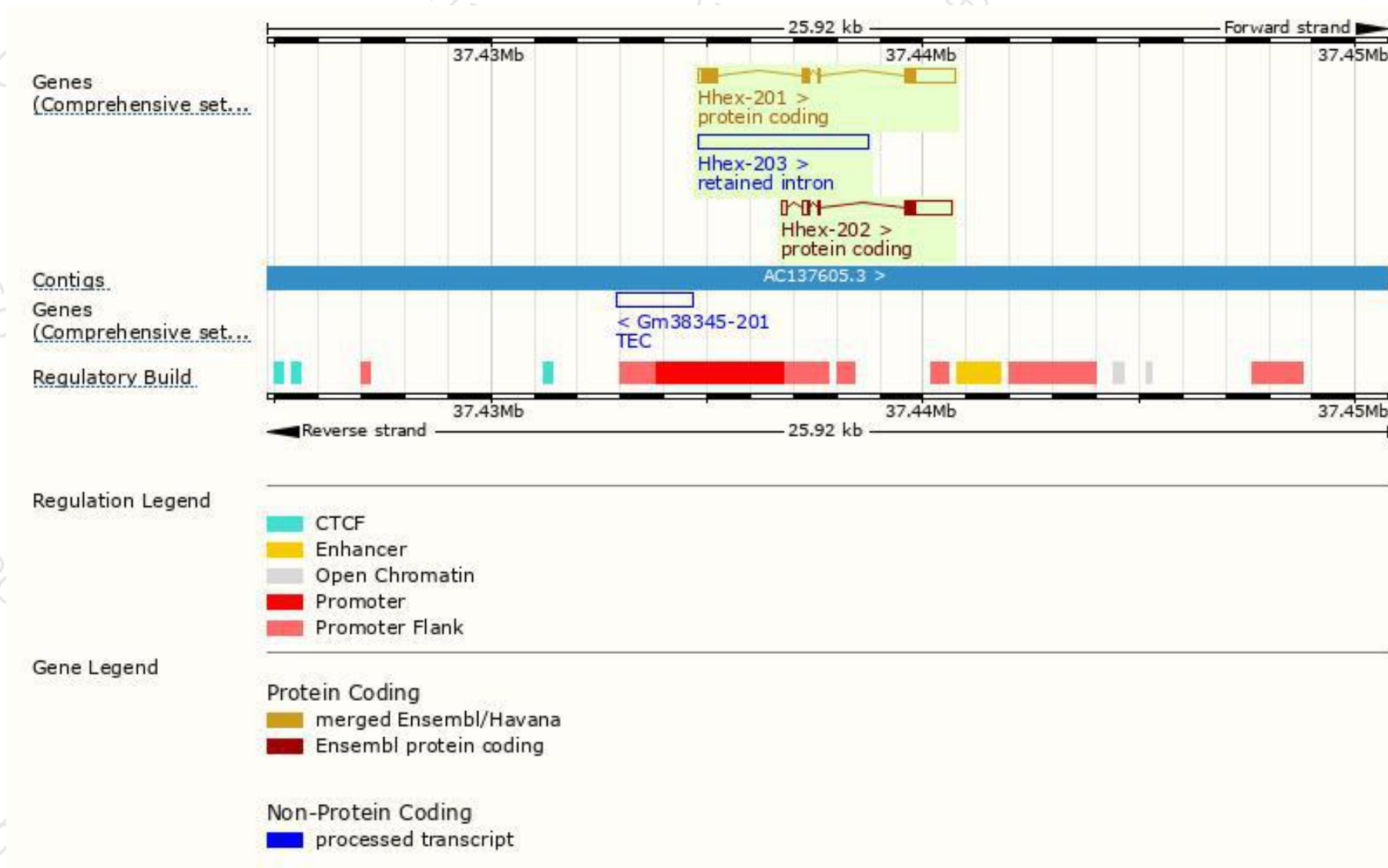
The gene has 3 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|--------------------------------------|------|-----------------------|-----------------|---------------------------|------------------------|---|
| Hhex-201 | ENSMUST00000025944.8 | 1802 | 271aa | Protein coding | CCDS29778 | P43120 | 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 |
| Hhex-202 | ENSMUST00000128184.2 | 1435 | 98aa | Protein coding | - | G3UXH1 | TSL:2 GENCODE basic |
| Hhex-203 | ENSMUST00000237452.1 | 3908 | No protein | Retained intron | - | - | |

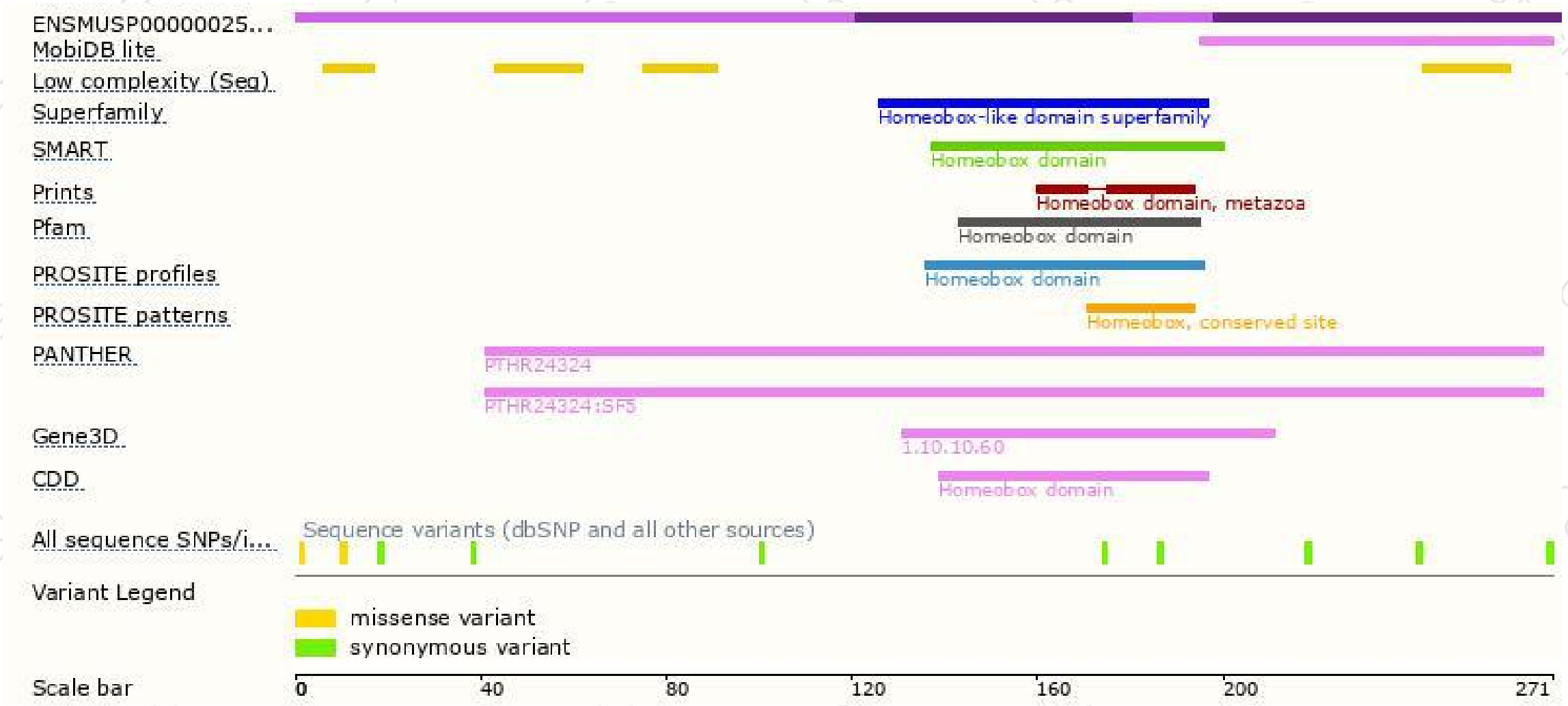
The strategy is based on the design of *Hhex-201* transcript,the transcription is shown below:



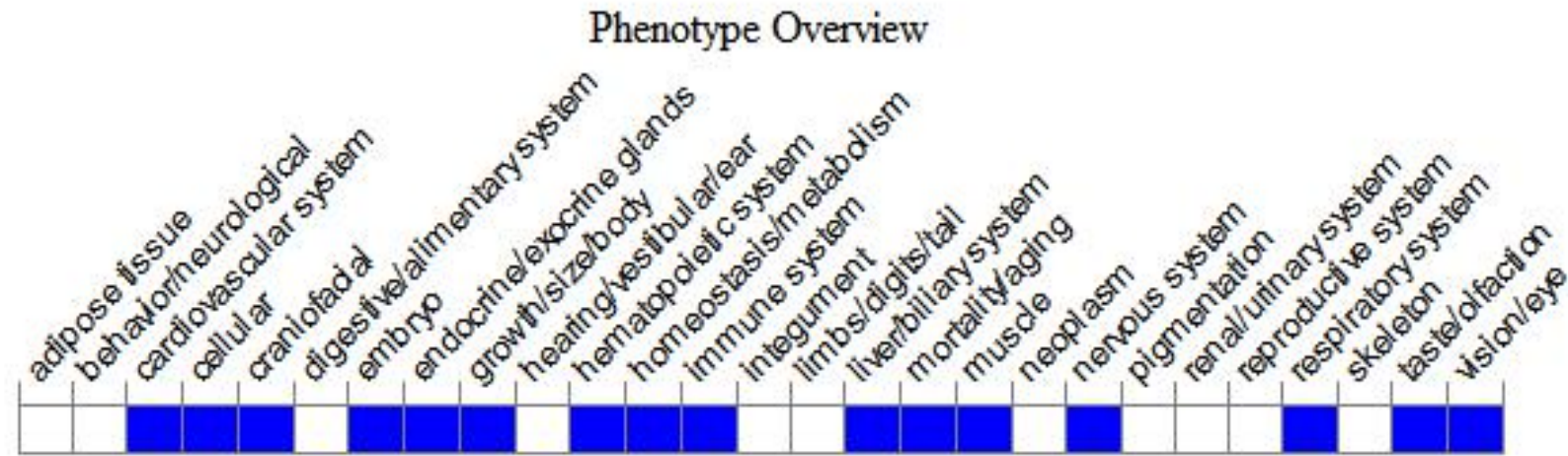
Genomic location distribution



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 exhibit embryonic lethality associated with abnormal embryogenesis and cardiac development. Mice homozygous for another knock-out allele exhibit embryonic lethality, fetal lethality and abnormal nervous system development.

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

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