

Eif3e Cas9-KO Strategy

Designer: Huan Wang

Reviewer: Yumeng Wang

Design Date: 2021-9-27

Project Overview

Project Name

Eif3e

Project type

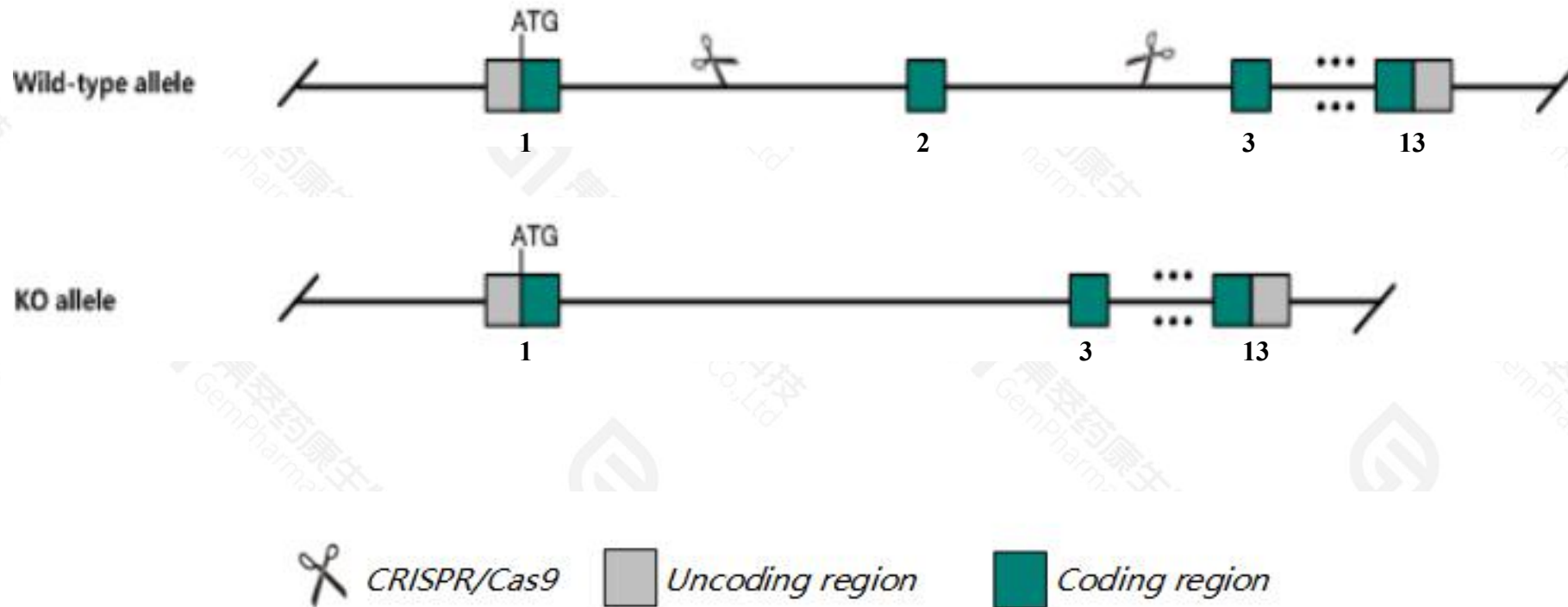
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eif3e* gene. The schematic diagram is as follows:



- The *Eif3e* gene has 4 transcripts. According to the structure of *Eif3e* gene, exon2 of *Eif3e-201*(ENSMUST00000022960.4) transcript is recommended as the knockout region. The region contains 115bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eif3e* 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 a null allele exhibit prenatal lethality with reduced embryo size, cell size and fetal membranes. Mice heterozygous for a null allele exhibit reduced size, weight, MEF cell proliferation and MEF translation.
- The *Eif3e* 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.

Eif3e eukaryotic translation initiation factor 3, subunit E [Mus musculus (house mouse)]

Gene ID: 16341, updated on 13-Mar-2020

Summary

Official Symbol Eif3e provided by [MGI](#)

Official Full Name eukaryotic translation initiation factor 3, subunit E provided by [MGI](#)

Primary source [MGI:MGI:99257](#)

See related [Ensembl:ENSMUSG00000022336](#)

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 48kDa, Eif3s6, Int6, eIF3-p46, eIF3-p48

Expression Broad expression in CNS E11.5 (RPKM 59.0), placenta adult (RPKM 52.0) and 22 other tissues [See more](#)

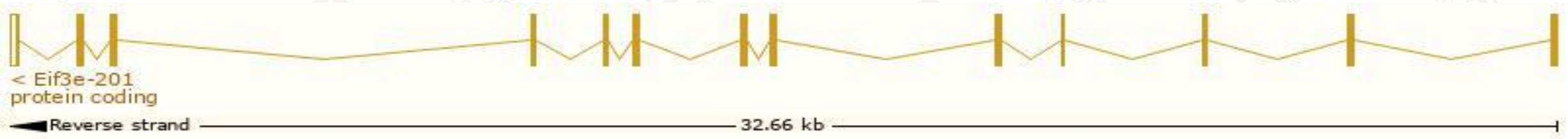
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

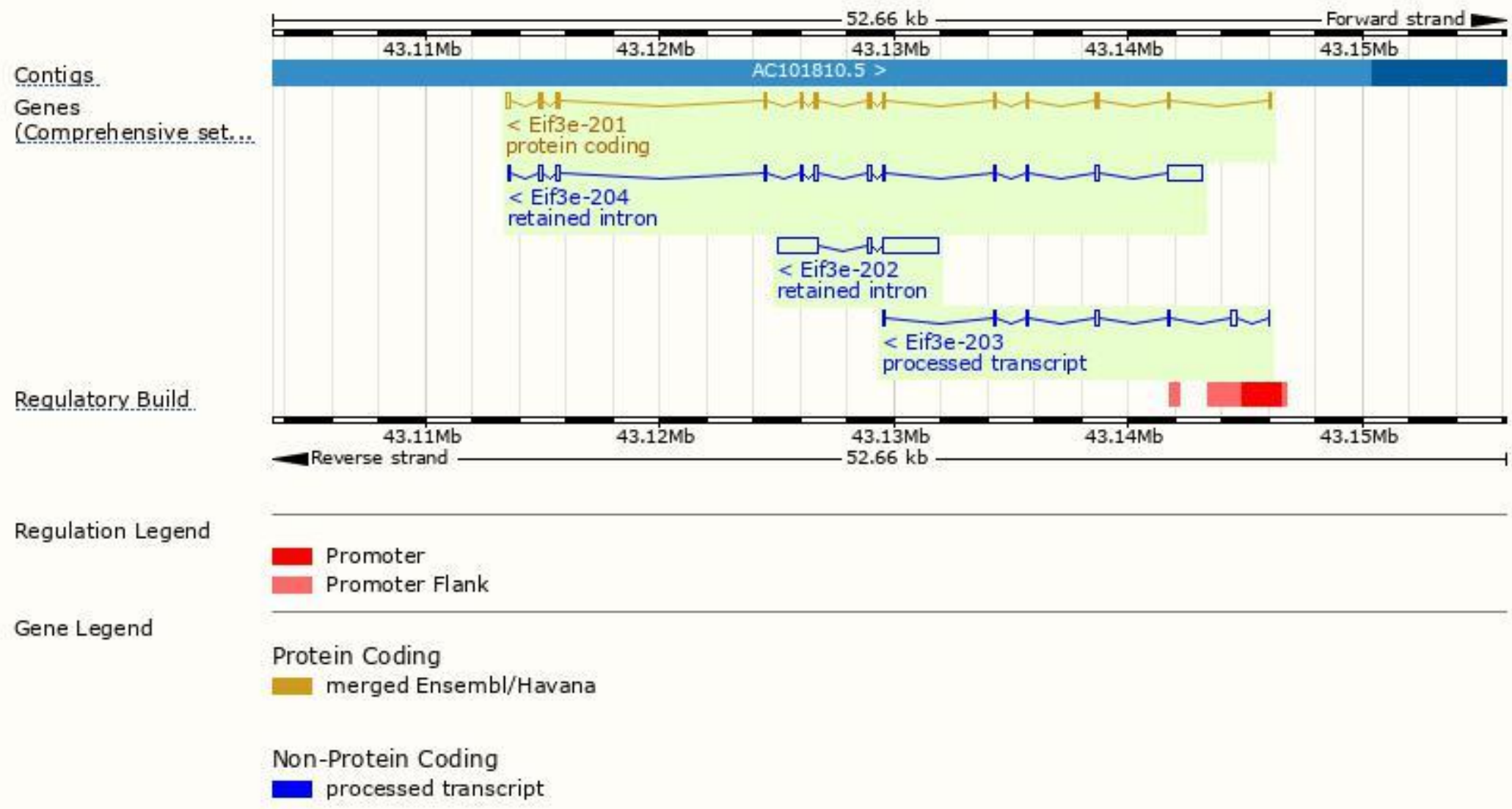
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eif3e-201	ENSMUST00000022960.3	1506	445aa	Protein coding	CCDS27452	P60229_Q3UIG0	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
Eif3e-203	ENSMUST000000226415.1	717	No protein	Processed transcript	-	-	
Eif3e-202	ENSMUST000000226281.1	4123	No protein	Retained intron	-	-	
Eif3e-204	ENSMUST000000228892.1	2633	No protein	Retained intron	-	-	

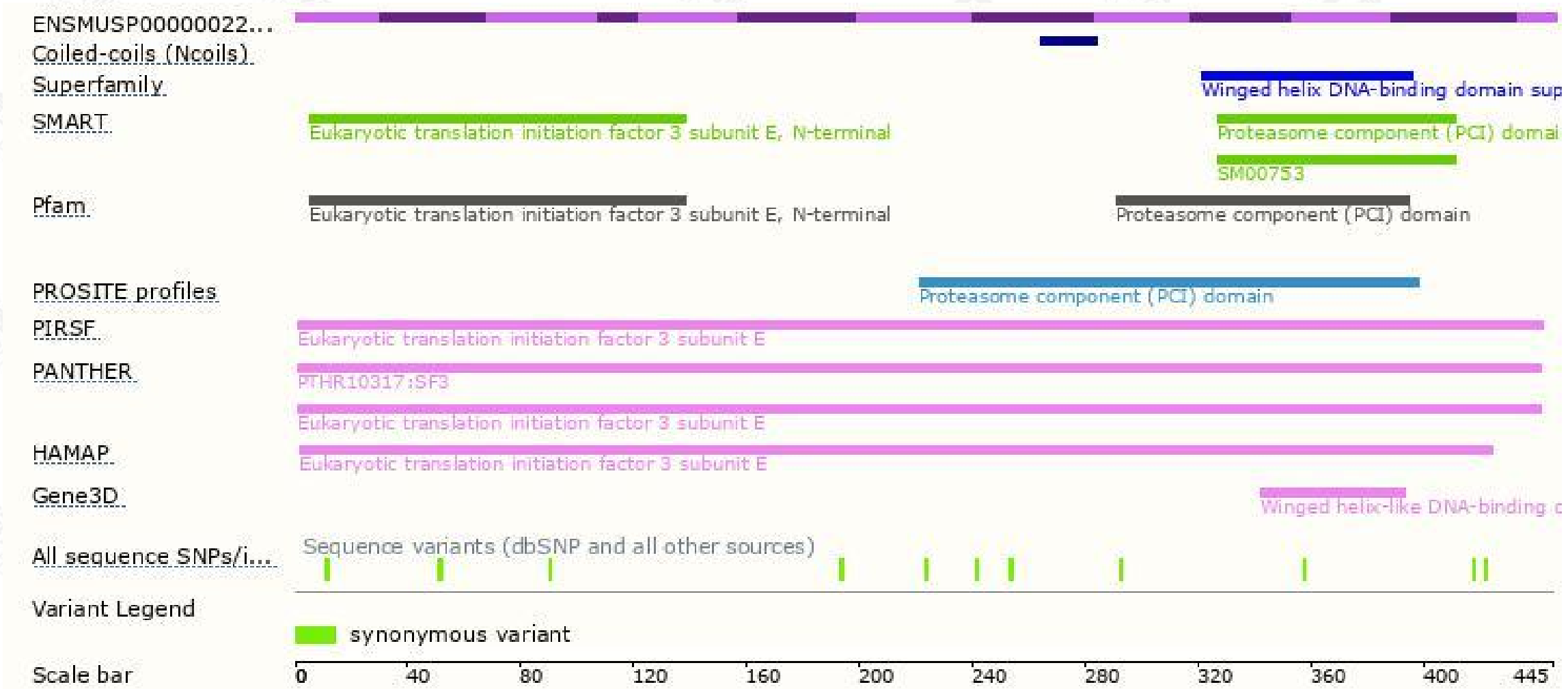
The strategy is based on the design of *Eif3e-201* transcript,the transcription is shown below:



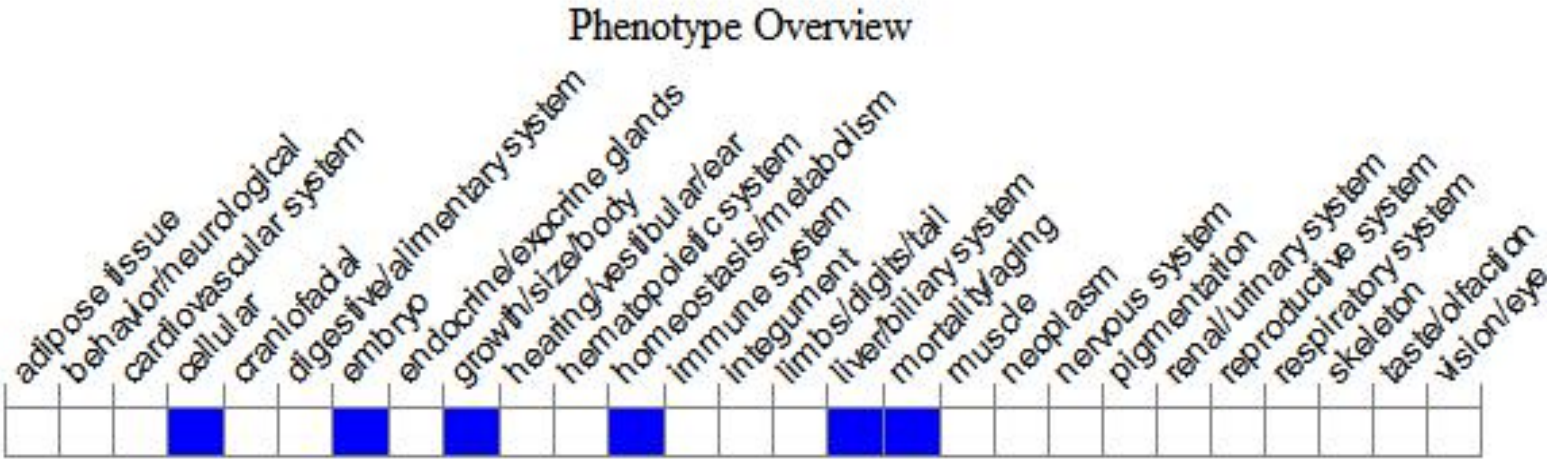
Genomic location distribution



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/>).

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If you have any questions, you are welcome to inquire.
Tel: 400-9660890

