

Zc3h4 Cas9-KO Strategy

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Reviewer: 2021-8-23

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Project Overview

Project Name

Zc3h4

Project type

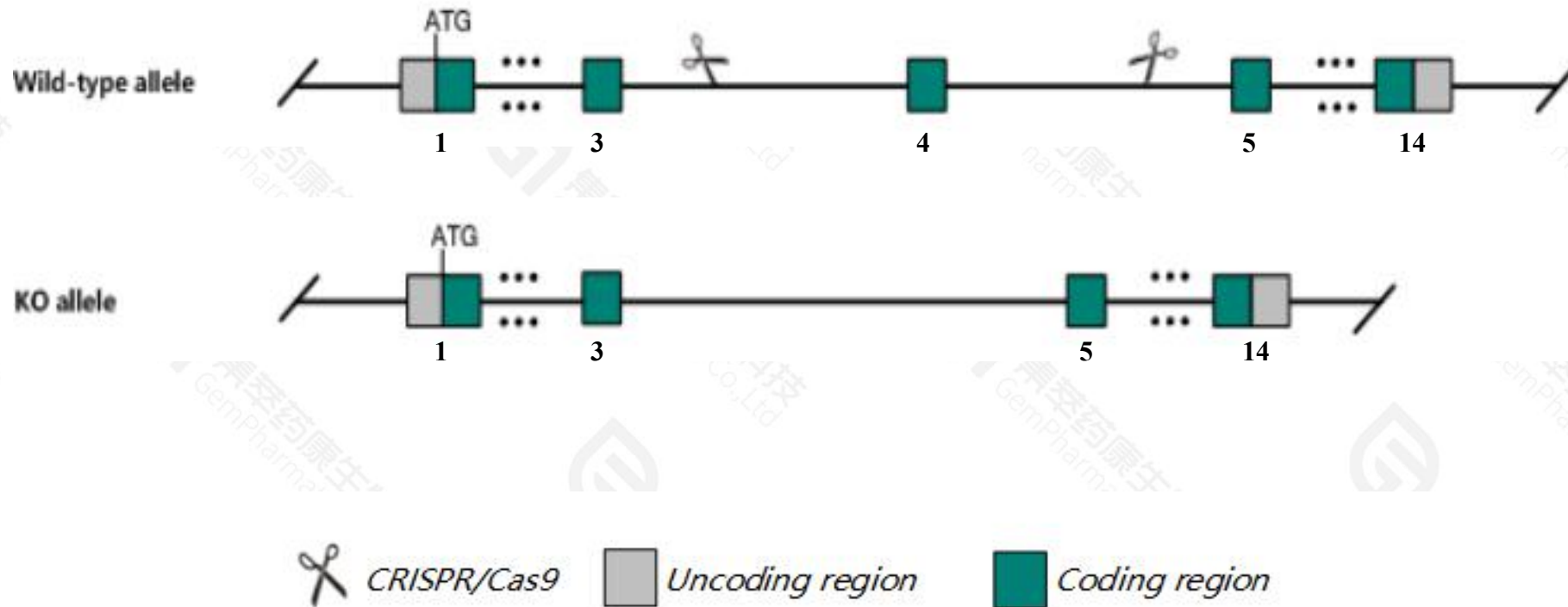
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zc3h4* gene. The schematic diagram is as follows:



- The *Zc3h4* gene has 4 transcripts. According to the structure of *Zc3h4* gene, exon4 of *Zc3h4-201*(ENSMUST00000098789.5) transcript is recommended as the knockout region. The region contains 223bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zc3h4* 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 knock-out allele show complete embryonic lethality between implantation and somite formation and failure of blastocysts to hatch from the zona pellucida and form typical outgrowth colonies.
- The effect is unknown of 203,204.
- The *Zc3h4* gene is located on the Chr7. 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.

Zc3h4 zinc finger CCCH-type containing 4 [Mus musculus (house mouse)]

Gene ID: 330474, updated on 2-Mar-2021

Summary



Official Symbol Zc3h4 provided by [MGI](#)

Official Full Name zinc finger CCCH-type containing 4 provided by [MGI](#)

Primary source [MGI:MGI:2682314](#)

See related [Ensembl:ENSMUSG00000059273](#)

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 Bwq1, Gm768, Kiaa1064-hp

Expression Ubiquitous expression in thymus adult (RPKM 20.9), spleen adult (RPKM 16.4) and 28 other tissues [See more](#)

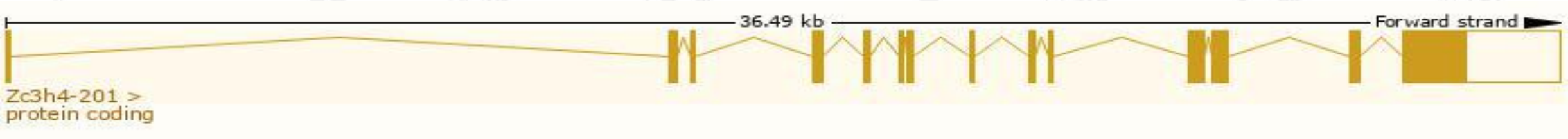
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

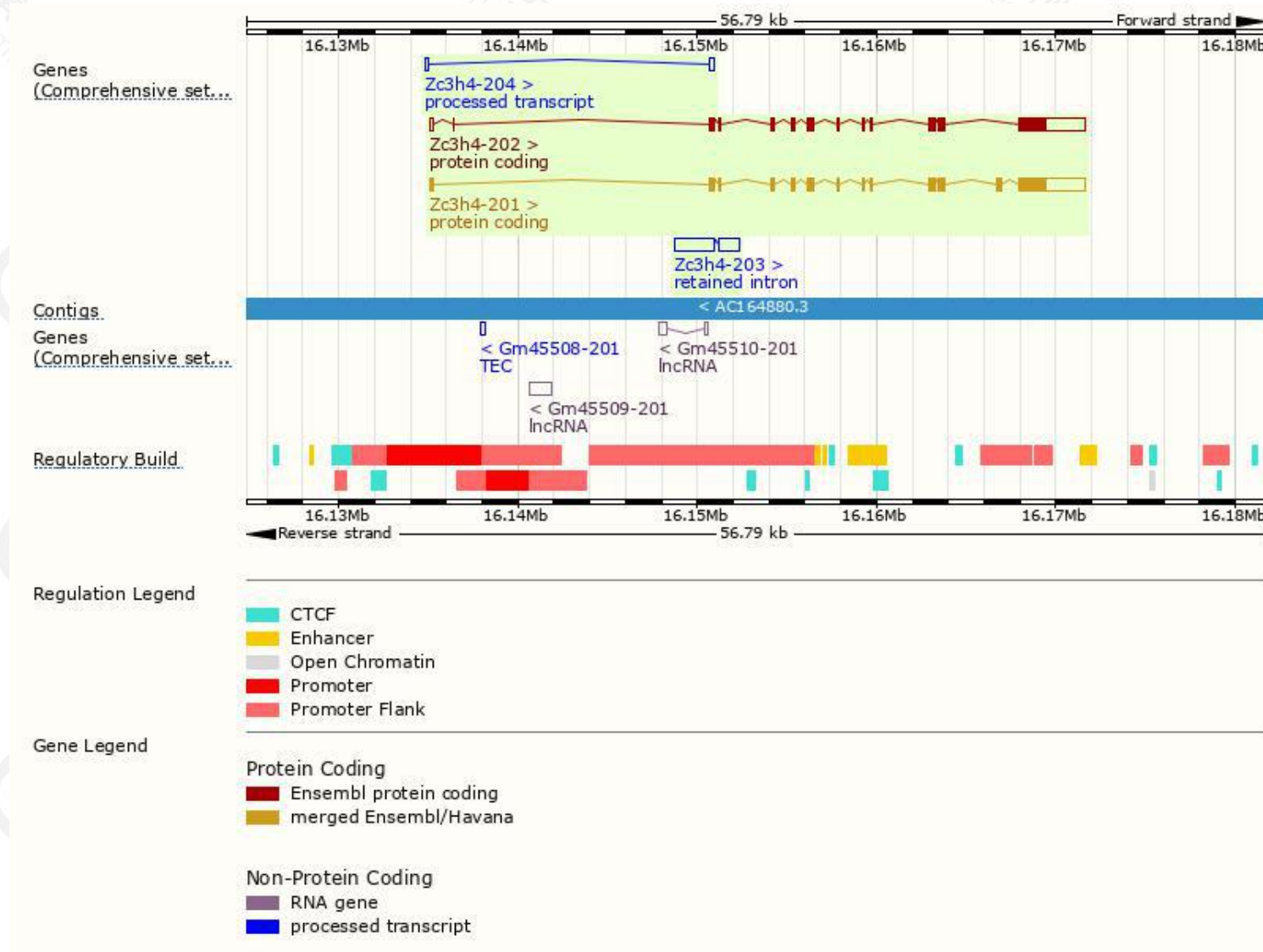
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zc3h4-201	ENSMUST00000098789.5	6039	1255aa	Protein coding	CCDS52040		TSL:5 , GENCODE basic , APPRIS P2 ,
Zc3h4-202	ENSMUST00000209289.2	5853	1180aa	Protein coding	-		TSL:5 , GENCODE basic , APPRIS ALT2 ,
Zc3h4-204	ENSMUST00000214735.2	333	No protein	Processed transcript	-		TSL:3 ,
Zc3h4-203	ENSMUST00000209374.2	3244	No protein	Retained intron	-		TSL:1 ,

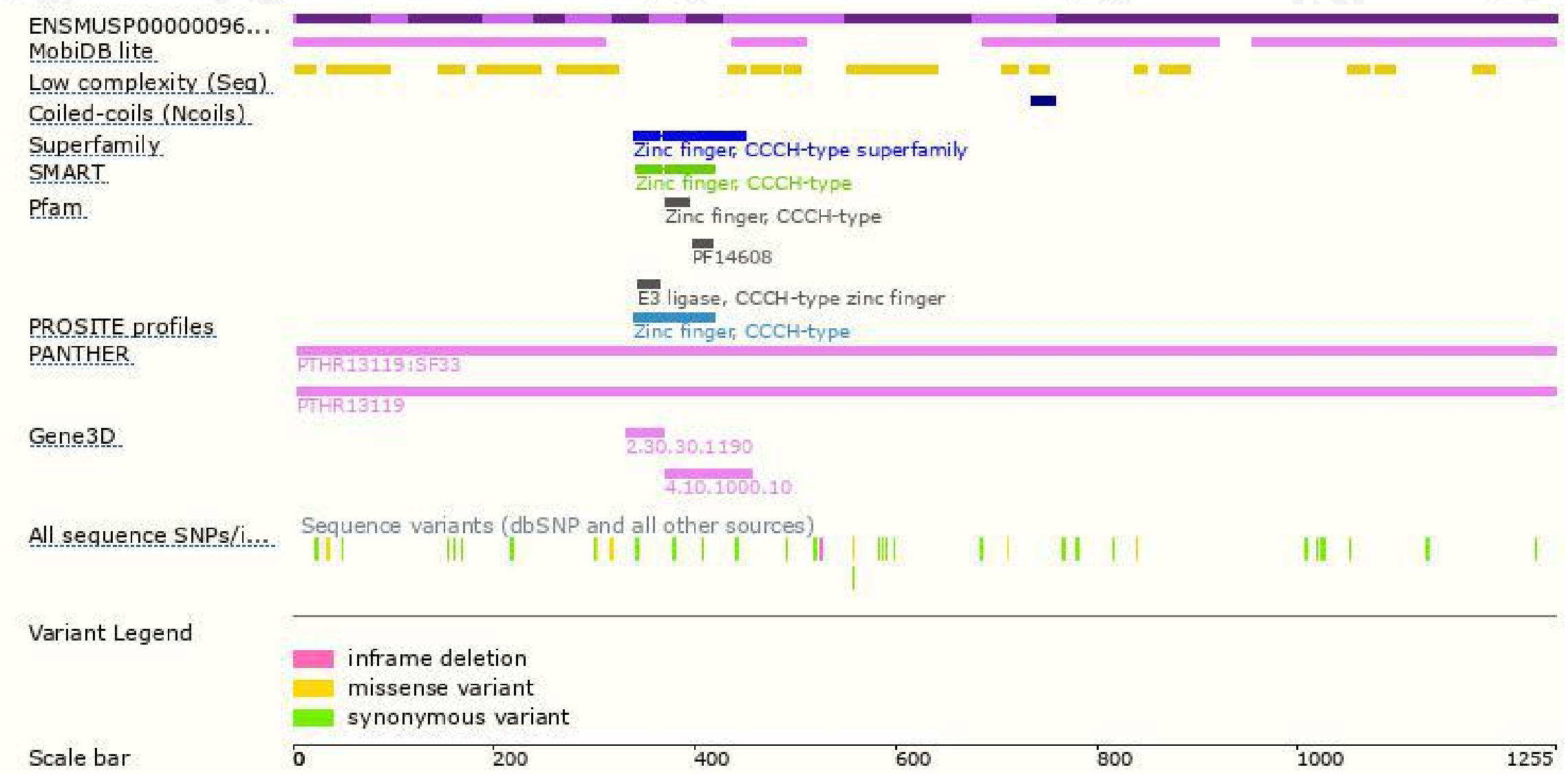
The strategy is based on the design of *Zc3h4-201* transcript,the transcription is shown below:



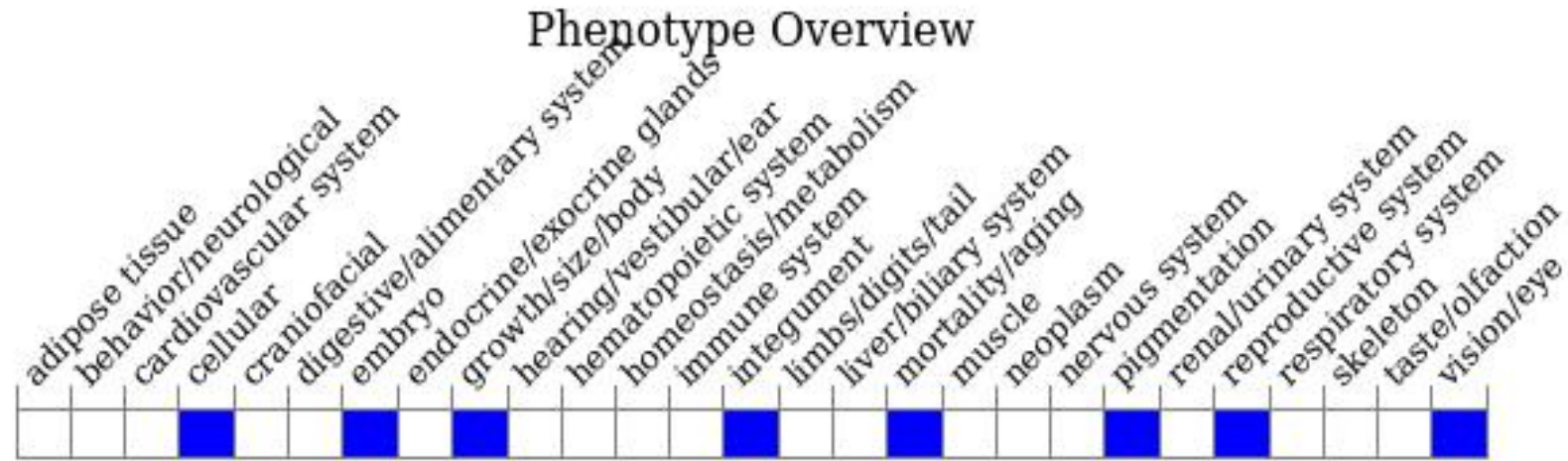
Genomic location distribution



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 show complete embryonic lethality between implantation and somite formation and failure of blastocysts to hatch from the zona pellucida and form typical outgrowth colonies.

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