

Hic2 Cas9-CKO Strategy

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Design Date: 2021-2-26

Project Overview

Project Name

Hic2

Project type

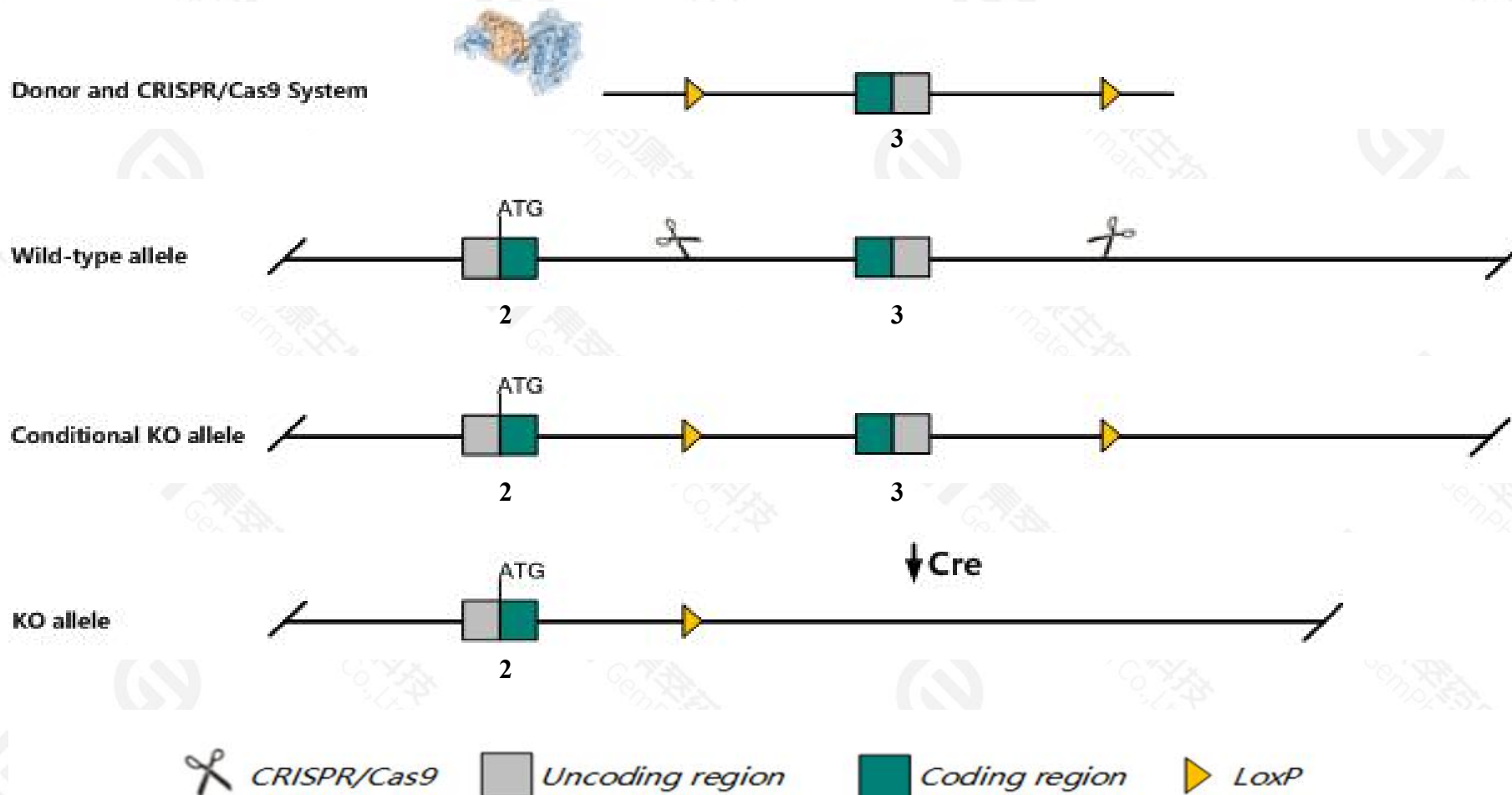
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hic2* gene. The schematic diagram is as follows:



- The *Hic2* gene has 2 transcripts. According to the structure of *Hic2* gene, exon3 of *Hic2-201*(ENSMUST00000090190.13) transcript is recommended as the knockout region. The region contains 1834bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hic2* 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, homozygous inactivation of this gene results in embryonic lethality. A subset of mice heterozygous for a knock-out allele exhibit prenatal lethality and cardiac defects including a ventricular septal defect with overriding aortic valve, and thin myocardial and trabecular layers.
- The KO region contains intron of the *Gm49573* gene. Knockout the region may affect the function of *Gm49573* gene.
- The *Hic2* gene is located on the Chr16. 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)

Hic2 hypermethylated in cancer 2 [Mus musculus (house mouse)]

Gene ID: 58180, updated on 13-Mar-2020

Summary



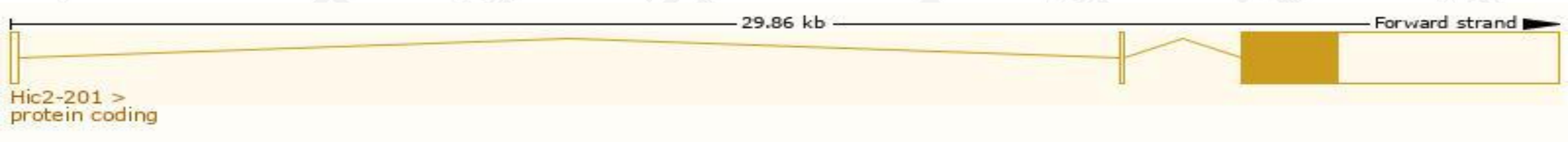
Official Symbol	Hic2 provided by MGI
Official Full Name	hypermethylated in cancer 2 provided by MGI
Primary source	MGI:MGI:1929869
See related	Ensembl:ENSMUSG00000050240
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA409108, HRG22, mKIAA1020
Expression	Broad expression in placenta adult (RPKM 11.4), CNS E11.5 (RPKM 5.1) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

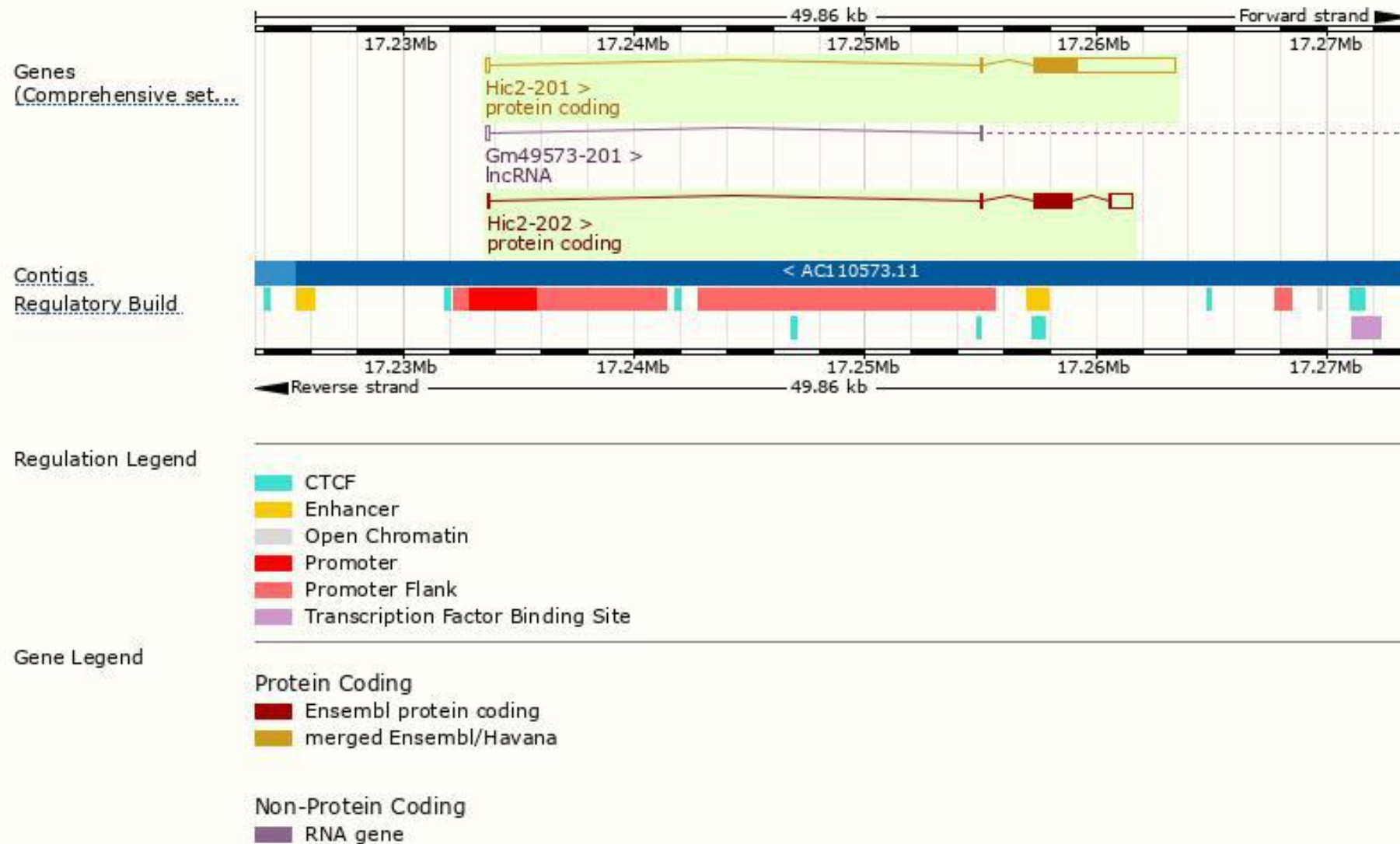
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hic2-201	ENSMUST00000090190.13	6354	619aa	Protein coding	CCDS27999	Q9JLZ6	TSL:1 GENCODE basic APPRIS P1
Hic2-202	ENSMUST00000232082.1	2765	566aa	Protein coding	-	Q9JLZ6	GENCODE basic

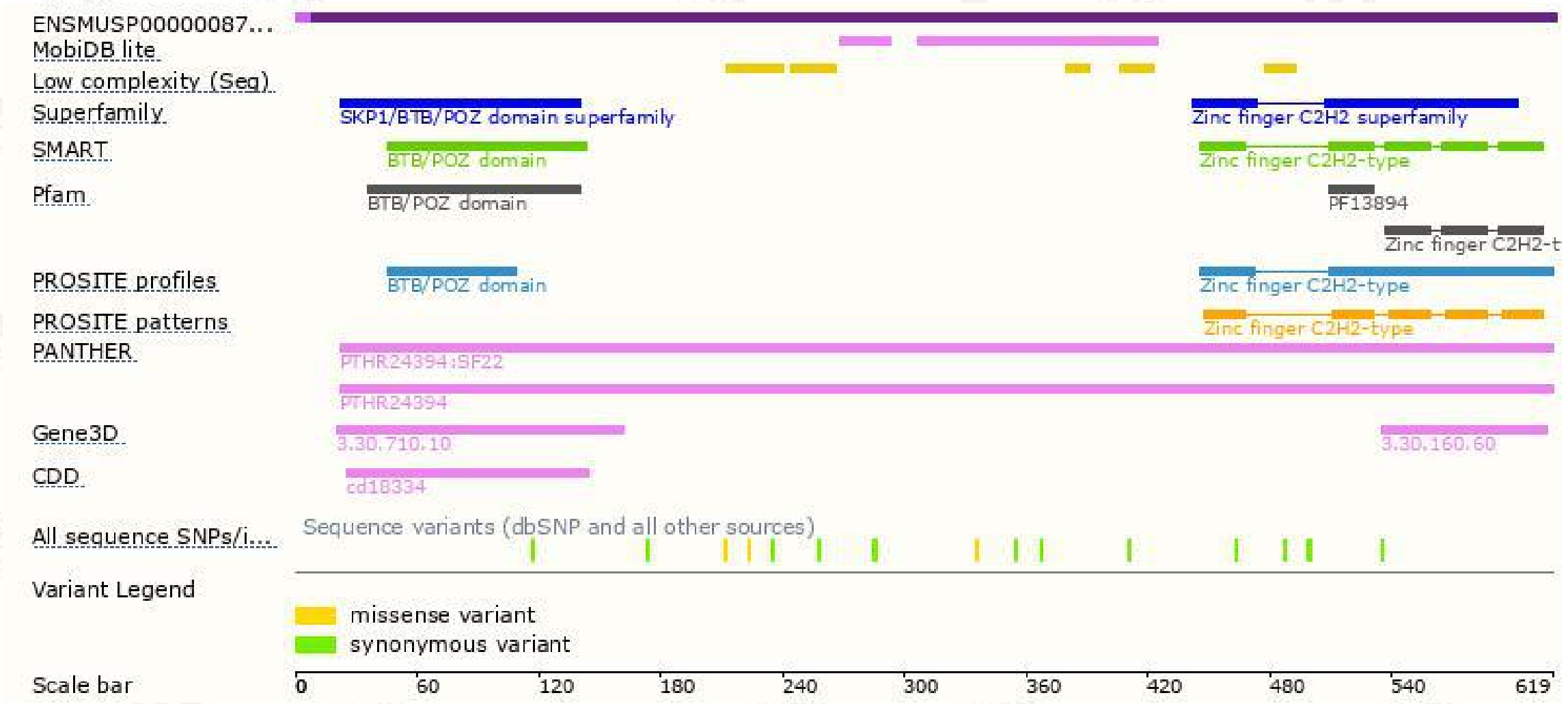
The strategy is based on the design of *Hic2-201* transcript,the transcription is shown below:



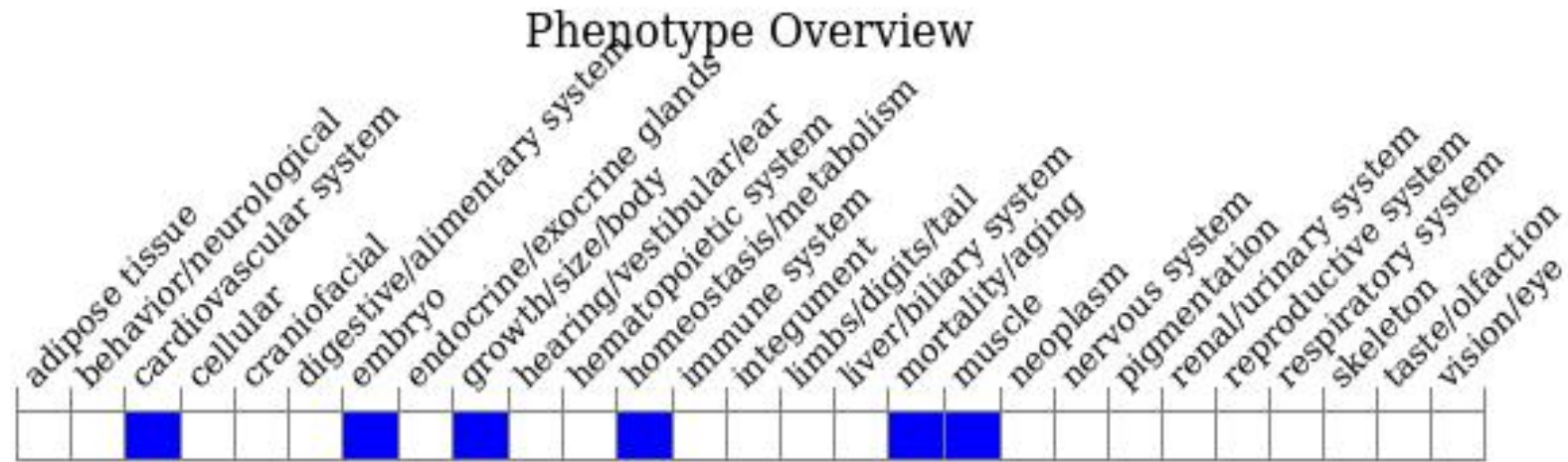
Genomic location distribution



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, homozygous inactivation of this gene results in embryonic lethality. A subset of mice heterozygous for a knock-out allele exhibit prenatal lethality and cardiac defects including a ventricular septal defect with overriding aortic valve, and thin myocardial and trabecular layers.

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