Hinfp Cas9-CKO Strategy

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Project Overview

Project Name	***Hinfp***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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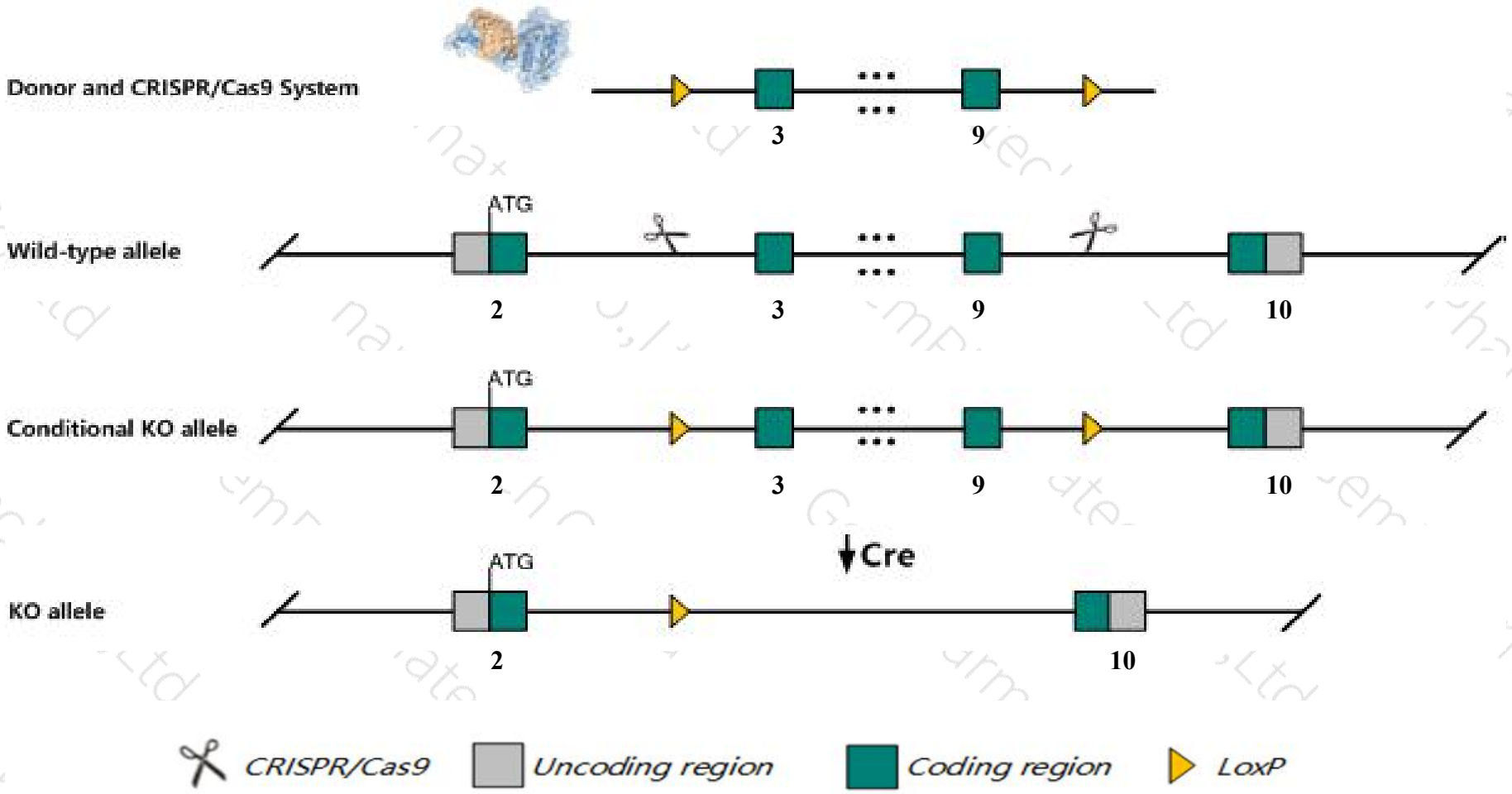
This model will use CRISPR/Cas9 technology to edit the *Hinfp* gene. The schematic diagram is as follows:



Technical routes

➢ The *Hinfp* gene has 8 transcripts. According to the structure of *Hinfp* gene, exon3-exon9 of *Hinfp-205*(ENSMUST00000216508.1) transcript is recommended as the knockout region.The region contains 958bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Hinfp* 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.

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele exhibit early embryonic lethality associated with delayed hatching and failure of the blastocyst to expand.

➢ The *Hinfp* gene is located on the Chr9. 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）

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Hinfp histone H4 transcription factor [Mus musculus (house mouse)]

Gene ID: 102423, updated on 13-Mar-2020

Summary

Official Symbol	Hinfp provided by MGI
Official Full Name	histone H4 transcription factor provided byMGI
Primary source	MGI:MGI:2429620
See related	Ensembl:ENSMUSG00000032119
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	AA589481, HiNF-P, Mizf
Expression	Ubiquitous expression in CNS E11.5 (RPKM 5.6), CNS E14 (RPKM 5.0) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

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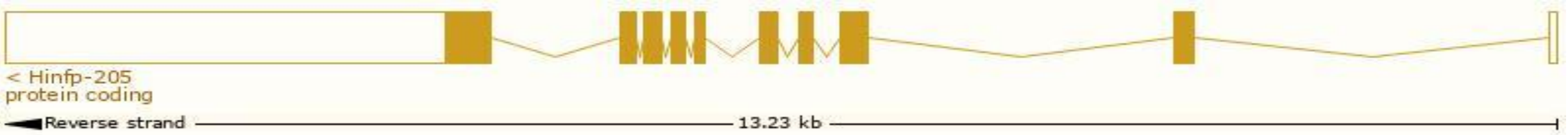
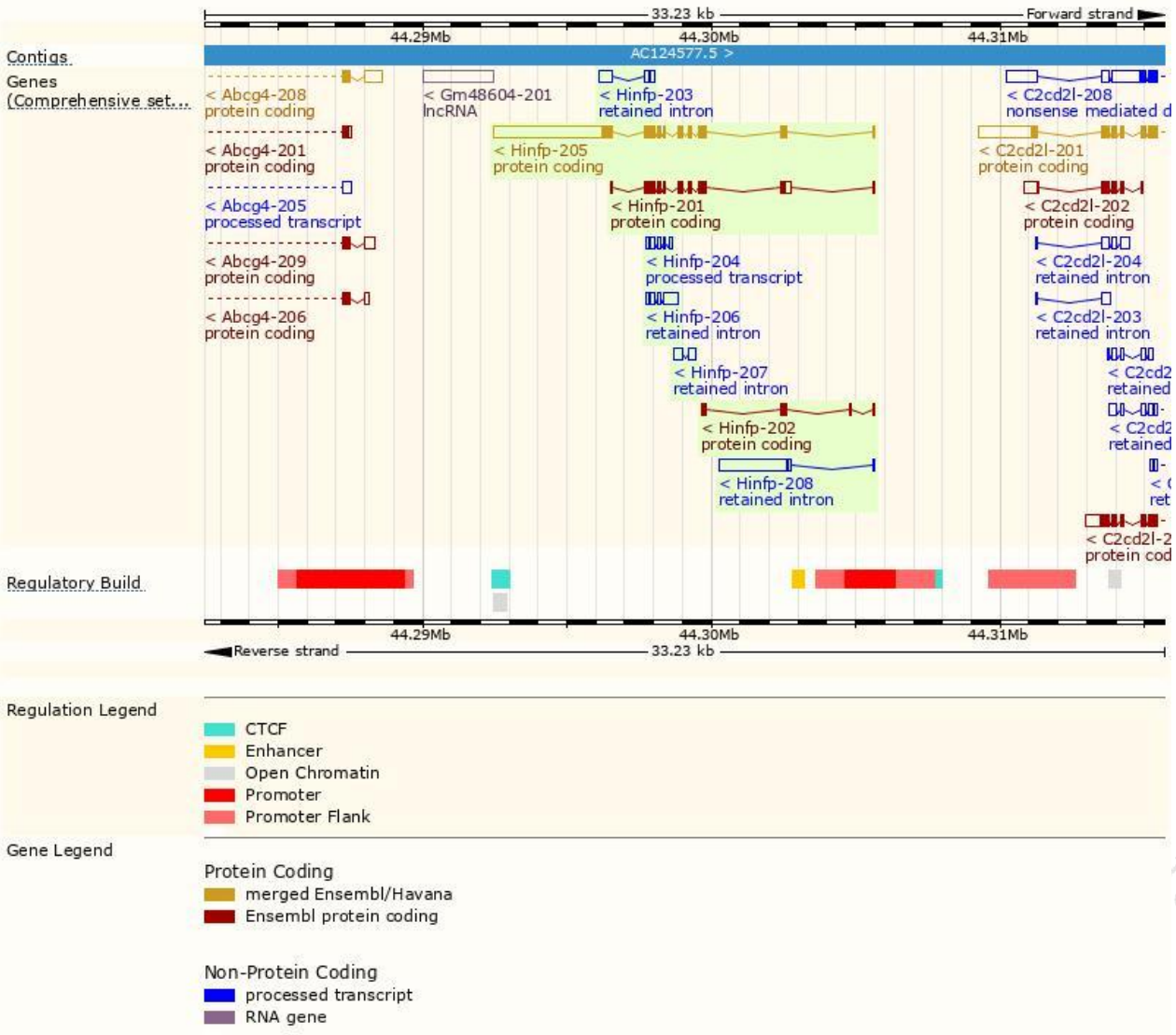
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hinfp-205	ENSMUST00000216508.1	5333	503aa	Protein coding	CCDS23102	Q8K1K9	TSL:1 GENCODE basic APPRIS P1
Hinfp-201	ENSMUST00000034629.5	1439	404aa	Protein coding	-	A0A1N9M8B2	CDS 3' incomplete TSL:1
Hinfp-202	ENSMUST00000214660.1	392	95aa	Protein coding	-	A0A1L1STC1	CDS 3' incomplete TSL:5
Hinfp-204	ENSMUST00000215665.1	508	No protein	Processed transcript	-	-	TSL:3
Hinfp-208	ENSMUST00000217605.1	2468	No protein	Retained intron	-	-	TSL:5
Hinfp-206	ENSMUST00000217137.1	887	No protein	Retained intron	-	-	TSL:2
Hinfp-203	ENSMUST00000215637.1	741	No protein	Retained intron	-	-	TSL:2
Hinfp-207	ENSMUST00000217205.1	551	No protein	Retained intron	-	-	TSL:2

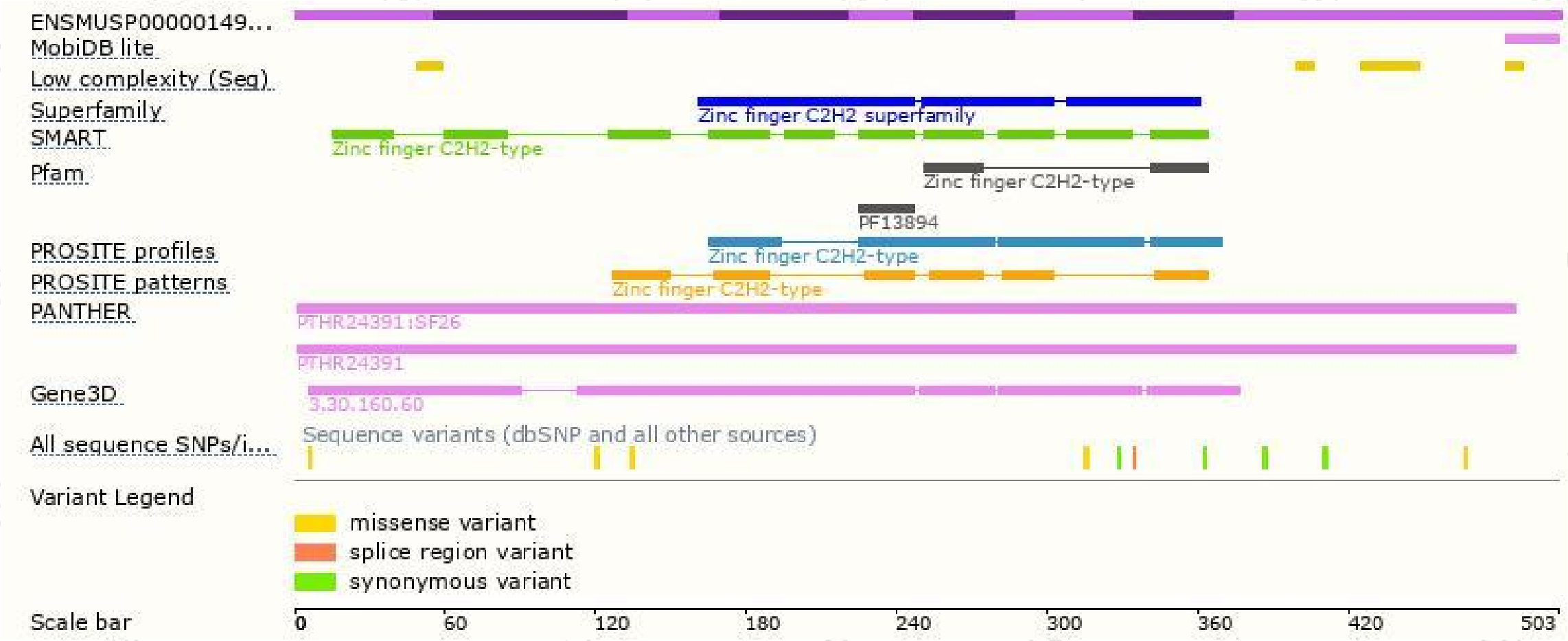
The strategy is based on the design of *Hinfp-205* transcript,the transcription is shown below:



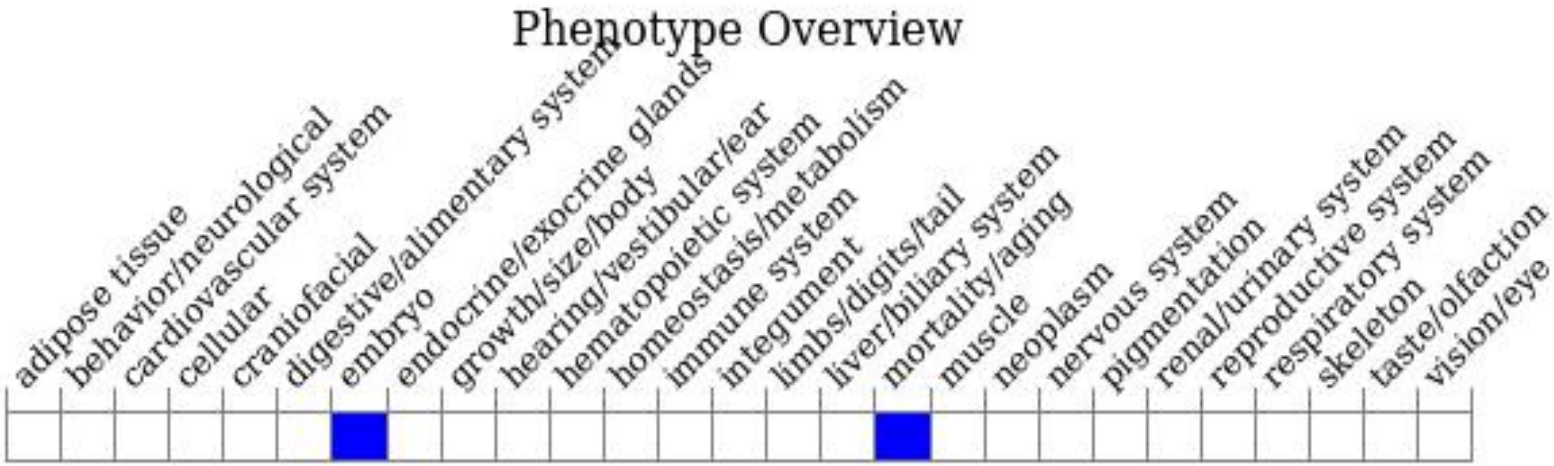
Genomic location distribution



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 early embryonic lethality associated with delayed hatching and failure of the blastocyst to expand.

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