Cebpb Cas9-KO Strategy

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Reviewer: Huimin Su

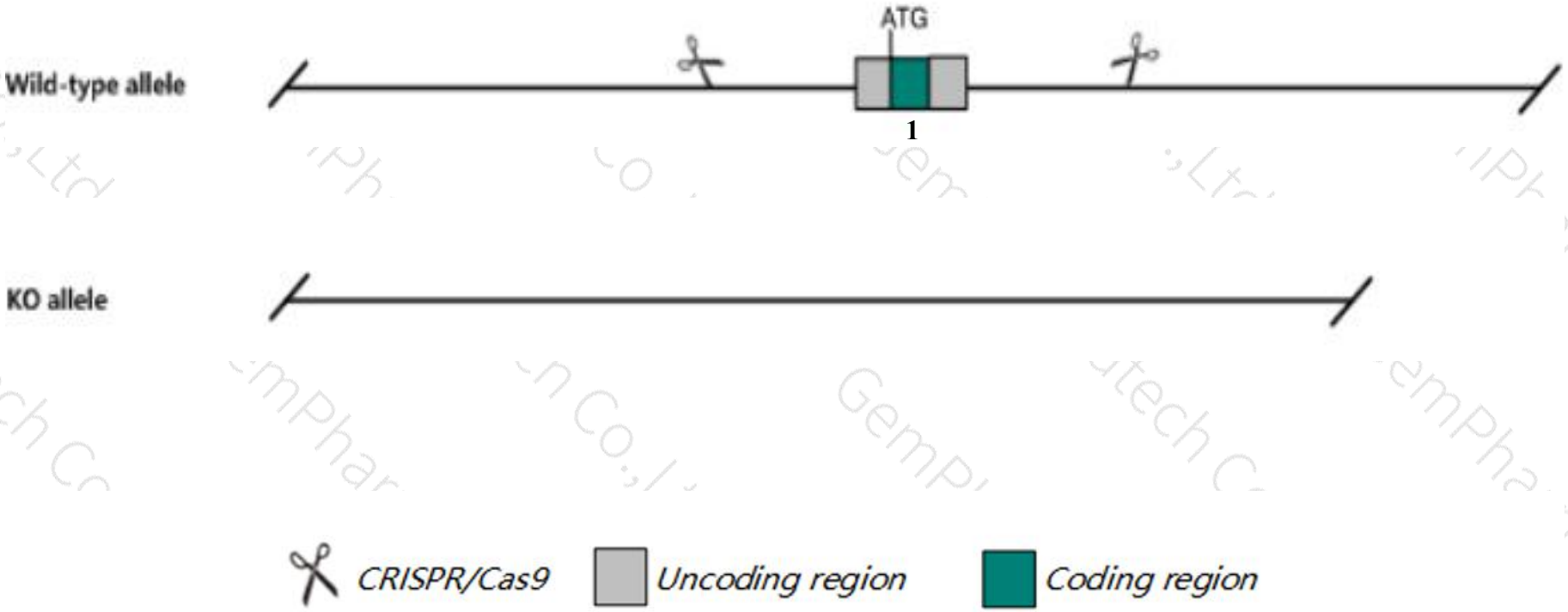
Design Date: 2020-5-9

Project Overview

Project Name	***Cebpb***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Cebpb* gene has 1 transcript. According to the structure of *Cebpb* gene, exon1 of *Cebpb-201* (ENSMUST00000070642.3) 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 *Cebpb* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,homozygotes for targeted null mutations exhibit high neonatal hypoglycemia and mortality, reduced epididymal fat pad weight, susceptibility to listeria monocytogenes, female sterility, impaired mammary development, and resistance to skin carcinogenesis.

➢ The KO region contains functional region of the *Tmem189 and A530013C23Rik* gene.Knockout the region may affect the function of *Tmem189 and A530013C23Rik* gene.

➢ The *Cebpb* gene is located on the Chr2. 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）

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Cebpb CCAAT/enhancer binding protein (C/EBP), beta [Mus musculus (house mouse)]

Gene ID: 12608, updated on 22-Mar-2020

Summary

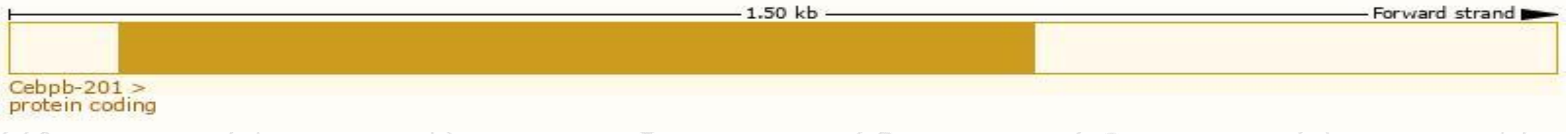
Official Symbol	Cebpb provided by MGI
Official Full Name	CCAAT/enhancer binding protein (C/EBP), beta provided byMGI
Primary source	MGI:MGI:88373
See related	Ensembl:ENSMUSG00000056501
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C/EBPbeta, CRP2, IL-6DBP, LAP, LIP, NF-IL6, NF-M, Nfil6
Orthologs	human all

Transcript information（Ensembl）

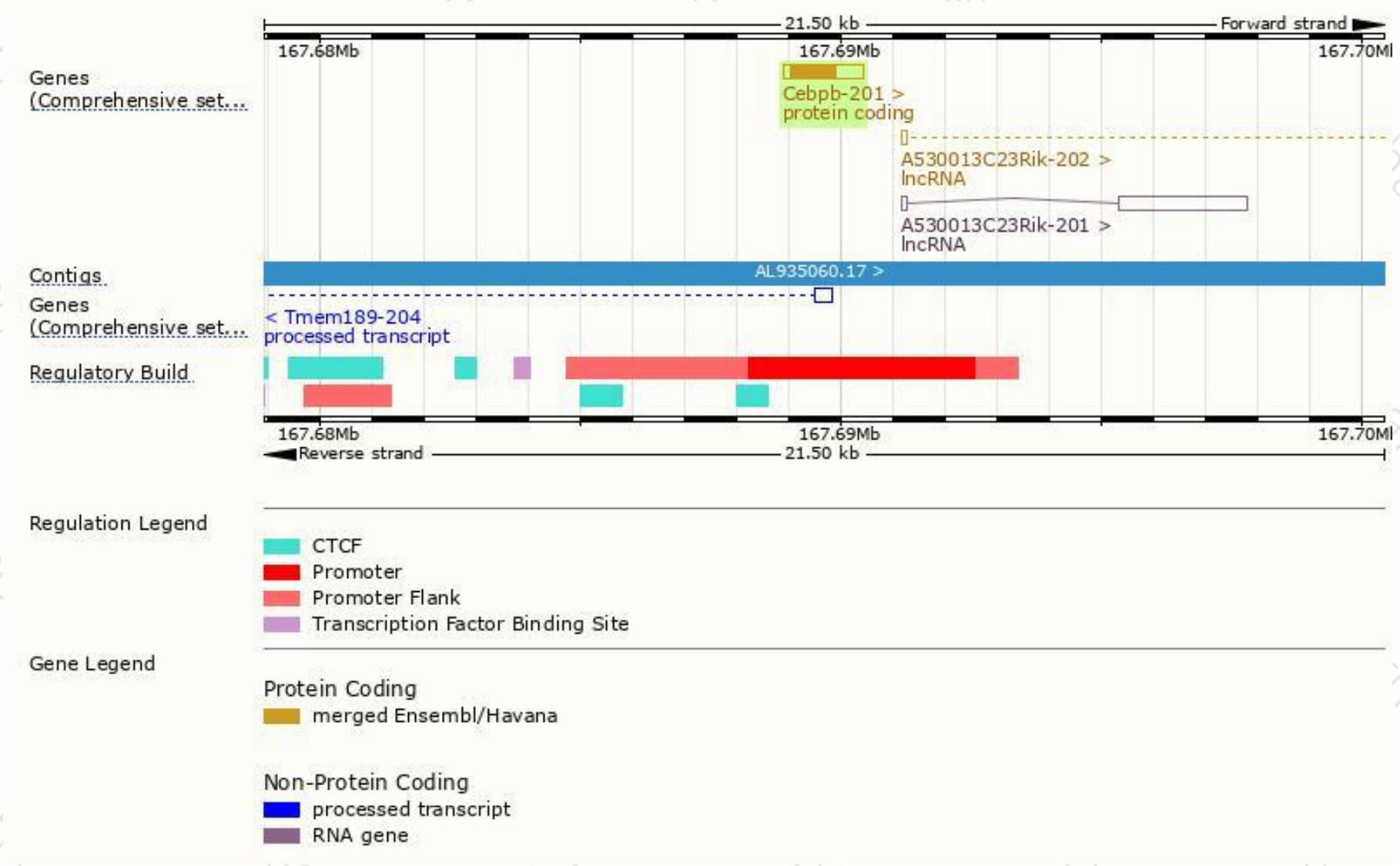
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cebpb-201	ENSMUST00000070642.3	1504	296aa	Protein coding	CCDS17105	P28033 Q3UPN9	TSL:NA 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

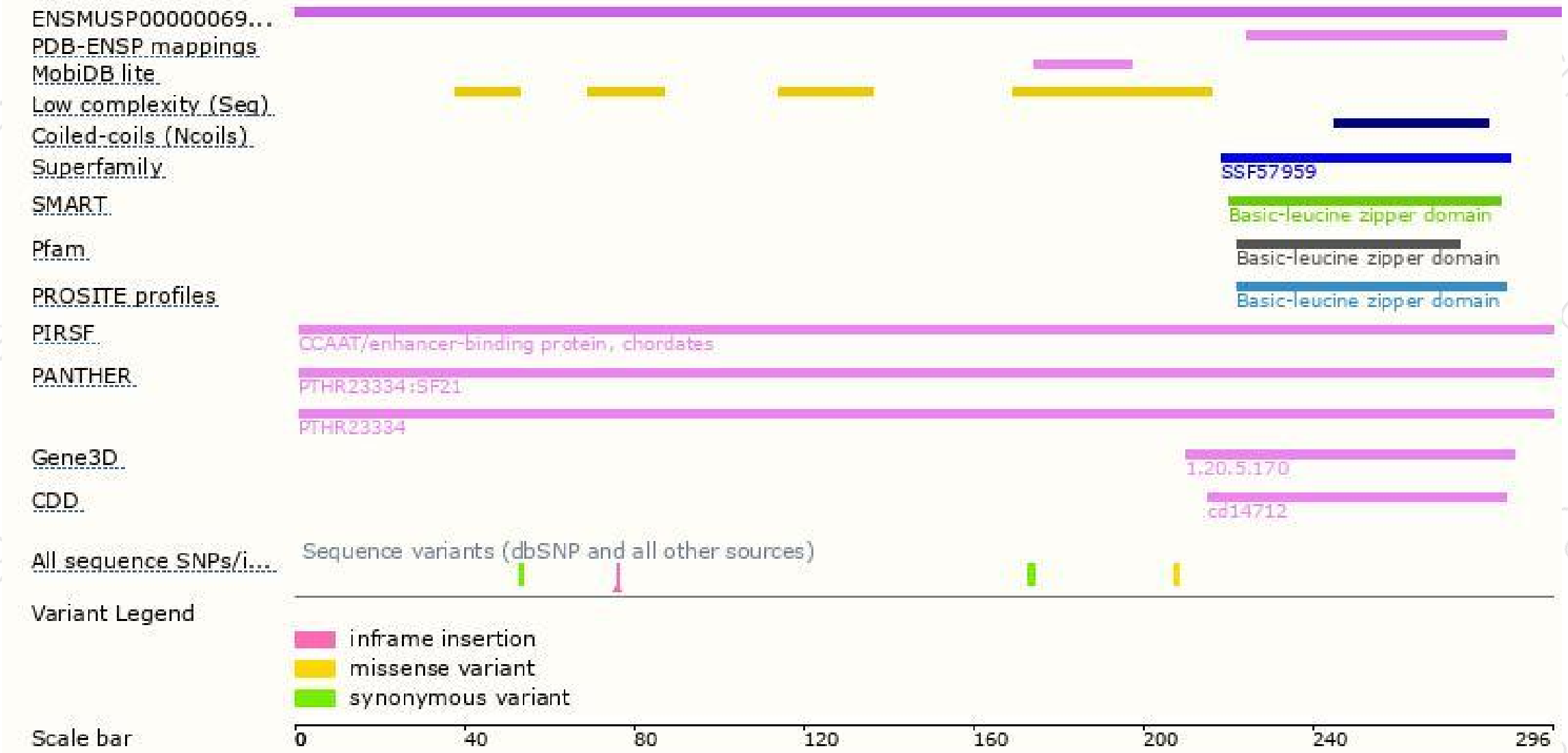
The strategy is based on the design of *Cebpb-201* transcript,The transcription is shown below



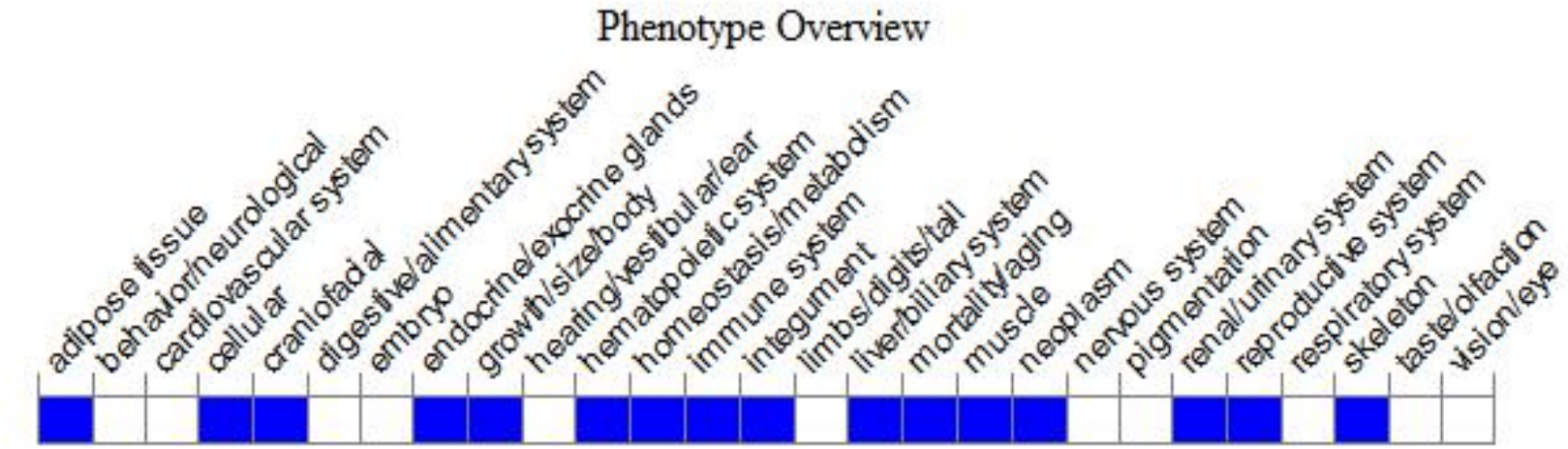
Genomic location distribution



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.

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