

Hoxb8 Cas9-KO Strategy

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Design Date: 2022-4-22

Project Overview

Project Name

Hoxb8

Project type

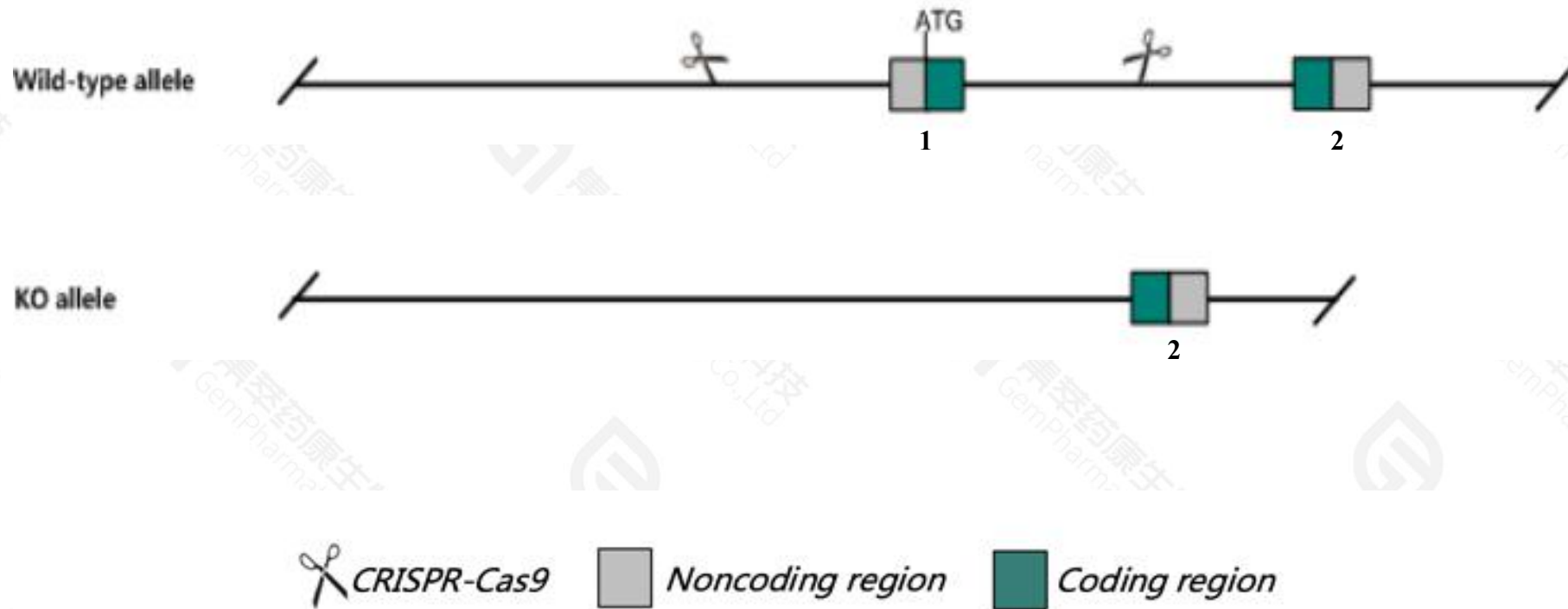
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Hoxb8* gene. The schematic diagram is as follows:



- The *Hoxb8* gene has 3 transcripts. According to the structure of *Hoxb8* gene, exon1 of *Hoxb8*-201(ENSMUST00000052650.4) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Hoxb8* 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, most homozygotes for targeted null mutations exhibit delayed preweaning growth, degeneration of the second spinal ganglion, axial skeletal defects, impaired clasping, an altered gait, and excessive grooming.
- This strategy may affect the 5-terminal regulation of *Hoxb7* gene.
- The *Hoxb8* gene is located on the Chr11. 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)

Hoxb8 homeobox B8 [*Mus musculus* (house mouse)]

Gene ID: 15416, updated on 1-Apr-2022

[Download Datasets](#)

Summary

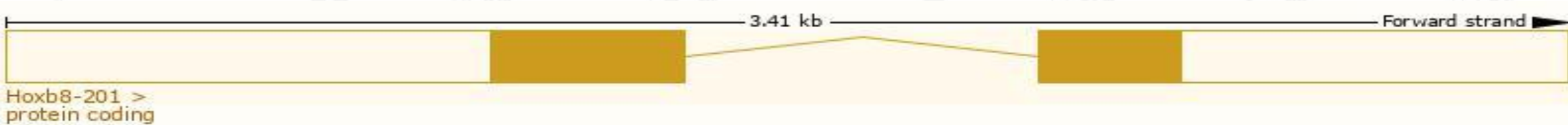
Official Symbol	Hoxb8 provided by MGI
Official Full Name	homeobox B8 provided by MGI
Primary source	MGI:MGI:96189
See related	Ensembl:ENSMUSG00000056648 AllianceGenome:MGI:96189
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Hox-2.4
Summary	Enables DNA-binding transcription repressor activity, RNA polymerase II-specific and sequence-specific DNA binding activity. Involved in negative regulation of myeloid cell differentiation and negative regulation of transcription by RNA polymerase II. Acts upstream of or within several processes, including dorsal spinal cord development; embryonic skeletal system morphogenesis; and grooming behavior. Predicted to be located in nucleoplasm. Predicted to be active in nucleus. Is expressed in several structures, including embryo mesenchyme; extraembryonic component; genitourinary system; nervous system; and neural ectoderm. Used to study trichotillomania. Orthologous to human HOXB8 (homeobox B8). [provided by Alliance of Genome Resources, Nov 2021]
Expression	Biased expression in adrenal adult (RPKM 49.5), genital fat pad adult (RPKM 24.0) and 6 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

Transcript information (Ensembl)

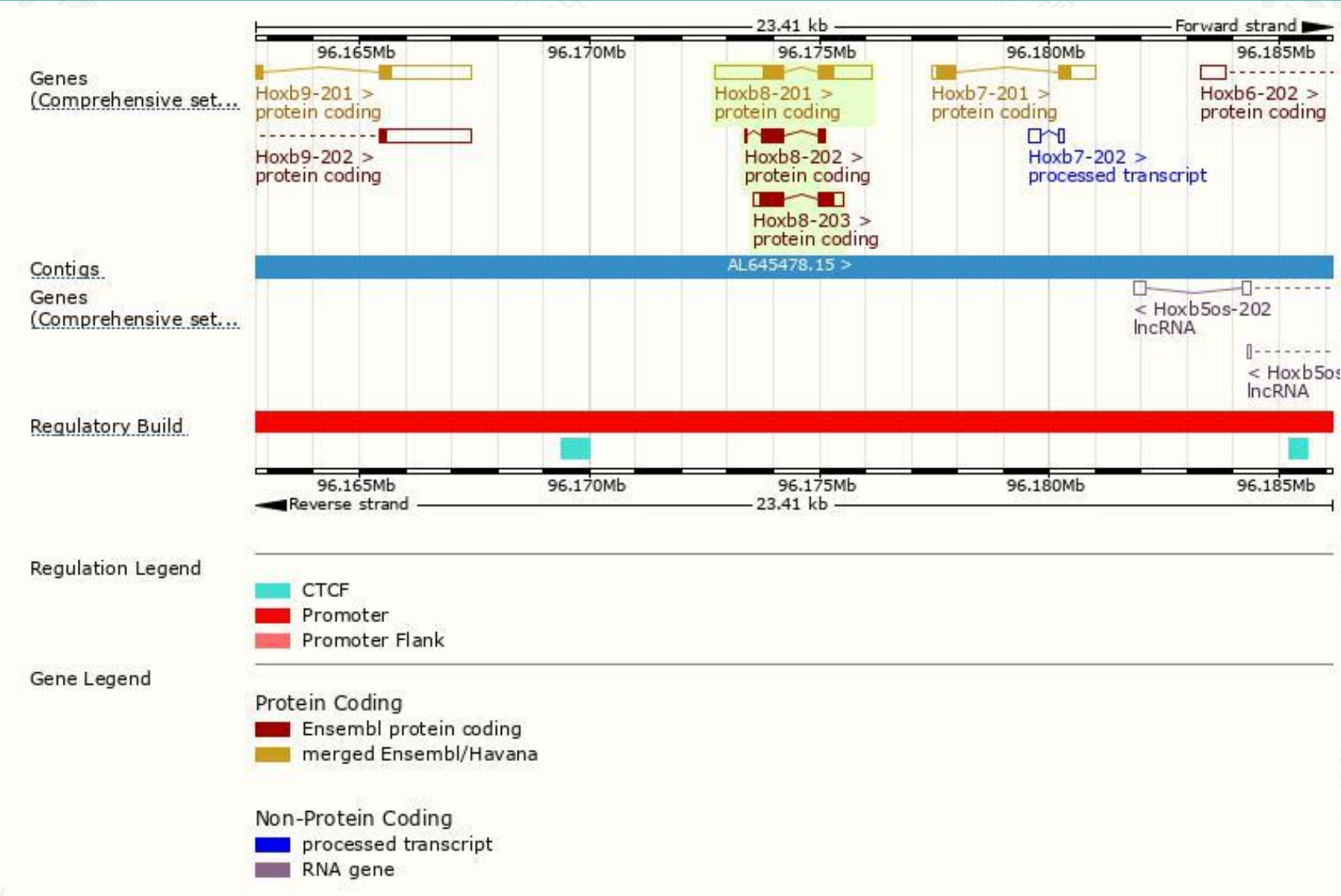
The gene has 3 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000052650.4	Hoxb8-201	2635	243aa	Protein coding	CCDS25293	A2A9Z8 P09632	Ensembl Canonical Gencode basic APPRIS P1 TSL:1
ENSMUST00000125410.2	Hoxb8-202	664	191aa	Protein coding	-	F6W0B3	TSL:5 CDS 3' incomplete
ENSMUST00000168043.2	Hoxb8-203	1141	243aa	Protein coding	CCDS25293	A2A9Z8 P09632	Gencode basic APPRIS P1 TSL:5

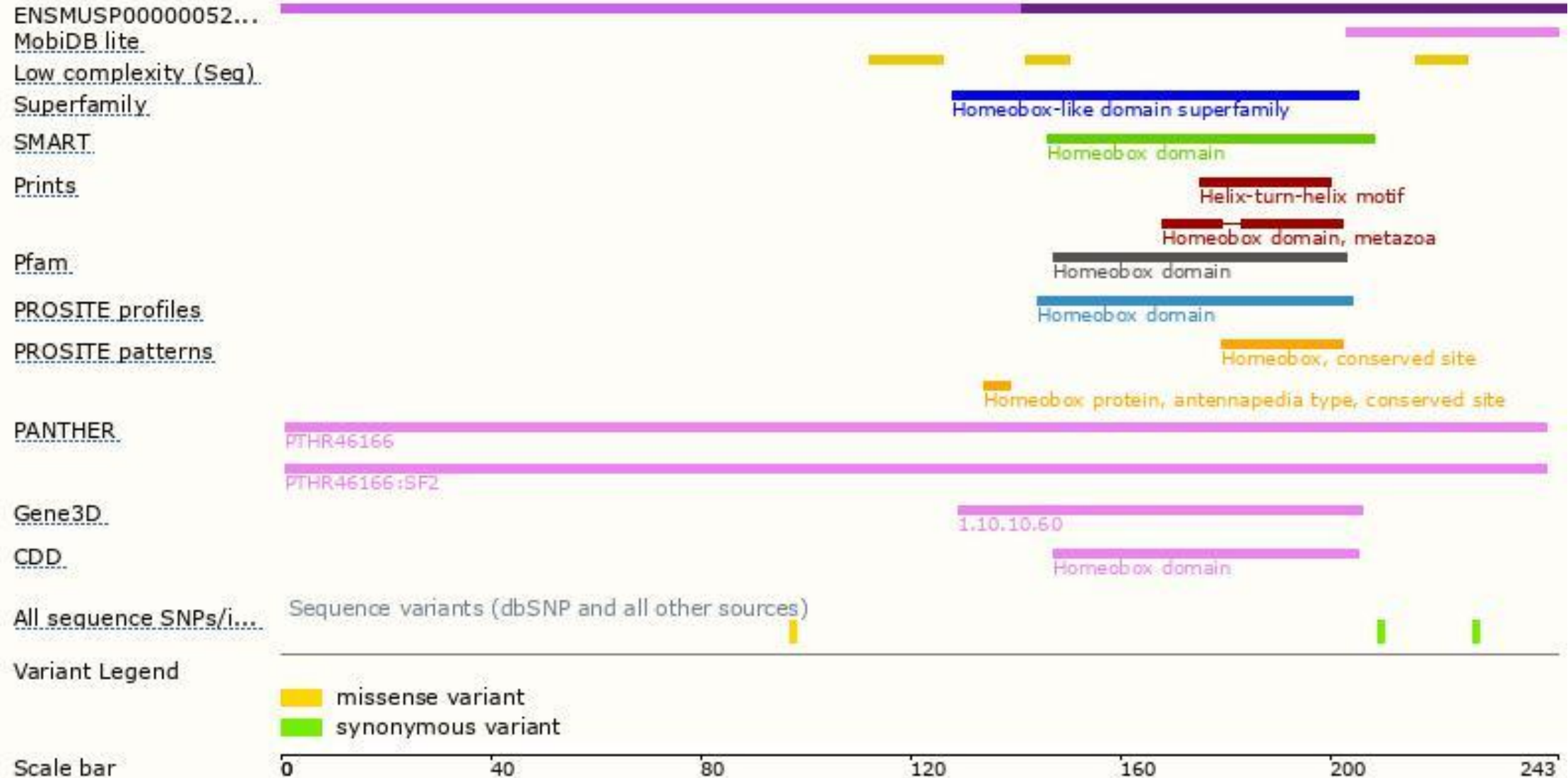
The strategy is based on the design of *Hoxb8-201* transcript,the transcription is shown below:



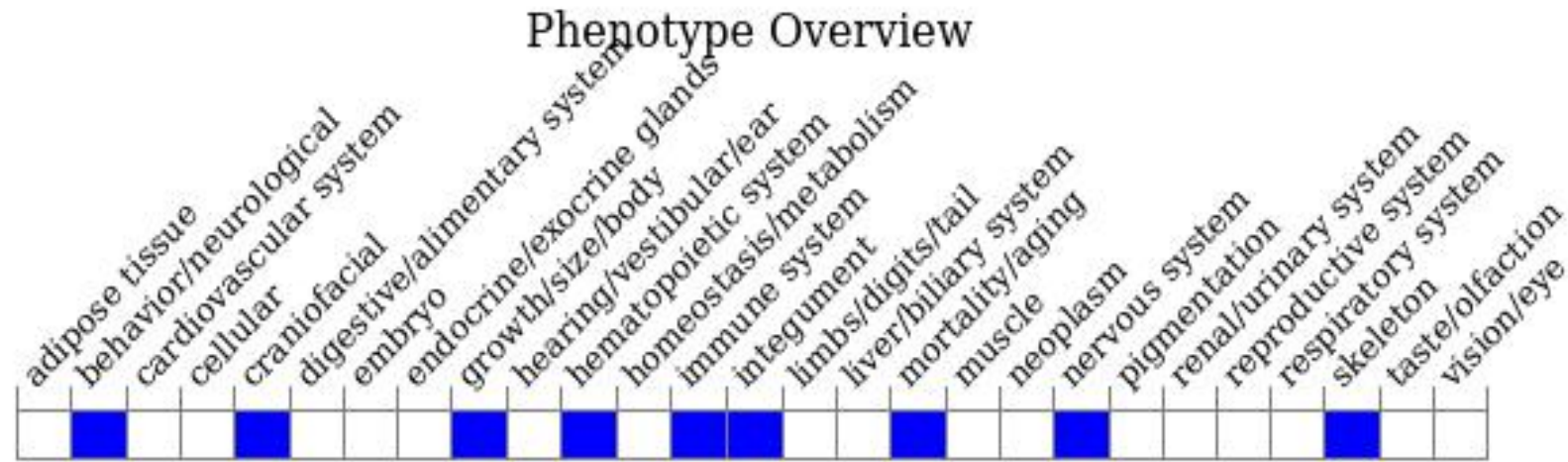
Genomic location distribution



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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