

Bcor Cas9-KO Strategy

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Project Overview

Project Name

Bcor

Project type

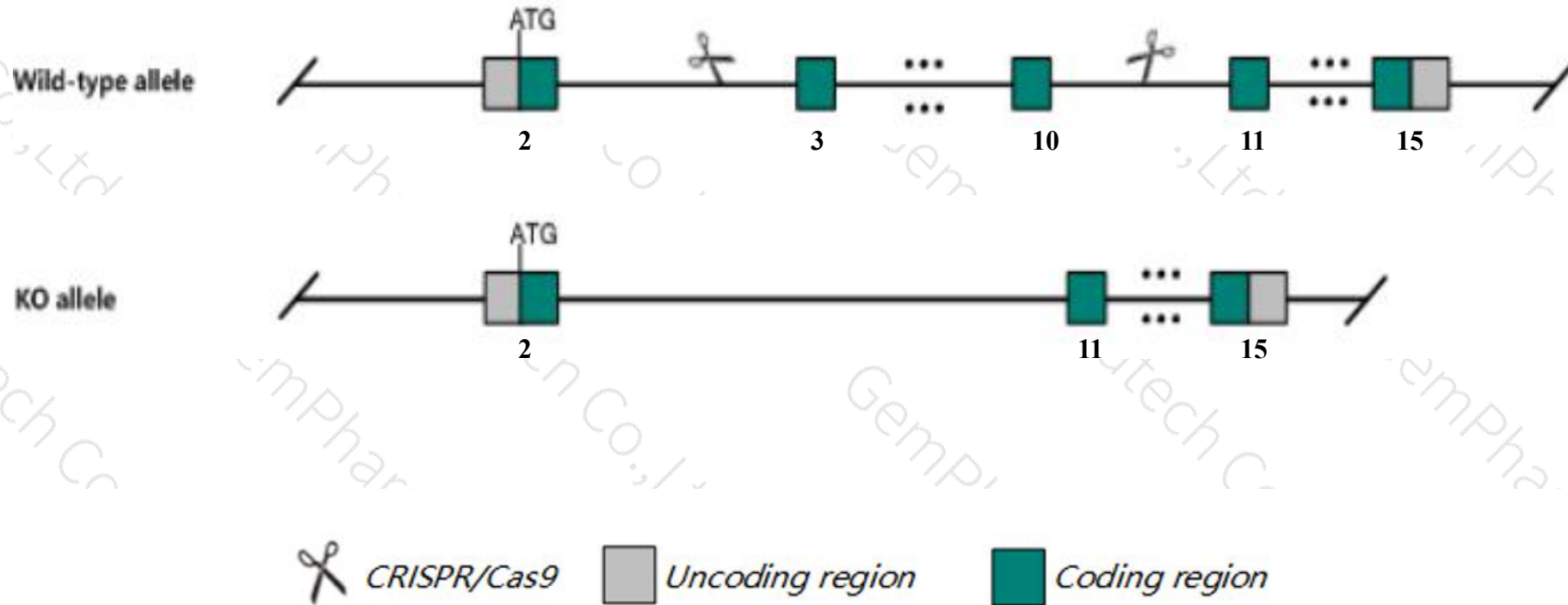
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Bcor* gene has 8 transcripts. According to the structure of *Bcor* gene, exon3-exon10 of *Bcor-204* (ENSMUST00000115513.8) transcript is recommended as the knockout region. The region contains 4354bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bcor* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Male chimeras hemizygous for either of two different gene trapped alleles die by E9.5 exhibiting anomalies in somite formation and heart looping, forebrain fusion, and microcephaly. Hemizygosity for other gene trapped alleles can cause patterning and embryo turning defects or abnormal gastrulation.
- The *Bcor* gene is located on the ChrX. 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)

Bcor BCL6 interacting corepressor [Mus musculus (house mouse)]

Gene ID: 71458, updated on 13-Mar-2020

Summary



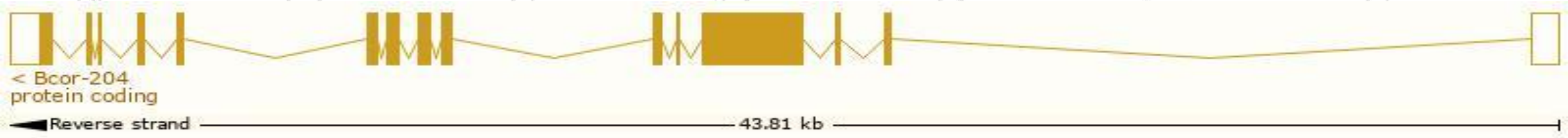
Official Symbol	Bcor provided by MGI
Official Full Name	BCL6 interacting corepressor provided by MGI
Primary source	MGI:MGI:1918708
See related	Ensembl:ENSMUSG00000040363
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2900008C10Rik, 5830466J11Rik, 8430401K06Rik, BcorR, D930024N20Rik, mKIAA1575
Expression	Ubiquitous expression in thymus adult (RPKM 7.4), CNS E11.5 (RPKM 5.8) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

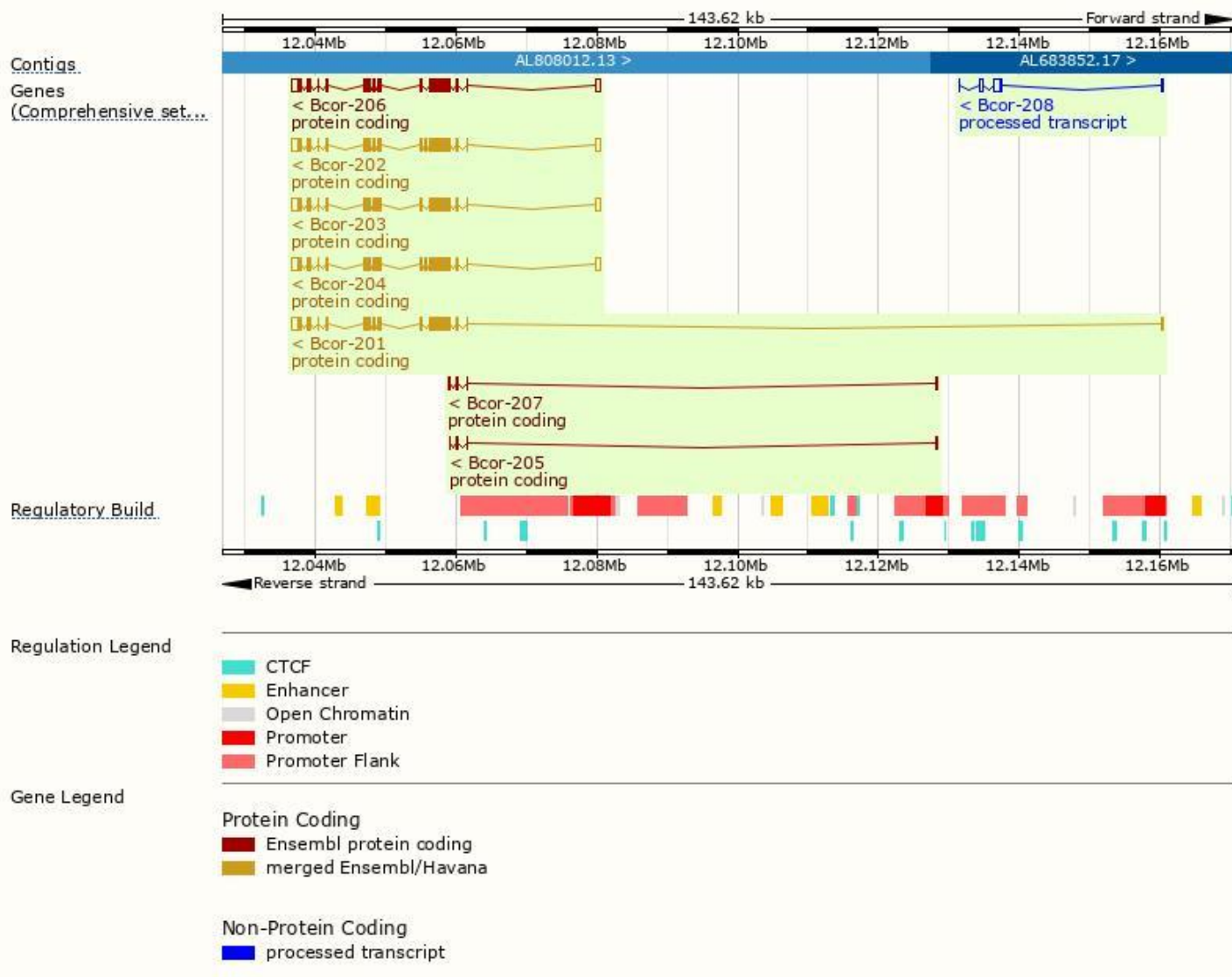
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bcor-204	ENSMUST00000115513.8	6941	1759aa	Protein coding	CCDS40873	Q8CGN4	TSL:1 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 ALT2
Bcor-203	ENSMUST00000115512.8	6887	1741aa	Protein coding	CCDS40872	Q8CGN4	TSL:1 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 ALT2
Bcor-202	ENSMUST00000065143.13	6839	1725aa	Protein coding	CCDS30021	Q8CGN4	TSL:1 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 P4
Bcor-206	ENSMUST00000124033.7	6785	1707aa	Protein coding	CCDS30022	Q8CGN4	TSL:1 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 ALT2
Bcor-201	ENSMUST00000043441.12	6113	1707aa	Protein coding	CCDS30022	Q8CGN4	TSL:5 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 ALT2
Bcor-207	ENSMUST00000145872.7	573	125aa	Protein coding	-	F7BEN2	CDS 3' incomplete TSL:2
Bcor-205	ENSMUST00000123004.1	456	95aa	Protein coding	-	F6XPR4	CDS 3' incomplete TSL:3
Bcor-208	ENSMUST00000209776.1	1534	No protein	Processed transcript	-	-	TSL:5

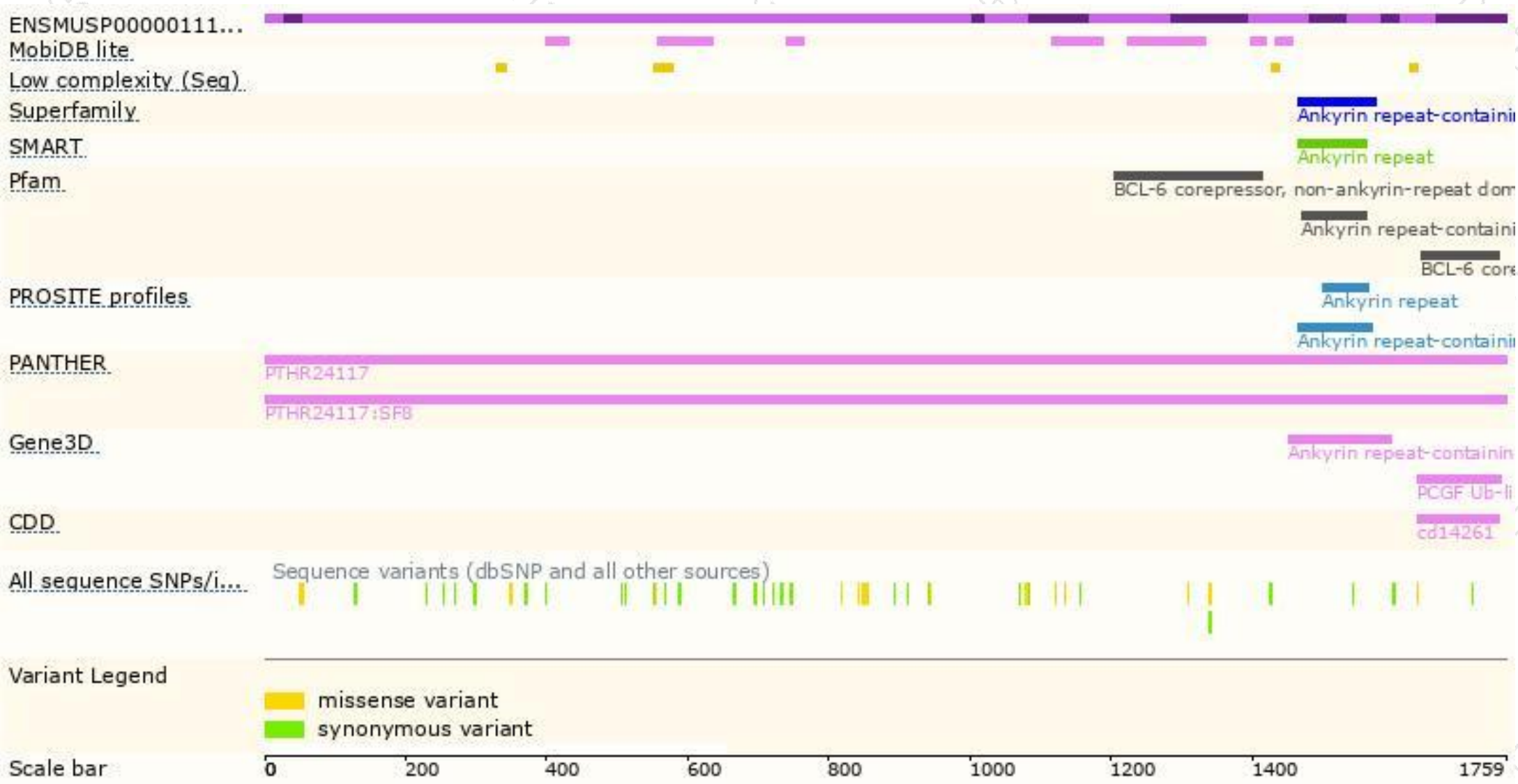
The strategy is based on the design of *Bcor-204* transcript,The transcription is shown below



Genomic location distribution

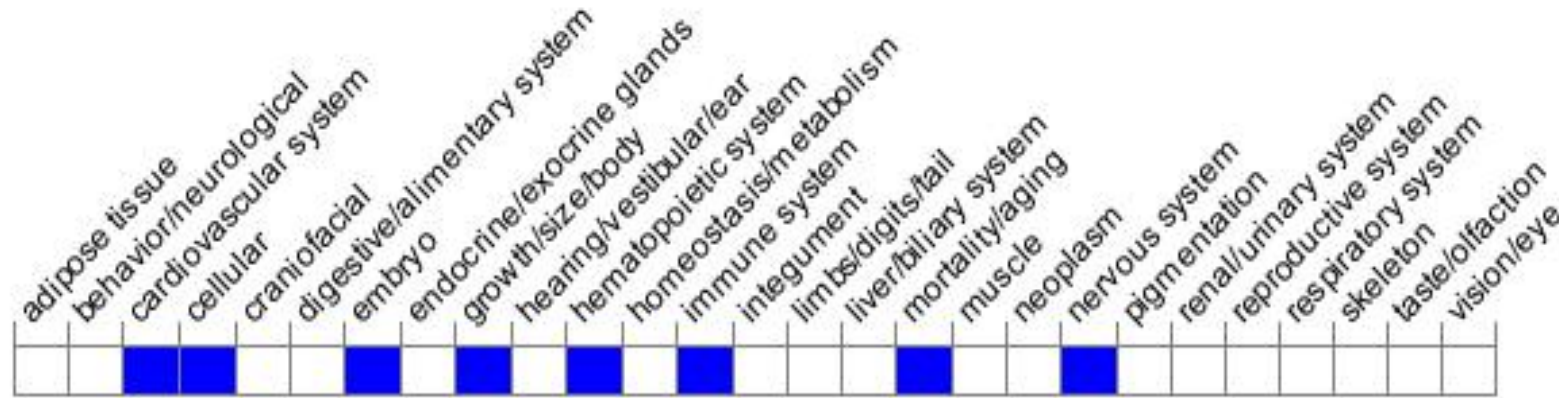


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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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