

Ubqln1 Cas9-CKO Strategy

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Project Overview

Project Name

Ubqln1

Project type

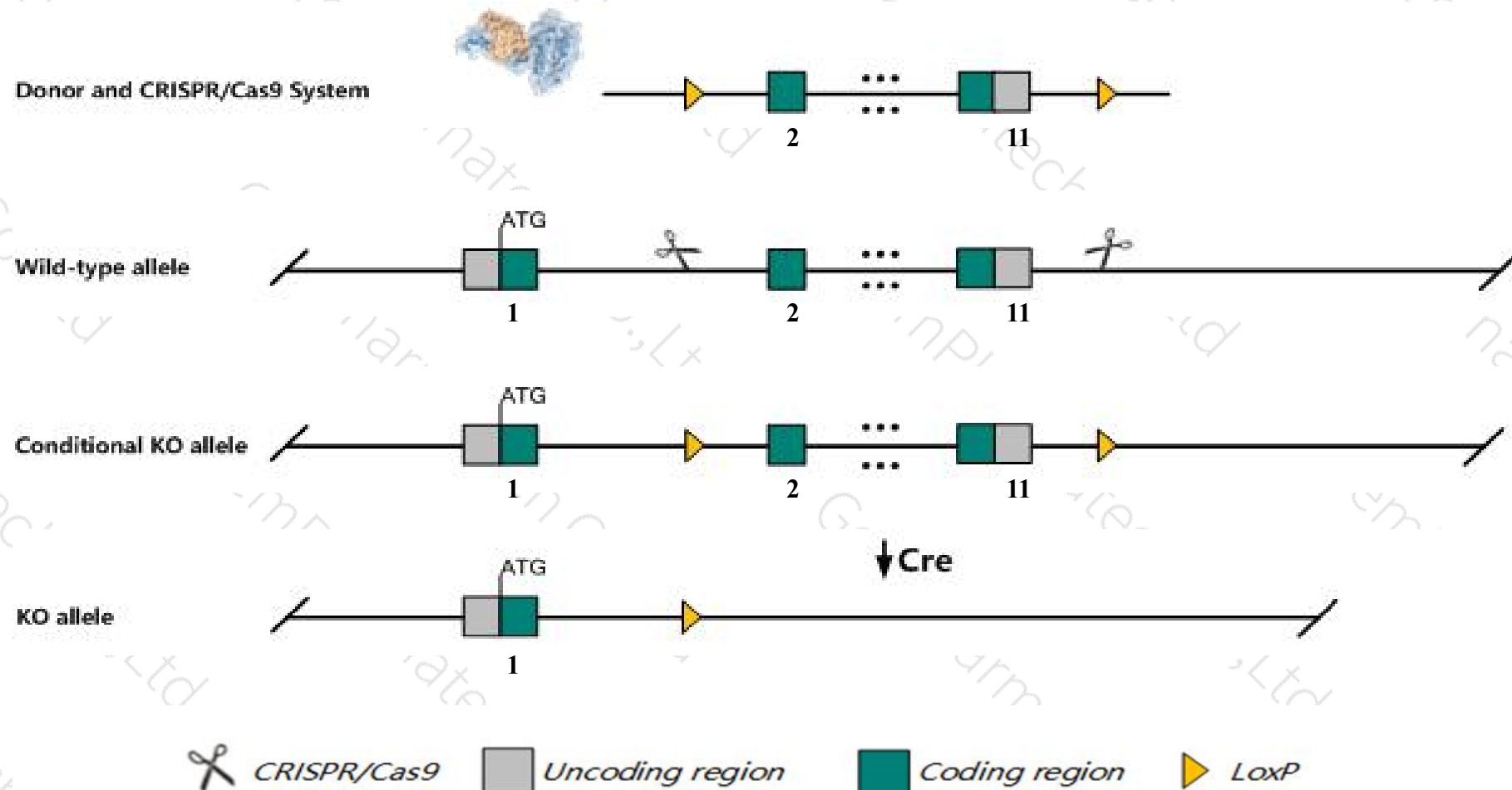
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ubqln1* gene. The schematic diagram is as follows:



- The *Ubqln1* gene has 4 transcripts. According to the structure of *Ubqln1* gene, exon2-exon11 of *Ubqln1-201* (ENSMUST00000058735.11) transcript is recommended as the knockout region. The region contains most 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 *Ubqln1* 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 null animals display impaired degradation of ubiquitinated proteins in the brain, increased ischemia/reperfusion-caused brain injury, and slower functional recovery after injury.
- The KO region contains *Gm48357-201* gene. Knockout the region may affect the function of *Gm48357-201* gene.
- The *Ubqln1* gene is located on the Chr13. 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.

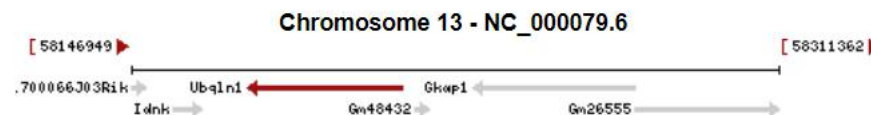
Gene information (NCBI)

Ubqln1 ubiquilin 1 [*Mus musculus* (house mouse)]

Gene ID: 56085, updated on 3-Sep-2019

Summary

Official Symbol Ubqln1 provided by MGI
Official Full Name ubiquilin 1 provided by MGI
Primary source MGI:MGI:1860276
See related Ensembl:ENSMUSG00000005312
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 Da41; Dsk2; Plc1; Xdrp1; C77538; Plc-1; AU019746; D13Ert372e; 1110046H03Rik; 1810030E05Rik
Expression Ubiquitous expression in ovary adult (RPKM 72.0), adrenal adult (RPKM 65.9) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)

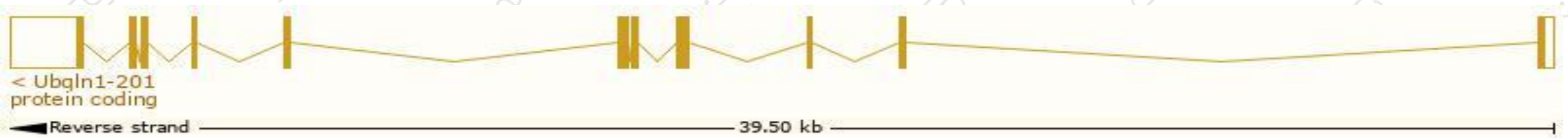


Transcript information (Ensembl)

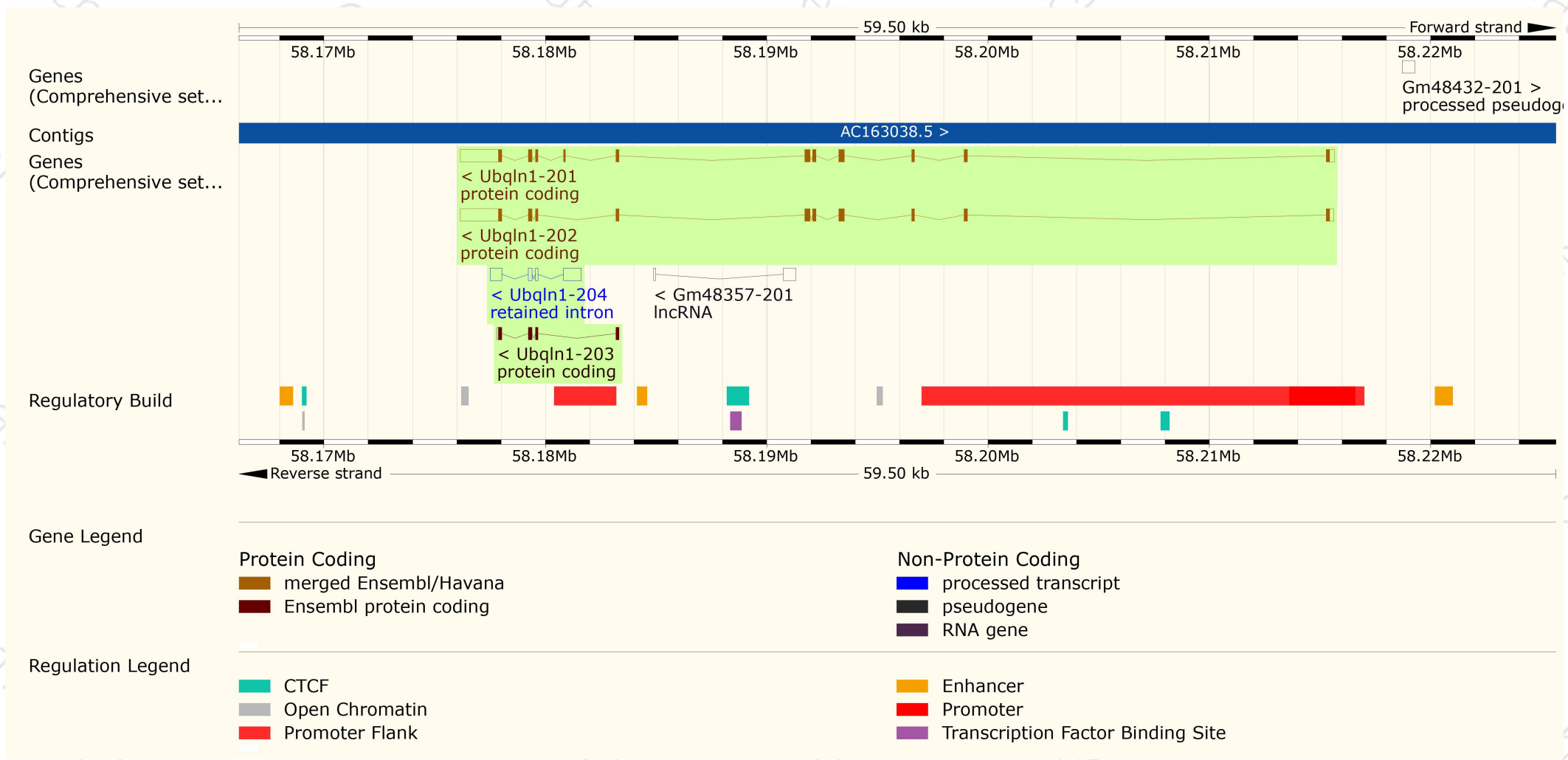
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Ubqln1-201	ENSMUST00000058735.11	3686	582aa	ENSMUSP00000050191.5	Protein coding	CCDS49281	Q8R317	TSL:1 GENCODE basic APPRIS ALT2
Ubqln1-202	ENSMUST00000076454.7	3561	554aa	ENSMUSP00000075782.6	Protein coding	CCDS26569	Q8R317	TSL:1 GENCODE basic APPRIS P3
Ubqln1-203	ENSMUST00000225645.1	631	190aa	ENSMUSP00000153666.1	Protein coding	-	A0A286YE09	CDS 5' incomplete
Ubqln1-204	ENSMUST00000225818.1	1596	No protein	-	Retained intron	-	-	-

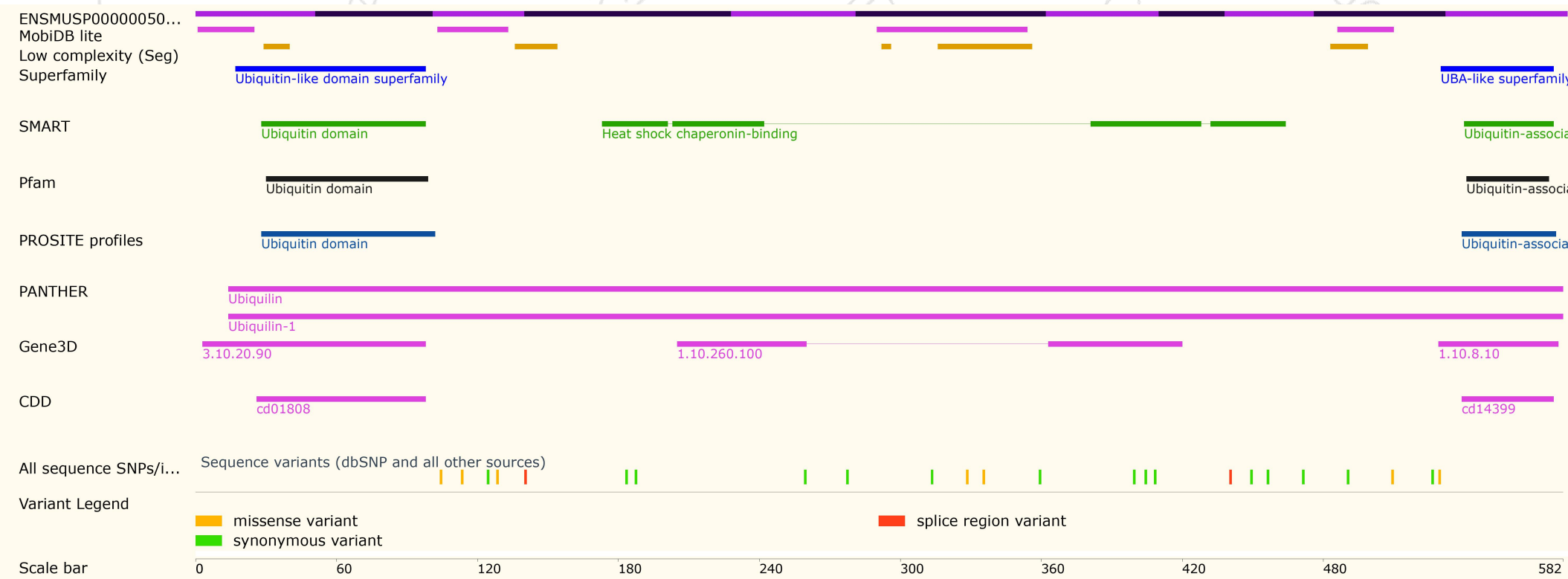
The strategy is based on the design of *Ubqln1-201* transcript,The transcription is shown below



Genomic location distribution

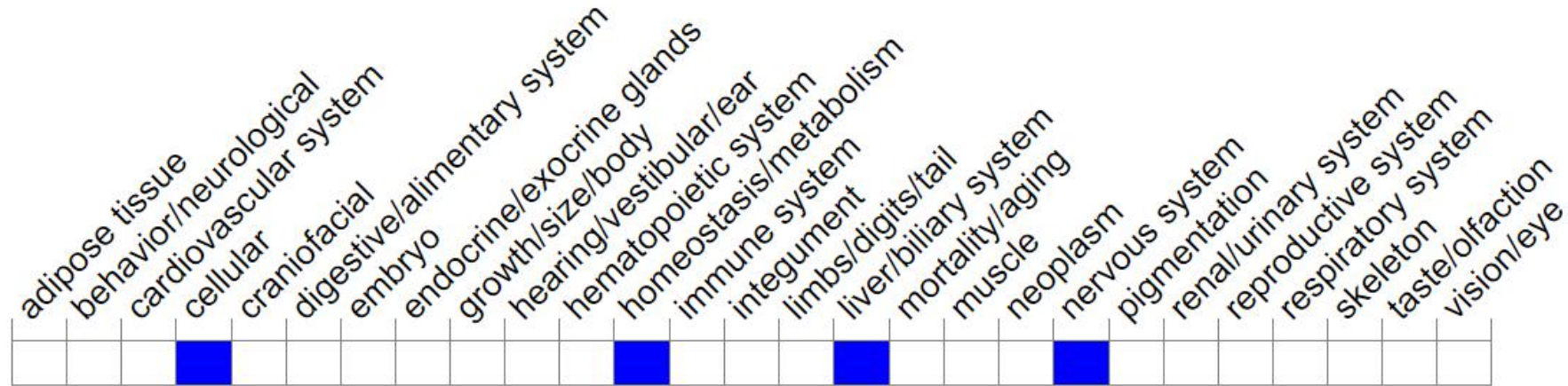


Protein domain



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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