

Ascc2 Cas9-CKO Strategy

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Project Overview

Project Name

Ascc2

Project type

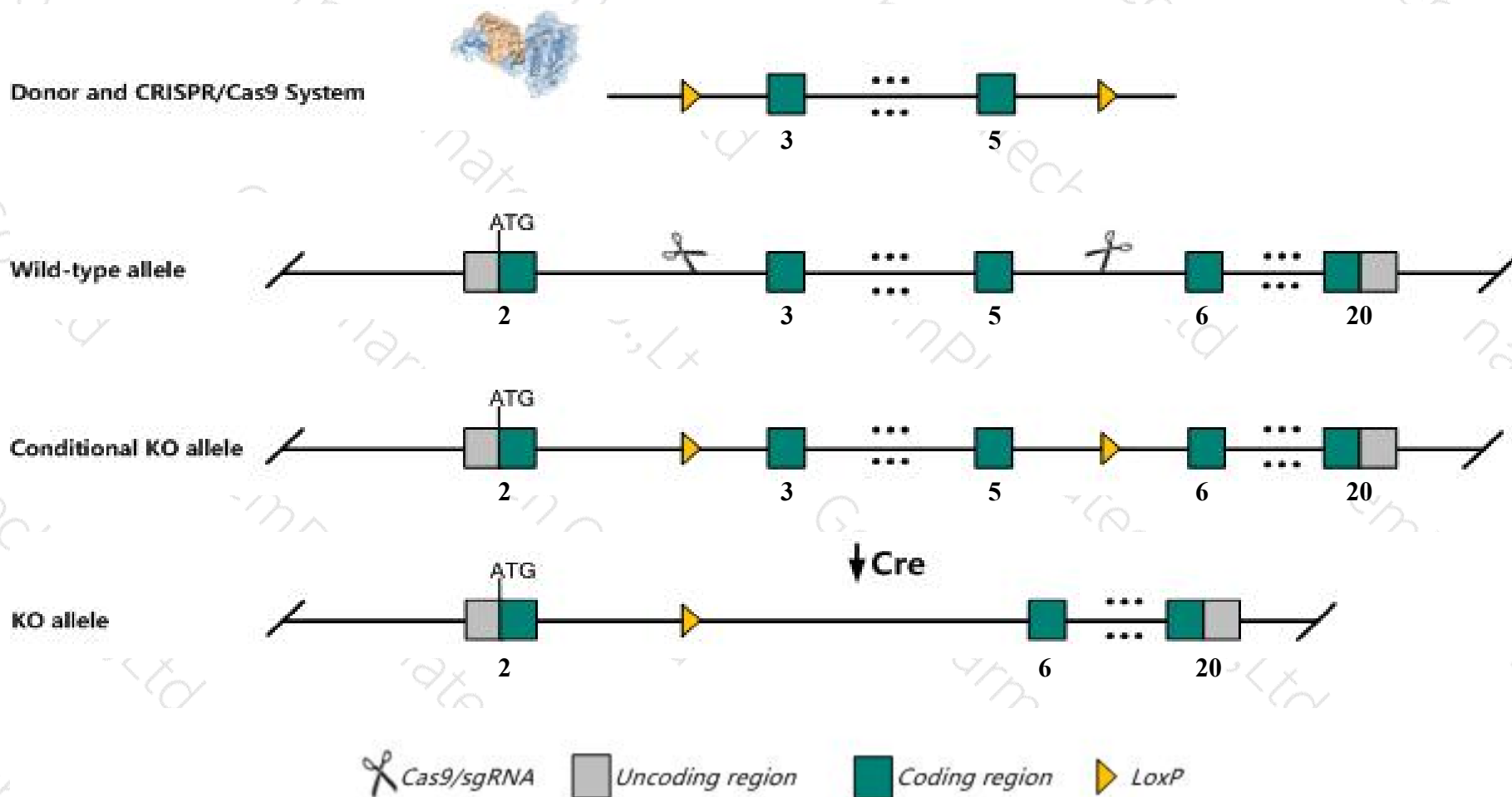
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ascc2* gene. The schematic diagram is as follows:



- The *Ascc2* gene has 2 transcripts. According to the structure of *Ascc2* gene, exon3-exon5 of *Ascc2-201* (ENSMUST00000070257.13) transcript is recommended as the knockout region. The region contains 460bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ascc2* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was 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.

- The *Ascc2* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

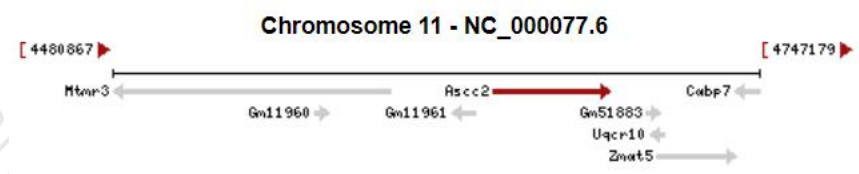
Gene information (NCBI)

Ascc2 activating signal cointegrator 1 complex subunit 2 [*Mus musculus* (house mouse)]

Gene ID: 75452, updated on 12-Aug-2019

Summary

- Official Symbol** Ascc2 provided by [MGI](#)
- Official Full Name** activating signal cointegrator 1 complex subunit 2 provided by [MGI](#)
- Primary source** [MGI:MGI:1922702](#)
- See related** [Ensembl:ENSMUSG00000020412](#)
- Gene type** protein coding
- RefSeq status** PROVISIONAL
- Organism** [Mus musculus](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as** AI482016; ASC1p100; AW046480; 1700011111Rik; 2610034L15Rik
- Expression** Ubiquitous expression in testis adult (RPKM 15.3), bladder adult (RPKM 12.2) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

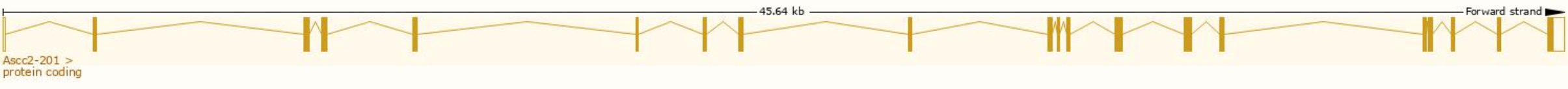


Transcript information (Ensembl)

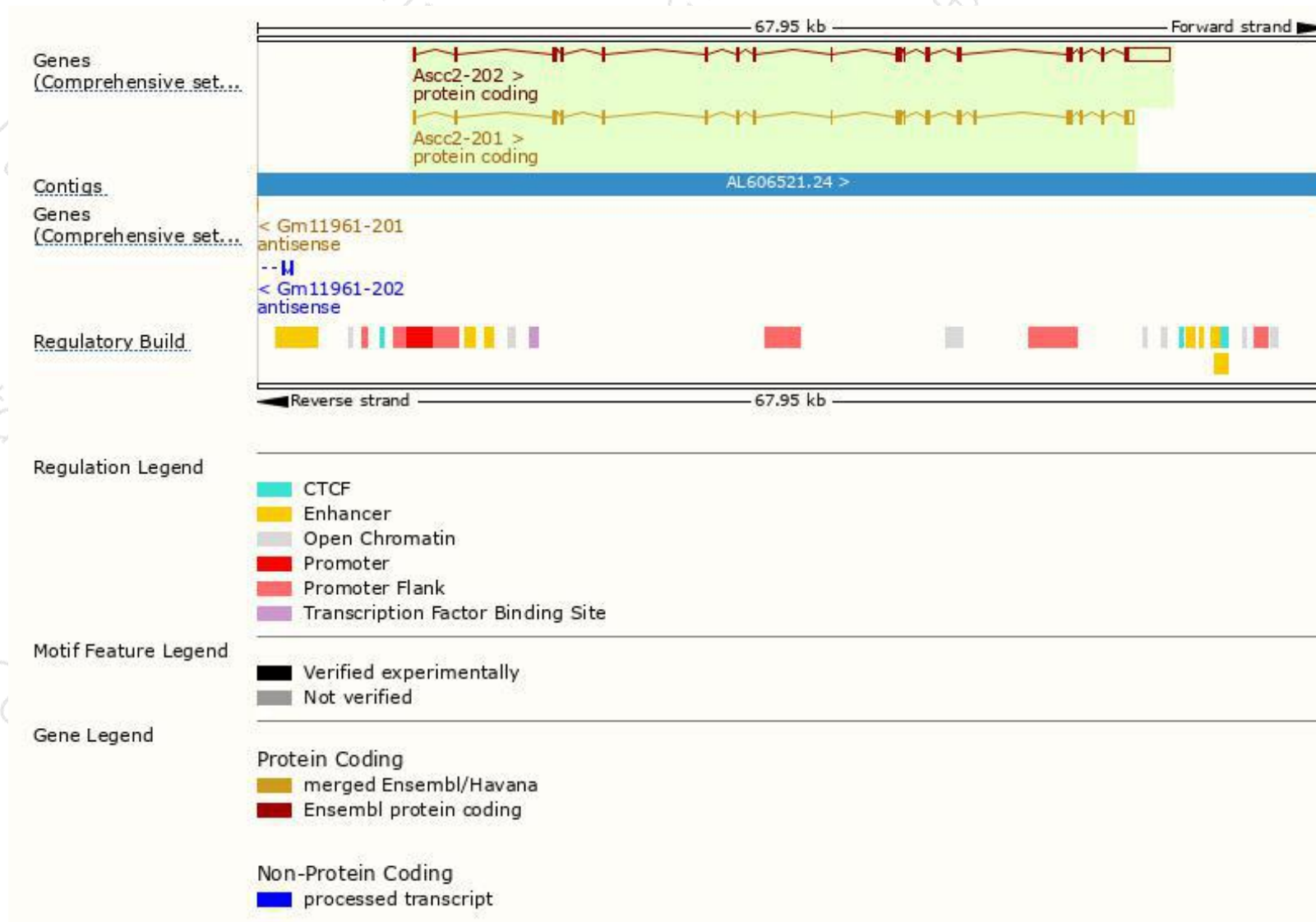
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Ascc2-201	ENSMUST00000070257.13	2650	749aa	ENSMUSP000000063272.7	Protein coding	CCDS24387	Q91WR3	TSL:1 GENCODE basic APPRIS P2
Ascc2-202	ENSMUST00000109930.2	4844	709aa	ENSMUSP00000105556.2	Protein coding	-	Q91WR3	TSL:1 GENCODE basic APPRIS ALT2

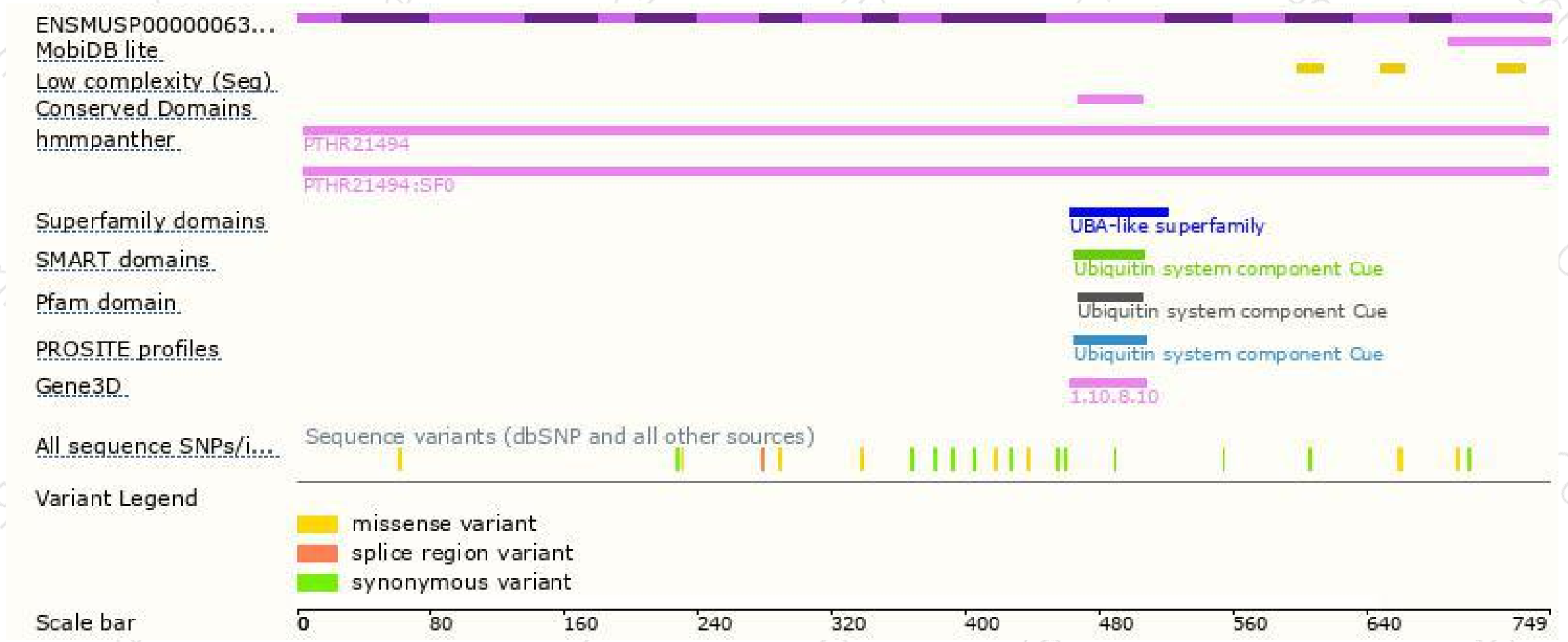
The strategy is based on the design of *Ascc2-201* transcript,The transcription is shown below



Genomic location distribution

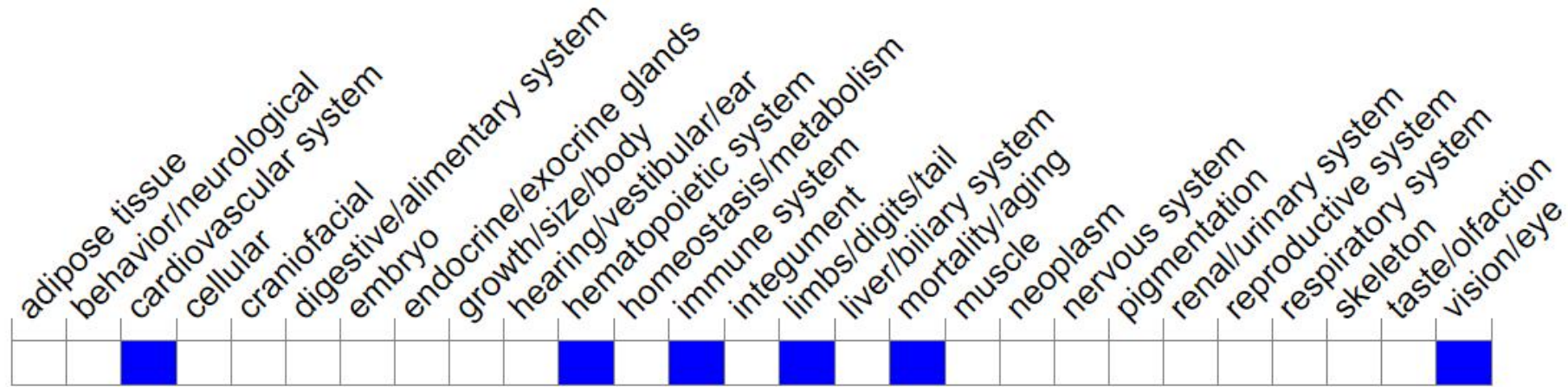


Protein domain



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/>).

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

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