

Cwc27 Cas9-CKO Strategy

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Project Overview

Project Name

Cwc27

Project type

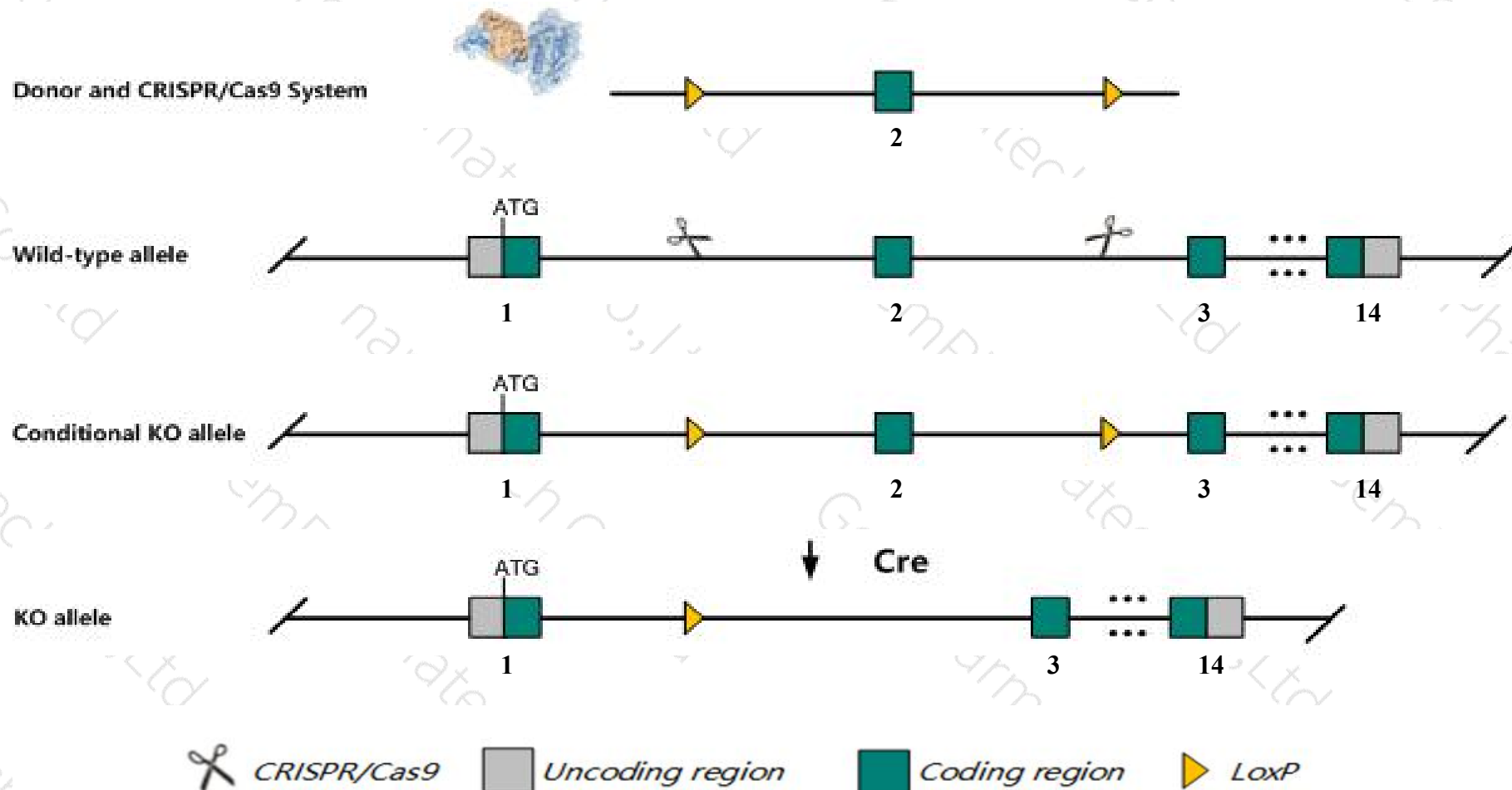
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cwc27* gene. The schematic diagram is as follows:



- The *Cwc27* gene has 4 transcripts. According to the structure of *Cwc27* gene, exon2 of *Cwc27-201* (ENSMUST00000022228.12) transcript is recommended as the knockout region. The region contains 97bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cwc27* 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.

Notice

- According to the existing MGI data, homozygous mutant mice exhibit reduced viability. Survivors after birth show signs of growth retardation and retinal depigmentation, along with numerous neurological, immunological, and blood chemistry abnormalities.
- The partial intron of transcript *Sreklip1*-203 will be deleted together in this strategy.
- The floxed region is near to the N-terminal of *Sreklip1* gene, this strategy may influence the regulatory function of the N-terminal of *Sreklip1* gene.
- Transcript *Cwc27*-202&203 may not be affected.
- The *Cwc27* 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)

Cwc27 CWC27 spliceosome-associated protein [Mus musculus (house mouse)]

Gene ID: 67285, updated on 13-Mar-2020

Summary



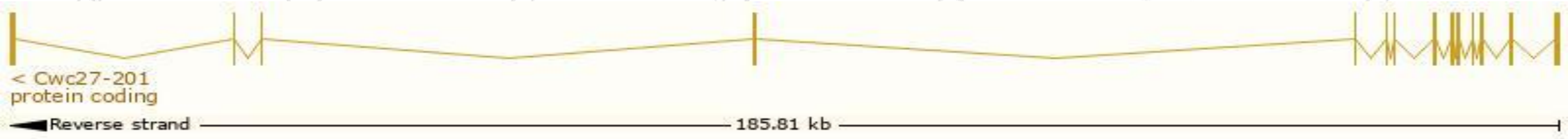
| | |
|---------------------------|---|
| Official Symbol | Cwc27 provided by MGI |
| Official Full Name | CWC27 spliceosome-associated protein provided by MGI |
| Primary source | MGI:MGI:1914535 |
| See related | Ensembl:ENSMUSG000000021715 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | 3110009E13Rik, NY-CO-10, Sdccag10 |
| Expression | Broad expression in CNS E11.5 (RPKM 1.3), CNS E14 (RPKM 0.7) and 21 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

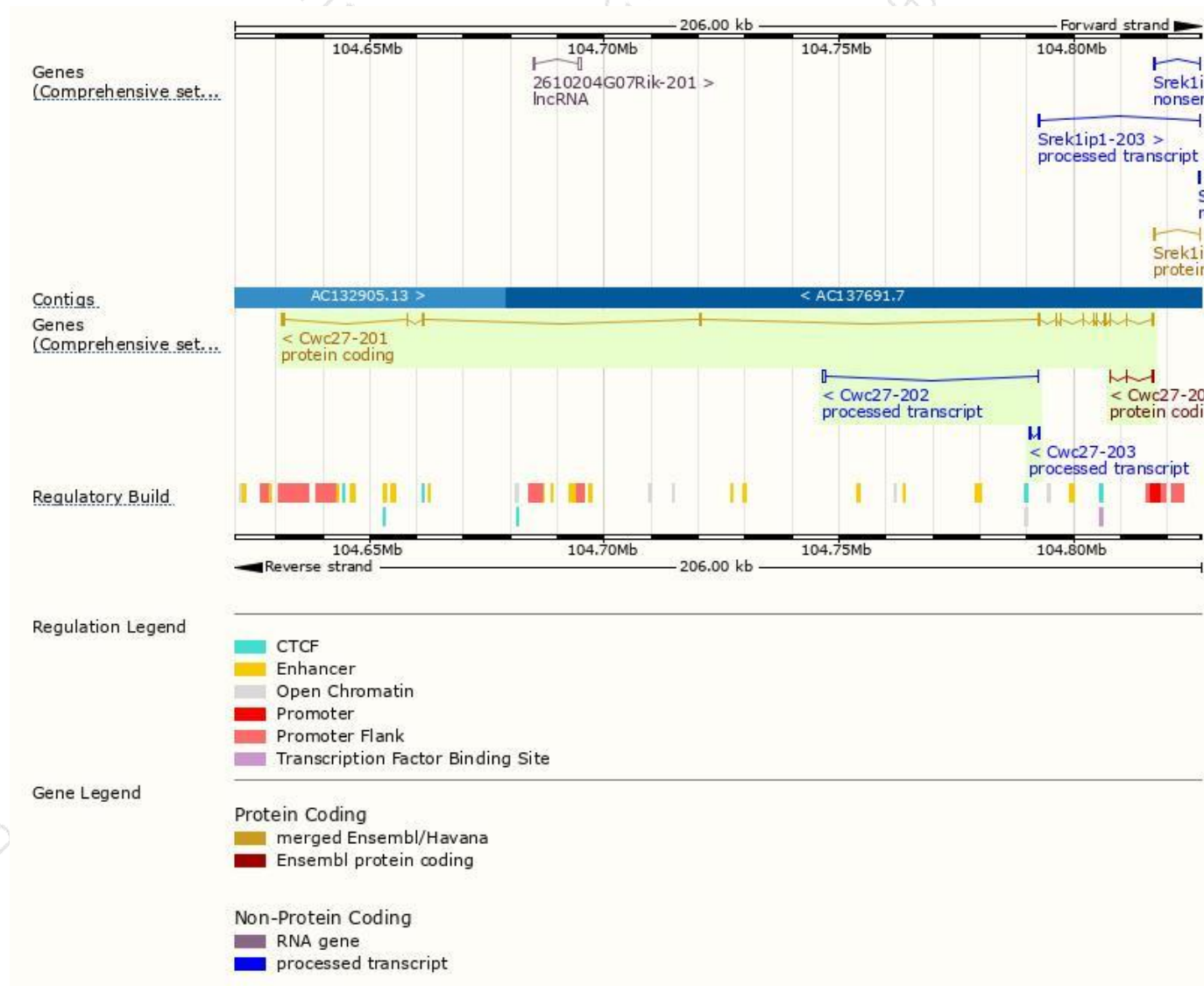
The gene has 4 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|---------------------------------------|------|-----------------------|----------------------|---------------------------|------------------------|---|
| Cwc27-201 | ENSMUST00000022228.12 | 2071 | 469aa | Protein coding | CCDS26752 | Q3TKY6 | 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 P1 |
| Cwc27-204 | ENSMUST00000154165.1 | 353 | 83aa | Protein coding | - | D3Z2U3 | CDS 3' incomplete TSL:3 |
| Cwc27-202 | ENSMUST00000141495.1 | 588 | No protein | Processed transcript | - | - | TSL:3 |
| Cwc27-203 | ENSMUST00000147514.1 | 451 | No protein | Processed transcript | - | - | TSL:3 |

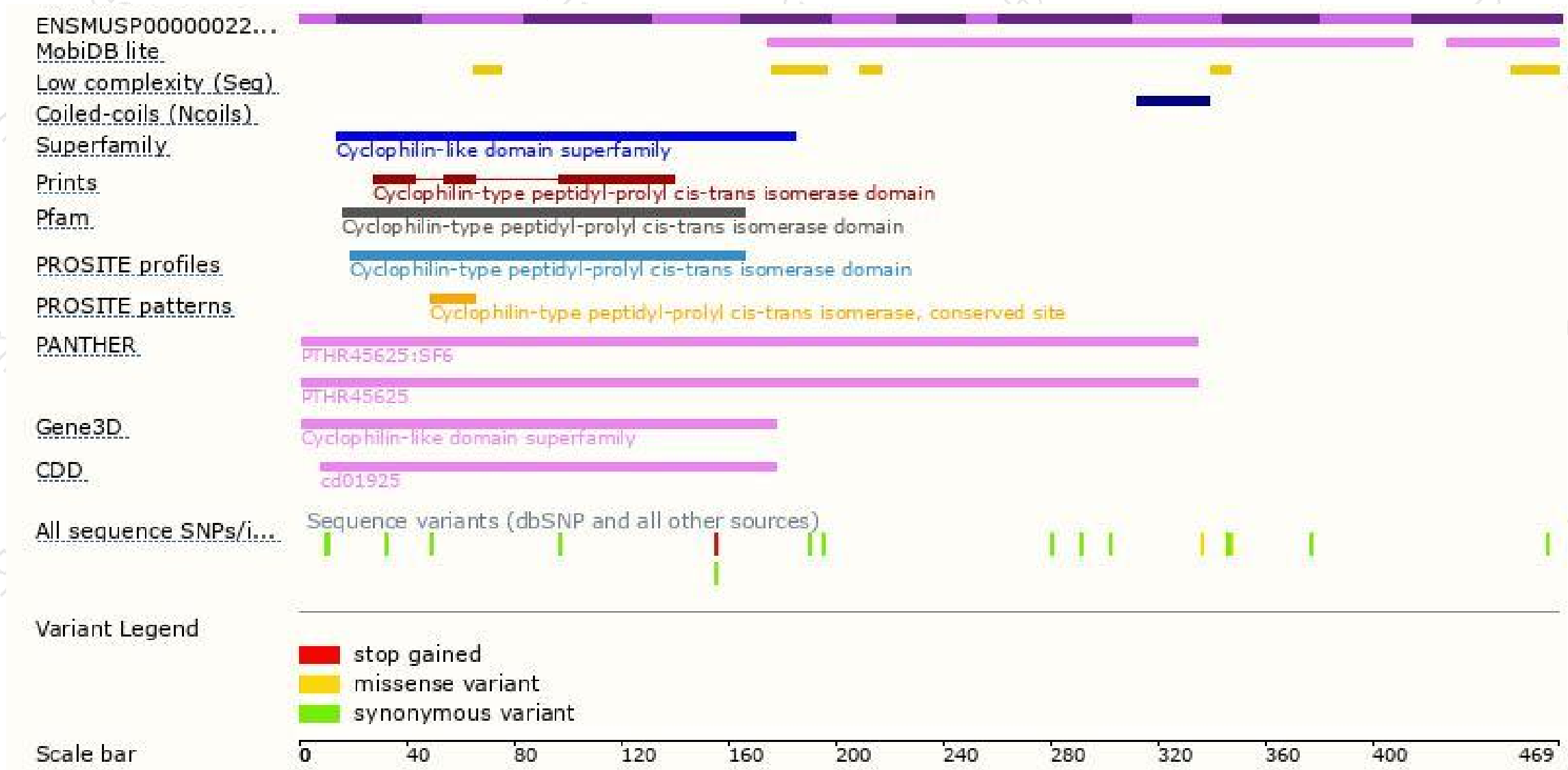
The strategy is based on the design of *Cwc27-201* transcript,The transcription is shown below



Genomic location distribution

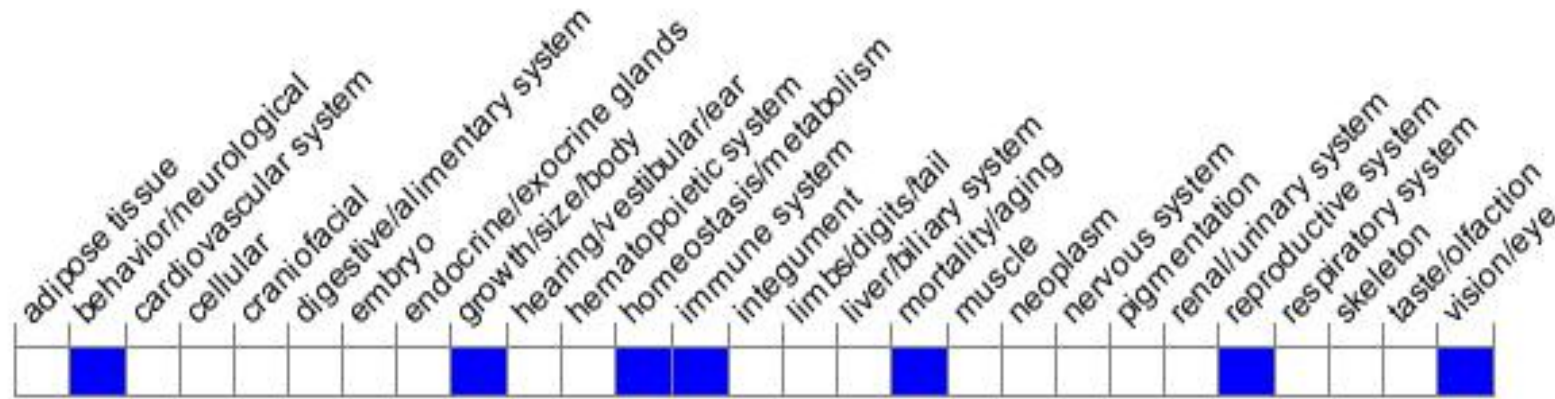


Protein domain



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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