

Pus7-D293A cas9-ki(PM) Mouse Model Strategy-CRISPR/Cas9 technology

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Reviewer: Jia Yu

Design Date: 2021-3-22

Project Overview

Project Name

Pus7-D293A

Project type

cas9-ki(PM)

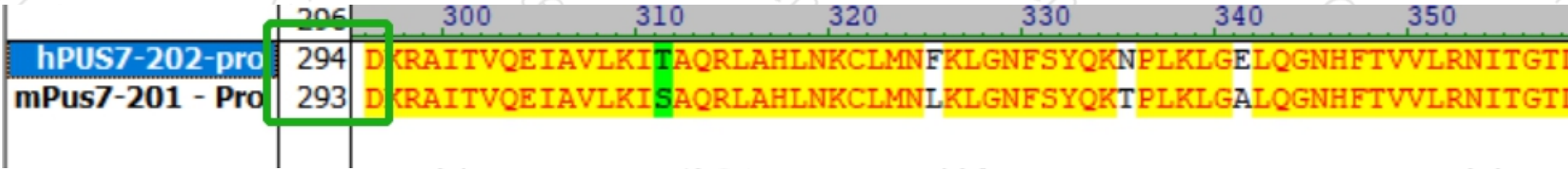
Strain background

C57BL/6JGpt

Technical Description

- The mouse *Pus7* gene has 9 transcripts. The human *PUS7* gene has 6 transcripts.
- According to the structure of *Pus7* gene and requirements of customer, the 294th amino acid(D) of human *PUS7* gene corresponds to the 293th amino acid(D) of mouse *Pus7* gene after comparing homology of mouse *Pus7* gene and human *PUS7* gene. This project produced *Pus7*-D293A point mutation on exon7 of the transcript of *Pus7*-201(ENSMUST00000119946.8, NM_178403.5 → NP_848490.2, 660aa). The 293th amino acids will be mutated from D to A, and the corresponding codon will be mutated to GCC by the GAC.
- The mouse *Pus7*-201 transcript contains 16 exons. The translation initiation site ATG is located at exon2, and the translation termination site TGA is located at exon16, encoding 660aa.
- In this project, *Pus7* gene will be modified by CRISPR/Cas9 technology. The brief process is as follows: In vitro, sgRNA and donor vectors were constructed. Cas9, sgRNA and donor were injected into the fertilized eggs of C57BL/6JGpt mice for homologous recombination, and obtained positive F0 mice identified by PCR and sequencing analysis. The stable inheritable positive F1 mice model was obtained by mating F0 mice with C57BL/6JGpt mice.

A comparison of the aa homology of human and mouse *Pus7* gene



consensus positions: 91.9% identity positions: 88.2%

The 294th amino acid(D) of human *PUS7* gene corresponds to the 293th amino acid(D) of mouse *Pus7* gene after comparing homology of mouse *Pus7* gene and human *PUS7* gene.

Targeted Mutation Site

Before mutation

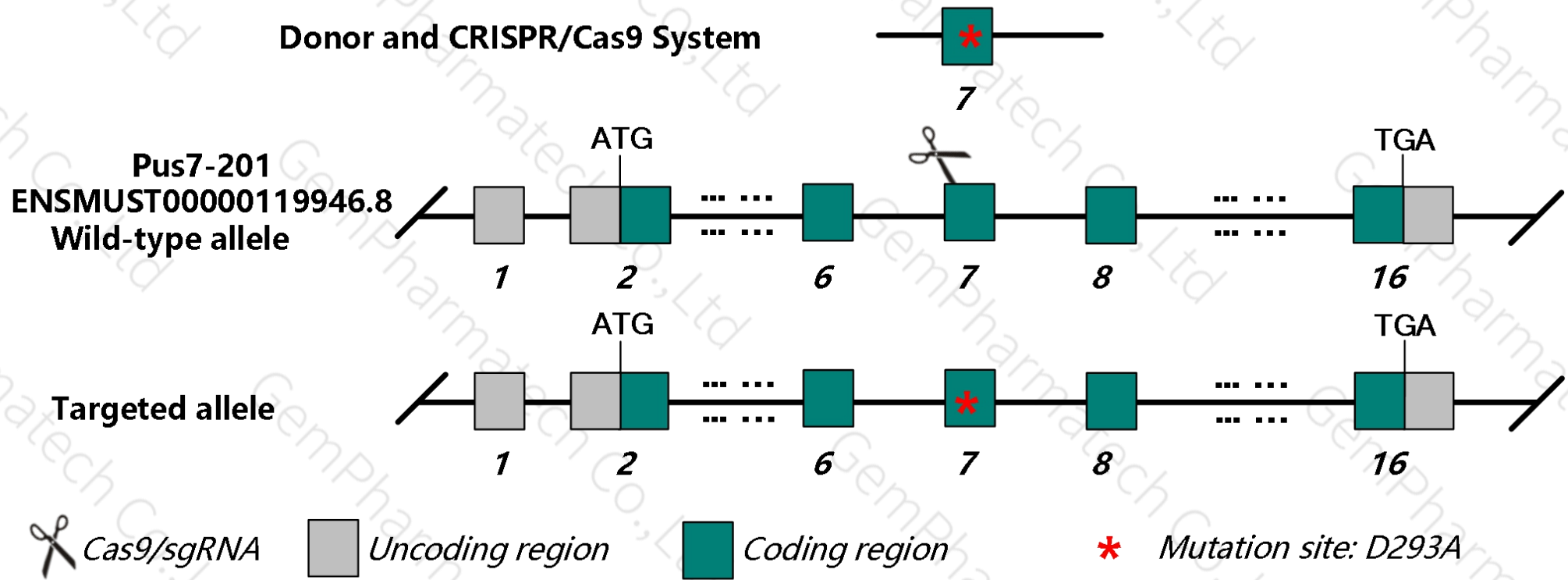
| | +1 | V | K | P | N | I | F | S | Y | M | G | T | K | D | K | R | A | I | T | V | Q | E | I | A | V | L | |
|-------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-------------|------------|------------|------------|------------|-------------|------------|------------|------------|---|---|---|---|---|---|--|
| 43401 | GTGTCTCATC | AGGGTAAAGC | CAAACATATT | CTCCTATATG | GGAACCAAAG | ACAAAAGGGC | AATCACAGTC | CAGGAGATTG | CTGTTCTCAA | GTAAGTGGAG | CACAGAGTAG | TCCCATTTTCG | GTTTGTATAA | GAGGATATAC | CCTTGGTTTC | TGTTTTCCCG | TTAGTGTCTAG | GTCCTCTAAC | GACAAGAGTT | CATTACCTC | | | | | | | |
| 43501 | TGCCCGCCCA | GACTGACAGT | GCACAGCCTC | AGCTCTGCTT | TAACGAACTT | ACCGCTTTCA | GCTTTGCATG | GTCTCTCTGC | CTTTTAAAAT | CTTGTAGACG | ACGGGCGGGT | CTGACTGTCA | CGTGTCGGAG | TCGAGACGAA | ATTGCTTGAA | TGGCGAAAGT | CGAAACGTAC | CAGAGAGACG | GAAAATTTTA | GAACATCTGC | | | | | | | |

After mutation

| | +1 | V | K | P | N | I | F | S | Y | M | G | T | K | A | K | R | A | I | T | V | Q | E | I | A | V | L | |
|-------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-------------|------------|------------|------------|------------|-------------|------------|------------|------------|---|---|---|---|---|---|--|
| 43401 | GTGTCTCATC | AGGGTAAAGC | CAAACATATT | CTCCTATATG | GGAACCAAAG | CCAAAAGGGC | AATCACAGTC | CAGGAGATTG | CTGTTCTCAA | GTAAGTGGAG | CACAGAGTAG | TCCCATTTTCG | GTTTGTATAA | GAGGATATAC | CCTTGGTTTC | GGTTTTCCCG | TTAGTGTCTAG | GTCCTCTAAC | GACAAGAGTT | CATTACCTC | | | | | | | |
| 43501 | TGCCCGCCCA | GACTGACAGT | GCACAGCCTC | AGCTCTGCTT | TAACGAACTT | ACCGCTTTCA | GCTTTGCATG | GTCTCTCTGC | CTTTTAAAAT | CTTGTAGACG | ACGGGCGGGT | CTGACTGTCA | CGTGTCGGAG | TCGAGACGAA | ATTGCTTGAA | TGGCGAAAGT | CGAAACGTAC | CAGAGAGACG | GAAAATTTTA | GAACATCTGC | | | | | | | |

The green region is exon7 of *Pus7-201*, the yellow region represents the mutation site.

This model uses CRISPR/Cas9 technology to edit the *Pus7* gene and the schematic diagram is as follow:



- One or Two synonymous mutations of amino acids will be introduced on exon7 of *Pus7*.
- Mouse *Pus7* gene is located on Chr5. Please take the loci in consideration when breeding this mutation mice with other gene modified strains, if the other gene is also on Chr5, it may be extremely hard to get double gene positive homozygotes.
- The scheme is designed according to the genetic information in the existing database. Due to the complex process of gene transcription and translation, it cannot be predicted completely at the present technology level.

Gene name and location (NCBI)

Pus7 pseudouridylate synthase 7 [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 78697, updated on 17-Dec-2020

Summary

Official Symbol Pus7 provided by [MGI](#)
Official Full Name pseudouridylate synthase 7 provided by [MGI](#)
Primary source [MGI:MGI:1925947](#)
See related [Ensembl:ENSMUSG00000057541](#)
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 C330017I15Rik
Expression Ubiquitous expression in bladder adult (RPKM 4.8), CNS E11.5 (RPKM 4.6) and 26 other tissues [See more](#)
Orthologs [human](#) [all](#)

NEW Try the new [Gene table](#)
Try the new [Transcript table](#)

Genomic context

Location: 5; 5 A3

Exon count: 19

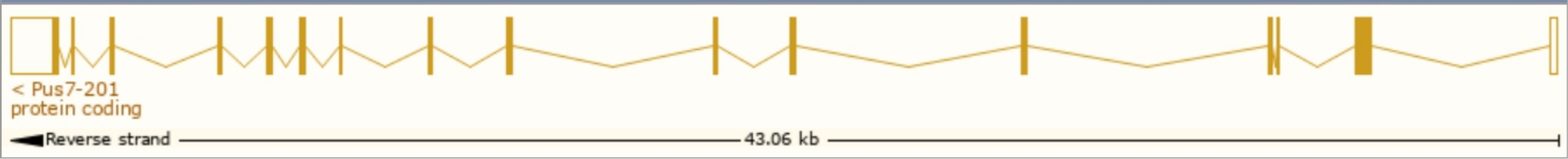
See Pus7 in [Genome Data Viewer](#)

Transcript information (Ensembl)

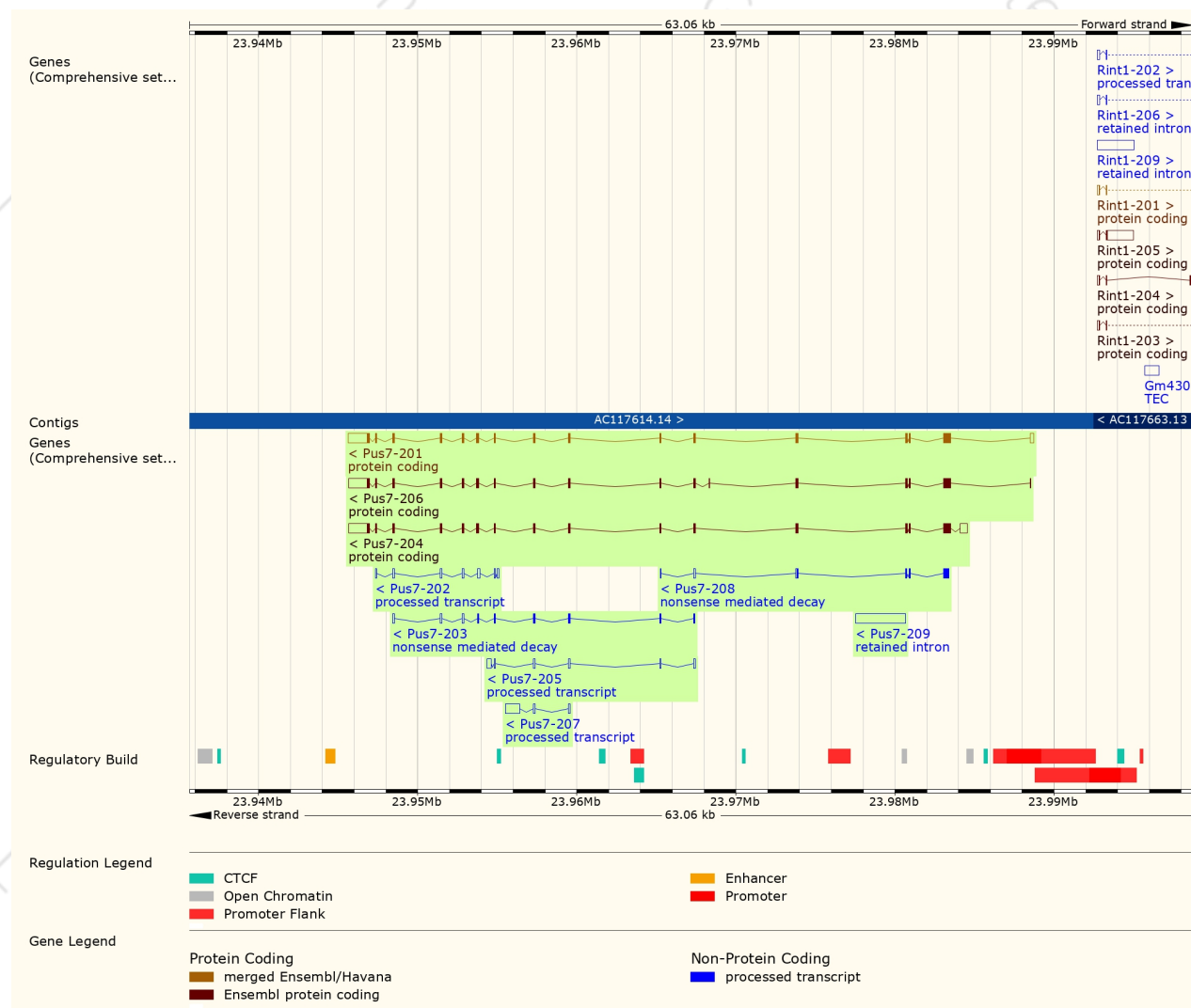
The gene has 9 transcripts, and all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt Match | Flags |
|----------|--------------------------------------|------|-----------------------|-------------------------|---------------------------|--------------------------|---------------------------------|
| Pus7-204 | ENSMUST00000131992.8 | 3645 | 660aa | Protein coding | CCDS51431 | Q91VU7-1 | TSL:1 GENCODE basic APPRIS P3 |
| Pus7-201 | ENSMUST00000119946.8 | 3407 | 660aa | Protein coding | CCDS51431 | Q91VU7-1 | TSL:1 GENCODE basic APPRIS P3 |
| Pus7-206 | ENSMUST00000148618.8 | 3266 | 666aa | Protein coding | CCDS80219 | Q91VU7-2 | TSL:1 GENCODE basic APPRIS ALT2 |
| Pus7-203 | ENSMUST00000131404.2 | 888 | 185aa | Nonsense mediated decay | - | F7CG42 | CDS 5' incomplete TSL:5 |
| Pus7-208 | ENSMUST00000151449.2 | 750 | 176aa | Nonsense mediated decay | - | F6XMS4 | CDS 5' incomplete TSL:3 |
| Pus7-207 | ENSMUST00000148921.2 | 1114 | No protein | Processed transcript | - | - | TSL:3 |
| Pus7-202 | ENSMUST00000129848.8 | 773 | No protein | Processed transcript | - | - | TSL:3 |
| Pus7-205 | ENSMUST00000147922.8 | 721 | No protein | Processed transcript | - | - | TSL:3 |
| Pus7-209 | ENSMUST00000195909.2 | 3118 | No protein | Retained intron | - | - | TSL:NA |

The strategy is based on the design of *Pus7-201* transcript, the transcription is shown below:



Genomic location distribution

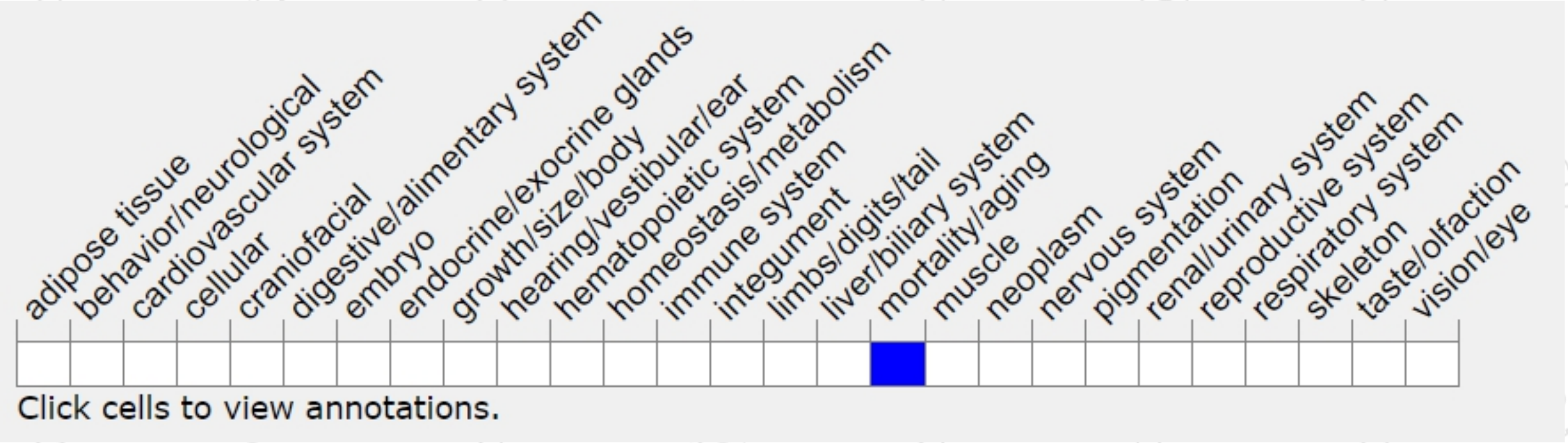


Protein domain



Mouse phenotype description(MGI)

URL link is as follows:
<http://www.informatics.jax.org/marker/MGI:1925947>



If you have any questions, please feel free to contact us.

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