

Atf5 Cas9-CKO Strategy

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Design Date: 2020-3-16

Project Overview

Project Name

Atf5

Project type

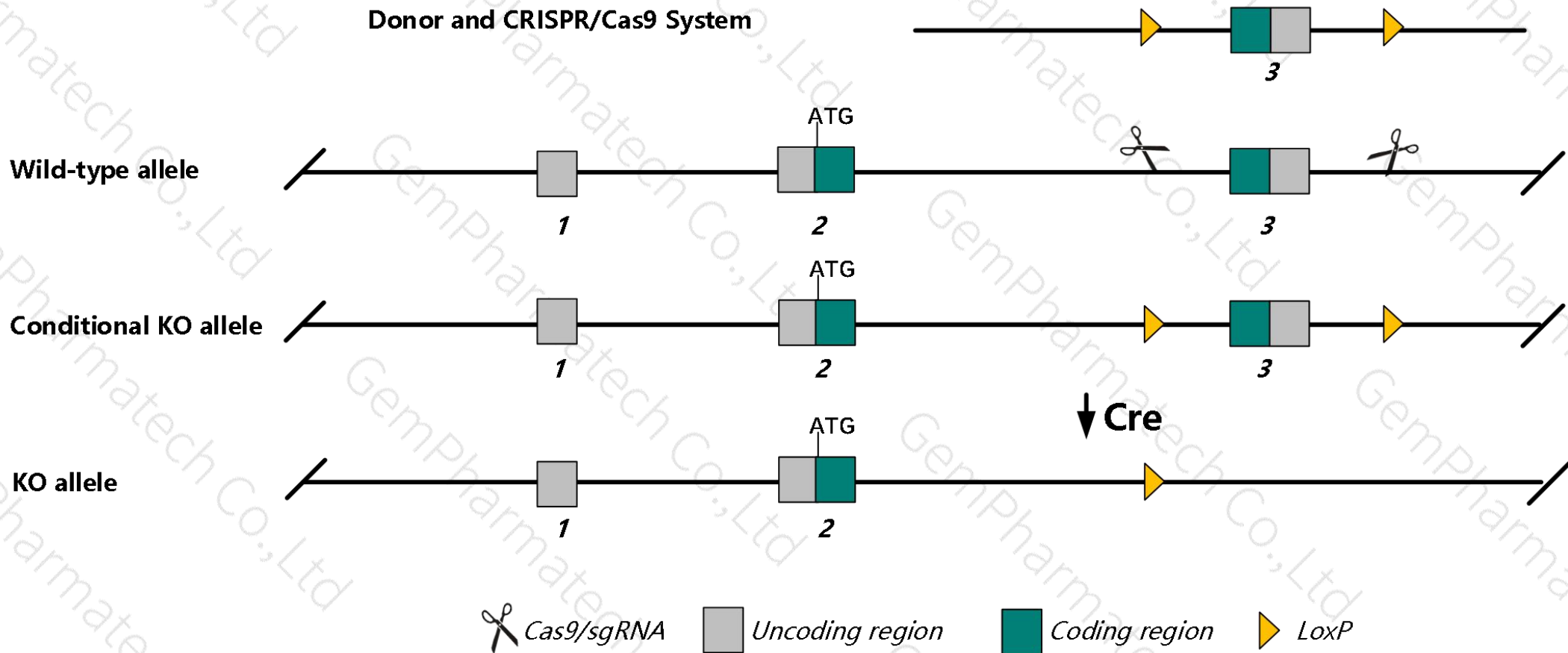
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atf5* gene. The schematic diagram is as follows:



Technical routes

- The *Atf5* gene has 3 transcripts. According to the structure of *Atf5* gene, exon3 of *Atf5-201* (ENSMUST00000047356.10) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atf5* 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, Mice homozygous for a knock-out allele exhibit partial neonatal and postnatal lethality, absence of gastric milk in some mice, decreased body weight in mice that survive and loss of mature olfactory sensory neurons with increased apoptosis in olfactory epithelium.
- The flox region is about 2.4 kb from the 5th end of the *Nup62* gene, which may affect the 5-terminal regulation of the gene.
- The flox region is about 2.8 kb from the 5th end of the *Il4i1* gene, which may affect the 5-terminal regulation of the gene.
- The *Atf5* gene is located on the Chr7. 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)

Atf5 activating transcription factor 5 [*Mus musculus* (house mouse)]

Gene ID: 107503, updated on 13-Mar-2020

Summary

| | |
|--------------------|---|
| Official Symbol | Atf5 provided by MGI |
| Official Full Name | activating transcription factor 5 provided by MGI |
| Primary source | MGI:MGI:2141857 |
| See related | Ensembl:ENSMUSG000000038539 |
| 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 | AFTA; Atf7; Atfx; ODA-10 |
| Expression | Broad expression in liver adult (RPKM 173.6), adrenal adult (RPKM 143.8) and 21 other tissues See more |
| Orthologs | human all |

Genomic context

Location: 7; 7 B3

Exon count: 4

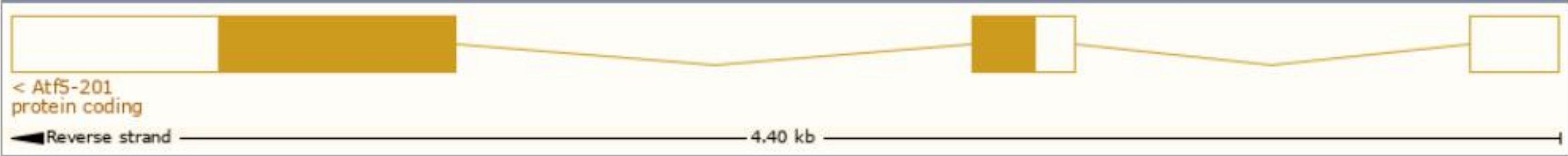
See Atf5 in [Genome Data Viewer](#)

Transcript information (Ensembl)

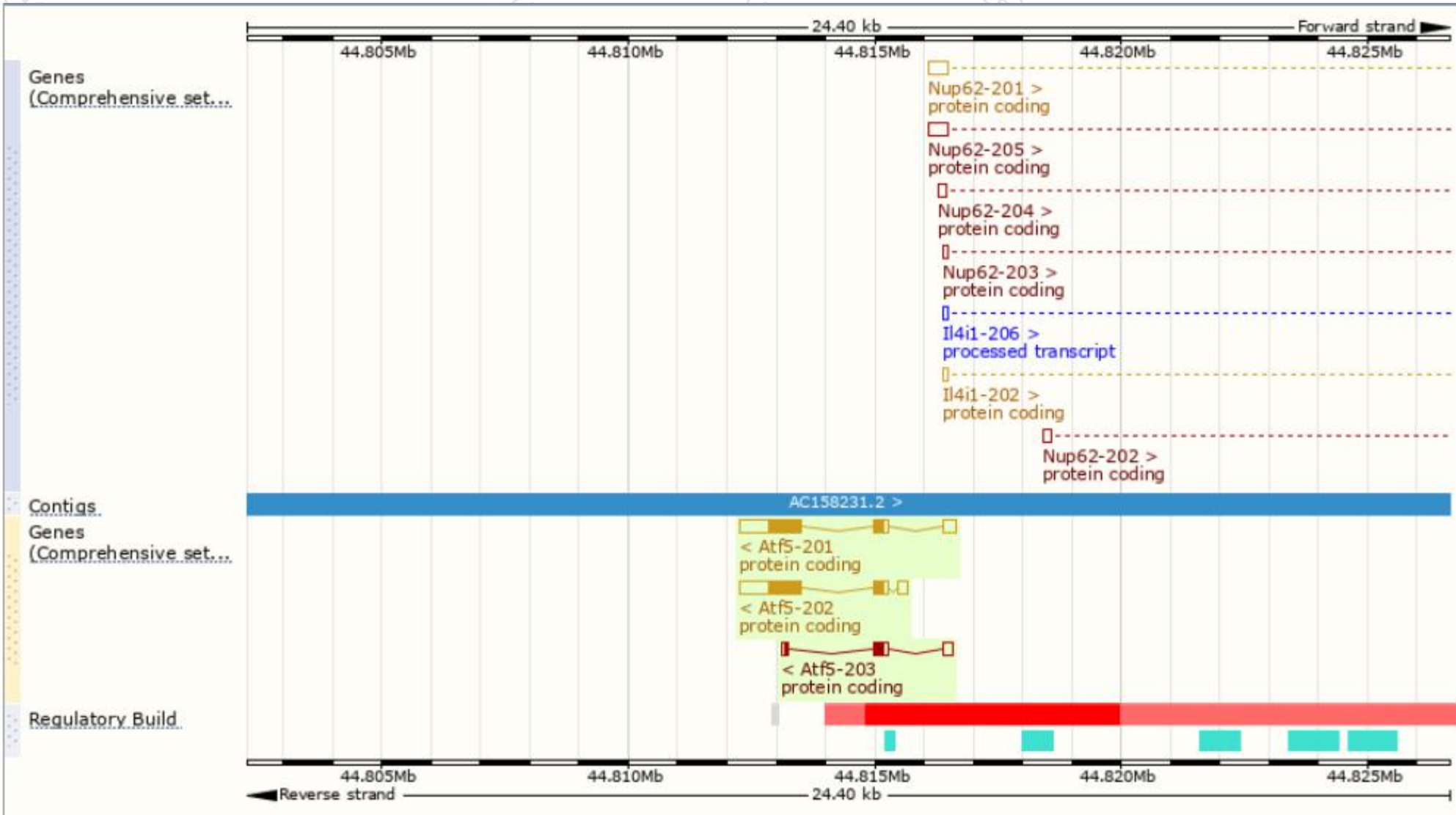
The gene has 3 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|---------------------------------------|------|-----------------------|----------------|---------------------------|---|-------------------------------|
| Atf5-201 | ENSMUST00000047356.10 | 1816 | 283aa | Protein coding | CCDS21215 | O70191 Q3UJF3 | TSL:1 GENCODE basic APPRIS P1 |
| Atf5-202 | ENSMUST00000107893.8 | 1735 | 283aa | Protein coding | CCDS21215 | O70191 Q3UJF3 | TSL:1 GENCODE basic APPRIS P1 |
| Atf5-203 | ENSMUST00000209072.1 | 595 | 75aa | Protein coding | - | A0A140LIB7 | TSL:5 GENCODE basic |

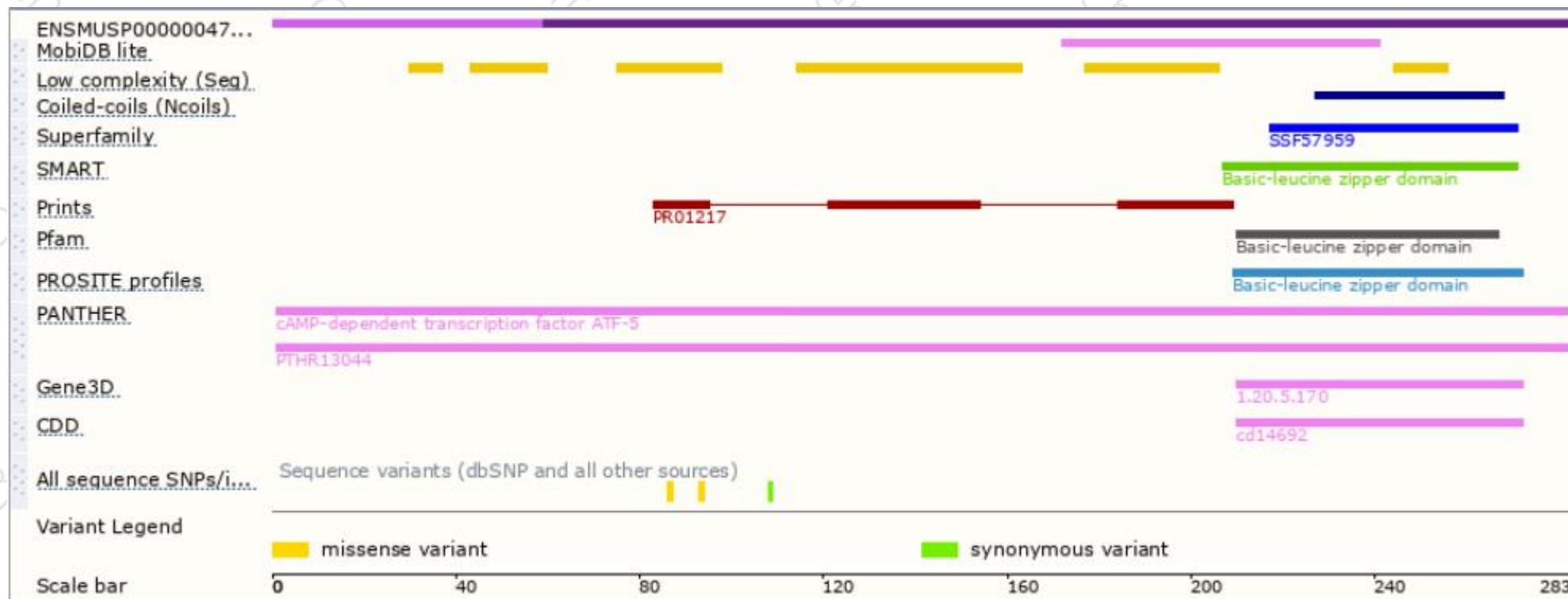
The strategy is based on the design of *Atf5-201* transcript,The transcription is shown below



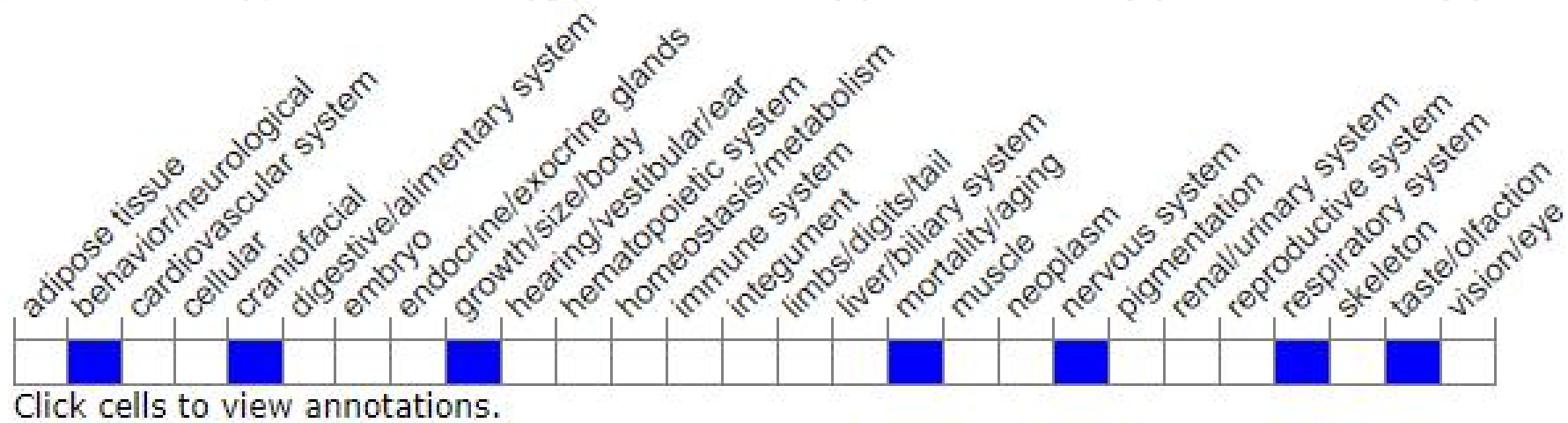
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Mice homozygous for a knock-out allele exhibit partial neonatal and postnatal lethality, absence of gastric milk in some mice, decreased body weight in mice that survive and loss of mature olfactory sensory neurons with increased apoptosis in olfactory epithelium.

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

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