

Dpf2 Cas9-CKO Strain Strategy

Designer: Lixin Lu

Reviewer: Linyan Wu

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Overview

Target Gene Name

- Dpf2

Project Type

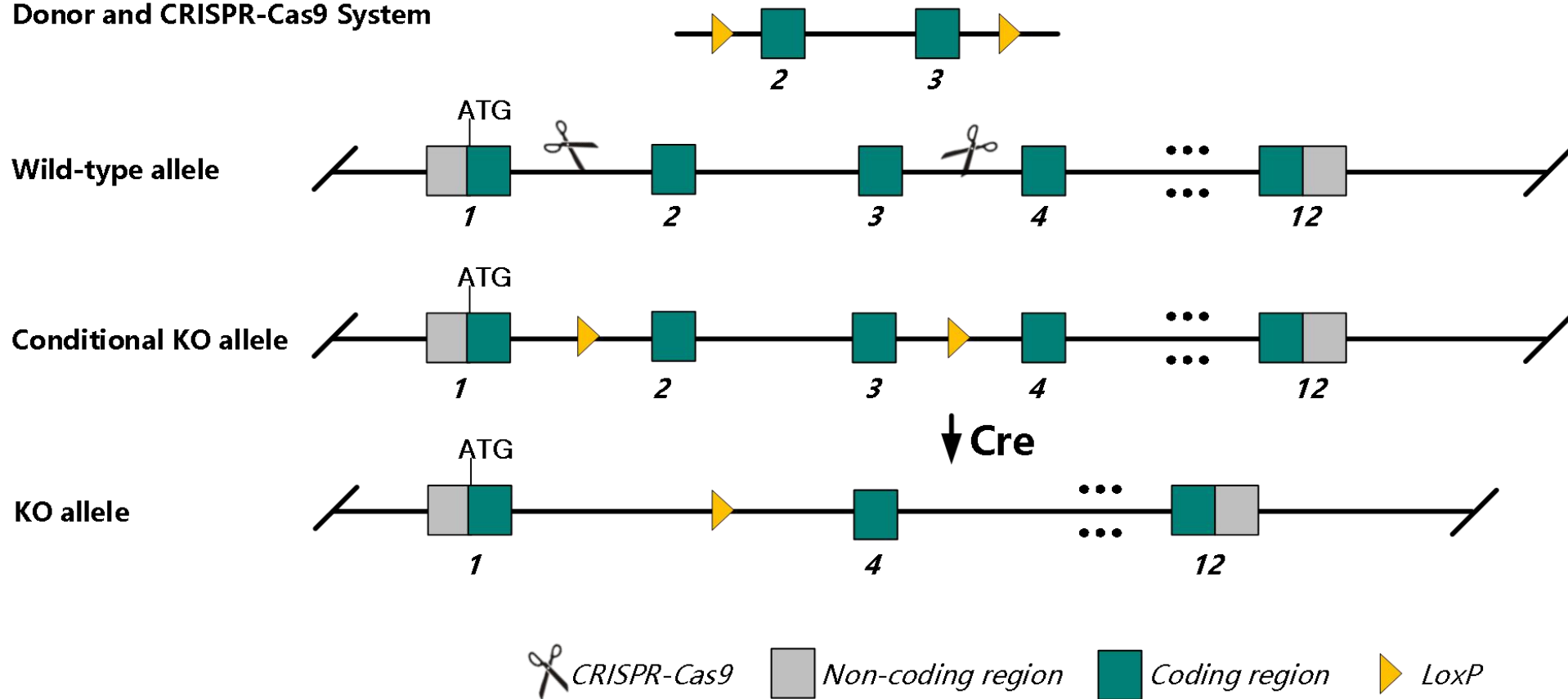
- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy

Donor and CRISPR-Cas9 System



Schematic representation of CRISPR-Cas9 engineering used to edit the *Dpf2* gene.

Technical Information

- The *Dpf2* gene has 10 transcripts. According to the structure of *Dpf2* gene, exon2-3 of *Dpf2*-202 (ENSMUST00000118623.1) transcript is recommended as the knockout region. The region contains 269 bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Dpf2* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Dpf2 double PHD fingers 2 [*Mus musculus* (house mouse)]

Gene ID: 19708, updated on 8-Dec-2022

[Download Datasets](#)

Summary

| | |
|---------------------------|---|
| Official Symbol | Dpf2 provided by MGI |
| Official Full Name | double PHD fingers 2 provided by MGI |
| Primary source | MGI:MGI:109529 |
| See related | Ensembl:ENSMUSG000000024826 AllianceGenome:MGI:109529 |
| 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 | Req; BAF45D; ubi-d4; 2210010M07Rik |
| Summary | Predicted to enable H3K9me3 modified histone binding activity; lysine-acetylated histone binding activity; and transcription coregulator activity. Predicted to be involved in negative regulation of myeloid progenitor cell differentiation; nervous system development; and regulation of transcription, DNA-templated. Predicted to act upstream of or within apoptotic process and chromatin organization. Located in cytoplasm and nucleus. Is expressed in several structures, including alimentary system; central nervous system; genitourinary system; integumental system; and sensory organ. Orthologous to human DPF2 (double PHD fingers 2). [provided by Alliance of Genome Resources, Apr 2022] |
| Expression | Ubiquitous expression in thymus adult (RPKM 38.7), limb E14.5 (RPKM 38.1) and 28 other tissues See more |
| Orthologs | human all |
| NEW | Try the new Gene table Try the new Transcript table |

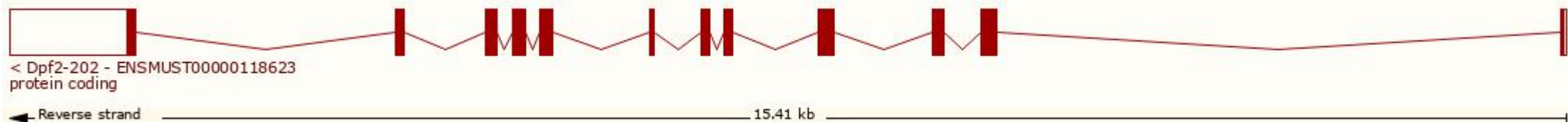
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 10 transcripts, all transcripts are shown below:

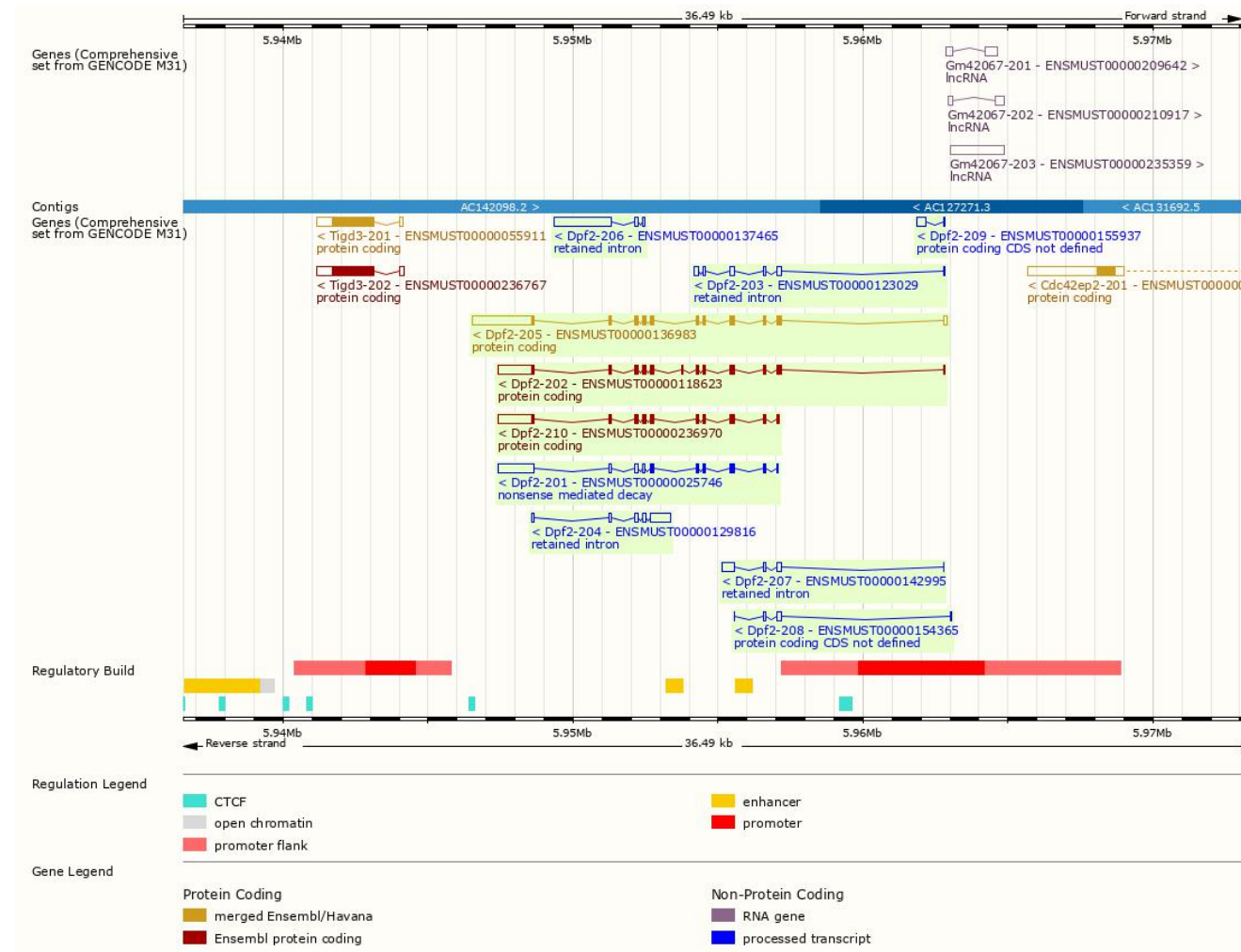
| Show/hide columns (1 hidden) | | | | | | | Filter | |
|---------------------------------------|----------|------|-----------------------|--------------------------------|---------------------------|----------------------------|-------------------------|---------------------|
| Transcript ID | Name | bp | Protein | Biotype | CCDS | UniProt Match | Flags | |
| ENSMUST00000025746.14 | Dpf2-201 | 2153 | 214aa | Nonsense mediated decay | | F8WIP7 | TSL:1 | CDS 5' incomplete |
| ENSMUST00000118623.2 | Dpf2-202 | 2406 | 405aa | Protein coding | CCDS70920 | D3Z5N6 | Ensembl Canonical | GENCODE basic TSL:5 |
| ENSMUST00000123029.8 | Dpf2-203 | 735 | No protein | Retained intron | | - | TSL:2 | |
| ENSMUST00000129816.8 | Dpf2-204 | 1115 | No protein | Retained intron | | - | TSL:2 | |
| ENSMUST00000136983.8 | Dpf2-205 | 3314 | 391aa | Protein coding | CCDS37892 | Q61103 | GENCODE basic APPRIS P1 | TSL:1 |
| ENSMUST00000137465.2 | Dpf2-206 | 2167 | No protein | Retained intron | | - | TSL:2 | |
| ENSMUST00000142995.8 | Dpf2-207 | 725 | No protein | Retained intron | | - | TSL:2 | |
| ENSMUST00000154365.2 | Dpf2-208 | 314 | No protein | Protein coding CDS not defined | | - | TSL:5 | |
| ENSMUST00000155937.2 | Dpf2-209 | 370 | No protein | Protein coding CDS not defined | | - | TSL:1 | |
| ENSMUST00000236970.2 | Dpf2-210 | 2217 | 349aa | Protein coding | | A0A494BBF7 | CDS 5' incomplete | |

The strategy is based on the design of *Dpf2*-202 transcript, the transcription is shown below:

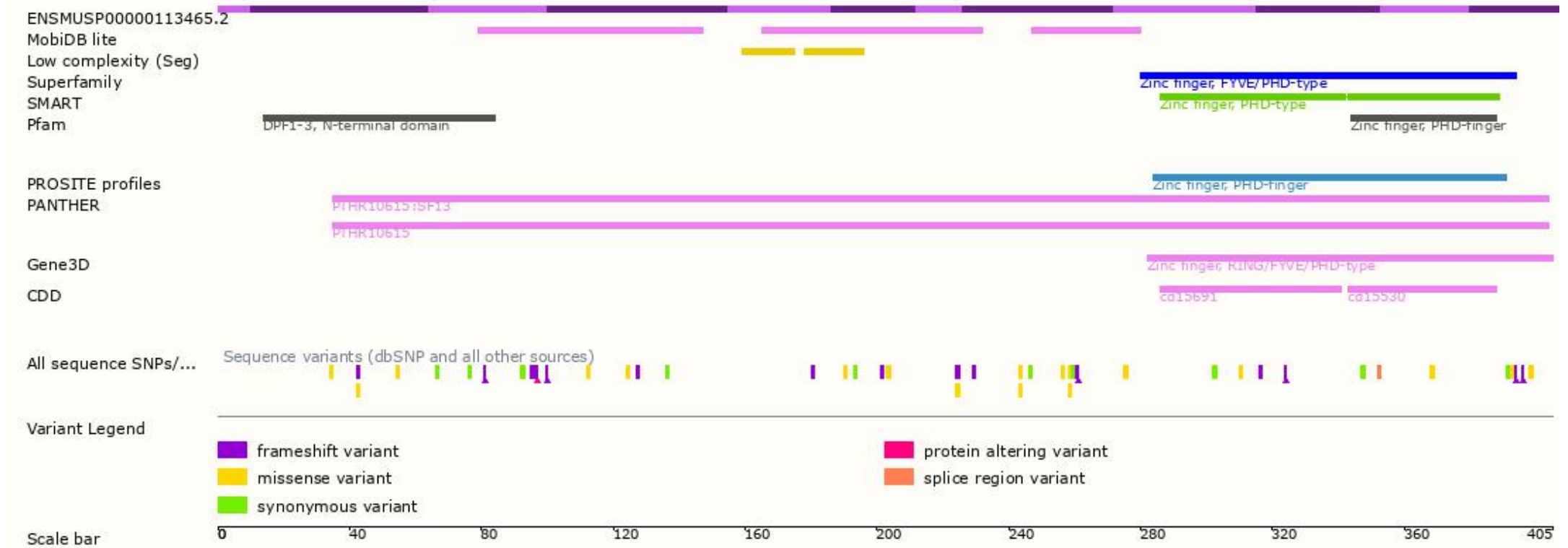


Source: <https://www.ensembl.org>

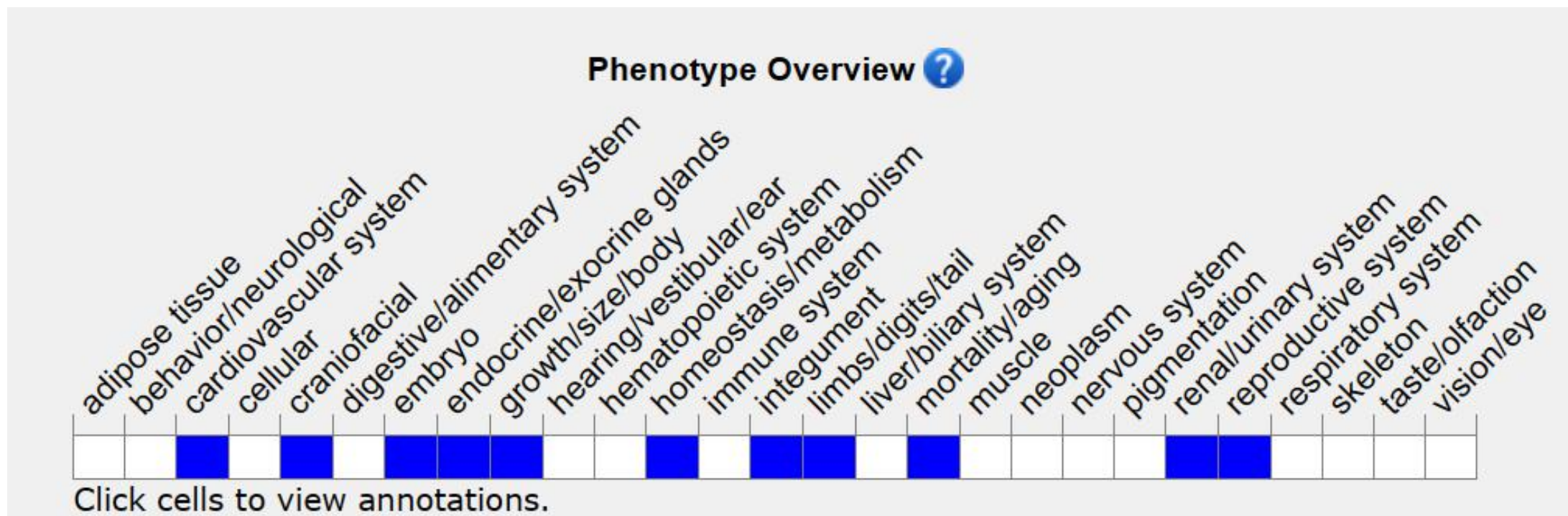
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



Important Information

- This strategy do not effect the transcription *Dpf2*-204, 206 and 209, the risk is unknown .
- *Dpf2* is located on Chr19. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.