GemPharmatech™

Yod1 Cas9-KO Strategy

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Reviewer: Jing Chen

Design Date: 2023-10-16

Overview

Target Gene Name

- Yod1

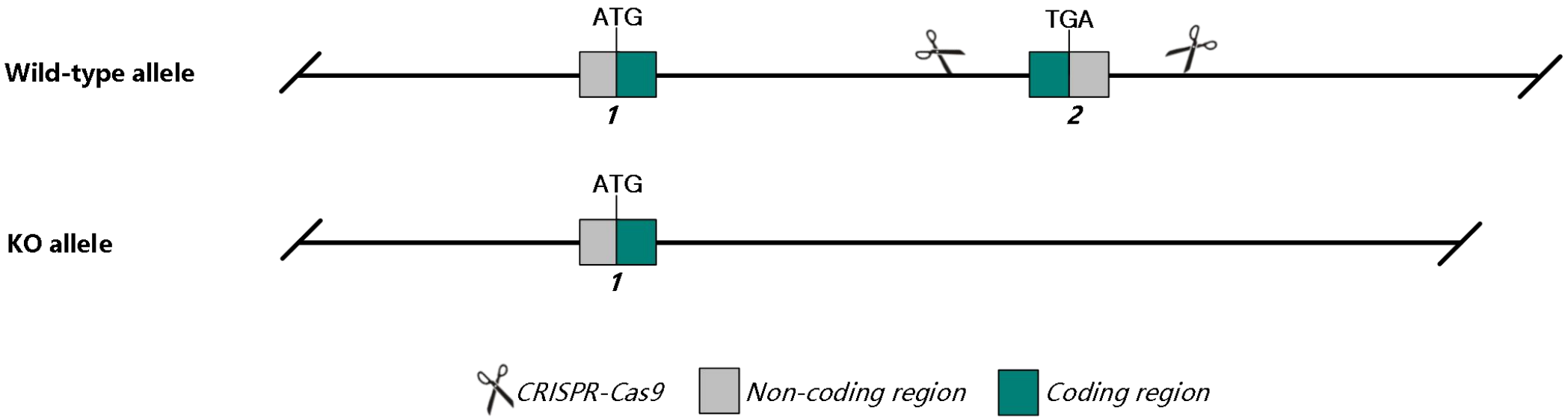
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy

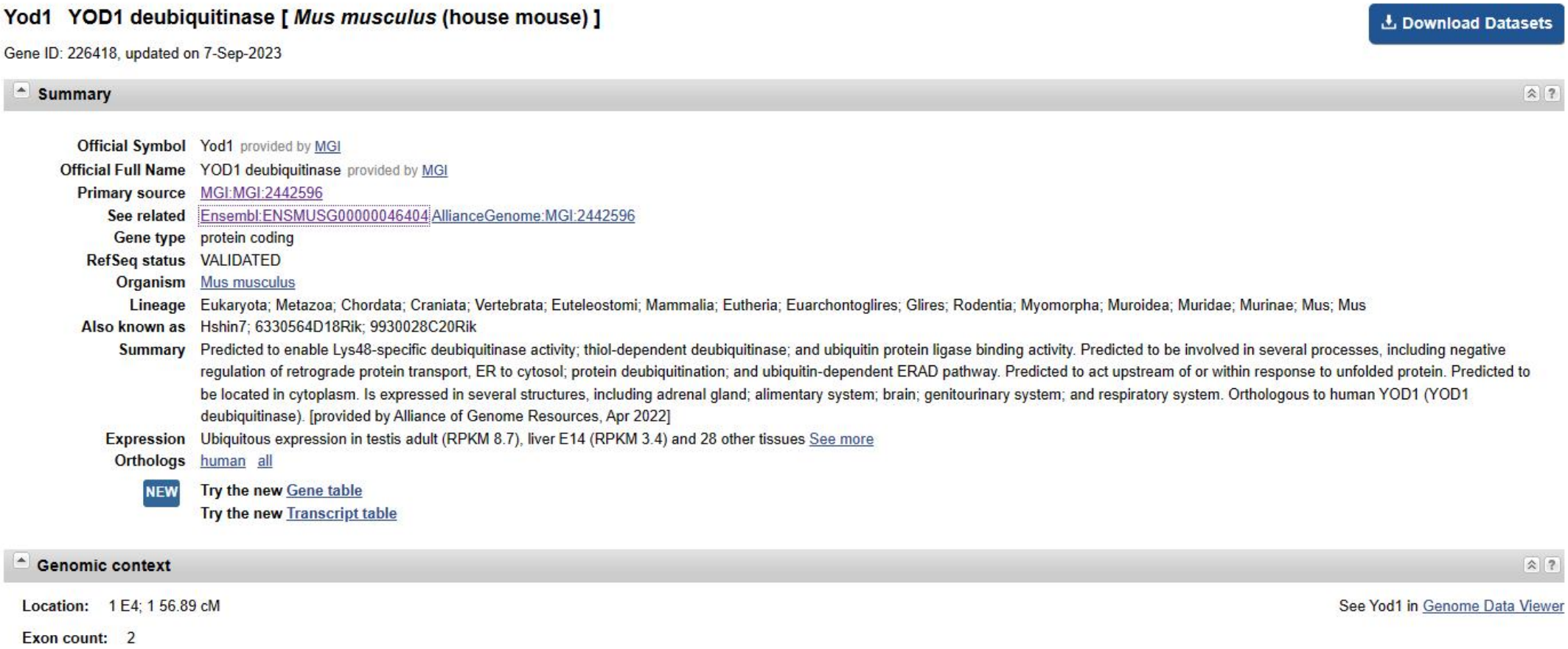


Schematic representation of CRISPR-Cas9 engineering used to edit the *Yod1* gene.

Technical Information

- The *Yod1* gene has 1 transcript. According to the structure of *Yod1* gene, exon 2 of *Yod1*-201 (NSMUST00000049813.6) transcript is recommended as the knockout region. The region contains 704 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 *Yod1* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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.

Gene Information



Yod1 YOD1 deubiquitinase [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 226418, updated on 7-Sep-2023

Summary

Official Symbol	Yod1 provided by MGI
Official Full Name	YOD1 deubiquitinase provided by MGI
Primary source	MGI:MGI:2442596
See related	Ensembl:ENSMUSG00000046404 AllianceGenome:MGI:2442596
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	Hshin7; 6330564D18Rik; 9930028C20Rik
Summary	Predicted to enable Lys48-specific deubiquitinase activity; thiol-dependent deubiquitinase; and ubiquitin protein ligase binding activity. Predicted to be involved in several processes, including negative regulation of retrograde protein transport, ER to cytosol; protein deubiquitination; and ubiquitin-dependent ERAD pathway. Predicted to act upstream of or within response to unfolded protein. Predicted to be located in cytoplasm. Is expressed in several structures, including adrenal gland; alimentary system; brain; genitourinary system; and respiratory system. Orthologous to human YOD1 (YOD1 deubiquitinase). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in testis adult (RPKM 8.7), liver E14 (RPKM 3.4) and 28 other tissues See more
Orthologs	human all

NEW Try the new Gene table

Try the new Transcript table

Genomic context

Location: 1 E4; 1 56.89 cM

See Yod1 in Genome Data Viewer

Exon count: 2

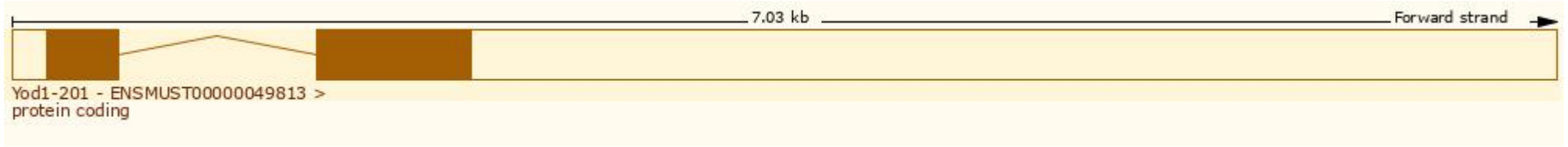
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 1 transcript, the transcript is shown below:

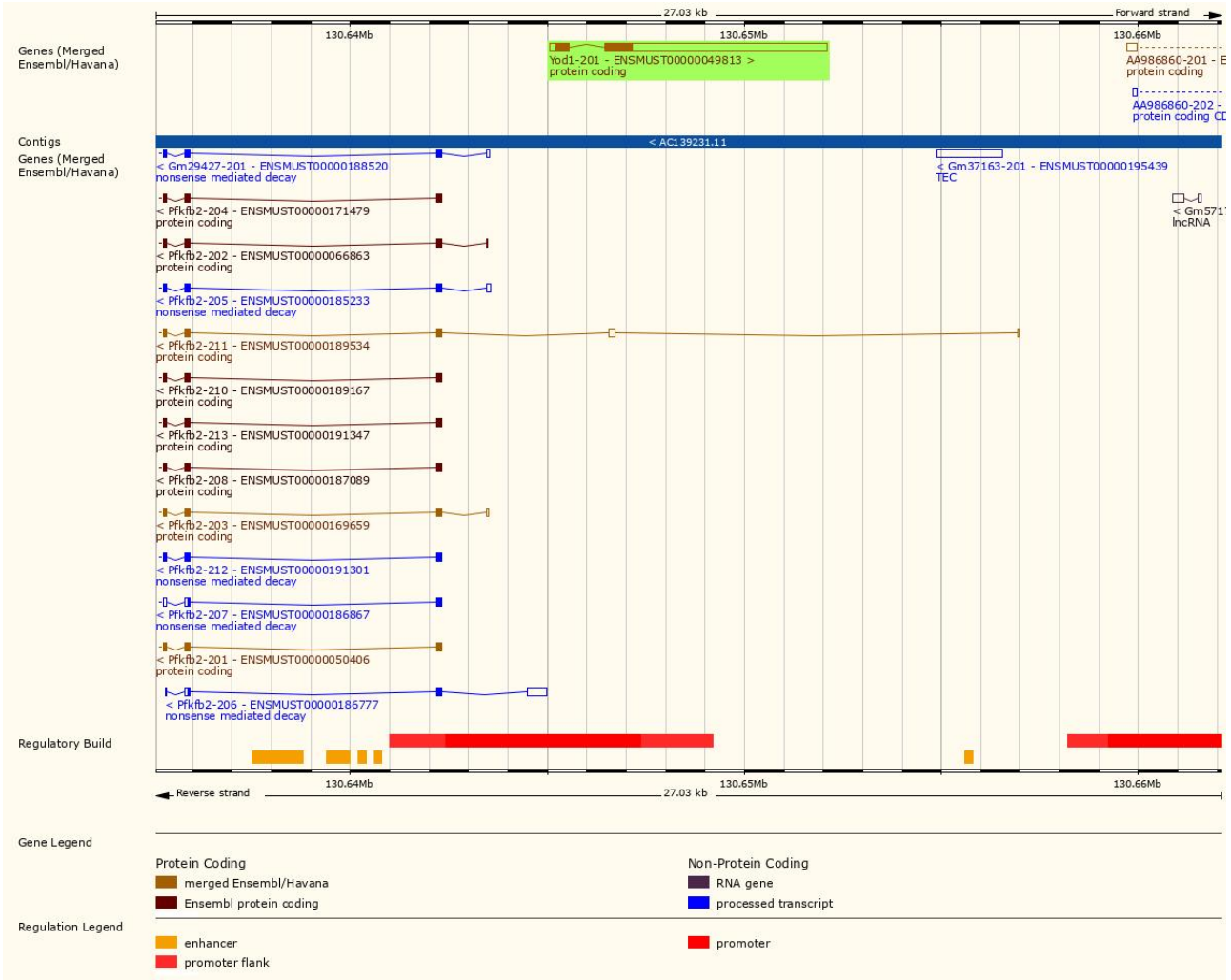
Transcript ID	Name ▲	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000049813.6	Yod1-201	6128	343aa	Protein coding	CCDS48351	Q8CB27	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1

The strategy is based on the design of *Yod1-201* transcript, the transcription is shown below:



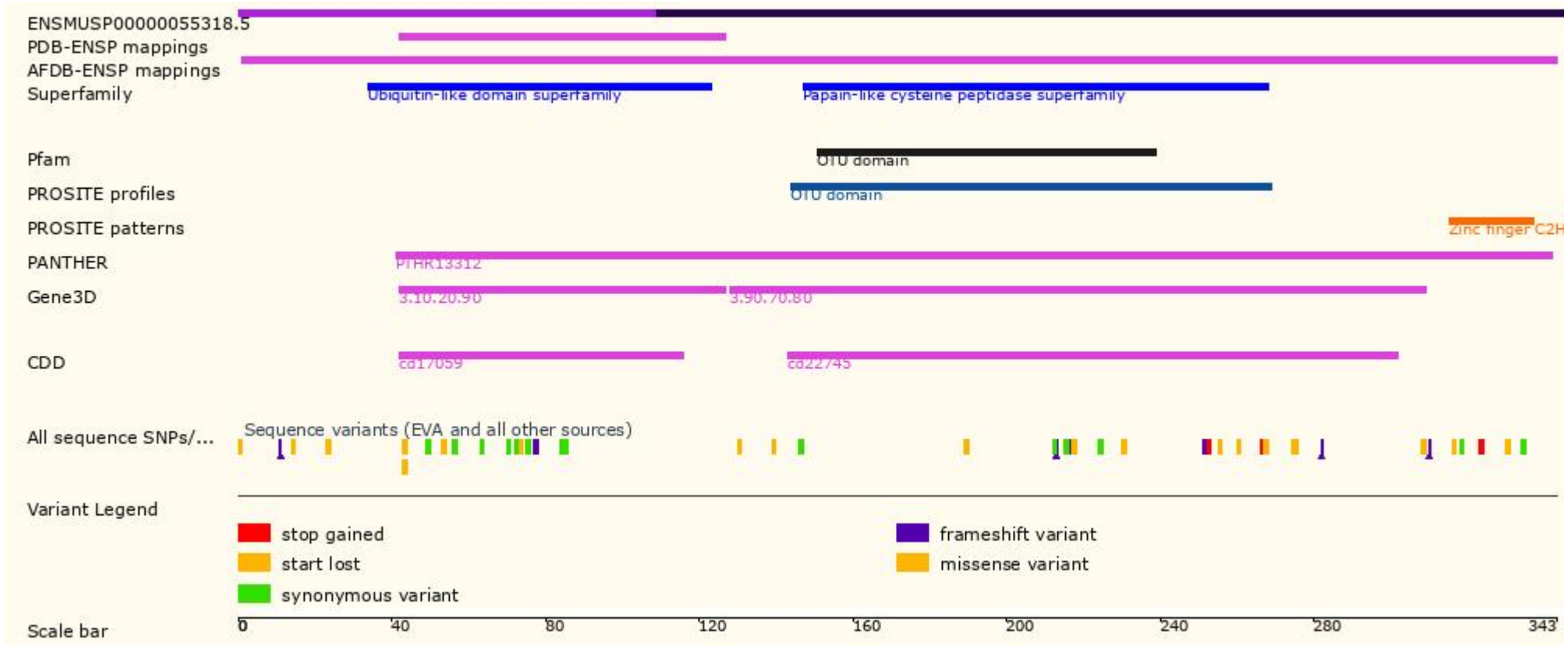
Source: https://www.ensembl.org

Genomic Information



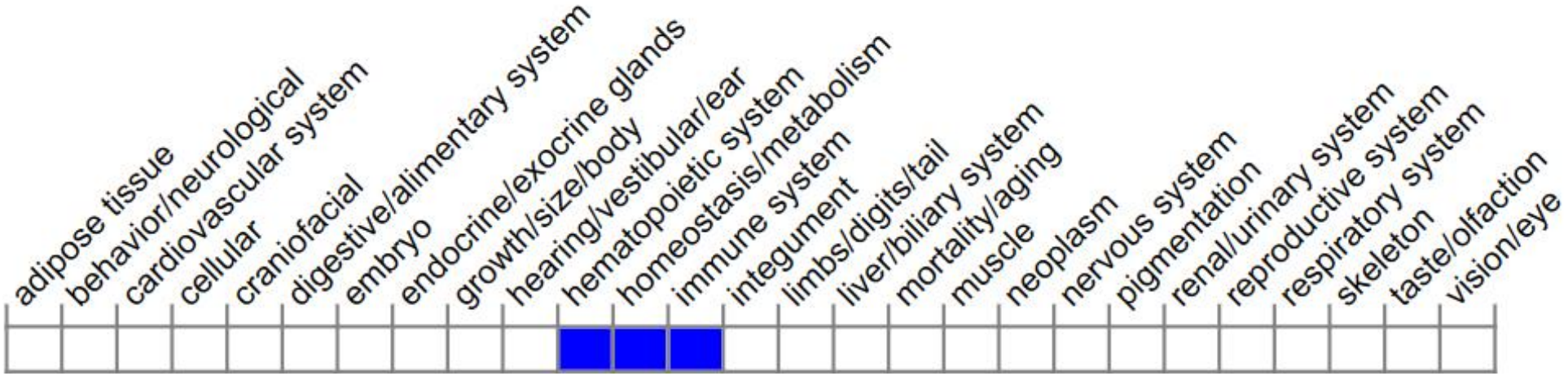
Source: : https://www.ensembl.org

Protein Information



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

Mouse Phenotype Information (MGI)



Source: https://www.informatics.jax.org

Important Information

- The N-terminal of *Yod1* gene will remain 109 aa, it may remain the partial function of *Yod1*.
- The knockout region will delete part of the 5' of *Pfkfb2*, which may affect the expression of *Pfkfb2*.
- The knockout region is about 7.5 kb away from the 5' of *AA986860*, which may affect the regulation of this gene.
- The knockout region is about 4.3 kb away from the 5' of *Gm37163*, which may affect the regulation of this gene.
- *Yod1* is located on Chr 1. 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 risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.