

Pdhb Cas9-CKO Strategy

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Overview

Target Gene Name

- *Pdhb*

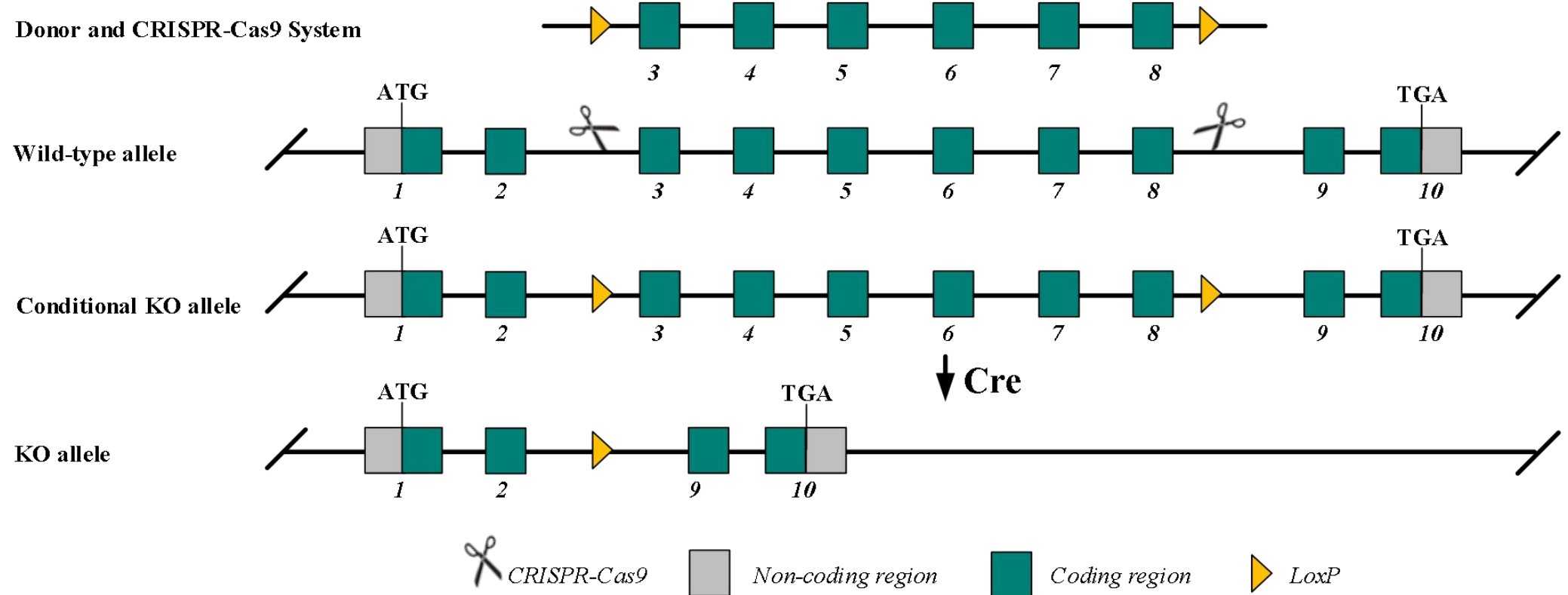
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



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

Technical Information

- The *Pdhb* gene has 7 transcripts. According to the structure of *Pdhb* gene, exon 3-8 of *Pdhb*-201 (ENSMUST00000022268.10) transcript is recommended as the knockout region. The region contains most of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Pdhb* 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

Pdhb pyruvate dehydrogenase (lipoamide) beta [*Mus musculus* (house mouse)]

[Download Datasets](#)

Gene ID: 68263, updated on 7-Sep-2023

Summary

Official Symbol	Pdhb provided by MGI
Official Full Name	pyruvate dehydrogenase (lipoamide) beta provided by MGI
Primary source	MGI:MGI:1915513
See related	Ensembl:ENSMUSG00000021748 AllianceGenome:MGI:1915513
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	2610103L06Rik
Summary	Predicted to enable pyruvate dehydrogenase (acetyl-transferring) activity. Predicted to contribute to pyruvate dehydrogenase (NAD+) activity. Predicted to be involved in acetyl-CoA biosynthetic process from pyruvate. Predicted to act upstream of or within mitochondrial acetyl-CoA biosynthetic process from pyruvate. Located in mitochondrion. Is expressed in several structures, including alimentary system; genitourinary system; heart; integumental system; and nervous system. Human ortholog(s) of this gene implicated in pyruvate decarboxylase deficiency. Orthologous to human PDHB (pyruvate dehydrogenase E1 subunit beta). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in heart adult (RPKM 138.5), placenta adult (RPKM 75.5) and 25 other tissues See more
Orthologs	human all

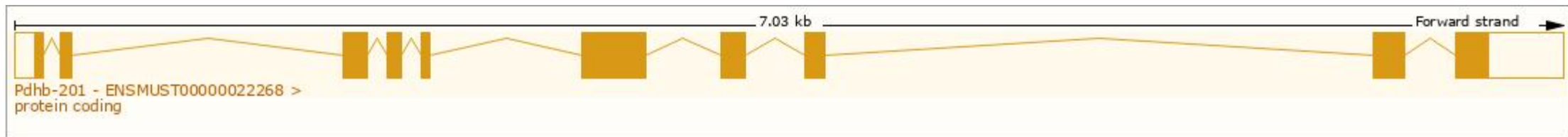
Source: <https://www.ncbi.nlm.nih.gov/gene/68263>

Transcript Information

The gene has 7 transcripts, all transcripts are shown below:

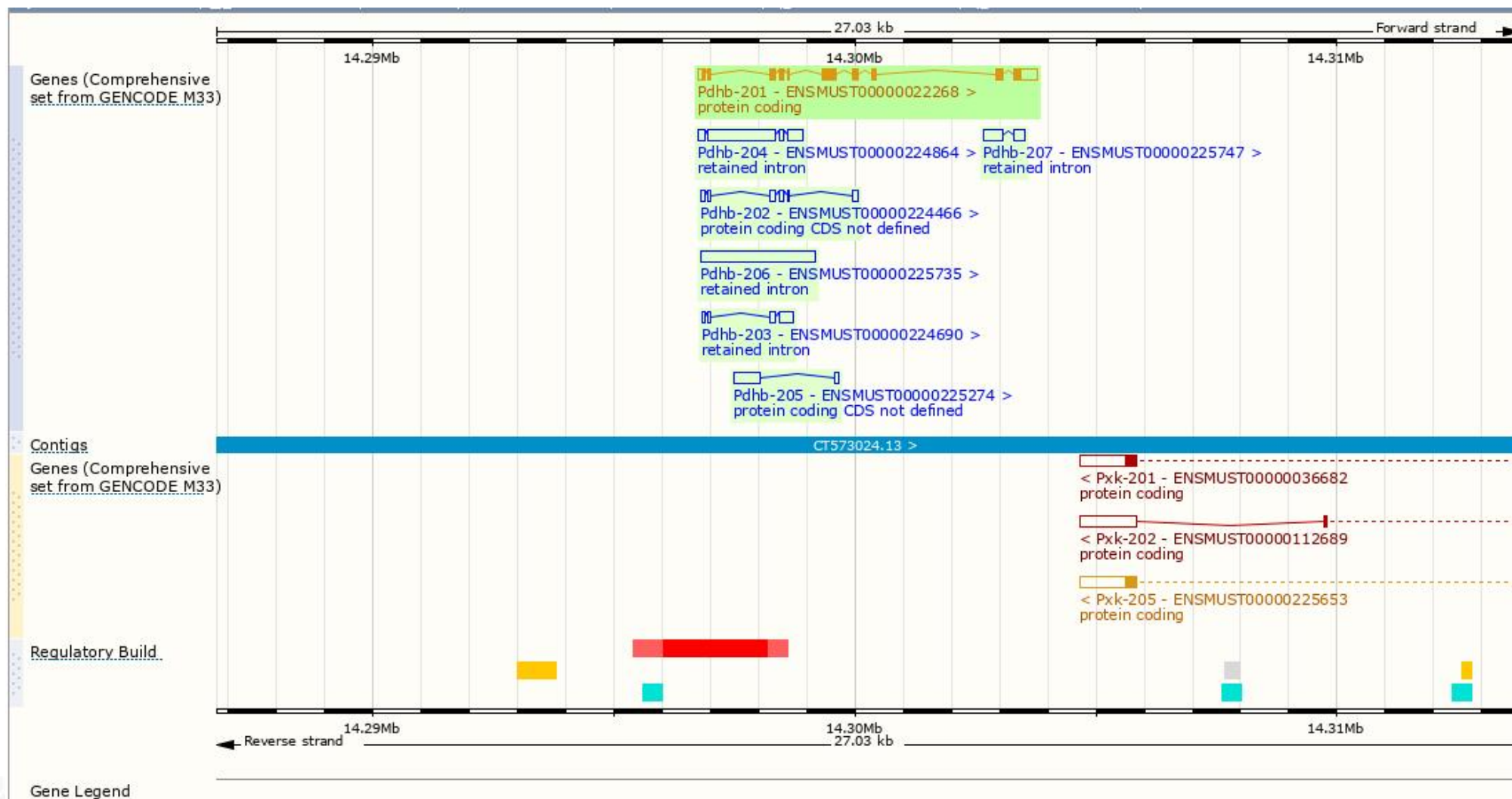
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags			
ENSMUST00000022268.10	Pdhb-201	1513	359aa	Protein coding	CCDS36800	Q9D051	Ensembl Canonical	GENCODE basic	APPRIS P1	TSL:1
ENSMUST000000225274.2	Pdhb-205	644	No protein	Protein coding CDS not defined		-	-	-	-	-
ENSMUST000000224466.2	Pdhb-202	459	No protein	Protein coding CDS not defined		-	-	-	-	-
ENSMUST000000225735.2	Pdhb-206	2377	No protein	Retained intron		-	-	-	-	-
ENSMUST000000224864.2	Pdhb-204	1914	No protein	Retained intron		-	-	-	-	-
ENSMUST000000225747.2	Pdhb-207	620	No protein	Retained intron		-	-	-	-	-
ENSMUST000000224690.2	Pdhb-203	482	No protein	Retained intron		-	-	-	-	-

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

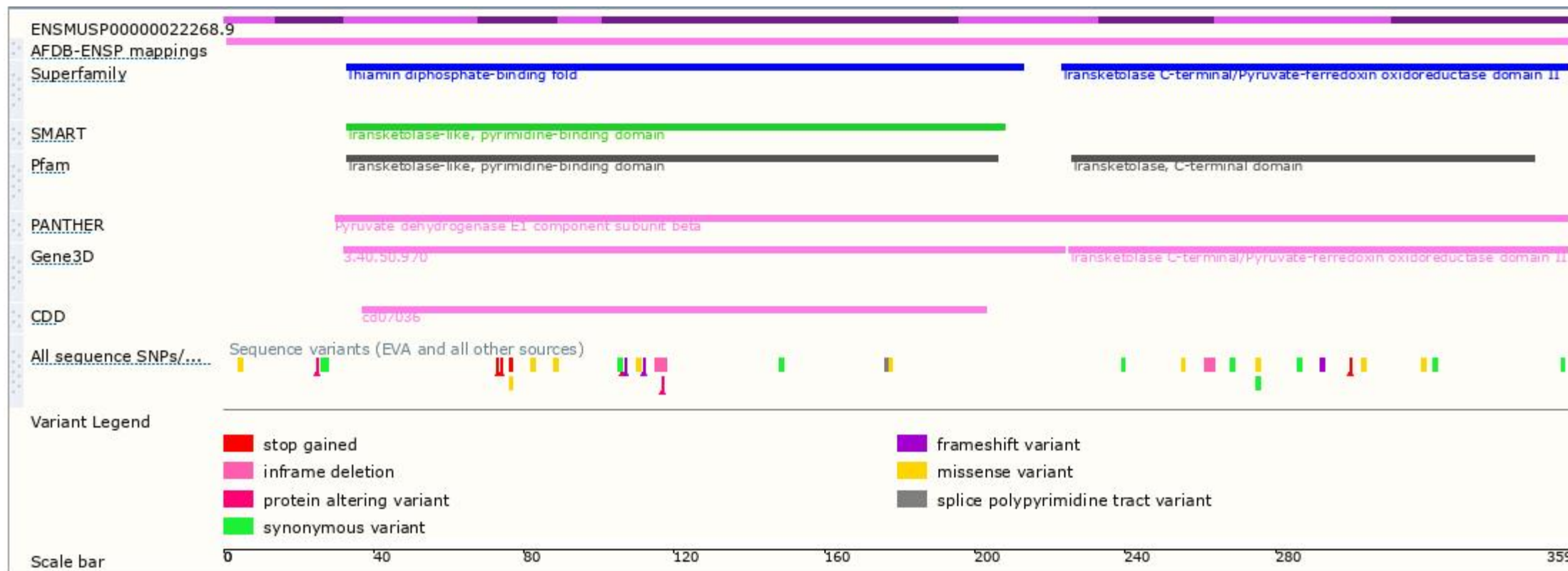


Source: <https://www.ensembl.org>

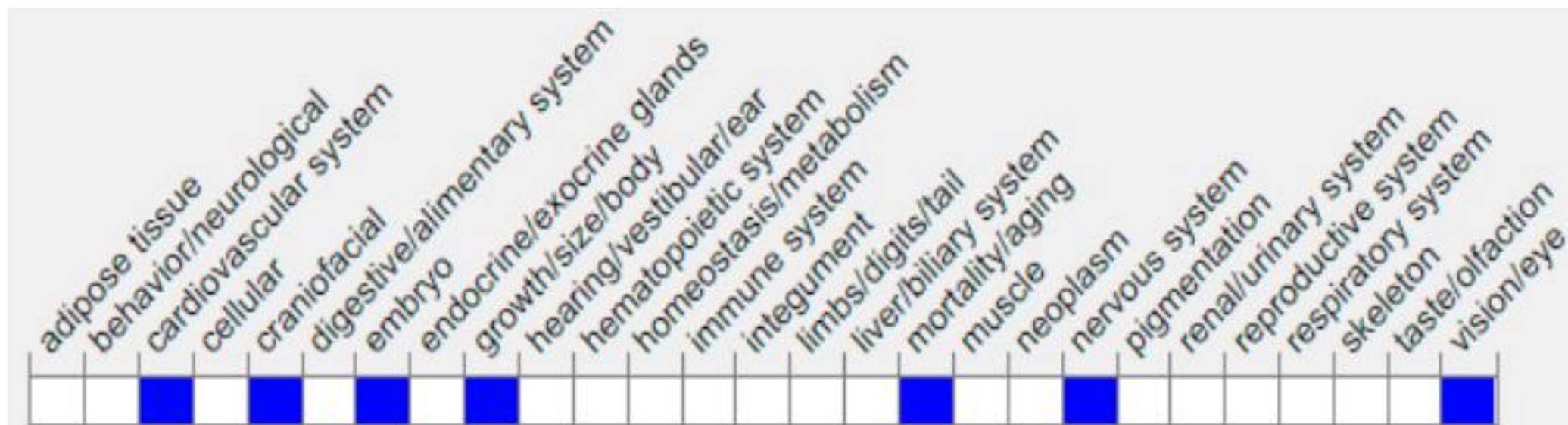
Genomic Information



Protein Information



Mouse Phenotype Description(MGI)



Important Information

- This strategy may result in truncated PDHB proteins.
- The knockout region close to the 3' of *Pxk*, which may affect the regulation of this gene.
- *Pdhb* is located on Chr14. 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.