

Dld Cas9-KO Strategy

Designer:

JiaYu

Reviewer:

Xiaojing Li

Design Date:

2020-1-19

Project Overview

Project Name

Dld

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Dld* gene has 4 transcripts. According to the structure of *Dld* gene, exon2-exon5 of *Dld*-201 (ENSMUST00000110857.4) transcript is recommended as the knockout region. The region contains 298bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dld* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Embryos homozygous for a targeted null mutation exhibit a developmental delay at 7.5 days postcoitum and are resorbed by 9.5 days postcoitum.
- The *Dld* gene is located on the Chr12. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Dld dihydrolipoamide dehydrogenase [Mus musculus (house mouse)]

Gene ID: 13382, updated on 7-Apr-2019

Summary



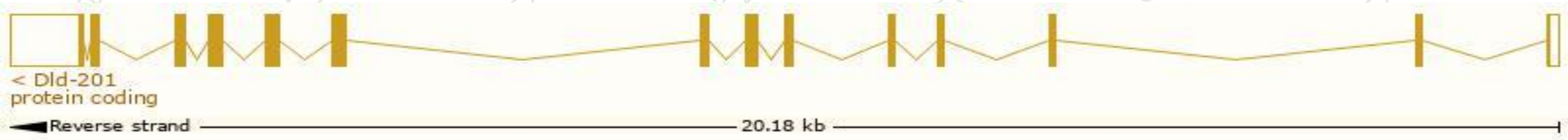
Official Symbol	Dld provided by MGI
Official Full Name	dihydrolipoamide dehydrogenase provided by MGI
Primary source	MGI:MGI:107450
See related	Ensembl:ENSMUSG00000020664
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	This gene encodes a member of the class-I pyridine nucleotide-disulfide oxidoreductase family. The encoded protein has been identified as a moonlighting protein based on its ability to perform mechanistically distinct functions. In homodimeric form, the encoded protein functions as a dehydrogenase and is found in several multi-enzyme complexes that regulate energy metabolism. However, as a monomer, this protein can function as a protease. [provided by RefSeq, Jan 2014]
Expression	Ubiquitous expression in placenta adult (RPKM 46.8), heart adult (RPKM 46.1) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

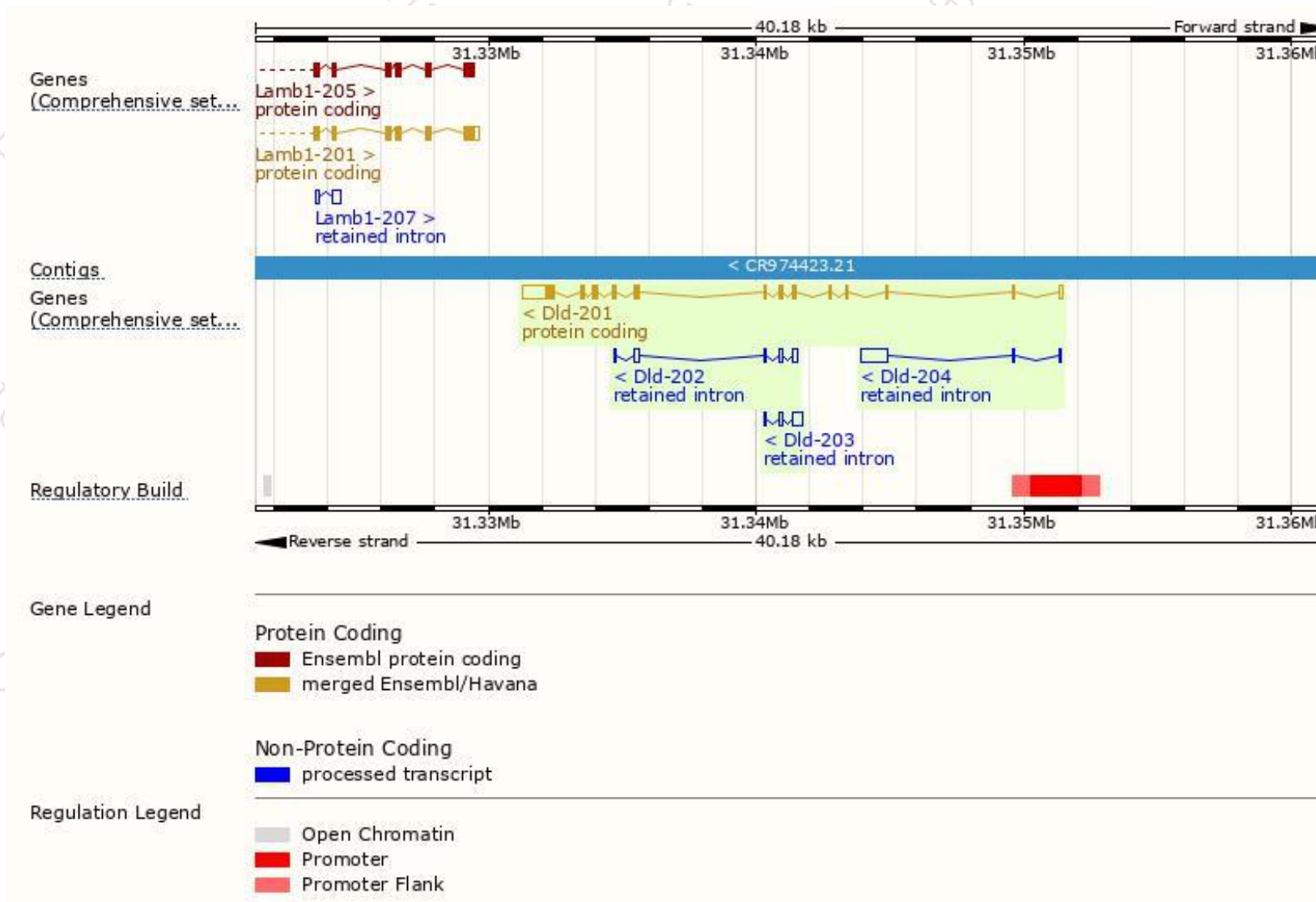
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dld-201	ENSMUST00000110857.4	2544	509aa	Protein coding	CCDS36428	O08749	TSL:1 GENCODE basic APPRIS P1
Dld-204	ENSMUST00000220415.1	1176	No protein	Retained intron	-	-	TSL:1
Dld-202	ENSMUST00000218624.1	661	No protein	Retained intron	-	-	TSL:2
Dld-203	ENSMUST00000219213.1	583	No protein	Retained intron	-	-	TSL:3

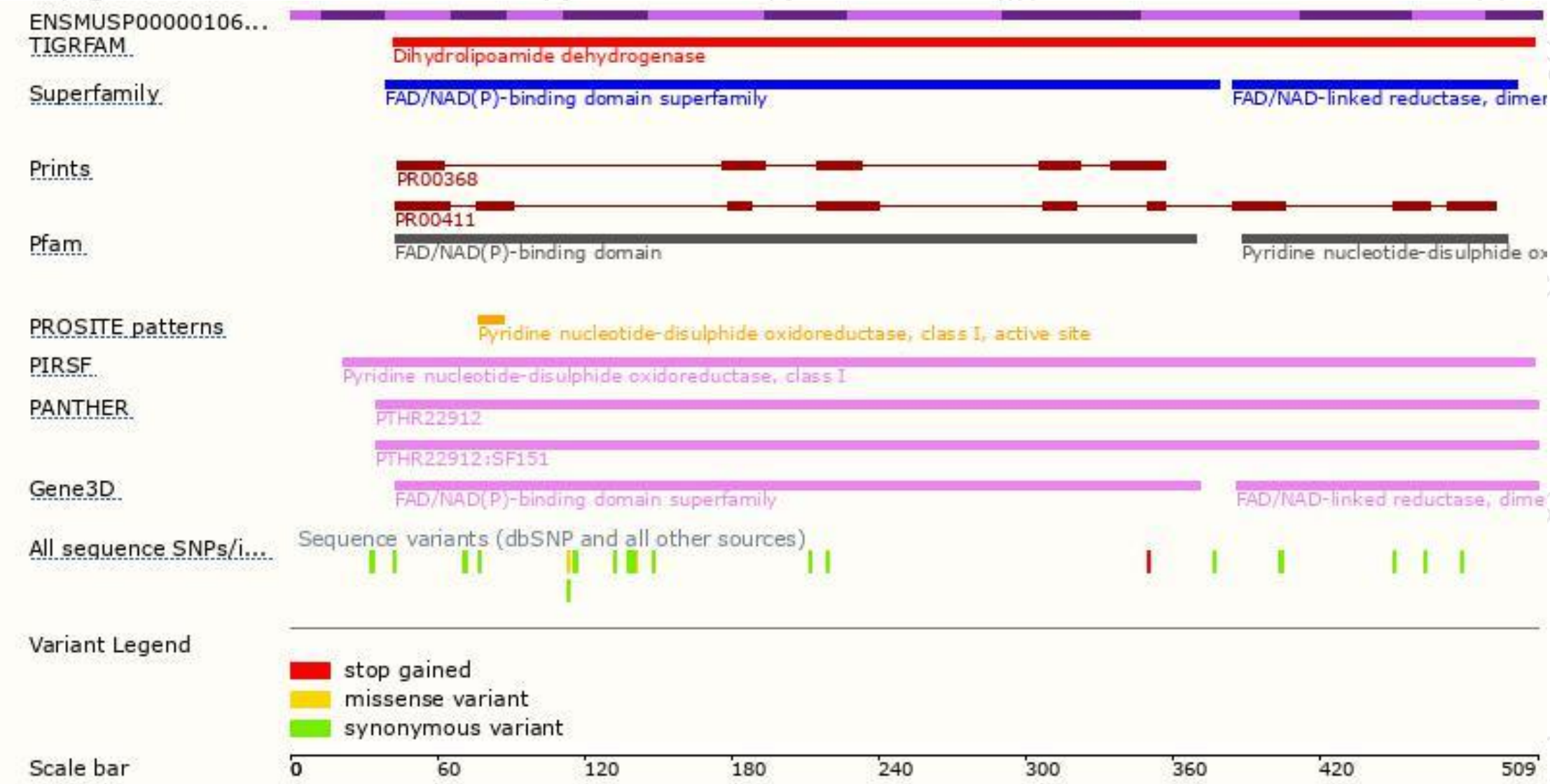
The strategy is based on the design of *Dld-201* transcript,The transcription is shown below



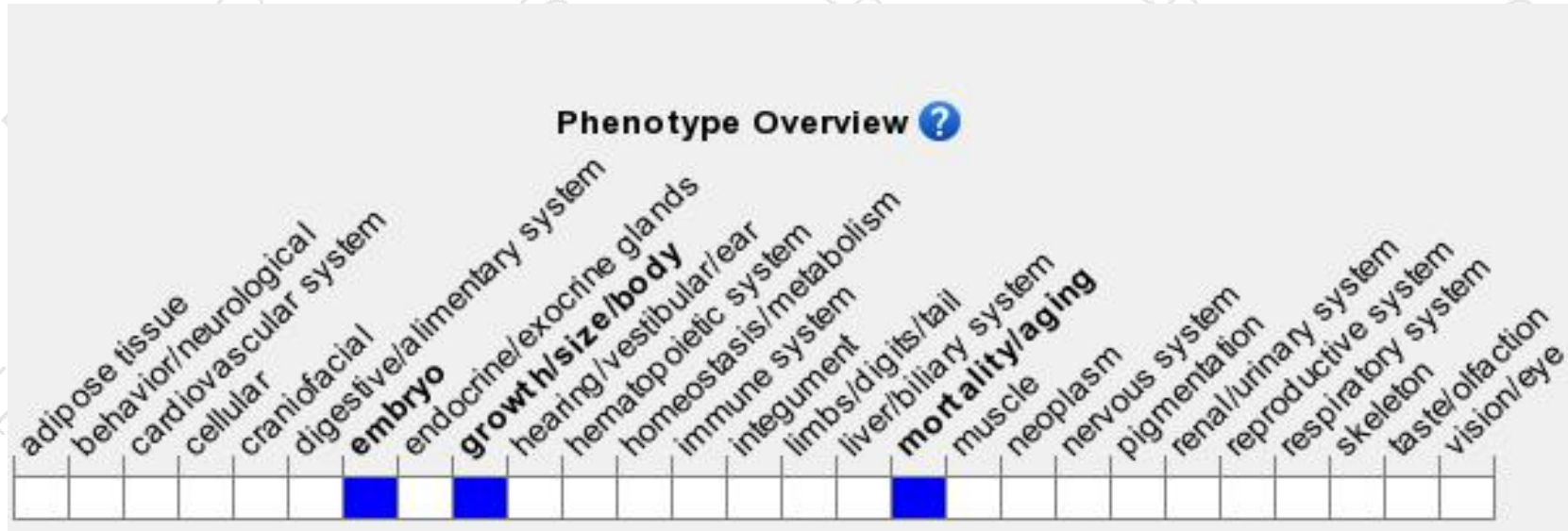
Genomic location distribution



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, Embryos homozygous for a targeted null mutation exhibit a developmental delay at 7.5 days postcoitum and are resorbed by 9.5 days postcoitum.

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

Tel: 400-9660890

