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Pfdn2 Cas9-CKO Strategy

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Design Date: 2022-10-17

Overview

Target Gene Name

- Pfdn2

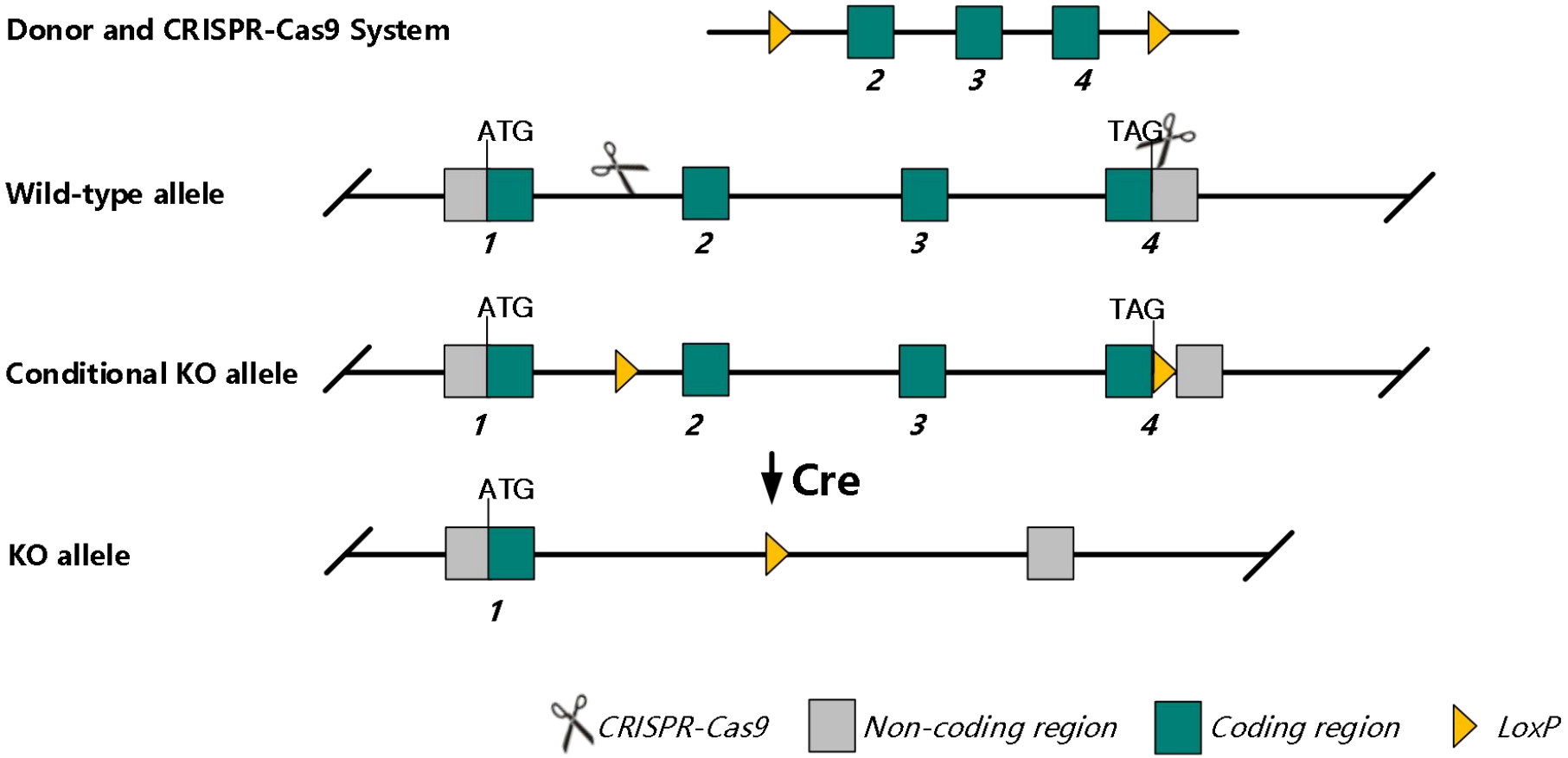
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Pfdn2* gene.

Technical Information

- The *Pfdn2* gene has 3 transcripts. According to the structure of *Pfdn2* gene, exon2-4 of *Pfdn2*-202 (ENSMUST00000135941.8) transcript is recommended as the knockout region. The region contains most of the coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Pfdn2* 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

Pfdn2 prefoldin 2 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 18637, updated on 26-Sep-2022

Summary

Official Symbol	Pfdn2 provided by MGI
Official Full Name	prefoldin 2 provided by MGI
Primary source	MGI:MGI:1276111
See related	Ensembl:ENSMUSG00000006412 AllianceGenome:MGI:1276111
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	ESTM27
Summary	Predicted to enable amyloid-beta binding activity; protein folding chaperone; and unfolded protein binding activity. Acts upstream of or within protein folding. Predicted to be located in cytosol; mitochondrion; and nucleus. Predicted to be part of prefoldin complex. Predicted to be active in cytoplasm. Orthologous to human PFDN2 (prefoldin subunit 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in CNS E11.5 (RPKM 48.2), CNS E14 (RPKM 27.8) and 28 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

Genomic context

Location: 1 H3; 1 79.35 cM — See Pfdn2 in Genome Data Viewer

Exon count: 5

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

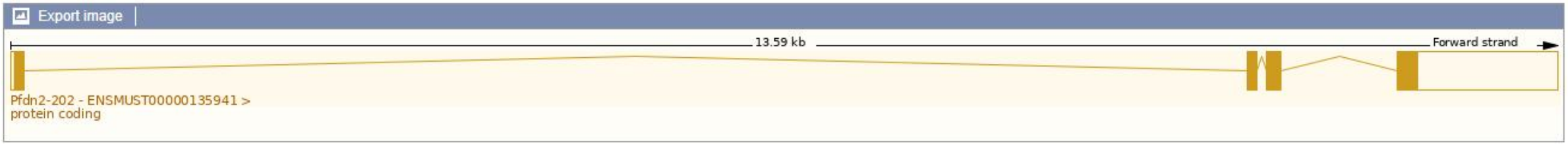
Transcript Information

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

Show/hide columns (1 hidden) Filter

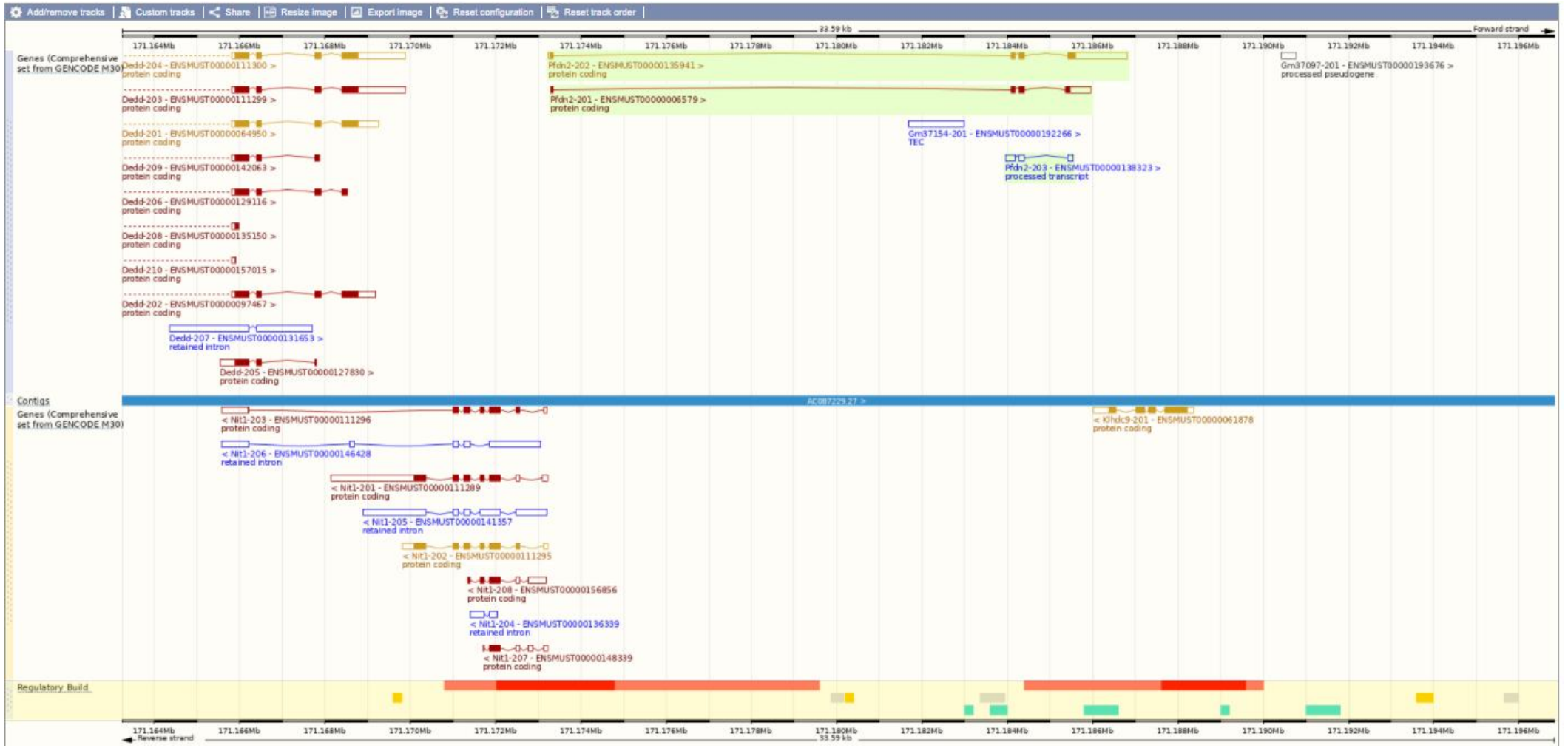
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match ▲	Flags
ENSMUST00000006579.5	Pfdn2-201	885	129aa	Protein coding		F8WJ30	TSL:3 CDS 5' incomplete
ENSMUST00000135941.8	Pfdn2-202	1735	154aa	Protein coding	CCDS15491	O70591	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000138323.2	Pfdn2-203	474	No protein	Processed transcript		-	TSL:2

The strategy is based on the design of *Pfdn2*-202 transcript, the transcription is shown below:



Source: https://www.ensembl.org

Genomic Information



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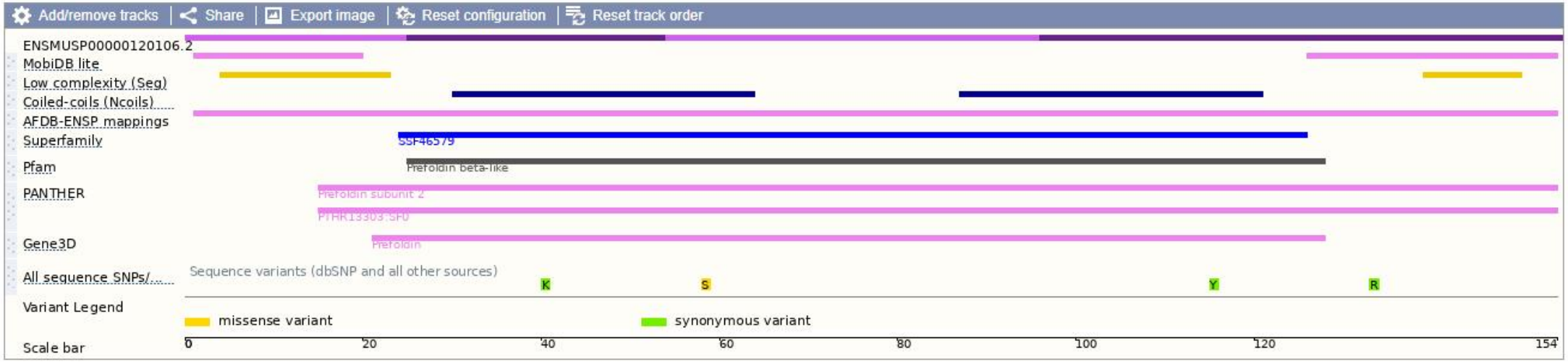
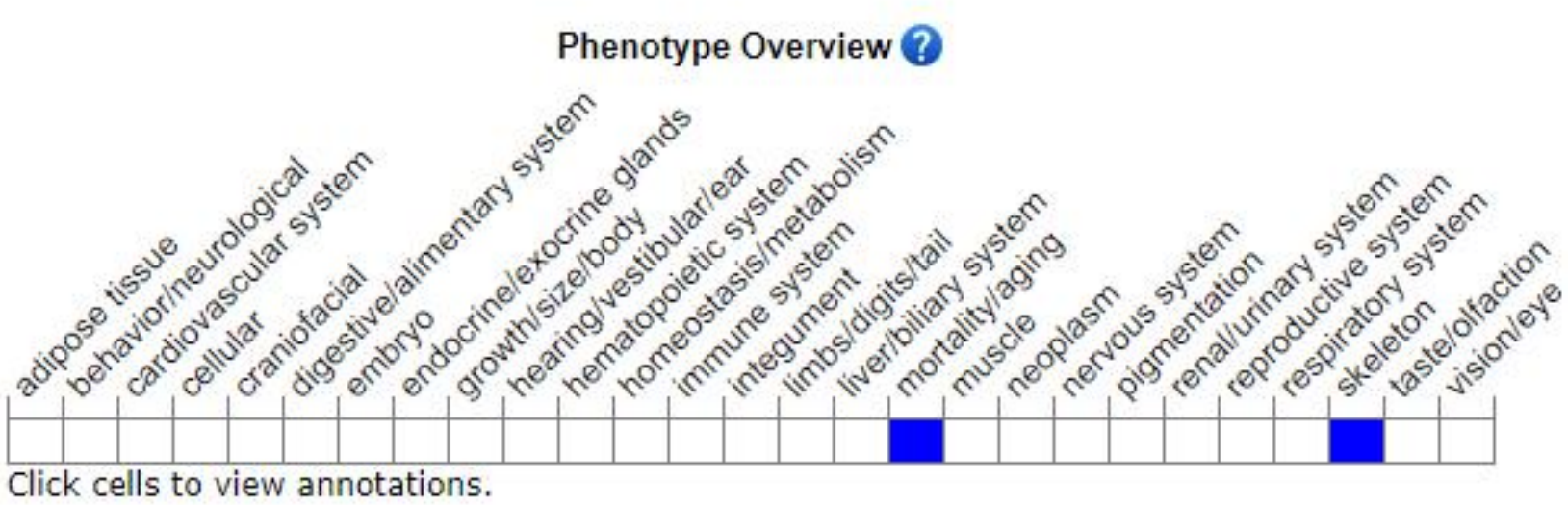
Source: : https://www.ensembl.org

Protein Information



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

Mouse Phenotype Information (MGI)



- Phenotypes affected by the mutations of *Pfdn2* gene are marked in blue. Mice homozygous for a transgenic gene disruption exhibit embryonic lethality at E6.

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

Important Information

- The second Loxp site is inserted after the stop coden, may affect the *Pfdn2* gene regulation function.
- Knockout the region may affect its function of *Klhdc9* gene.
- *Pfdn2* is located on Chr1. 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.