GemPharmatech™

Far1 Cas9-KO Strategy

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Reviewer: Xingkai Xiao

Design Date: 2024-1-22

Overview

Target Gene Name

- *Far1*

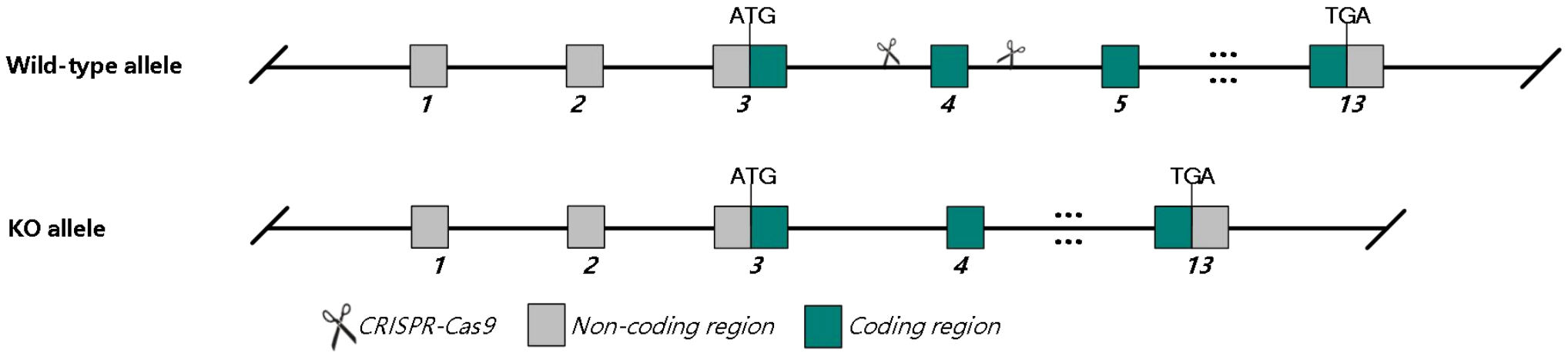
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Far1* gene.

Technical Information

- The *Far1* gene has 11 transcripts. According to the structure of *Far1* gene, exon 4 of *Far1*-201 (ENSMUST00000033018.15) is recommended as the knockout region. The region contains 176 bp of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Far1* 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

Far1 fatty acyl CoA reductase 1 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 67420, updated on 23-Nov-2023

Summary

Official Symbol	Far1 provided by MGI
Official Full Name	fatty acyl CoA reductase 1 provided by MGI
Primary source	MGI:MGI:1914670
See related	Ensembl:ENSMUSG00000030759 AllianceGenome:MGI:1914670
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	Mlstd2; 2600011M19Rik; 2900034E22Rik; 3732409C05Rik
Summary	Enables fatty-acyl-CoA reductase (alcohol-forming) activity. Involved in wax biosynthetic process. Located in peroxisome. Orthologous to human FAR1 (fatty acyl-CoA reductase 1). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in bladder adult (RPKM 22.8), CNS E18 (RPKM 14.0) and 22 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**
Try the new Transcript table

Genomic context

Location: 7 F1; 7 59.21 cM — See Far1 in Genome Data Viewer

Exon count: 15

https://www.ncbi.nlm.nih.gov/gene/67420

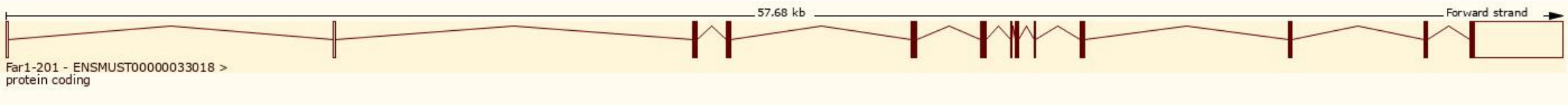
Transcript Information

The gene has 11 transcripts, all transcripts are shown below:

Show/hide columns (1 hidden) Filter

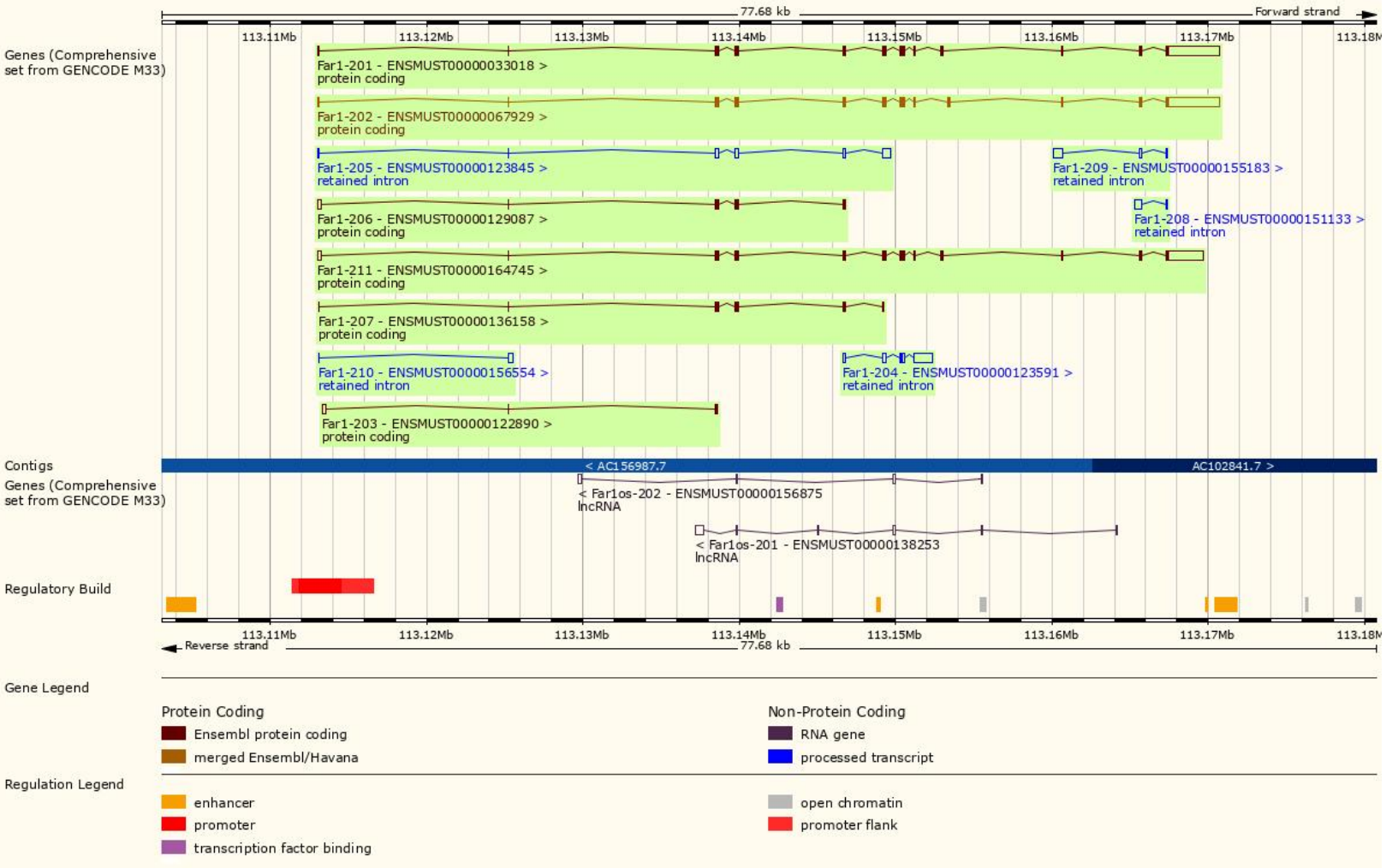
Transcript ID	Name ▲	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000033018.15	Far1-201	4962	515aa	Protein coding	CCDS40093	Q922J9	Ensembl Canonical GENCODE basic APPRIS P3 TSL:1
ENSMUST00000067929.15	Far1-202	4935	515aa	Protein coding	CCDS72024	Q922J9-3	GENCODE basic APPRIS ALT1 TSL:1
ENSMUST00000122890.2	Far1-203	445	37aa	Protein coding		D3Z072	TSL:3 CDS 3' incomplete
ENSMUST00000123591.2	Far1-204	1674	No protein	Retained intron		-	TSL:1
ENSMUST00000123845.8	Far1-205	1218	No protein	Retained intron		-	TSL:1
ENSMUST00000129087.8	Far1-206	769	181aa	Protein coding		D3Z5W6	TSL:3 CDS 3' incomplete
ENSMUST00000136158.8	Far1-207	733	206aa	Protein coding		D3Z4N9	TSL:3 CDS 3' incomplete
ENSMUST00000151133.2	Far1-208	524	No protein	Retained intron		-	TSL:2
ENSMUST00000155183.2	Far1-209	775	No protein	Retained intron		-	TSL:2
ENSMUST00000156554.2	Far1-210	413	No protein	Retained intron		-	TSL:2
ENSMUST00000164745.8	Far1-211	3972	515aa	Protein coding	CCDS40093	Q922J9	GENCODE basic APPRIS P3 TSL:5

The strategy is based on the design of *Far1*-201 transcript, the transcription is shown below:



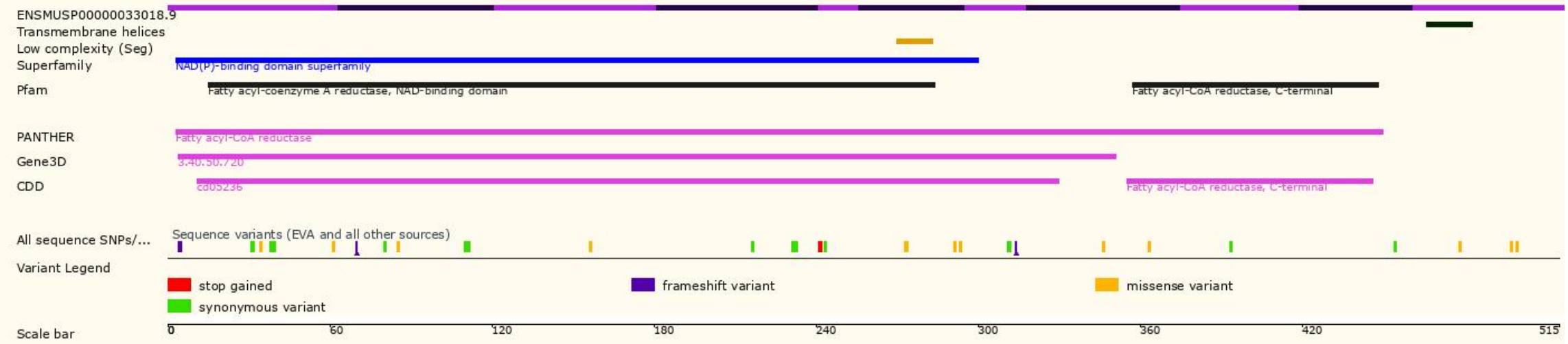
Source: http://asia.ensembl.org/

Genomic Information



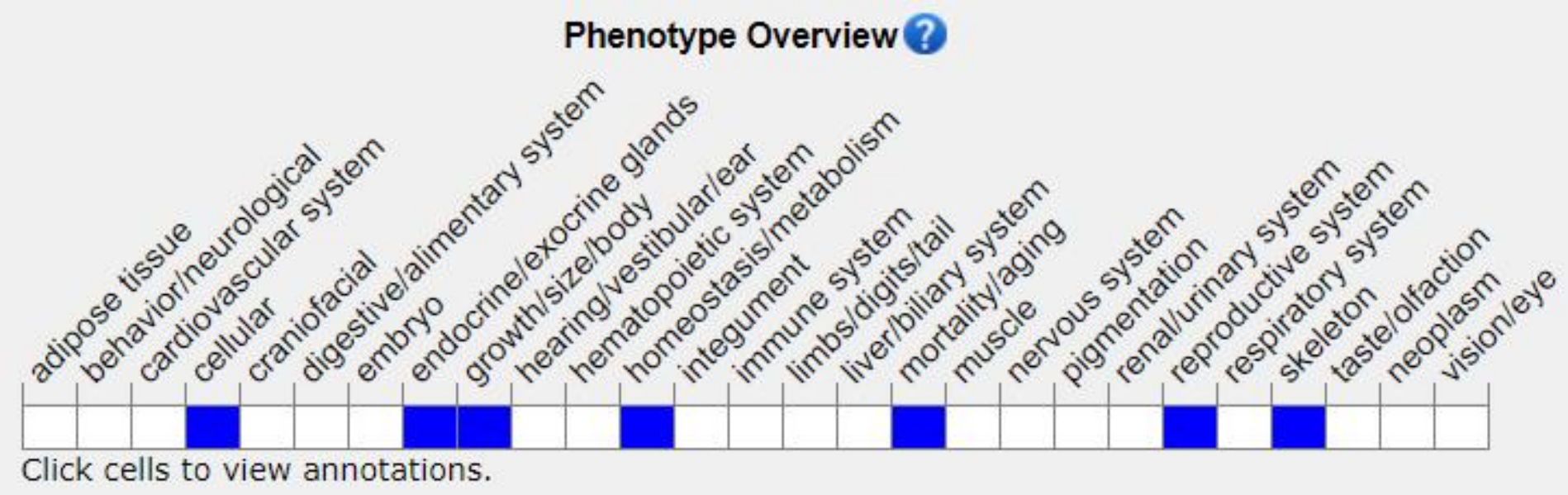
Source: http://asia.ensembl.org/

Protein Information



Source: https://www.ensembl.org

Mouse Phenotype Information (MGI)



Mice homozygous for a null allele show partial preweaning lethality, postnatal growth retardation, small testes, and male infertility associated with azoospermia, spermatogenesis arrest, disrupted intercellular bridge formation, multinucleated giant germ cells, and increased male germ cell apoptosis.

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

Important Information

- The knockout region overlaps with *Far1os* gene, which may affect the function of this gene.
- This stratergy may not affect *Far1*-203, *Far1*-204, *Far1*-208 and *Far1*-209 transcript.
- *Far1* is located on Chr 7. 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.