

Atp5f1d Cas9-KO Strategy

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Overview

Target Gene Name

- Atp5f1d

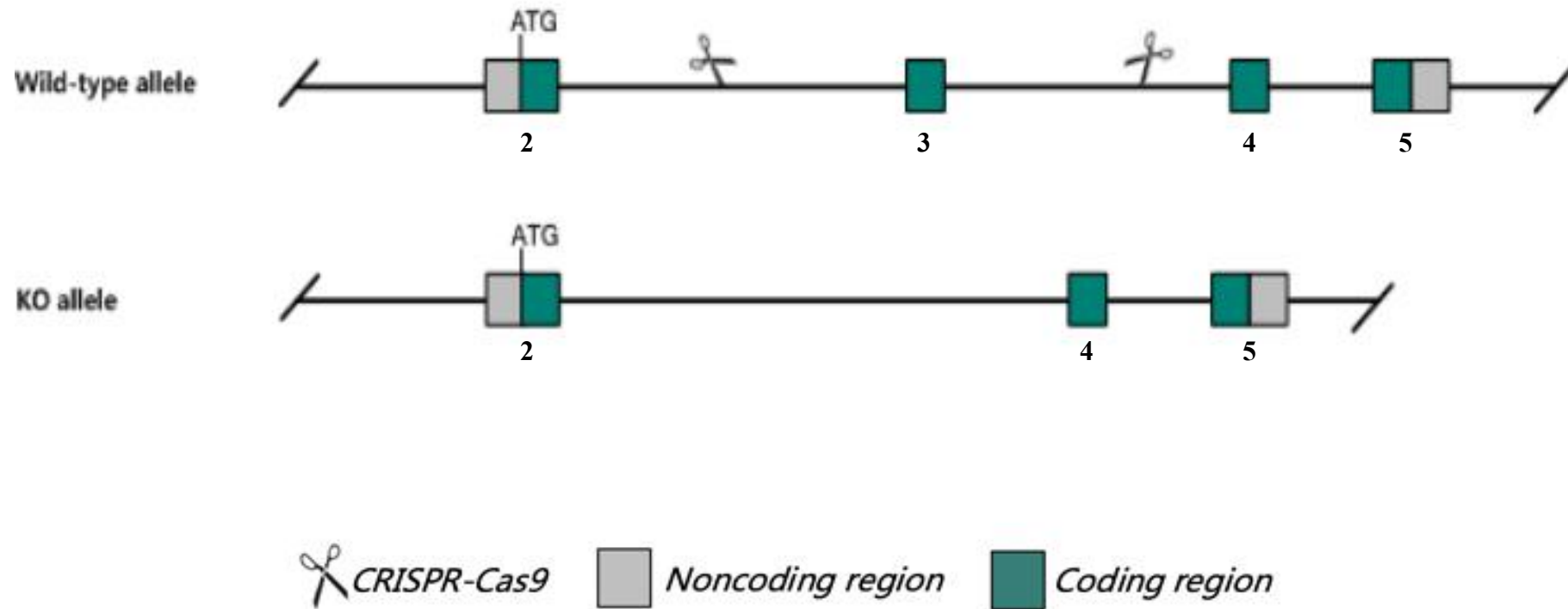
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Technical Information

- The *Atp5f1d* gene has 4 transcripts. According to the structure of *Atp5f1d* gene, exon3 of *Atp5d-203* (ENSMUST00000105367.8) transcript is recommended as the knockout region. The region contains 154bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Atp5f1d* 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

Atp5f1d ATP synthase F1 subunit delta [*Mus musculus* (house mouse)]

Gene ID: 66043, updated on 11-Apr-2024

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Summary

Official Symbol	Atp5f1d provided by MGI
Official Full Name	ATP synthase F1 subunit delta provided by MGI
Primary source	MGI:MGI:1913293
See related	Ensembl:ENSMUSG00000003072 AllianceGenome:MGI:1913293
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	Atp5d; 0610008F14Rik; 1500000I11Rik
Summary	Predicted to enable proton transmembrane transporter activity. Predicted to contribute to ATP hydrolysis activity and proton-transporting ATP synthase activity, rotational mechanism. Predicted to be involved in mitochondrial ATP synthesis coupled proton transport and mitochondrial proton-transporting ATP synthase complex assembly. Predicted to act upstream of or within proton transmembrane transport. Located in mitochondrial inner membrane. Is expressed in several structures, including alimentary system; eye; genitourinary system; integumental system; and nervous system. Human ortholog(s) of this gene implicated in mitochondrial complex V (ATP synthase) deficiency. Orthologous to human ATP5F1D (ATP synthase F1 subunit delta). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in duodenum adult (RPKM 1424.1), adrenal adult (RPKM 1222.1) and 23 other tissues See more
Orthologs	human all
NEW	Try the new Gene table
	Try the new Transcript table

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

Transcript Information

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

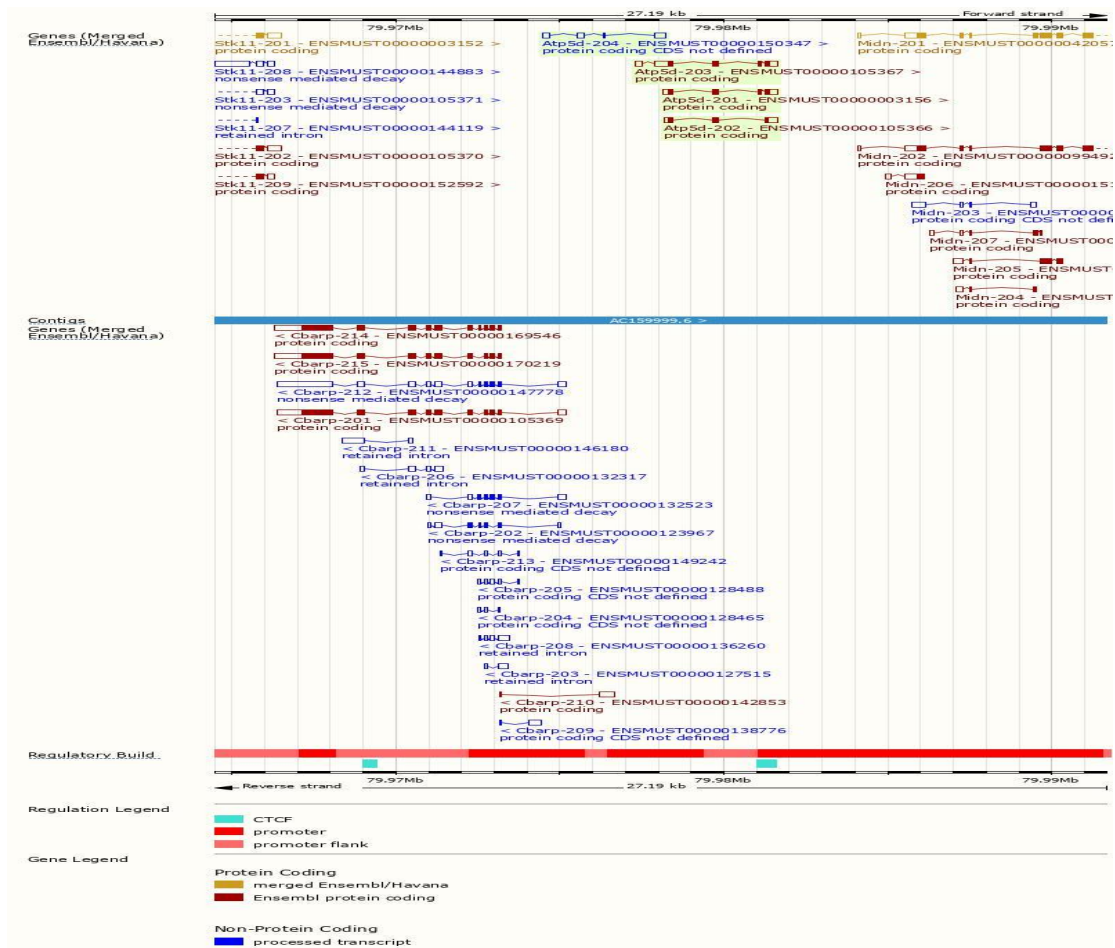
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000105367.8	Atp5f1d-203	1410	168aa	Protein coding	CCDS24010	Q4FK74 Q9D3D9	Ensembl Canonical Gencode basic APPRIS P1 TSL:5
ENSMUST00000003156.15	Atp5f1d-201	931	168aa	Protein coding	CCDS24010	Q4FK74 Q9D3D9	Gencode basic APPRIS P1 TSL:1
ENSMUST00000105366.2	Atp5f1d-202	781	121aa	Protein coding	CCDS83726	D3Z7S4	Gencode basic TSL:2
ENSMUST00000150347.2	Atp5f1d-204	873	No protein	Protein coding CDS not defined		-	TSL:3

The strategy is based on the design of *Atp5f1d*-203 transcript, the transcription is shown below:

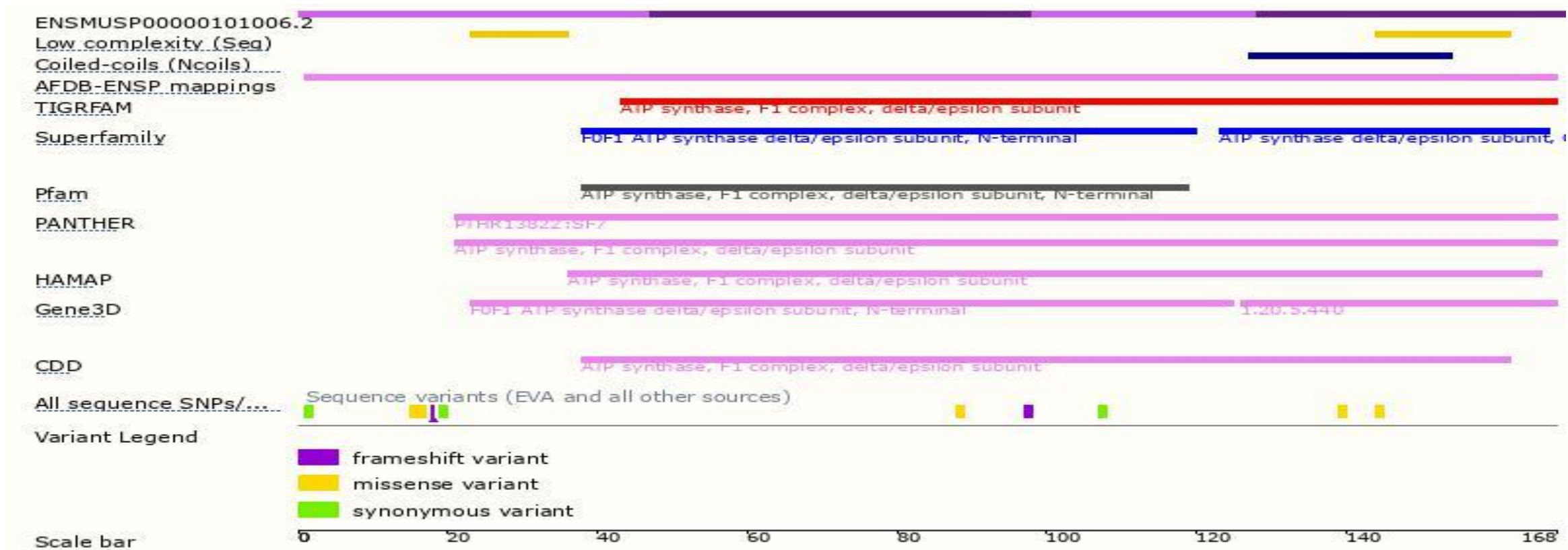


Source: <https://www.ensembl.org>

Genomic Information



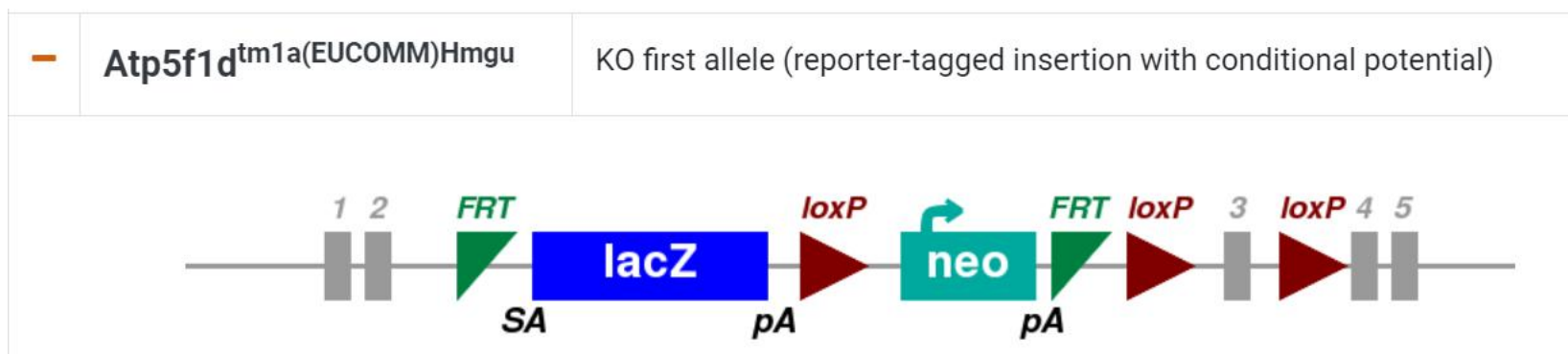
Protein Information



Important Information

- According to MGI information, the gene knockout homozygous mice died before weaning.
- The knockout region of this strategy is closer to the 5-terminus of the *Cbap* and *Midn* genes, which may affect the regulation of the 5-terminus of the *Cbap* and *Midn* genes.
- *Atp5f1d* is located on Chr10. 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.

Reference



<https://www.mousephenotype.org/data/genes/MGI:1913293>