

Atp5h Cas9-KO Strategy

Designer: Fang Wang

Reviewer: DaoHua Xu

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Overview

Target Gene Name

- Atp5h

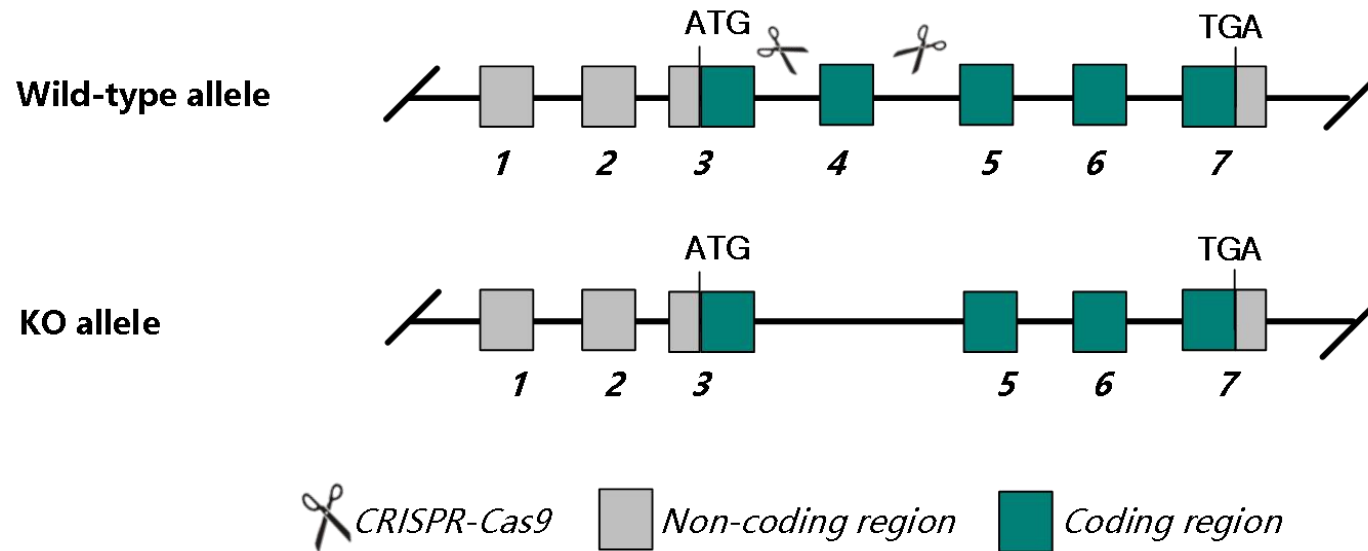
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Atp5h* gene.

Technical Information

- The *Atp5b* gene has 8 transcripts. According to the structure of *Atp5b* gene, exon 4 of *Atp5b*-203(ENSMUST00000106537.8) transcript is recommended as the knockout region. The region contains 97bp coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Atp5b* 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

Atp5h ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit D [*Mus musculus* (house mouse)]

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Gene ID: 71679, updated on 15-Mar-2023

Summary

Official Symbol	Atp5h provided by MGI
Official Full Name	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit D provided by MGI
Primary source	MGI:MGI:1918929
See related	Ensembl:ENSMUSG00000034566 AllianceGenome:MGI:1918929
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	Atp5pd; 0610009D10Rik
Summary	Predicted to enable proton transmembrane transporter activity. Predicted to contribute to proton-transporting ATP synthase activity, rotational mechanism. Predicted to be involved in mitochondrial ATP synthesis coupled proton transport. Predicted to act upstream of or within ion transport. Located in mitochondrion. Is expressed in several structures, including alimentary system; integumental system; nervous system; respiratory system; and sensory organ. Orthologous to human ATP5PD (ATP synthase peripheral stalk subunit d). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in heart adult (RPKM 94.5), CNS E11.5 (RPKM 81.5) and 25 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

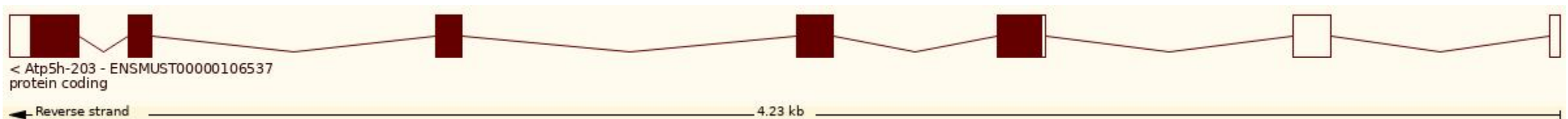
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 8 transcripts, all transcripts are shown below:

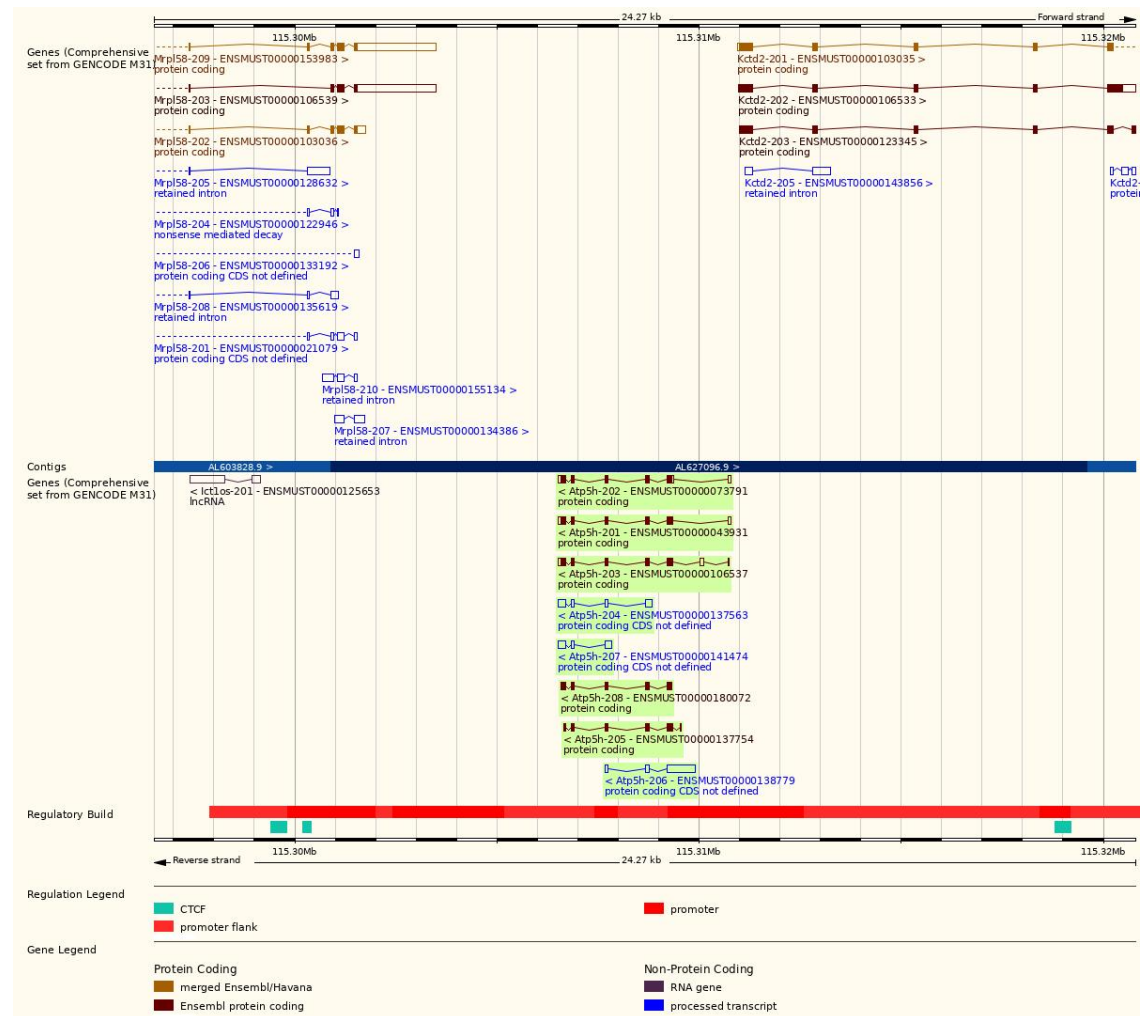
Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
ENSMUST00000043931.9	Atp5h-201	625	161aa	Protein coding	CCDS25633	Q9DCX2	GENCODE basic	APPRIS P1 TSL:1
ENSMUST00000073791.10	Atp5h-202	659	161aa	Protein coding	CCDS25633	Q9DCX2	GENCODE basic	APPRIS P1 TSL:5
ENSMUST00000106537.8	Atp5h-203	682	161aa	Protein coding	CCDS25633	Q9DCX2	Ensembl Canonical	GENCODE basic APPRIS P1 TSL:5
ENSMUST00000137563.8	Atp5h-204	510	No protein	Protein coding CDS not defined		-	TSL:2	
ENSMUST00000137754.2	Atp5h-205	468	138aa	Protein coding		B1ASE2	TSL:3 CDS 3' incomplete	
ENSMUST00000138779.2	Atp5h-206	857	No protein	Protein coding CDS not defined		-	TSL:2	
ENSMUST00000141474.8	Atp5h-207	420	No protein	Protein coding CDS not defined		-	TSL:2	
ENSMUST00000180072.8	Atp5h-208	486	161aa	Protein coding	CCDS25633	Q9DCX2	GENCODE basic	APPRIS P1 TSL:2

The strategy is based on the design of *Atp5h*-203 transcript, the transcription is shown below:

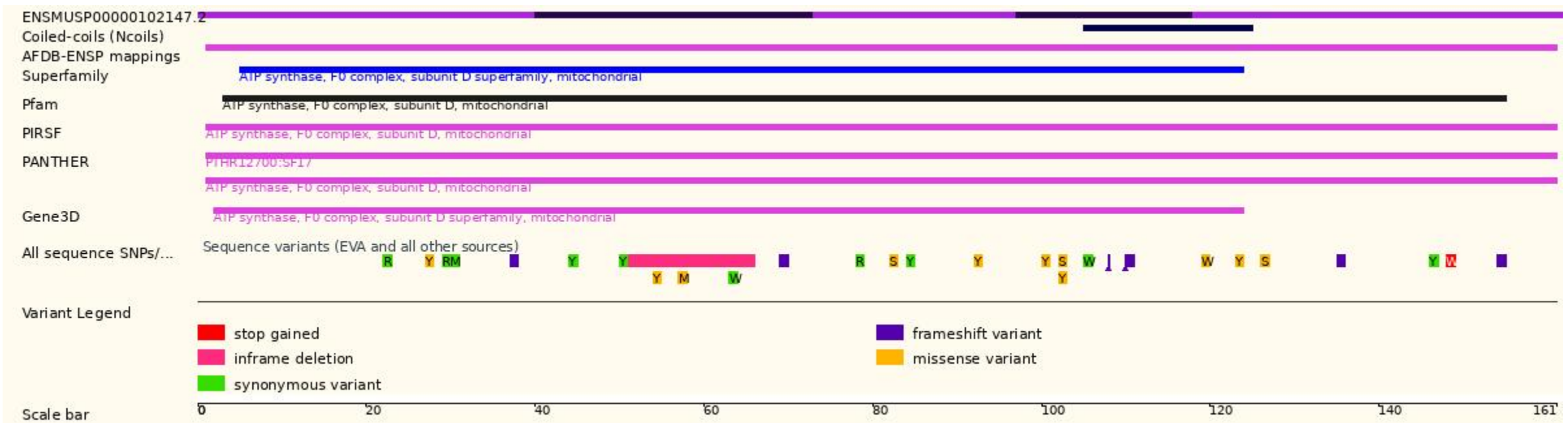


Source: <https://www.ensembl.org>

Genomic Information



Protein Information



Important Information

- The effect of *Kctd2* gene is unknown.
- The effect of this strategy on the *Atp5b* -207 transcript is unknown.
- *Atp5b* is located on Chr 11. 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.