

Atp5h Cas9-CKO Strategy

Designer: Fang Wang

Reviewer: DaoHua Xu

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Overview

Target Gene Name

- Atp5h

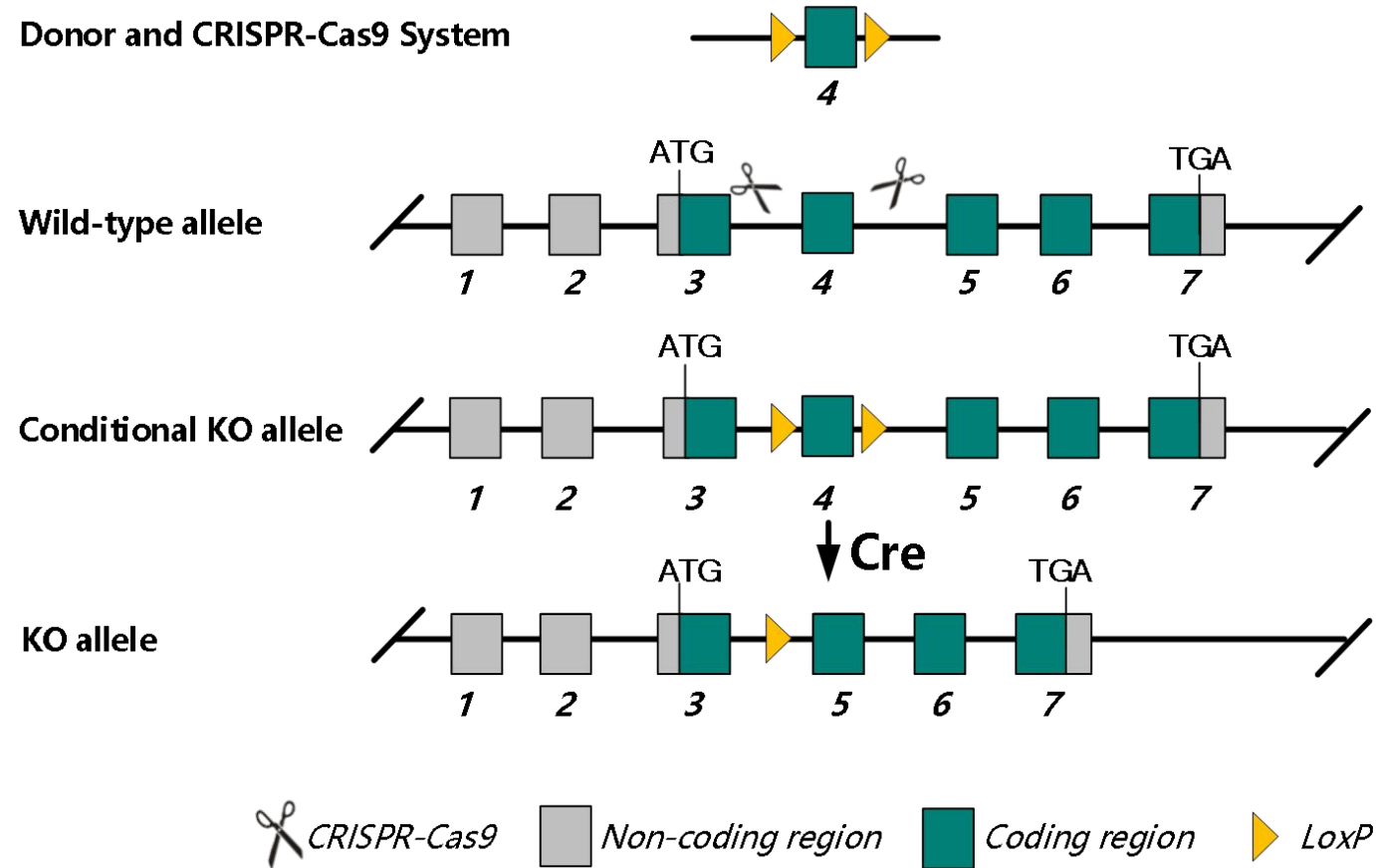
Project Type

- Cas9-CKO

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: 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

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](#)

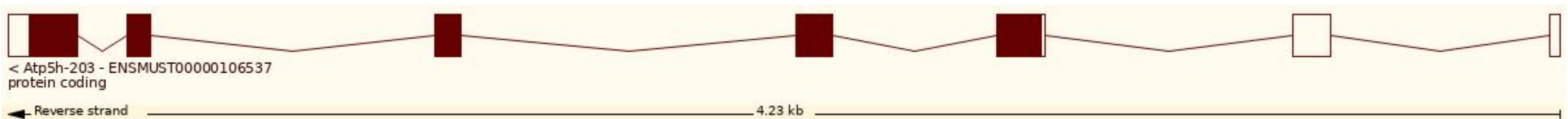
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

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

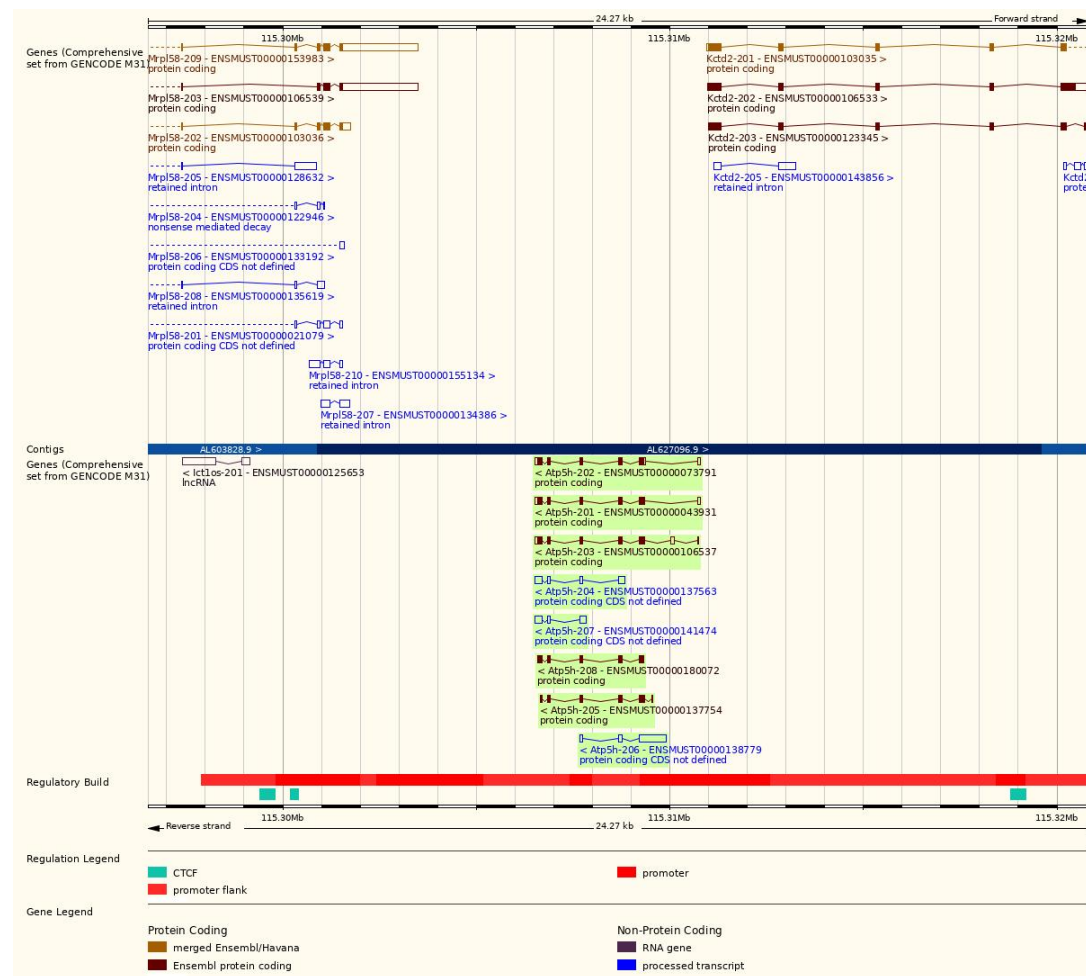
Show/hide columns (1 hidden) Filter							
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000043931.9	Atp5h-201	625	161aa	Protein coding	CCDS25633	Q9DCX2	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000073791.10	Atp5h-202	659	161aa	Protein coding	CCDS25633	Q9DCX2	GENCODE basic APPRIS 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:

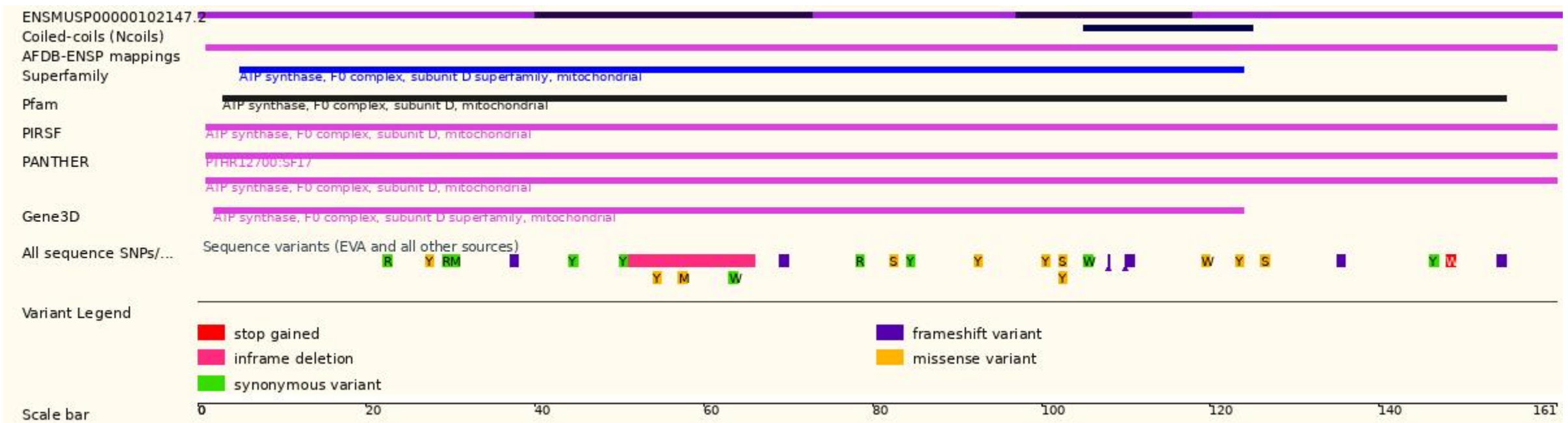


Source: <https://www.ensembl.org>

Genomic Information



Protein Information



Important Information

- A loxp site is about 2kb from the 5 'end of *Kctd2* gene , which may affect the function of the gene.
- 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 risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.