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Atp5c1 Cas9-CKO Strategy

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Design Date: 2023-9-6

Overview

Target Gene Name

- Atp5c1

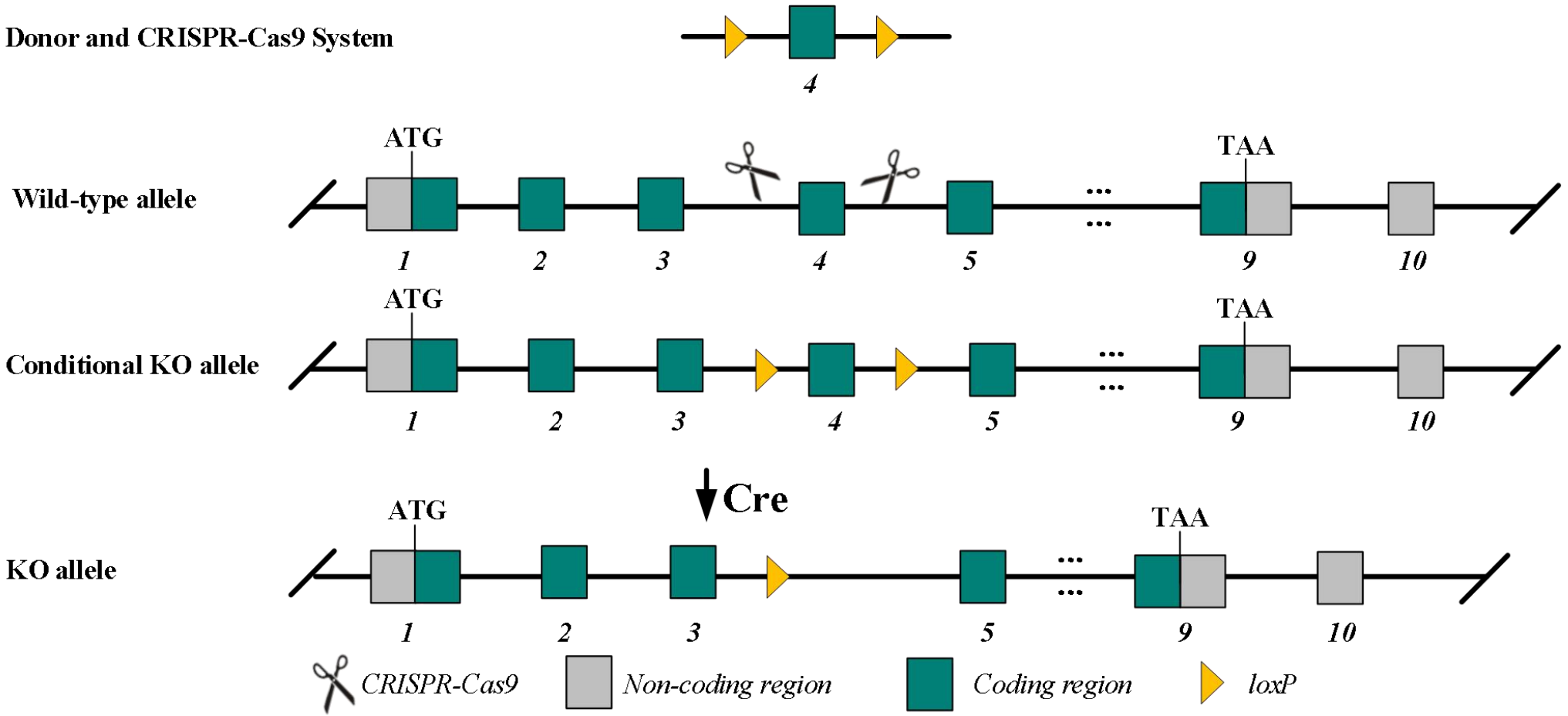
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Atp5c1* gene.

Technical Information

- The *Atp5c1* gene has 7 transcripts. According to the structure of *Atp5c1* gene, exon 4 of *Atp5c1-203* (ENSMUST00000114897.9) transcript is recommended as the knockout region. The region contains 205 bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Atp5c1* 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

Atp5f1c ATP synthase F1 subunit gamma [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 11949, updated on 18-Aug-2023

Summary

Official Symbol	Atp5f1c provided by MGI
Official Full Name	ATP synthase F1 subunit gamma provided by MGI
Primary source	MGI:MGI:1261437
See related	Ensembl:ENSMUSG00000025781 AllianceGenome:MGI:1261437
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	Atp5c1; 1700094F02Rik
Summary	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. Predicted to act upstream of or within ATP biosynthetic process and ion transport. Located in mitochondrial inner membrane and myelin sheath. Is expressed in several structures, including alimentary system; genitourinary system; integumental system; nervous system; and sensory organ. Orthologous to human ATP5F1C (ATP synthase F1 subunit gamma). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in heart adult (RPKM 316.7), kidney adult (RPKM 177.9) and 28 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**

Try the new Transcript table

Genomic context

Location: 2 A1; 2 6.86 cM — See Atp5f1c in Genome Data Viewer

Exon count: 10

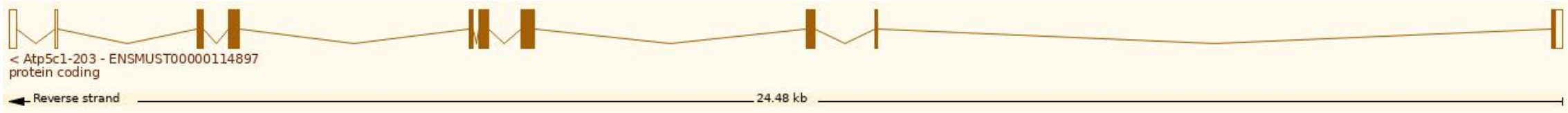
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 7 transcripts, all transcripts are shown below:

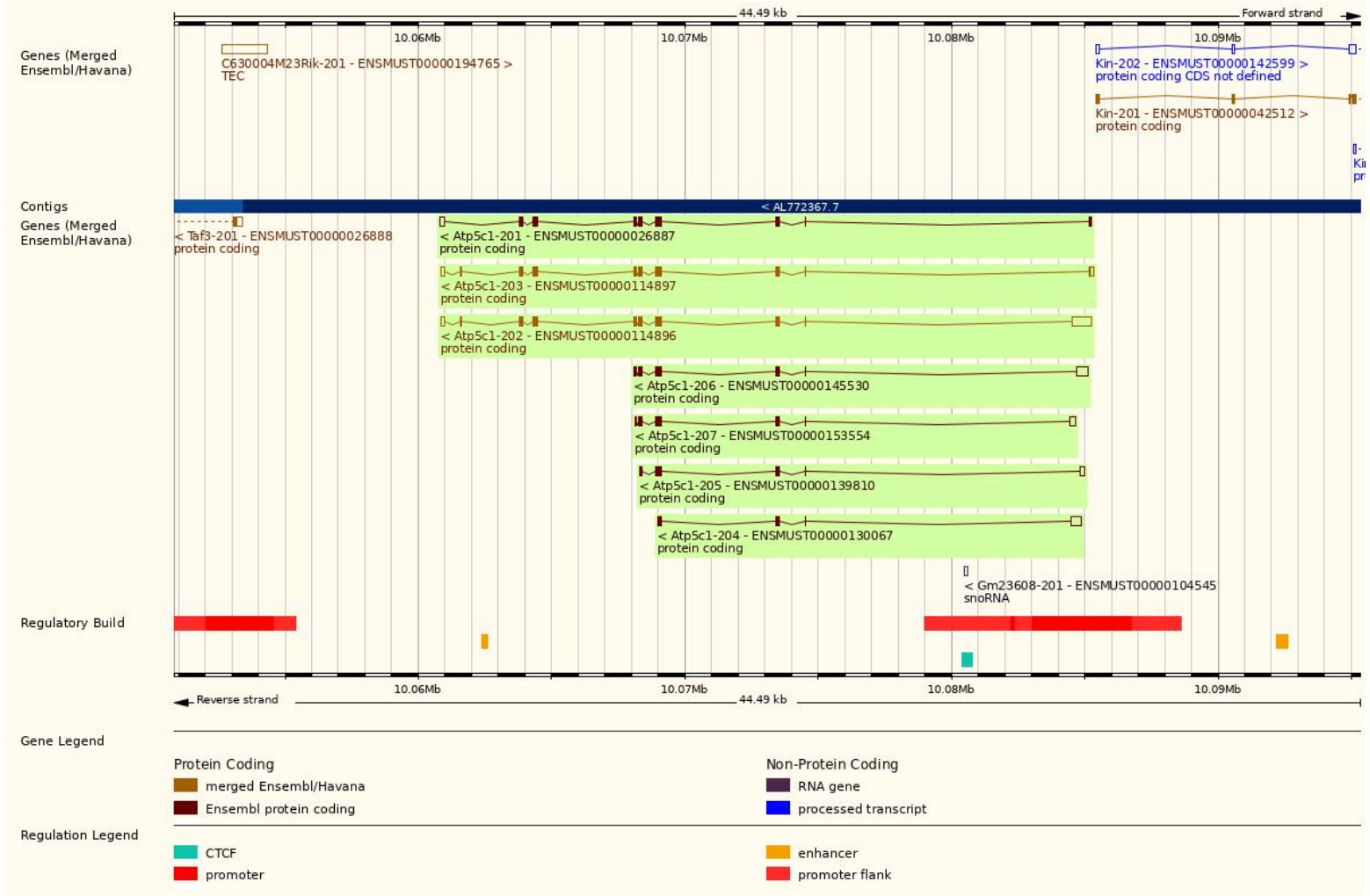
Transcript ID	Name	bp	Protein	Translation ID	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000114897.9	Atp5c1-203	1166	298aa	ENSMUSP00000110547.3	Protein coding	CCDS38045	Q3UD06 Q91VR2	Ensembl Canonical GENCODE basic APPRIS P4 TSL:1
ENSMUST00000114896.8	Atp5c1-202	1735	274aa	ENSMUSP00000110546.2	Protein coding	CCDS50497	Q8C2Q8	GENCODE basic TSL:1
ENSMUST00000026887.14	Atp5c1-201	1060	297aa	ENSMUSP00000026887.8	Protein coding		A2AKU9	GENCODE basic APPRIS ALT1 TSL:5
ENSMUST00000145530.8	Atp5c1-206	1000	188aa	ENSMUSP00000116508.2	Protein coding		A2AKV3	TSL:5 CDS 3' incomplete
ENSMUST00000153554.8	Atp5c1-207	770	171aa	ENSMUSP00000116368.2	Protein coding		A2AKV2	TSL:3 CDS 3' incomplete
ENSMUST00000130067.2	Atp5c1-204	690	101aa	ENSMUSP00000117182.2	Protein coding		A2AKV0	TSL:3 CDS 3' incomplete
ENSMUST00000139810.8	Atp5c1-205	635	154aa	ENSMUSP00000123100.2	Protein coding		A2AKV1	TSL:5 CDS 3' incomplete

The strategy is based on the design of *Atp5c1*-203 transcript, the transcription is shown below:



Source: https://www.ensembl.org

Genomic Information



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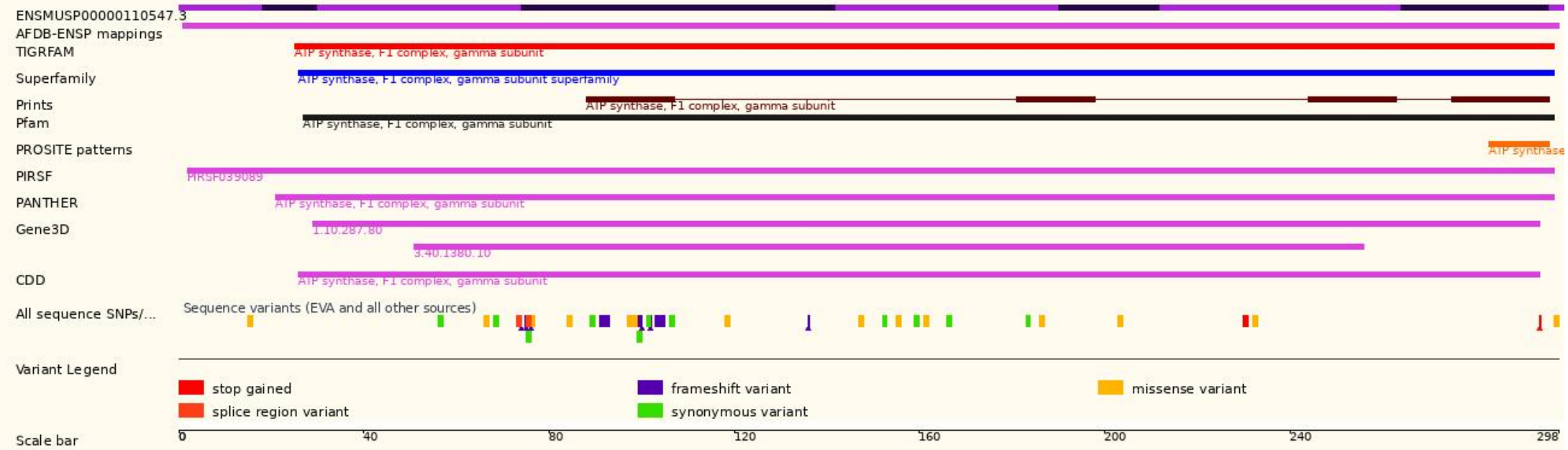
Source: : https://www.ensembl.org

Protein Information



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

Important Information

- The N-terminal of *Atp5c1* gene will remain 74 aa, it may remain the partial function of *Atp5c1*.
- The intron 4-5 of *Atp5c1*-203 is 520 bp, the loxp insertion may affect the regulation of this gene.
- The targeting region has a repetitive structure TAGA, which may introduce mutations.
- *Atp5c1* is located on Chr 2. 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 dsigned 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.