GemPharmatech™

Atp5f1b Cas9-KO Strategy

Designer: Jing Chen

Reviewer: Xingkai Xiao

Design Date: 2024-4-19

Overview

Target Gene Name

- Atp5f1b

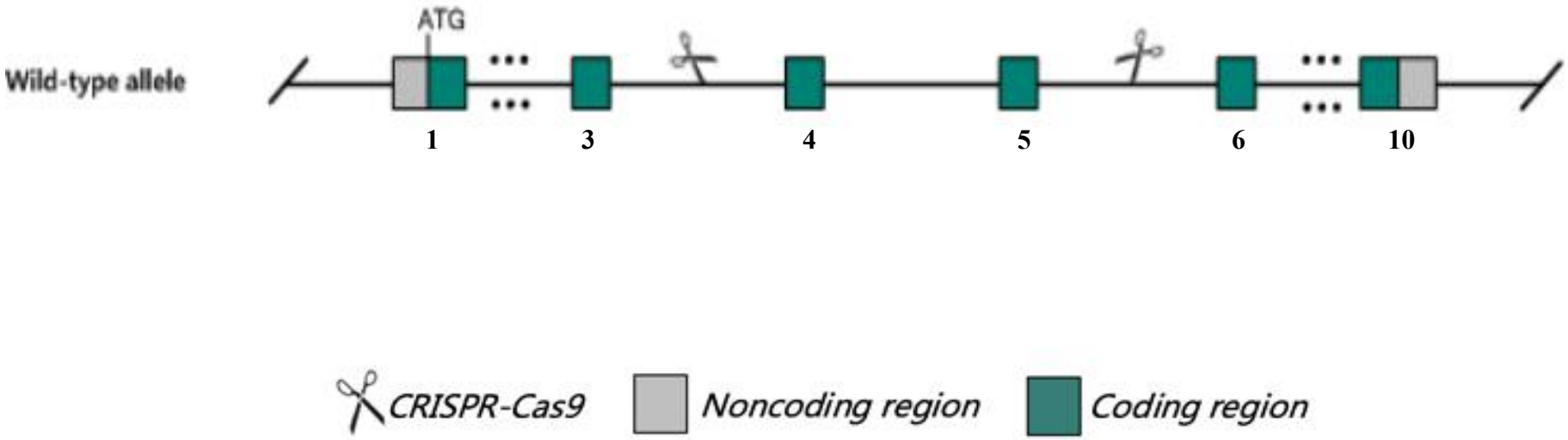
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy

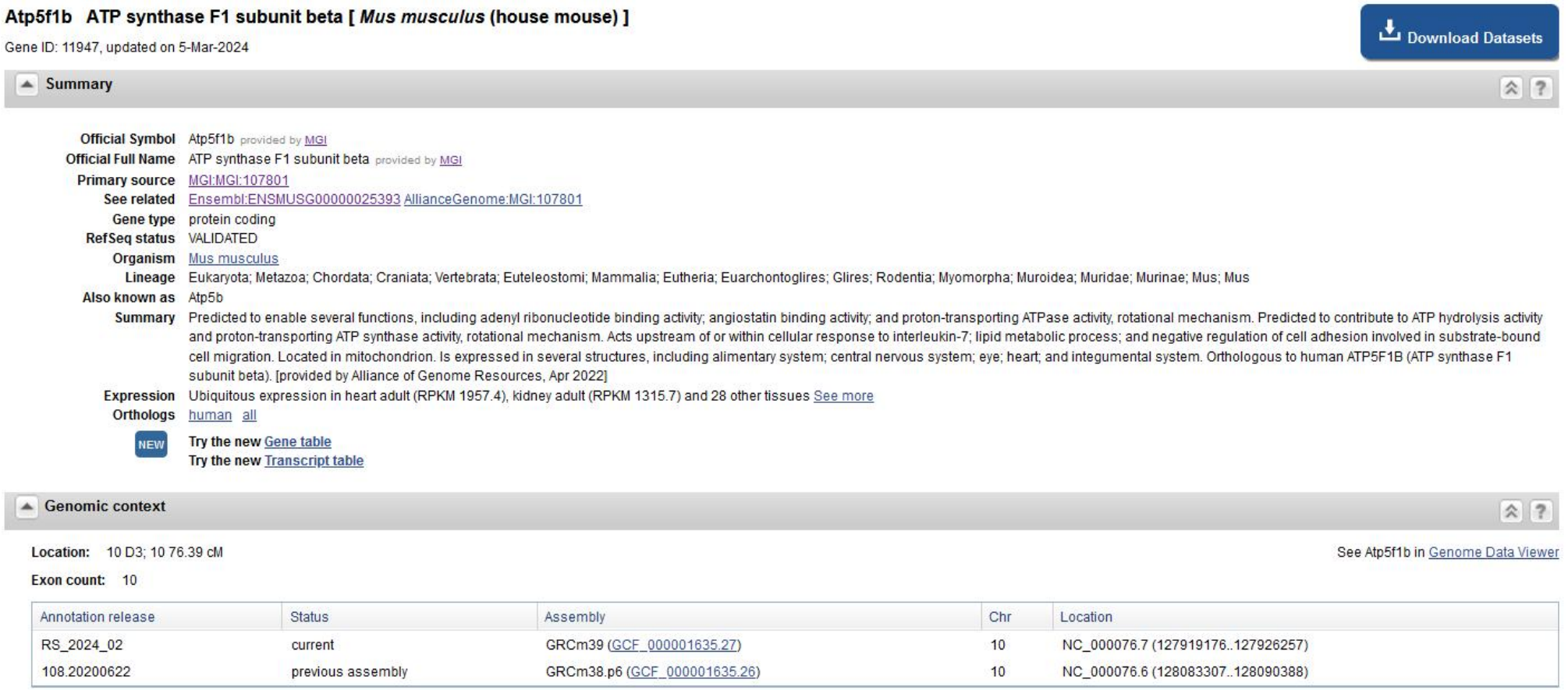


Schematic representation of CRISPR-Cas9 engineering used to edit the *Atp5f1b* gene.

Technical Information

- The *Atp5f1b* gene has 9 transcripts. According to the structure of *Atp5f1b* gene, exon4-exon5 of *Atp5f1b*-201 (ENSMUST00000026459.6) transcript is recommended as the knockout region. The region contains 307bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Atp5f1b* 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



Atp5f1b ATP synthase F1 subunit beta [*Mus musculus* (house mouse)]

Gene ID: 11947, updated on 5-Mar-2024

Download Datasets

Summary

Official Symbol	Atp5f1b provided by MGI
Official Full Name	ATP synthase F1 subunit beta provided by MGI
Primary source	MGI:MGI:107801
See related	Ensembl:ENSMUSG00000025393 AllianceGenome:MGI:107801
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	Atp5b
Summary	Predicted to enable several functions, including adenyl ribonucleotide binding activity; angiostatin binding activity; and proton-transporting ATPase activity, rotational mechanism. Predicted to contribute to ATP hydrolysis activity and proton-transporting ATP synthase activity, rotational mechanism. Acts upstream of or within cellular response to interleukin-7; lipid metabolic process; and negative regulation of cell adhesion involved in substrate-bound cell migration. Located in mitochondrion. Is expressed in several structures, including alimentary system; central nervous system; eye; heart; and integumental system. Orthologous to human ATP5F1B (ATP synthase F1 subunit beta). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in heart adult (RPKM 1957.4), kidney adult (RPKM 1315.7) and 28 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

Genomic context

Location: 10 D3; 10 76.39 cM

See Atp5f1b in Genome Data Viewer

Exon count: 10

Annotation release	Status	Assembly	Chr	Location
RS_2024_02	current	GRCm39 (GCF_000001635.27)	10	NC_000076.7 (127919176..127926257)
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (128083307..128090388)

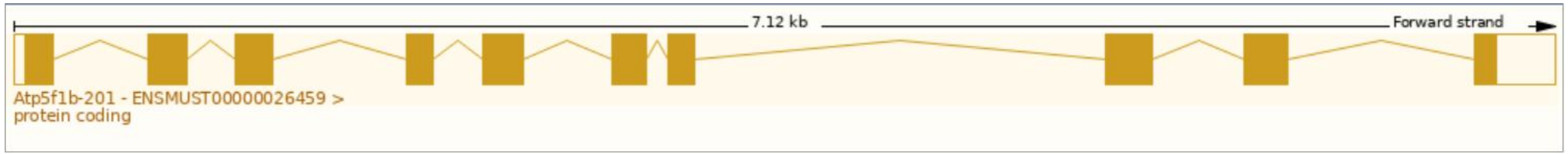
https://www.ncbi.nlm.nih.gov/gene/11947

Transcript Information

The gene has 9 transcripts,all transcripts are shown below:

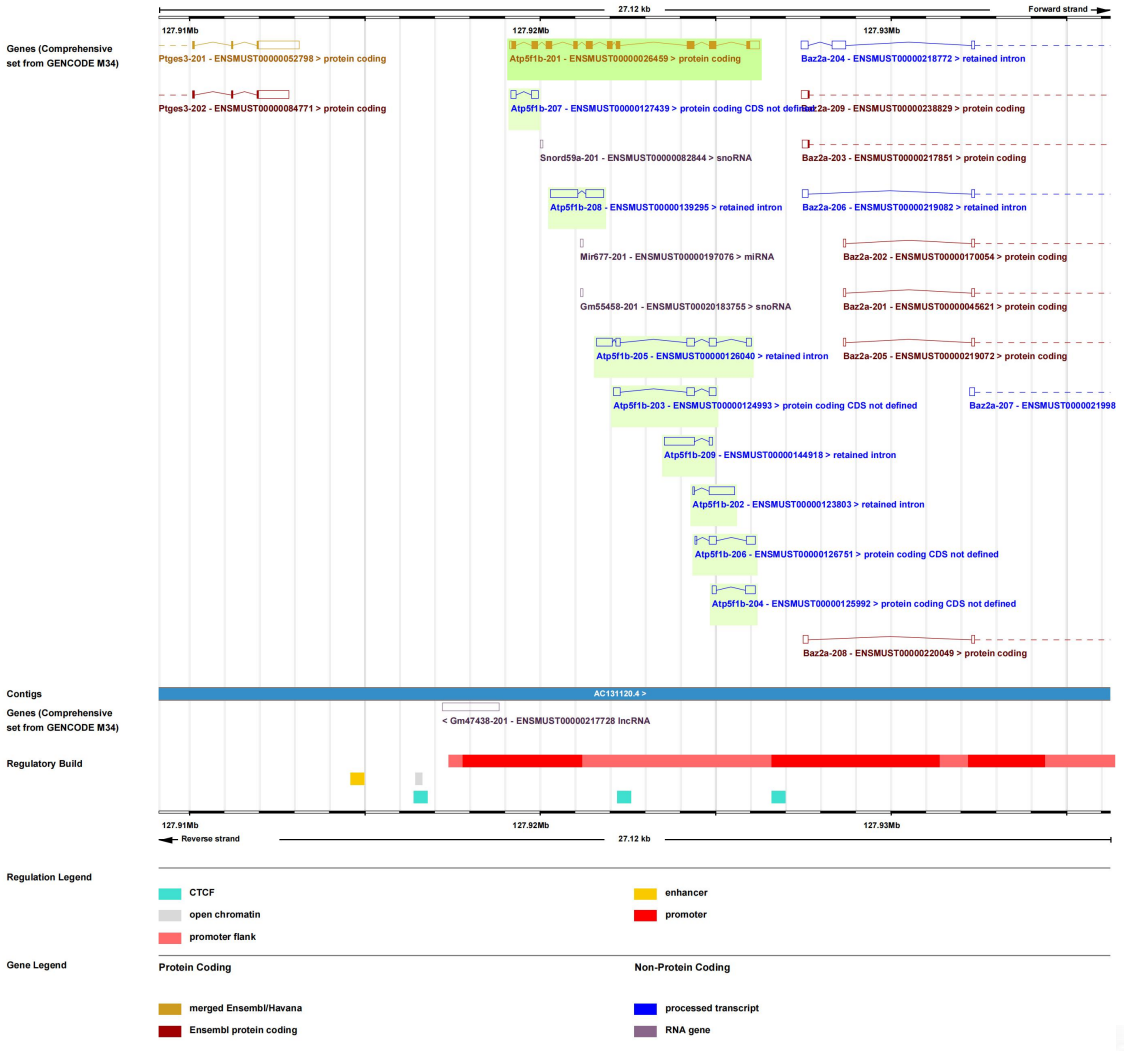
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000026459.6	Atp5f1b-201	1916	529aa	Protein coding	CCDS24259	P56480	Ensembl Canonical, GENCODE basic, APPRIS P1, TSL:1
ENSMUST00000123803.2	Atp5f1b-202	768	No protein	Retained intron		-	TSL:1
ENSMUST00000124993.2	Atp5f1b-203	600	No protein	Protein coding CDS not defined		-	TSL:2
ENSMUST00000125992.2	Atp5f1b-204	399	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000126040.8	Atp5f1b-205	1131	No protein	Retained intron		-	TSL:2
ENSMUST00000126751.2	Atp5f1b-206	478	No protein	Protein coding CDS not defined		-	TSL:2
ENSMUST00000127439.2	Atp5f1b-207	343	No protein	Protein coding CDS not defined		-	TSL:2
ENSMUST00000139295.3	Atp5f1b-208	1288	No protein	Retained intron		-	TSL:2
ENSMUST00000144918.2	Atp5f1b-209	948	No protein	Retained intron		-	TSL:1

The strategy is based on the design of *Atp5f1b*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org

Genomic Information



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

Protein Information

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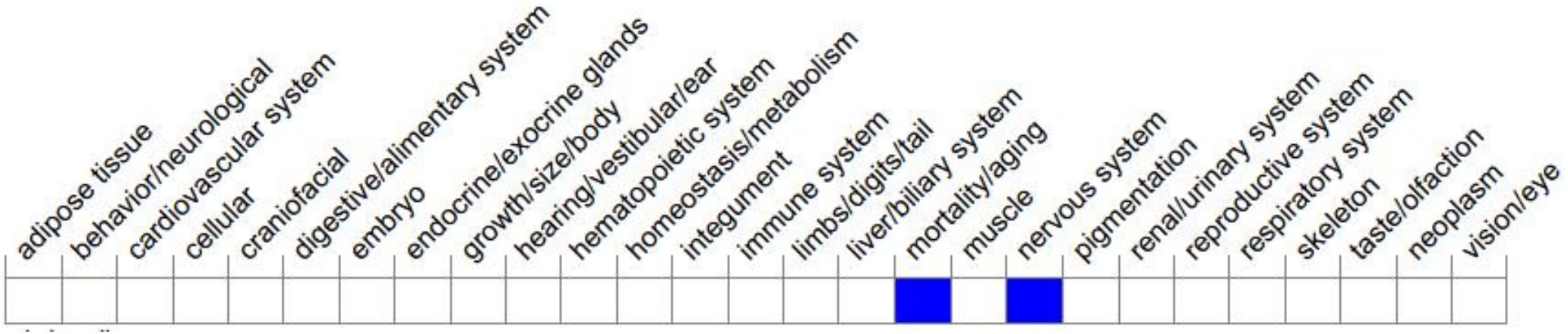
Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



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

Important Information

- According to MGI, mice homozygous for *Atp5f1b* knockout exhibit embryonic lethality.
- The knockout region is about 0.5 kb away from the 3' of the *Snord59a* gene, 1.7 kb away from the 5' of the *Gm47438* gene, 5.7 kb away from the 5' of the *Baz2a* gene,which may affect the regulation of this gene.
- A part of amino acid sequence (162 aa) will still remain at the N-terminal of *Atp5f1b*-201.
- The knockout region contains the *Mir677* and *Gm55458* gene, which are knocked out together.
- *Atp5f1b* 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.