

Atp5g3 Cas9-KO Strategy

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Project Overview

Project Name

Atp5g3

Project type

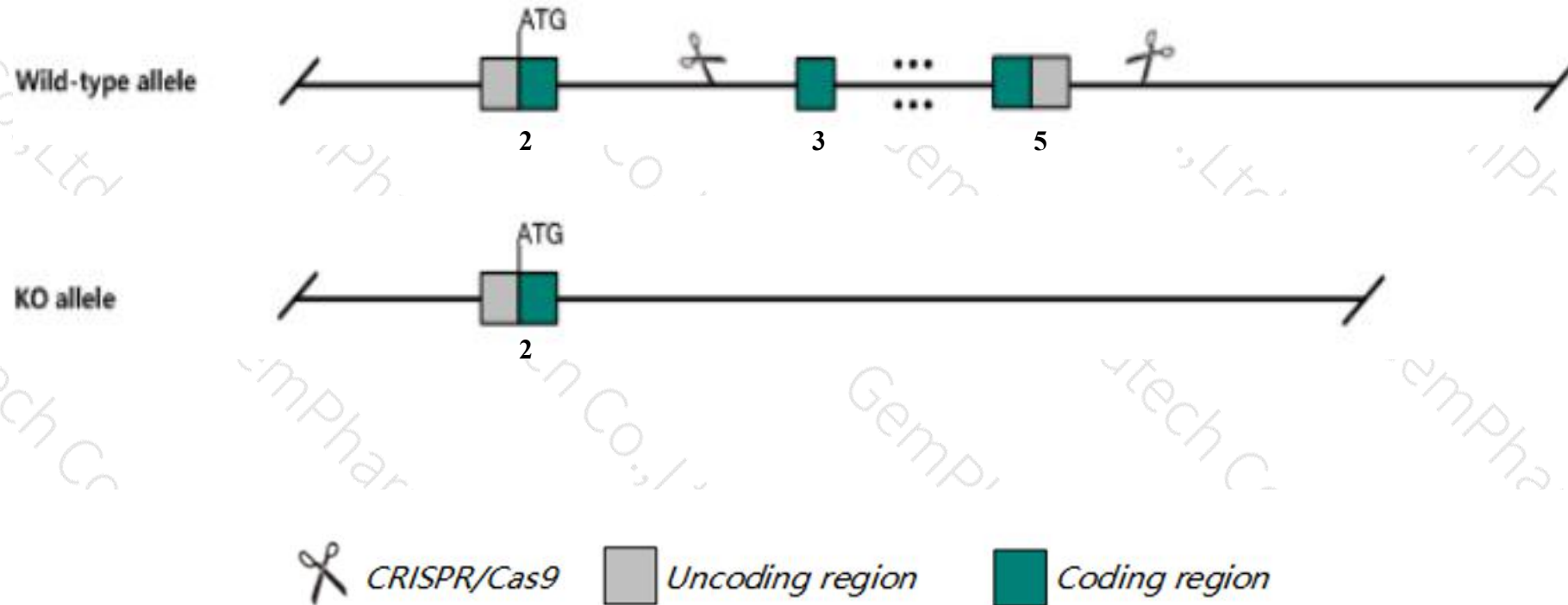
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp5g3* gene. The schematic diagram is as follows:



- The *Atp5g3* gene has 5 transcripts. According to the structure of *Atp5g3* gene, exon3-exon5 of *Atp5g3-202* (ENSMUST00000111996.7) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp5g3* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Atp5g3* gene is located on the Chr2. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Atp5g3 ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit C3 (subunit 9) [*Mus musculus* (house mouse)]

Gene ID: 228033, updated on 13-Mar-2020

Summary



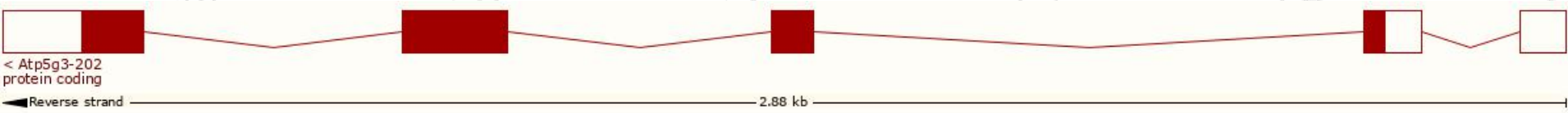
Official Symbol	Atp5g3 provided by MGI
Official Full Name	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit C3 (subunit 9) provided by MGI
Primary source	MGI:MGI:2442035
See related	Ensembl:ENSMUSG00000018770
Gene type	protein coding
RefSeq status	REVIEWED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Atp5mc3; 6030447M23
Summary	The protein encoded by this gene is a subunit of mitochondrial membrane ATP synthase, the enzyme that catalyzes ATP synthesis during oxidative phosphorylation. This gene encodes subunit 9, which is present in multiple copies in the transmembrane part of the ATP synthase complex. Phenotype and gene expression profiles suggest correlations between this gene and alcoholism- and obesity-related phenotypes. Alternative splicing results in multiple transcript variants and protein isoforms. [provided by RefSeq, Sep 2014]
Expression	Ubiquitous expression in heart adult (RPKM 896.5), kidney adult (RPKM 502.3) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

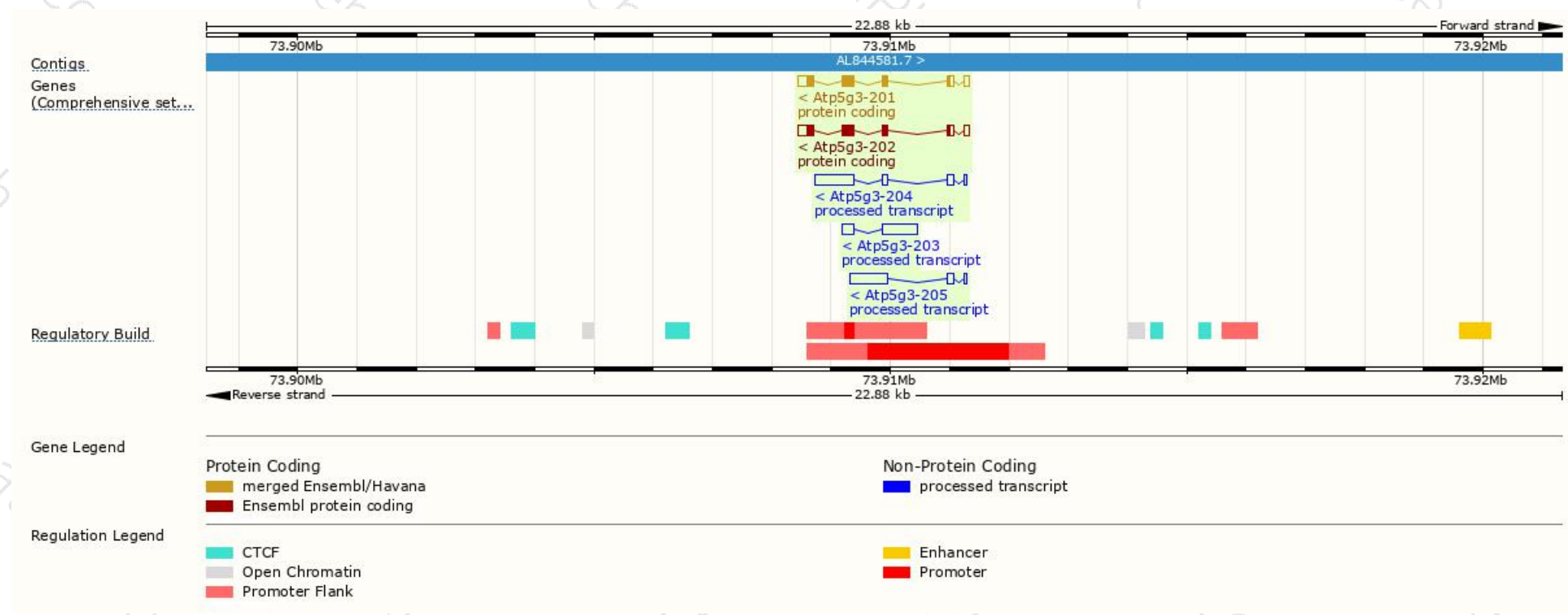
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp5g3-202	ENSMUST00000111996.7	723	141aa	Protein coding	CCDS16136	P56384 Q14BC2	TSL:2 GENCODE basic APPRIS P1
Atp5g3-201	ENSMUST0000018914.2	714	141aa	Protein coding	CCDS16136	P56384 Q14BC2	TSL:1 GENCODE basic APPRIS P1
Atp5g3-204	ENSMUST00000142768.7	862	No protein	Processed transcript	-	-	TSL:2
Atp5g3-203	ENSMUST00000131045.1	791	No protein	Processed transcript	-	-	TSL:2
Atp5g3-205	ENSMUST00000155474.1	770	No protein	Processed transcript	-	-	TSL:2

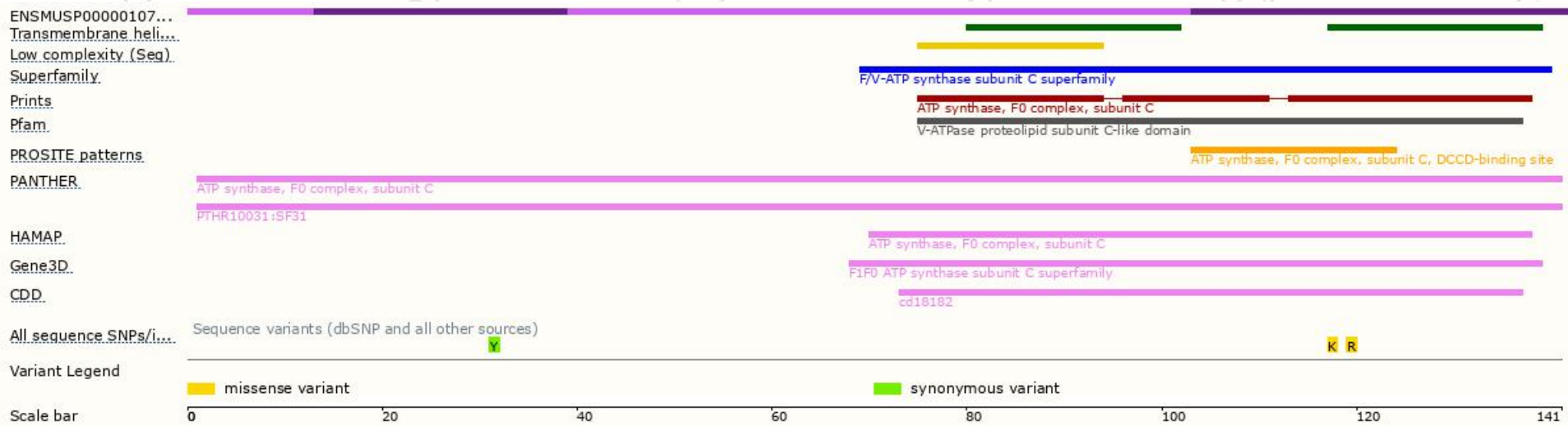
The strategy is based on the design of *Atp5g3-202* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



If you have any questions, you are welcome to inquire.

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