

***Atp5e* Cas9-KO Strategy**

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Reviewer:

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Design Date:

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Project Overview

Project Name

Atp5e

Project type

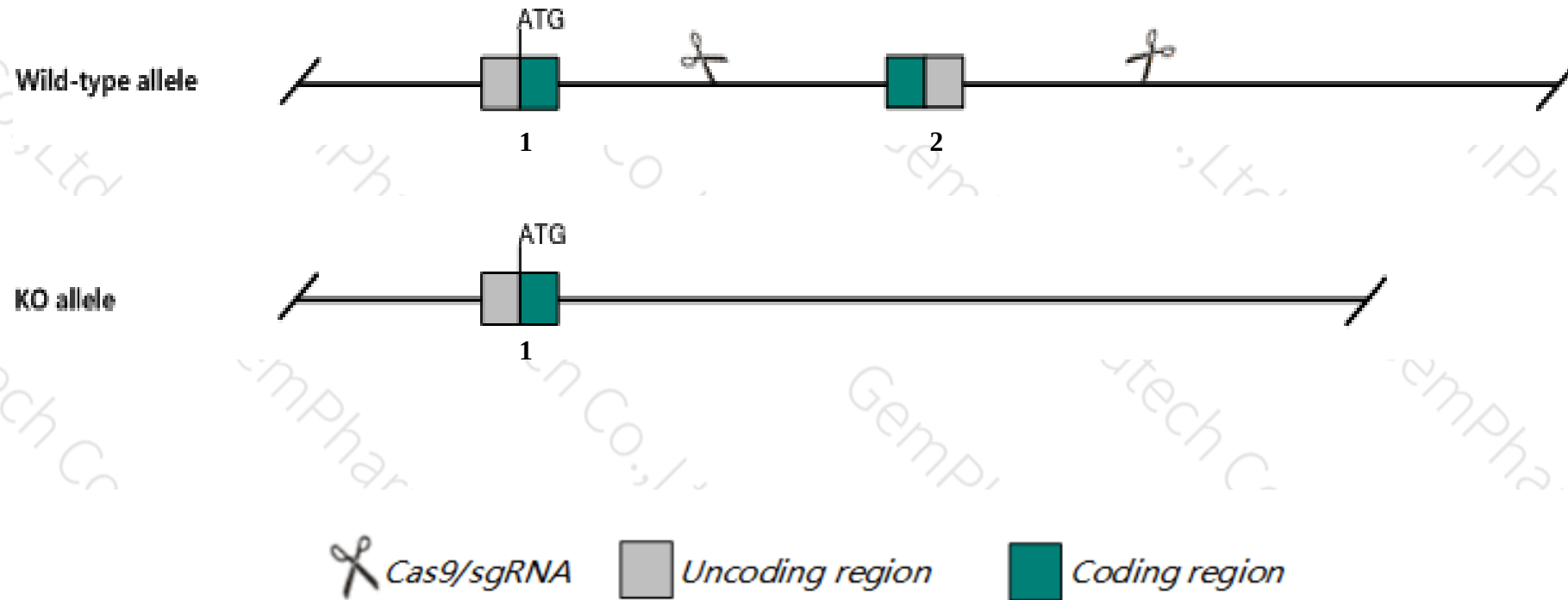
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp5e* gene. The schematic diagram is as follows:



- The *Atp5e* gene has 3 transcripts. According to the structure of *Atp5e* gene, exon2 of *Atp5e*-201(ENSMUST00000016396.7) 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 *Atp5e* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The *Atp5e* 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)

Atp5e ATP synthase, H⁺ transporting, mitochondrial F1 complex, epsilon subunit [Mus musculus (house mouse)]

Gene ID: 67126, updated on 13-Mar-2020

Summary



Official Symbol Atp5e provided by [MGI](#)

Official Full Name ATP synthase, H⁺ transporting, mitochondrial F1 complex, epsilon subunit provided by [MGI](#)

Primary source [MGI:MGI:1855697](#)

See related [Ensembl:ENSMUSG00000016252](#)

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 2410043G19Rik, ATPE, AV000645, Atp5f1e

Expression Ubiquitous expression in heart adult (RPKM 220.7), kidney adult (RPKM 213.5) and 28 other tissues [See more](#)

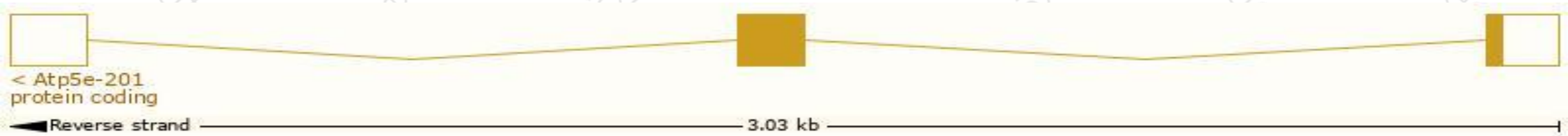
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

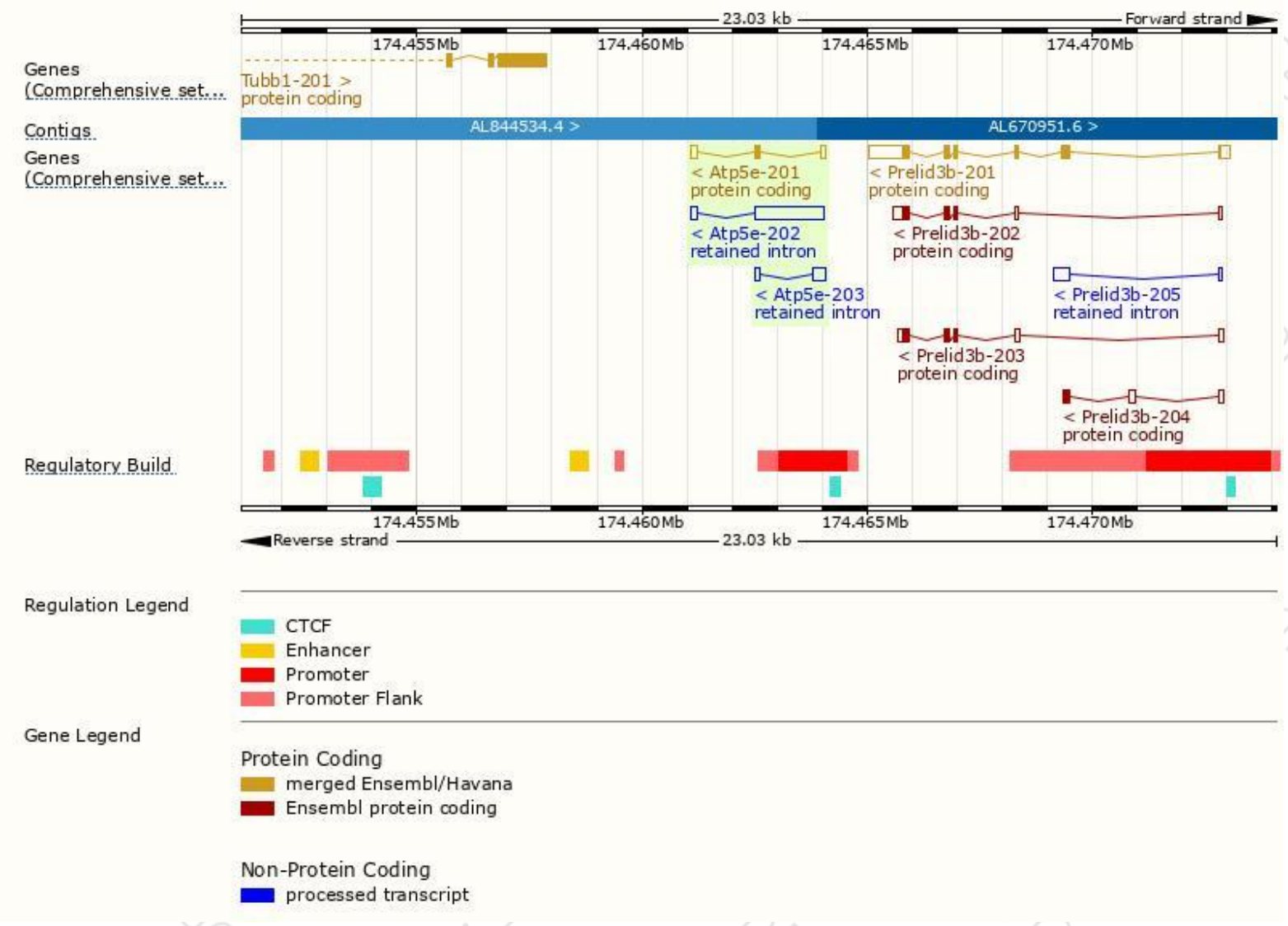
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp5e-201	ENSMUST00000016396.7	421	52aa	Protein coding	CCDS38360	P56382 Q545F5	TSL:1 GENCODE basic APPRIS P1
Atp5e-202	ENSMUST000000149191.1	1697	No protein	Retained intron	-	-	TSL:1
Atp5e-203	ENSMUST000000153132.1	402	No protein	Retained intron	-	-	TSL:3

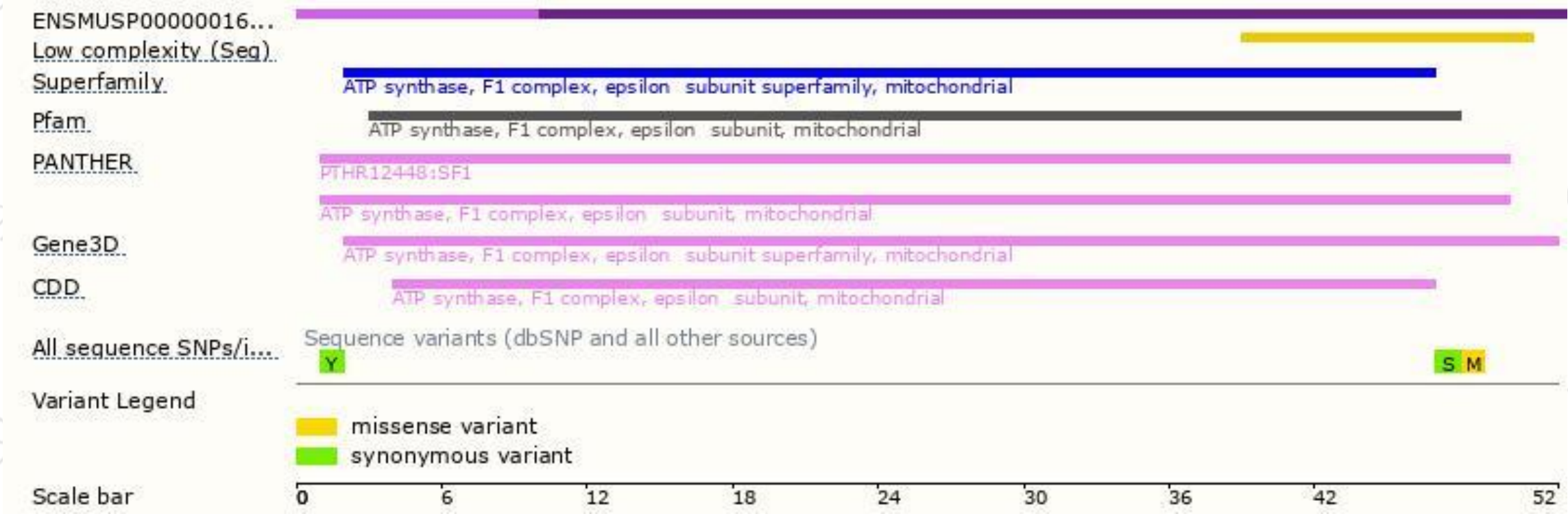
The strategy is based on the design of *Atp5e-201* transcript,the transcription is shown below:



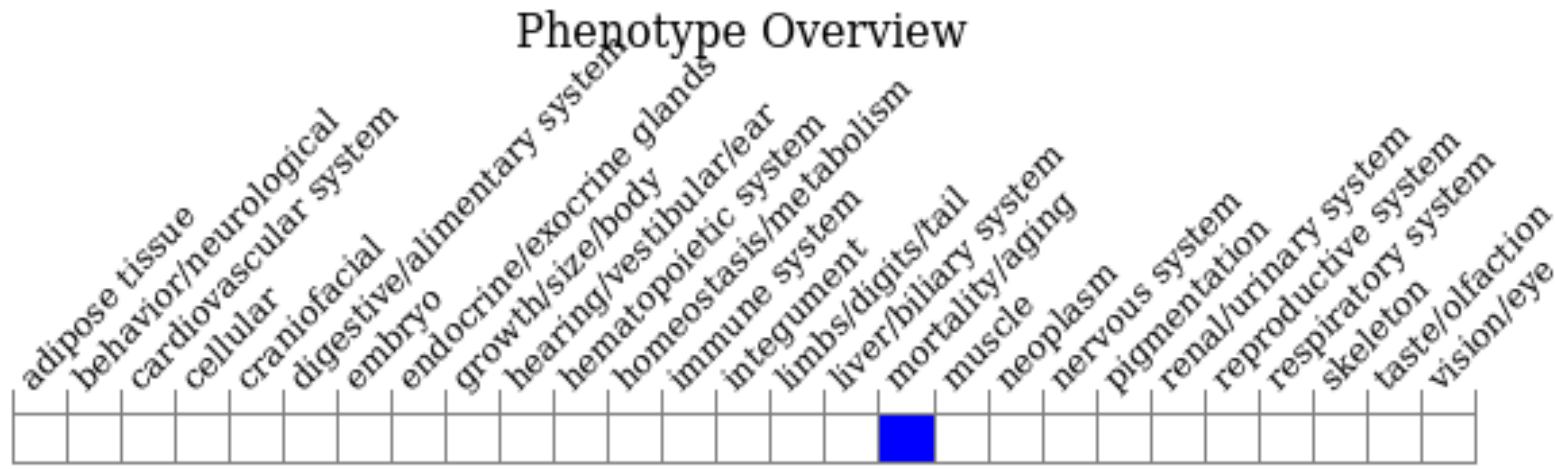
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(<http://www.informatics.jax.org/>).

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

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