

# *Atp5e* Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Atp5e*

**Project type**

**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

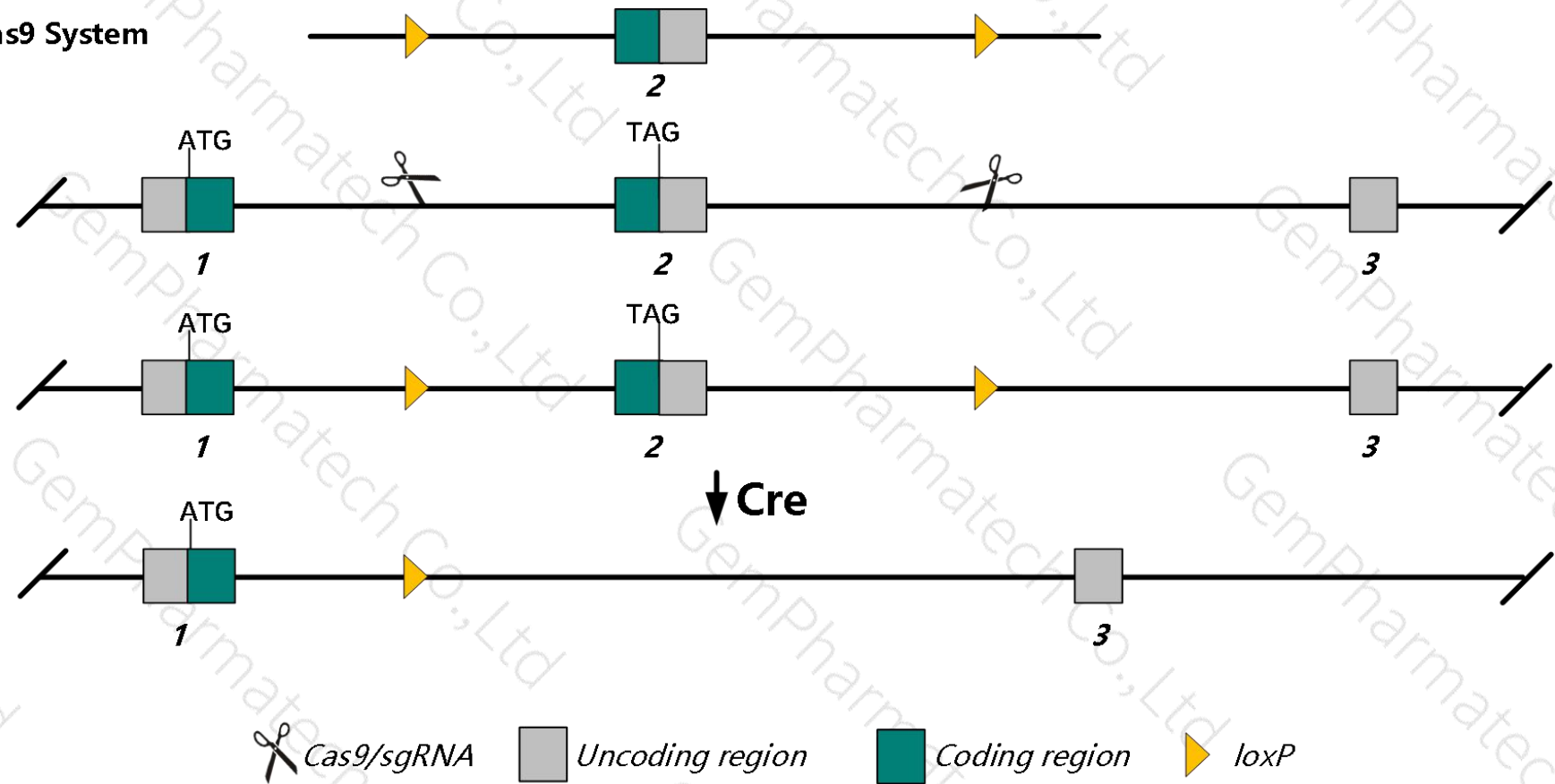
This model will use CRISPR/Cas9 technology to edit the *Atp5e* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System

Wild-type allele

Floxed allele

KO allele



# Technical routes

- 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 stop codon TAG. 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, donor vector was constructed. Cas9, sgRNA 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice was 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.

- The KO region is close to *Prelid3b* gene .Knockout the region may affect the regulatory function of *Prelid3b* gene.
- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



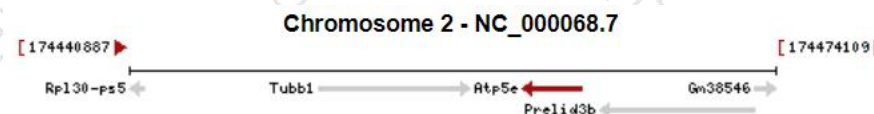
# Gene information (NCBI)

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

Gene ID: 67126, updated on 12-Aug-2019

## Summary

**Official Symbol** Atp5e provided by [MGI](#)  
**Official Full Name** ATP synthase, H<sup>+</sup> 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** ATPE; Atp5f1e; AV000645; 2410043G19Rik  
**Expression** Ubiquitous expression in heart adult (RPKM 220.7), kidney adult (RPKM 213.5) and 28 other tissues [See more](#)  
**Orthologs** [human](#) [all](#)

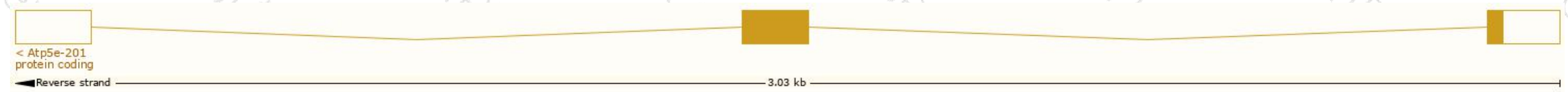


# Transcript information (Ensembl)

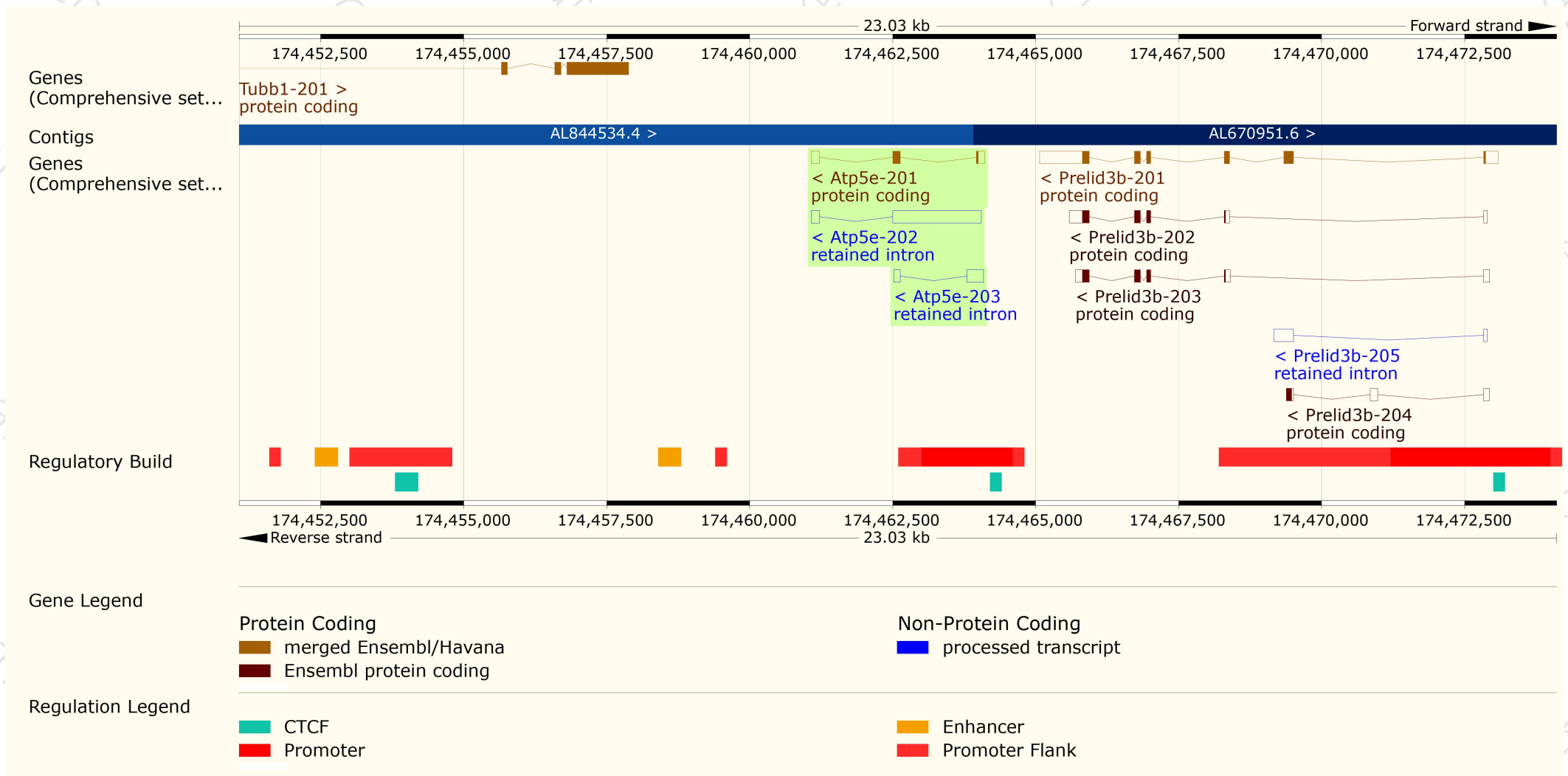
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Atp5e-201	<a href="#">ENSMUST00000016396.7</a>	421	<a href="#">52aa</a>	<a href="#">ENSMUSP00000016396.7</a>	Protein coding	<a href="#">CCDS38360</a>	<a href="#">P56382</a> <a href="#">Q545F5</a>	TSL:1 GENCODE basic APPRIS P1
Atp5e-202	<a href="#">ENSMUST00000149191.1</a>	1697	No protein	-	Retained intron	-	-	TSL:1
Atp5e-203	<a href="#">ENSMUST00000153132.1</a>	402	No protein	-	Retained intron	-	-	TSL:3

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

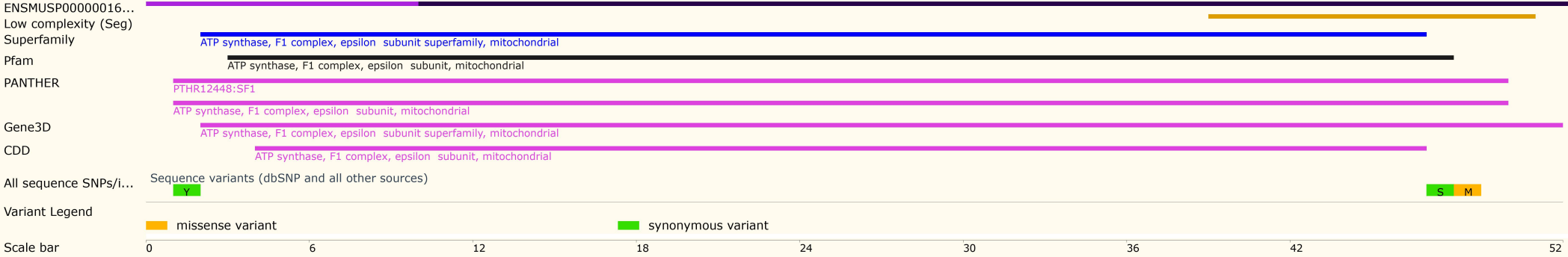


# Genomic location distribution

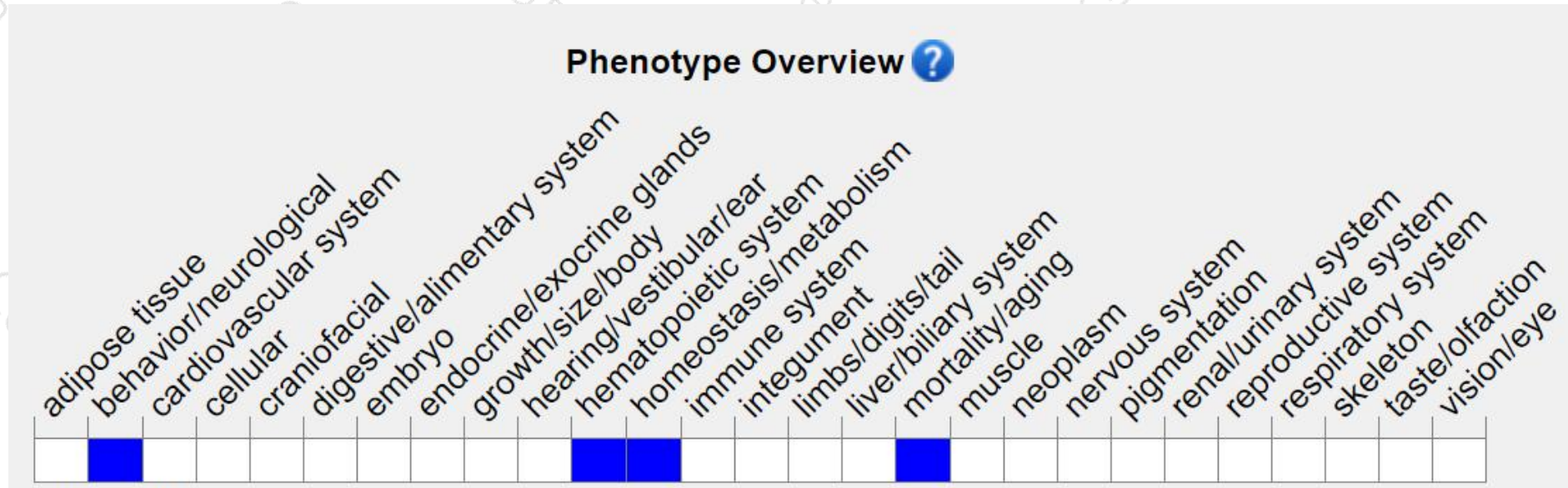




# Protein domain



# 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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