

# *Atp5c1* Cas9-KO Strategy

**Designer:**

**Daohua Xu**

**Reviewer:**

**Huimin Su**

**Design Date:**

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# Project Overview

**Project Name**

*Atp5c1*

**Project type**

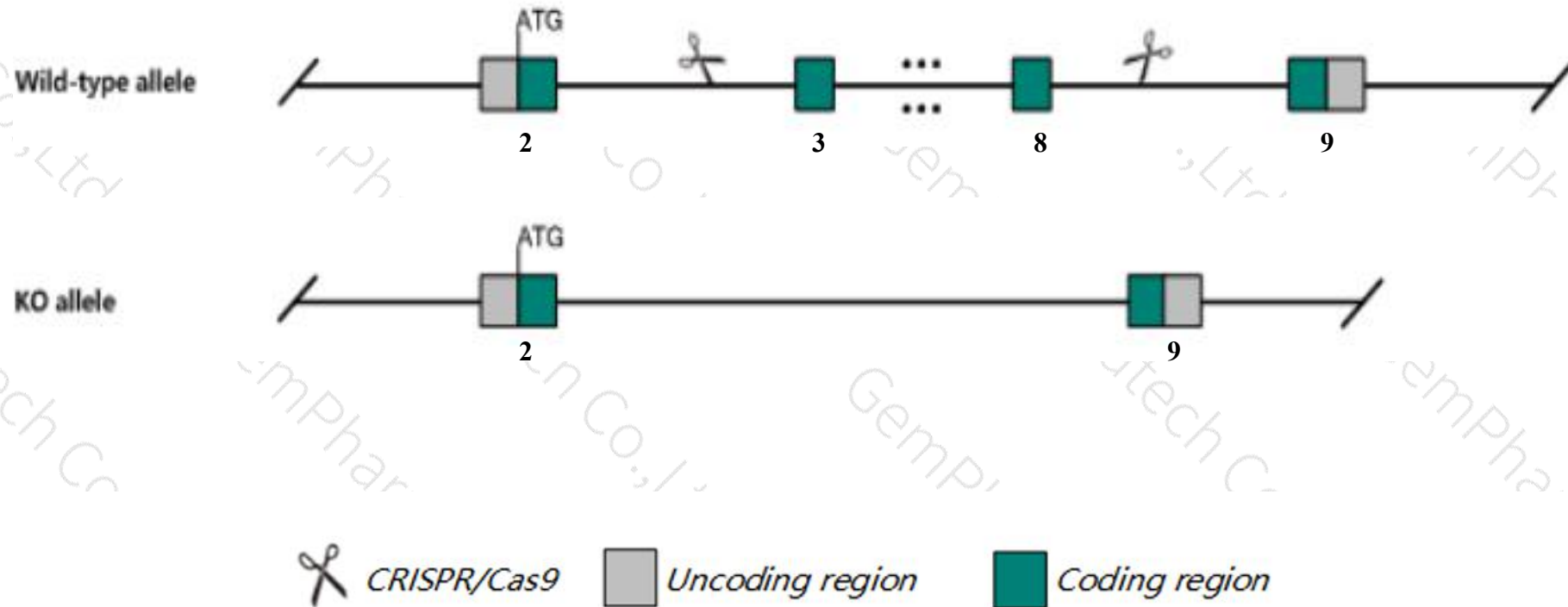
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp5c1* gene. The schematic diagram is as follows:



- The *Atp5c1* gene has 7 transcripts. According to the structure of *Atp5c1* gene, exon3-exon8 of *Atp5c1*-202 (ENSMUST00000114896.7) transcript is recommended as the knockout region. The region contains 799bp coding sequence. Knock 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

- The *Atp5c1* 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)

**Atp5c1** ATP synthase, H<sup>+</sup> transporting, mitochondrial F1 complex, gamma polypeptide 1 [ *Mus musculus* (house mouse) ]

Gene ID: 11949, updated on 13-Mar-2020

## Summary

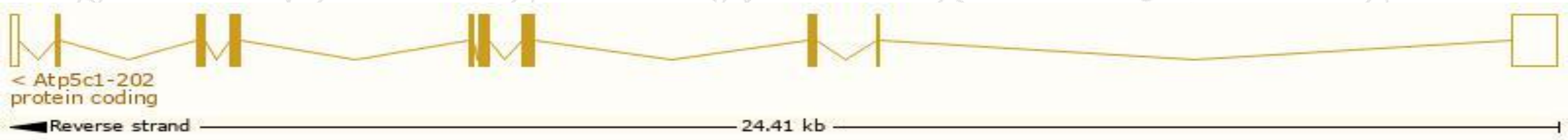
|                    |                                                                                                                                                                           |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Official Symbol    | Atp5c1 provided by <a href="#">MGI</a>                                                                                                                                    |
| Official Full Name | ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, gamma polypeptide 1 provided by <a href="#">MGI</a>                                                  |
| Primary source     | <a href="#">MGI:MGI:1261437</a>                                                                                                                                           |
| See related        | <a href="#">Ensembl:ENSMUSG000000025781</a>                                                                                                                               |
| Gene type          | protein coding                                                                                                                                                            |
| RefSeq status      | VALIDATED                                                                                                                                                                 |
| Organism           | <a href="#">Mus musculus</a>                                                                                                                                              |
| Lineage            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as      | Atp5f1c; 1700094F02Rik                                                                                                                                                    |
| Expression         | Ubiquitous expression in heart adult (RPKM 316.7), kidney adult (RPKM 177.9) and 28 other tissues <a href="#">See more</a>                                                |
| Orthologs          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

# Transcript information (Ensembl)

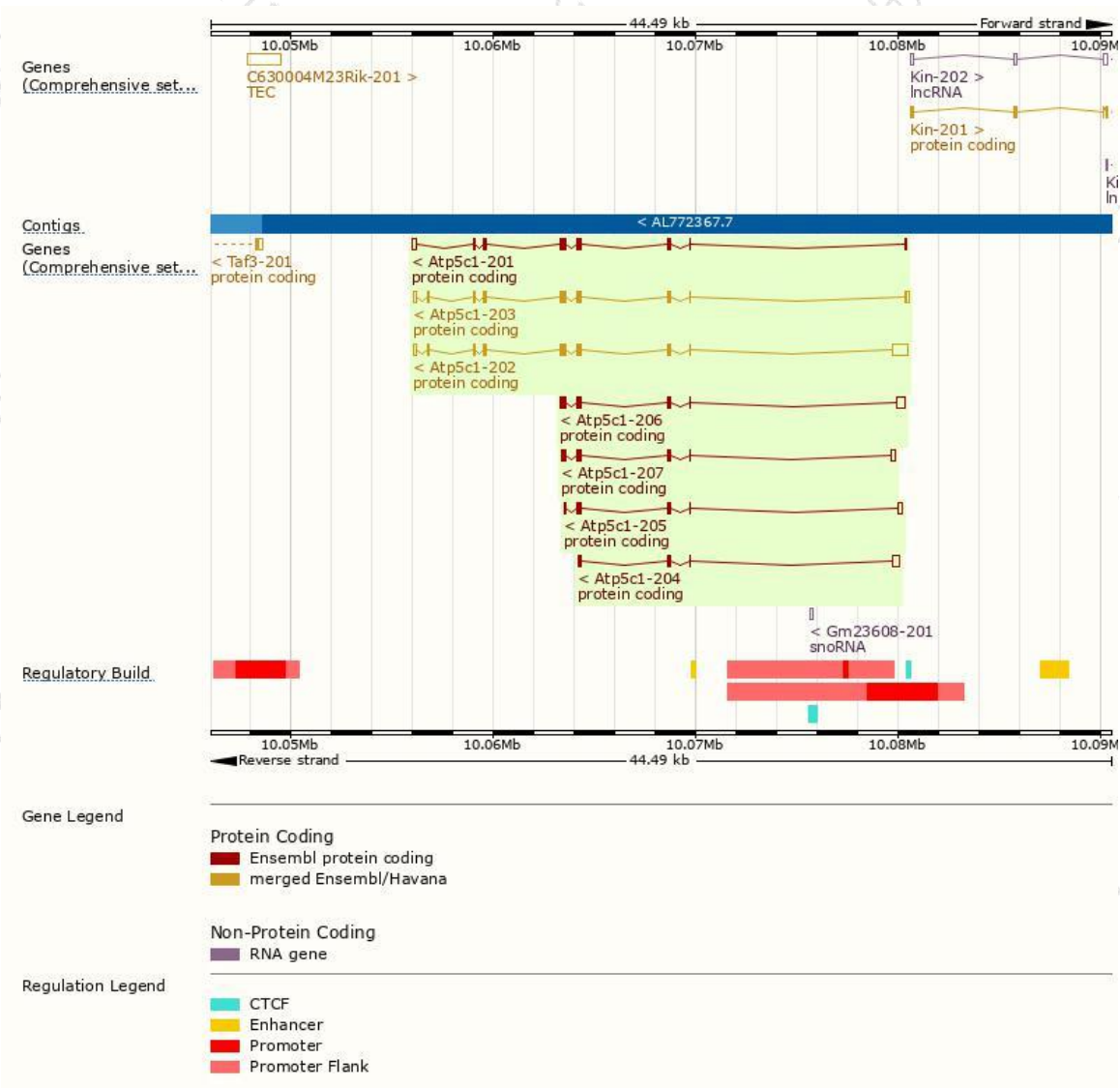
The gene has 7 transcripts,all transcripts are shown below:

| Name       | Transcript ID                         | bp   | Protein               | Biotype        | CCDS                      | UniProt                                       | Flags                           |
|------------|---------------------------------------|------|-----------------------|----------------|---------------------------|-----------------------------------------------|---------------------------------|
| Atp5c1-202 | <a href="#">ENSMUST00000114896.7</a>  | 1735 | <a href="#">274aa</a> | Protein coding | <a href="#">CCDS50497</a> | <a href="#">Q8C2Q8</a>                        | TSL:1 GENCODE basic             |
| Atp5c1-203 | <a href="#">ENSMUST00000114897.8</a>  | 1166 | <a href="#">298aa</a> | Protein coding | <a href="#">CCDS38045</a> | <a href="#">Q3UD06</a> <a href="#">Q91VR2</a> | TSL:1 GENCODE basic APPRIS P2   |
| Atp5c1-201 | <a href="#">ENSMUST00000026887.13</a> | 1060 | <a href="#">297aa</a> | Protein coding | -                         | <a href="#">A2AKU9</a>                        | TSL:5 GENCODE basic APPRIS ALT1 |
| Atp5c1-206 | <a href="#">ENSMUST00000145530.7</a>  | 1000 | <a href="#">188aa</a> | Protein coding | -                         | <a href="#">A2AKV3</a>                        | CDS 3' incomplete TSL:5         |
| Atp5c1-207 | <a href="#">ENSMUST00000153554.7</a>  | 770  | <a href="#">171aa</a> | Protein coding | -                         | <a href="#">A2AKV2</a>                        | CDS 3' incomplete TSL:3         |
| Atp5c1-204 | <a href="#">ENSMUST00000130067.1</a>  | 690  | <a href="#">101aa</a> | Protein coding | -                         | <a href="#">A2AKV0</a>                        | CDS 3' incomplete TSL:3         |
| Atp5c1-205 | <a href="#">ENSMUST00000139810.7</a>  | 635  | <a href="#">154aa</a> | Protein coding | -                         | <a href="#">A2AKV1</a>                        | CDS 3' incomplete TSL:5         |

The strategy is based on the design of *Atp5c1-202* transcript,The transcription is shown below

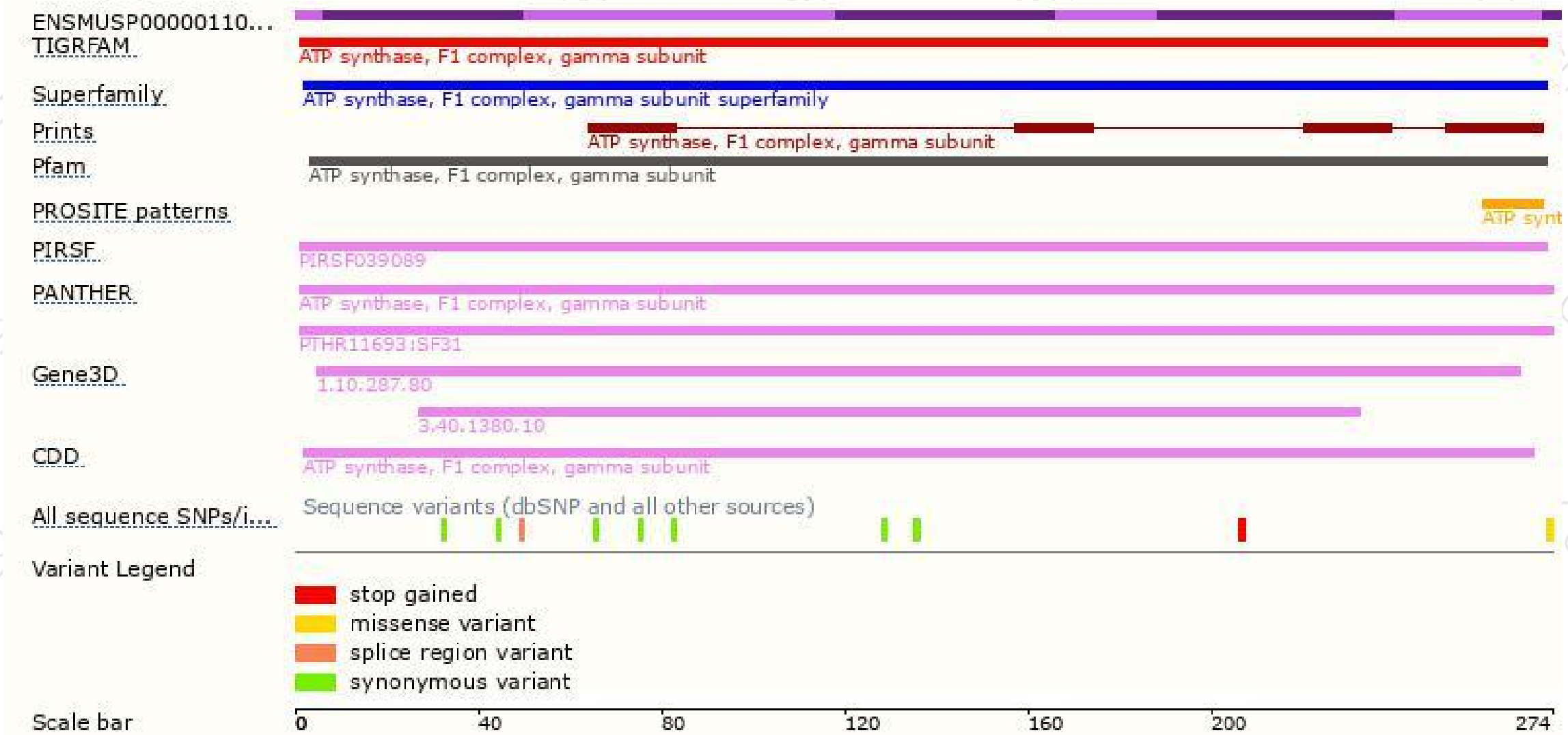


# Genomic location distribution





# Protein domain



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

Tel: 400-9660890

