

# ***Atp6v0e2 Cas9-KO Strategy***

**Designer:**

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# Project Overview

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**Project Name**

*Atp6v0e2*

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**Project type**

**Cas9-KO**

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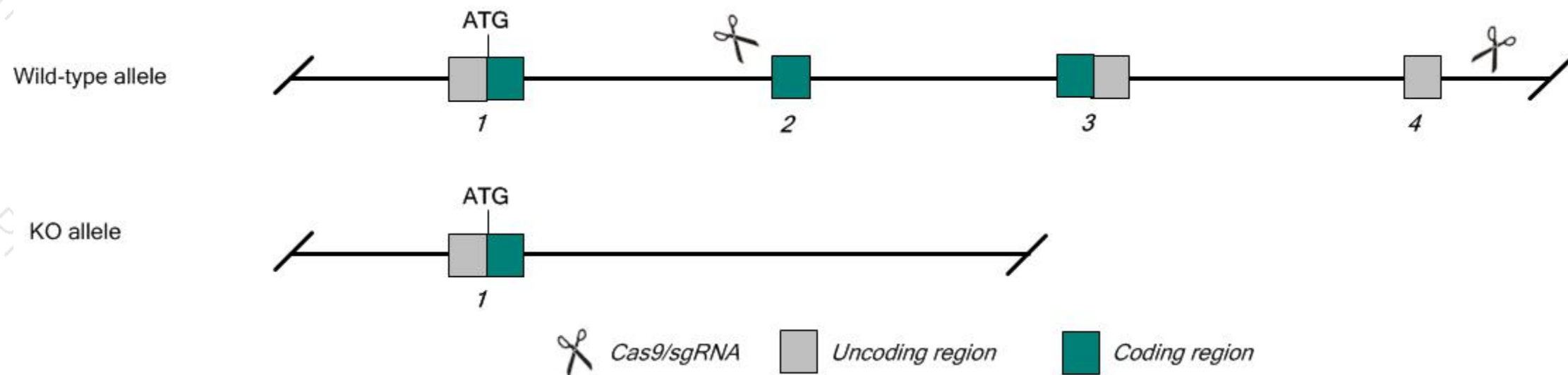
**Strain background**

**C57BL/6J**

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# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp6v0e2* gene. The schematic diagram is as follows:



- The *Atp6v0e2* gene has 3 transcripts. According to the structure of *Atp6v0e2* gene, exon2-4 of *Atp6v0e2*-201 (ENSMUST00000040361.7) transcript is recommended as the knockout region. The region 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 *Atp6v0e2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- The *Atp6v0e2* gene is located on the Chr6. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

# Gene information (NCBI)

## Atp6v0e2 ATPase, H<sup>+</sup> transporting, lysosomal V0 subunit E2 [ *Mus musculus* (house mouse) ]

Gene ID: 76252, updated on 4-Jun-2019

### Summary

|                    |                                                                                                                                                                           |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Official Symbol    | Atp6v0e2 provided by <a href="#">MGI</a>                                                                                                                                  |
| Official Full Name | ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit E2 provided by <a href="#">MGI</a>                                                                              |
| Primary source     | <a href="#">MGI:MGI:1923502</a>                                                                                                                                           |
| See related        | <a href="#">Ensembl:ENSMUSG000000039347</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      | NM9.2; 0610006O14Rik                                                                                                                                                      |
| Expression         | Broad expression in cortex adult (RPKM 116.9), cerebellum adult (RPKM 109.2) and 20 other tissues <a href="#">See more</a>                                                |
| Orthologs          | <a href="#">human</a> <a href="#">all</a>                                                                                                                                 |

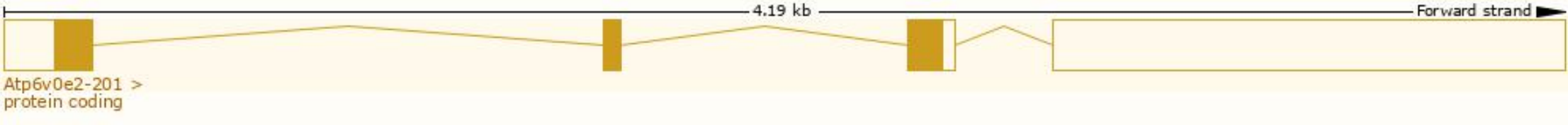


# Transcript information (Ensembl)

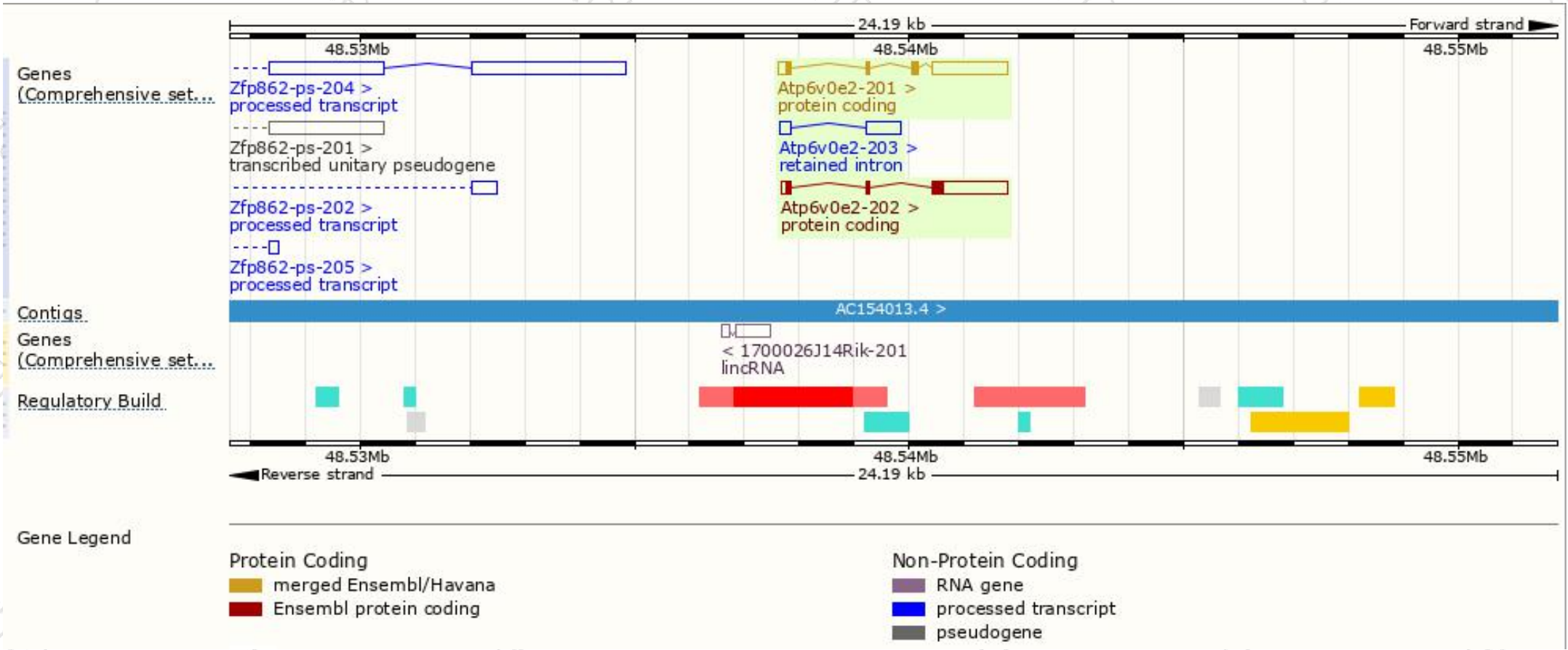
The gene has 3 transcripts, and all transcripts are shown below :

| Name         | Transcript ID                         | bp   | Protein               | Biotype         | CCDS                      | UniProt                    | Flags                         |
|--------------|---------------------------------------|------|-----------------------|-----------------|---------------------------|----------------------------|-------------------------------|
| Atp6v0e2-201 | <a href="#">ENSMUST00000040361.7</a>  | 1789 | <a href="#">81aa</a>  | Protein coding  | <a href="#">CCDS20103</a> | <a href="#">Q91XE7</a>     | TSL:1 GENCODE basic APPRIS P1 |
| Atp6v0e2-202 | <a href="#">ENSMUST000000203011.1</a> | 1612 | <a href="#">112aa</a> | Protein coding  | <a href="#">CCDS85039</a> | <a href="#">ADA0N4SVQ2</a> | TSL:2 GENCODE basic           |
| Atp6v0e2-203 | <a href="#">ENSMUST000000204277.1</a> | 857  | No protein            | Retained intron | -                         | -                          | TSL:2                         |

The strategy is based on the design of *Atp6v0e2-201* transcript, The transcription is shown below

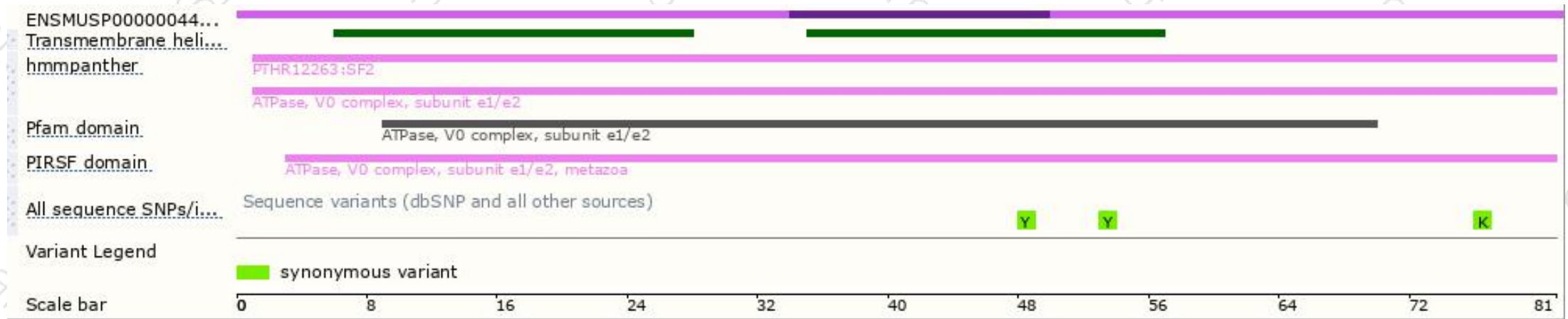


# Genomic location (Ensembl)





# Protein domain (Ensembl)



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

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