

Atp6v0e2 Cas9-CKO Strategy

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Design Date: 2022-09-23

Overview

Target Gene Name

- *Atp6v0e2*

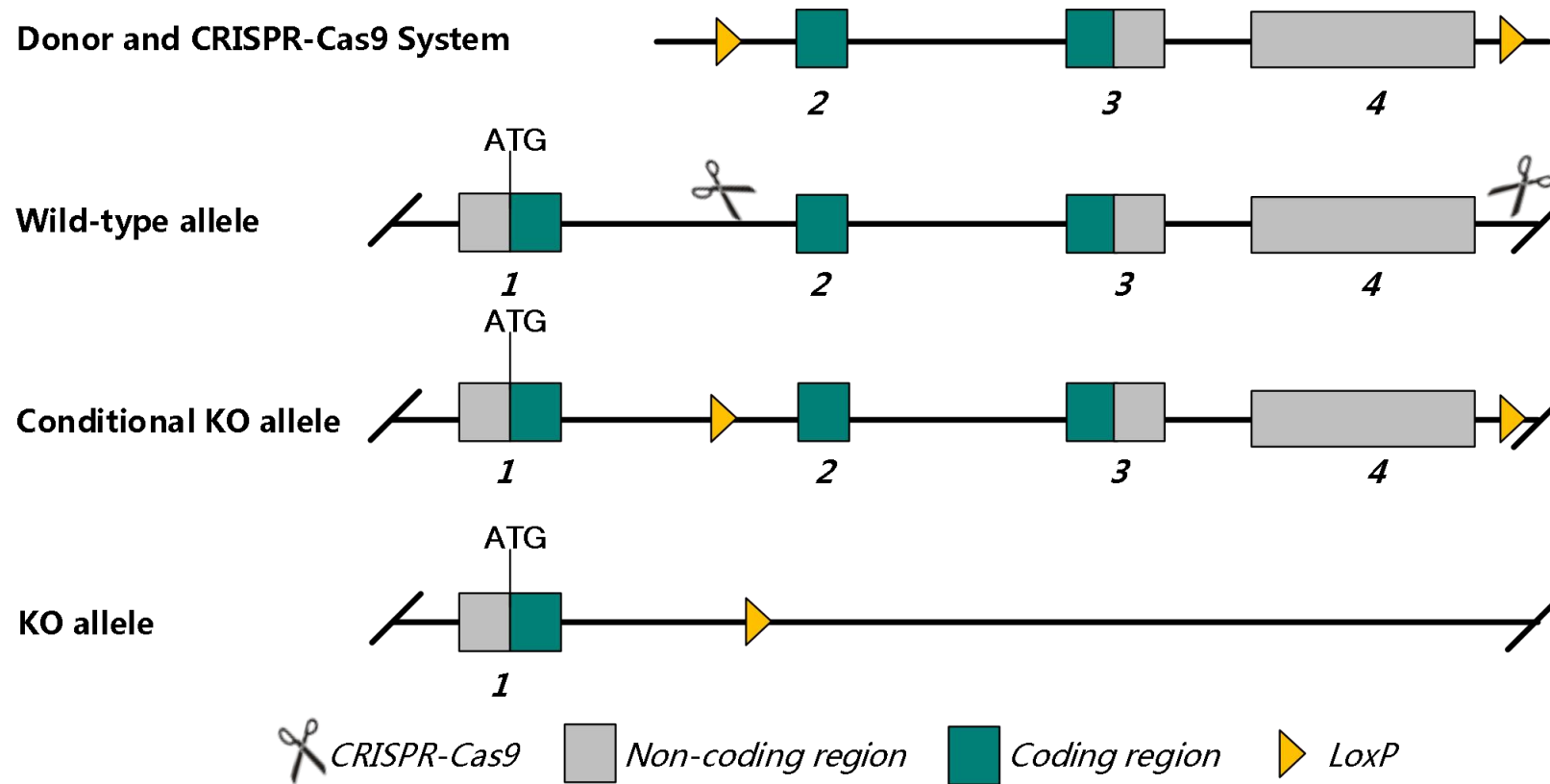
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Atp6v0e2* gene.

Technical Information

- The *Atp6v0e2* gene has 3 transcripts. According to the structure of *Atp6v0e2* gene, exon2-4 of *Atp6v0e2*-201(ENSMUST00000040361.8) transcript is recommended as the knockout region. The region contains 142 bp coding sequence. Knocking 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: CRISPR-Cas9 system 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be 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.

Gene Information

Atp6v0e2 ATPase, H⁺ transporting, lysosomal V0 subunit E2 [*Mus musculus* (house mouse)]

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Gene ID: 76252, updated on 30-Aug-2022

Summary

Official Symbol	Atp6v0e2 provided by MGI
Official Full Name	ATPase, H ⁺ transporting, lysosomal V0 subunit E2 provided by MGI
Primary source	MGI:MGI:1923502
See related	Ensembl:ENSMUSG00000039347 AllianceGenome:MGI:1923502
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	NM9.2; 0610006O14Rik
Summary	Predicted to enable proton-transporting ATPase activity, rotational mechanism. Predicted to be involved in proton transmembrane transport. Predicted to act upstream of or within ion transport. Predicted to be located in membrane. Predicted to be integral component of membrane. Predicted to be part of proton-transporting V-type ATPase, V0 domain. Is expressed in several structures, including genitourinary system; nervous system; sensory organ; and tongue. Orthologous to human ATP6V0E2 (ATPase H ⁺ transporting V0 subunit e2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in cortex adult (RPKM 116.9), cerebellum adult (RPKM 109.2) and 20 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

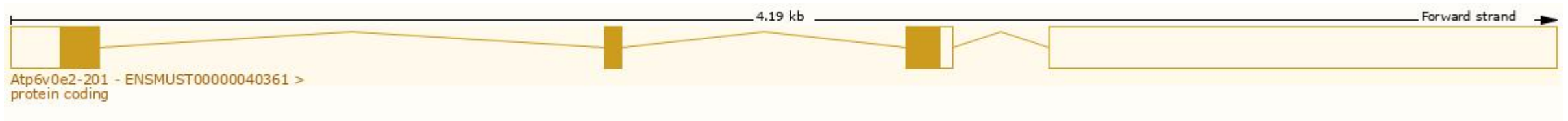
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

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

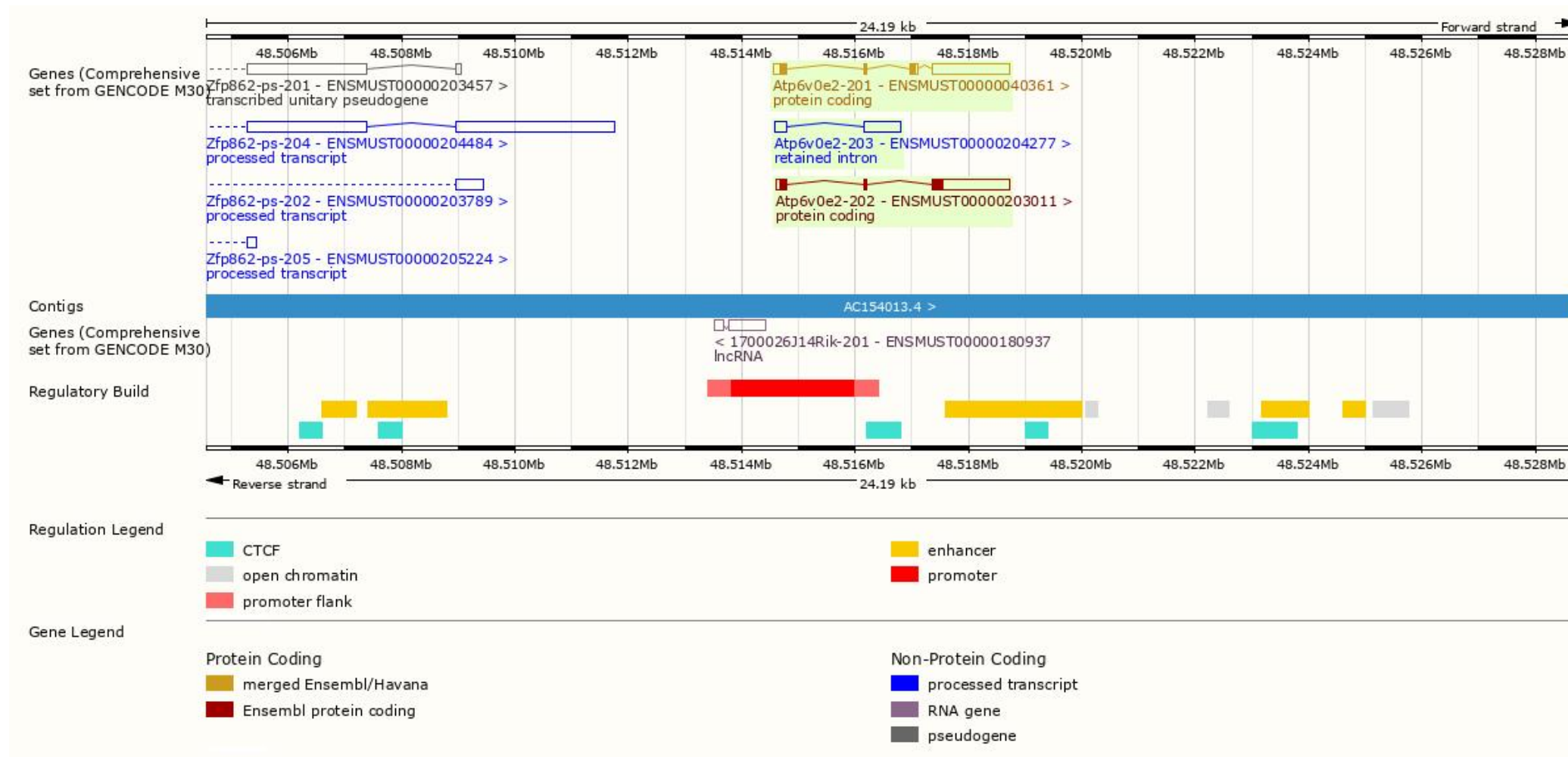
Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
ENSMUST00000203011.2	Atp6v0e2-202	1612	112aa	Protein coding	CCDS85039	ADA0N4SVQ2	Ensembl Canonical	GENCODE basic TSL:2
ENSMUST00000040361.8	Atp6v0e2-201	1789	81aa	Protein coding	CCDS20103	Q91XE7	GENCODE basic	APPRIS P1 TSL:1
ENSMUST00000204277.2	Atp6v0e2-203	857	No protein	Retained intron			TSL:2	

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

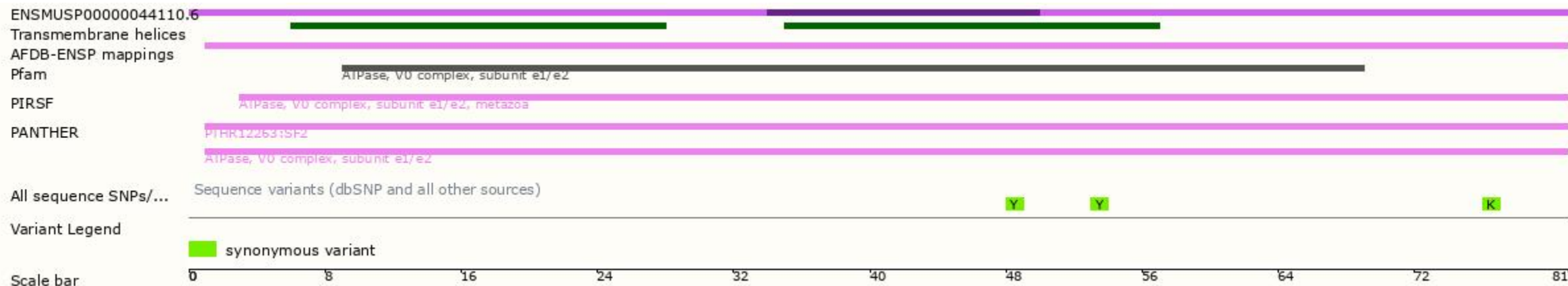


Source: <https://www.ensembl.org>

Genomic Information



Protein Information



Mouse Phenotype Information (MGI)

- The phenotype of mice homozygous for this gene is unknown

Important Information

- According to MGI, the phenotype of mice homozygous for this gene is unknown.
- The insertion site was about 1.5 kb from the 5' end of *1700026J14Rik* gene, and this strategy may affect the regulation of the 5' end of *1700026J14Rik* gene.
- *Atp6v0e2* is located on Chr6. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.