

Atp6v1e1 Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Atp6v1e1

Project type

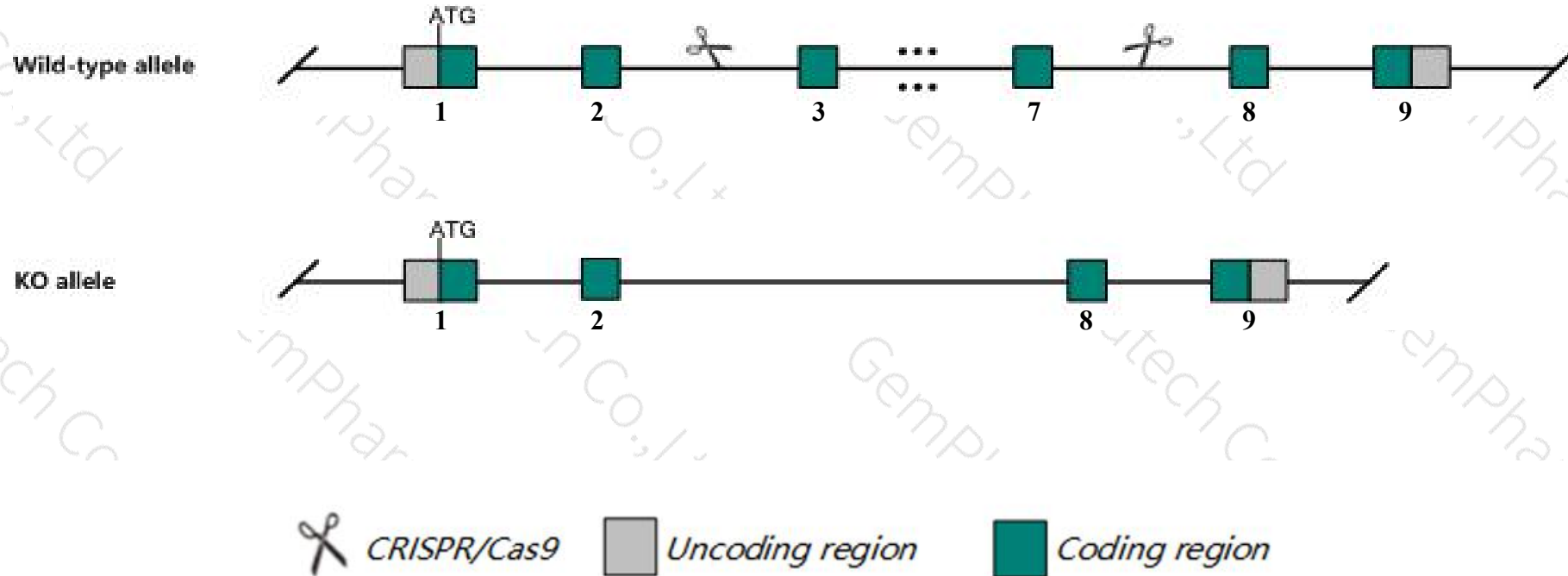
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp6v1e1* gene. The schematic diagram is as follows:



- The *Atp6v1e1* gene has 6 transcripts. According to the structure of *Atp6v1e1* gene, exon3-exon7 of *Atp6v1e1-201* (ENSMUST00000019354.10) transcript is recommended as the knockout region. The region contains 431bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp6v1e1* gene. The brief process is as follows: CRISPR/Cas9 syst

- The *Atp6v1e1* 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.
- Transcript 204 CDS 5' incomplete the influences is unknown; Transcript 205,206 CDS 3' incomplete the influences is unknown
- 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)

Atp6v1e1 ATPase, H⁺ transporting, lysosomal V1 subunit E1 [Mus musculus (house mouse)]

Gene ID: 11973, updated on 7-Apr-2019

Summary

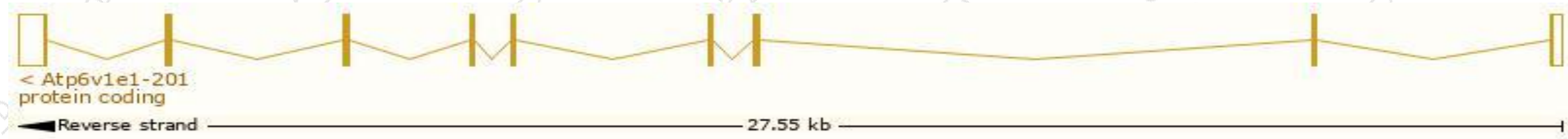
Official Symbol	Atp6v1e1 provided by MGI
Official Full Name	ATPase, H ⁺ transporting, lysosomal V1 subunit E1 provided by MGI
Primary source	MGI:MGI:894326
See related	Ensembl:ENSMUSG00000019210
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410029D23Rik, Atp6e, Atp6e2, Atp6v1e, D6Ert385e, Vma4, p31
Expression	Ubiquitous expression in cortex adult (RPKM 139.1), frontal lobe adult (RPKM 137.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

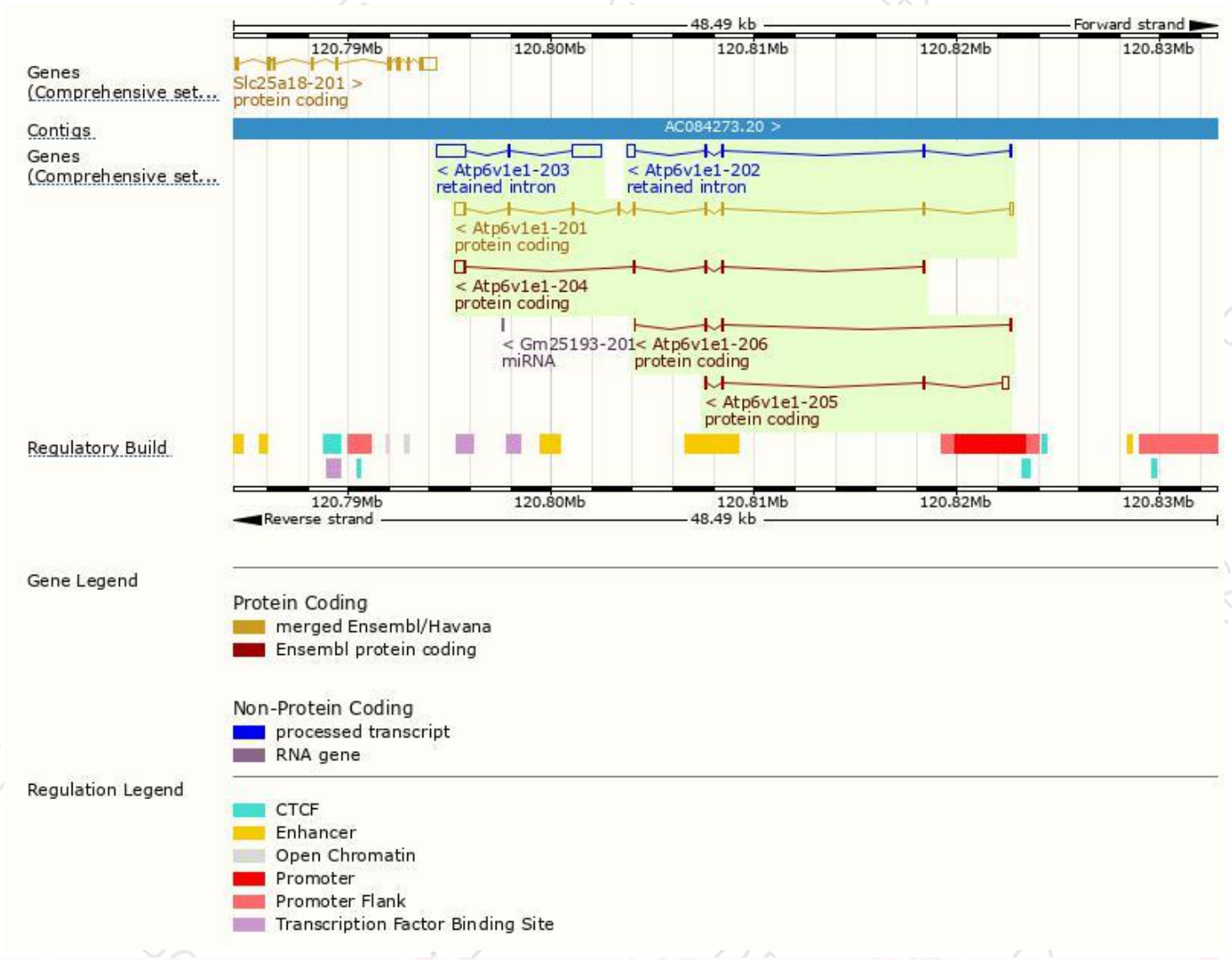
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp6v1e1-201	ENSMUST00000019354.10	1312	226aa	Protein coding	CCDS20484	P50518	TSL:1 Gencode basic APPRIS P1
Atp6v1e1-204	ENSMUST000000203783.2	835	128aa	Protein coding	-	A0A0N4SW07	CDS 5' incomplete TSL:5
Atp6v1e1-205	ENSMUST000000204699.1	517	78aa	Protein coding	-	A0A0N4SWA3	CDS 3' incomplete TSL:3
Atp6v1e1-206	ENSMUST000000205049.2	334	87aa	Protein coding	-	A0A0N4SW34	CDS 3' incomplete TSL:3
Atp6v1e1-203	ENSMUST000000203527.1	2928	No protein	Retained intron	-	-	TSL:1
Atp6v1e1-202	ENSMUST000000203432.1	731	No protein	Retained intron	-	-	TSL:2

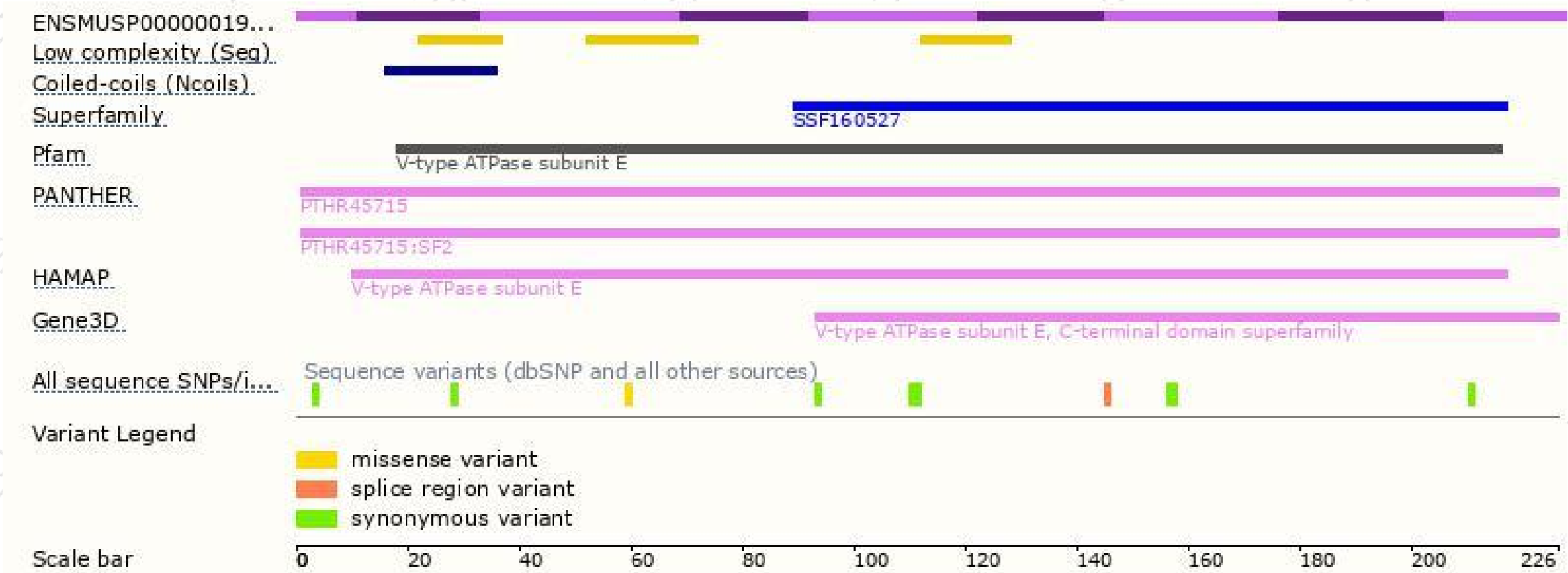
The strategy is based on the design of *Atp6v1e1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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