Atp6v0e Cas9-KO Strategy Romphamaxoch Collins

Designer: Comphannax Co./

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Project Overview



Project Name

Atp6v0e

Project type

Cas9-KO

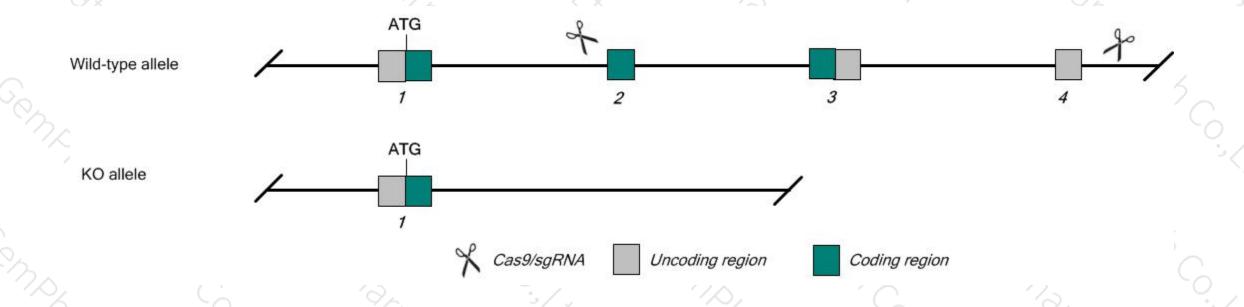
Strain background

C57BL/6J

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Atp6v0e gene. The schematic diagram is as follows:



Technical routes



- The *Atp6v0e* gene has 5 transcripts. According to the structure of *Atp6v0e* gene, exon2-4 of *Atp6v0e*-201 (ENSMUST00000015719.15) transcript is recommended as the knockout region. The region contains 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 *Atp6v0e* 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.

Notice



- The *Atp6v0e* gene is located on the Chr17. 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)



Atp6v0e ATPase, H+ transporting, lysosomal V0 subunit E [Mus musculus (house mouse)]

Gene ID: 11974, updated on 8-Jun-2019

Summary

Official Symbol Atp6v0e provided by MGI

Official Full Name ATPase, H+ transporting, lysosomal VO subunit E provided by MGI

Primary source MGI:MGI:1328318

See related Ensembl: ENSMUSG00000015575

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 M9.2; Atp6k; Atp6v0e1

Expression Ubiquitous expression in genital fat pad adult (RPKM 163.1), kidney adult (RPKM 139.8) and 28 other tissues See more

Orthologs human all

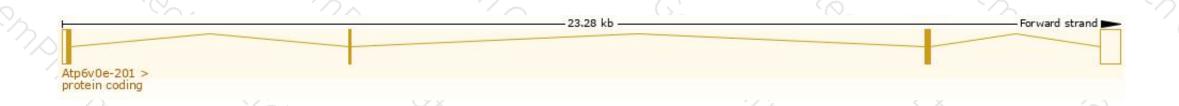
Transcript information (Ensembl)



The gene has 5 transcripts, and all transcripts are shown below:

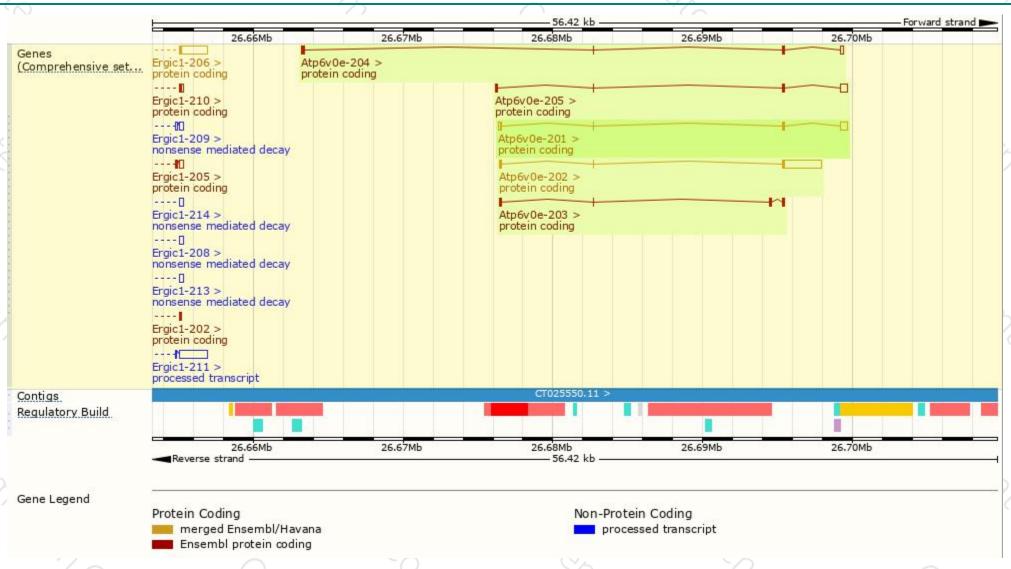
Name 🝦	Transcript ID 👙	bp 🌲	Protein 🍦	Biotype 🍦	CCDS 🍦	UniProt 🌲	Flags
Atp6v0e-202	ENSMUST00000167352.1	2812	<u>81aa</u>	Protein coding	CCDS28554 ₽	<u>Q9CQD8</u> ₽	TSL:1 GENCODE basic APPRIS P1
Atp6v0e-201	ENSMUST00000015719.15	823	<u>81aa</u>	Protein coding	CCDS28554 ₽	Q9CQD8₽	TSL:1 GENCODE basic APPRIS P1
Atp6v0e-205	ENSMUST00000236867.1	772	<u>86aa</u>	Protein coding	2	62	GENCODE basic
Atp6∨0e-204	ENSMUST00000236346.1	494	<u>80aa</u>	Protein coding	8	12	GENCODE basic
Atp6v0e-203	ENSMUST00000236299.1	442	<u>104aa</u>	Protein coding	2	79	GENCODE basic

The strategy is based on the design of *Atp6v0e-201* transcript, The transcription is shown below



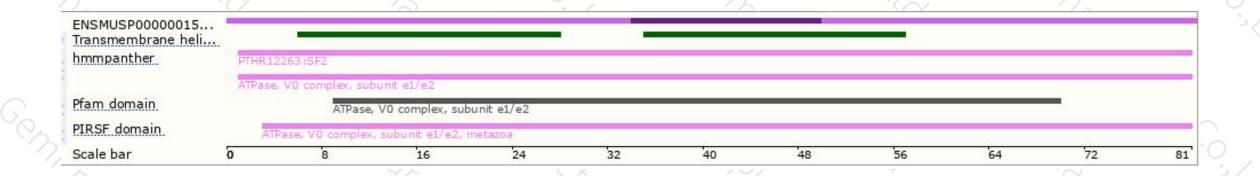
Genomic location (Ensembl)





Protein domain (Ensembl)





If you have any questions, you are welcome to inquire. Tel: 025-5864 1534





