

Atp6v0c Cas9-KO Strategy

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Project Overview

Project Name

Atp6v0c

Project type

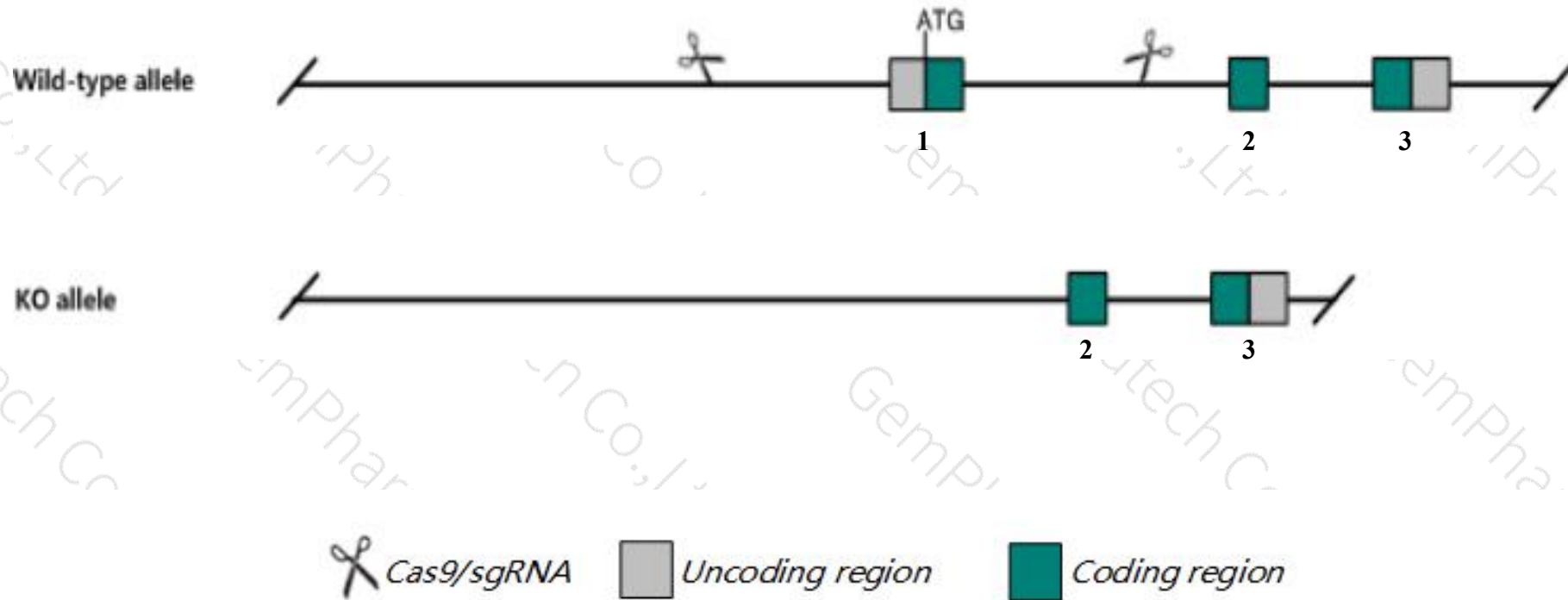
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp6v0c* gene. The schematic diagram is as follows:



- The *Atp6v0c* gene has 6 transcripts. According to the structure of *Atp6v0c* gene, exon1 of *Atp6v0c-201* (ENSMUST00000024932.11) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp6v0c* 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.

- According to the existing MGI data, Homozygous mutation of this gene results in embryonic lethality.
- The *Atp6v0c* 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 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)

Atp6v0c ATPase, H⁺ transporting, lysosomal V0 subunit C [Mus musculus (house mouse)]

Gene ID: 11984, updated on 31-Jan-2019

Summary



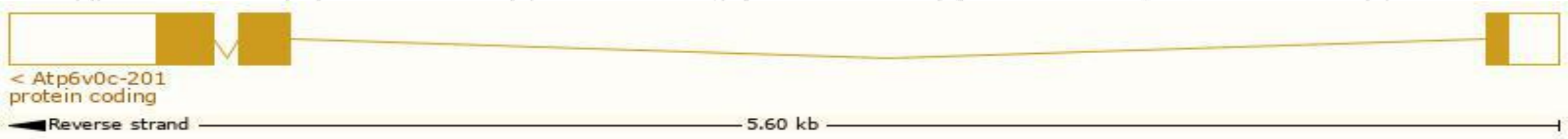
Official Symbol	Atp6v0c provided by MGI
Official Full Name	ATPase, H ⁺ transporting, lysosomal V0 subunit C provided by MGI
Primary source	MGI:MGI:88116
See related	Ensembl:ENSMUSG00000024121
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Atp6c, Atp6c2, Atp6l, Atpl, Atpl-rs1, PL16, VATL, Vma3
Expression	Ubiquitous expression in kidney adult (RPKM 768.5), adrenal adult (RPKM 629.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

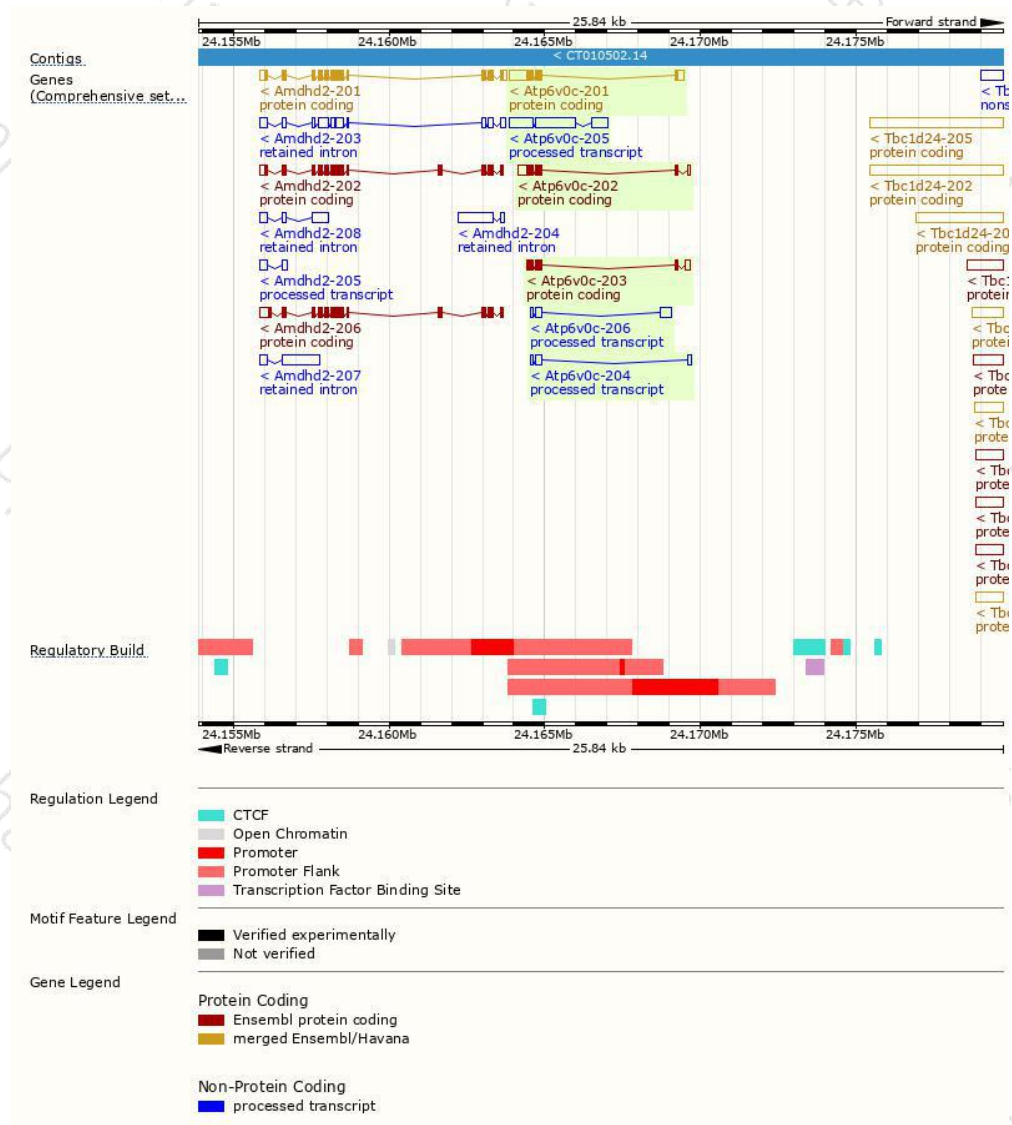
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp6v0c-201	ENSMUST00000024932.11	1183	155aa	Protein coding	CCDS28476	A3KML5 P63082	TSL:1 GENCODE basic APPRIS P1
Atp6v0c-202	ENSMUST00000098862.8	796	155aa	Protein coding	CCDS28476	A3KML5 P63082	TSL:2 GENCODE basic APPRIS P1
Atp6v0c-203	ENSMUST00000148541.7	609	150aa	Protein coding	-	E9Q9C5	CDS 3' incomplete TSL:3
Atp6v0c-205	ENSMUST00000151061.1	2567	No protein	Processed transcript	-	-	TSL:5
Atp6v0c-206	ENSMUST00000156061.1	607	No protein	Processed transcript	-	-	TSL:2
Atp6v0c-204	ENSMUST00000150647.1	351	No protein	Processed transcript	-	-	TSL:3

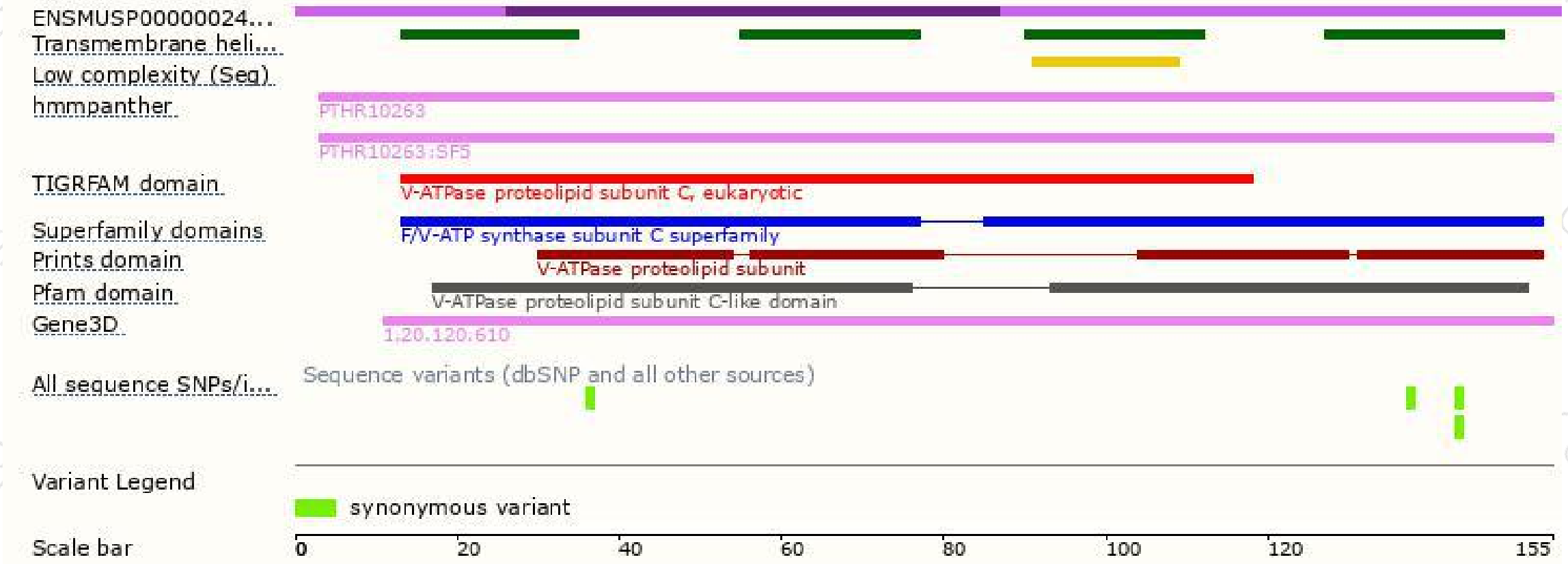
The strategy is based on the design of *Atp6v0c-201* transcript,The transcription is shown below



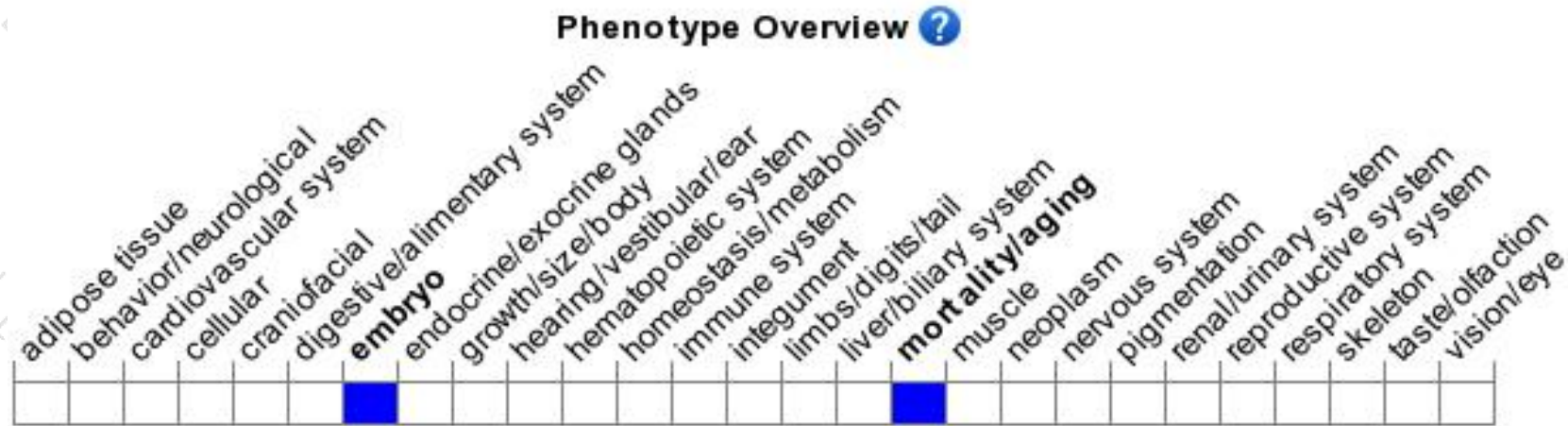
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Homozygous mutation of this gene results in embryonic lethality.

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

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