

Atp6v1a Cas9-CKO Strategy

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Project Overview

Project Name

Atp6v1a

Project type

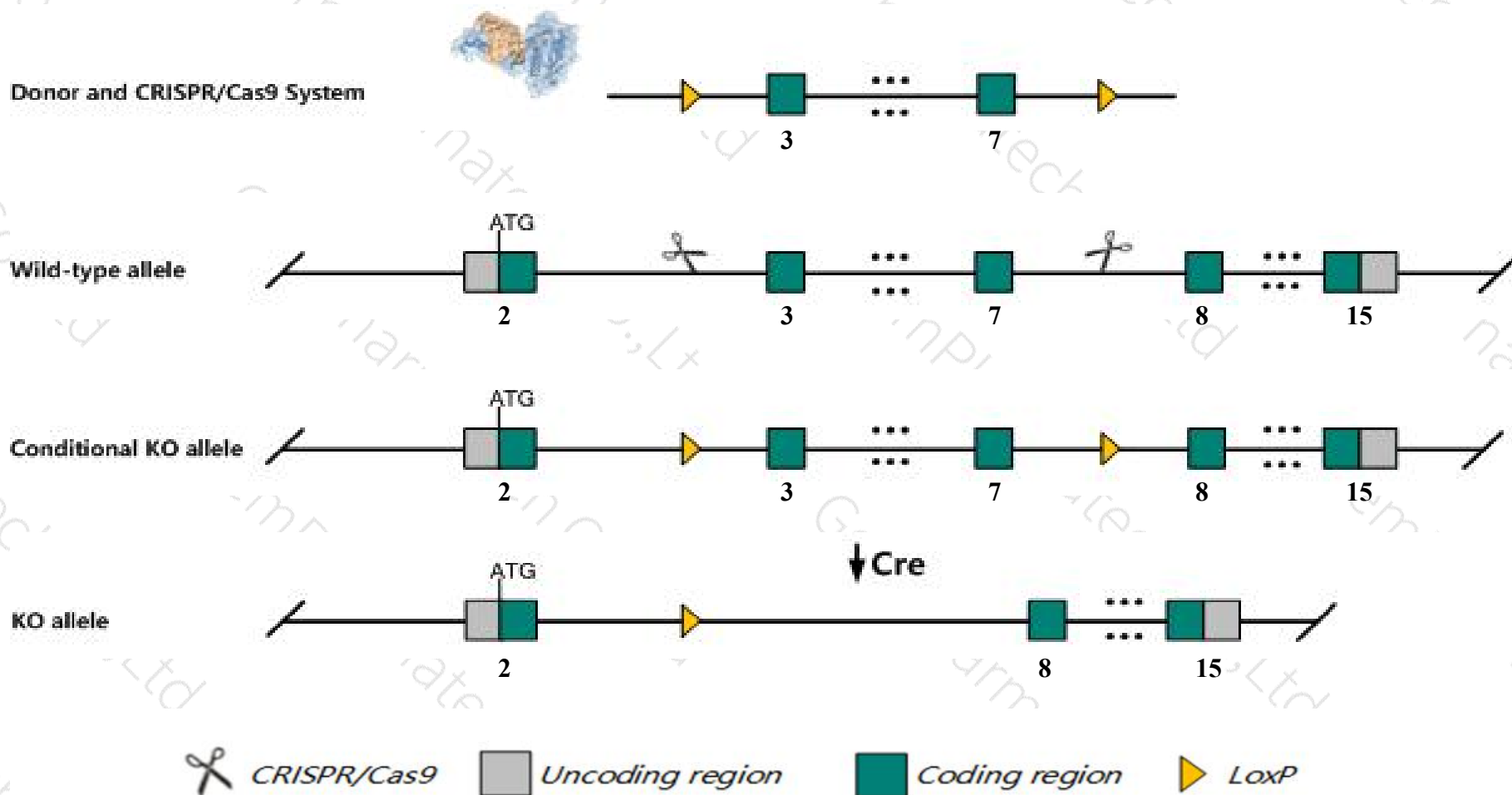
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp6v1a* gene. The schematic diagram is as follows:



- The *Atp6v1a* gene has 6 transcripts. According to the structure of *Atp6v1a* gene, exon3-exon7 of *Atp6v1a*-202 (ENSMUST00000114666.8) transcript is recommended as the knockout region. The region contains 797bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp6v1a* 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- 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.

Notice

- The *Atp6v1a* gene is located on the Chr16. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Atp6v1a ATPase, H⁺ transporting, lysosomal V1 subunit A [*Mus musculus* (house mouse)]

Gene ID: 11964, updated on 9-Feb-2020

Summary

- Official Symbol** Atp6v1a provided by [MGI](#)
- Official Full Name** ATPase, H⁺ transporting, lysosomal V1 subunit A provided by [MGI](#)
- Primary source** [MGI:MGI:1201780](#)
- See related** [Ensembl:ENSMUSG00000052459](#)
- 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** VA68; VPP2; Atp6a1; Atp6a2; AI647066; Atp6v1a1
- Expression** Broad expression in cerebellum adult (RPKM 59.0), frontal lobe adult (RPKM 52.8) and 24 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 16; 16 B4 [See Atp6v1a in Genome Data Viewer](#)

Exon count: 16

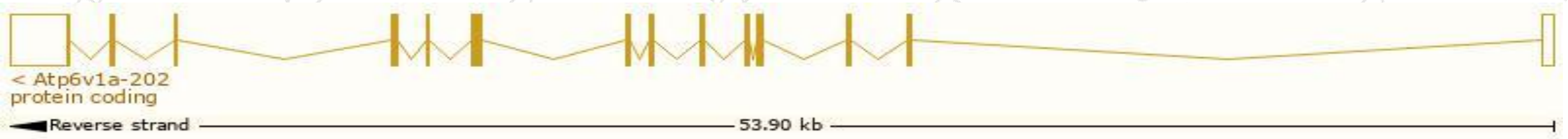
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	16	NC_000082.6 (44085402..44139702, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	16	NC_000082.5 (44085517..44139132, complement)

Transcript information (Ensembl)

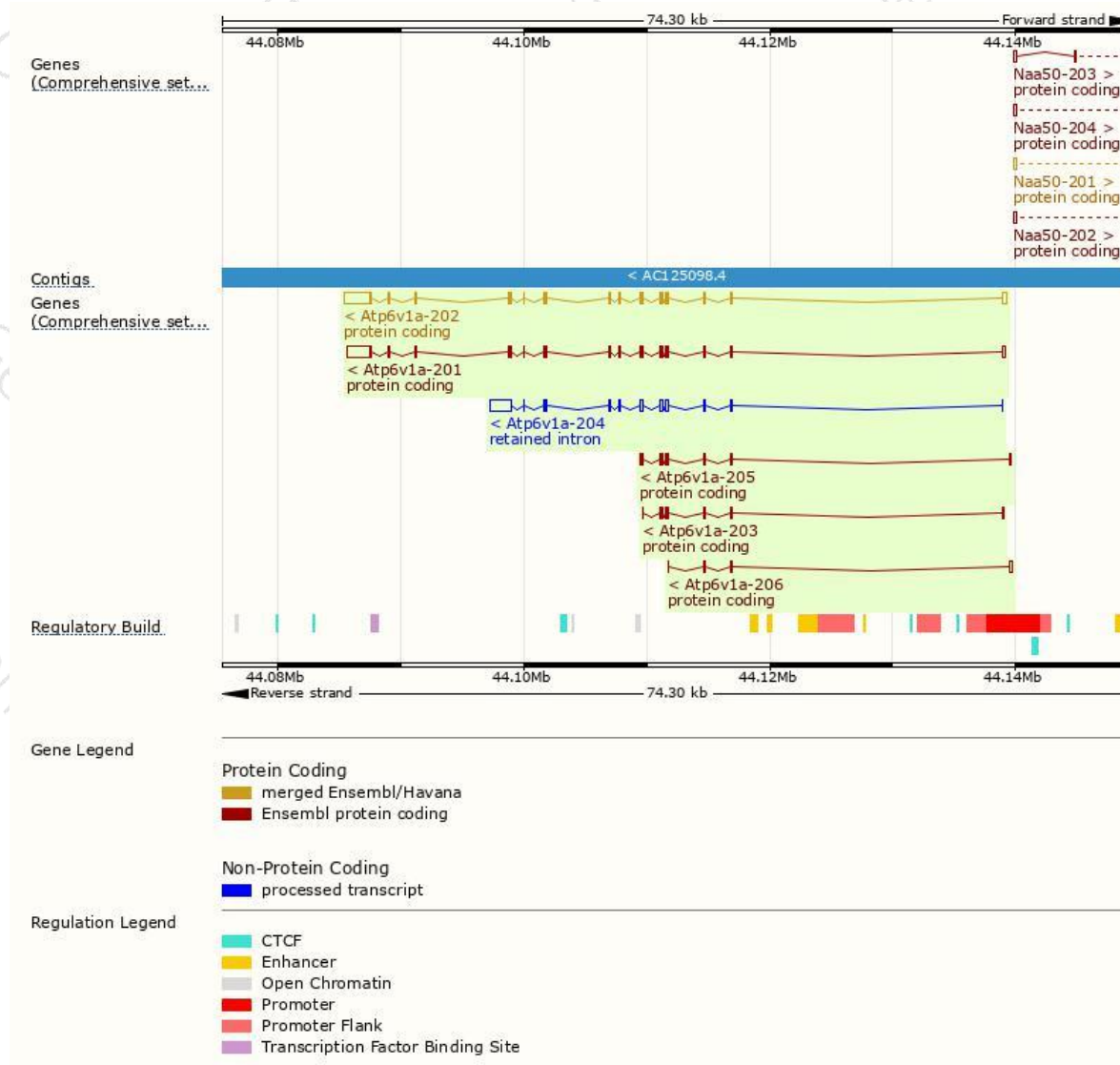
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp6v1a-202	ENSMUST00000114666.8	4234	617aa	Protein coding	CCDS28182	P50516	TSL:1 GENCODE basic APPRIS P1
Atp6v1a-201	ENSMUST00000063661.12	3896	617aa	Protein coding	CCDS28182	P50516	TSL:1 GENCODE basic APPRIS P1
Atp6v1a-205	ENSMUST00000137557.7	894	237aa	Protein coding	-	D3Z1B9	CDS 3' incomplete TSL:3
Atp6v1a-203	ENSMUST00000124102.7	629	196aa	Protein coding	-	D3YWH3	CDS 3' incomplete TSL:5
Atp6v1a-206	ENSMUST00000147025.1	440	77aa	Protein coding	-	D3YZ23	CDS 3' incomplete TSL:5
Atp6v1a-204	ENSMUST00000130036.1	3093	No protein	Retained intron	-	-	TSL:1

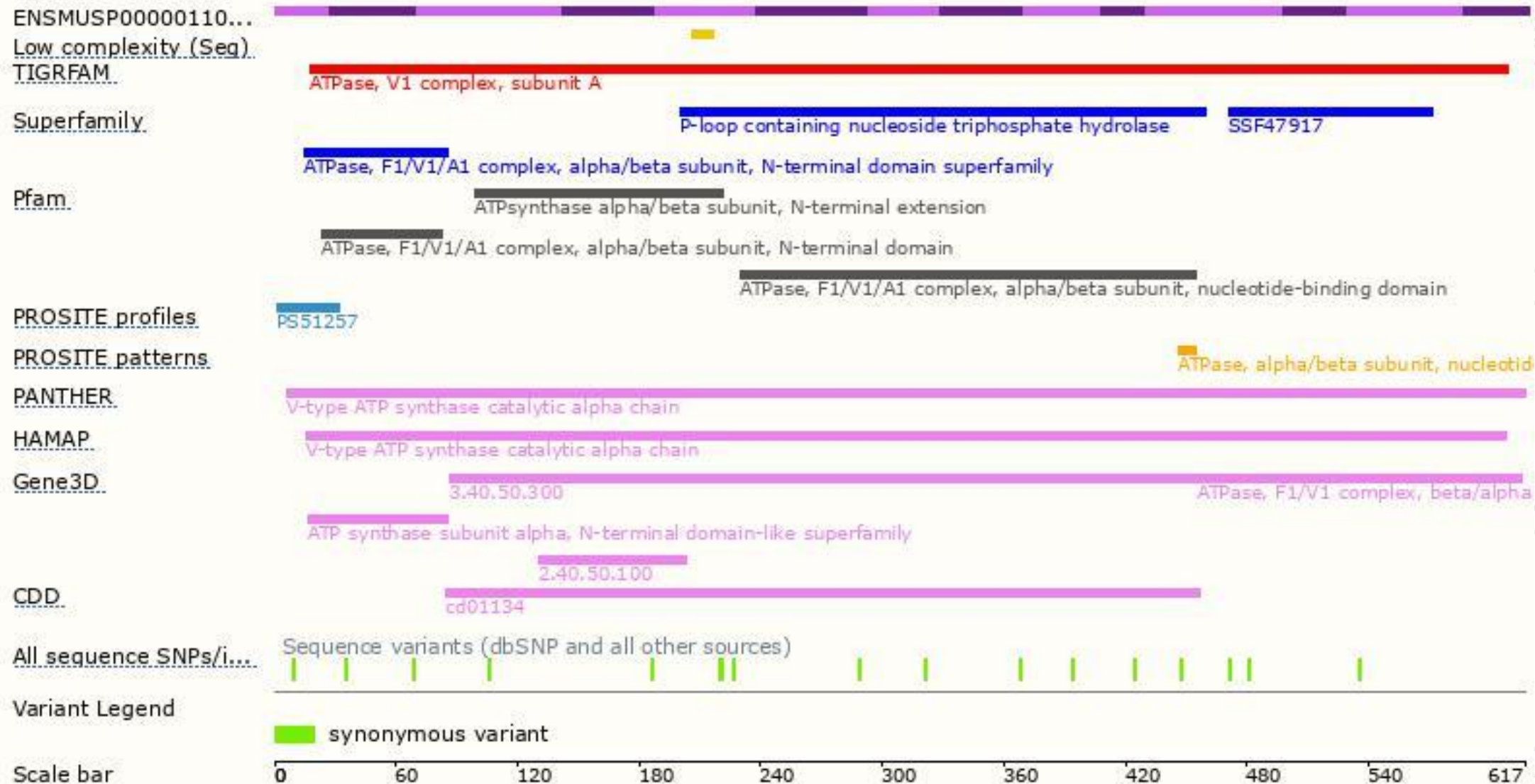
The strategy is based on the design of *Atp6v1a-202* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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