Atp6v0e Cas9-CKO *Strategy*

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Project Overview

Project Name	***Atp6v0e***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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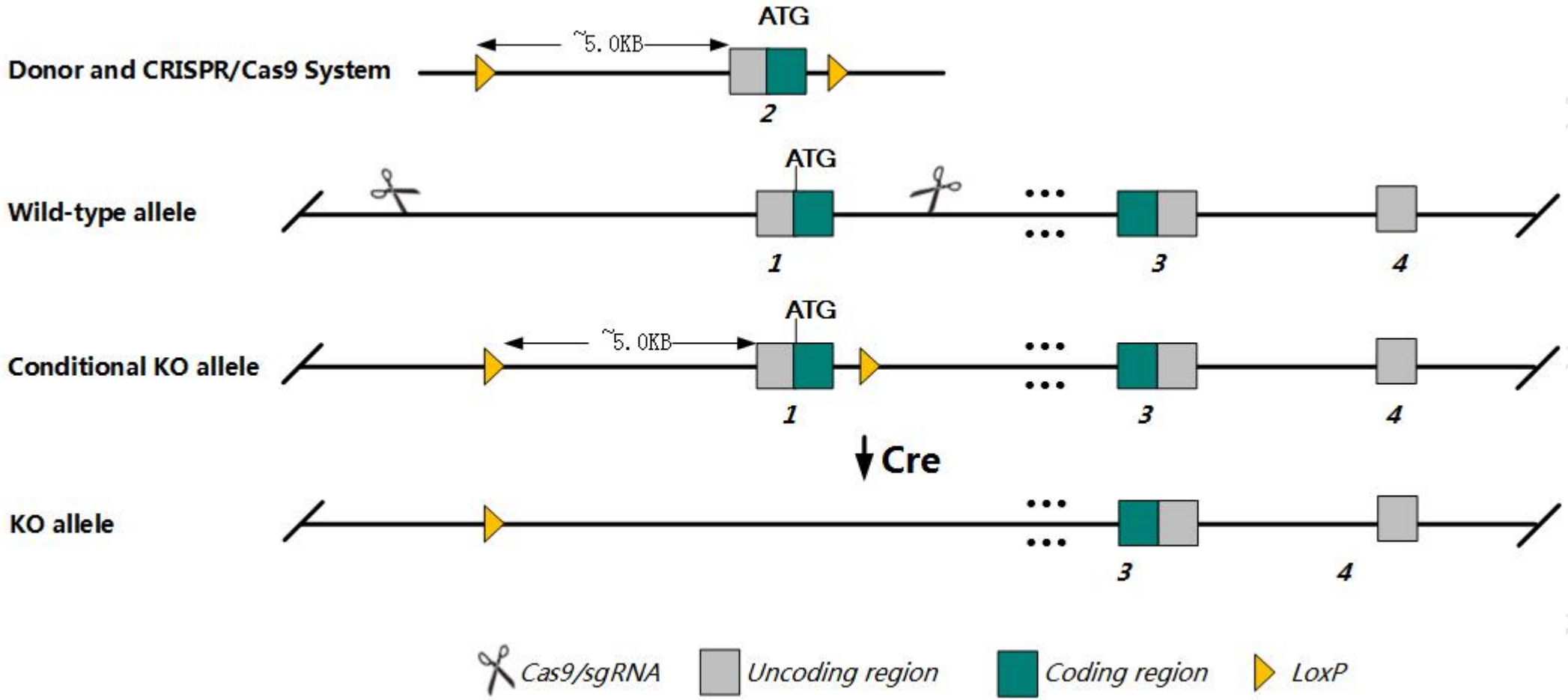
This model will use CRISPR/Cas9 technology to edit the *Atp6v0e* gene. The schematic diagram is as follows:



Technical routes

- The *Atp6v0e* gene has 5 transcript.According to the structure of *Atp6v0e* gene, *Atp6v0e*-201 (ENSMUST00000015719.15) transcript is recommended as the knockout region.The region contains the predicted promoter region and E1.Knock out the region will result in disruption of the gene.

- In this project we use CRISPR/Cas9 technology to modify *Atp6v0e* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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 or cell types.

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 biological processes, all risk of the loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

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

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

Summary

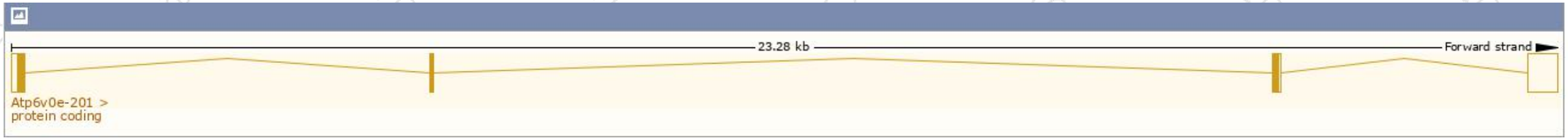
Official Symbol	Atp6v0e provided by MGI
Official Full Name	ATPase, H+ transporting, lysosomal V0 subunit E provided by MGI
Primary source	MGI:MGI:1328318
See related	Ensembl:ENSMUSG00000015575
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; 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）

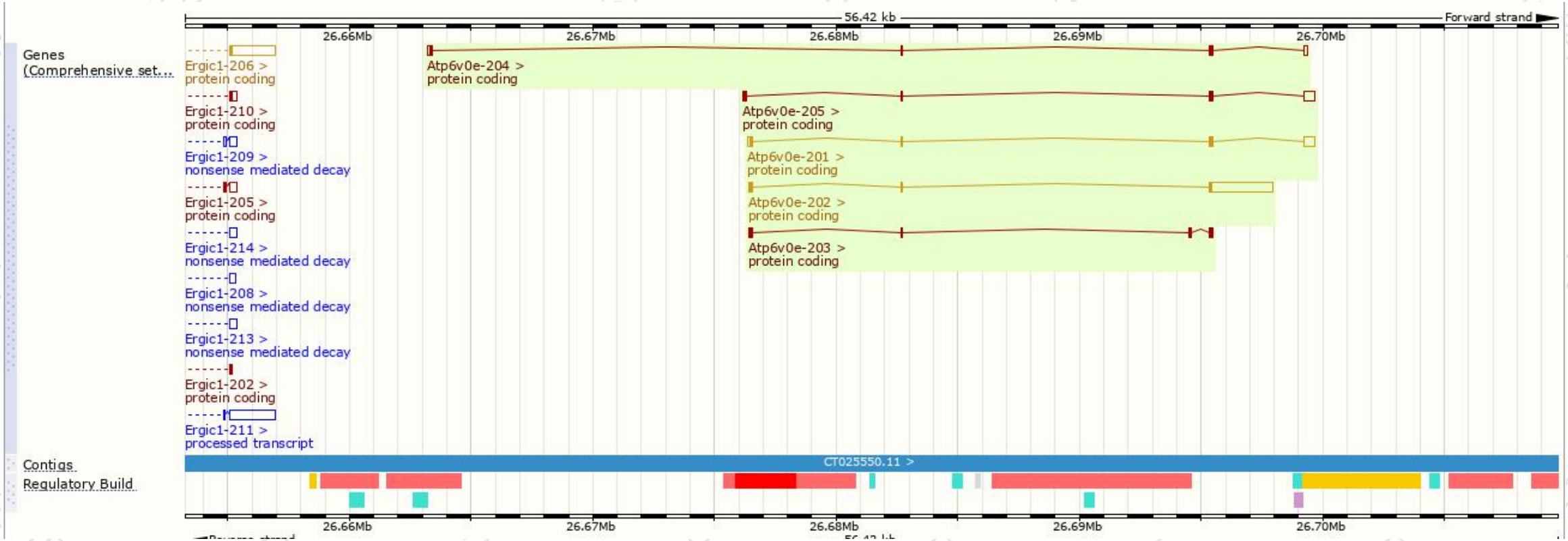
The gene has 5 transcripts, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp6v0e-201	ENSMUST00000015719.15	823	81aa	Protein coding	CCDS28554	Q9CQD8	TSL:1 GENCODE basic APPRIS P1
Atp6v0e-202	ENSMUST00000167352.1	2812	81aa	Protein coding	CCDS28554	Q9CQD8	TSL:1 GENCODE basic APPRIS P1
Atp6v0e-203	ENSMUST00000236299.1	442	104aa	Protein coding	-	-	GENCODE basic
Atp6v0e-204	ENSMUST00000236346.1	494	80aa	Protein coding	-	-	GENCODE basic
Atp6v0e-205	ENSMUST00000236867.1	772	86aa	Protein coding	-	-	GENCODE basic

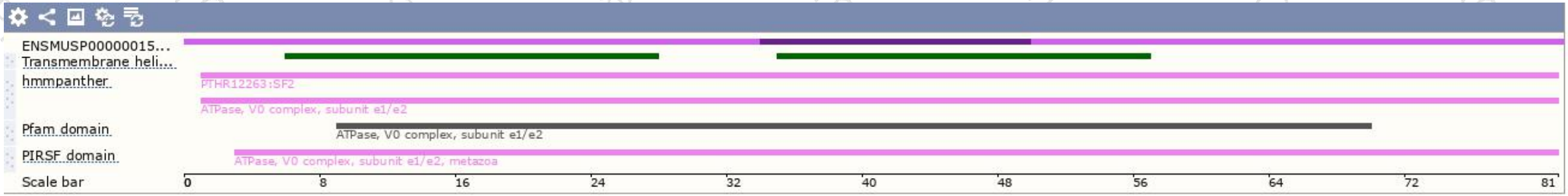
The strategy is based on the design of *Atp6v0e*-201 transcript,The transcription is shown below



Genomic location distribution



Protein domain



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