

***Atp5l* Cas9-CKO Strategy**

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Project Overview

Project Name

Atp5l

Project type

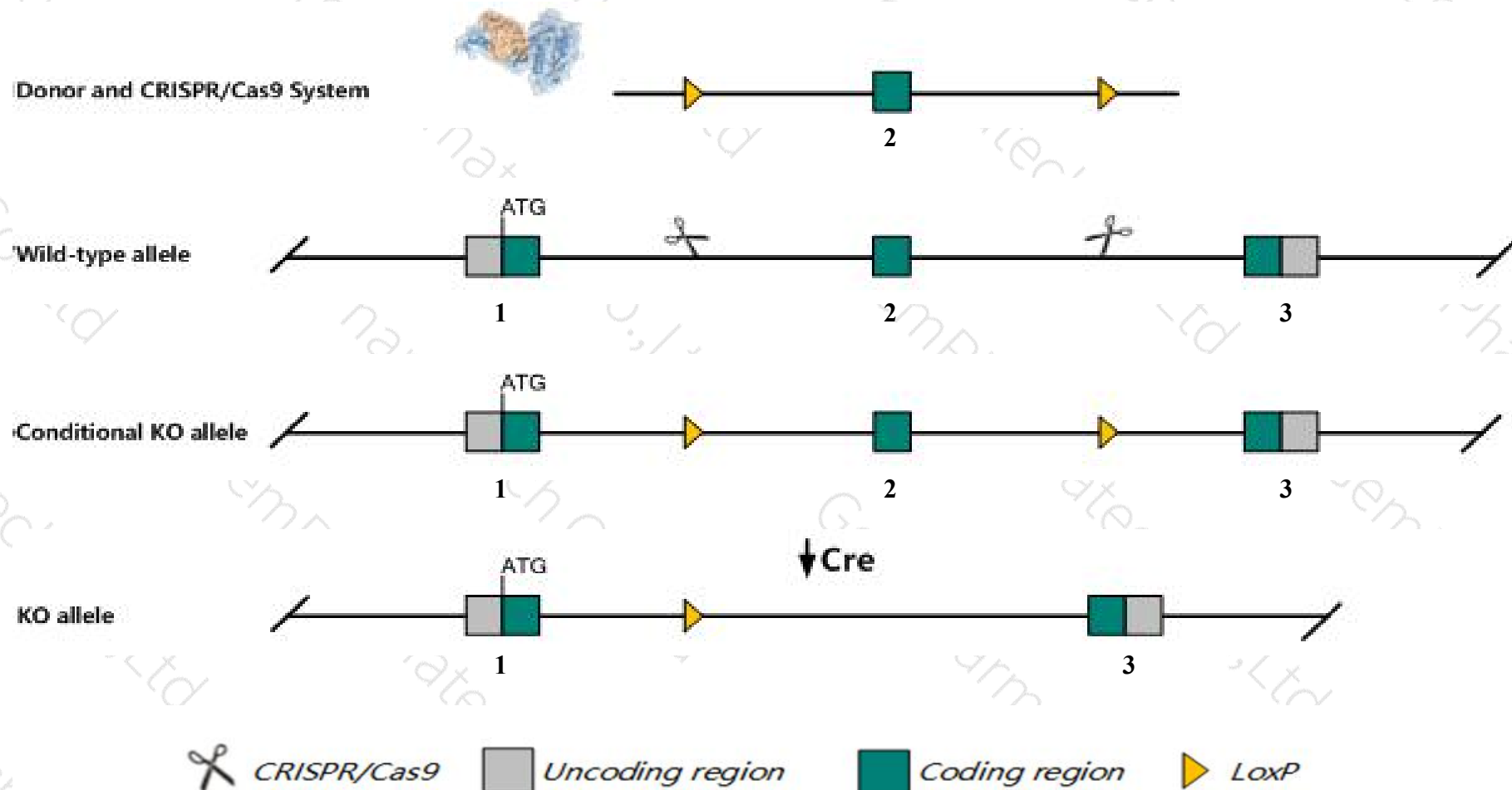
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp5l* gene. The schematic diagram is as follows:



Technical routes

- The *Atp5l* gene has 4 transcripts. According to the structure of *Atp5l* gene, exon2 of *Atp5l-201*(ENSMUST00000043675.8) transcript is recommended as the knockout region. The region contains 161bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp5l* 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 *Atp5l* gene is located on the Chr9. 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)

Atp5l ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit G [Mus musculus (house mouse)]

Gene ID: 27425, updated on 13-Mar-2020

Summary



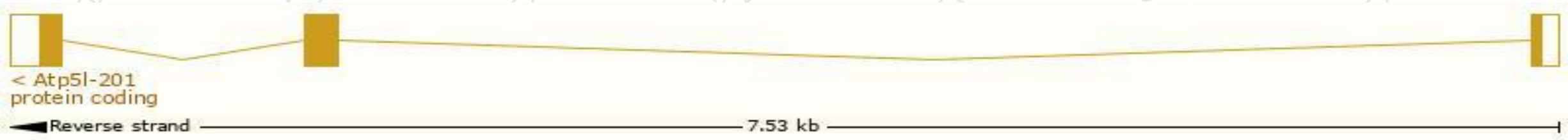
Official Symbol	Atp5l provided by MGI
Official Full Name	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit G provided by MGI
Primary source	MGI:MGI:1351597
See related	Ensembl:ENSMUSG00000038717
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4933437C06Rik, Atp5mg
Expression	Ubiquitous expression in heart adult (RPKM 309.5), kidney adult (RPKM 211.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

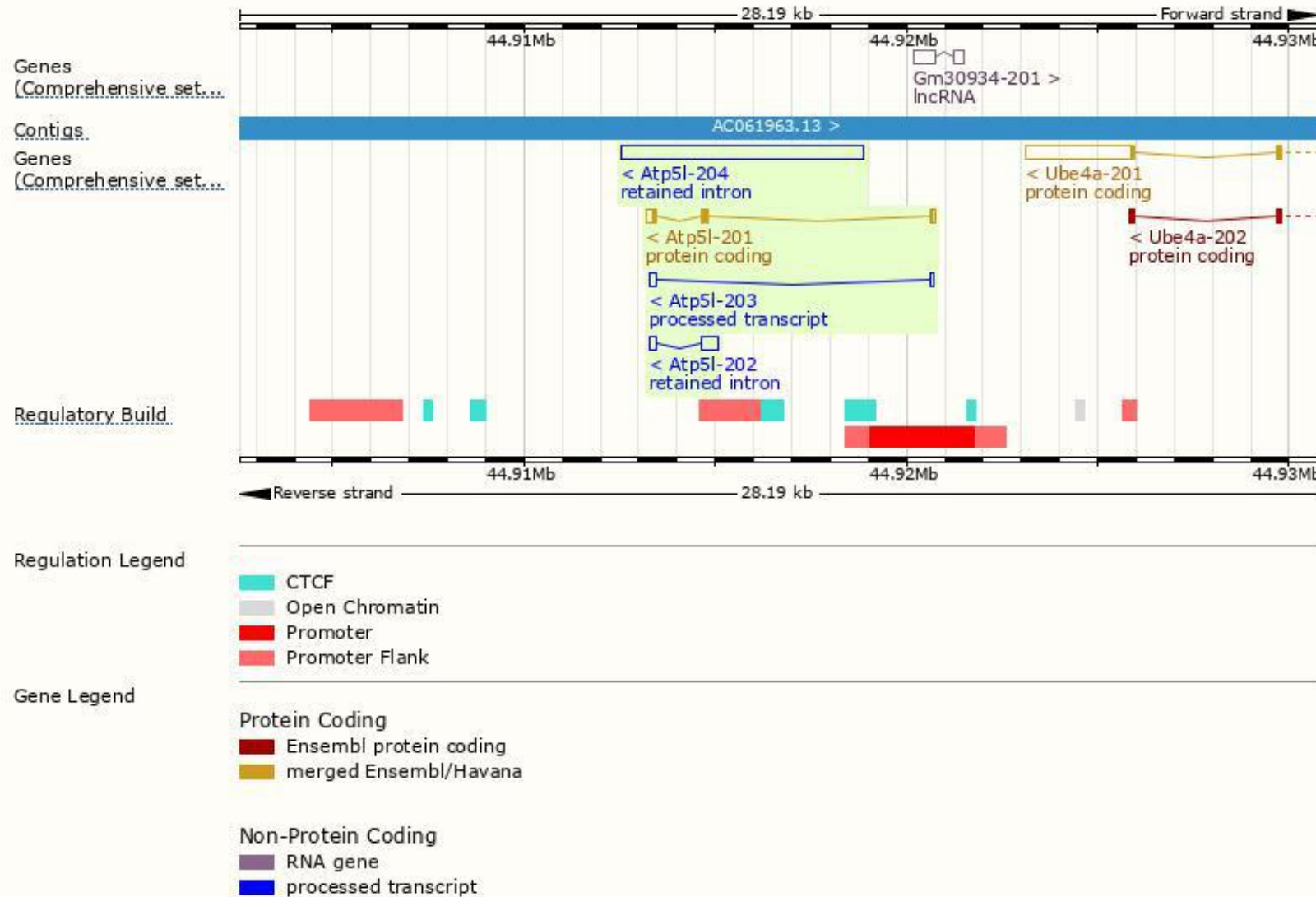
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp5l-201	ENSMUST00000043675.8	544	103aa	Protein coding	CCDS40604	Q9CPQ8	TSL:1 GENCODE basic APPRIS P1
Atp5l-203	ENSMUST00000216380.1	295	No protein	Processed transcript	-	-	TSL:1
Atp5l-204	ENSMUST00000216815.1	6310	No protein	Retained intron	-	-	TSL:NA
Atp5l-202	ENSMUST00000213999.1	608	No protein	Retained intron	-	-	TSL:2

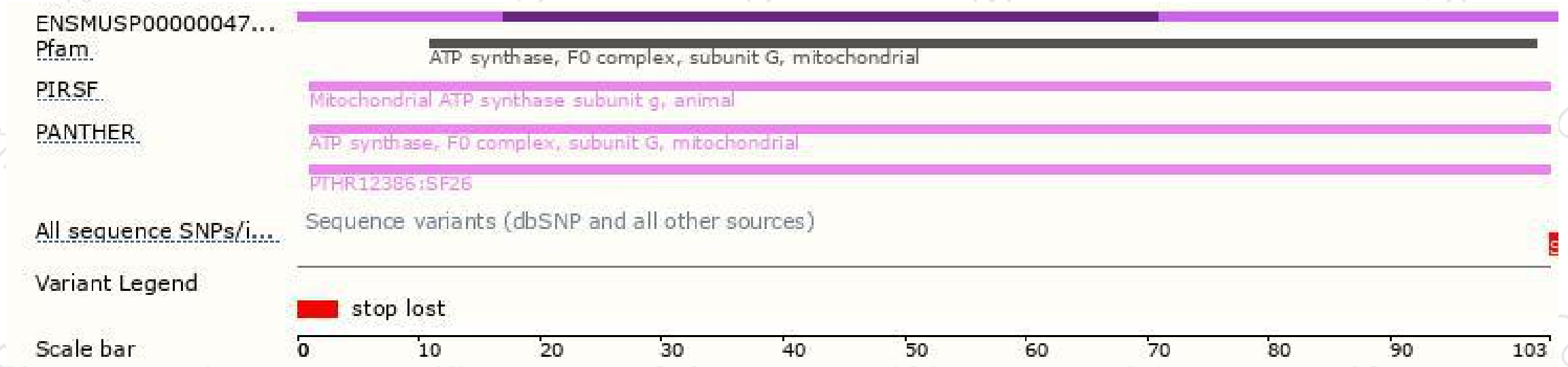
The strategy is based on the design of *Atp5l-201* transcript,the transcription is shown below:



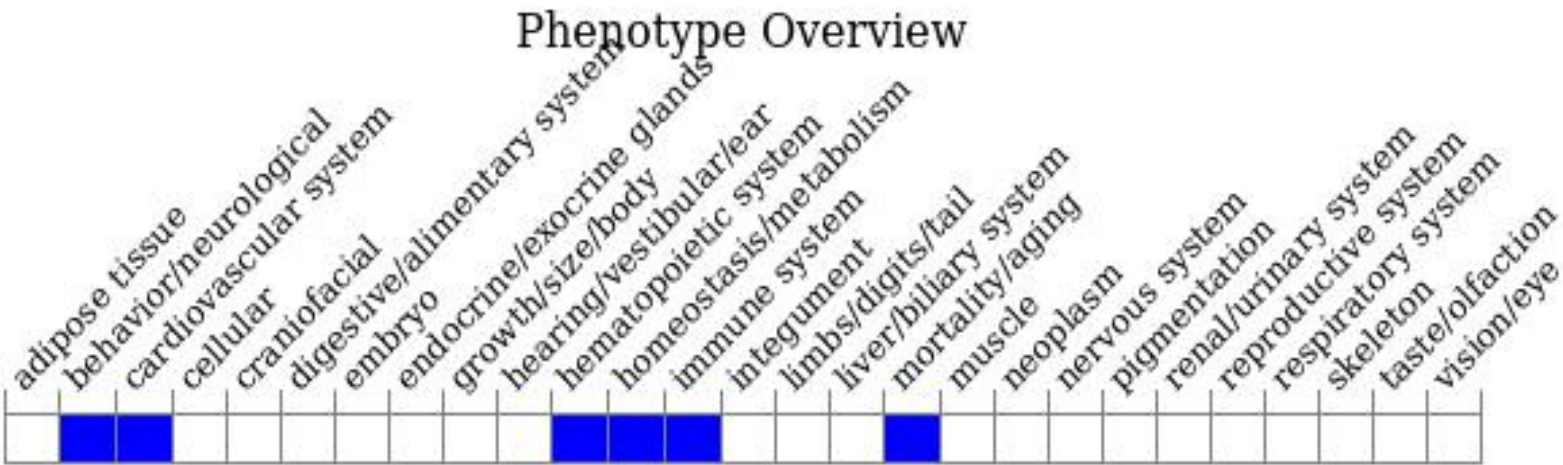
Genomic location distribution



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/>).

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

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