

Atp5g2 Cas9-KO Strategy

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Project Overview

Project Name

Atp5g2

Project type

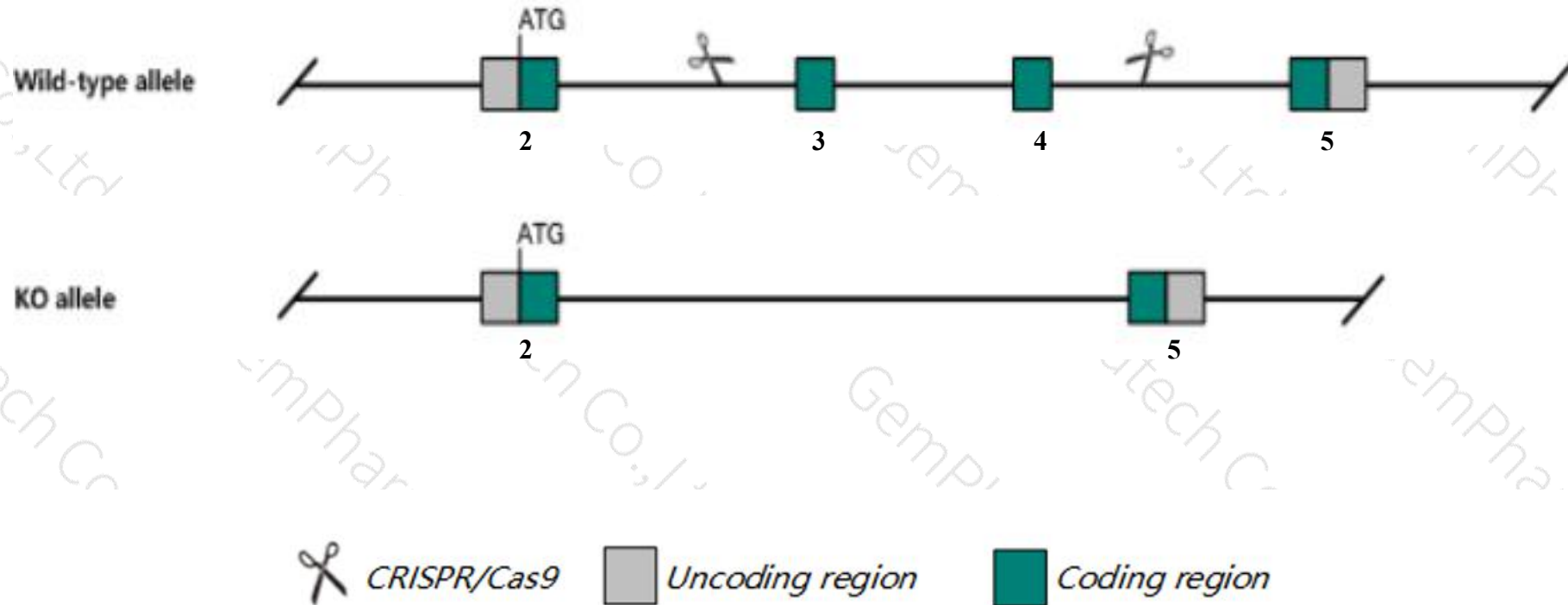
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp5g2* gene. The schematic diagram is as follows:



- The *Atp5g2* gene has 4 transcripts. According to the structure of *Atp5g2* gene, exon3-exon4 of *Atp5g2-202* (ENSMUST00000185641.6) transcript is recommended as the knockout region. The region contains 287bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp5g2* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Atp5g2* gene is located on the Chr15. 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)

Atp5g2 ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit C2 (subunit 9) [*Mus musculus* (house mouse)]

Gene ID: 67942, updated on 13-Mar-2020

Summary



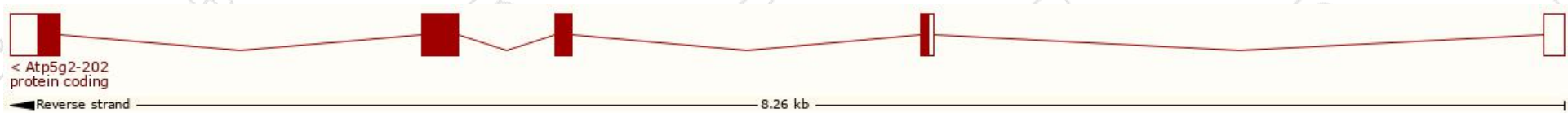
Official Symbol	Atp5g2 provided by MGI
Official Full Name	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit C2 (subunit 9) provided by MGI
Primary source	MGI:MGI:1915192
See related	Ensembl:ENSMUSG00000062683
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Atp5mc2; 1810041M08Rik
Expression	Ubiquitous expression in colon adult (RPKM 306.9), kidney adult (RPKM 301.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

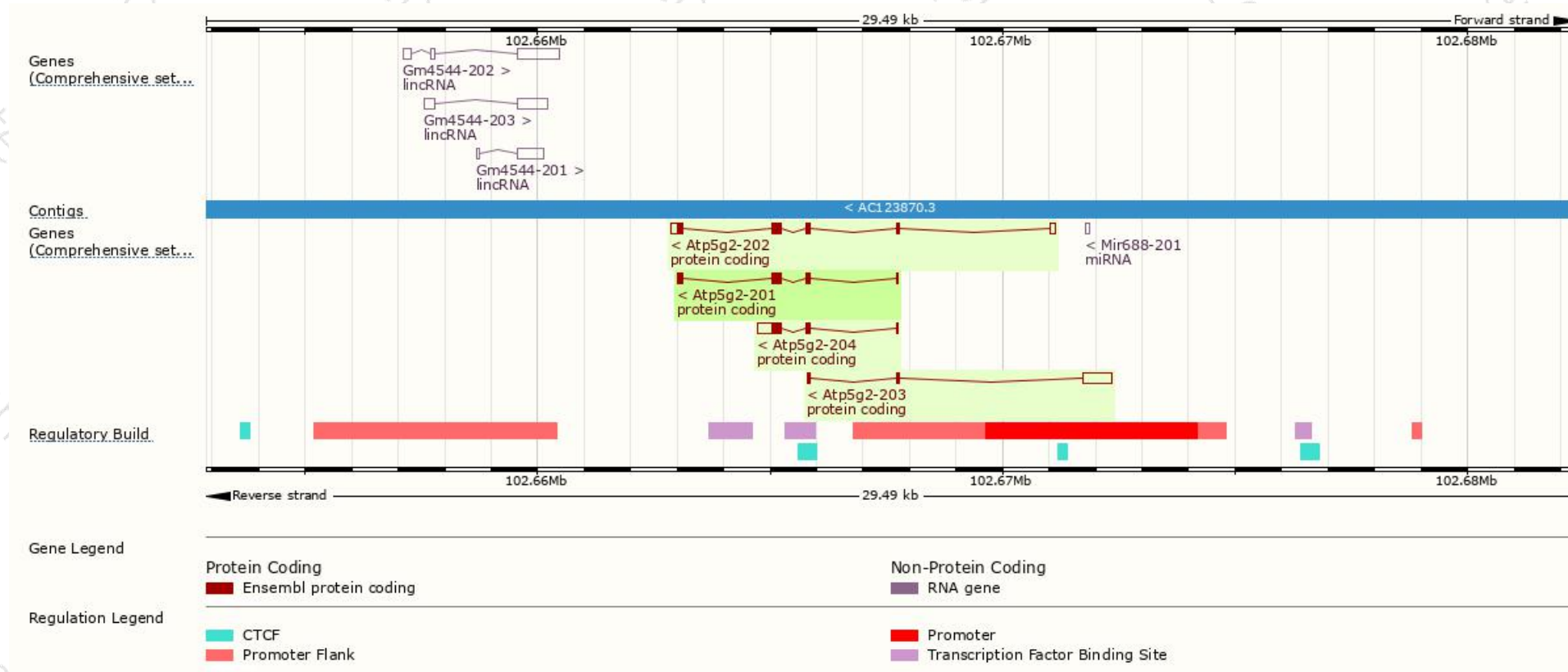
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp5g2-202	ENSMUST00000185641.6	731	146aa	Protein coding	CCDS27888	P56383	TSL:1 GENCODE basic APPRIS P1
Atp5g2-201	ENSMUST00000075630.9	441	146aa	Protein coding	CCDS27888	P56383	TSL:1 GENCODE basic APPRIS P1
Atp5g2-203	ENSMUST00000186952.1	753	31aa	Protein coding	-	A0A087WSE2	CDS 3' incomplete TSL:3
Atp5g2-204	ENSMUST00000187160.1	635	107aa	Protein coding	-	A0A087WQS5	CDS 5' incomplete TSL:2

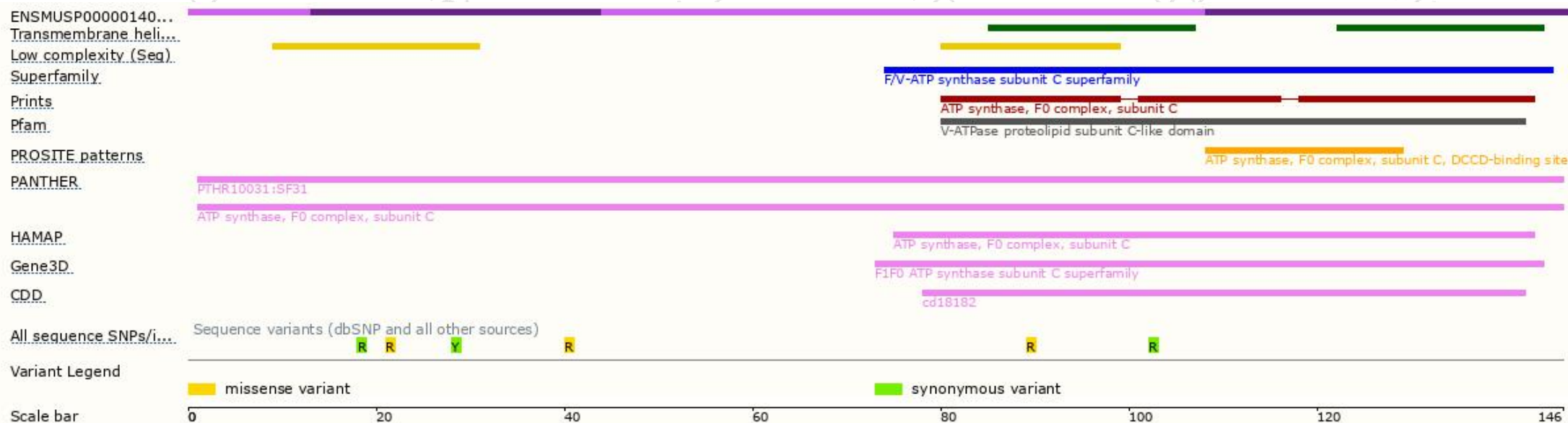
The strategy is based on the design of *Atp5g2-202* transcript,the transcription is shown below:



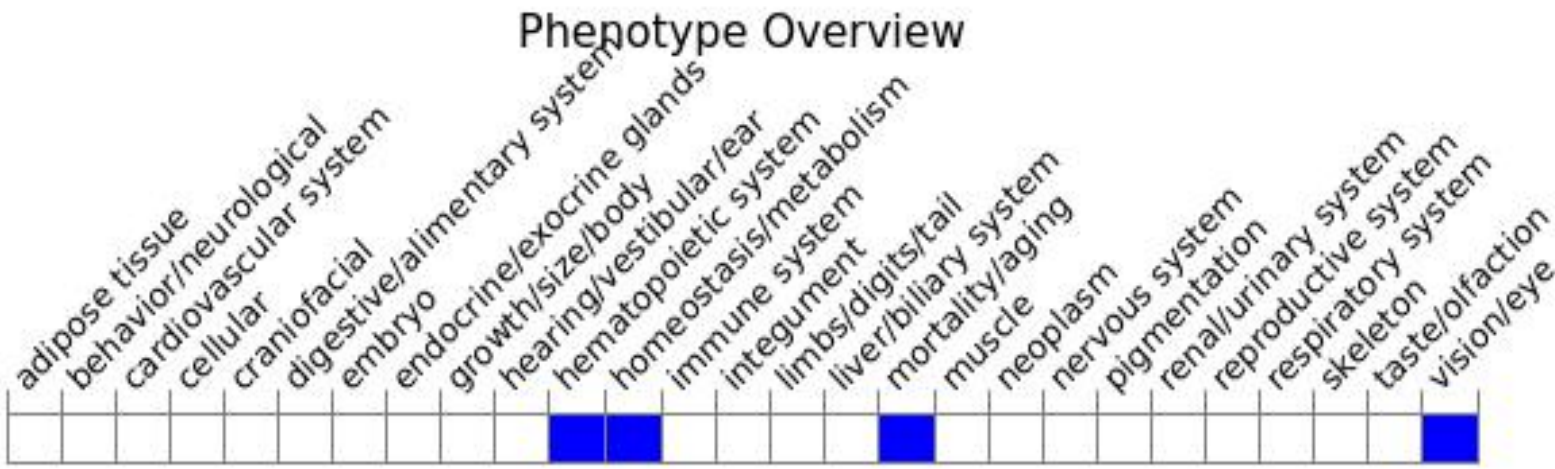
Genomic location distribution



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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