

Atp9a Cas9-KO Strategy

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Project Overview

Project Name

Atp9a

Project type

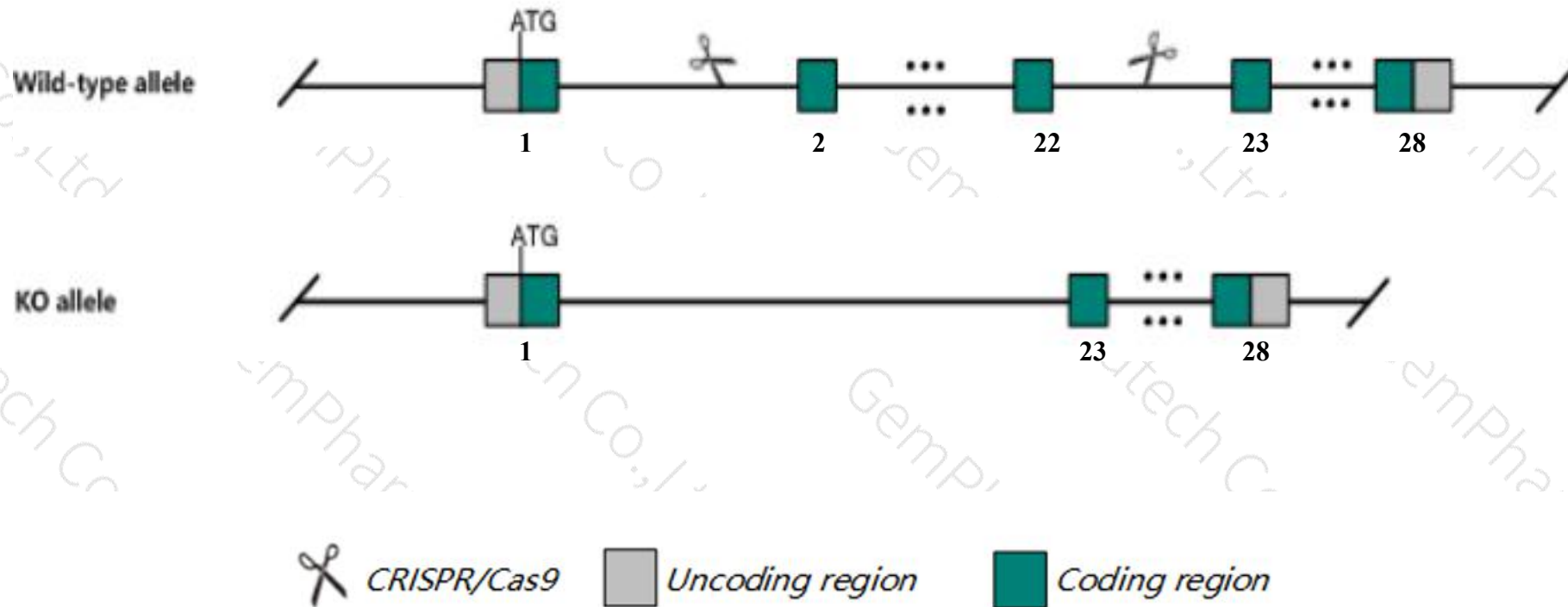
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp9a* gene. The schematic diagram is as follows:



- The *Atp9a* gene has 11 transcripts. According to the structure of *Atp9a* gene, exon2-exon22 of *Atp9a-201* (ENSMUST00000029060.10) transcript is recommended as the knockout region. The region contains 2347bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp9a* gene. The brief process is as follows: CRISPR/Cas9 system

- The KO region contains functional region of the Atp9a gene. Knockout the region may affect the function of LOC109280124.
- The *Atp9a* gene is located on the Chr2. 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)

Atp9a ATPase, class II, type 9A [Mus musculus (house mouse)]

Gene ID: 11981, updated on 13-Mar-2020

Summary



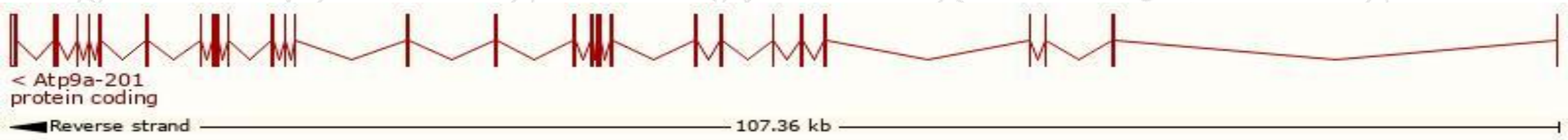
Official Symbol	Atp9a provided by MGI
Official Full Name	ATPase, class II, type 9A provided by MGI
Primary source	MGI:MGI:1330826
See related	Ensembl:ENSMUSG000000027546
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ila
Expression	Ubiquitous expression in colon adult (RPKM 66.0), CNS E18 (RPKM 56.7) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

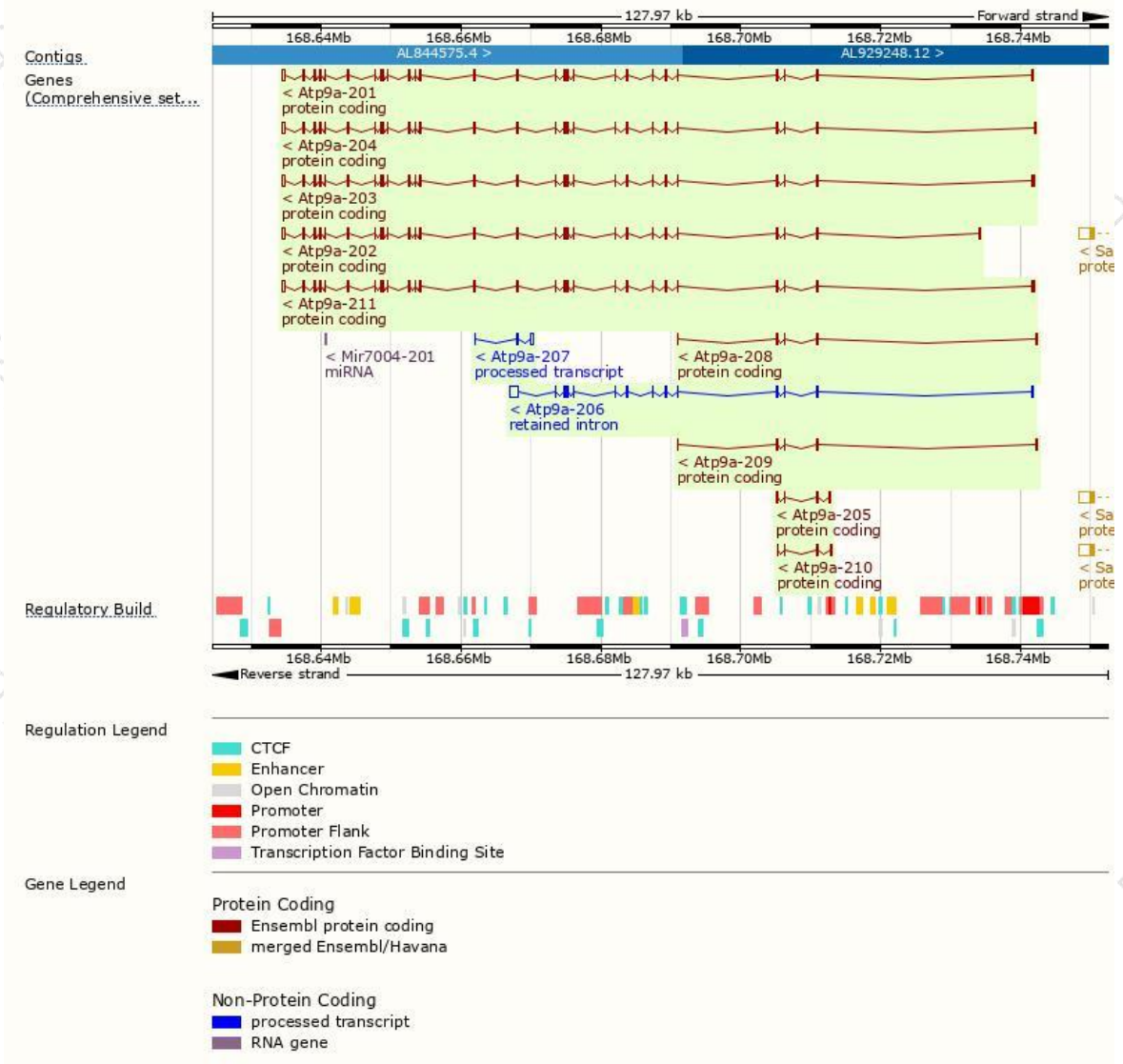
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp9a-202	ENSMUST00000109175.8	3729	1031aa	Protein coding	CCDS71202	Q8C288	TSL:1 GENCODE basic APPRIS ALT 2
Atp9a-201	ENSMUST00000029060.10	3529	1047aa	Protein coding	CCDS38345	O70228	TSL:1 GENCODE basic APPRIS P3
Atp9a-204	ENSMUST00000109177.7	3456	1029aa	Protein coding	CCDS71203	Q8C4G3	TSL:1 GENCODE basic
Atp9a-203	ENSMUST00000109176.7	3691	1105aa	Protein coding	-	A2AQC3	TSL:1 GENCODE basic
Atp9a-211	ENSMUST00000178504.7	3668	1047aa	Protein coding	-	O70228	TSL:5 GENCODE basic APPRIS ALT 2
Atp9a-209	ENSMUST00000156397.7	655	189aa	Protein coding	-	A2AQC9	CDS 3' incomplete TSL:3
Atp9a-208	ENSMUST00000151610.7	634	62aa	Protein coding	-	B2FDH4	CDS 3' incomplete TSL:3
Atp9a-205	ENSMUST00000123156.7	603	112aa	Protein coding	-	A2AUZ0	CDS 3' incomplete TSL:3
Atp9a-210	ENSMUST00000156555.1	481	88aa	Protein coding	-	A2AUZ1	CDS 3' incomplete TSL:3
Atp9a-207	ENSMUST00000147757.1	568	No protein	Processed transcript	-	-	TSL:5
Atp9a-206	ENSMUST00000140188.7	2484	No protein	Retained intron	-	-	TSL:1

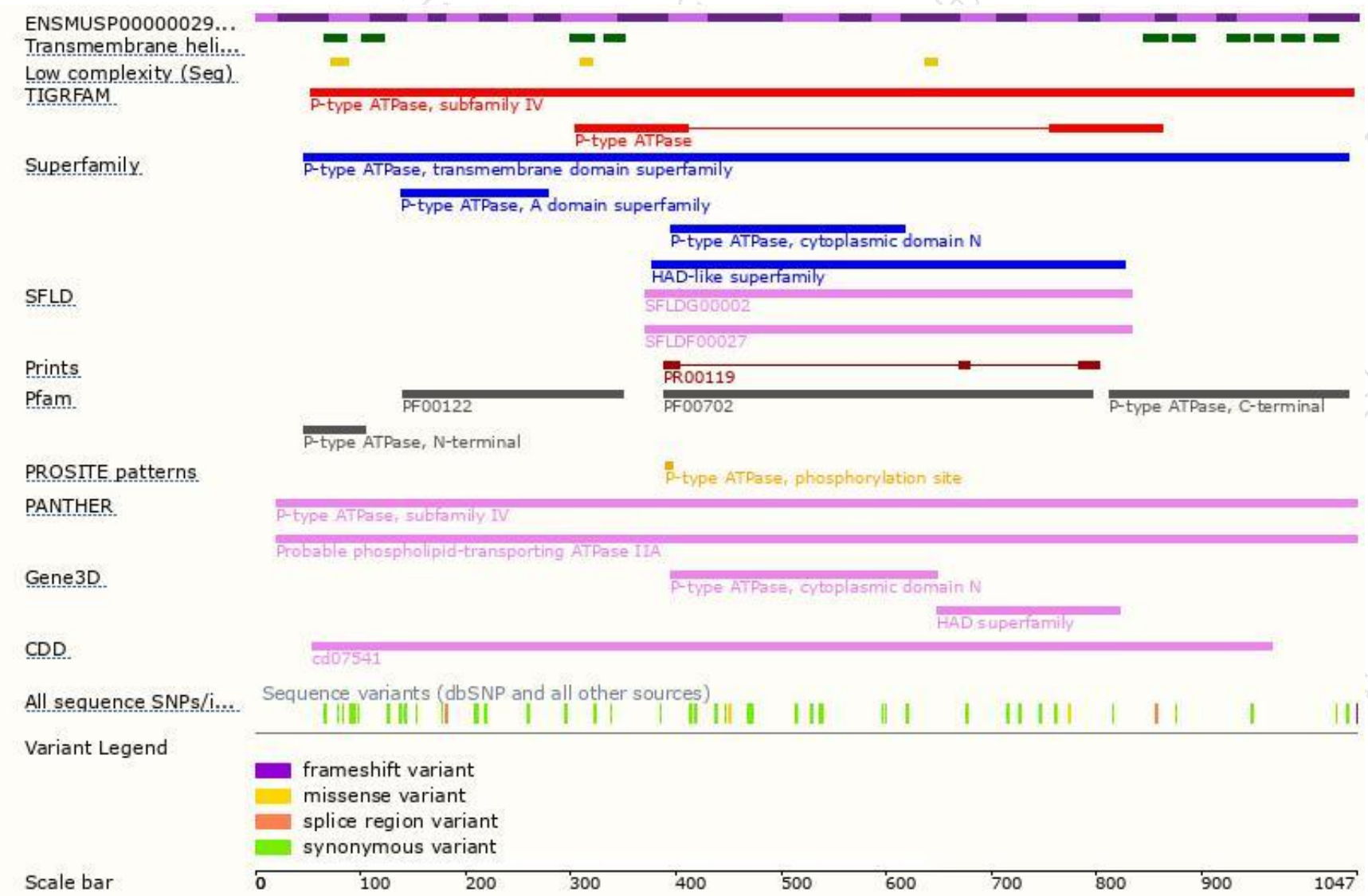
The strategy is based on the design of *Atp9a-201* transcript,the transcription is shown below:



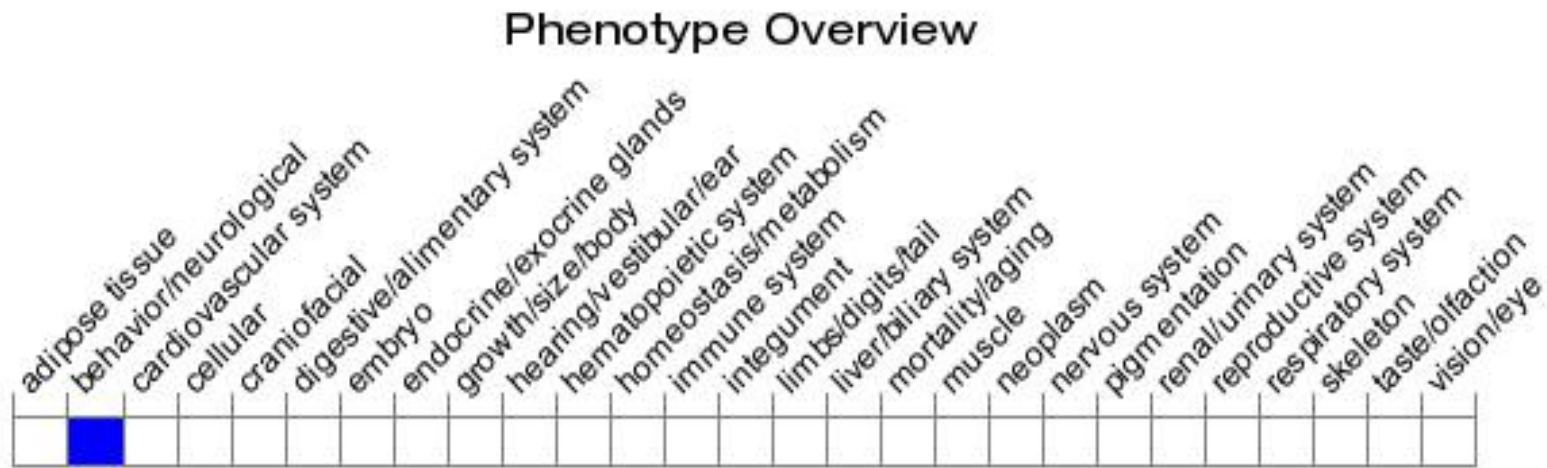
Genomic location distribution



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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