

Atp8a1 Cas9-KO Strategy

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Project Overview

Project Name

Atp8a1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp8a1* gene. The schematic diagram is as follows:



- The *Atp8a1* gene has 14 transcripts. According to the structure of *Atp8a1* gene, exon2-exon4 of *Atp8a1-201* (ENSMUST00000037380.14) transcript is recommended as the knockout region. The region contains 314bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp8a1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutant mice are viable, fertile and phenotypically normal.
- The *Atp8a1* gene is located on the Chr5. 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)

Atp8a1 ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 [*Mus musculus* (house mouse)]

Gene ID: 11980, updated on 4-Dec-2019

Summary

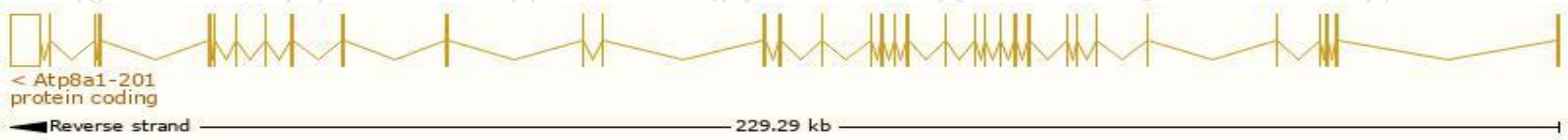
Official Symbol	Atp8a1 provided by MGI
Official Full Name	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 provided by MGI
Primary source	MGI:MGI:1330848
See related	Ensembl:ENSMUSG00000037685
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	APLT; Atp3a2; ClassI; AI481521; AI853962; AW743152; AW822227; B230107D19Rik
Expression	Broad expression in lung adult (RPKM 16.4), cortex adult (RPKM 15.1) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

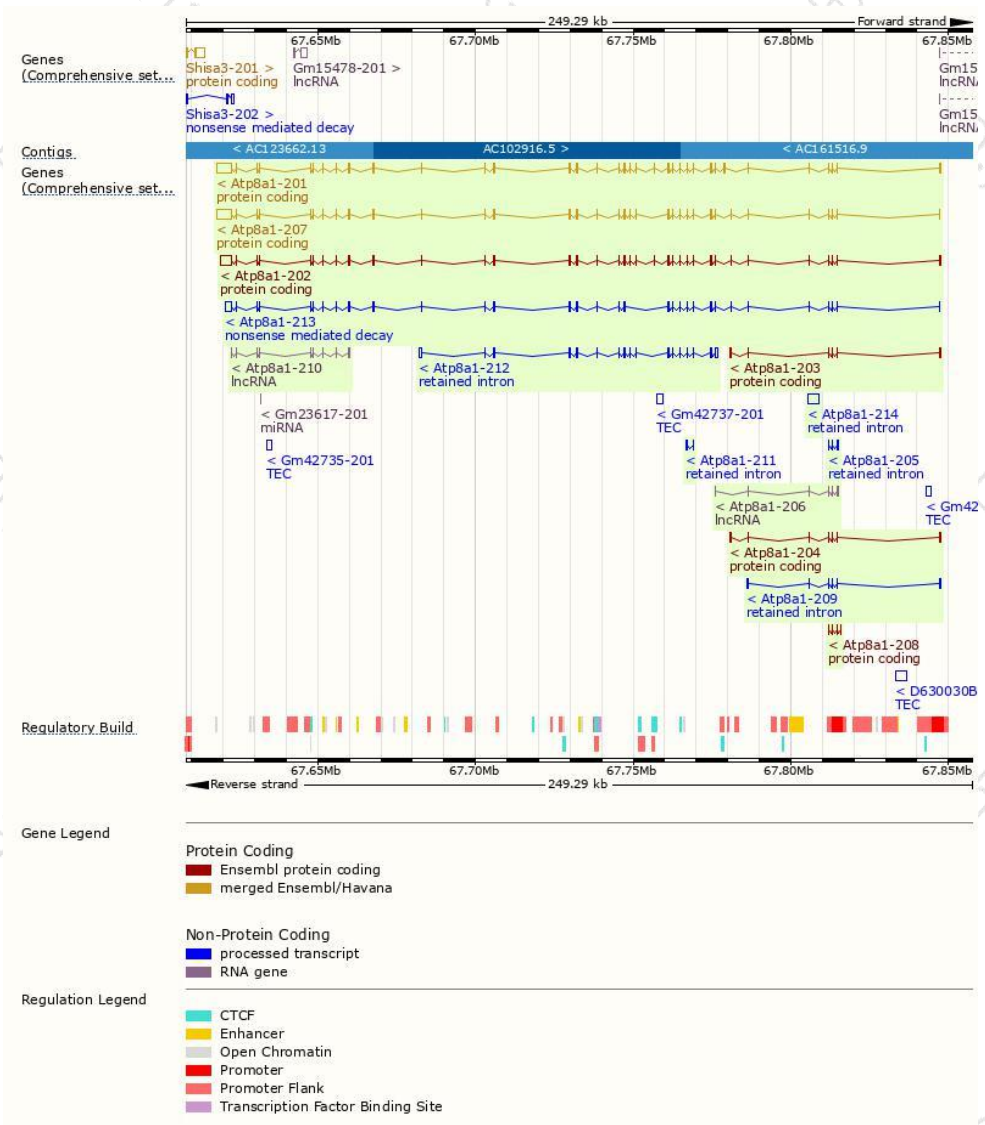
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp8a1-201	ENSMUST00000037380.14	8178	1164aa	Protein coding	CCDS39104	P70704	TSL:1 GENCODE basic APPRIS P4
Atp8a1-207	ENSMUST00000135930.7	8069	1149aa	Protein coding	CCDS39105	P70704	TSL:1 GENCODE basic APPRIS ALT 1
Atp8a1-202	ENSMUST00000072971.12	7154	1164aa	Protein coding	CCDS80295	A0A0M3HEP7	TSL:1 GENCODE basic APPRIS ALT 2
Atp8a1-204	ENSMUST00000113652.7	854	175aa	Protein coding	-	Q3U9N5	TSL:1 GENCODE basic
Atp8a1-203	ENSMUST00000113651.7	808	122aa	Protein coding	-	E9Q4J5	TSL:5 GENCODE basic
Atp8a1-208	ENSMUST00000141443.1	368	106aa	Protein coding	-	F6Q8P7	CDS 3' incomplete TSL:5
Atp8a1-213	ENSMUST00000200955.3	5373	441aa	Nonsense mediated decay	-	A0A0J9YV34	TSL:5
Atp8a1-214	ENSMUST00000202248.1	3360	No protein	Retained intron	-	-	TSL:NA
Atp8a1-212	ENSMUST00000155911.1	2932	No protein	Retained intron	-	-	TSL:1
Atp8a1-209	ENSMUST00000143013.7	1014	No protein	Retained intron	-	-	TSL:2
Atp8a1-205	ENSMUST00000128726.1	750	No protein	Retained intron	-	-	TSL:5
Atp8a1-211	ENSMUST00000152433.1	617	No protein	Retained intron	-	-	TSL:3
Atp8a1-210	ENSMUST00000149501.1	762	No protein	lncRNA	-	-	TSL:3
Atp8a1-206	ENSMUST00000130652.7	469	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Atp8a1-201* transcript,The transcription is shown below



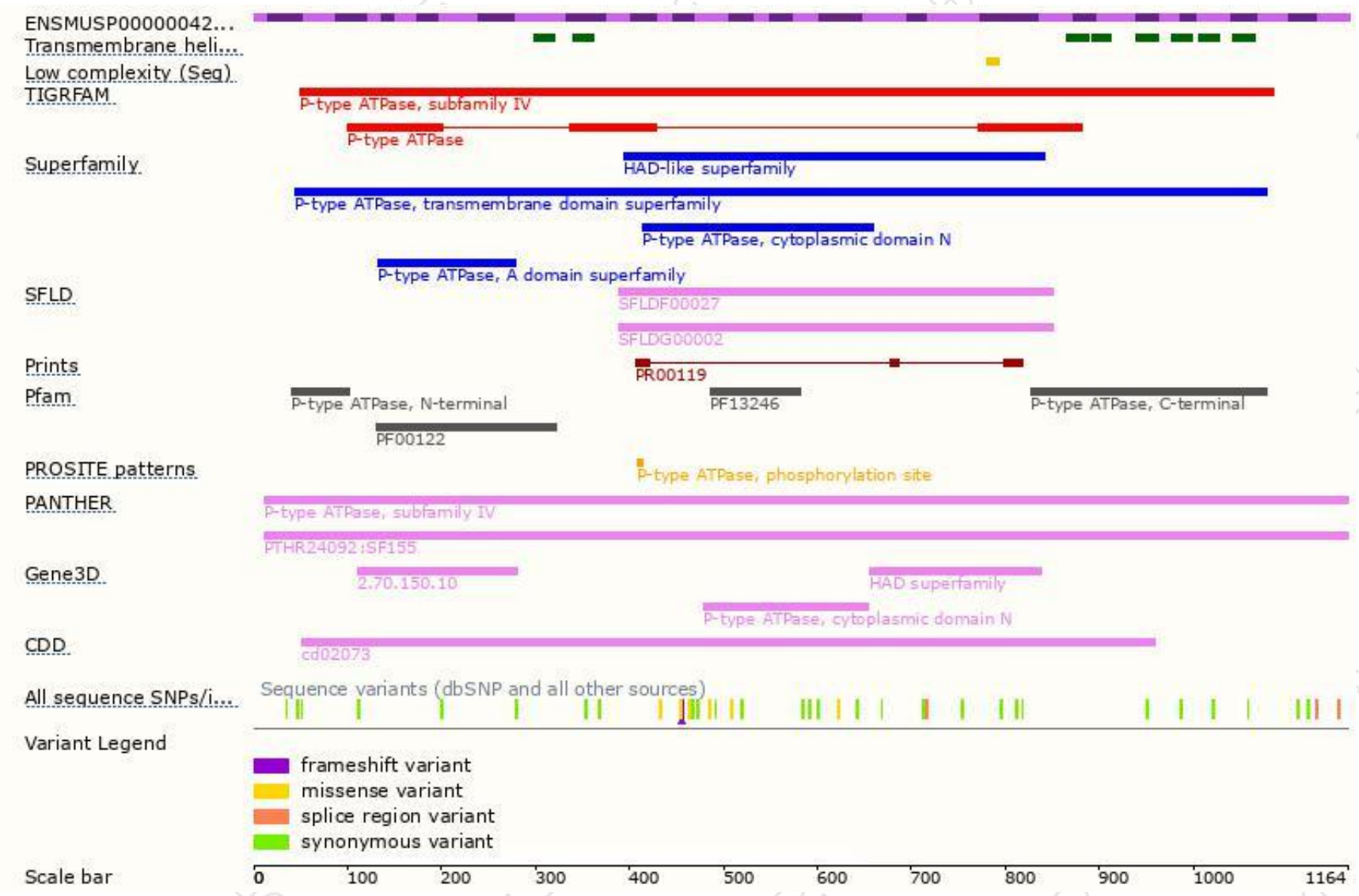
Genomic location distribution



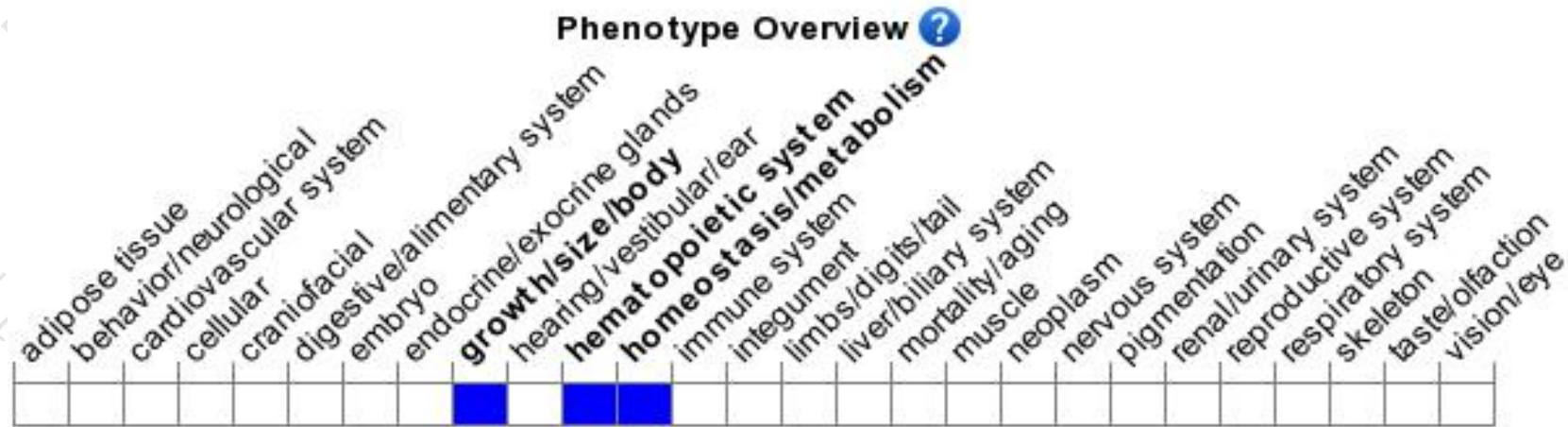
Protein domain



集萃药康
GemPharmatech



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Homozygous mutant mice are viable, fertile and phenotypically normal.

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

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