

# *Atp4a* Cas9-KO Strategy

**Designer:**

**JiaYu**

**Reviewer:**

**Xiaojing Li**

**Design Date:**

**2019-8-27**

# Project Overview

**Project Name**

*Atp4a*

**Project type**

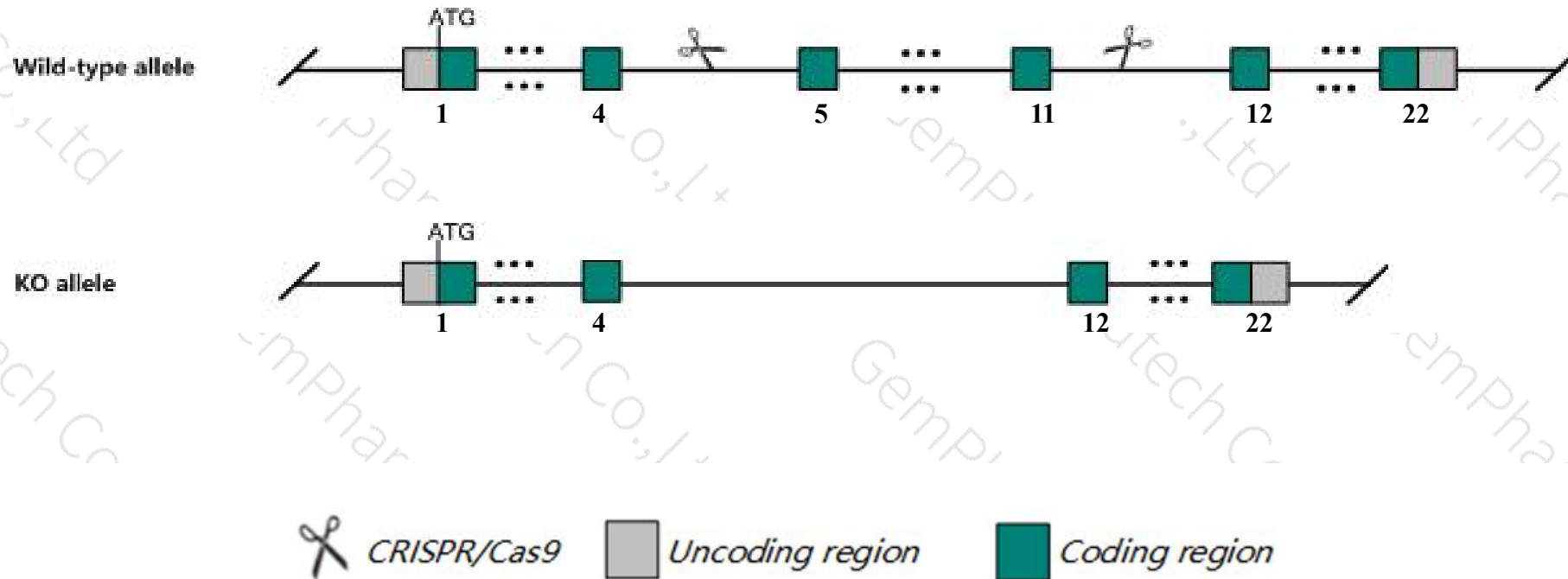
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp4a* gene. The schematic diagram is as follows:



- The *Atp4a* gene has 5 transcripts. According to the structure of *Atp4a* gene, exon5-exon11 of *Atp4a-201* (ENSMUST00000005692.13) transcript is recommended as the knockout region. The region contains 1273bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp4a* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutation of this gene results in achlorhydria, hypergastrinemia, and abnormalities of the parietal cells. Mice homozygous for an ENU-induced allele exhibit iron-deficiency anemia.
- The *Atp4a* gene is located on the Chr7. 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)

## Atp4a ATPase, H<sup>+</sup>/K<sup>+</sup> exchanging, gastric, alpha polypeptide [Mus musculus (house mouse)]

Gene ID: 11944, updated on 5-Mar-2019

### Summary



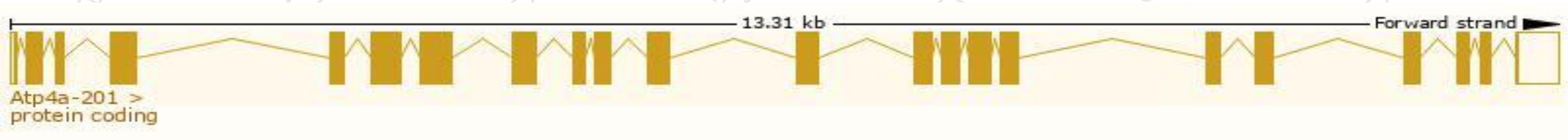
<b>Official Symbol</b>	Atp4a provided by <a href="#">MGI</a>
<b>Official Full Name</b>	ATPase, H <sup>+</sup> /K <sup>+</sup> exchanging, gastric, alpha polypeptide provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:88113</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000005553</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Expression</b>	Restricted expression toward stomach adult (RPKM 485.0) <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

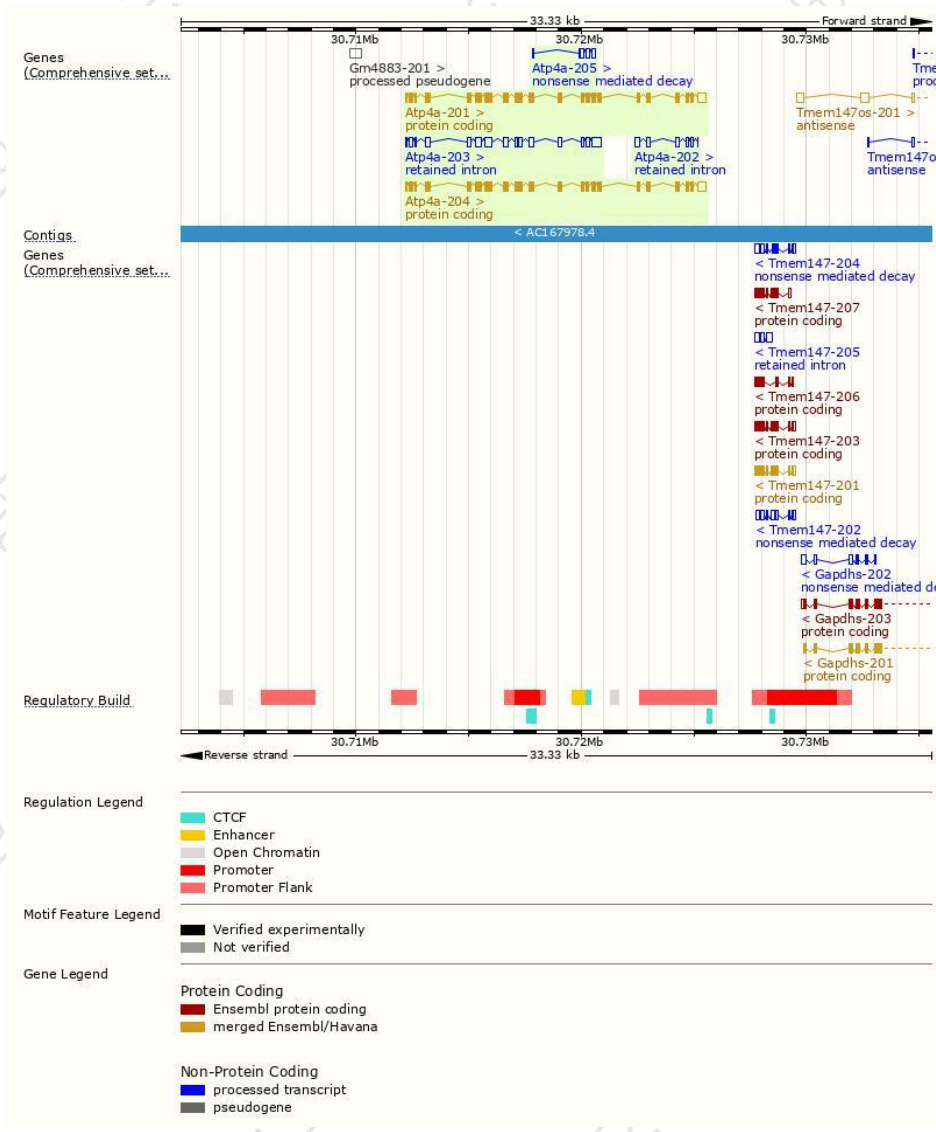
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp4a-201	<a href="#">ENSMUST00000005692.13</a>	3485	<a href="#">1034aa</a>	Protein coding	<a href="#">CCDS71932</a>	<a href="#">E9QNX7</a>	TSL:5 GENCODE basic APPRIS P1
Atp4a-204	<a href="#">ENSMUST00000170371.1</a>	3447	<a href="#">1025aa</a>	Protein coding	<a href="#">CCDS52182</a>	<a href="#">Q91WH7</a>	TSL:1 GENCODE basic
Atp4a-205	<a href="#">ENSMUST00000171014.1</a>	564	<a href="#">32aa</a>	Nonsense mediated decay	-	<a href="#">F6S7B0</a>	CDS 5' incomplete TSL:3
Atp4a-203	<a href="#">ENSMUST00000167761.7</a>	2601	No protein	Retained intron	-	-	TSL:1
Atp4a-202	<a href="#">ENSMUST00000165410.1</a>	738	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Atp4a-201* transcript,The transcription is shown below

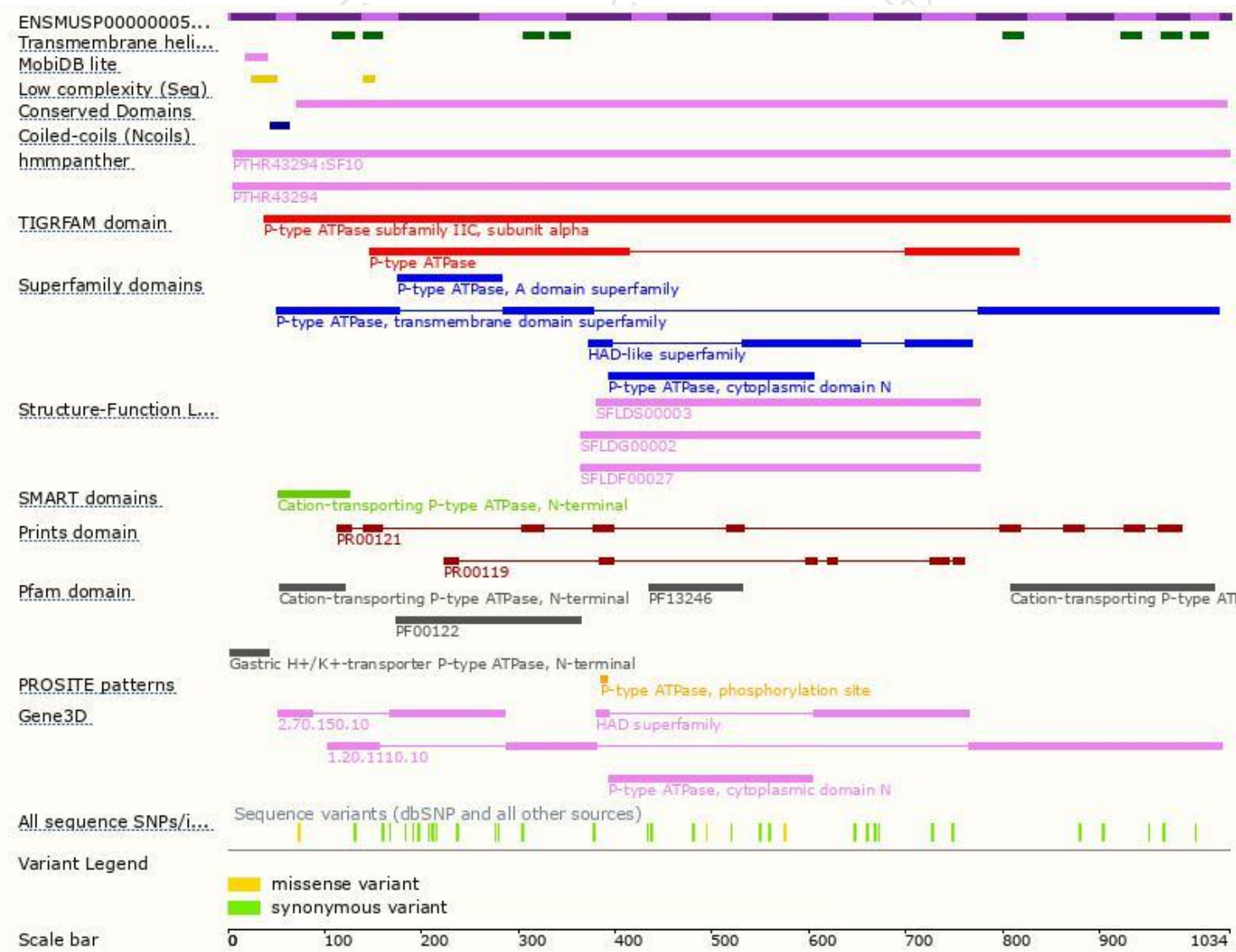


# Genomic location distribution

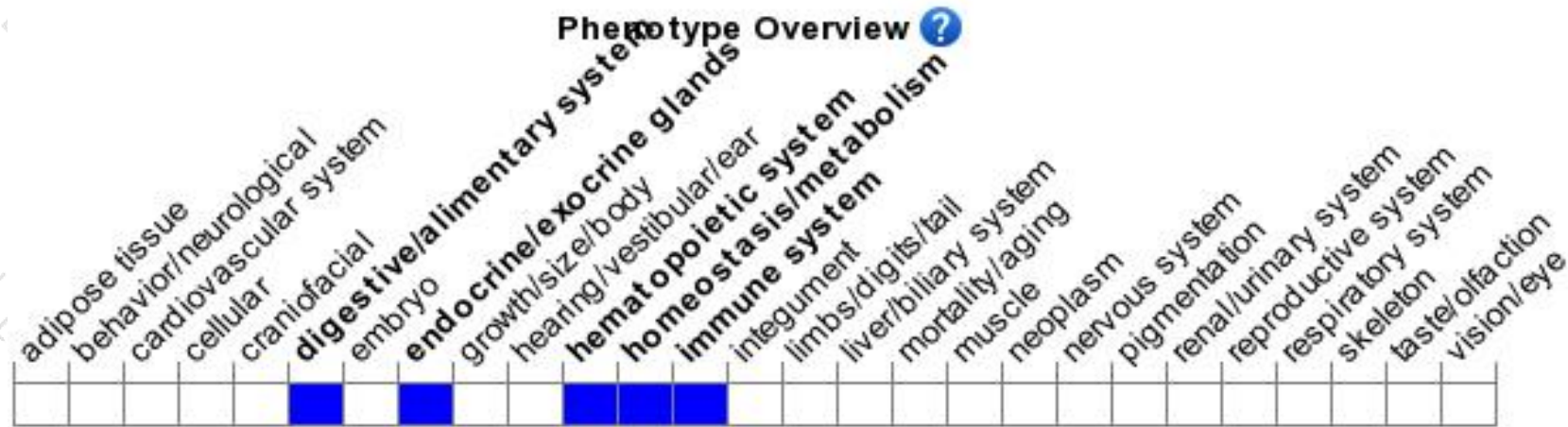




# Protein domain



# Mouse phenotype description(MGI )



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

According to the existing MGI data, Homozygous mutation of this gene results in achlorhydria, hypergastrinemia, and abnormalities of the parietal cells. Mice homozygous for an ENU-induced allele exhibit iron-deficiency anemia.

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

Tel: 400-9660890

