

# *Atp11a* Cas9-KO Strategy

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<b>Design Date:</b>	<b>2019-11-16</b>

# Project Overview

**Project Name**

*Atp11a*

**Project type**

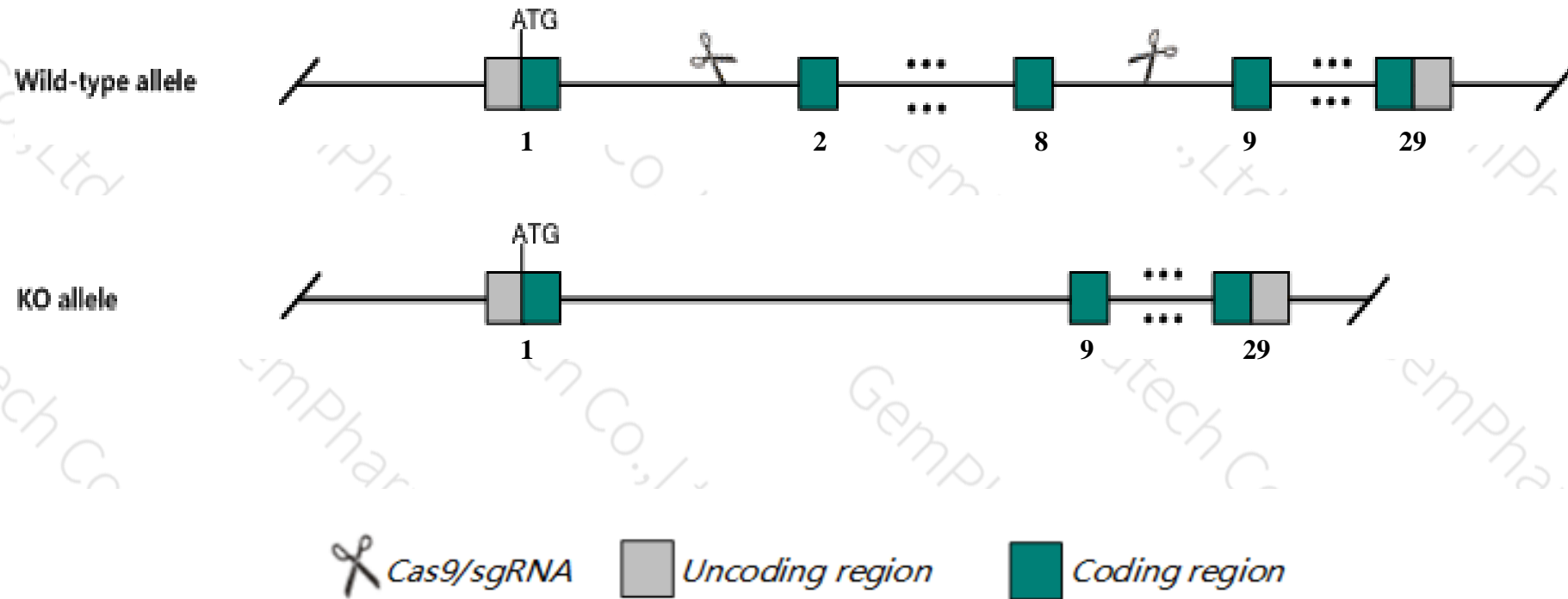
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atp11a* gene. The schematic diagram is as follows:



- The *Atp11a* gene has 11 transcripts. According to the structure of *Atp11a* gene, exon2-exon8 of *Atp11a*-202(ENSMUST00000091237.11) transcript is recommended as the knockout region. The region contains 686bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atp11a* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, mice homozygous for a conditional allele activated in muscle cells exhibit abnormal myoblast function in culture and abnormal skeletal muscle regeneration.
- The *Atp11a* gene is located on the Chr8. 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)

## Atp11a ATPase, class VI, type 11A [Mus musculus (house mouse)]

Gene ID: 50770, updated on 13-Mar-2020

### Summary



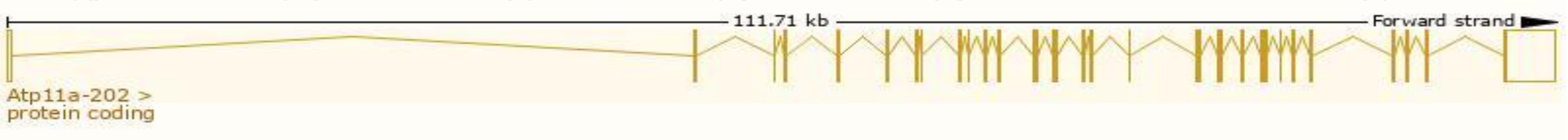
<b>Official Symbol</b>	Atp11a provided by <a href="#">MGI</a>
<b>Official Full Name</b>	ATPase, class VI, type 11A provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1354735</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000031441</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>Also known as</b>	4930558F19Rik, AU040868, Atpc1h, Ih
<b>Expression</b>	Broad expression in lung adult (RPKM 80.2), kidney adult (RPKM 45.0) and 21 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

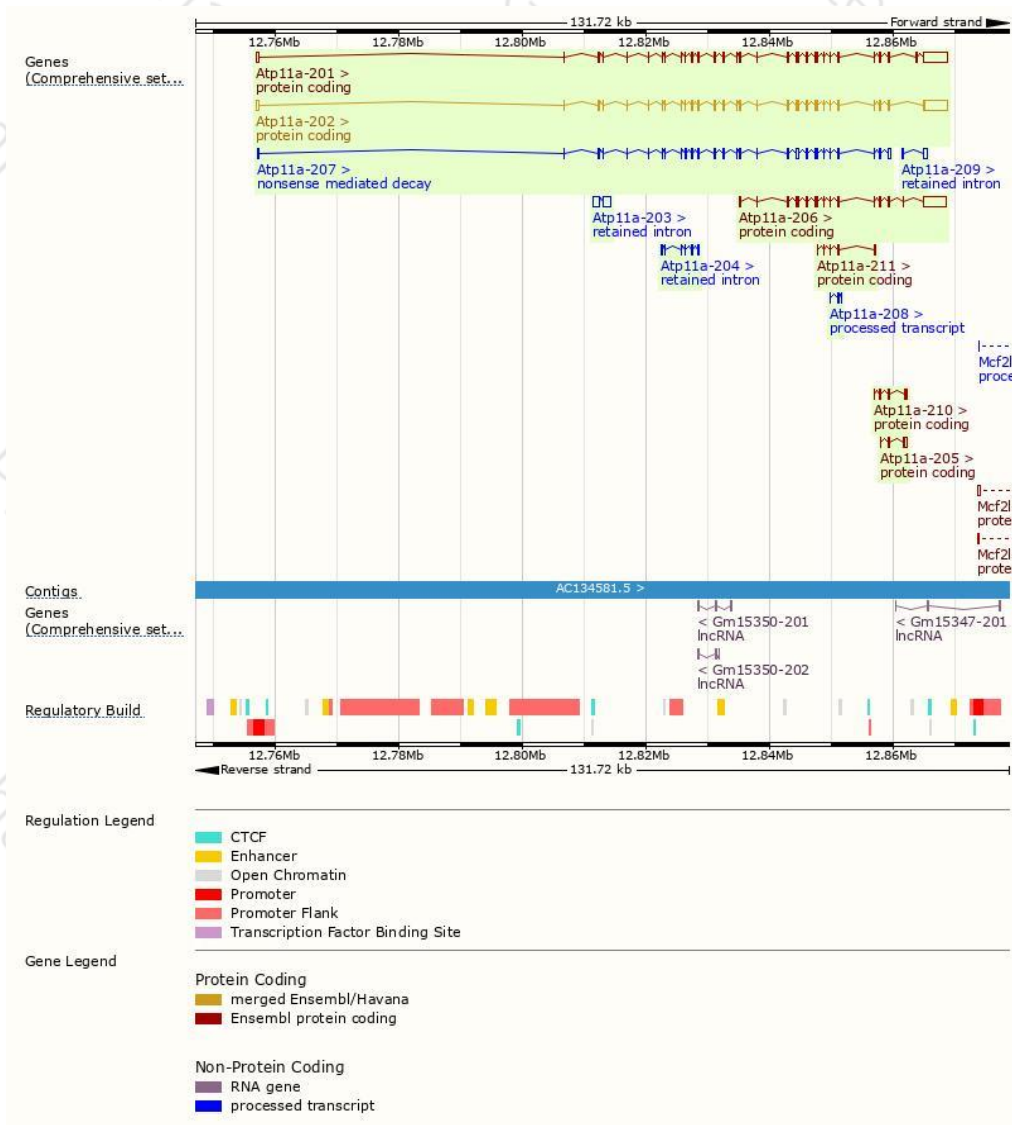
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atp11a-201	<a href="#">ENSMUST00000033818.9</a>	7549	<a href="#">1142aa</a>	Protein coding	<a href="#">CCDS80858</a>	<a href="#">E9Q3G7</a>	TSL:1 GENCODE basic APPRIS ALT2
Atp11a-202	<a href="#">ENSMUST00000091237.11</a>	7443	<a href="#">1187aa</a>	Protein coding	<a href="#">CCDS40223</a>	<a href="#">P98197</a>	TSL:1 GENCODE basic APPRIS P3
Atp11a-206	<a href="#">ENSMUST00000132974.7</a>	5528	<a href="#">590aa</a>	Protein coding	-	<a href="#">F6Z4J2</a>	CDS 5' incomplete TSL:1
Atp11a-211	<a href="#">ENSMUST00000152273.1</a>	692	<a href="#">163aa</a>	Protein coding	-	<a href="#">F6R5M4</a>	CDS 5' incomplete TSL:3
Atp11a-210	<a href="#">ENSMUST00000143359.7</a>	604	<a href="#">131aa</a>	Protein coding	-	<a href="#">F6Z063</a>	CDS 5' incomplete TSL:3
Atp11a-205	<a href="#">ENSMUST00000131804.1</a>	567	<a href="#">89aa</a>	Protein coding	-	<a href="#">F6QJS5</a>	CDS 5' incomplete TSL:5
Atp11a-207	<a href="#">ENSMUST00000133338.7</a>	4028	<a href="#">291aa</a>	Nonsense mediated decay	-	<a href="#">D6RII8</a>	TSL:1
Atp11a-208	<a href="#">ENSMUST00000136918.1</a>	290	No protein	Processed transcript	-	-	TSL:5
Atp11a-203	<a href="#">ENSMUST00000125031.1</a>	2295	No protein	Retained intron	-	-	TSL:1
Atp11a-209	<a href="#">ENSMUST00000139545.1</a>	811	No protein	Retained intron	-	-	TSL:2
Atp11a-204	<a href="#">ENSMUST00000127197.1</a>	755	No protein	Retained intron	-	-	TSL:3

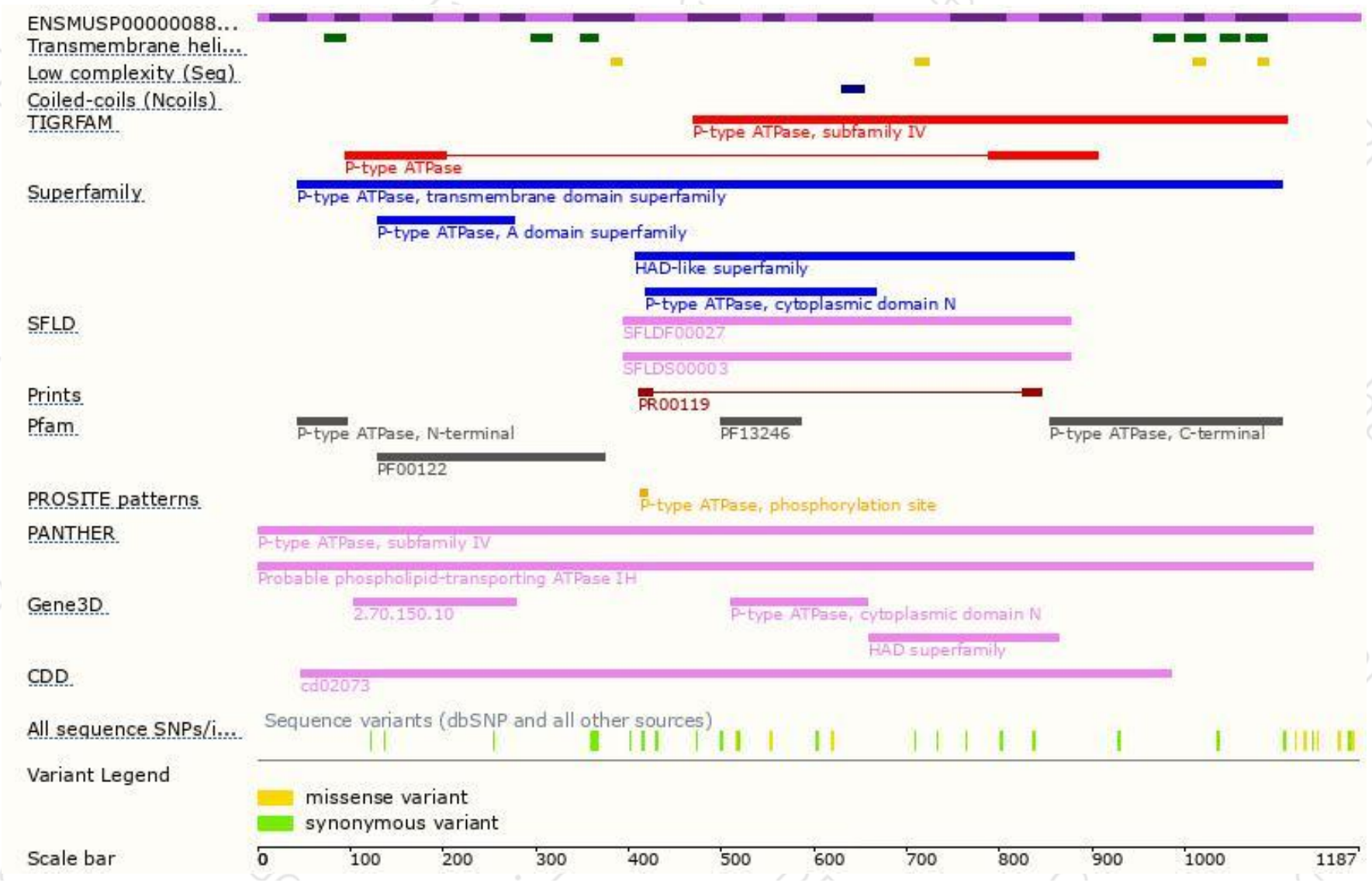
The strategy is based on the design of *Atp11a-202* transcript,the transcription is shown below:



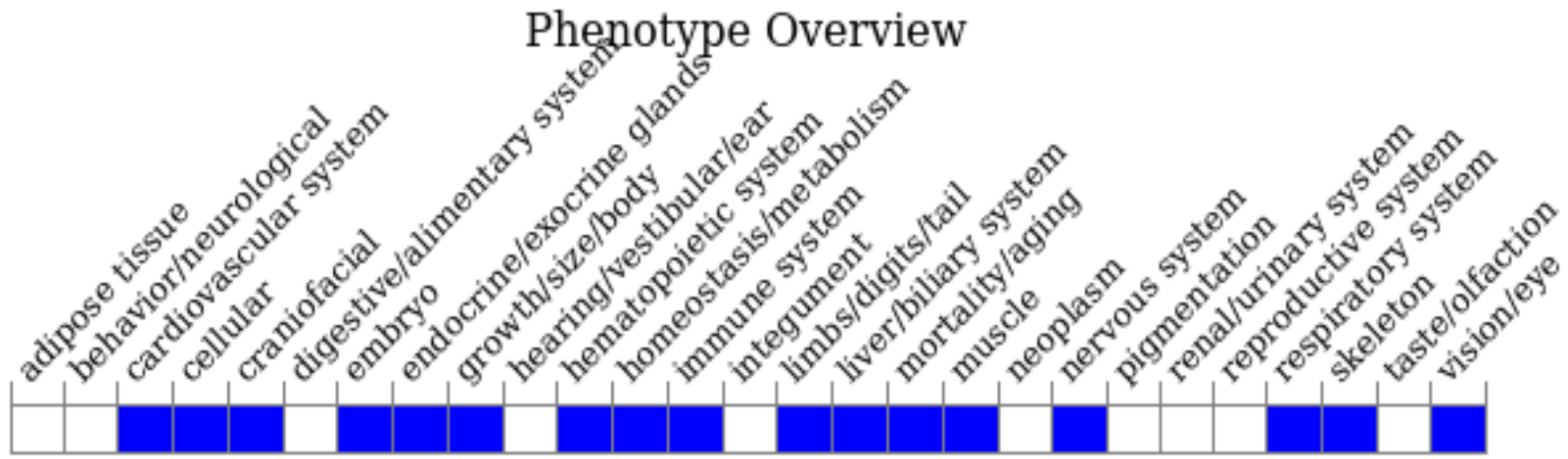
# Genomic location distribution



# 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/>).*

According to the existing MGI data,mice homozygous for a conditional allele activated in muscle cells exhibit abnormal myoblast function in culture and abnormal skeletal muscle regeneration.

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

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