

# *Agbl3* Cas9-KO Strategy

**Designer:**

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**Design Date:**

**2019-10-18**

# Project Overview

**Project Name**

*Agbl3*

**Project type**

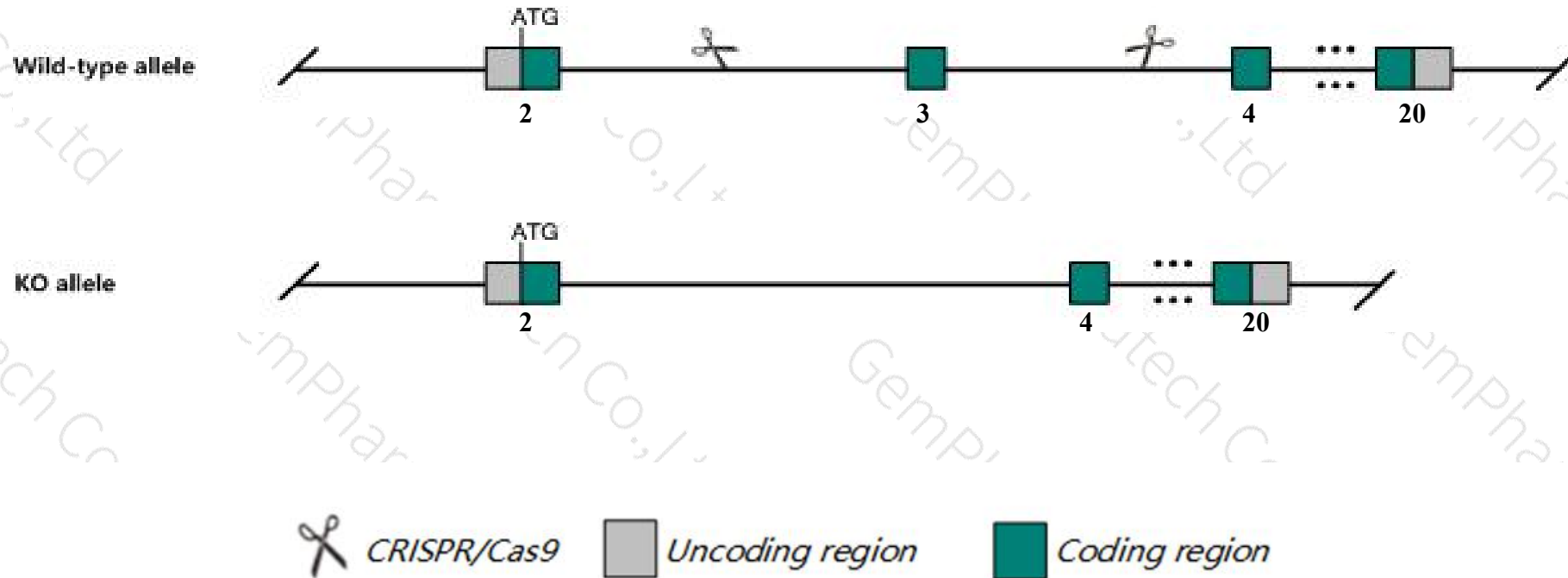
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Agbl3* gene. The schematic diagram is as follows:



- The *Agbl3* gene has 11 transcripts. According to the structure of *Agbl3* gene, exon3 of *Agbl3-204* (ENSMUST00000115016.7) transcript is recommended as the knockout region. The region contains 61bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Agbl3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mice for a targeted allele are viable and fertile. Mice homozygous for a knock-out allele exhibit normal response to herpes simplex virus (HSV) and vaccinia virus (VACV) infection.
- The *Agbl3* gene is located on the Chr6. 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)

## Agbl3 ATP/GTP binding protein-like 3 [Mus musculus (house mouse)]

Gene ID: 76223, updated on 31-Jan-2019

### Summary



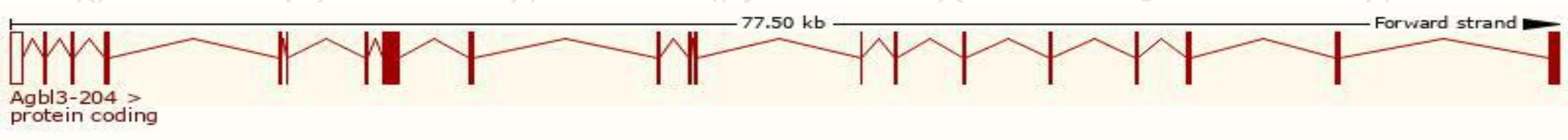
<b>Official Symbol</b>	Agbl3 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	ATP/GTP binding protein-like 3 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1923473</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000038836</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	2900053G10Rik, 4930431N21Rik, 6530406M24Rik, CCP3
<b>Expression</b>	Broad expression in testis adult (RPKM 4.2), CNS E18 (RPKM 1.2) and 21 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

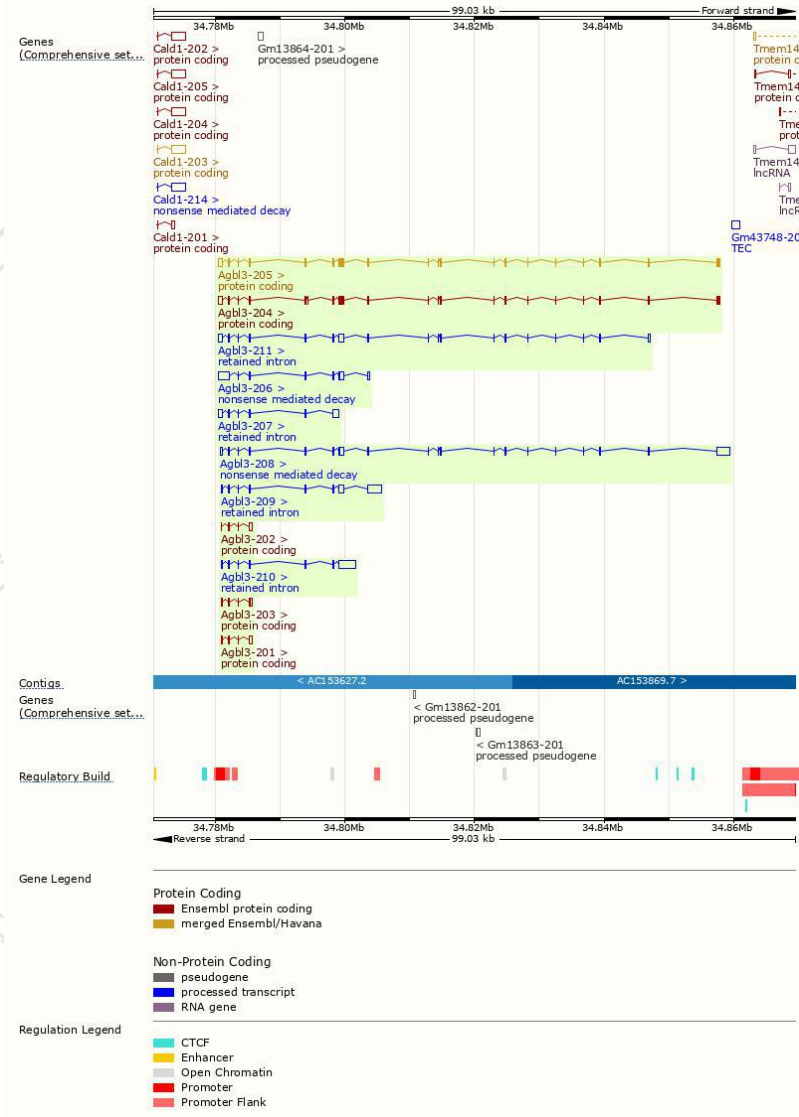
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Agbl3-204	<a href="#">ENSMUST00000115016.7</a>	3734	<a href="#">1006aa</a>	Protein coding	<a href="#">CCDS80515</a>	<a href="#">Q8CDP0</a>	TSL:1 GENCODE basic APPRIS ALT2
Agbl3-205	<a href="#">ENSMUST00000115017.7</a>	3719	<a href="#">1001aa</a>	Protein coding	<a href="#">CCDS19995</a>	<a href="#">Q8CDP0</a>	TSL:1 GENCODE basic APPRIS P3
Agbl3-203	<a href="#">ENSMUST00000115014.7</a>	805	<a href="#">129aa</a>	Protein coding	<a href="#">CCDS80516</a>	<a href="#">Q8CDP0</a>	TSL:1 GENCODE basic
Agbl3-201	<a href="#">ENSMUST00000115009.1</a>	806	<a href="#">49aa</a>	Protein coding	-	<a href="#">D3Z4P1</a>	TSL:5 GENCODE basic
Agbl3-202	<a href="#">ENSMUST00000115012.7</a>	790	<a href="#">49aa</a>	Protein coding	-	<a href="#">D3Z4P1</a>	TSL:3 GENCODE basic
Agbl3-208	<a href="#">ENSMUST00000148834.7</a>	4819	<a href="#">185aa</a>	Nonsense mediated decay	-	<a href="#">D6RI59</a>	TSL:1
Agbl3-206	<a href="#">ENSMUST00000135304.7</a>	3384	<a href="#">185aa</a>	Nonsense mediated decay	-	<a href="#">D6RI59</a>	TSL:1
Agbl3-209	<a href="#">ENSMUST00000155726.7</a>	3764	No protein	Retained intron	-	-	TSL:2
Agbl3-211	<a href="#">ENSMUST00000202017.3</a>	3397	No protein	Retained intron	-	-	TSL:2
Agbl3-210	<a href="#">ENSMUST00000155890.1</a>	3264	No protein	Retained intron	-	-	TSL:2
Agbl3-207	<a href="#">ENSMUST00000143474.7</a>	1931	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Agbl3-204* transcript,The transcription is shown below

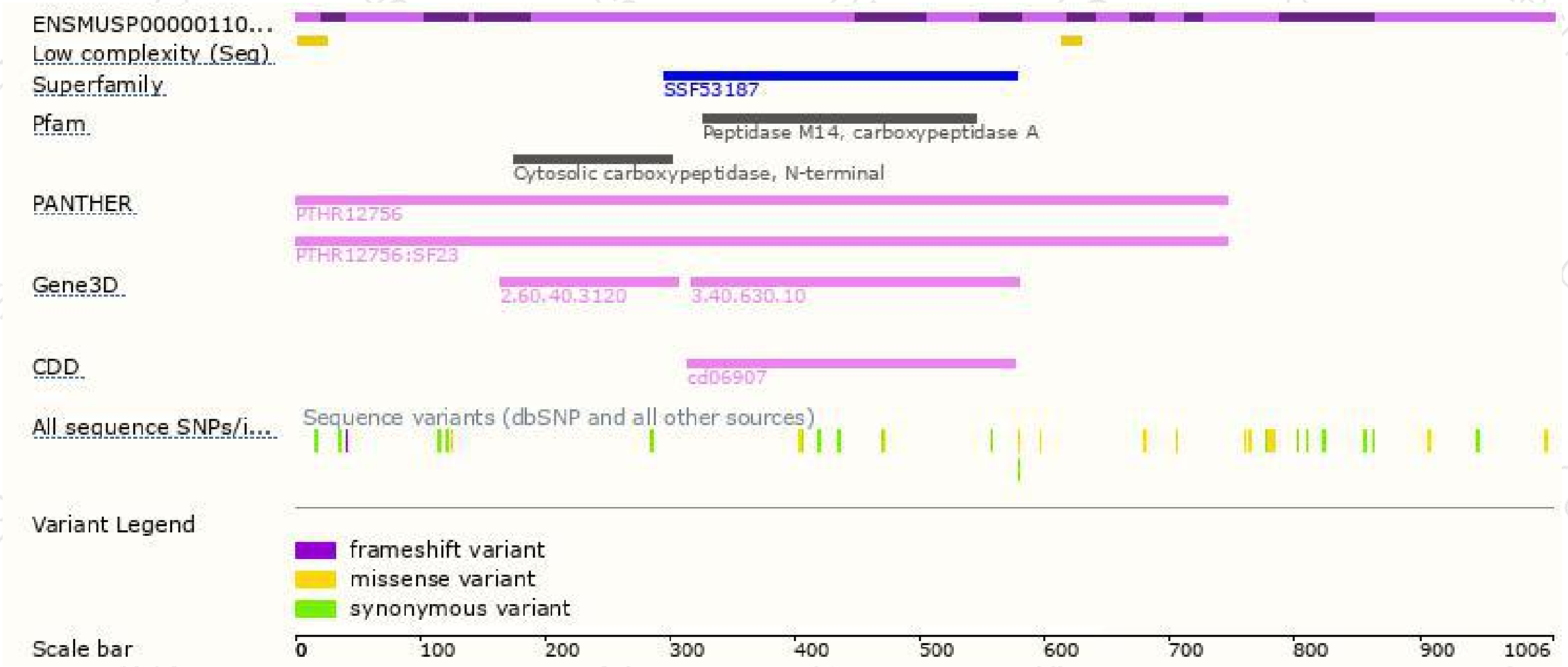


# Genomic location distribution





# Protein domain



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

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