

Ap3m1 Cas9-KO Strategy

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Design Date:

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Project Overview

Project Name

Ap3m1

Project type

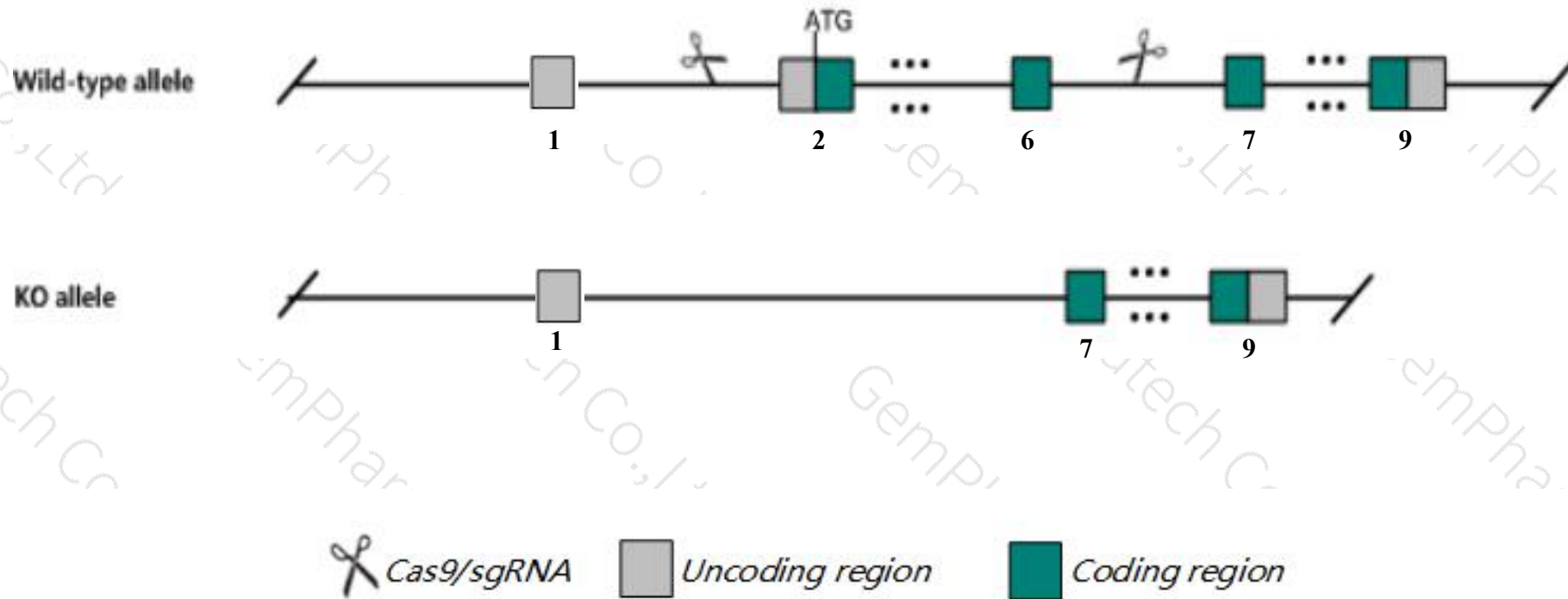
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ap3m1* gene. The schematic diagram is as follows:



- The *Ap3m1* gene has 8 transcripts. According to the structure of *Ap3m1* gene, exon2-exon6 of *Ap3m1-206* (ENSMUST00000154460.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ap3m1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Ap3m1* gene is located on the Chr14. 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)

Ap3m1 adaptor-related protein complex 3, mu 1 subunit [*Mus musculus* (house mouse)]

Gene ID: 55946, updated on 29-Mar-2020

Summary

Official Symbol Ap3m1 provided by [MGI](#)
Official Full Name adaptor-related protein complex 3, mu 1 subunit provided by [MGI](#)
Primary source [MGI:MGI:1929212](#)
See related [Ensembl:ENSMUSG00000021824](#)
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 C78982; R75378; 1200013D09Rik
Expression Ubiquitous expression in placenta adult (RPKM 16.1), CNS E11.5 (RPKM 13.4) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)

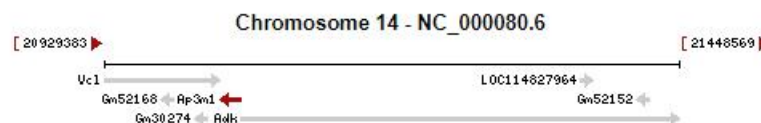
Genomic context

Location: 14 A3; 14 11.58 cM

See Ap3m1 in [Genome Data Viewer](#)

Exon count: 10

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	14	NC_000080.6 (21033106..21052553, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	14	NC_000080.5 (21852964..21871664, complement)

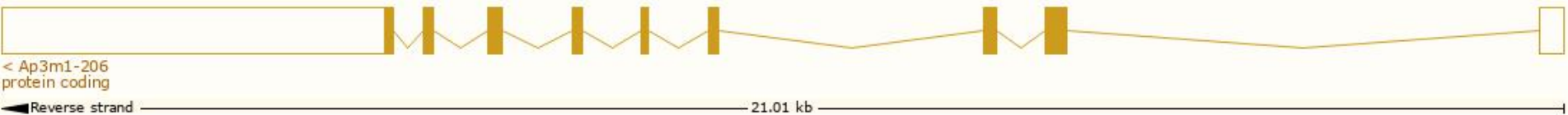


Transcript information (Ensembl)

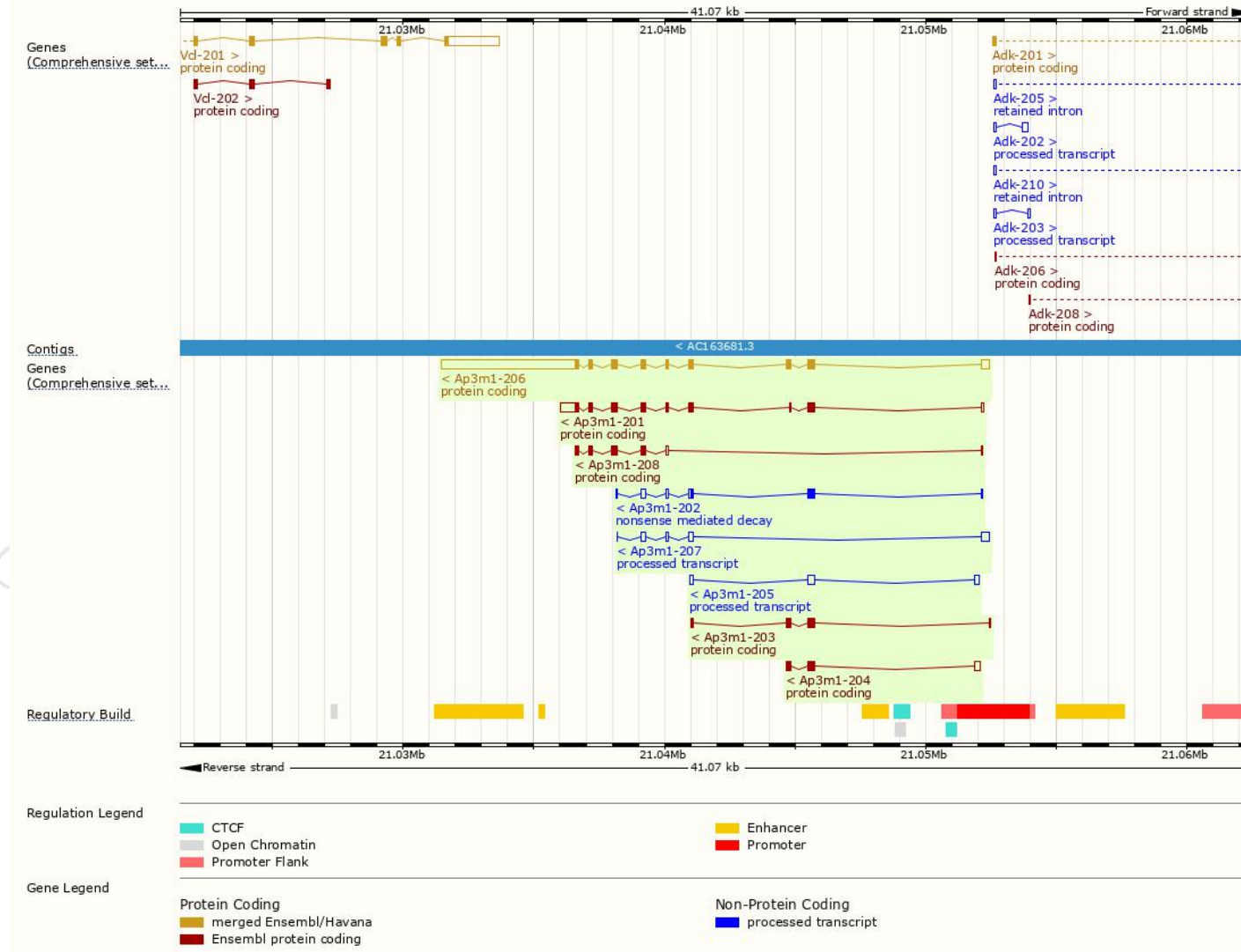
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ap3m1-206	ENSMUST00000154460.7	6732	418aa	Protein coding	CCDS26861	Q9JKC8	TSL:1 GENCODE basic APPRIS P1
Ap3m1-201	ENSMUST00000022371.9	1770	364aa	Protein coding	-	H7BWY2	TSL:5 GENCODE basic
Ap3m1-208	ENSMUST00000224016.1	764	204aa	Protein coding	-	A0A286YDZ6	GENCODE basic
Ap3m1-204	ENSMUST00000130370.2	673	148aa	Protein coding	-	D3YWU3	CDS 3' incomplete TSL:2
Ap3m1-203	ENSMUST00000130291.7	579	174aa	Protein coding	-	D3YXV9	CDS 3' incomplete TSL:2
Ap3m1-202	ENSMUST00000126536.7	737	114aa	Nonsense mediated decay	-	D6RI63	TSL:3
Ap3m1-207	ENSMUST00000156716.1	693	No protein	Processed transcript	-	-	TSL:5
Ap3m1-205	ENSMUST00000148886.1	562	No protein	Processed transcript	-	-	TSL:3

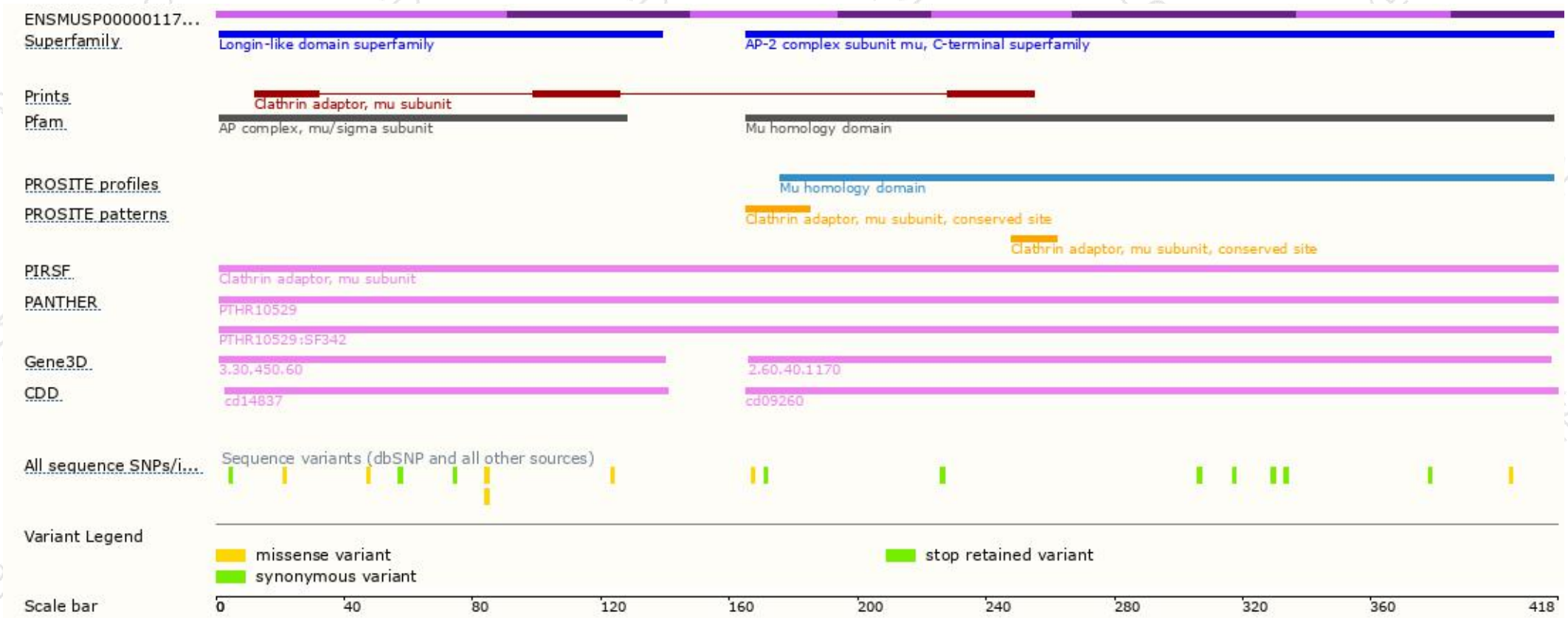
The strategy is based on the design of *Ap3m1-206* transcript,the transcription is shown below



Genomic location distribution



Protein domain



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

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