

Ap3m1 Cas9-KO Strategy

Designer: Reviewer:

Design Date:

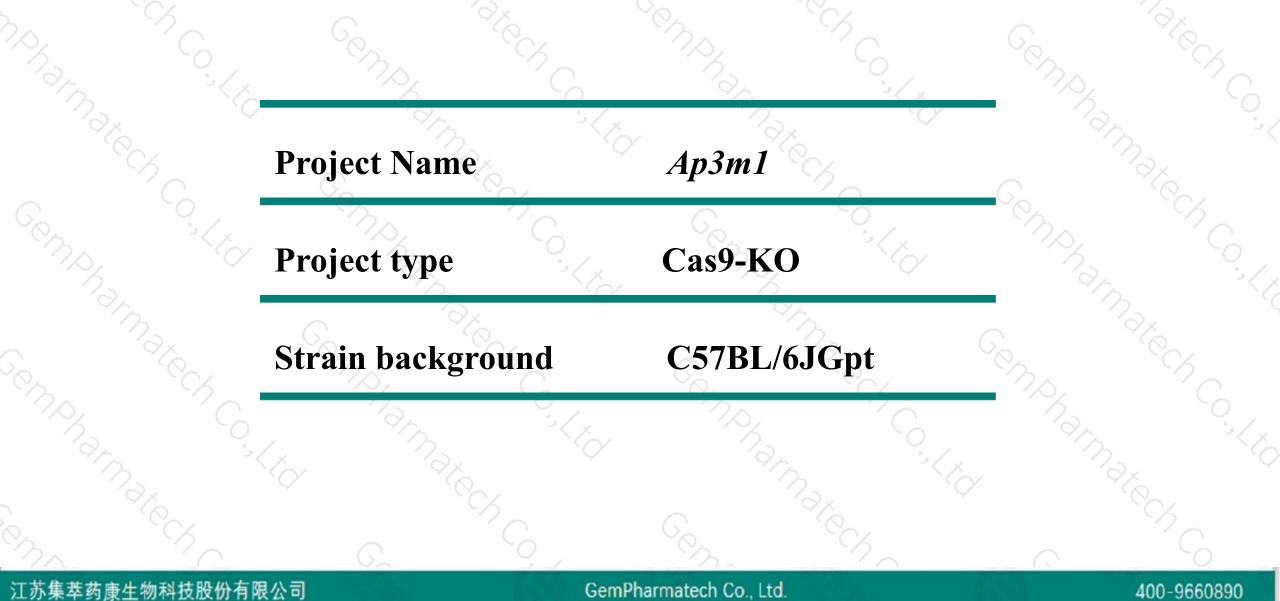
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2020-4-9

Project Overview

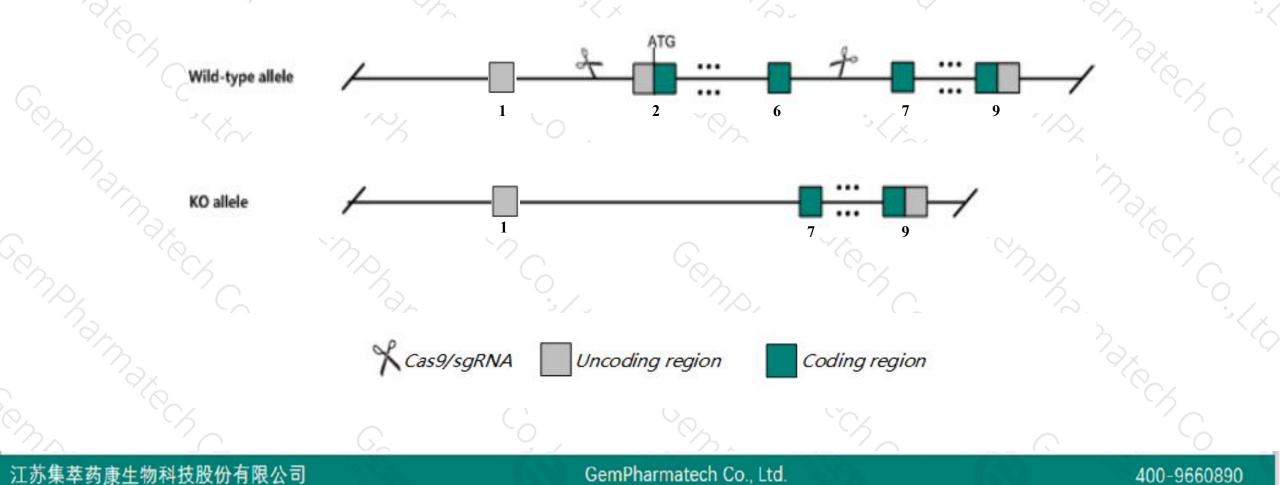




Knockout strategy



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.

Notice

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

2 ?

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:ENSMUSG0000021824
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

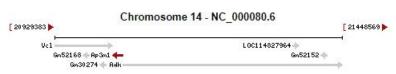
Location: 14 A3; 14 11.58 cM

≈ ?

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 (2103310621052553, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	14	NC_000080.5 (2185296421871664, complement)



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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	<u>418aa</u>	Protein coding	<u>CCDS26861</u> 교	Q9JKC8	TSL:1 GENCODE basic APPRIS P1
Ap3m1-201	ENSMUST0000022371.9	1770	<u>364aa</u>	Protein coding	-	<u>H7BWY2</u> &	TSL:5 GENCODE basic
Ap3m1-208	ENSMUST00000224016.1	764	<u>204aa</u>	Protein coding	121	A0A286YDZ6@	GENCODE basic
Ap3m1-204	ENSMUST00000130370.2	673	<u>148aa</u>	Protein coding	120	D3YWU3@	CDS 3' incomplete TSL:2
Ap3m1-203	ENSMUST00000130291.7	579	<u>174aa</u>	Protein coding	120	D3YXV9₽	CDS 3' incomplete TSL:2
Ap3m1-202	ENSMUST00000126536.7	737	<u>114aa</u>	Nonsense mediated decay		D6R163	TSL:3
Ap3m1-207	ENSMUST00000156716.1	693	No protein	Processed transcript	-	-	TSL:5
Ap3m1-205	ENSMUST00000148886.1	562	No protein	Processed transcript	5 7 6		TSL:3

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

< Ap3m1-206 protein coding

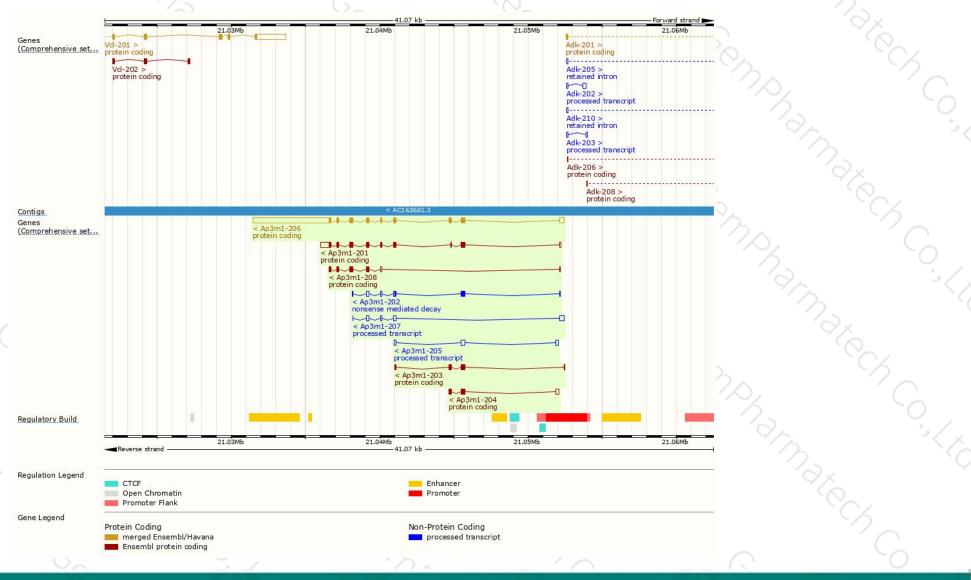
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Genomic location distribution







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Protein domain



Superfamily Longin-like domain superfamily AP-2 complex subunit mu, C-terminal superfamily Prints. Clathrin adaptor, mu subunit Mu homology domain PROSITE profiles. Mu homology domain PROSITE patterns. Clathrin adaptor, mu subunit PIRSE. Clathrin adaptor, mu subunit PIRSE. Clathrin adaptor, mu subunit PARTHER. PTHR10529 PIRSIDE statems. Clathrin adaptor, mu subunit CDD. 230,450.60 CDD. 230,450.60 CDD. 214537 All sequence. SNPs/in Sequence variants (dbSNP and all other sources) Variant Legend missense variant synonymous variant Scale bar 0 40 80 120 160 200 240 280 320 360 418	ISMUSP00000117 =		1 ° ° C/		20,	1C		Go.		
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



