

Ap3s2 Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Ap3s2

Project type

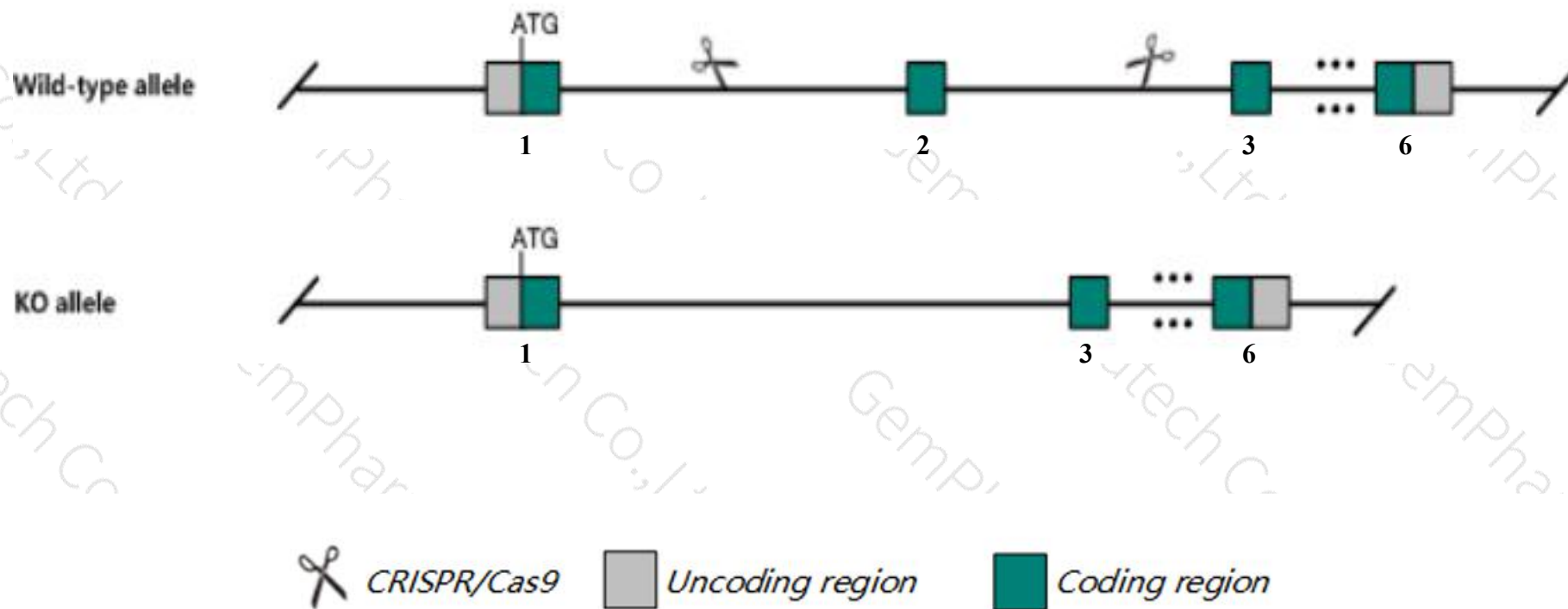
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ap3s2* gene. The schematic diagram is as follows:



- The *Ap3s2* gene has 2 transcripts. According to the structure of *Ap3s2* gene, exon2 of *Ap3s2-201* (ENSMUST00000075657.7) transcript is recommended as the knockout region. The region contains 92bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ap3s2* gene. The brief process is as follows: CRISPR/Cas9 system

- The 5-terminal regulatin of *5430400D12Rik* and *Gm26646* may be affect.
- The *Ap3s2* 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)

Ap3s2 adaptor-related protein complex 3, sigma 2 subunit [*Mus musculus* (house mouse)]

Gene ID: 11778, updated on 13-Mar-2020

Summary

Official Symbol Ap3s2 provided by [MGI](#)
Official Full Name adaptor-related protein complex 3, sigma 2 subunit provided by [MGI](#)
Primary source [MGI:1337060](#)
See related [Ensembl:ENSMUSG00000063801](#)
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 [s]3B
Expression Ubiquitous expression in whole brain E14.5 (RPKM 17.2), CNS E14 (RPKM 15.6) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)

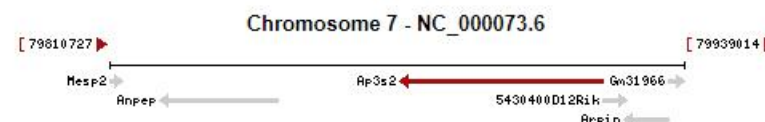
Genomic context

Location: 7; 7 D2

See Ap3s2 in [Genome Data Viewer](#)

Exon count: 6

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (79875325..79920640, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (87020211..87065526, complement)

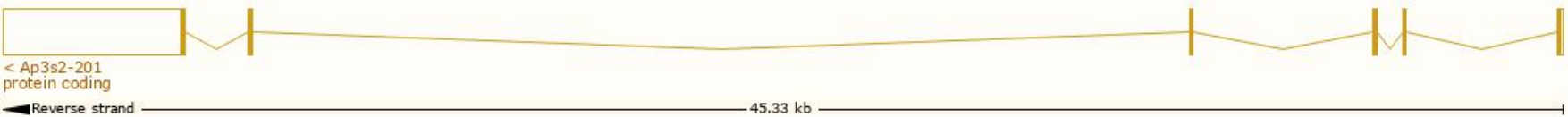


Transcript information (Ensembl)

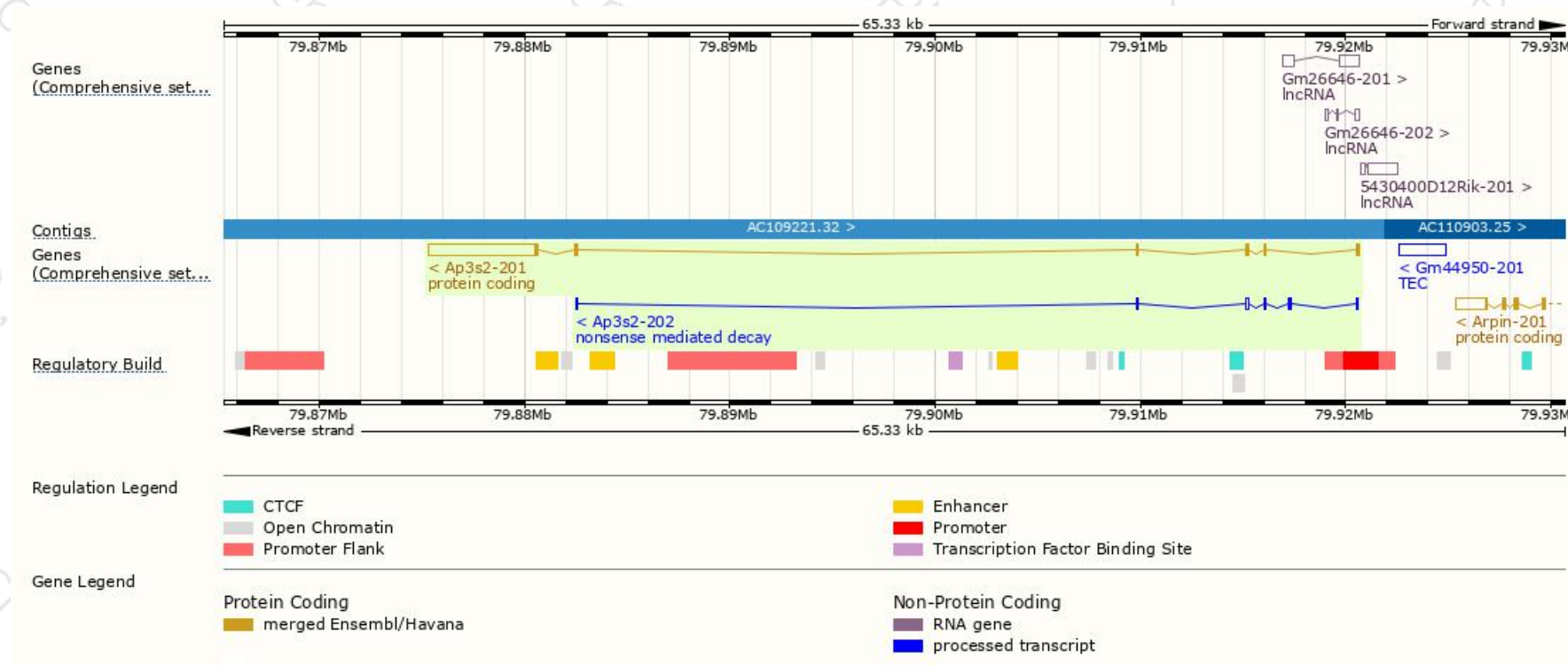
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ap3s2-201	ENSMUST00000075657.7	5813	193aa	Protein coding	CCDS21389	Q8BSZ2	TSL:1 GENCODE basic APPRIS P1
Ap3s2-202	ENSMUST00000206725.1	519	42aa	Nonsense mediated decay	-	A0A0U1RQ64	TSL:3

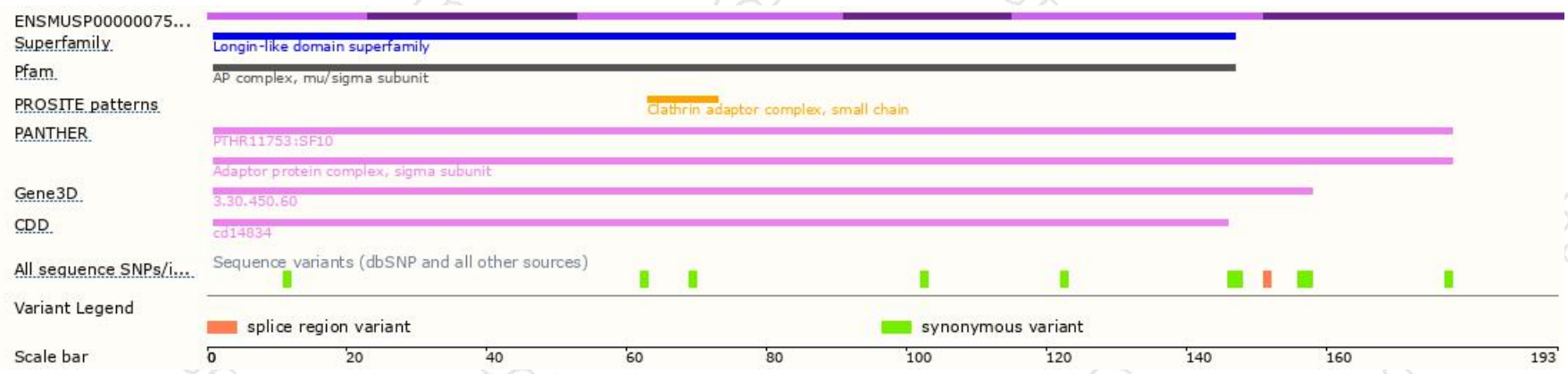
The strategy is based on the design of *Ap3s2-201* transcript,the transcription is shown below



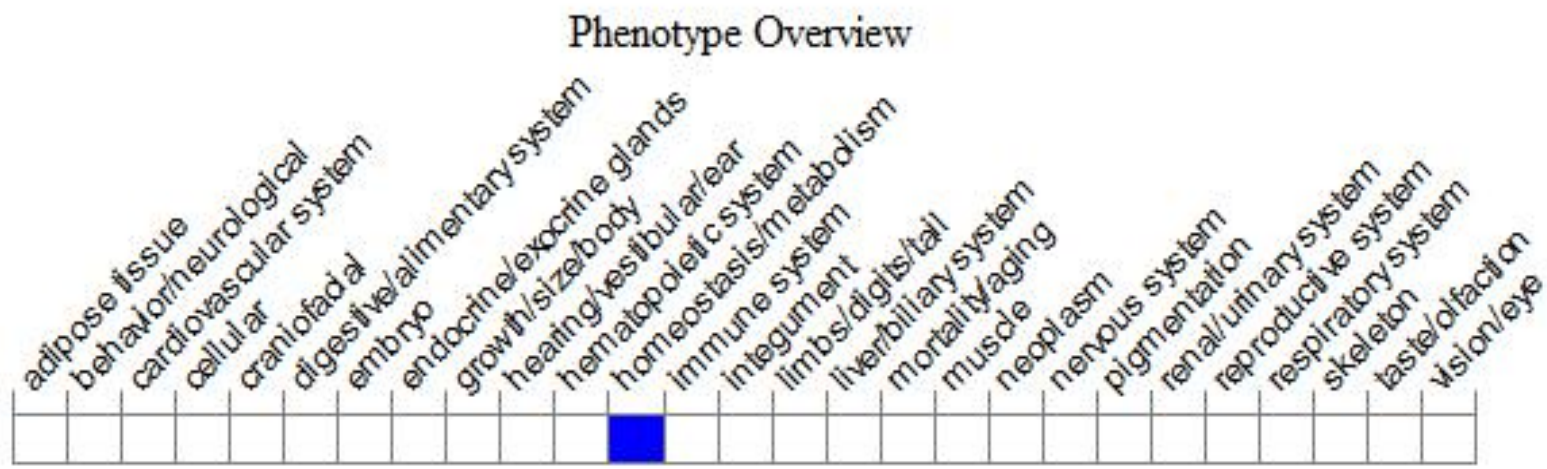
Genomic location distribution



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/>).

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

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