Ap3s1 Cas9-KO Strategy

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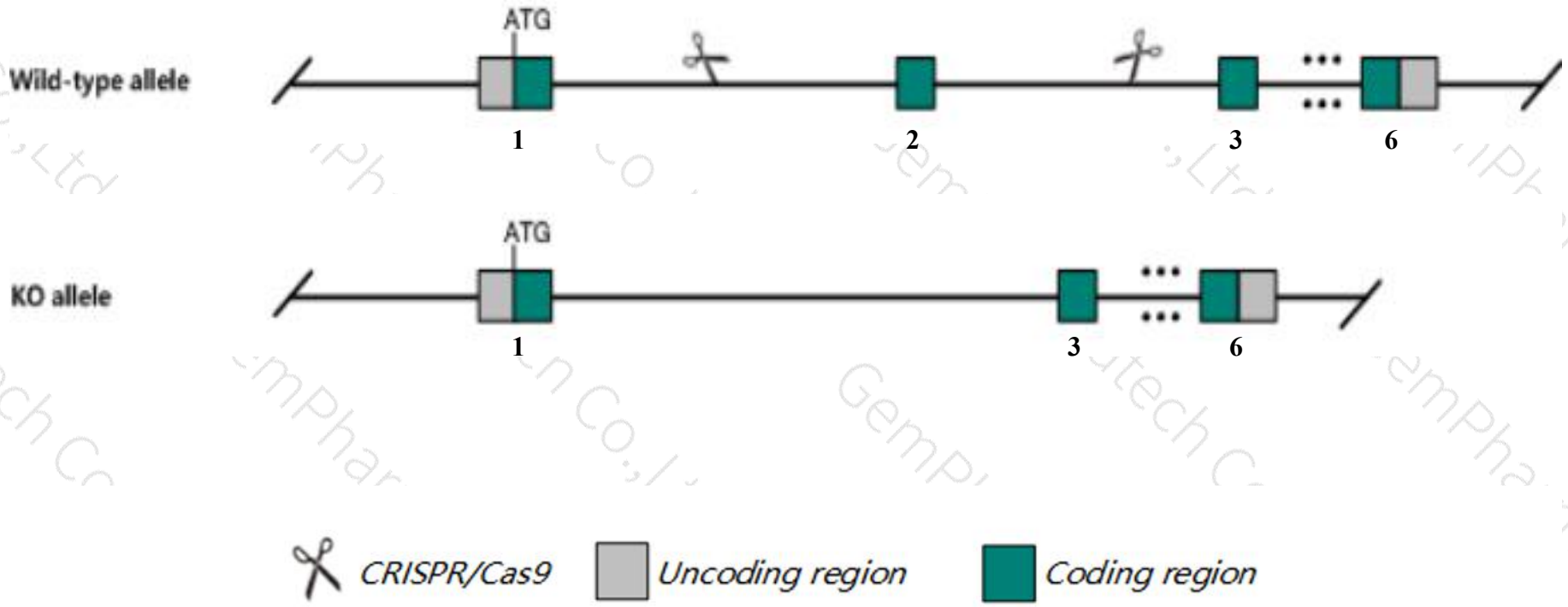
Design Date: **2020-4-9**

Project Overview

Project Name	***Ap3s1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ap3s1* gene. The schematic diagram is as follows:



Technical routes

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- The *Ap3s1* gene has 6 transcripts. According to the structure of *Ap3s1* gene, exon2 of *Ap3s1-201* (ENSMUST00000025357.8) 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 *Ap3s1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- The *Ap3s1* gene is located on the Chr18. 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）

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Ap3s1 adaptor-related protein complex 3, sigma 1 subunit [*Mus musculus* (house mouse)]

Gene ID: 11777, updated on 5-Apr-2020

Summary

Official Symbol	Ap3s1 provided by MGI
Official Full Name	adaptor-related protein complex 3, sigma 1 subunit provided by MGI
Primary source	MGI:MGI:1337062
See related	Ensembl:ENSMUSG00000024480
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	This gene encodes the sigma subunit of the heterotetrameric adaptor protein complex AP-3 which is involved in the formation of specialized lysosome-related compartments such as melanosomes. Alternate splicing of this gene results in multiple transcript variants encoding different isoforms. Pseudogenes of this gene are found on chromosomes 1, 8, 16, 17 and X. [provided by RefSeq, Dec 2014]
Expression	Ubiquitous expression in CNS E18 (RPKM 12.6), CNS E14 (RPKM 11.2) and 27 other tissues See more
Orthologs	human all

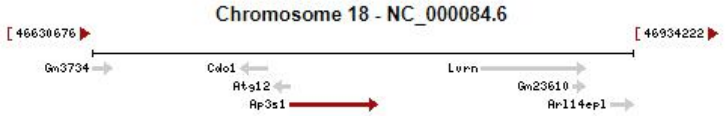
Genomic context

Location: 18; 18 C

See Ap3s1 in Genome Data Viewer

Exon count: 7

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (46741694..46790826)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (46901571..46950480)

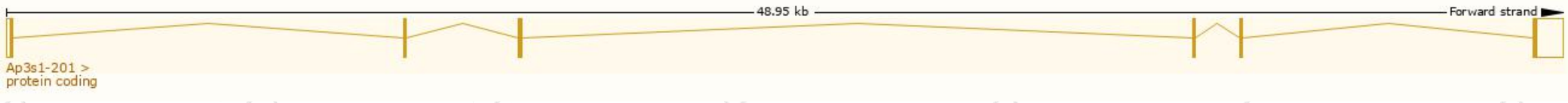


Transcript information（Ensembl）

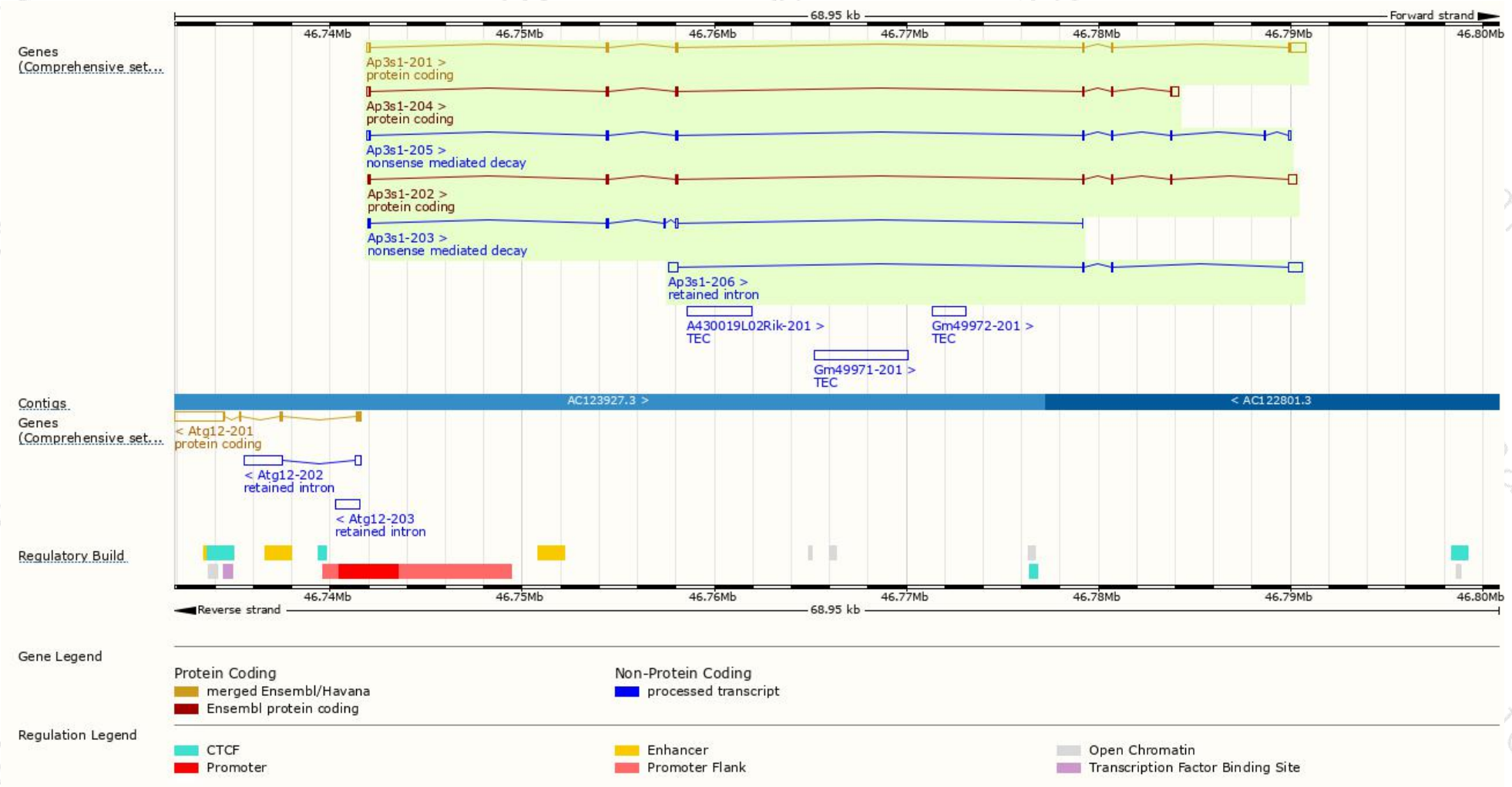
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ap3s1-201	ENSMUST00000025357.8	1520	193aa	Protein coding	CCDS29236	Q3U8S0 Q9DCR2	TSL:1 GENCODE basic APPRIS P1
Ap3s1-202	ENSMUST00000224622.1	978	162aa	Protein coding	-	A0A286YDU3	GENCODE basic
Ap3s1-204	ENSMUST00000225520.1	957	162aa	Protein coding	-	A0A286YDU3	GENCODE basic
Ap3s1-205	ENSMUST00000226108.1	743	162aa	Nonsense mediated decay	-	A0A286YDU3	-
Ap3s1-203	ENSMUST00000225415.1	417	54aa	Nonsense mediated decay	-	A0A286YD58	-
Ap3s1-206	ENSMUST00000234998.1	1407	No protein	Retained intron	-	-	-

The strategy is based on the design of *Ap3s1-201* transcript,the transcription is shown below

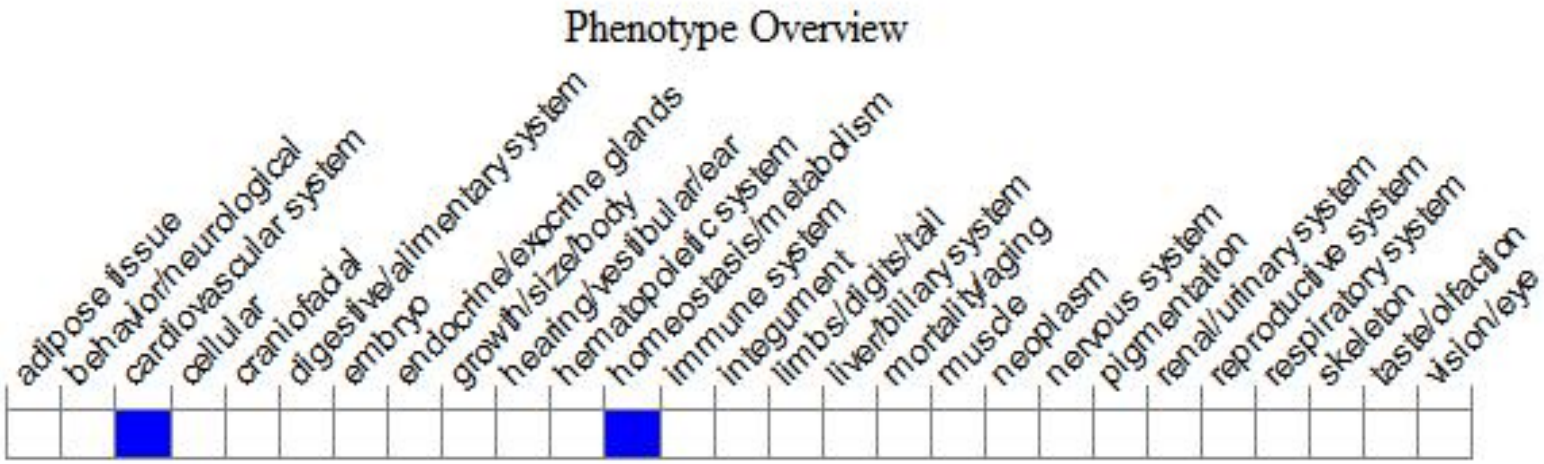


Genomic location distribution



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/).

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