

# *Ap4s1* Cas9-CKO Strategy

**Designer:**

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**Design Date:**

**2019-8-22**

# Project Overview

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**Project Name**

*Ap4s1*

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**Project type**

**Cas9-CKO**

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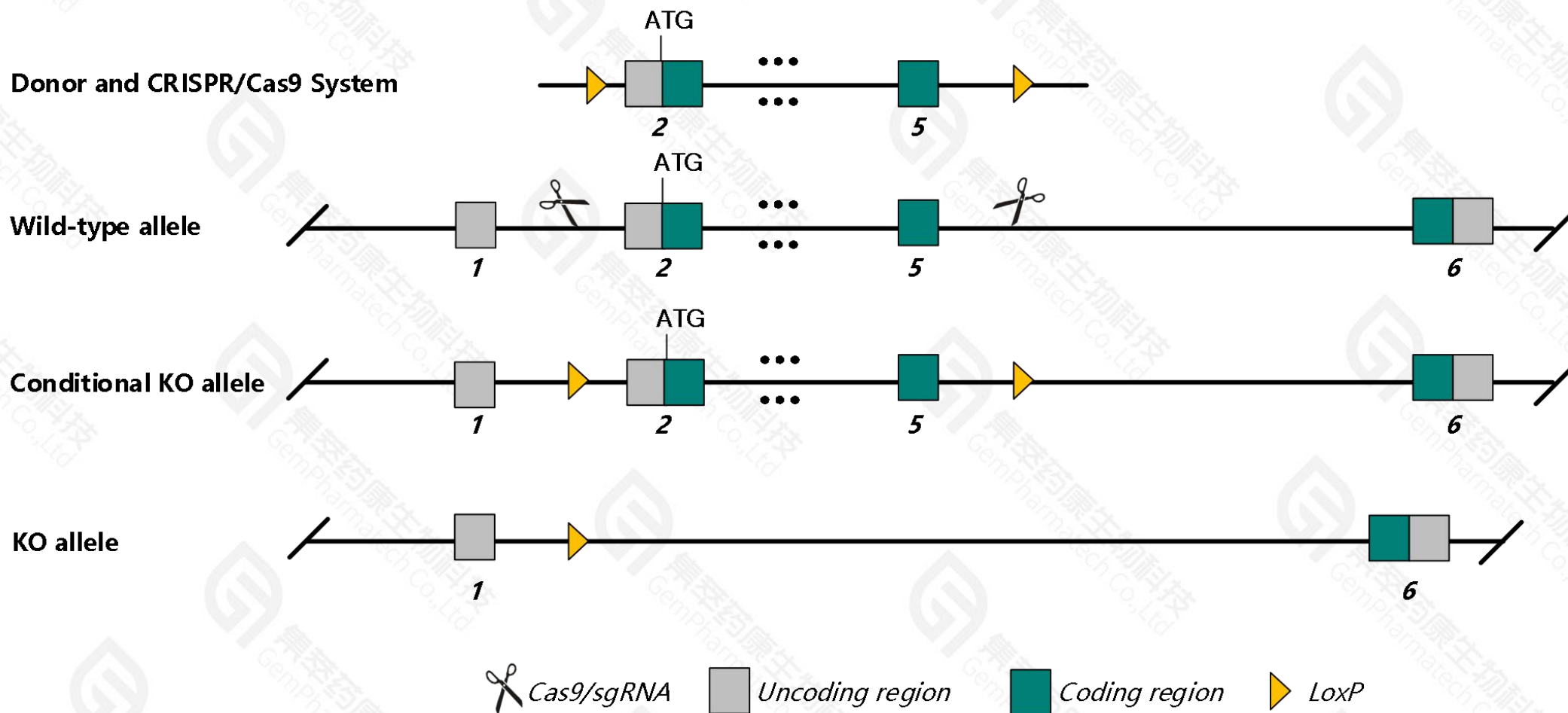
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ap4s1* gene. The schematic diagram is as follows:



# Technical routes

- The *Ap4s1* gene has 2 transcripts. According to the structure of *Ap4s1* gene, exon2-exon5 of *Ap4s1*-201(ENSMUST00000021338.10) 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 *Ap4s1* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- The *Ap4s1* gene is located on the Chr12. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

## Ap4s1 adaptor-related protein complex AP-4, sigma 1 [Mus musculus (house mouse)]

Gene ID: 11782, updated on 13-Mar-2020

### Summary

**Official Symbol** Ap4s1 provided by [MGI](#)

**Official Full Name** adaptor-related protein complex AP-4, sigma 1 provided by [MGI](#)

**Primary source** [MGI:MGI:1337065](#)

**See related** [Ensembl:ENSMUSG00000020955](#)

**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

**Also known as** AI314282

**Summary** This gene encodes the sigma subunit of the adaptor-related protein complex 4 which mediates intracellular membrane trafficking along the endocytic and secretory transport pathways. This complex contains four subunits, beta, epsilon, mu, and sigma, and belongs to a family of five adapter protein complexes, including three clathrin-associated complexes and two non clathrin-associated complexes, that localize to different intracellular compartments and mediate membrane vesicle trafficking using distinct pathways. In humans, loss-of-function mutations in this gene have been linked to specific adapter complex 4 deficiency disorders including hereditary spastic paraplegia. Alternate splicing results in multiple transcript variants. [provided by RefSeq, Jul 2016]

**Expression** Ubiquitous expression in cerebellum adult (RPKM 9.3), frontal lobe adult (RPKM 8.9) and 28 other tissues [See more](#)

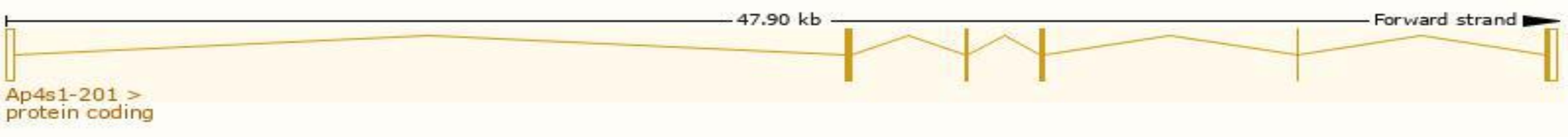
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

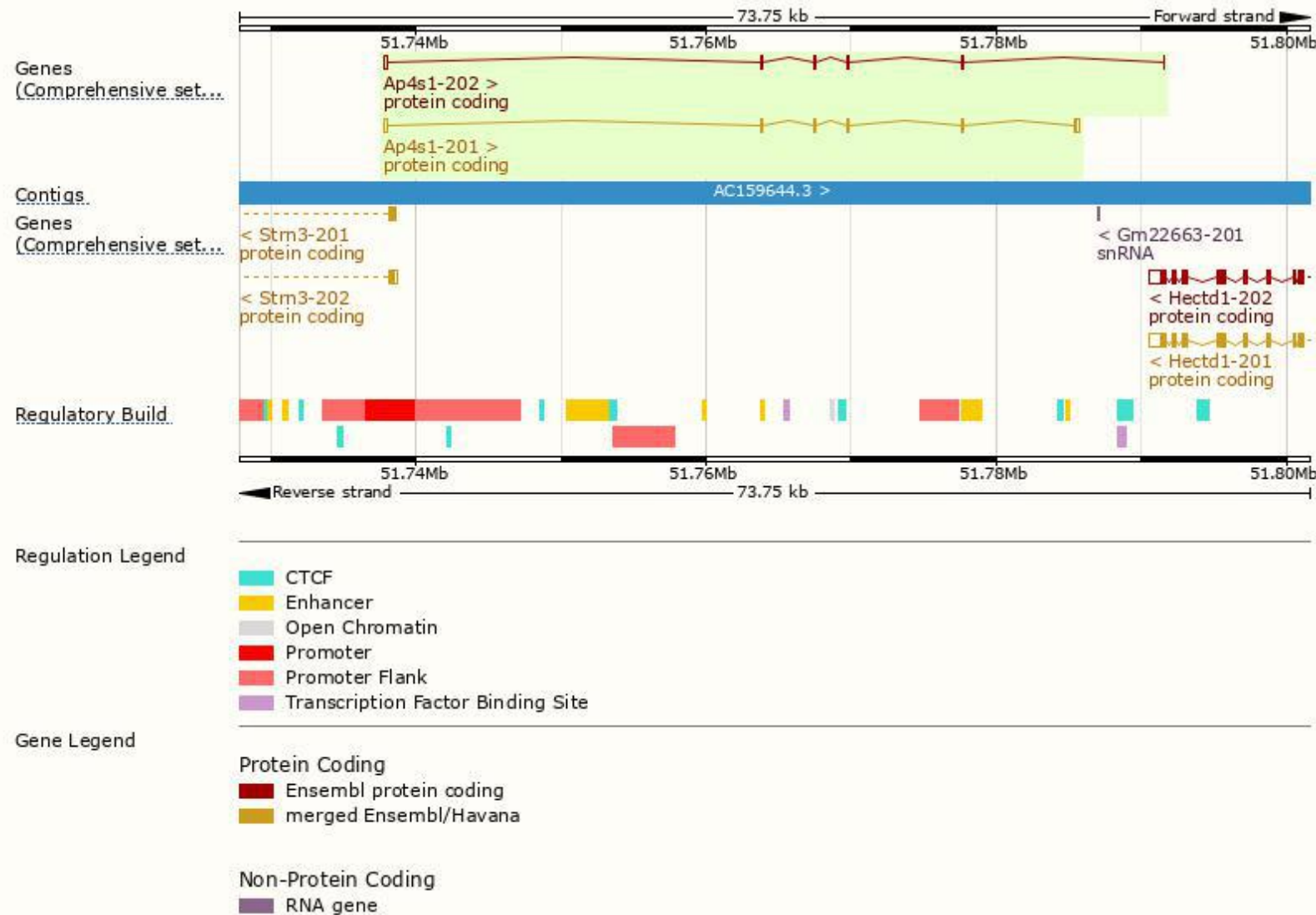
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ap4s1-201	<a href="#">ENSMUST00000021338.9</a>	1035	<a href="#">144aa</a>	Protein coding	<a href="#">CCDS36441</a>	<a href="#">Q9WVL1</a>	TSL:1 GENCODE basic APPRIS P1
Ap4s1-202	<a href="#">ENSMUST00000218820.1</a>	757	<a href="#">134aa</a>	Protein coding	-	<a href="#">A0A1W2P708</a>	CDS 3' incomplete TSL:5

The strategy is based on the design of *Ap4s1-201* transcript,the transcription is shown below:

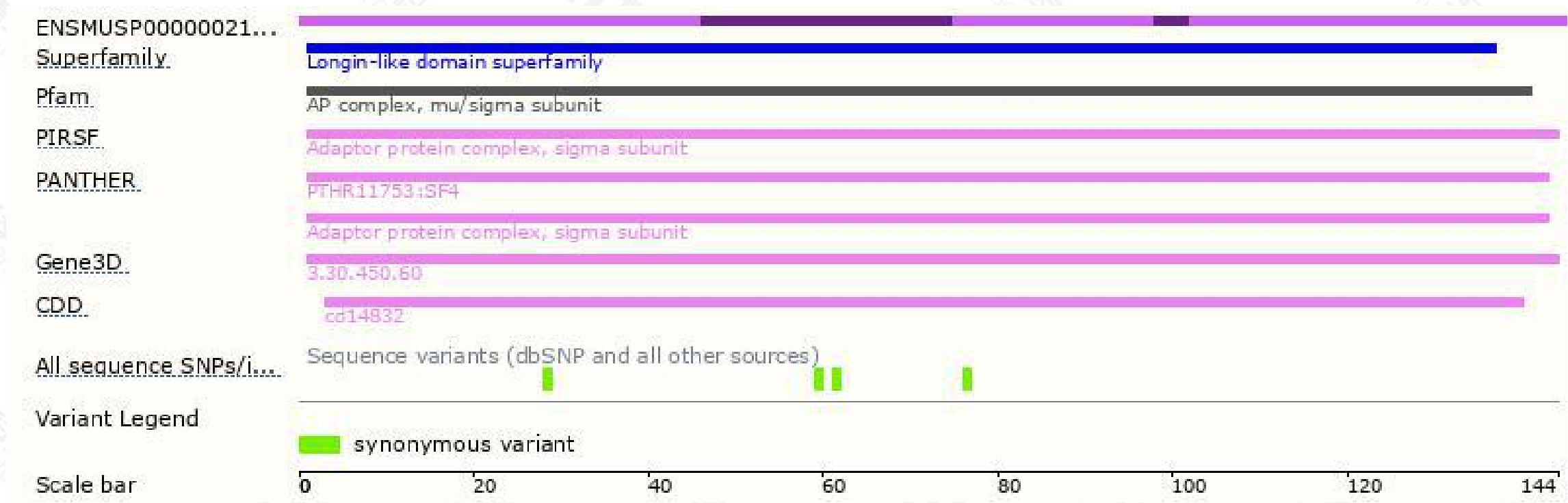


# Genomic location distribution





# Protein domain



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