Ap2s1 Cas9-CKO Strategy

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Project Overview

Project Name	***Ap2s1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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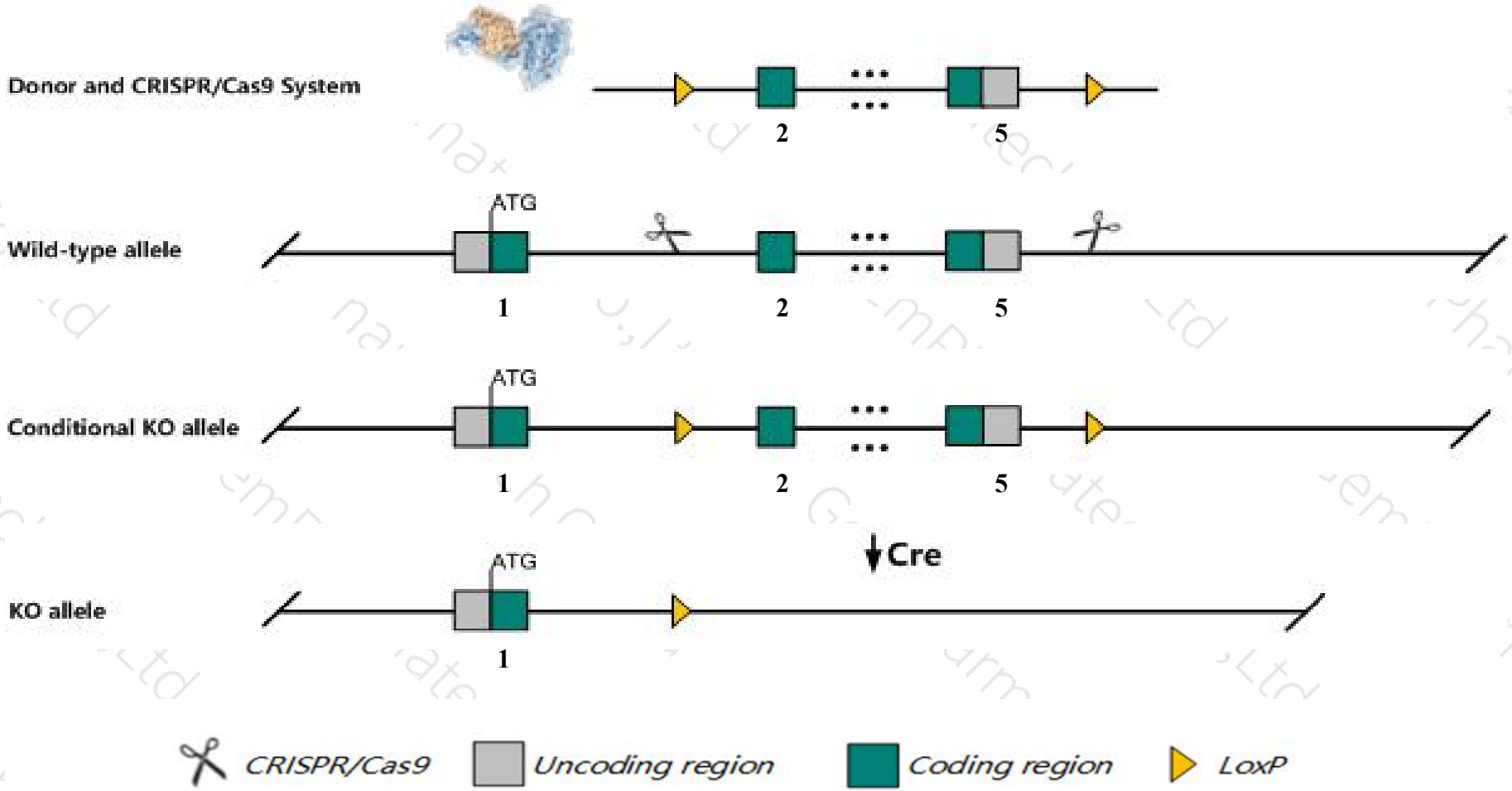
This model will use CRISPR/Cas9 technology to edit the *Ap2s1* gene. The schematic diagram is as follows:



Technical routes

- The *Ap2s1* gene has 5 transcripts. According to the structure of *Ap2s1* gene, exon2-exon5 of *Ap2s1-201* (ENSMUST00000086112.7) transcript is recommended as the knockout region.The region contains most of the coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ap2s1* 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.

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit decreased embryo size, a rudimentary egg cylinder, failure of primitive streak formation, absent primitive node and head folds, failure to gastrulate, and complete lethality prior to organogenesis.
- The *Ap2s1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Ap2s1 adaptor-related protein complex 2, sigma 1 subunit [*Mus musculus* (house mouse)]

Gene ID: 232910, updated on 7-Apr-2020

Summary

Official Symbol	Ap2s1 provided by MGI
Official Full Name	adaptor-related protein complex 2, sigma 1 subunit provided by MGI
Primary source	MGI:MGI:2141861
See related	Ensembl:ENSMUSG00000008036
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	AI043088
Expression	Ubiquitous expression in duodenum adult (RPKM 68.3), large intestine adult (RPKM 65.1) and 28 other tissues See more
Orthologs	human all

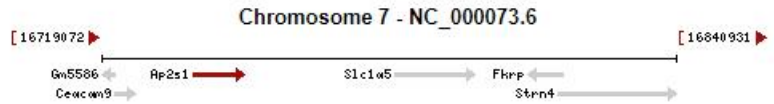
Genomic context

Location: 7; 7 A2

See Ap2s1 in Genome Data Viewer

Exon count: 5

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (16738444..16749290)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (17323793..17334639)



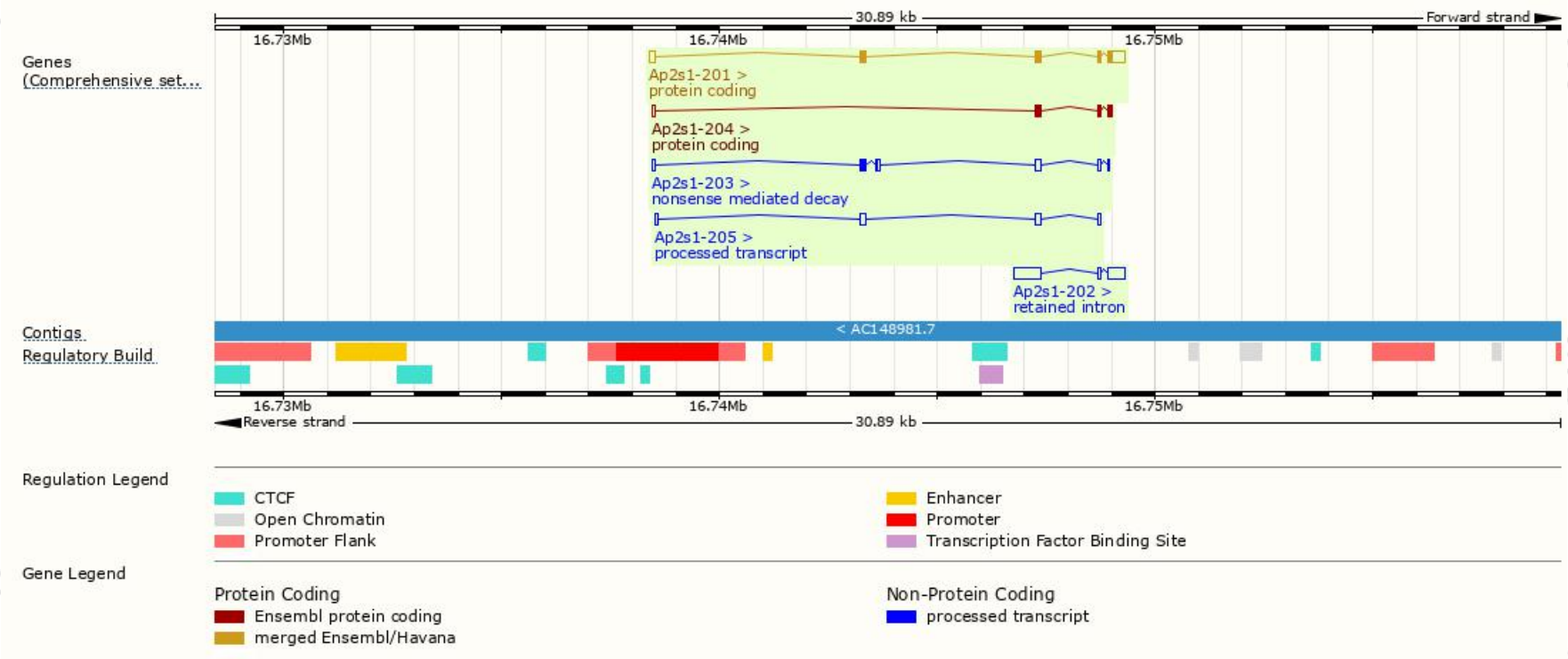
Transcript information（Ensembl）

The gene has 5 transcripts,all transcripts are shown below:

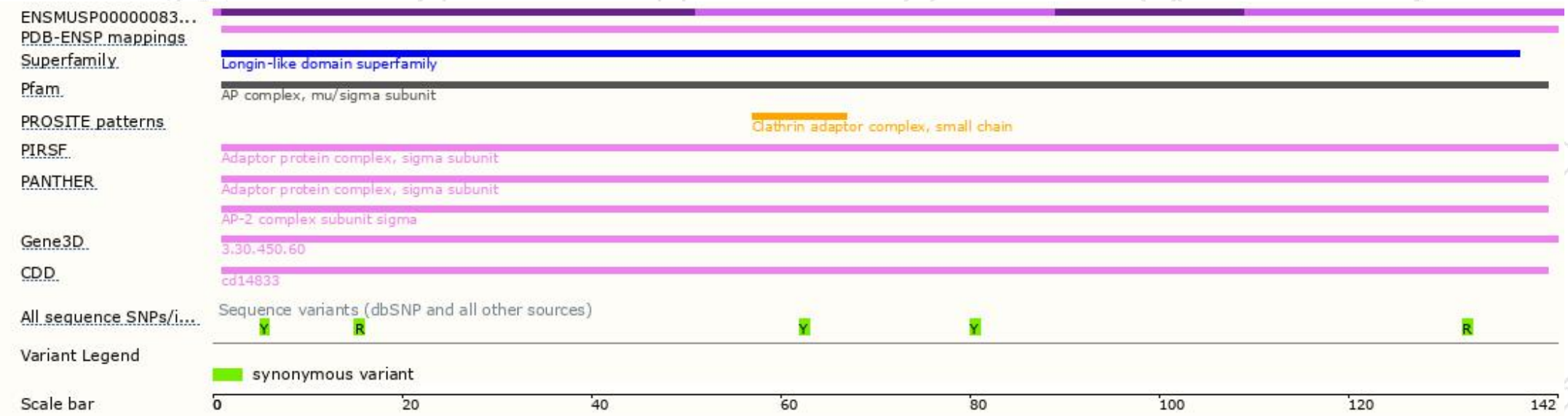
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ap2s1-201	ENSMUST00000086112.7	836	142aa	Protein coding	CCDS52042	P62743 Q3UJ76	TSL:1 GENCODE basic APPRIS P1
Ap2s1-204	ENSMUST00000205607.1	372	92aa	Protein coding	-	A0A0U1RQ06	TSL:3 GENCODE basic
Ap2s1-203	ENSMUST00000205590.1	504	60aa	Nonsense mediated decay	-	A0A0U1RPS0	TSL:3
Ap2s1-205	ENSMUST00000205673.1	374	No protein	Processed transcript	-	-	TSL:5
Ap2s1-202	ENSMUST00000141496.1	1054	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Ap2s1-201* transcript, the transcription is shown below

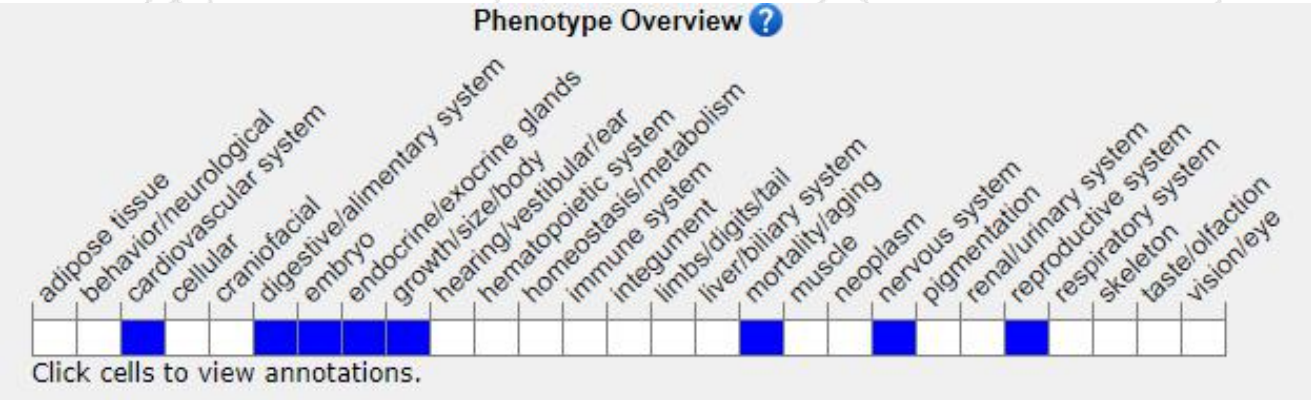
Genomic location distribution



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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