

Apcs Cas9-KO Strategy

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Project Overview

Project Name

Apcs

Project type

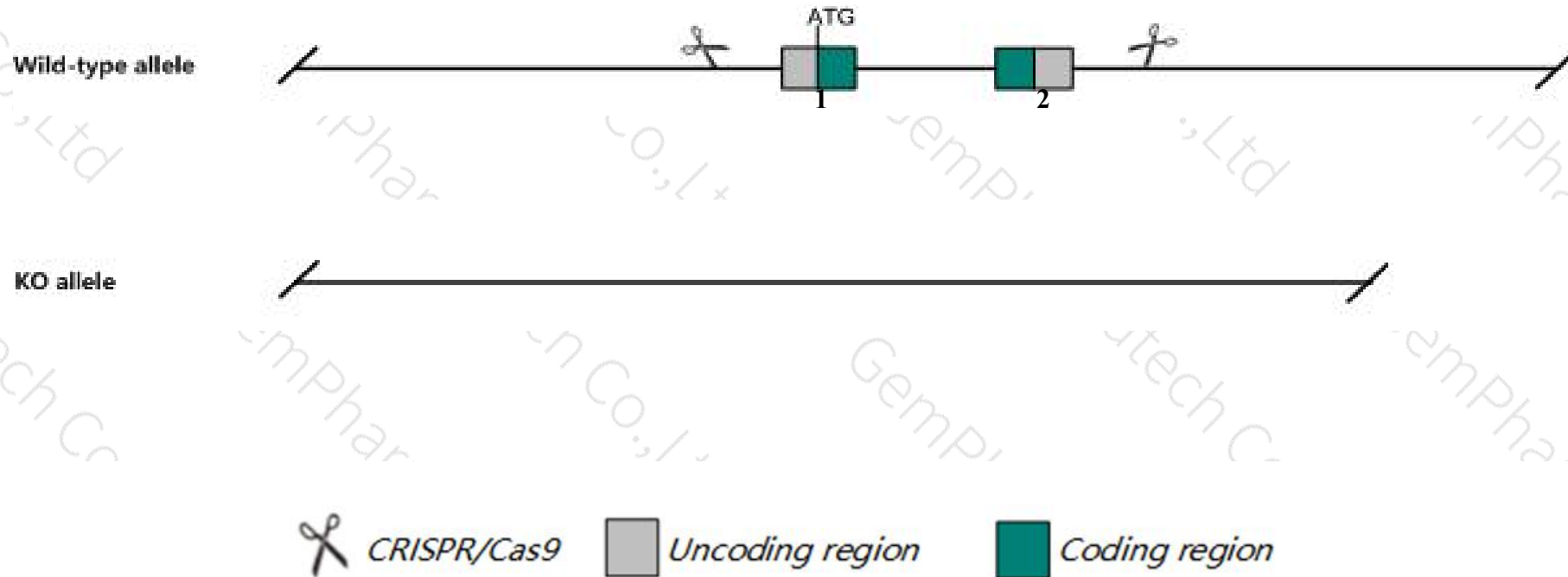
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Apcs* gene has 1 transcript. According to the structure of *Apcs* gene, exon1-exon2 of *Apcs-201* (ENSMUST00000027824.5) transcript is recommended as the knockout region. The region contains all 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 *Apcs* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a null allele exhibit decreased antibody productions, increased autoimmune antibodies, reduced amyloidosis and glomerulonephrosis depending on strain background.
- The *Apcs* gene is located on the Chr1. 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)

Apcs serum amyloid P-component [*Mus musculus* (house mouse)]

Gene ID: 20219, updated on 12-Aug-2019

Summary

- Official Symbol** Apcs provided by [MGI](#)
- Official Full Name** serum amyloid P-component provided by [MGI](#)
- Primary source** [MGI:MGI:98229](#)
- See related** [Ensembl:ENSMUSG00000026542](#)
- 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** Sap
- Expression** Restricted expression toward liver E18 (RPKM 530.3) [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 1 H3; 1 80.33 cM

See Apcs in [Genome Data Viewer](#)

Exon count: 2

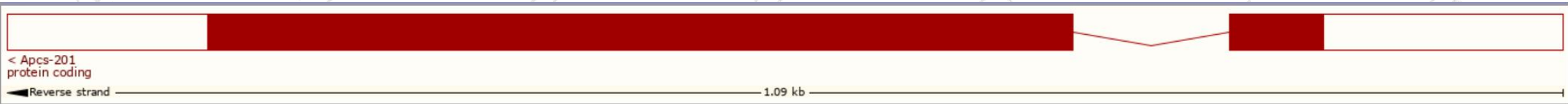
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (172893961..172895054, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (174824092..174825185, complement)

Transcript information (Ensembl)

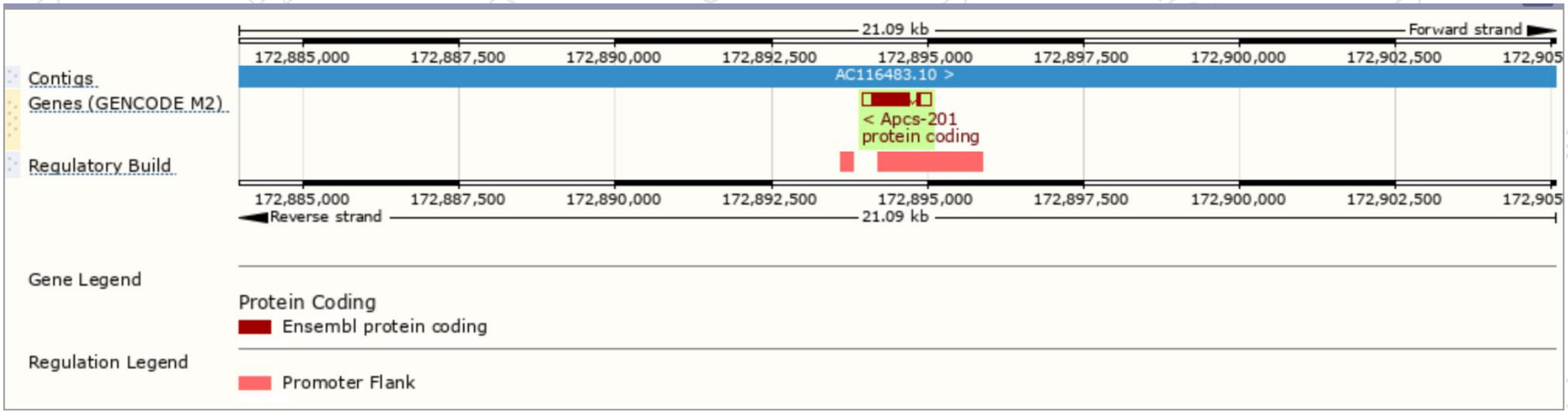
The gene has 1 transcript,the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Apcs-201	ENSMUST00000027824.5	983	224aa	Protein coding	CCDS15520	P12246 Q4JFI8	GENCODE basic

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



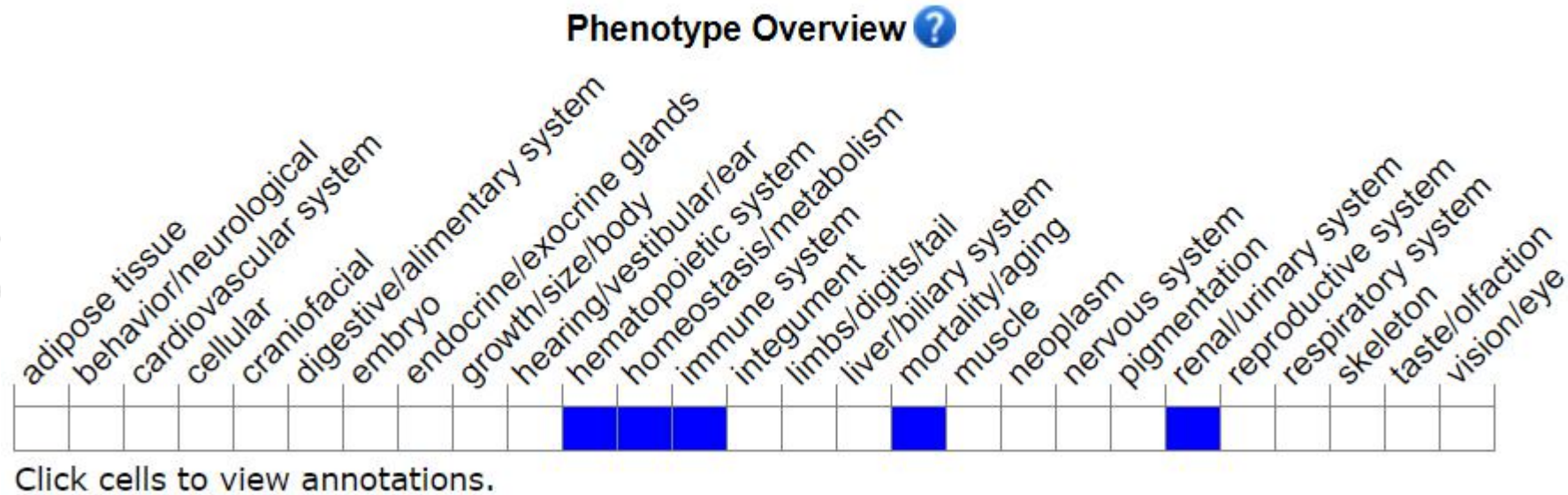
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for a null allele exhibit decreased antibody productions, increased autoimmune antibodies, reduced amyloidosis and glomerulonephrosis depending on strain background.

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

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