

Acp6 Cas9-KO Strategy

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Project Overview

Project Name

Acp6

Project type

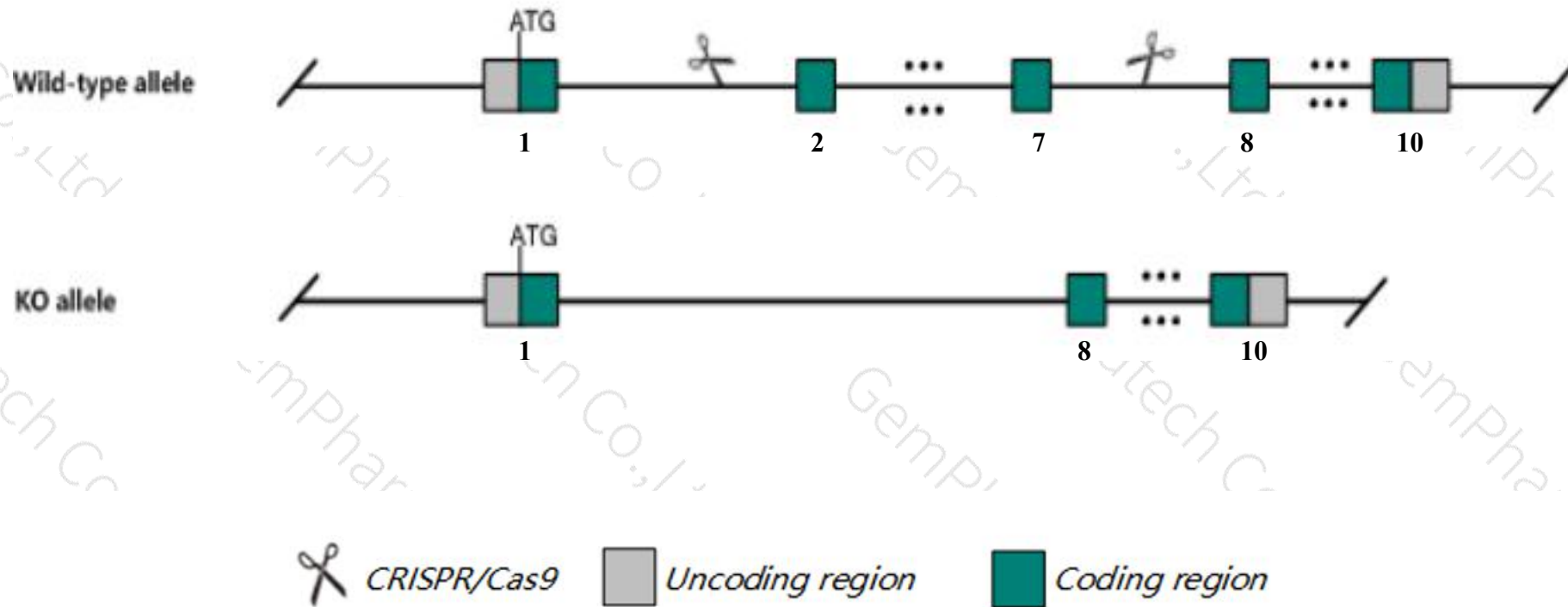
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Acp6* gene. The schematic diagram is as follows:



- The *Acp6* gene has 9 transcripts. According to the structure of *Acp6* gene, exon2-exon7 of *Acp6-201* (ENSMUST00000090759.4) transcript is recommended as the knockout region. The region contains 659bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Acp6* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, phenotypic analysis of mice homozygous for a gene trap allele indicates this mutation has no notable phenotype in any parameter tested.
- Transcripts 205,208 may not be affected.
- The *Acp6* gene is located on the Chr3. 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)

Acp6 acid phosphatase 6, lysophosphatidic [Mus musculus (house mouse)]

Gene ID: 66659, updated on 13-Mar-2020

Summary



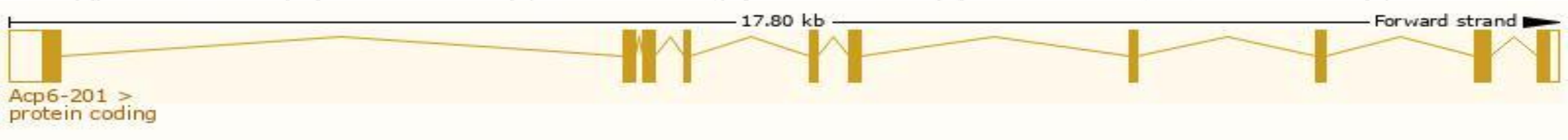
Official Symbol	Acp6 provided by MGI
Official Full Name	acid phosphatase 6, lysophosphatidic provided by MGI
Primary source	MGI:MGI:1931010
See related	Ensembl:ENSMUSG00000028093
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5730559A09Rik, ACPL1, AU022842, mPACPL1
Expression	Ubiquitous expression in duodenum adult (RPKM 20.3), large intestine adult (RPKM 18.8) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

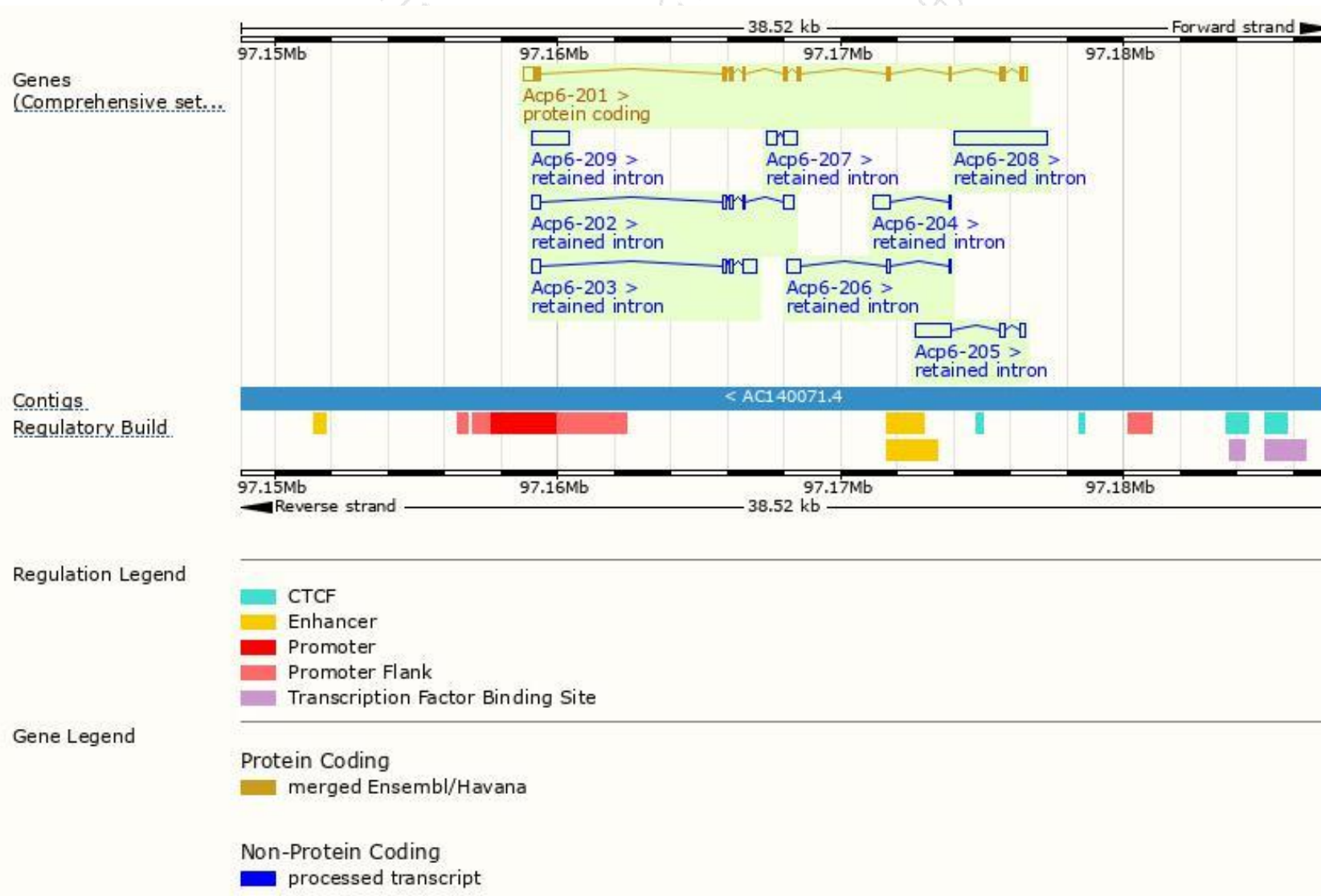
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Acp6-201	ENSMUST00000090759.4	1754	418aa	Protein coding	CCDS17653	Q8BP40	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Acp6-208	ENSMUST00000198329.1	3291	No protein	Retained intron	-	-	TSL:NA
Acp6-205	ENSMUST00000143234.1	1611	No protein	Retained intron	-	-	TSL:1
Acp6-209	ENSMUST00000199346.1	1300	No protein	Retained intron	-	-	TSL:NA
Acp6-203	ENSMUST00000133965.7	1033	No protein	Retained intron	-	-	TSL:2
Acp6-202	ENSMUST00000126438.1	924	No protein	Retained intron	-	-	TSL:2
Acp6-207	ENSMUST00000149900.1	852	No protein	Retained intron	-	-	TSL:3
Acp6-204	ENSMUST00000139898.1	689	No protein	Retained intron	-	-	TSL:1
Acp6-206	ENSMUST00000146143.1	648	No protein	Retained intron	-	-	TSL:2

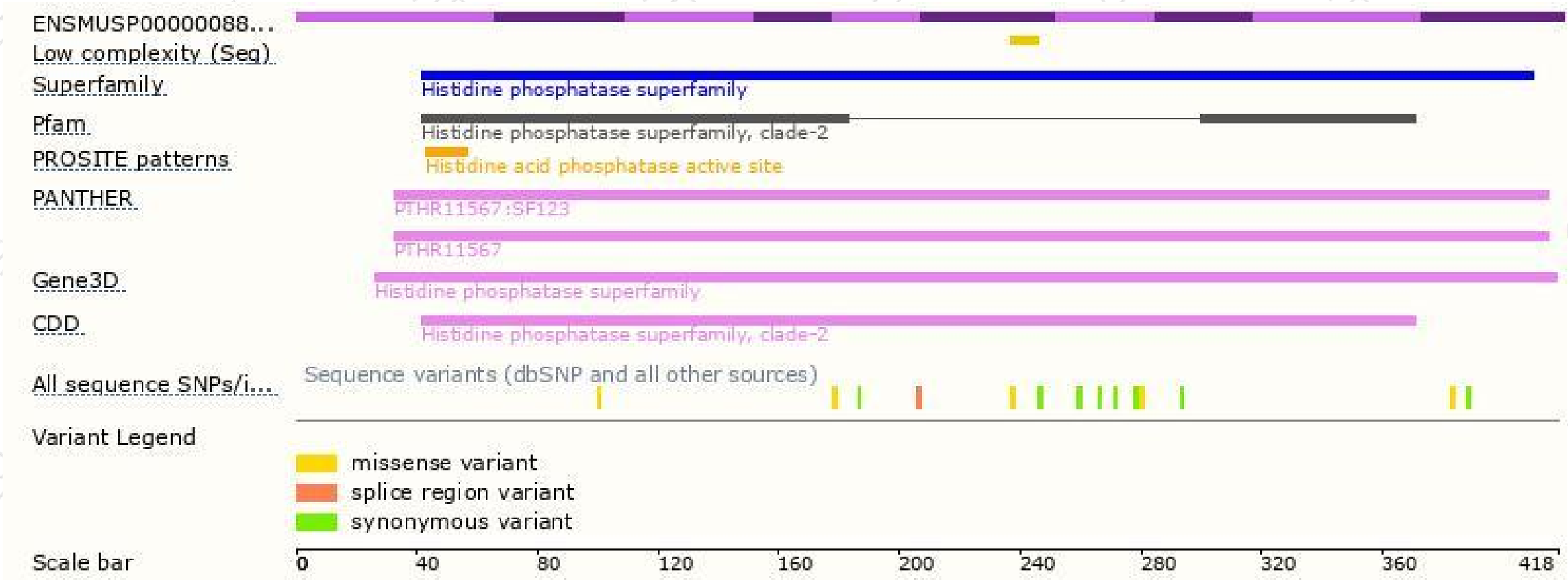
The strategy is based on the design of *Acp6-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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