

C8a Cas9-KO Strategy

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Project Overview

Project Name

C8a

Project type

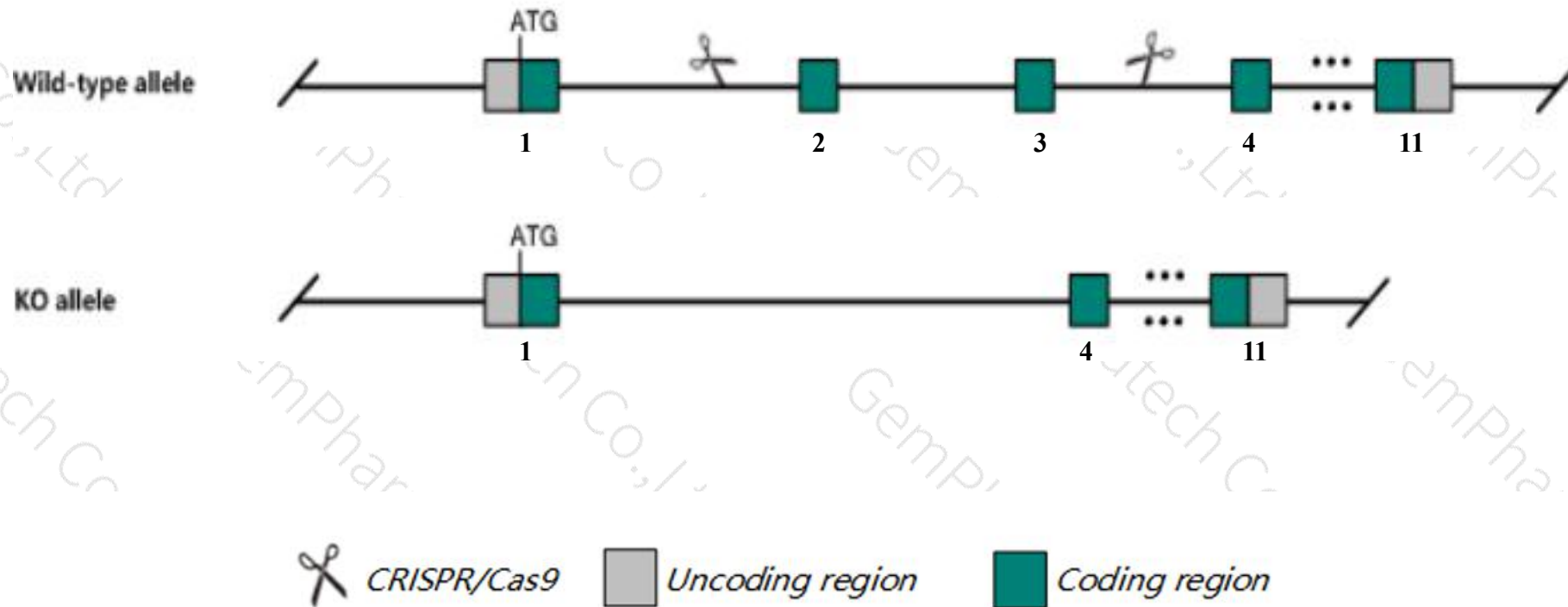
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *C8a* gene. The schematic diagram is as follows:



- The *C8a* gene has 4 transcripts. According to the structure of *C8a* gene, exon2-exon3 of *C8a-202* (ENSMUST00000064873.8) transcript is recommended as the knockout region. The region contains 239bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *C8a* gene. The brief process is as follows: CRISPR/Cas9 system w

- The *C8a* gene is located on the Chr4. 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.
- Transcript *C8a*-204 may not be affected.
- 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)

C8a complement component 8, alpha polypeptide [Mus musculus (house mouse)]

Gene ID: 230558, updated on 13-Mar-2020

Summary



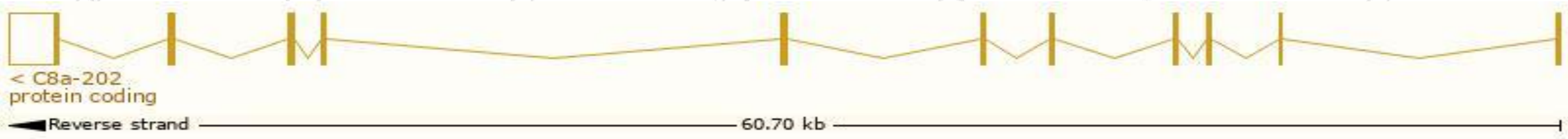
Official Symbol	C8a provided by MGI
Official Full Name	complement component 8, alpha polypeptide provided by MGI
Primary source	MGI:MGI:2668347
See related	Ensembl:ENSMUSG00000035031
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	This gene encodes the alpha subunit of complement component C8 that participates in the assembly of the complement membrane attack complex. The encoded preproprotein undergoes proteolytic processing to generate the alpha subunit, which associates with the beta and gamma subunits to form a trimeric complement component, C8. Alternative splicing results in multiple transcript variants encoding different isoforms that may undergo similar proteolytic processing. This gene is located adjacent to the gene encoding the beta subunit. [provided by RefSeq, Oct 2015]
Expression	Biased expression in liver adult (RPKM 25.6), liver E18 (RPKM 22.4) and 3 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

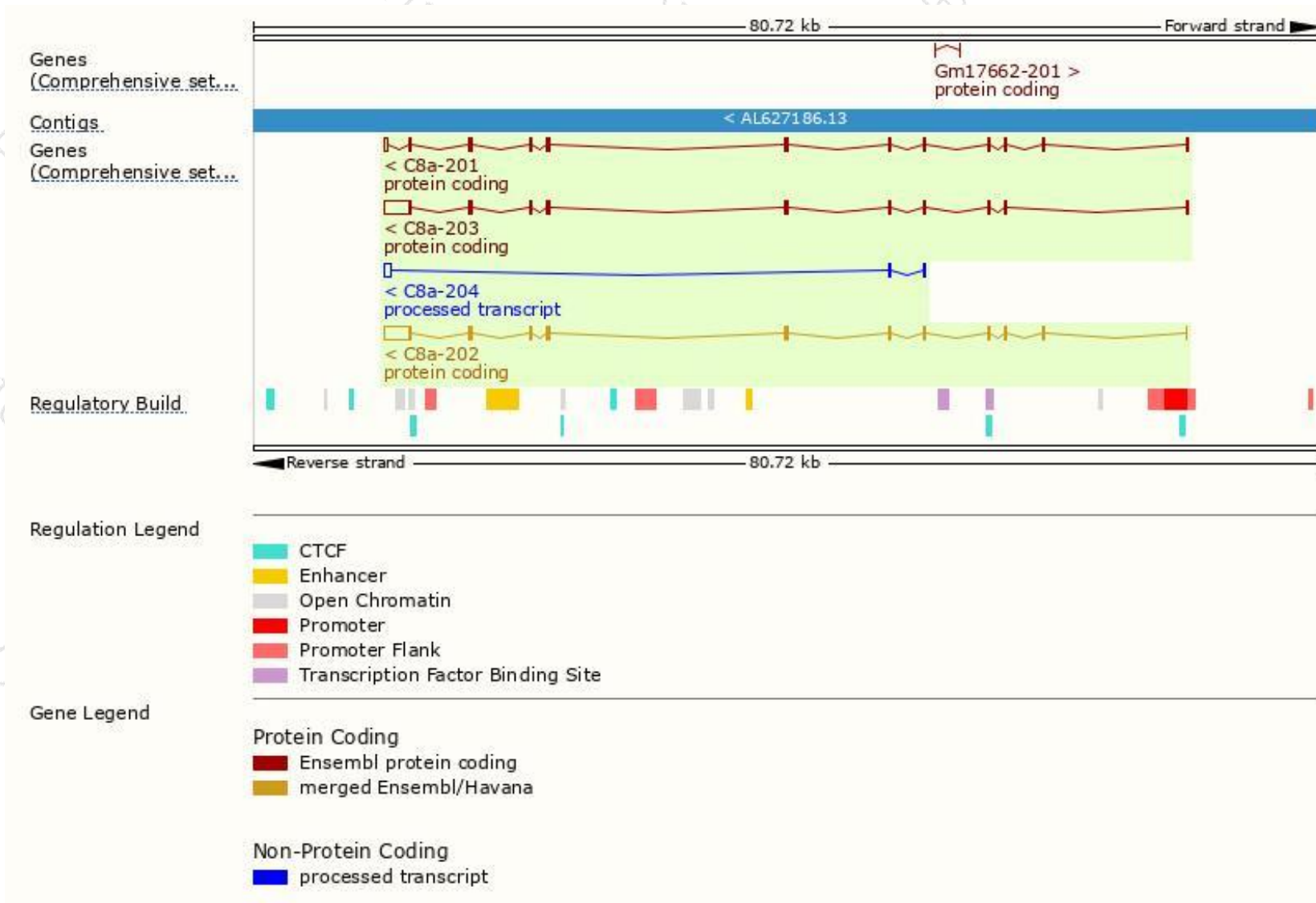
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
C8a-202	ENSMUST00000064873.8	3617	587aa	Protein coding	CCDS18415	Q8K182	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 P3
C8a-203	ENSMUST00000106808.9	3539	543aa	Protein coding	CCDS71433	A2A998	TSL:2 GENCODE basic
C8a-201	ENSMUST00000048947.14	1993	580aa	Protein coding	CCDS84763	A2A997	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 ALT2
C8a-204	ENSMUST00000152146.1	749	No protein	Processed transcript	-	-	TSL:5

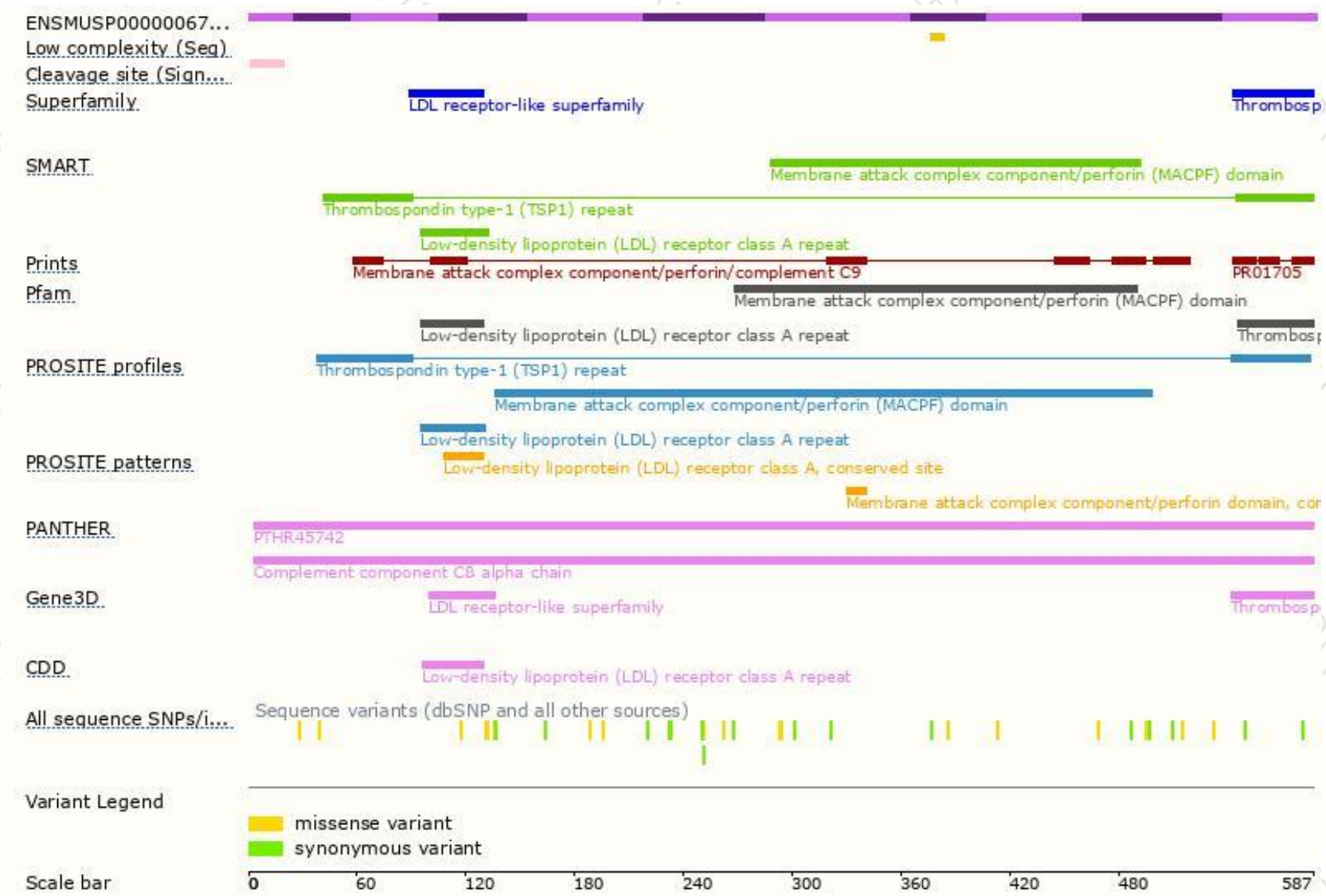
The strategy is based on the design of C8a-202 transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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