

C1qtnf12 Cas9-KO Strategy

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Reviewer:

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Design Date:

2020/2/17

Project Overview

Project Name

C1qtnf12

Project type

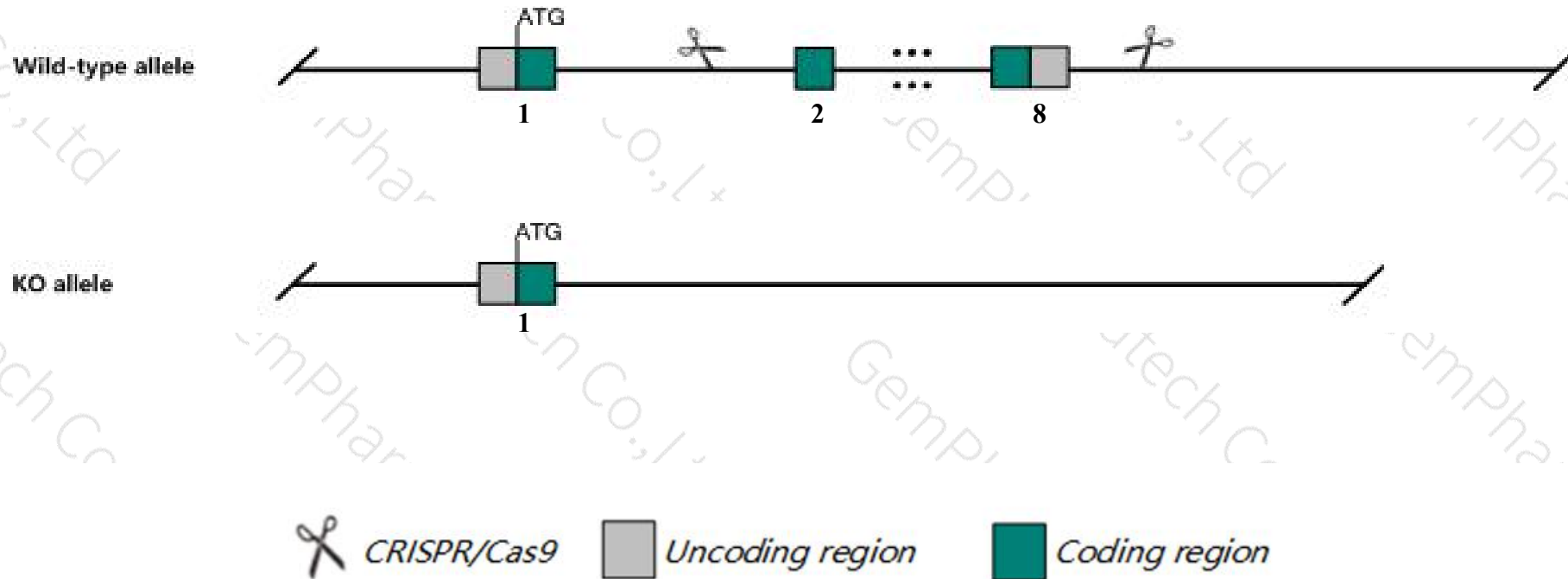
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Clqtnf12* gene. The schematic diagram is as follows:



- The *Clqtnf12* gene has 3 transcripts. According to the structure of *Clqtnf12* gene, exon2-exon8 of *Clqtnf12-201* (ENSMUST00000024338.4) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Clqtnf12* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Clqtnf12* 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.
- 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)

C1qtnf12 C1q and tumor necrosis factor related 12 [*Mus musculus* (house mouse)]

Gene ID: 67389, updated on 12-Aug-2019

Summary

Official Symbol C1qtnf12 provided by [MGI](#)
Official Full Name C1q and tumor necrosis factor related 12 provided by [MGI](#)
Primary source [MGI:MGI:1914639](#)
See related [Ensembl:ENSMUSG00000023571](#)
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 C1qdc2; CTRP12; Fam132a; alipolin; 1110035L05Rik
Expression Broad expression in duodenum adult (RPKM 84.1), adrenal adult (RPKM 49.9) and 23 other tissues [See more](#)
Orthologs [human](#) [all](#)

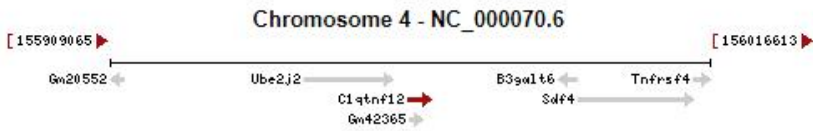
Genomic context

Location: 4 E2; 4 87.66 cM

See C1qtnf12 in [Genome Data Viewer](#)

Exon count: 8

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (155962312..155966629)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (155336427..155340738)

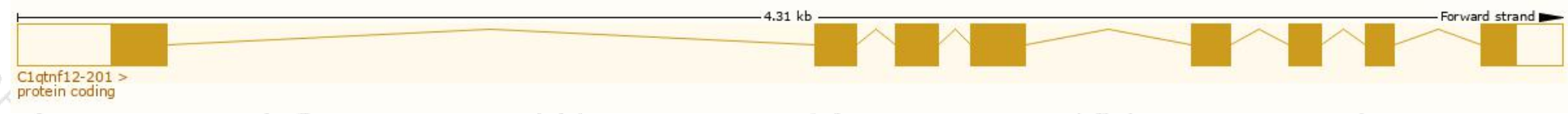


Transcript information (Ensembl)

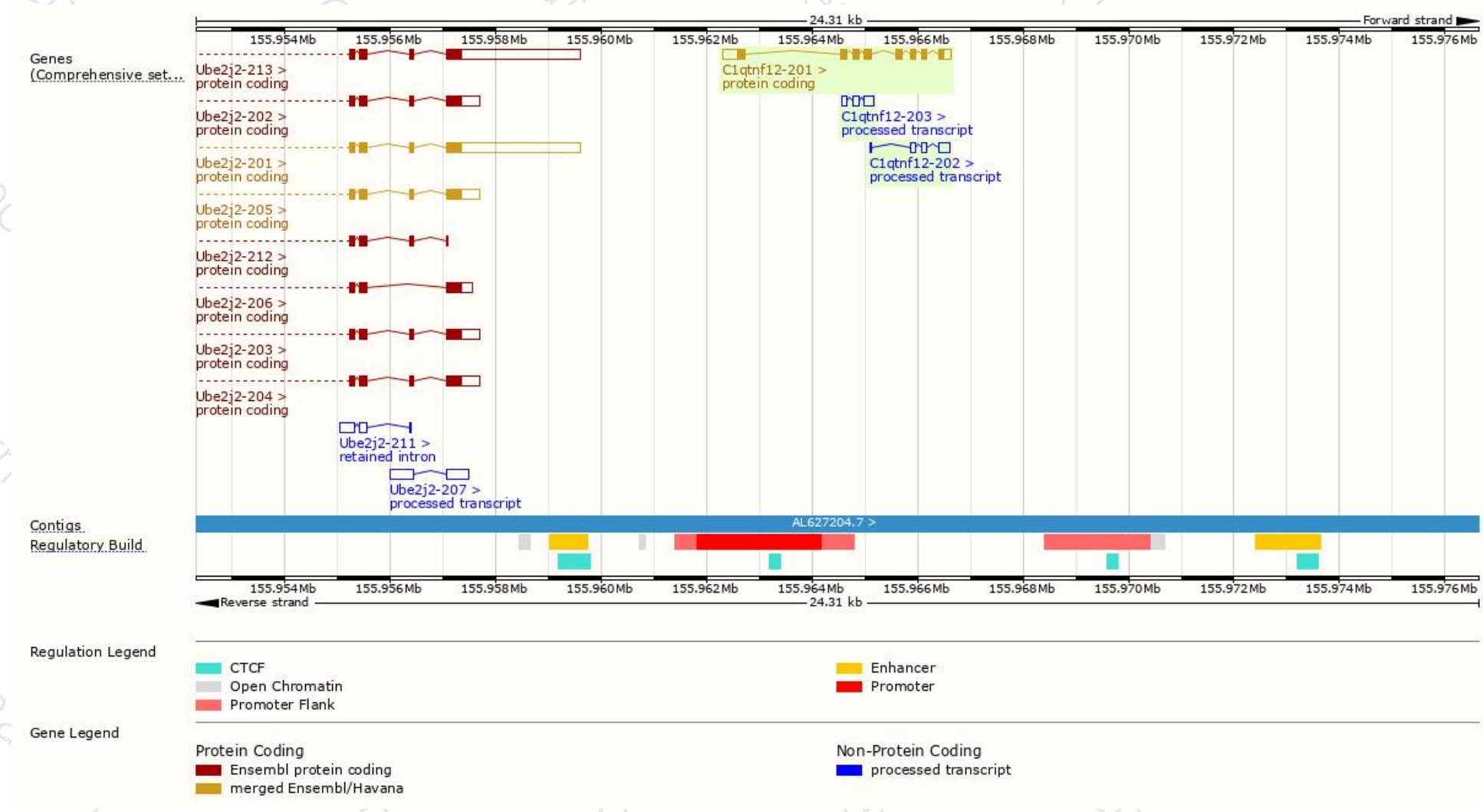
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
C1qtnf12-201	ENSMUST00000024338.4	1315	308aa	Protein coding	CCDS19052	Q8R2Z0	TSL:1 GENCODE basic APPRIS P1
C1qtnf12-202	ENSMUST00000127222.1	423	No protein	Processed transcript	-	-	TSL:2
C1qtnf12-203	ENSMUST00000149558.1	423	No protein	Processed transcript	-	-	TSL:3

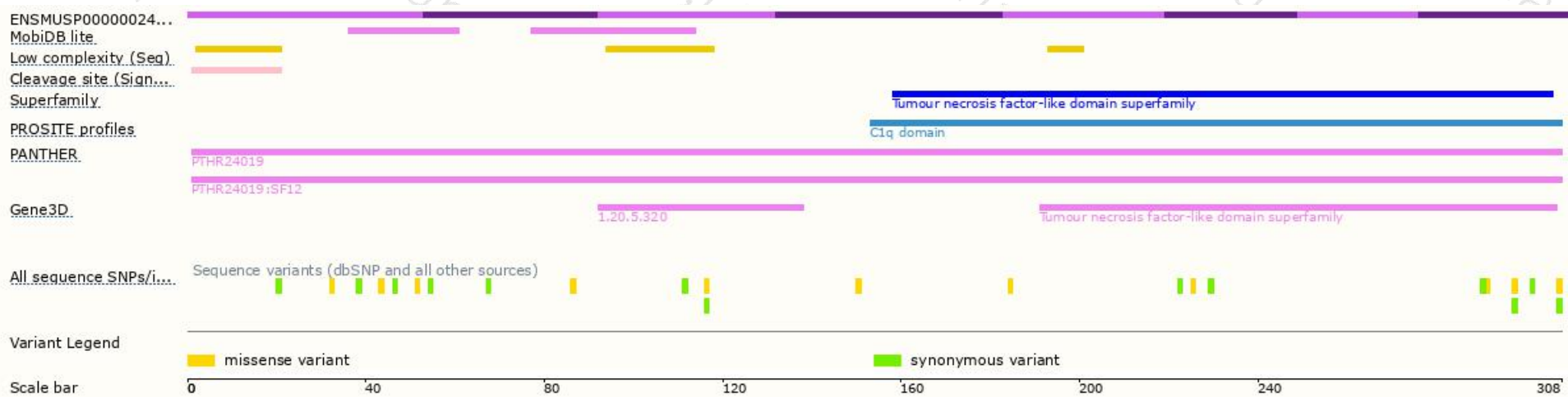
The strategy is based on the design of *C1qtnf12-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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