

# *C1qtnf12* Cas9-CKO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***C1qtnf12***

**Project type**

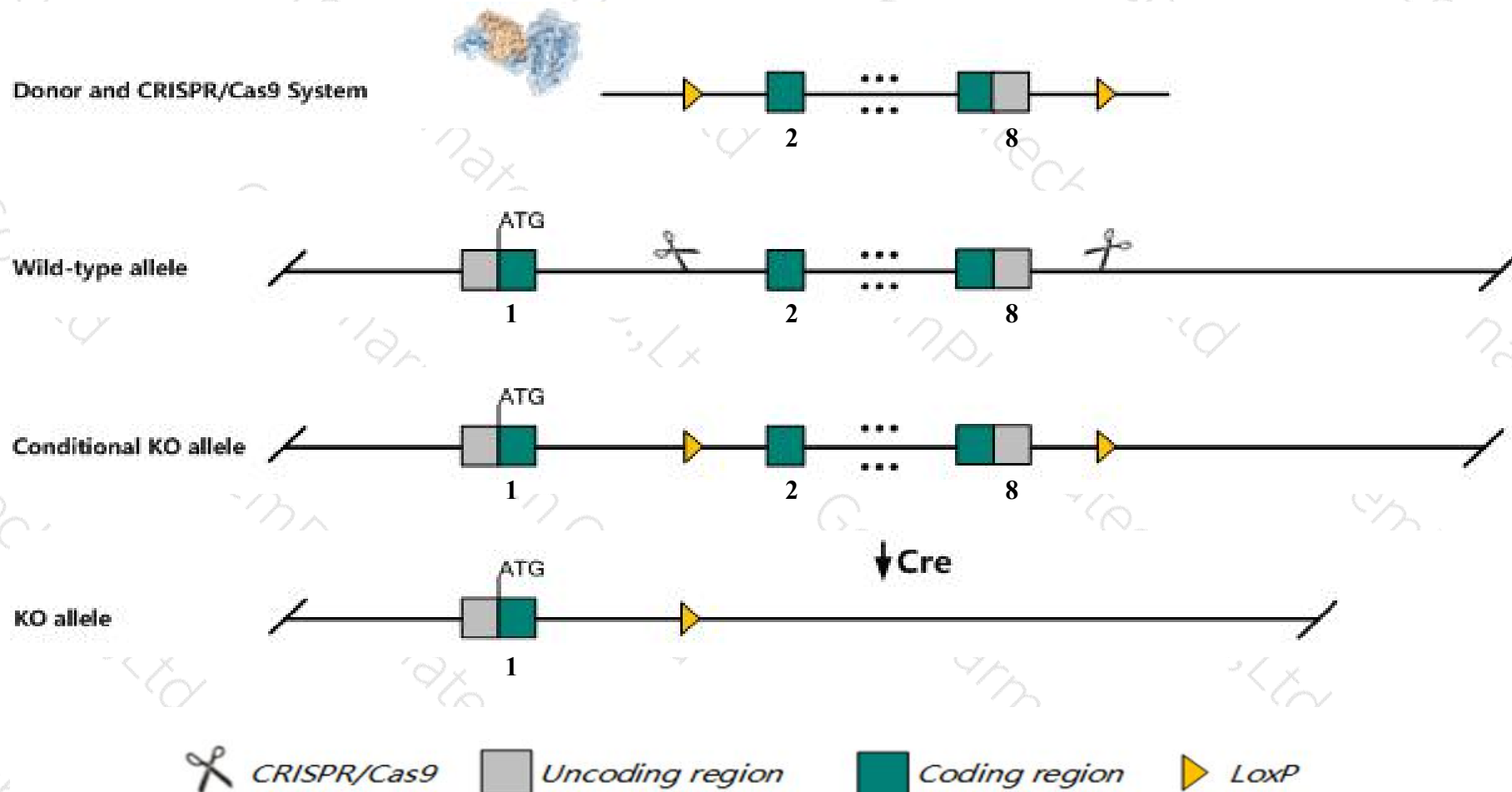
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



# Technical routes

- 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 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

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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](#)

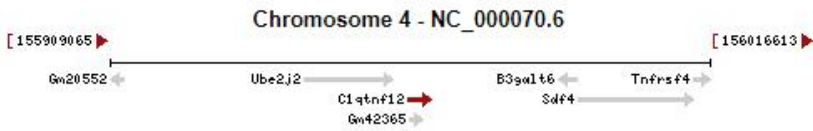
### Genomic context

**Location:** 4 E2; 4 87.66 cM

See C1qtnf12 in [Genome Data Viewer](#)

**Exon count:** 8

Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	4	NC_000070.6 (155962312..155966629)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	4	NC_000070.5 (155336427..155340738)

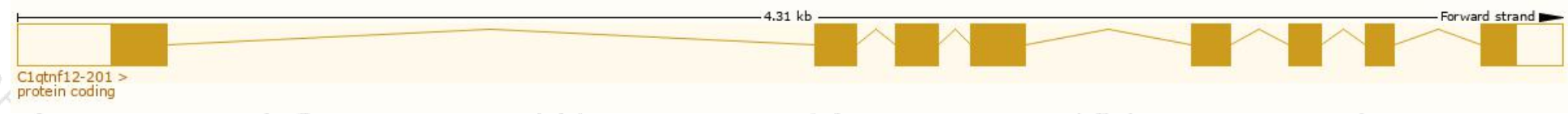


# Transcript information (Ensembl)

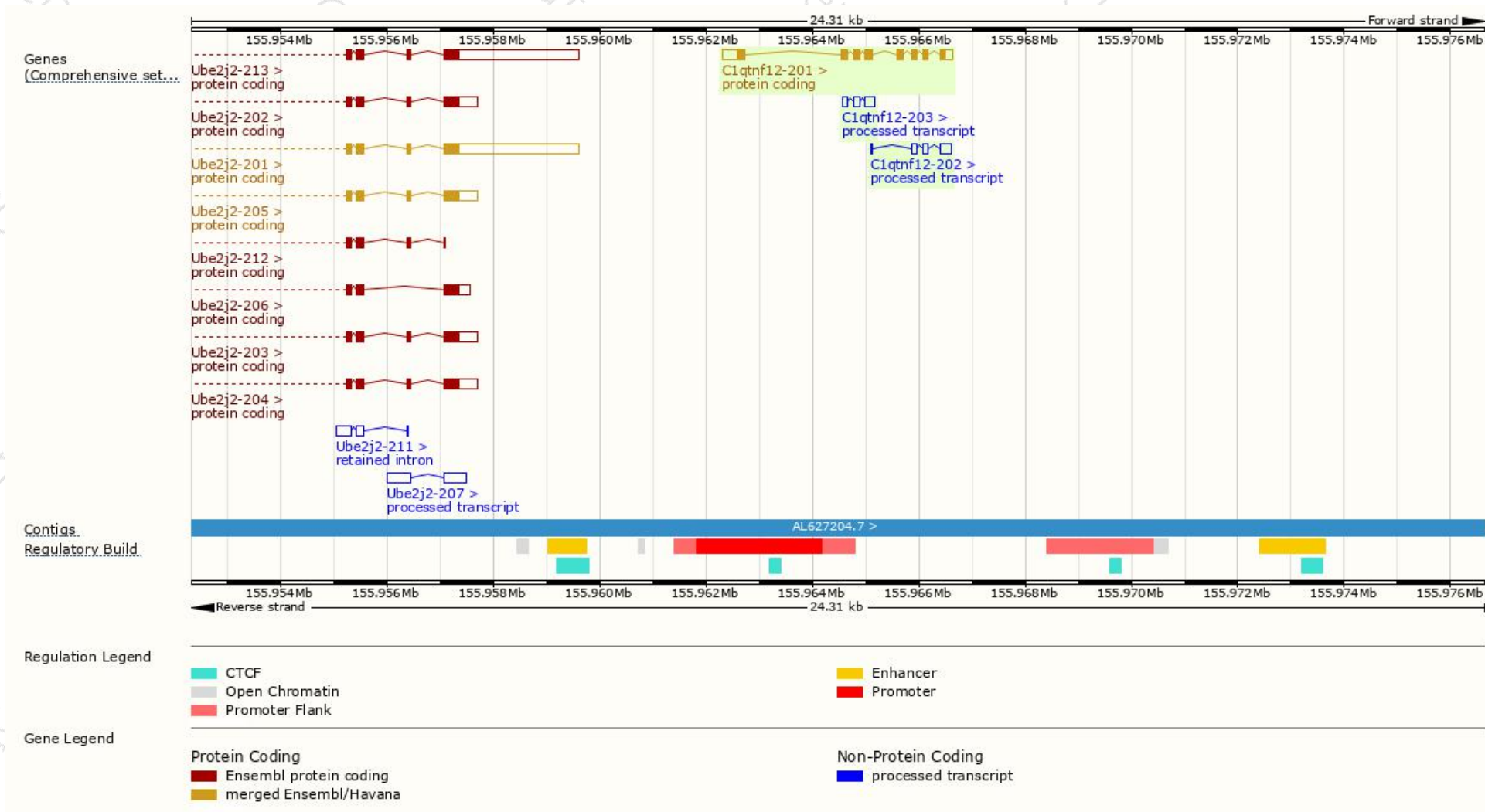
The gene has 3 transcripts,all transcripts are shown below:

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

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

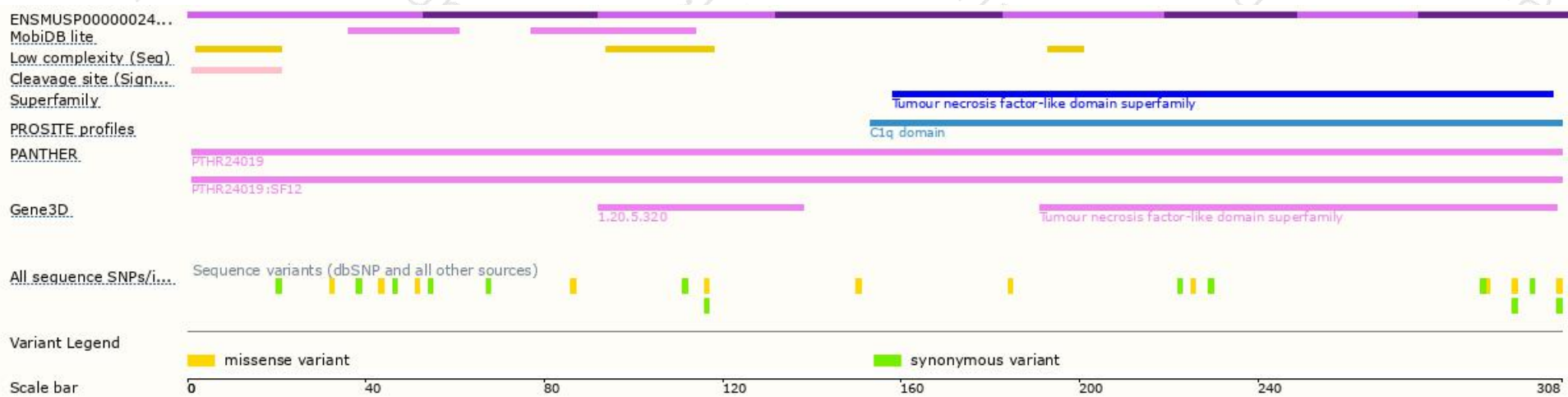


# Genomic location distribution





# Protein domain



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

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