

C1qtnf3 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

C1qtnf3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Clqtnf3* gene. The schematic diagram is as follows:



- The *C1qtnf3* gene has 2 transcripts. According to the structure of *C1qtnf3* gene, exon2 of *C1qtnf3-201* (ENSMUST00000022853.14) transcript is recommended as the knockout region. The region contains 112bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *C1qtnf3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit increased susceptibility to collagen-induced arthritis.
- The *Clqtnf3* gene is located on the Chr15. 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)

C1qtnf3 C1q and tumor necrosis factor related protein 3 [Mus musculus (house mouse)]

Gene ID: 81799, updated on 31-Jan-2019

Summary



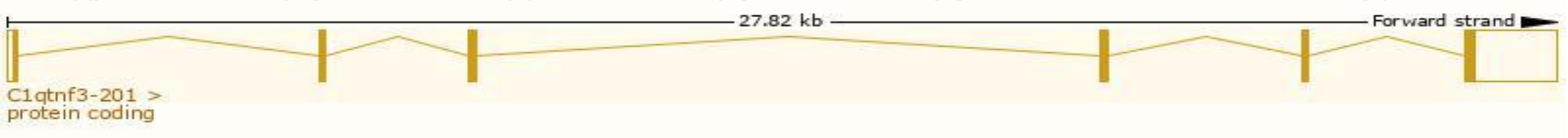
Official Symbol	C1qtnf3 provided by MGI
Official Full Name	C1q and tumor necrosis factor related protein 3 provided by MGI
Primary source	MGI:MGI:1932136
See related	Ensembl:ENSMUSG00000058914
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310005P21Rik, Adim, CORS-26, CORS26, CTRP3, Corcs, Cors
Expression	Biased expression in limb E14.5 (RPKM 35.7), subcutaneous fat pad adult (RPKM 12.5) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

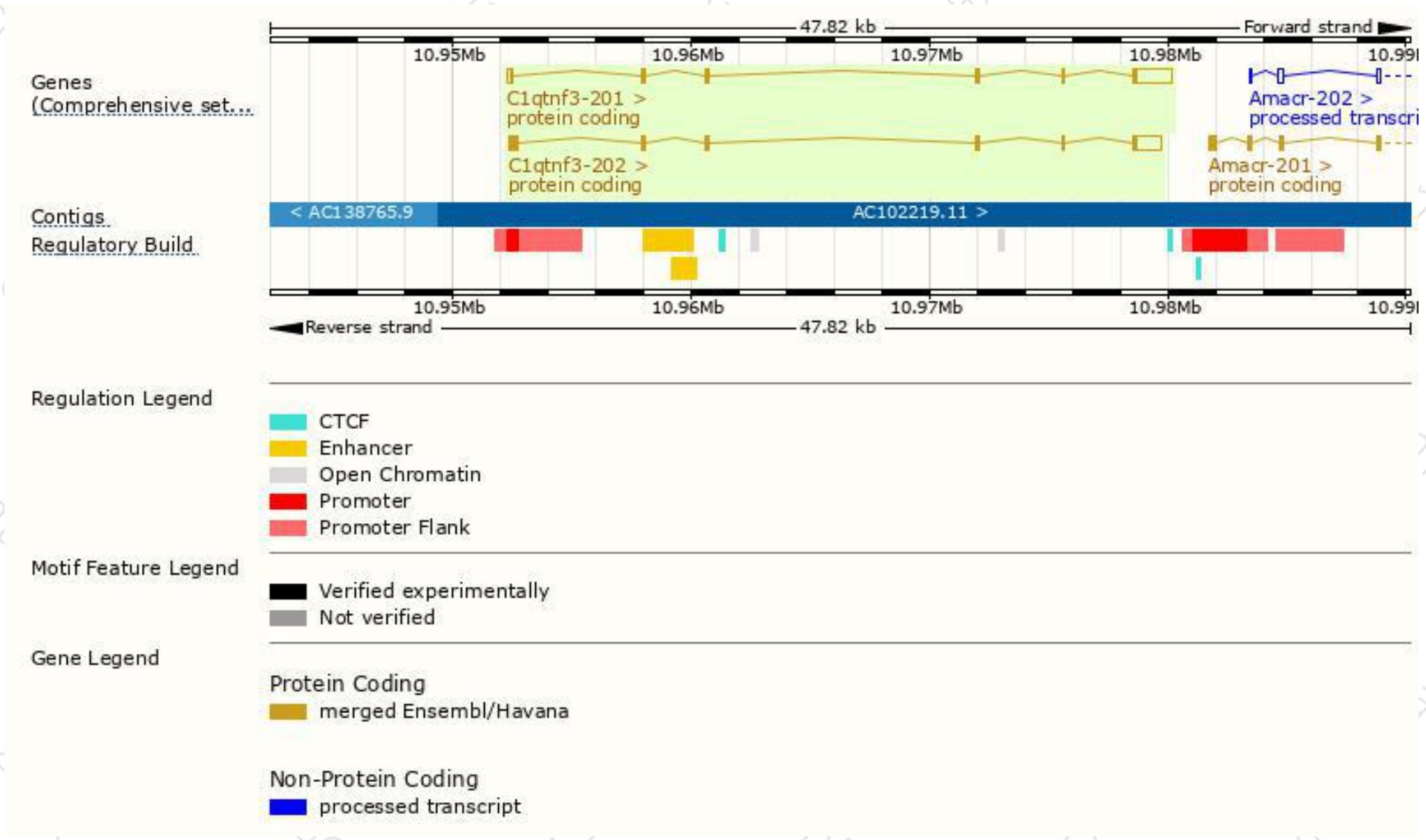
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
C1qtnf3-201	ENSMUST00000022853.14	2338	246aa	Protein coding	CCDS27380	Q4ZJN6 Q9ES30	TSL:1 GENCODE basic APPRIS P3
C1qtnf3-202	ENSMUST00000110523.1	2088	319aa	Protein coding	CCDS56977	D3YZ61	TSL:5 GENCODE basic APPRIS ALT 1

The strategy is based on the design of *C1qtnf3-201* transcript,The transcription is shown below



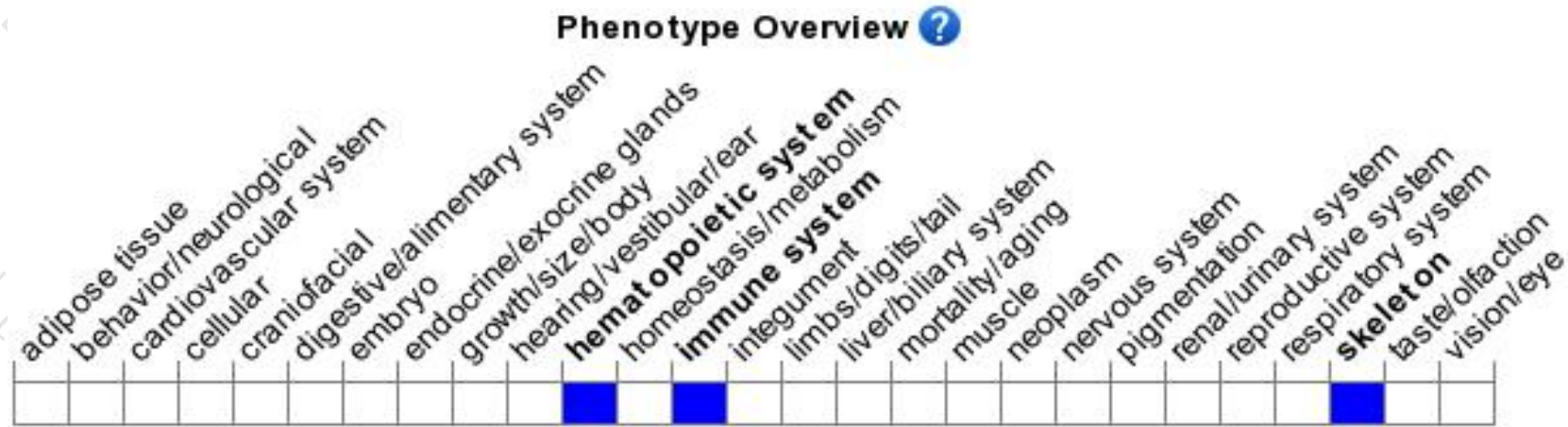
Genomic location distribution



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 knock-out allele exhibit increased susceptibility to collagen-induced arthritis.

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

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