

C1qtnf1 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

C1qtnf1

Project type

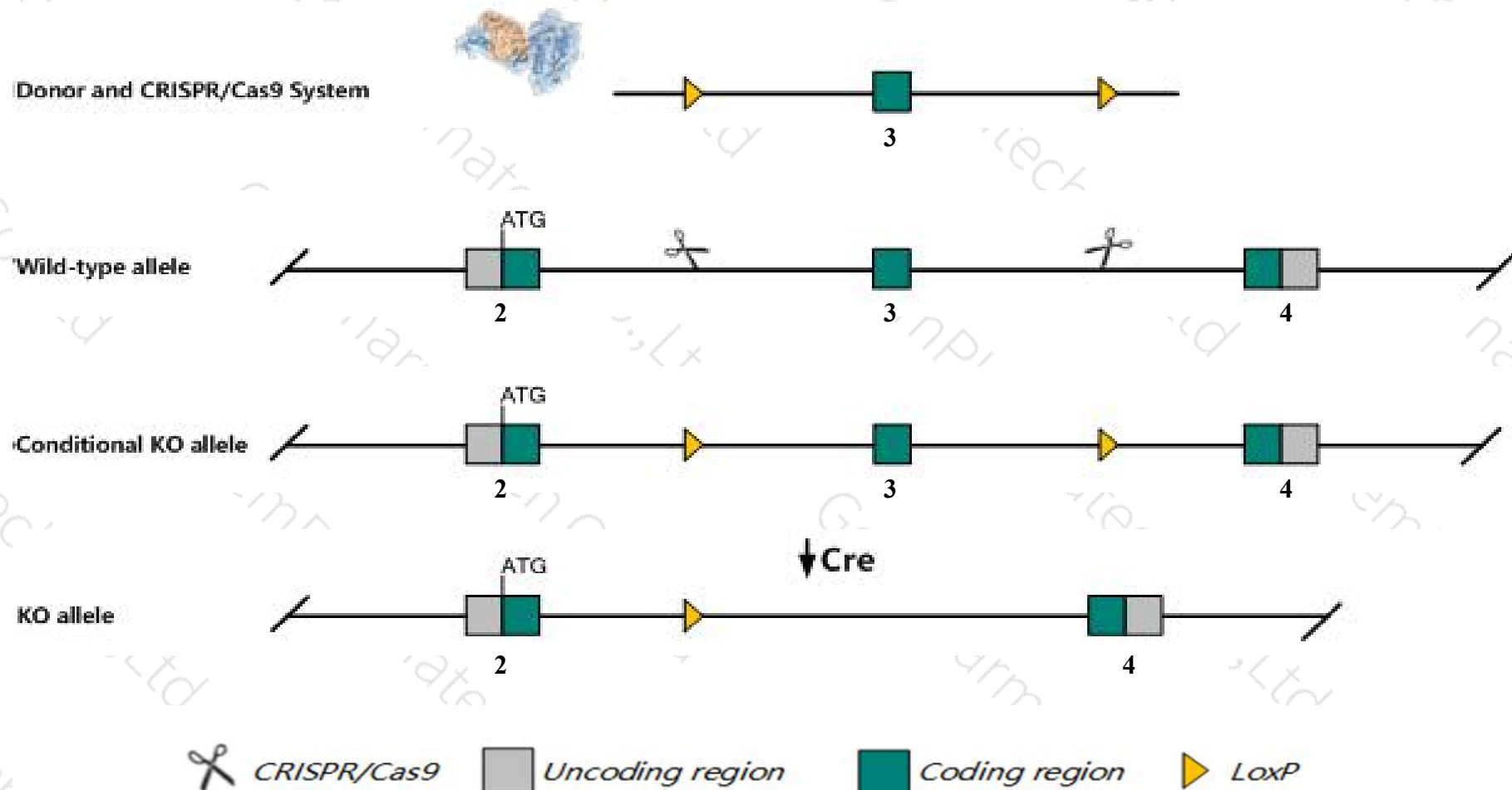
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Clqtnf1* gene. The schematic diagram is as follows:



Technical routes

- The *Clqtnf1* gene has 4 transcripts. According to the structure of *Clqtnf1* gene, exon3 of *Clqtnf1-201* (ENSMUST00000017590.8) transcript is recommended as the knockout region. The region contains 140bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Clqtnf1* 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.

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit altered glucose and lipid homeostasis.
- The flox region is in the intron of the Gm11747 gene, which may affect the regulation of this gene.
- Transcript 203,204 CDS 3' incomplete the influences is unknown.
- The *Clqtnfl* gene is located on the Chr11. 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)

C1qtnf1 C1q and tumor necrosis factor related protein 1 [*Mus musculus* (house mouse)]

Gene ID: 56745, updated on 13-Mar-2020

Summary

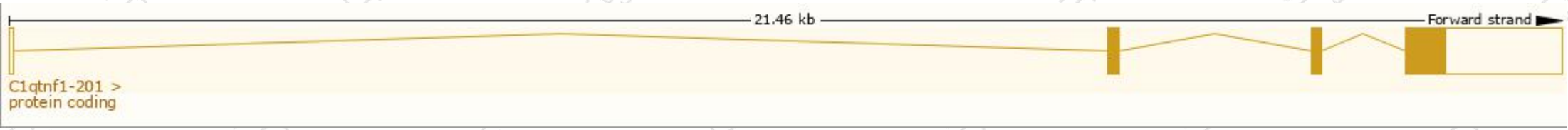
Official Symbol	C1qtnf1 provided by MGI
Official Full Name	C1q and tumor necrosis factor related protein 1 provided by MGI
Primary source	MGI:MGI:1919254
See related	Ensembl:ENSMUSG00000017446
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Adip; CTRP1; Zsig37; 1600017K21Rik
Expression	Broad expression in mammary gland adult (RPKM 21.5), subcutaneous fat pad adult (RPKM 17.9) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

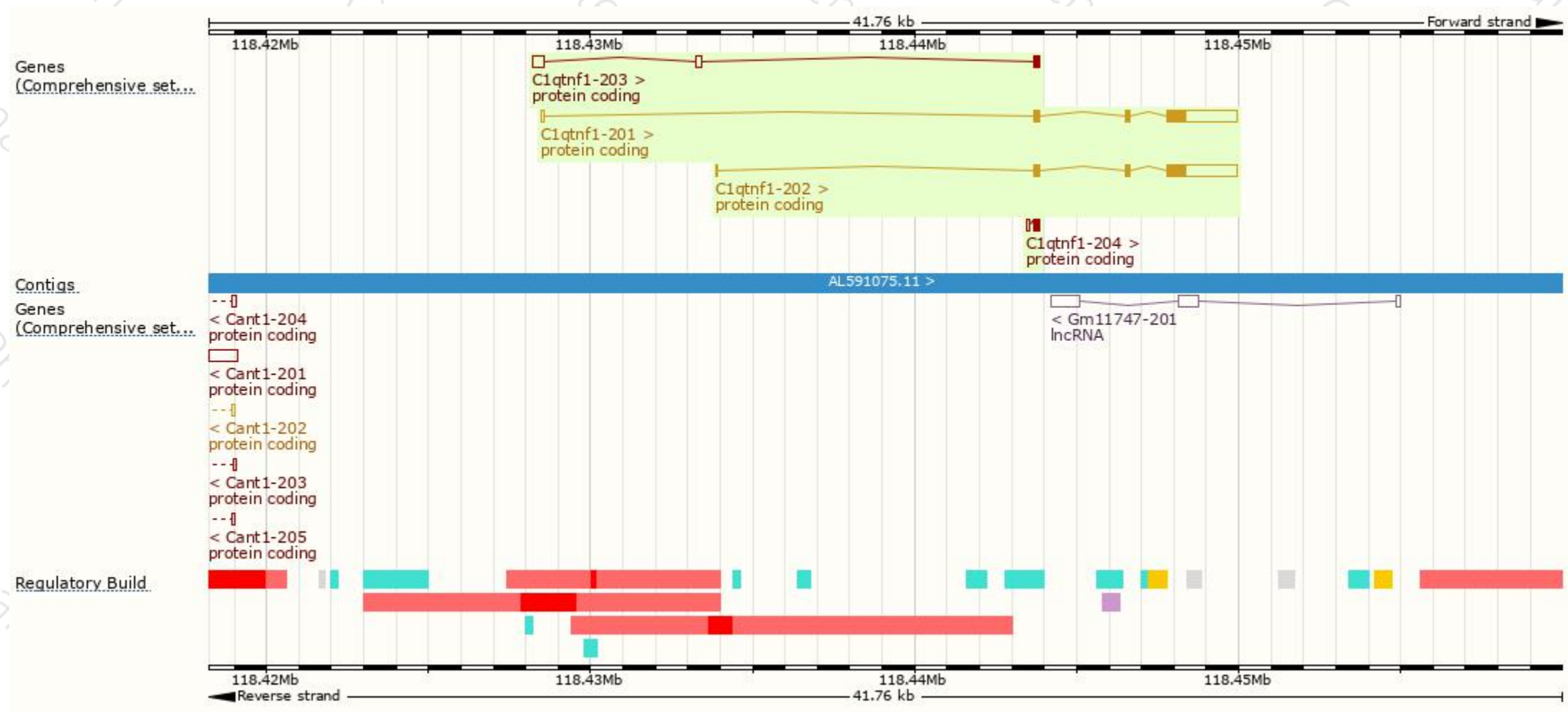
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
C1qtnf1-201	ENSMUST00000017590.8	2532	281aa	Protein coding	CCDS25703	A0A3B0J1J8 Q9QXP7	TSL:1 GENCODE basic APPRIS P1
C1qtnf1-202	ENSMUST000000106286.2	2512	281aa	Protein coding	CCDS25703	A0A3B0J1J8 Q9QXP7	TSL:1 GENCODE basic APPRIS P1
C1qtnf1-203	ENSMUST000000124861.1	684	49aa	Protein coding	-	A2A4W1	CDS 3' incomplete TSL:3
C1qtnf1-204	ENSMUST000000133558.2	246	51aa	Protein coding	-	A2A4W2	CDS 3' incomplete TSL:3

The strategy is based on the design of *C1qtnf1-201* transcript,The transcription is shown below



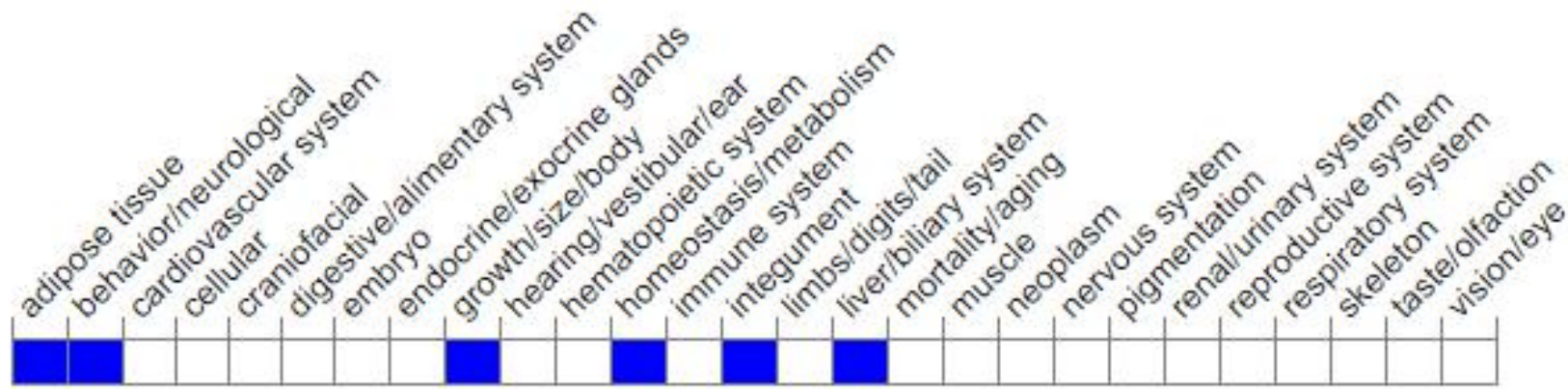
Genomic location distribution



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 altered glucose and lipid homeostasis.

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

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