

# *C1qtnf1* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview



**Project Name**

***C1qtnf1***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *C1qtnf1* gene has 4 transcripts. According to the structure of *C1qtnf1* gene, exon3 of *C1qtnf1-201* (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 *C1qtnf1* gene. The brief process is as follows: CRISPR/Cas9 system

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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

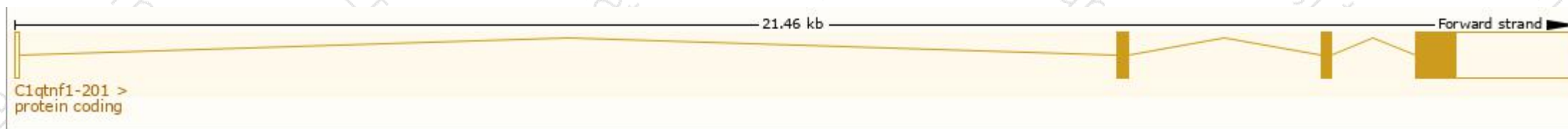
<b>Official Symbol</b>	C1qtnf1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	C1q and tumor necrosis factor related protein 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1919254</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000017446</a>
<b>Gene type</b>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

# Transcript information (Ensembl)

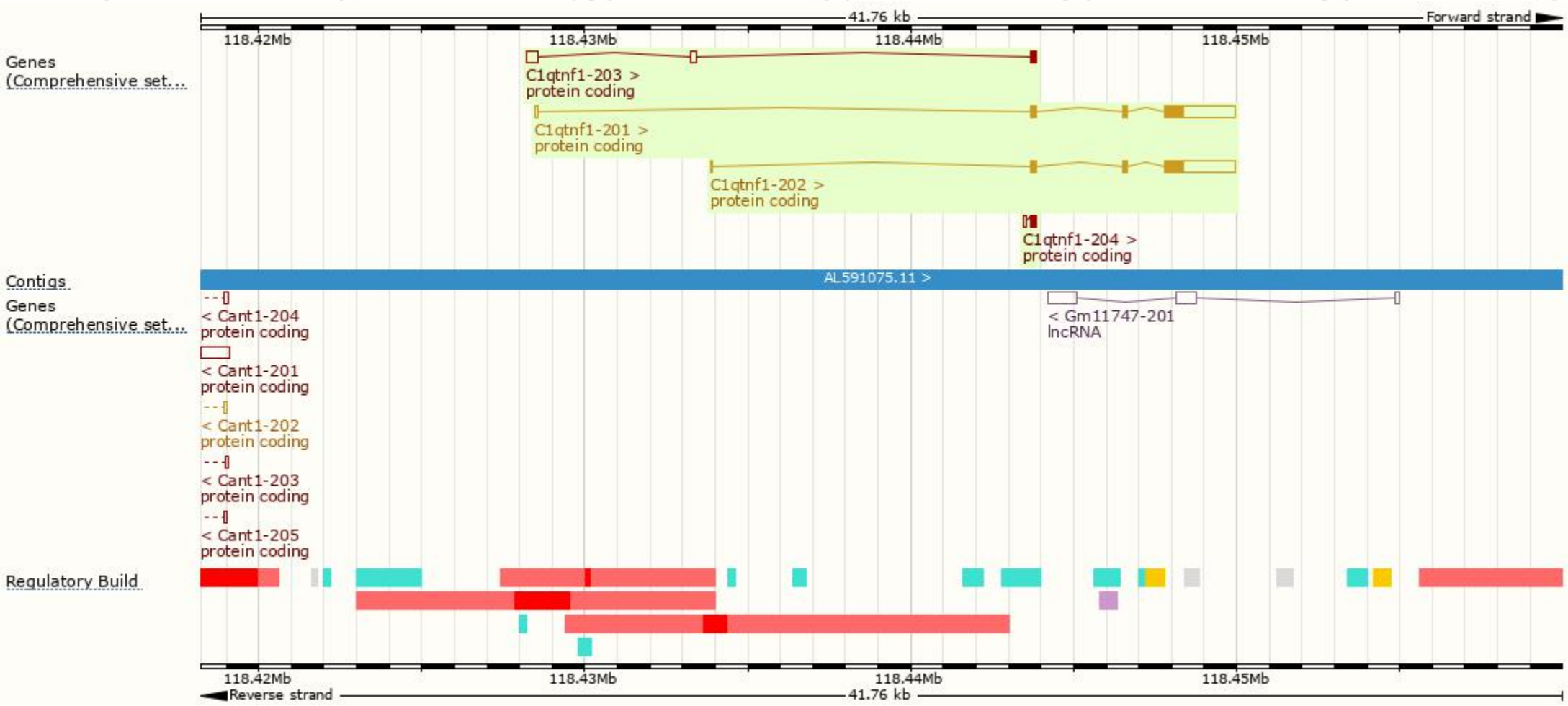
The gene has 4 transcripts, all transcripts are shown below:

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

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



# Genomic location distribution

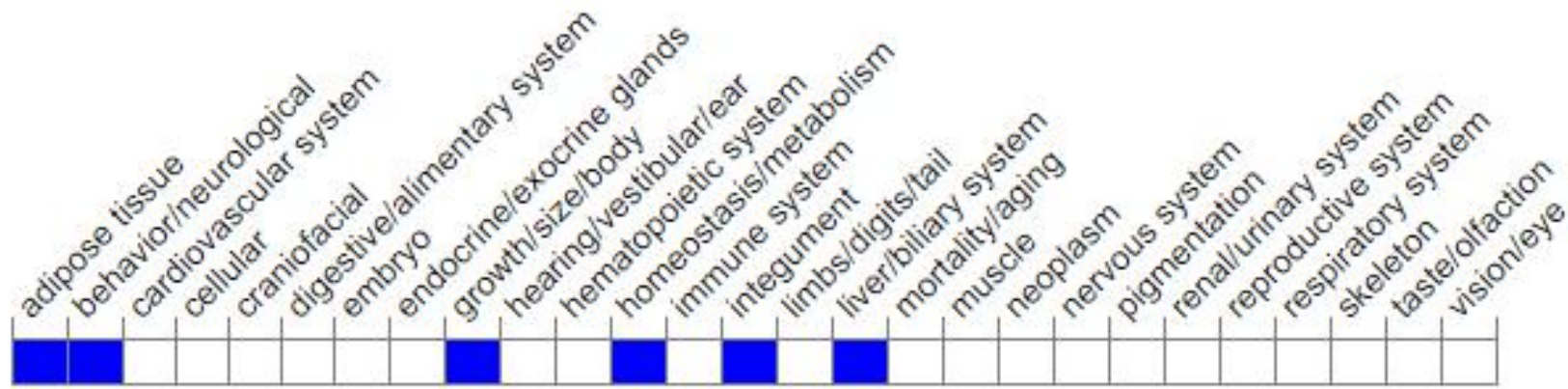




# Protein domain



# 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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