

C1qa Cas9-KO Strategy

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| Reviewer: | Huan Fan |
| Design Date: | 2020-5-22 |

Project Overview

Project Name

C1qa

Project type

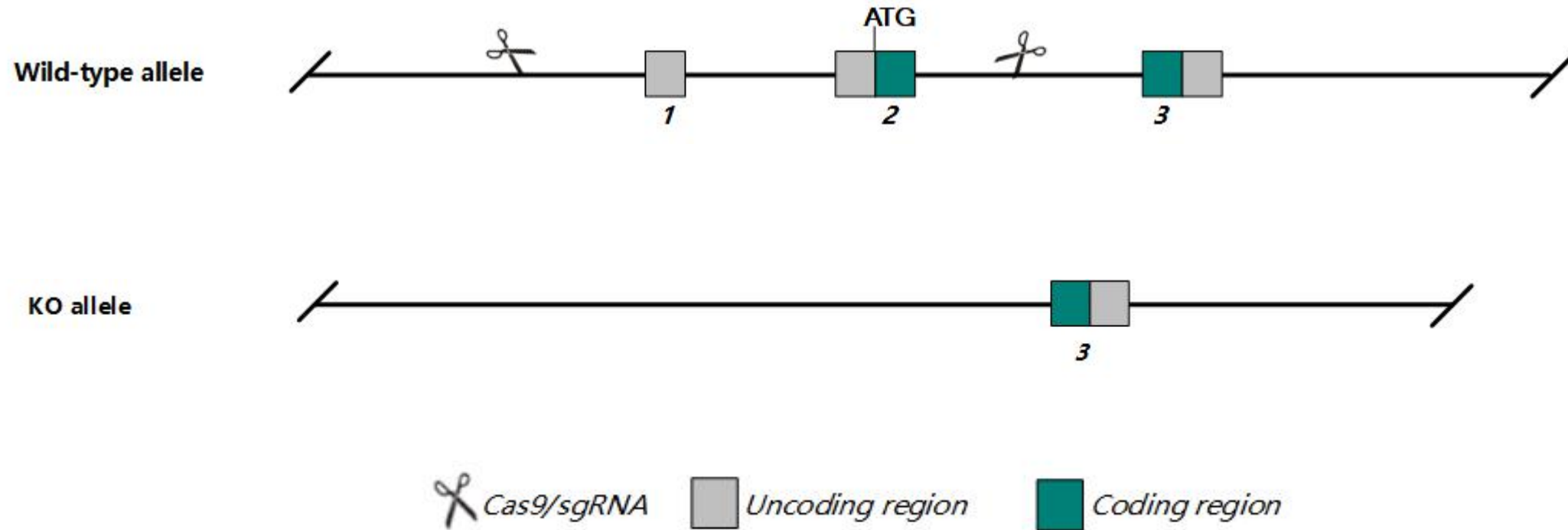
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Clqa* gene has 1 transcript. According to the structure of *Clqa* gene, exon1-exon2 of *Clqa-201* (ENSMUST00000046285.5) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Clqa* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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.

- According to the existing MGI data, mice homozygous for a knock-out allele display absence seizures, glomerulonephritis, increased numbers of glomerular apoptotic bodies, high autoantibody titres, and increased mortality, with severity affected by genetic background.
- The *Clqa* 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)

C1qa complement component 1, q subcomponent, alpha polypeptide [Mus musculus (house mouse)]

Gene ID: 12259, updated on 13-Mar-2020

Summary



Official Symbol C1qa provided by [MGI](#)

Official Full Name complement component 1, q subcomponent, alpha polypeptide provided by [MGI](#)

Primary source [MGI:MGI:88223](#)

See related [Ensembl:ENSMUSG00000036887](#)

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 AI255395, Adic, C1q

Expression Ubiquitous expression in mammary gland adult (RPKM 87.8), spleen adult (RPKM 86.7) and 25 other tissues [See more](#)

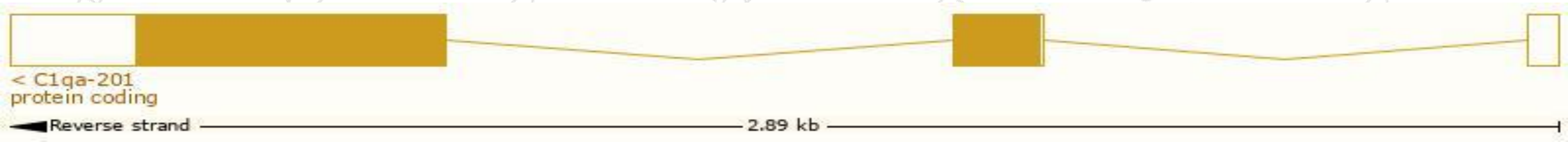
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

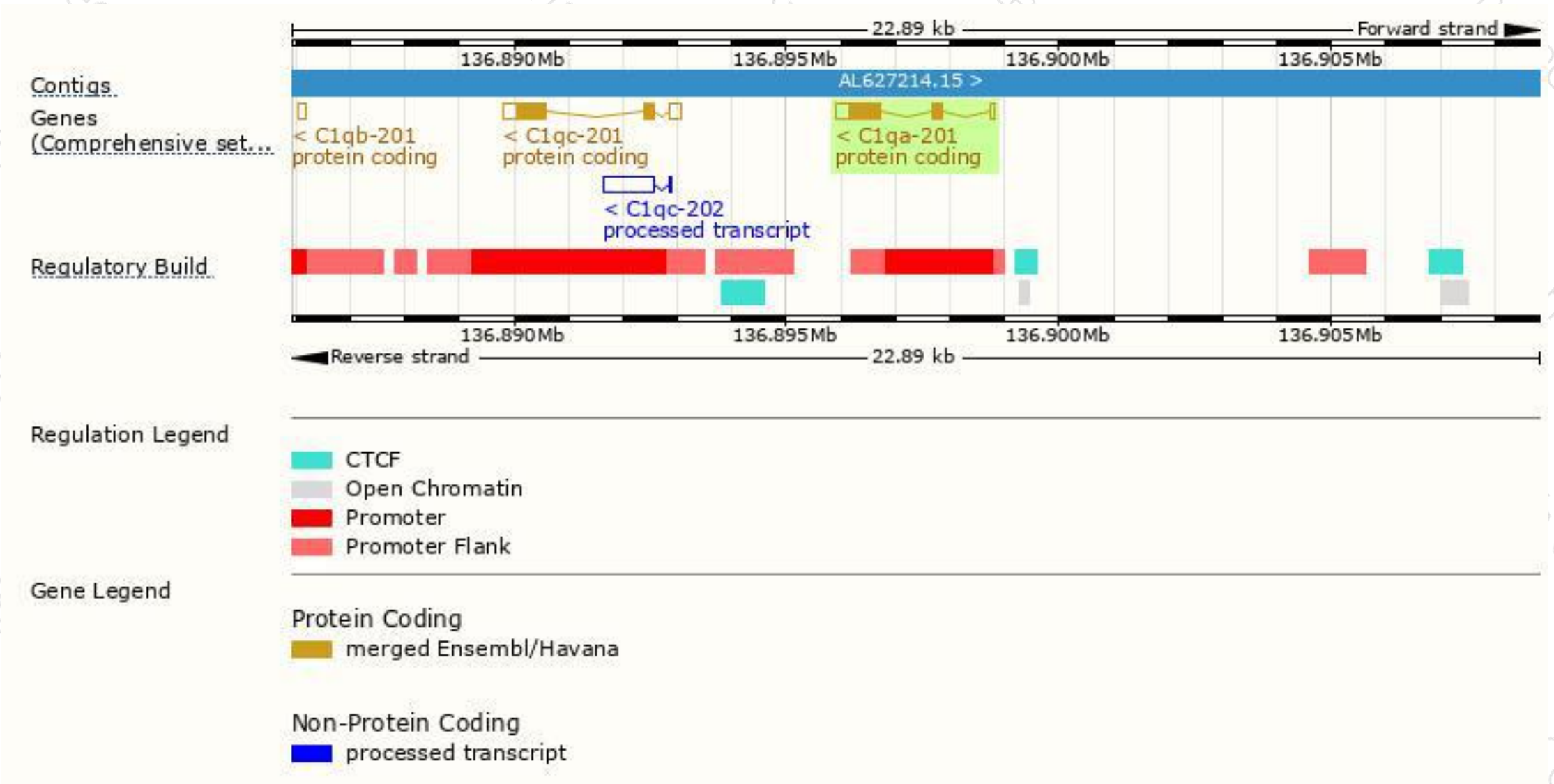
The gene has 1 transcript, and the transcript is shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|--------------------------------------|------|-----------------------|----------------|---------------------------|-----------------------------------|---|
| C1qa-201 | ENSMUST00000046285.5 | 1040 | 245aa | Protein coding | CCDS18812 | A0A3B0IP04 P98086 | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |

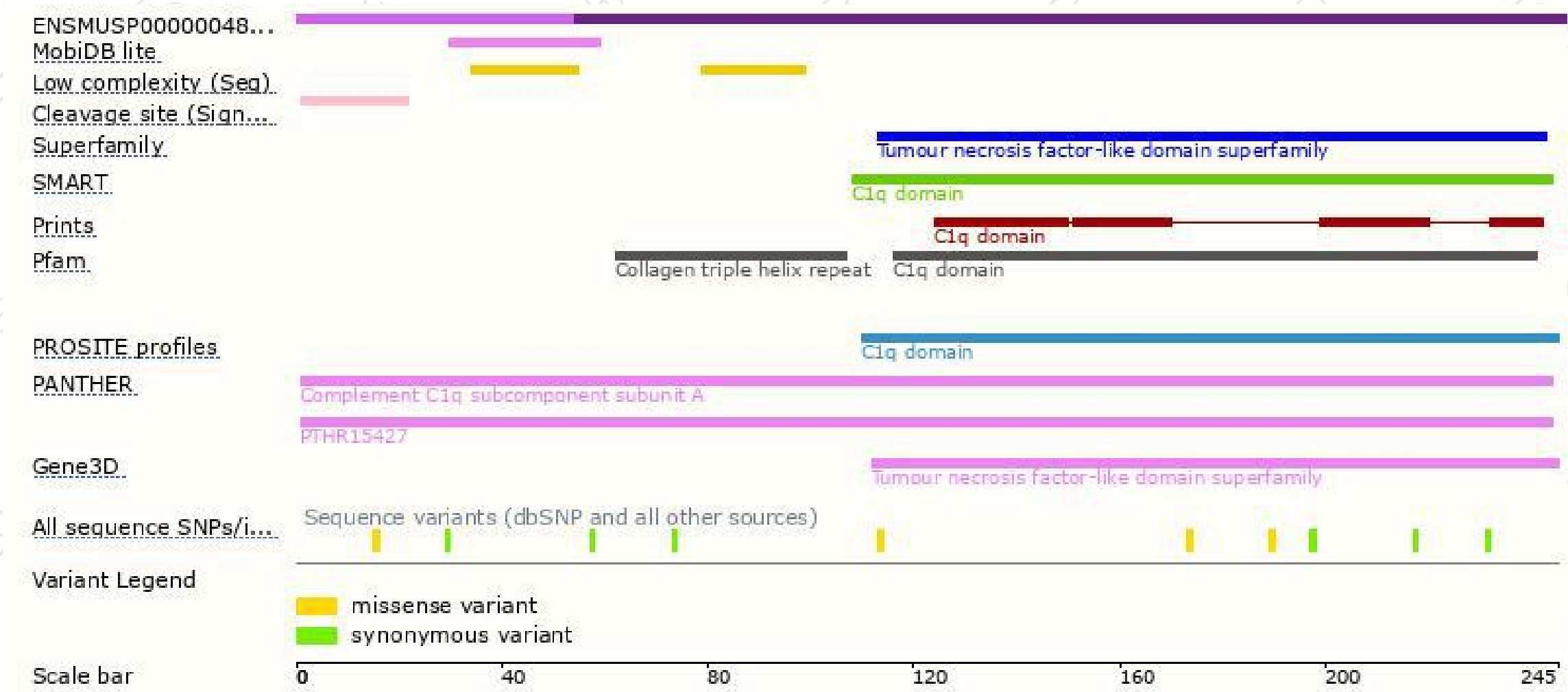
The strategy is based on the design of *C1qa-201* transcript, the transcription is shown below:



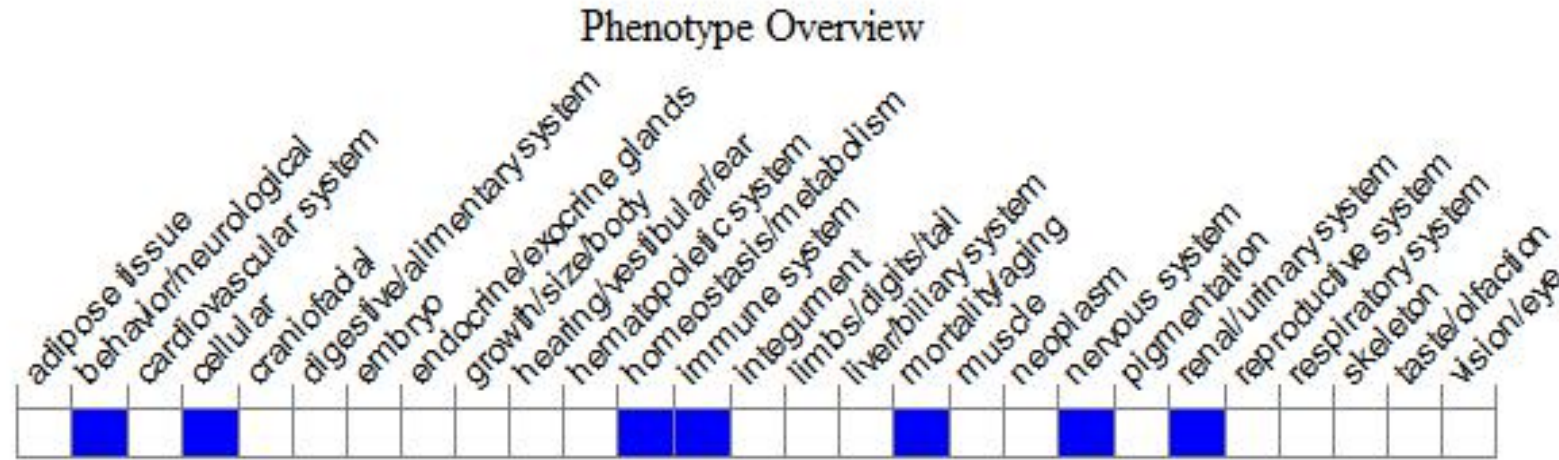
Genomic location distribution



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 display absence seizures, glomerulonephritis, increased numbers of glomerular apoptotic bodies, high autoantibody titres, and increased mortality, with severity affected by genetic background.

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

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