C1ql1 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Daohua Xu

Design Date: 2020-8-10

Project Overview

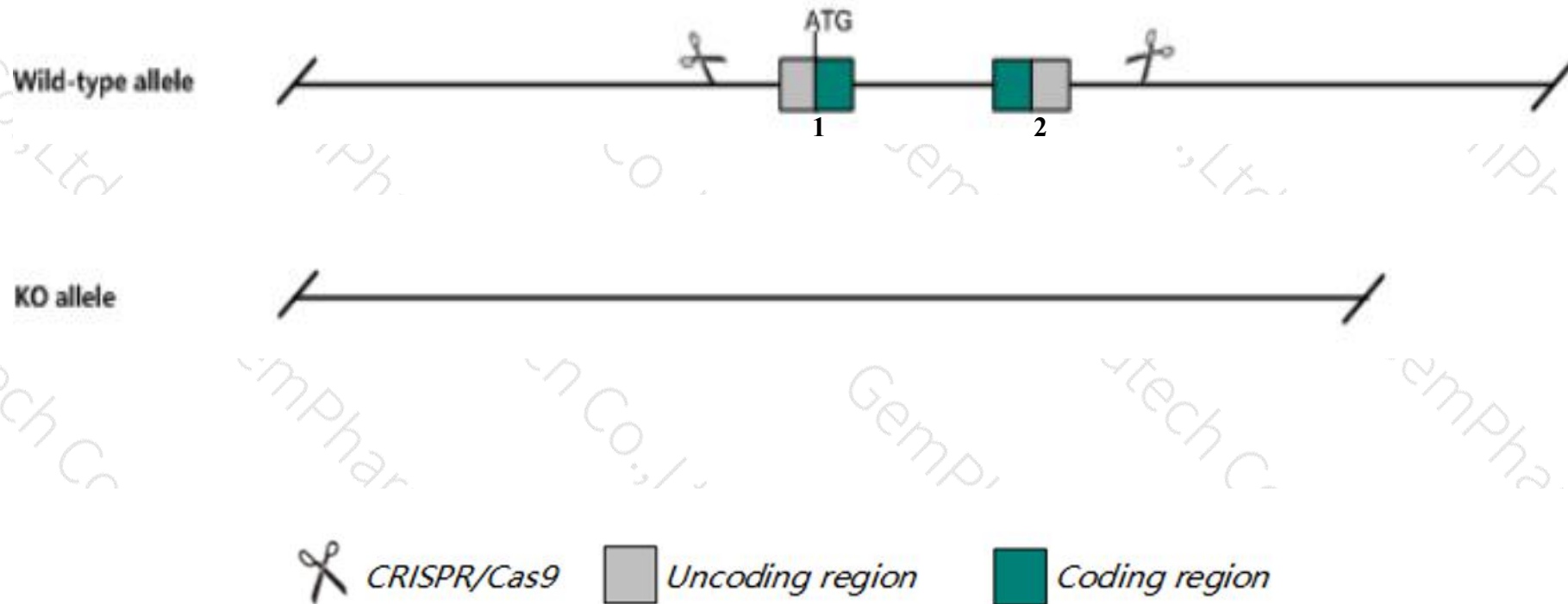|	
Project Name	*C1ql1*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *C1ql1* gene. The schematic diagram is as follows:

Technical routes

➤ The *C1ql1* gene has 1 transcript. According to the structure of *C1ql1* gene, exon1-exon2 of *C1ql1-201*(ENSMUST00000057849.5) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *C1ql1* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,mice homozygous for a null allele exhibit impaired motor learning with alterned climbing fiber electrophysiology.

➢ The *C1ql1* 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）

C1ql1 complement component 1, q subcomponent-like 1 [Mus musculus (house mouse)]

Gene ID: 23829, updated on 13-Mar-2020

Summary

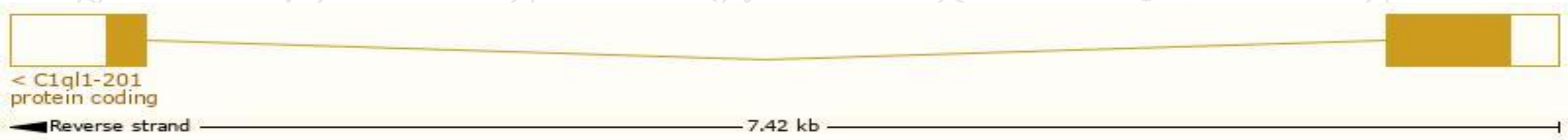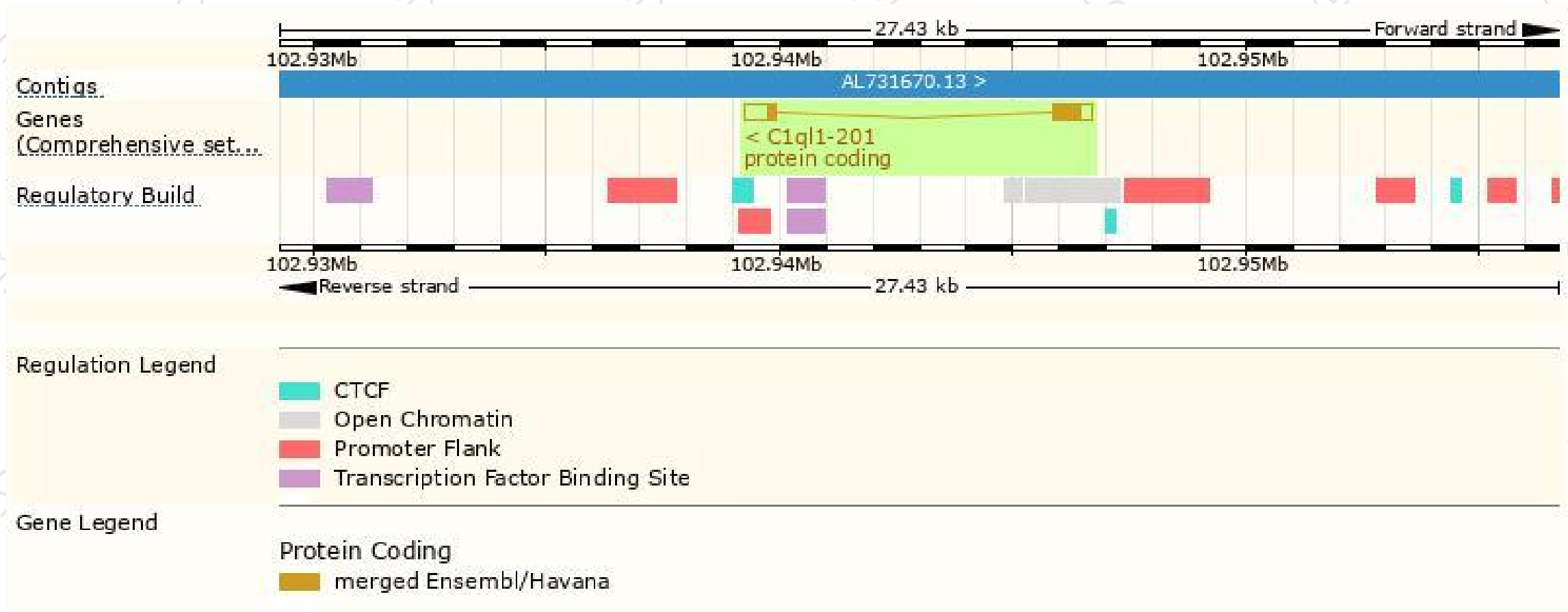|	
Official Symbol	C1ql1 provided by MGI
Official Full Name	complement component 1, q subcomponent-like 1 provided by MGI
Primary source	MGI:MGI:1344400
See related	Ensembl:ENSMUSG00000045532
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Adil, C1qrf, CRF, CTRP14, gliacolin
Expression	Biased expression in adrenal adult (RPKM 41.8), frontal lobe adult (RPKM 6.2) and 7 other tissuesSee 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
C1ql1-201	ENSMUST00000057849.5	1473	258aa	Protein coding	CCDS25509	A0A3B0ITH6 O88992	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 *C1ql1-201* transcript,the transcription is shown below:
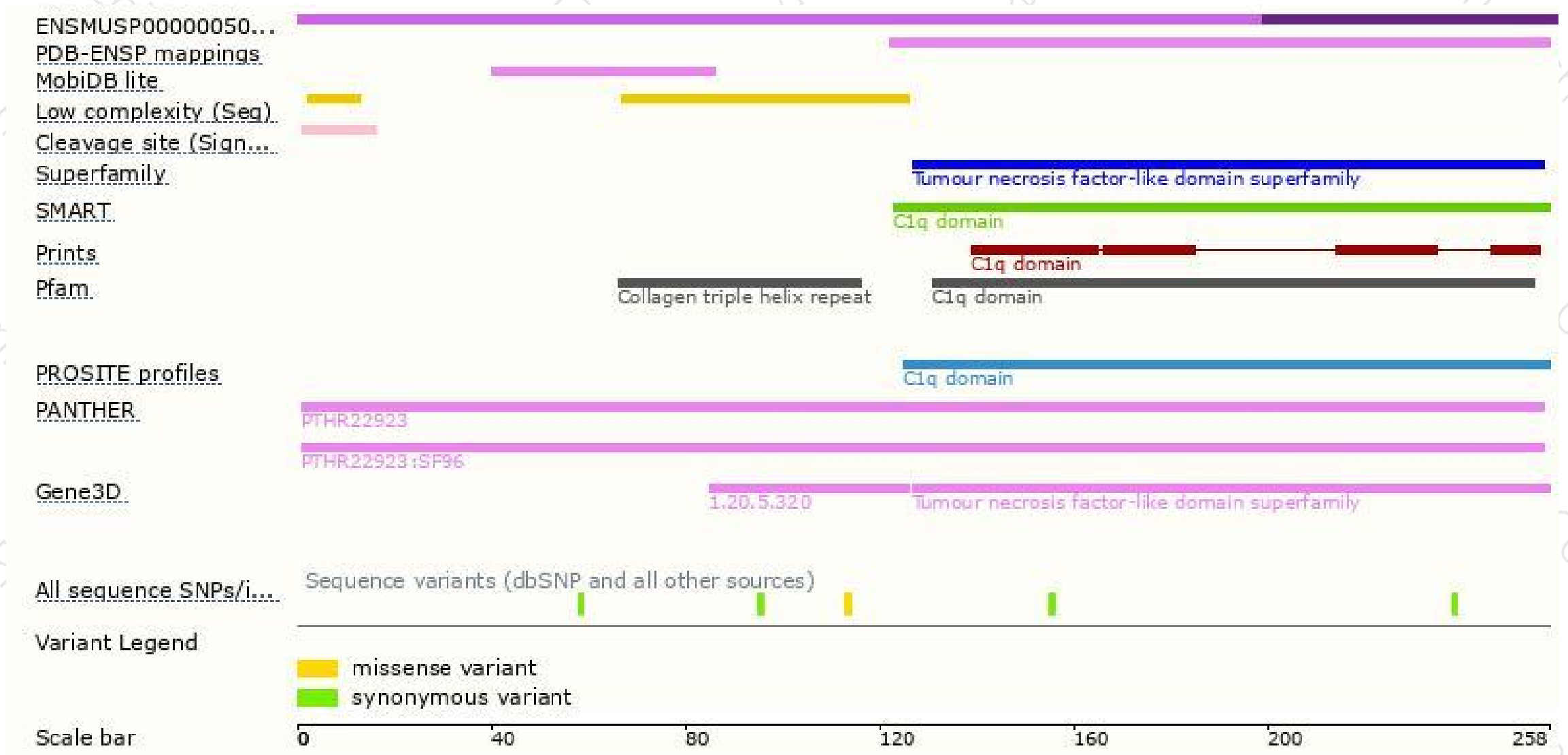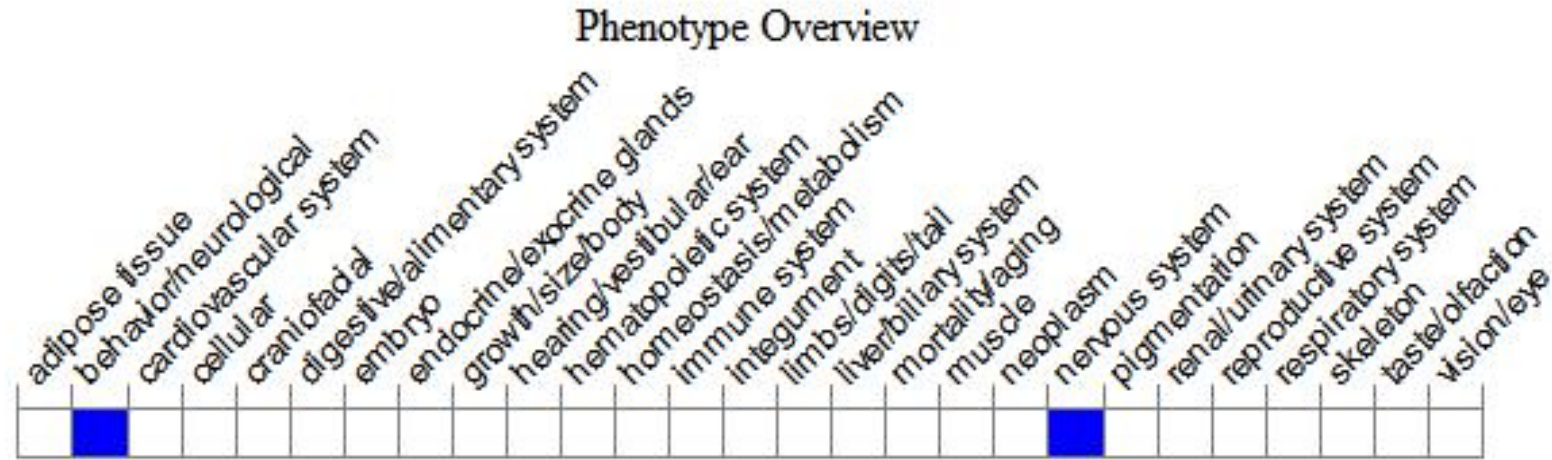

< C1ql1-201
protein coding

◄─── Reverse strand ─────────────────── 7.42 kb ───────────

Genomic location distribution

Protein domain

ENSMUSP00000050...						
PDB-ENSP mappings						
MobiDB lite						
Low complexity (Seg)						
Cleavage site (Sign...						
Superfamily			Tumour necrosis factor-like domain superfamily			
SMART			C1q domain			
Prints			C1q domain			
Pfam		Collagen triple helix repeat	C1q domain			
PROSITE profiles			C1q domain			
PANTHER	PTHR22923					
	PTHR22923:SF96					
Gene3D		1.20.5.320	Tumour necrosis factor-like domain superfamily			
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)					
Variant Legend						
	missense variant					
	synonymous variant					
Scale bar	0	40	80	120	160	200	258

Mouse phenotype description(MGI)

Phenotype Overview

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 null allele exhibit impaired motor learning with alterned climbing fiber electrophysiology.