

C1qtnf7 Cas9-CKO Strategy

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Project Overview

Project Name

C1qtnf7

Project type

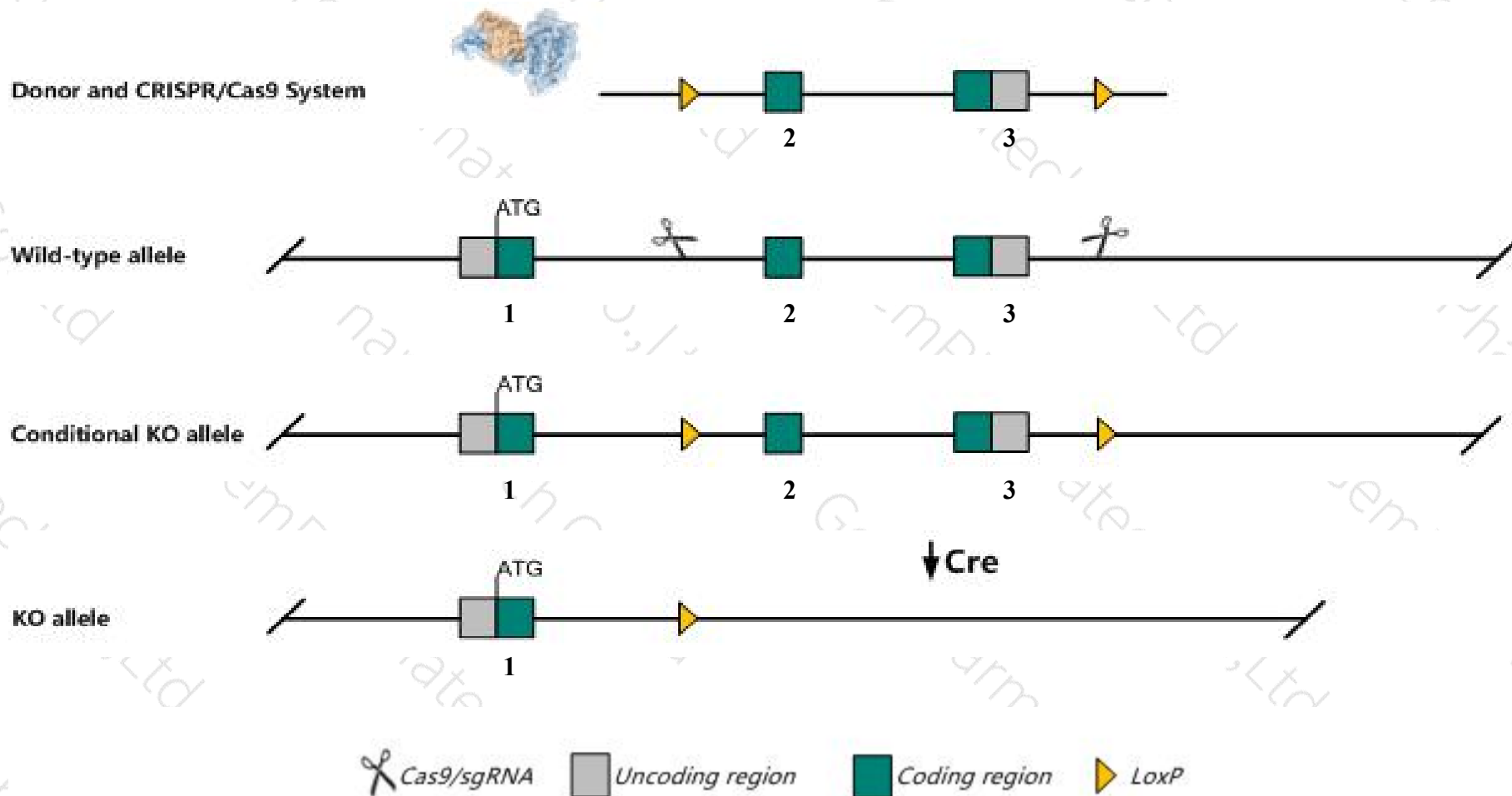
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Clqtnf7* gene. The schematic diagram is as follows:



Technical routes

- The *Clqtnf7* gene has 3 transcripts. According to the structure of *Clqtnf7* gene, exon2-exon3 of *Clqtnf7*-201(ENSMUST00000076939.9) transcript is recommended as the knockout region. The region contains most 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 *Clqtnf7* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was 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 decreased weight, liver fibrosis, male-specific glucose serum levels and adipose inflammation with male-specific improved glucose tolerance when fed a high-fat diet.
- The *Clqtnf7* gene is located on the Chr5. 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)

C1qtnf7 C1q and tumor necrosis factor related protein 7 [Mus musculus (house mouse)]

Gene ID: 109323, updated on 13-Mar-2020

Summary



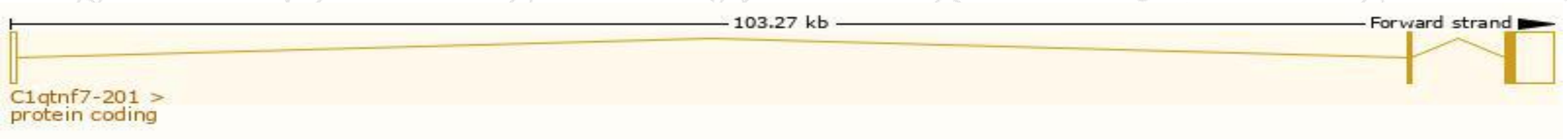
Official Symbol	C1qtnf7 provided by MGI
Official Full Name	C1q and tumor necrosis factor related protein 7 provided by MGI
Primary source	MGI:MGI:1925911
See related	Ensembl:ENSMUSG00000061535
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5530401N20Rik, 8430425G24Rik, Adig, Ctrp7
Expression	Biased expression in bladder adult (RPKM 5.7), lung adult (RPKM 3.9) and 11 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

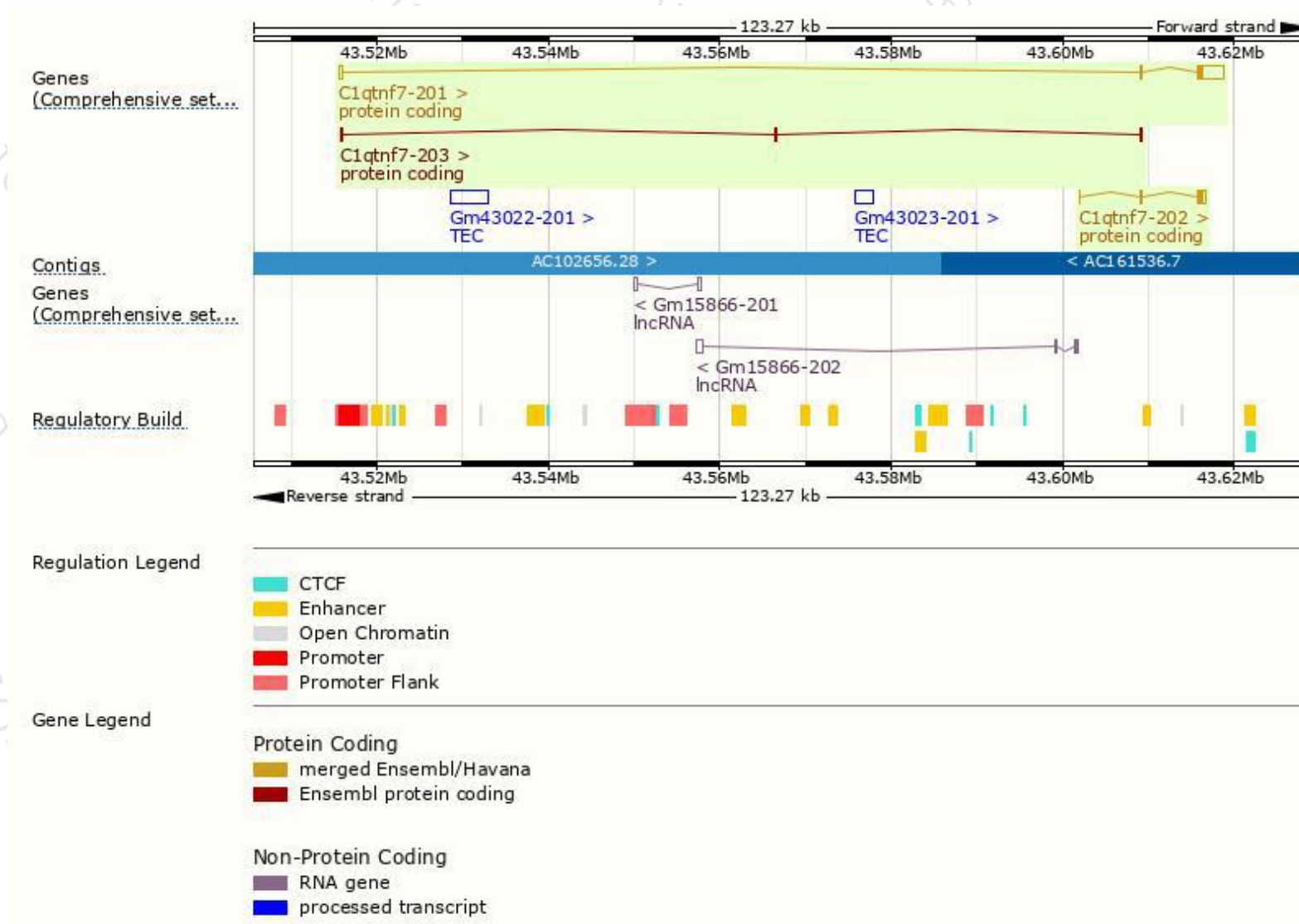
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
C1qtnf7-201	ENSMUST00000076939.9	3879	296aa	Protein coding	CCDS51488	E9PVG1	TSL:1 GENCODE basic APPRIS ALT1
C1qtnf7-202	ENSMUST00000121872.2	1283	289aa	Protein coding	CCDS19262	Q5BKS0 Q8BVD7	TSL:1 GENCODE basic APPRIS P3
C1qtnf7-203	ENSMUST00000144558.2	649	67aa	Protein coding	-	D3YZZ1	CDS 3' incomplete TSL:3

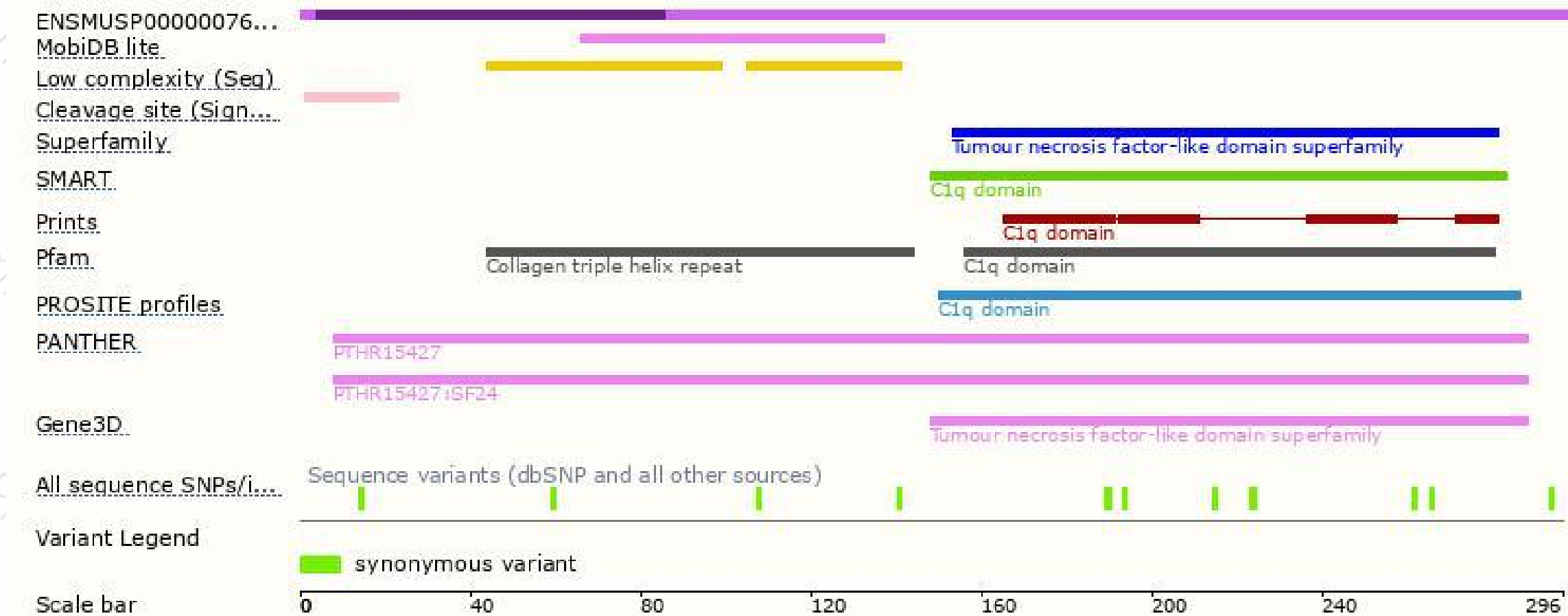
The strategy is based on the design of *C1qtnf7-201* transcript,the transcription is shown below:



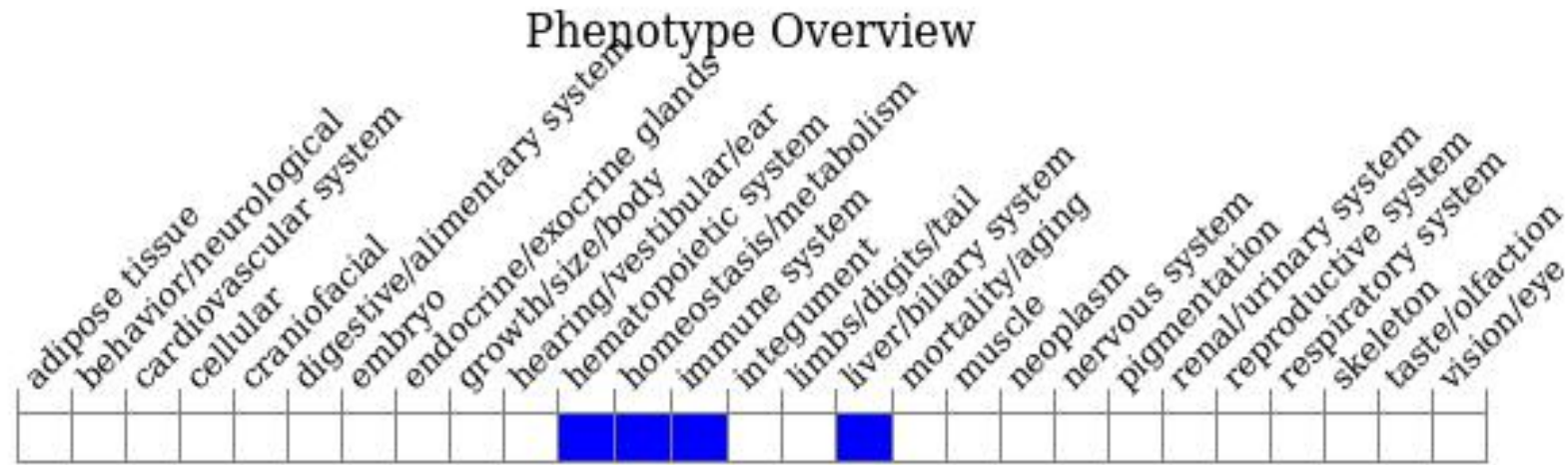
Genomic location distribution



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 decreased weight, liver fibrosis, male-specific glucose serum levels and adipose inflammation with male-specific improved glucose tolerance when fed a high-fat diet.

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

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