

Angptl4 Cas9-KO Strategy

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Project Overview

Project Name

Angptl4

Project type

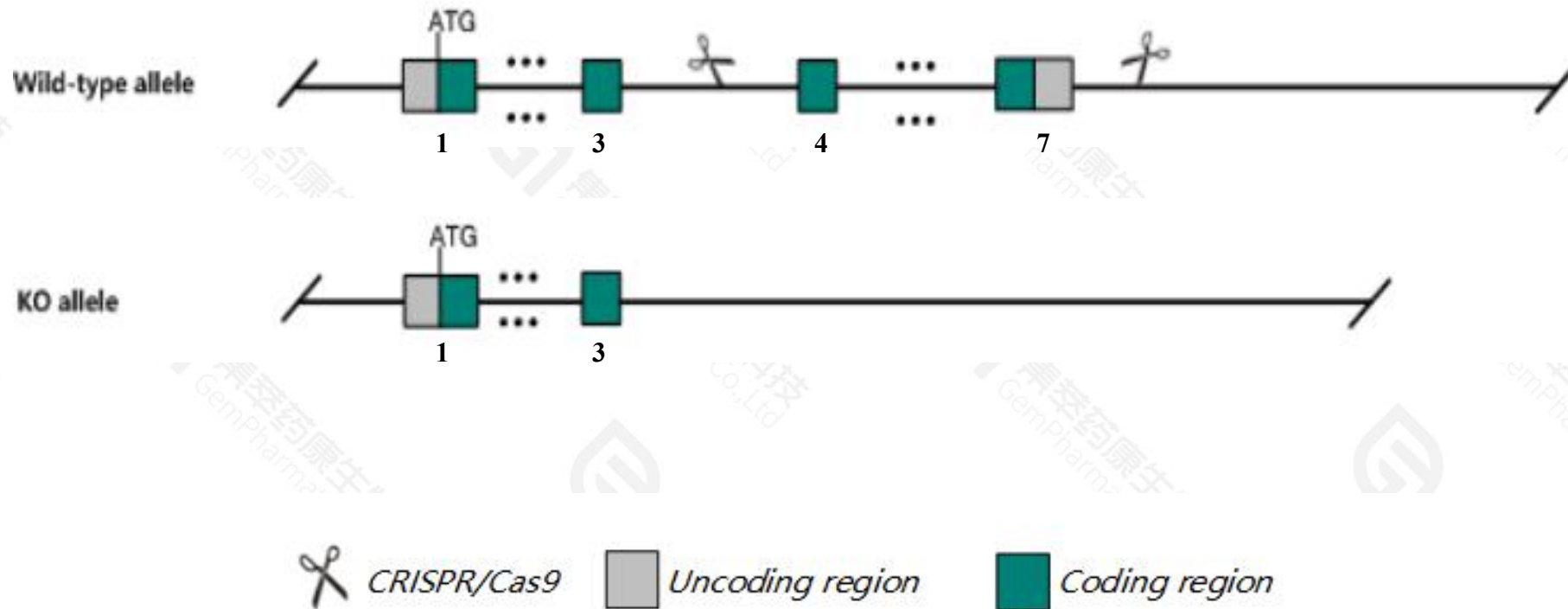
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Angptl4* gene. The schematic diagram is as follows:



- The *Angptl4* gene has 4 transcripts. According to the structure of *Angptl4* gene, exon4-exon7 of *Angptl4-201*(ENSMUST00000002360.17) transcript is recommended as the knockout region. The region contains 674bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Angptl4* 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.

- According to the existing MGI data, mice homozygous for disruptions in this gene display decreased levels of triglycerides and cholesterol and a lower increase in body fat after exposure to gut microbiota.
- The KO region contains functional region of the *Angptl4* gene. Knockout the region may affect the function of LOC118568328 gene.
- The *Angptl4* gene is located on the Chr17. 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.

Angptl4 angiotensin-like 4 [Mus musculus (house mouse)]

Gene ID: 57875, updated on 20-Dec-2020

Summary



Official Symbol Angptl4 provided by [MGI](#)

Official Full Name angiotensin-like 4 provided by [MGI](#)

Primary source [MGI:MGI:1888999](#)

See related [Ensembl:ENSMUSG00000002289](#)

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 Arp4, Bk89, FI, Fiaf, HF, Hfarp, NG2, Ng27, Pgar, Pgarg, Pp1158

Expression Biased expression in subcutaneous fat pad adult (RPKM 130.4), genital fat pad adult (RPKM 109.0) and 14 other tissues [See more](#)

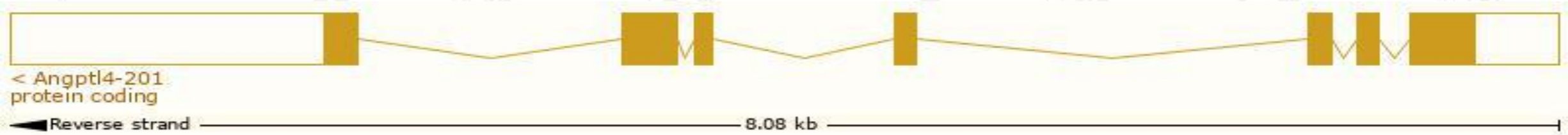
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

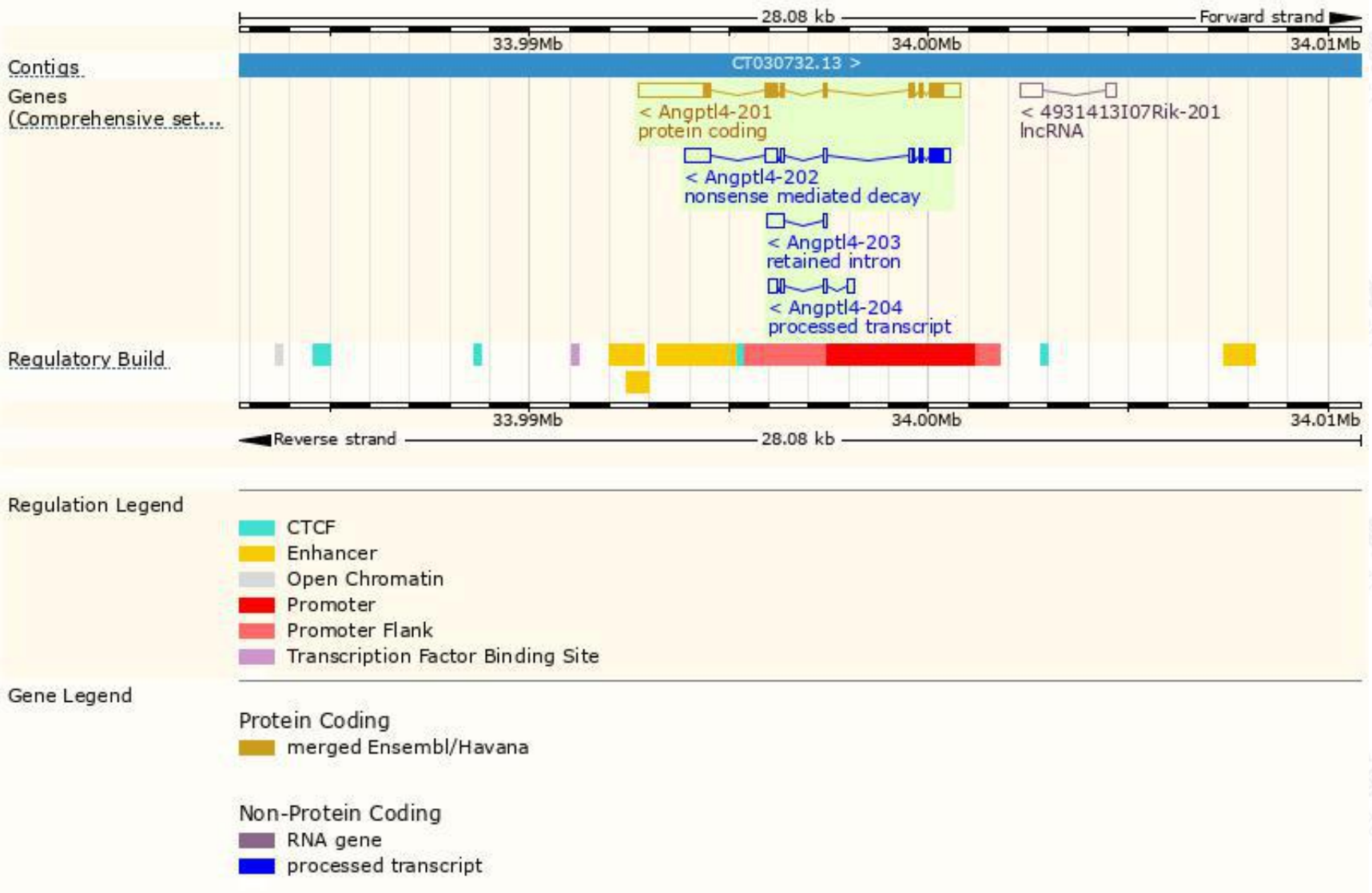
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Angptl4-201	ENSMUST00000002360.17	3308	410aa	Protein coding	CCDS28629		TSL:1 , GENCODE basic , APPRIS P1 ,
Angptl4-202	ENSMUST00000173869.8	1859	154aa	Nonsense mediated decay	-		TSL:1 ,
Angptl4-204	ENSMUST00000174872.2	575	No protein	Processed transcript	-		TSL:3 ,
Angptl4-203	ENSMUST00000174858.2	539	No protein	Retained intron	-		TSL:3 ,

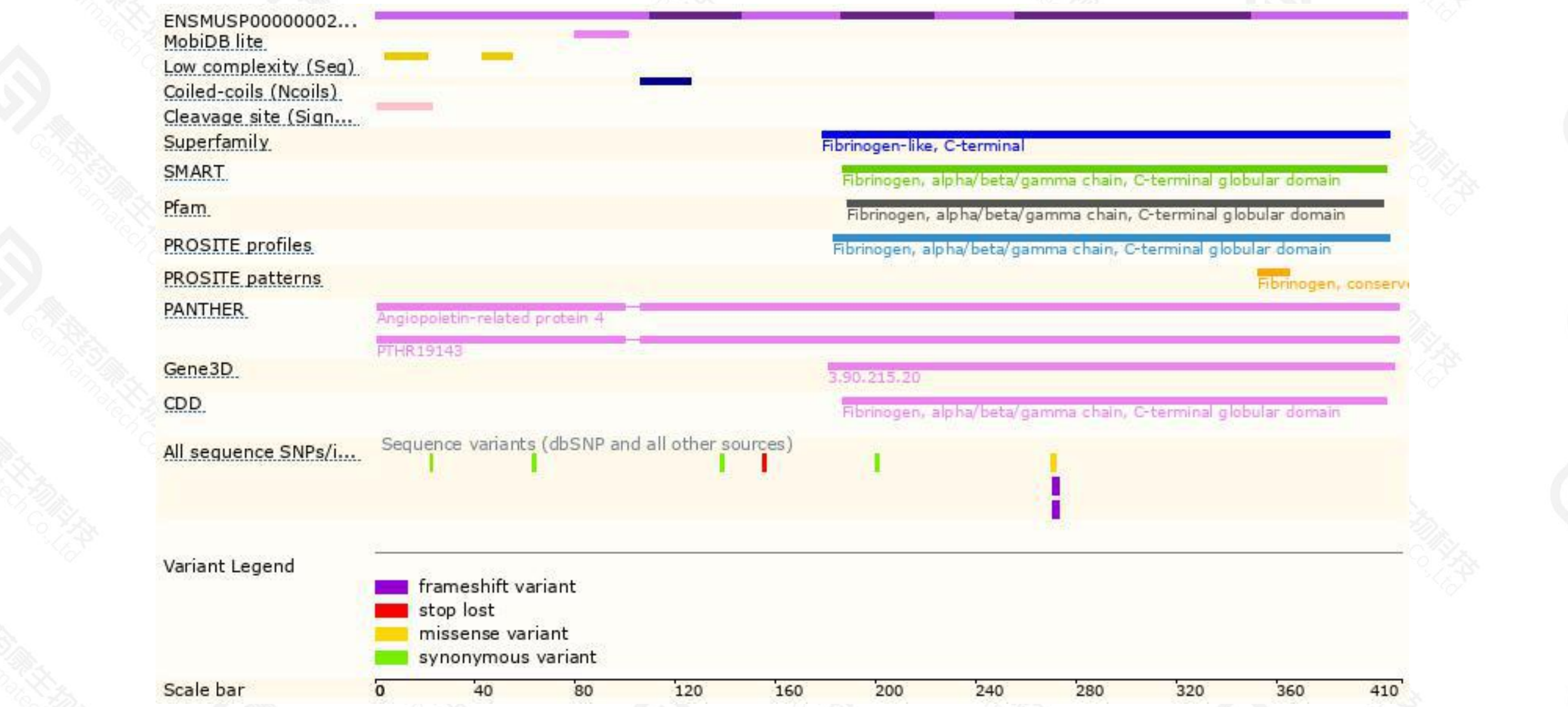
The strategy is based on the design of *Angptl4-201* transcript,the transcription is shown below:



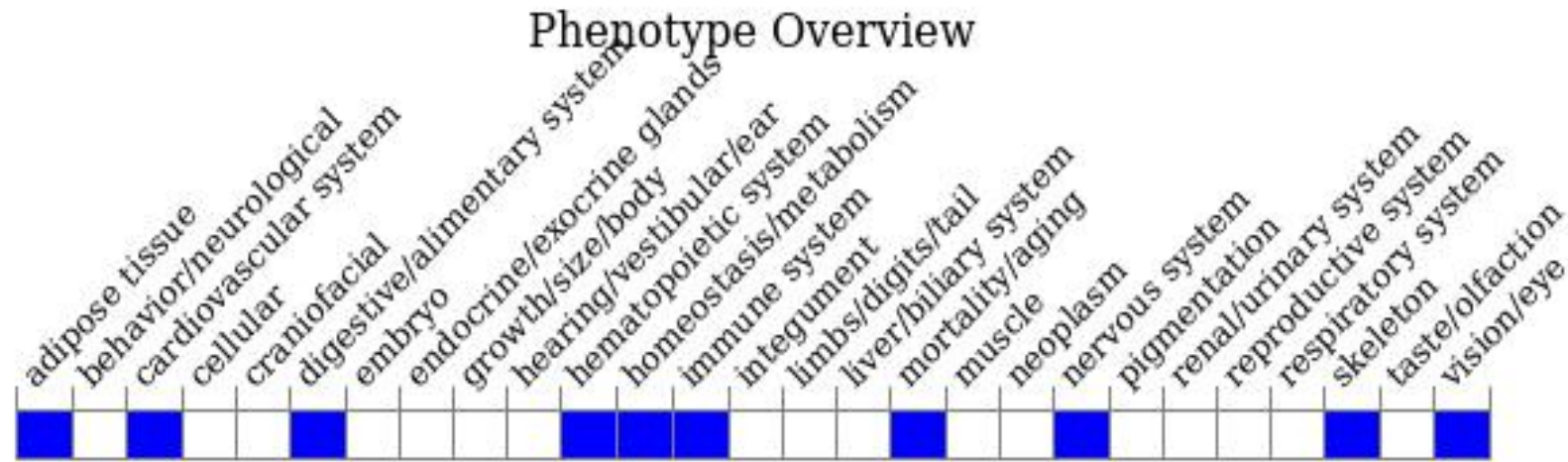
Genomic location distribution



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 disruptions in this gene display decreased levels of triglycerides and cholesterol and a lower increase in body fat after exposure to gut microbiota.

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