

# ***Lipa Cas9-CKO Strategy***

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# Project Overview

**Project Name**

*Lipa*

**Project type**

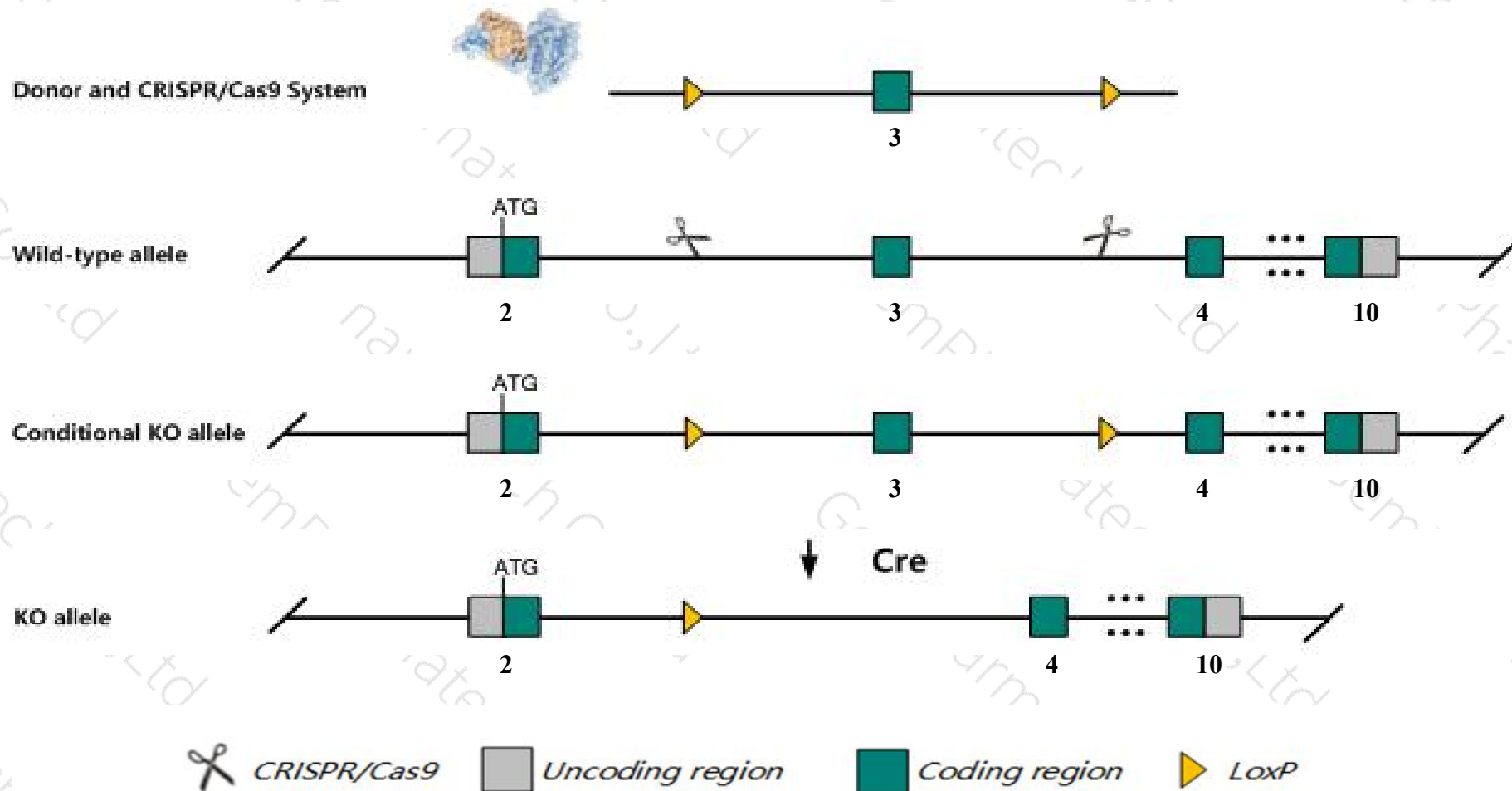
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



# Technical routes

- The *Lipa* gene has 6 transcripts. According to the structure of *Lipa* gene, exon3 of *Lipa*-201 (ENSMUST00000049572.14) transcript is recommended as the knockout region. The region contains 118bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lipa* gene. The brief process is as follows: CRISPR/Cas9 system 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 will be 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.

# Notice

- According to the existing MGI data, Homozygous null mice show massive accumulation of triglycerides and cholesteryl esters in several organs, depletion of white and brown fat, hepatosplenomegaly, increased energy intake and plasma free fatty acid levels, insulin resistance, lung inflammation, alveolar destruction and premature death.
- Transcript *Lipa*-203&204 may not be affected.
- The *Lipa* gene is located on the Chr19. 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)

## Lipa lysosomal acid lipase A [ *Mus musculus* (house mouse) ]

Gene ID: 16889, updated on 29-Oct-2019

Summary

- Official Symbol

Lipa provided by MGI
- Official Full Name

lysosomal acid lipase A provided by MGI
- Primary source

[MGI:MGI:96789](#)
- See related

[Ensembl:ENSMUSG00000024781](#)
- 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

Lal; Lip1; Lip-1; AA960673
- Expression

Broad expression in kidney adult (RPKM 86.1), liver adult (RPKM 55.5) and 24 other tissues [See more](#)
- Orthologs

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

Genomic context

Location: 19; 19 C1

See Lipa in [Genome Data Viewer](#)

Exon count: 10

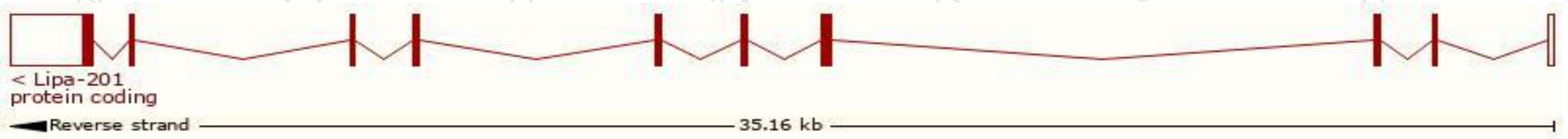
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	19	NC_000085.6 (34492316..34527474, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	19	NC_000085.5 (34566806..34601964, complement)

# Transcript information (Ensembl)

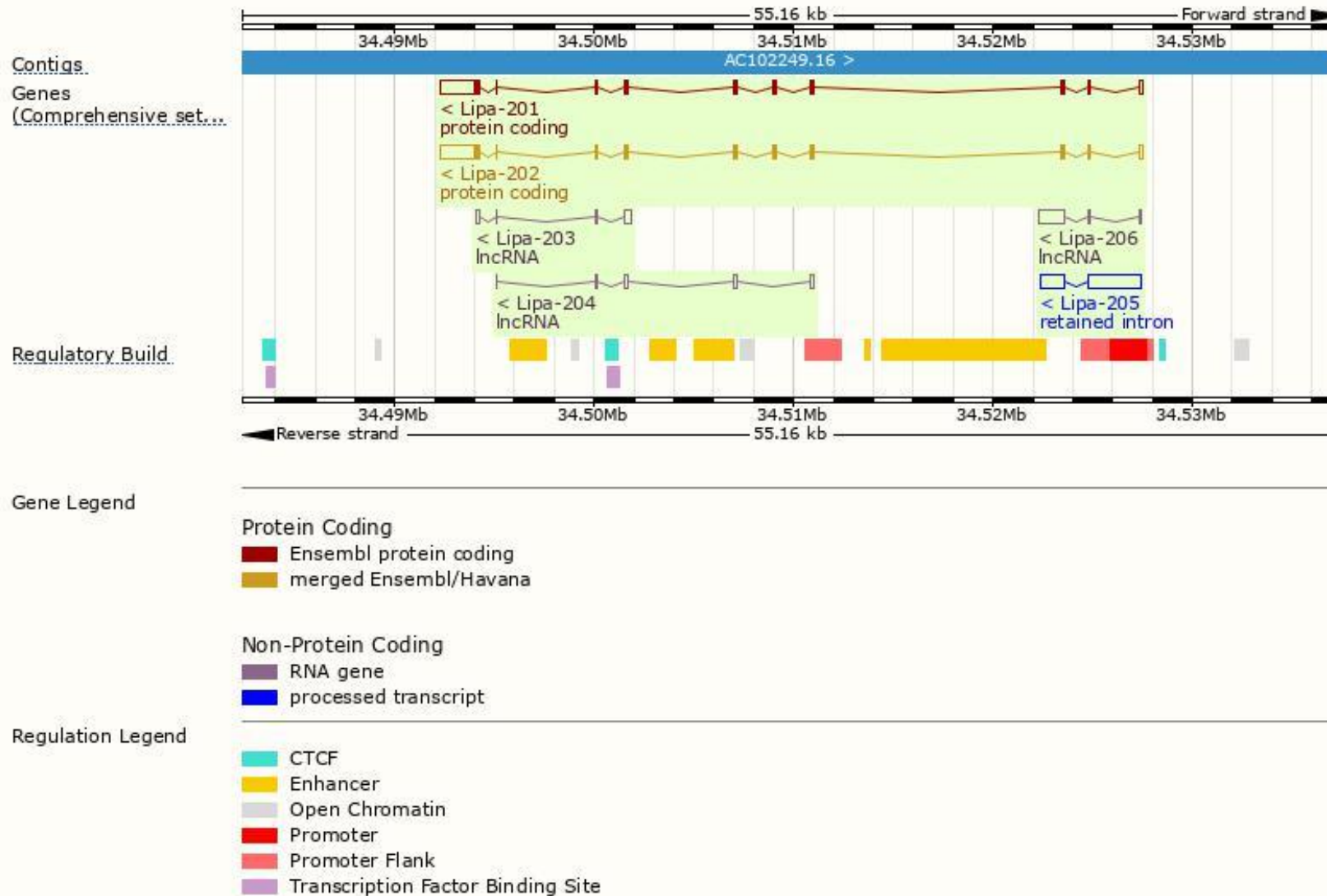
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lipa-201	<a href="#">ENSMUST00000049572.14</a>	2969	<a href="#">397aa</a>	Protein coding	<a href="#">CCDS29760</a>	<a href="#">Q9Z0M5</a>	TSL:1 GENCODE basic APPRIS P1
Lipa-202	<a href="#">ENSMUST00000178114.1</a>	2965	<a href="#">397aa</a>	Protein coding	<a href="#">CCDS29760</a>	<a href="#">Q9Z0M5</a>	TSL:1 GENCODE basic APPRIS P1
Lipa-205	<a href="#">ENSMUST00000237513.1</a>	3895	No protein	Retained intron	-	-	
Lipa-206	<a href="#">ENSMUST00000237617.1</a>	1361	No protein	lncRNA	-	-	
Lipa-203	<a href="#">ENSMUST00000236641.1</a>	663	No protein	lncRNA	-	-	
Lipa-204	<a href="#">ENSMUST00000237497.1</a>	586	No protein	lncRNA	-	-	

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

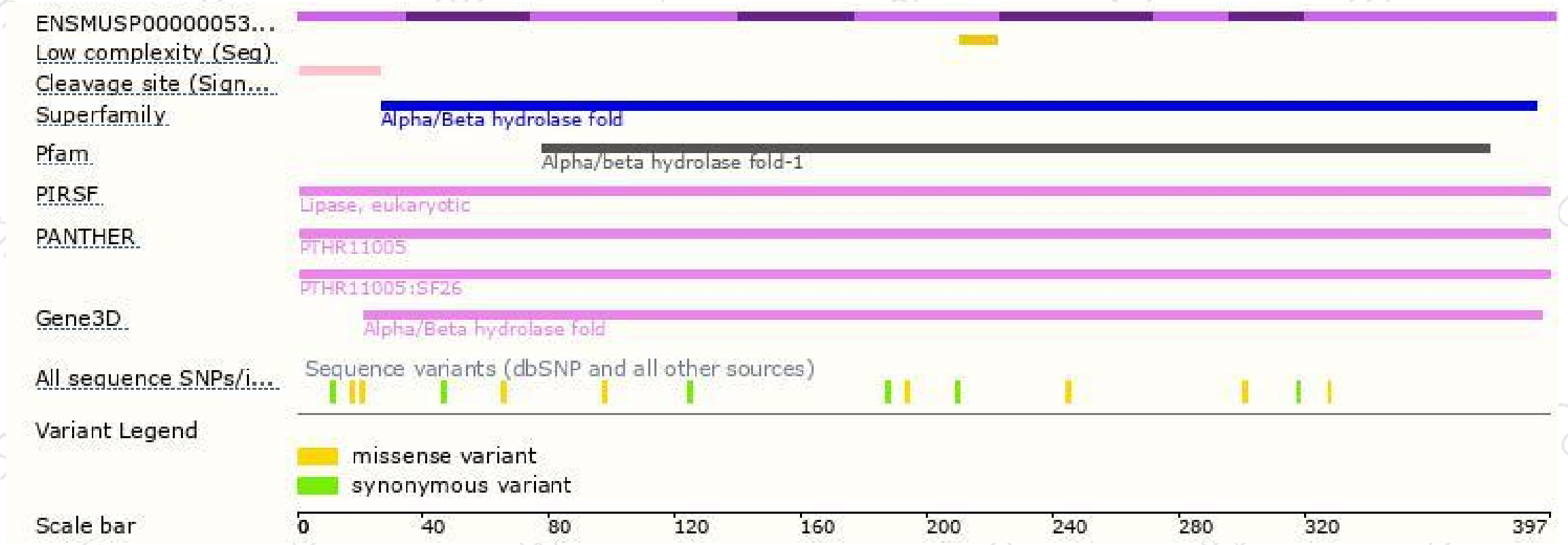


# Genomic location distribution

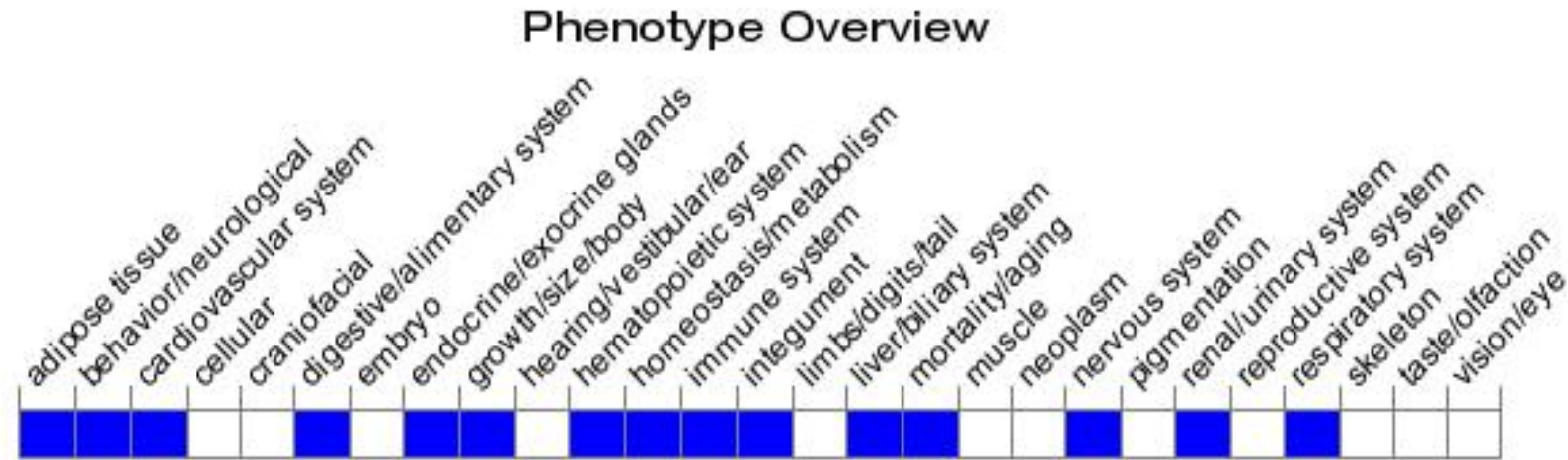




# Protein domain



# 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, Homozygous null mice show massive accumulation of triglycerides and cholesteryl esters in several organs, depletion of white and brown fat, hepatosplenomegaly, increased energy intake and plasma free fatty acid levels, insulin resistance, lung inflammation, alveolar destruction and premature death.

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

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