

# *Plin2* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Plin2*

**Project type**

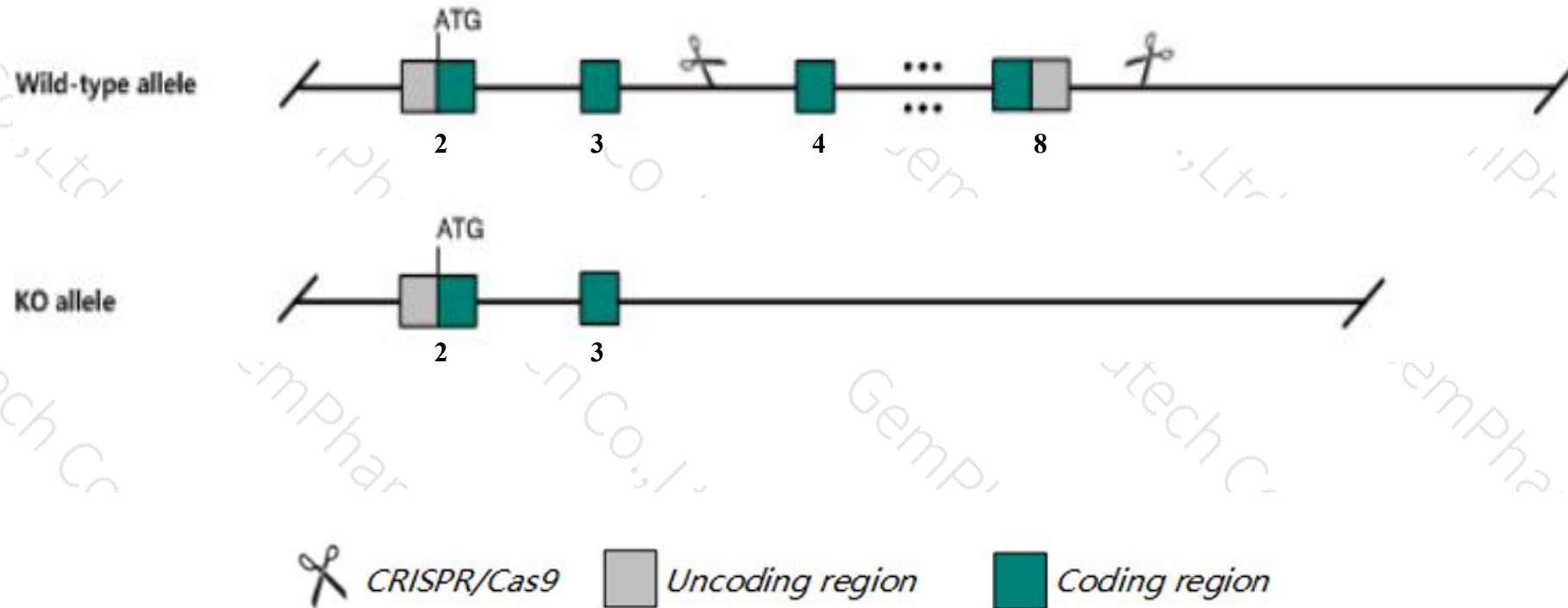
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Plin2* gene. The schematic diagram is as follows:



- The *Plin2* gene has 8 transcripts. According to the structure of *Plin2* gene, exon4-exon8 of *Plin2-201* (ENSMUST00000000466.12) transcript is recommended as the knockout region. The region contains 1052bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Plin2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for null mutations are resistant to diet-induced obesity and hepatic steatosis and may exhibit altered milk composition, vision abnormalities, or small sebaceous glands. Male mice homozygous for a gene trap allele are infertile.
- The *Plin2* 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)

## Plin2 perilipin 2 [Mus musculus (house mouse)]

Gene ID: 11520, updated on 31-Jan-2019

### Summary



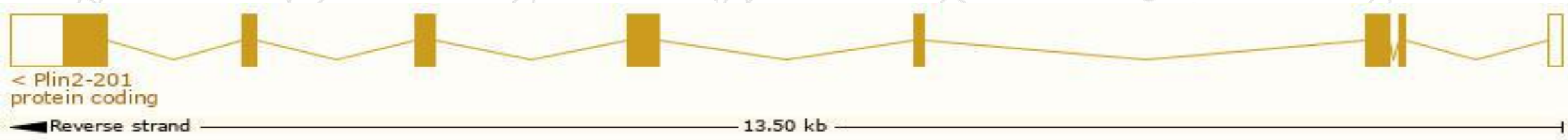
<b>Official Symbol</b>	Plin2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	perilipin 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:87920</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000028494</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	AA407157, ADPH, Adfp, Adrp
<b>Expression</b>	Broad expression in subcutaneous fat pad adult (RPKM 153.8), liver adult (RPKM 106.9) and 24 other tissues <a href="#">See more</a>

# Transcript information (Ensembl)

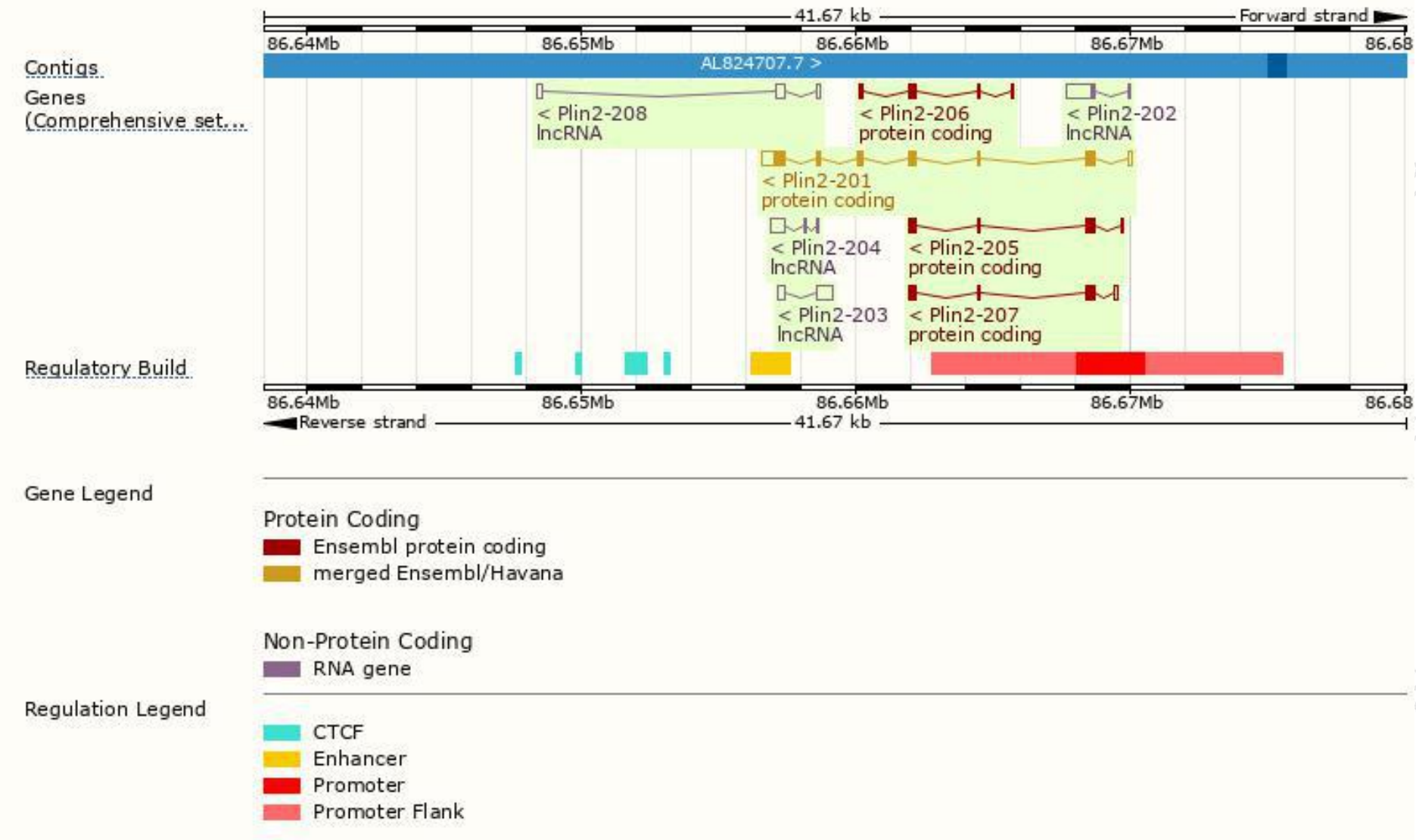
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plin2-201	<a href="#">ENSMUST00000000466.12</a>	1888	<a href="#">425aa</a>	Protein coding	<a href="#">CCDS18308</a>	<a href="#">P43883</a>	TSL:1 GENCODE basic APPRIS P1
Plin2-207	<a href="#">ENSMUST00000149700.7</a>	730	<a href="#">196aa</a>	Protein coding	-	<a href="#">B1AXR5</a>	CDS 3' incomplete TSL:2
Plin2-205	<a href="#">ENSMUST00000140382.2</a>	683	<a href="#">196aa</a>	Protein coding	-	<a href="#">B1AXR5</a>	CDS 3' incomplete TSL:3
Plin2-206	<a href="#">ENSMUST00000147097.2</a>	551	<a href="#">157aa</a>	Protein coding	-	<a href="#">B1AXR3</a>	CDS 3' incomplete TSL:5
Plin2-202	<a href="#">ENSMUST00000134094.1</a>	996	No protein	lncRNA	-	-	TSL:2
Plin2-203	<a href="#">ENSMUST00000134437.1</a>	817	No protein	lncRNA	-	-	TSL:2
Plin2-204	<a href="#">ENSMUST00000138605.1</a>	635	No protein	lncRNA	-	-	TSL:3
Plin2-208	<a href="#">ENSMUST00000154999.1</a>	588	No protein	lncRNA	-	-	TSL:3

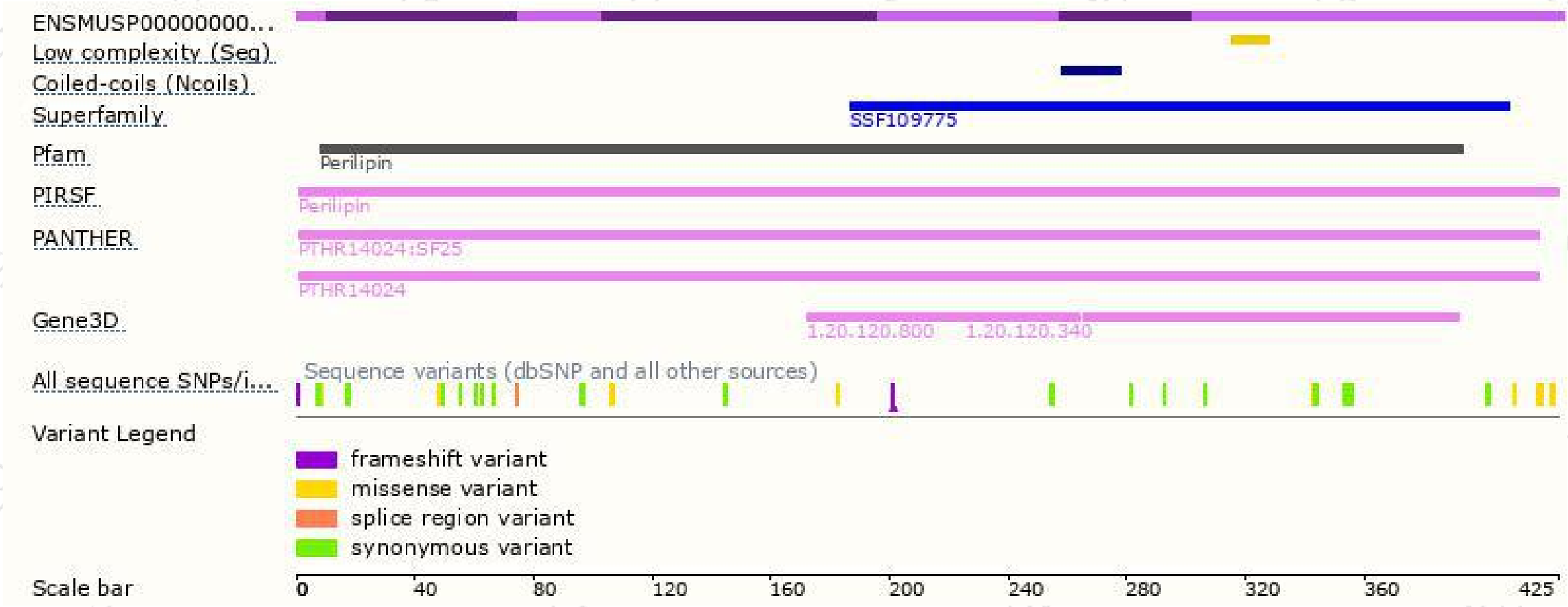
The strategy is based on the design of *Plin2-201* transcript,The transcription is shown below



# Genomic location distribution

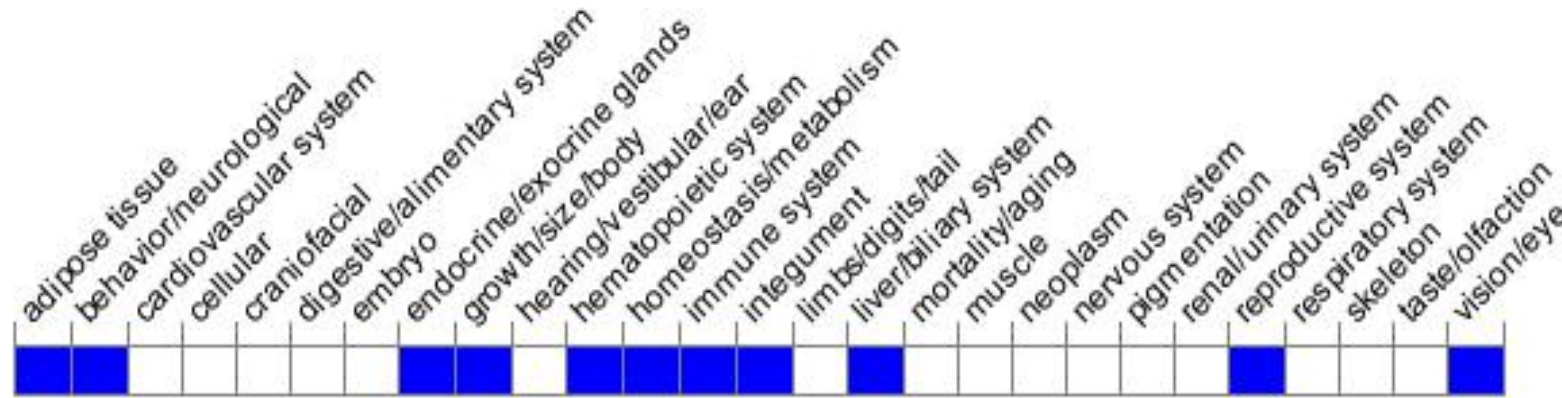


# Protein domain



# 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, Homozygotes for null mutations are resistant to diet-induced obesity and hepatic steatosis and may exhibit altered milk composition, vision abnormalities, or small sebaceous glands. Male mice homozygous for a gene trap allele are infertile.

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

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