

# *Acs11* Cas9-CKO Strategy

**Designer:**

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**Design Date:**

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# Project Overview

**Project Name**

*Acs11*

**Project type**

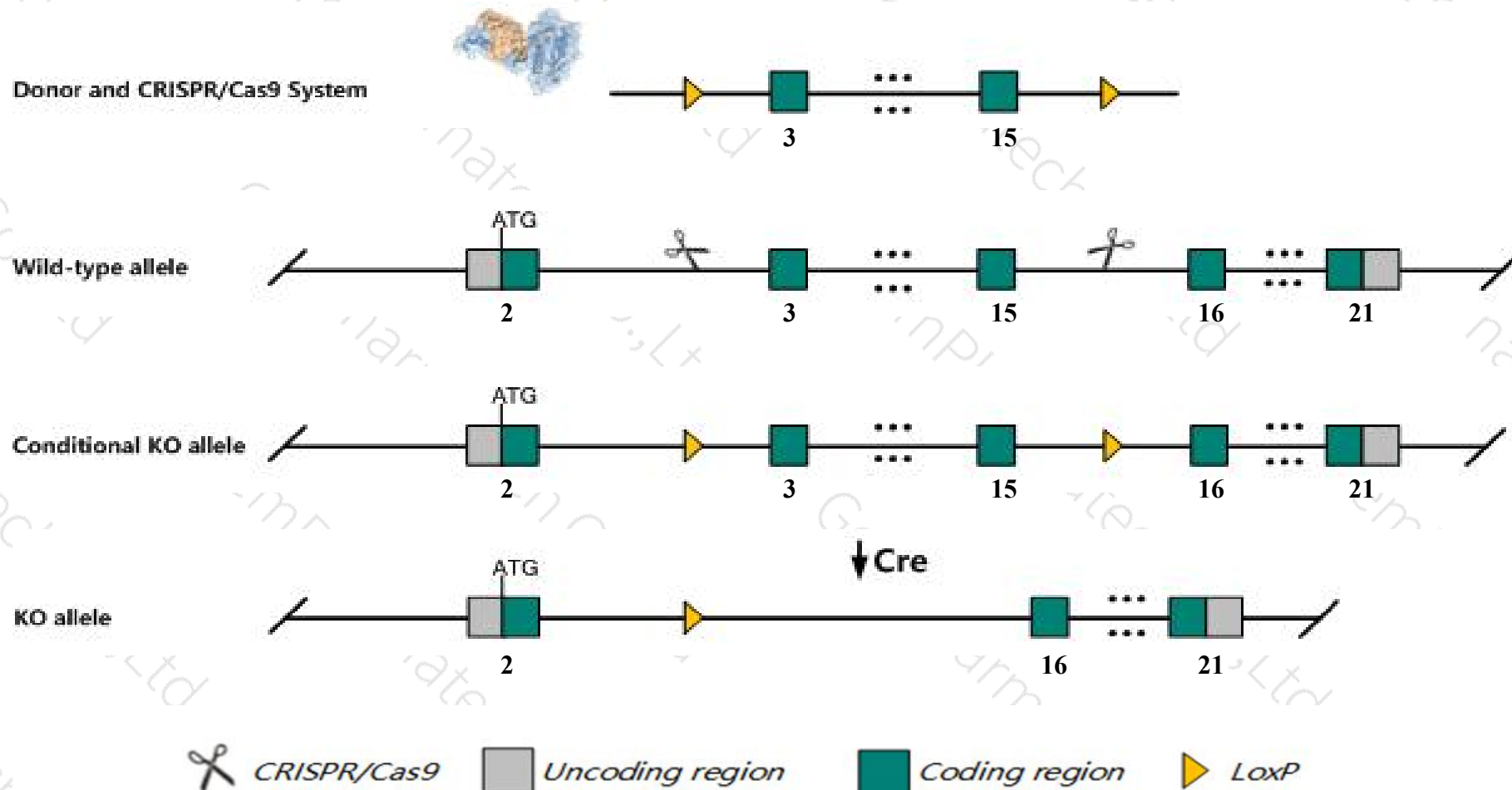
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Acs11* gene. The schematic diagram is as follows:



# Technical routes

- The *Acs11* gene has 11 transcripts. According to the structure of *Acs11* gene, exon3-exon15 of *Acs11-201* (ENSMUST00000034046.12) transcript is recommended as the knockout region. The region contains 1240bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Acs11* 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.

- According to the existing MGI data, Liver acyl-CoA levels are reduced when this gene is conditionally knocked out in the liver. Impaired adaptive thermogenesis when this gene is conditionally knocked out in adipose tissue.
- The *Acs11* gene is located on the Chr8. 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)

## Acs11 acyl-CoA synthetase long-chain family member 1 [Mus musculus (house mouse)]

Gene ID: 14081, updated on 31-Jan-2019

### Summary



**Official Symbol** Acs11 provided by [MGI](#)

**Official Full Name** acyl-CoA synthetase long-chain family member 1 provided by [MGI](#)

**Primary source** [MGI:MGI:102797](#)

**See related** [Ensembl:ENSMUSG00000018796](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** Acas, Acas1, Acs, FACS, Fac12, LACS 1, LACS1

**Summary** The protein encoded by this gene belongs to a family of acyl coenzyme A synthetase proteins, which convert long chain fatty acids to acyl CoA products via an ATP-dependent pathway. This enzyme is enriched in heart, liver and adipose tissue, where it functions in lipid synthesis and mitochondrial and peroxisomal beta-oxidation. In addition, it is expressed in monocytes and macrophages where it appears to have a functionally distinct role in mediating inflammatory and innate immune responses. A pseudogene of this gene is found on chromosome 5. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Oct 2014]

**Expression** Biased expression in liver E18 (RPKM 94.6), subcutaneous fat pad adult (RPKM 79.5) and 13 other tissues [See more](#)

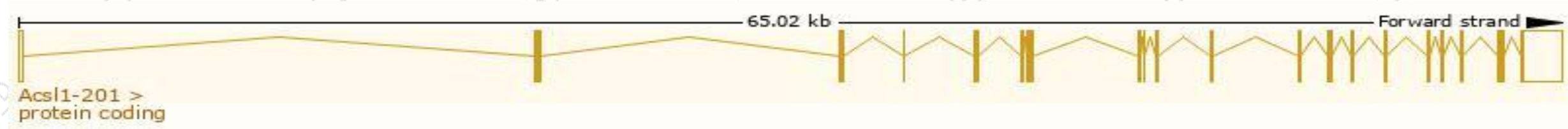
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

The gene has 11 transcripts,all transcripts are shown below:

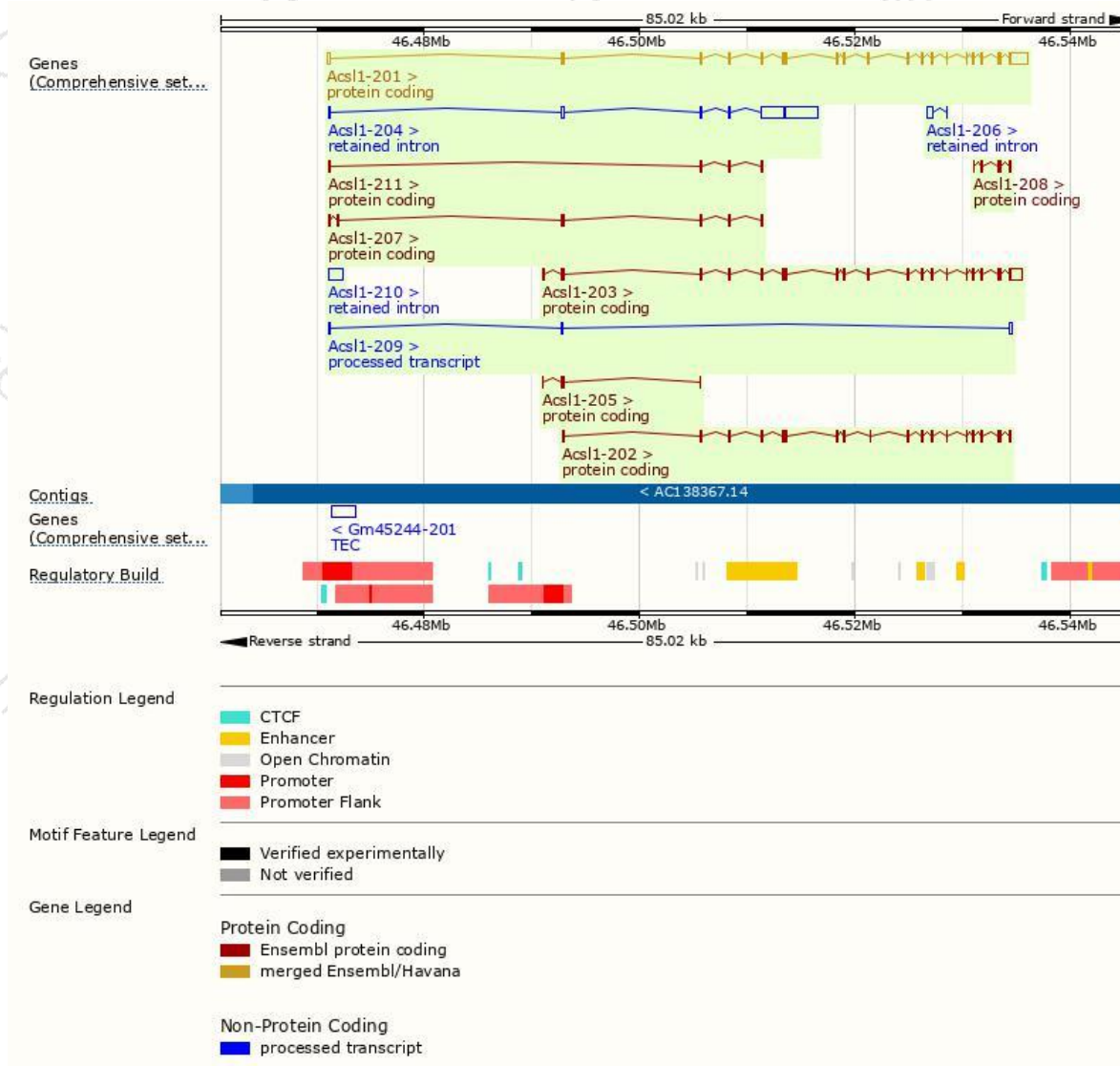
Show/hide columns (1 hidden)								Filter		
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags		
Acs11-201	<a href="#">ENSMUST00000034046.12</a>	3897	<a href="#">699aa</a>	Protein coding	<a href="#">CCDS22291</a>	<a href="#">P41216</a>	<a href="#">NM_007981</a> <a href="#">NP_032007</a>	TSL:1	GENCODE basic	APPRIS P2
Acs11-203	<a href="#">ENSMUST000000110372.8</a>	3429	<a href="#">699aa</a>	Protein coding	<a href="#">CCDS22291</a>	<a href="#">P41216</a>	<a href="#">NM_001302163</a> <a href="#">NP_001289092</a>	TSL:1	GENCODE basic	APPRIS P2
Acs11-202	<a href="#">ENSMUST000000110371.7</a>	2100	<a href="#">699aa</a>	Protein coding	-	<a href="#">D3Z041</a>	-	TSL:5	GENCODE basic	APPRIS ALT1
Acs11-207	<a href="#">ENSMUST000000135955.7</a>	673	<a href="#">136aa</a>	Protein coding	-	<a href="#">D3Z457</a>	-	CDS 3' incomplete	TSL:3	
Acs11-208	<a href="#">ENSMUST000000152423.1</a>	441	<a href="#">95aa</a>	Protein coding	-	<a href="#">F6WNZ2</a>	-	CDS 5' incomplete	TSL:5	
Acs11-205	<a href="#">ENSMUST000000130563.1</a>	368	<a href="#">86aa</a>	Protein coding	-	<a href="#">D3YVF6</a>	-	CDS 3' incomplete	TSL:2	
Acs11-211	<a href="#">ENSMUST000000211644.1</a>	343	<a href="#">58aa</a>	Protein coding	-	<a href="#">A0A1B0GRS8</a>	-	CDS 3' incomplete	TSL:2	
Acs11-209	<a href="#">ENSMUST000000210929.1</a>	474	No protein	Processed transcript	-	-	-	TSL:5		
Acs11-204	<a href="#">ENSMUST000000128746.2</a>	5676	No protein	Retained intron	-	-	-	TSL:2		
Acs11-210	<a href="#">ENSMUST000000211289.1</a>	1253	No protein	Retained intron	-	-	-	TSL:NA		
Acs11-206	<a href="#">ENSMUST000000133161.1</a>	573	No protein	Retained intron	-	-	-	TSL:3		

The strategy is based on the design of *Acs11-201* transcript,The transcription is shown below



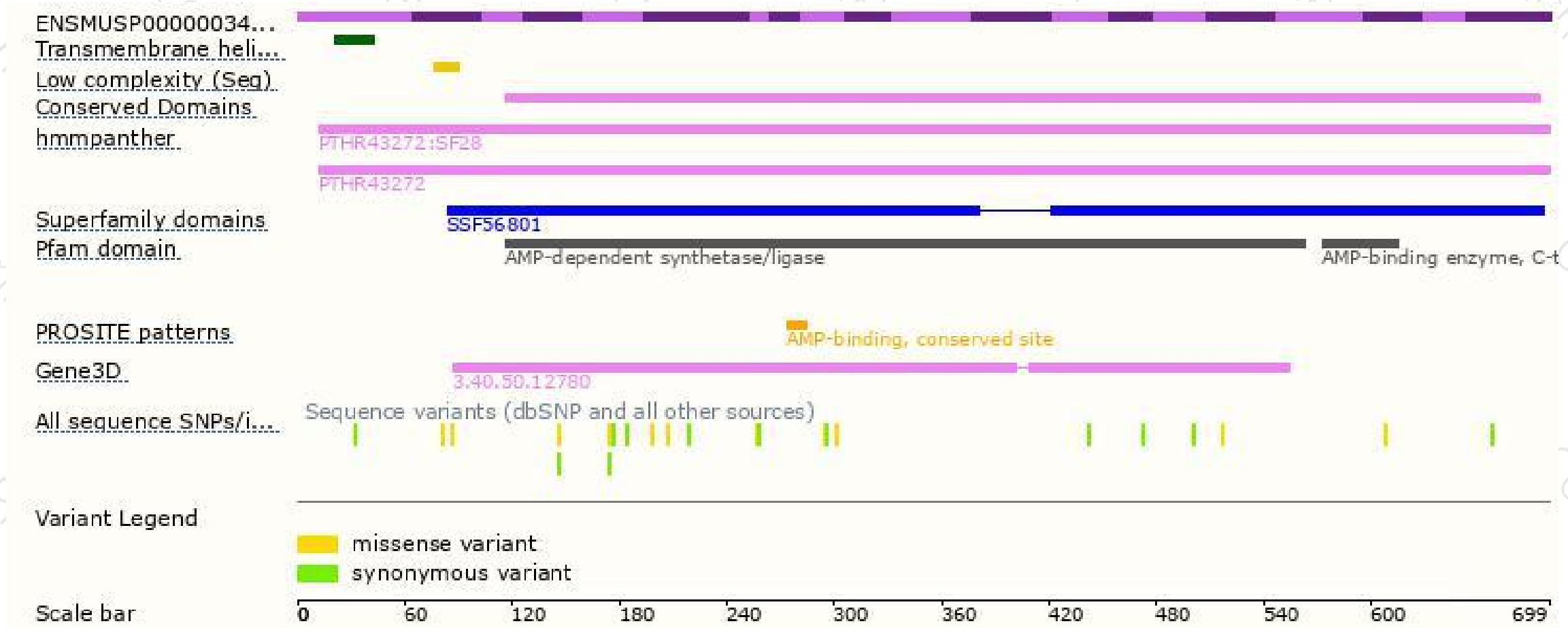


# Genomic location distribution

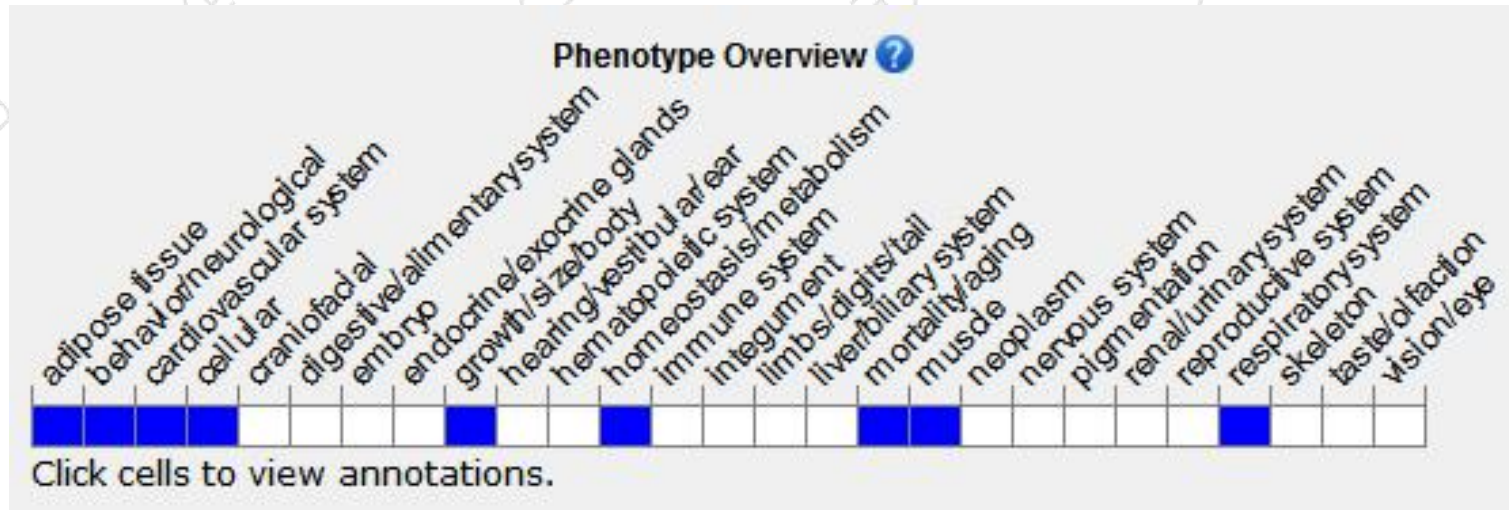




# Protein domain



# 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, Liver acyl-CoA levels are reduced when this gene is conditionally knocked out in the liver. Impaired adaptive thermogenesis when this gene is conditionally knocked out in adipose tissue.

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

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