

# *Acss1* Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Acss1*

**Project type**

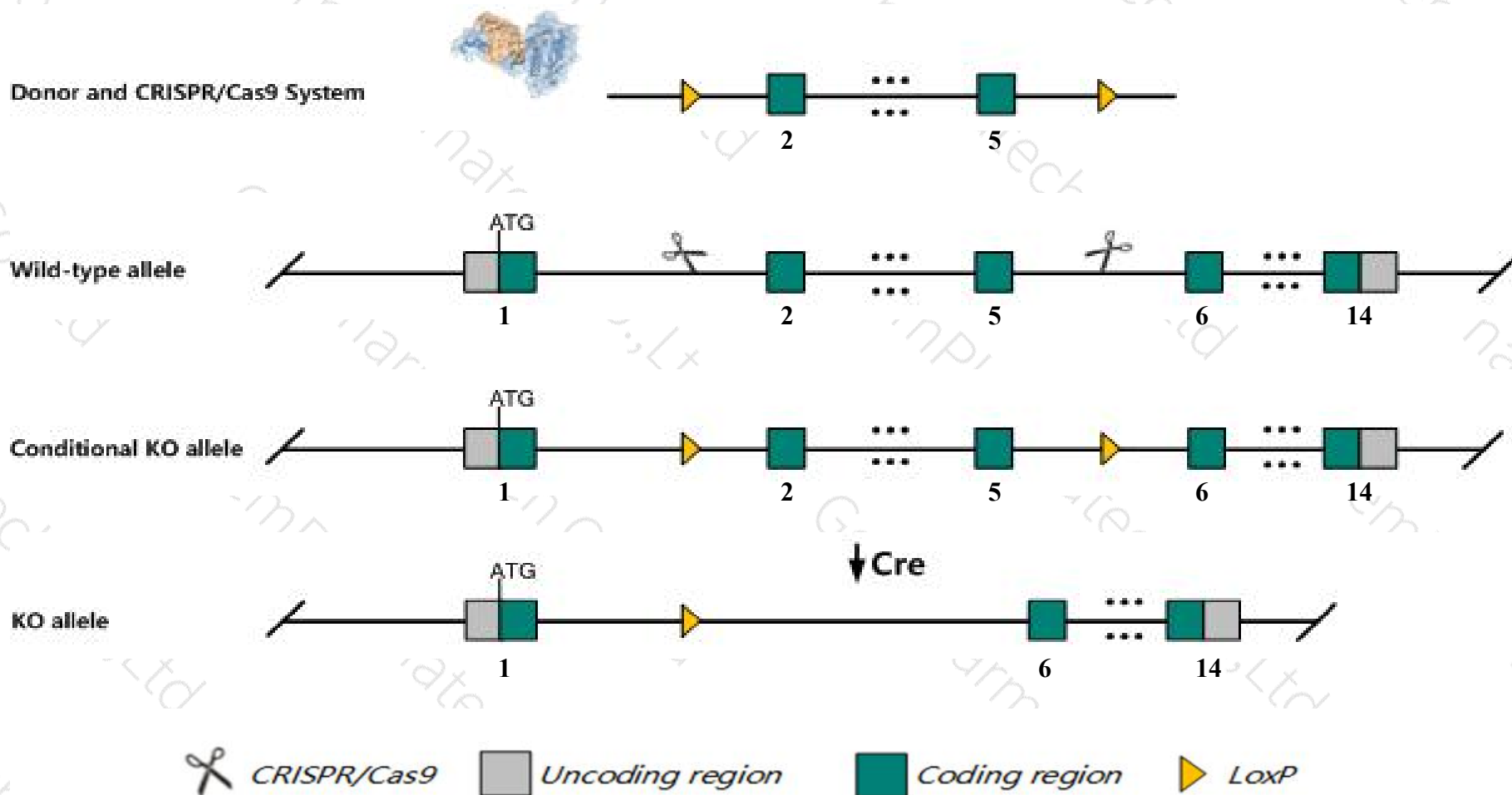
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Acsc1* gene. The schematic diagram is as follows:



# Technical routes

- The *Acss1* gene has 5 transcripts. According to the structure of *Acss1* gene, exon2-exon5 of *Acss1-201* (ENSMUST00000028944.3) transcript is recommended as the knockout region. The region contains 626bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Acss1* 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, Mice with disruptions in this gene display abnormalities in acetate metabolism. Ability to maintain body temperature under fasting conditions is reduced.
- The floxed region is near to the N-terminal of *E130215H24Rik* gene, this strategy may influence the regulatory function of the N-terminal of *E130215H24Rik* gene.
- The *Acss1* gene is located on the Chr2. 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)

## Acss1 acyl-CoA synthetase short-chain family member 1 [ *Mus musculus* (house mouse) ]

Gene ID: 68738, updated on 10-Oct-2019

### Summary

Official Symbol	Acss1 provided by MGI
Official Full Name	acyl-CoA synthetase short-chain family member 1 provided by MGI
Primary source	MGI:MGI:1915988
See related	Ensembl:ENSMUSG00000027452
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<i>Mus musculus</i>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Acas2; Acas2l; AceCS2; AI788978; 1110032O15Rik
Expression	Broad expression in kidney adult (RPKM 106.8), heart adult (RPKM 84.4) and 20 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

### Genomic context

Location: 2; 2 G3

See Acss1 in [Genome Data Viewer](#)

Exon count: 14

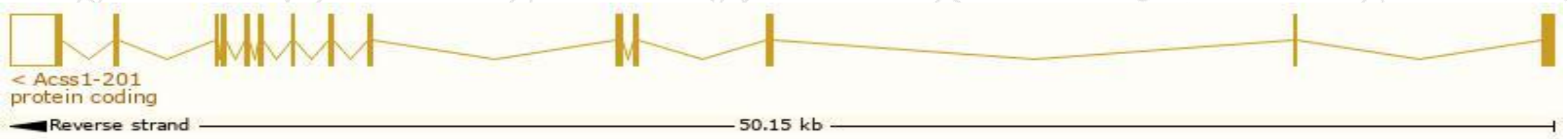
Annotation release	Status	Assembly	Chr	Location
<a href="#">108</a>	current	GRCm38.p6 ( <a href="#">GCF_000001635.26</a> )	2	NC_000068.7 (150618111..150668240, complement)
Build 37.2	previous assembly	MGSCv37 ( <a href="#">GCF_000001635.18</a> )	2	NC_000068.6 (150443847..150493976, complement)

# Transcript information (Ensembl)

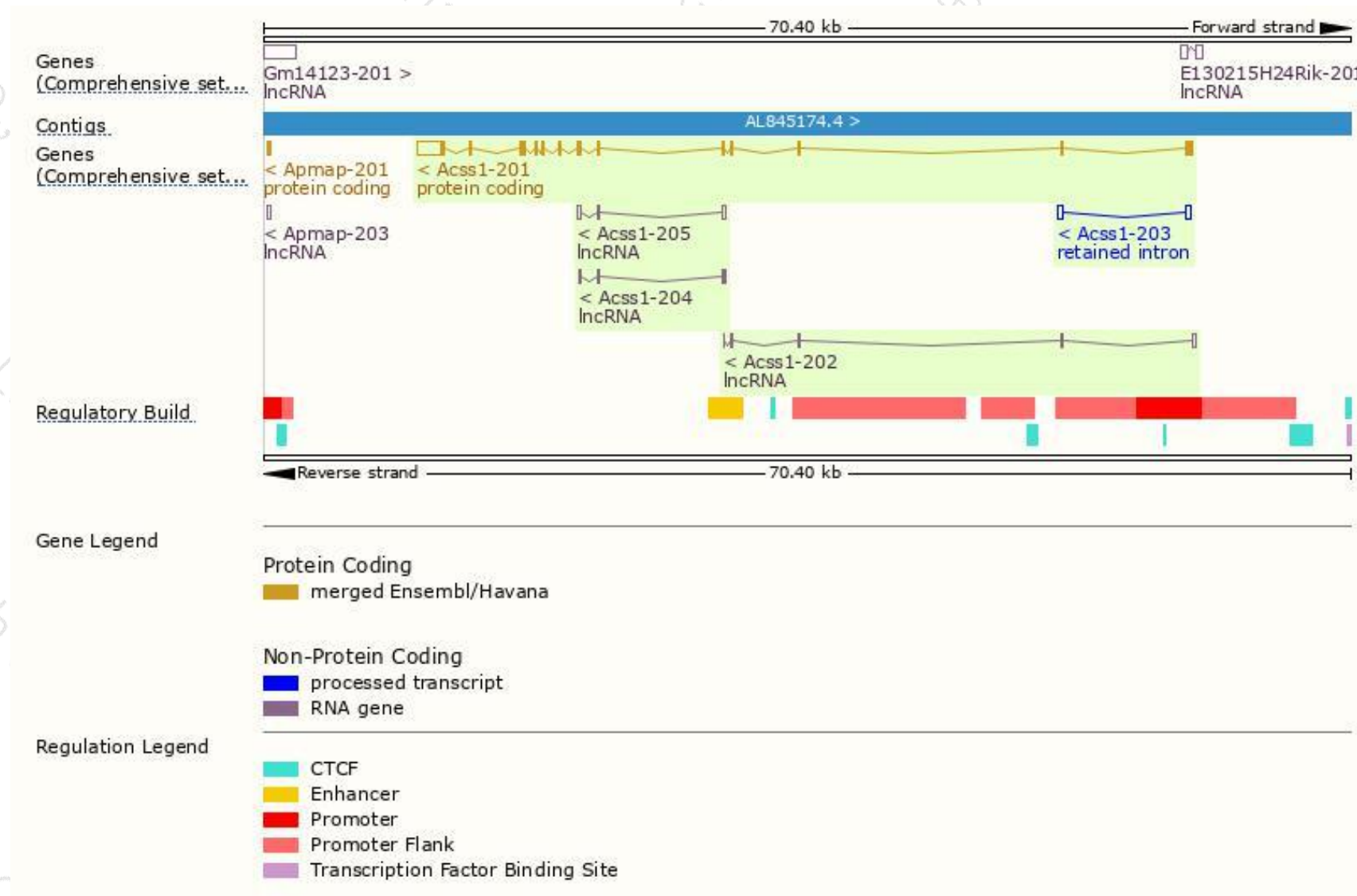
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Acss1-201	<a href="#">ENSMUST00000028944.3</a>	3618	<a href="#">682aa</a>	Protein coding	<a href="#">CCDS16859</a>	<a href="#">Q3UJ89</a> <a href="#">Q99NB1</a>	TSL:1 GENCODE basic APPRIS P1
Acss1-203	<a href="#">ENSMUST00000141785.1</a>	658	No protein	Retained intron	-	-	TSL:2
Acss1-202	<a href="#">ENSMUST00000141500.1</a>	656	No protein	lncRNA	-	-	TSL:5
Acss1-205	<a href="#">ENSMUST00000154328.7</a>	547	No protein	lncRNA	-	-	TSL:2
Acss1-204	<a href="#">ENSMUST00000147135.1</a>	392	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Acss1-201* transcript,The transcription is shown below

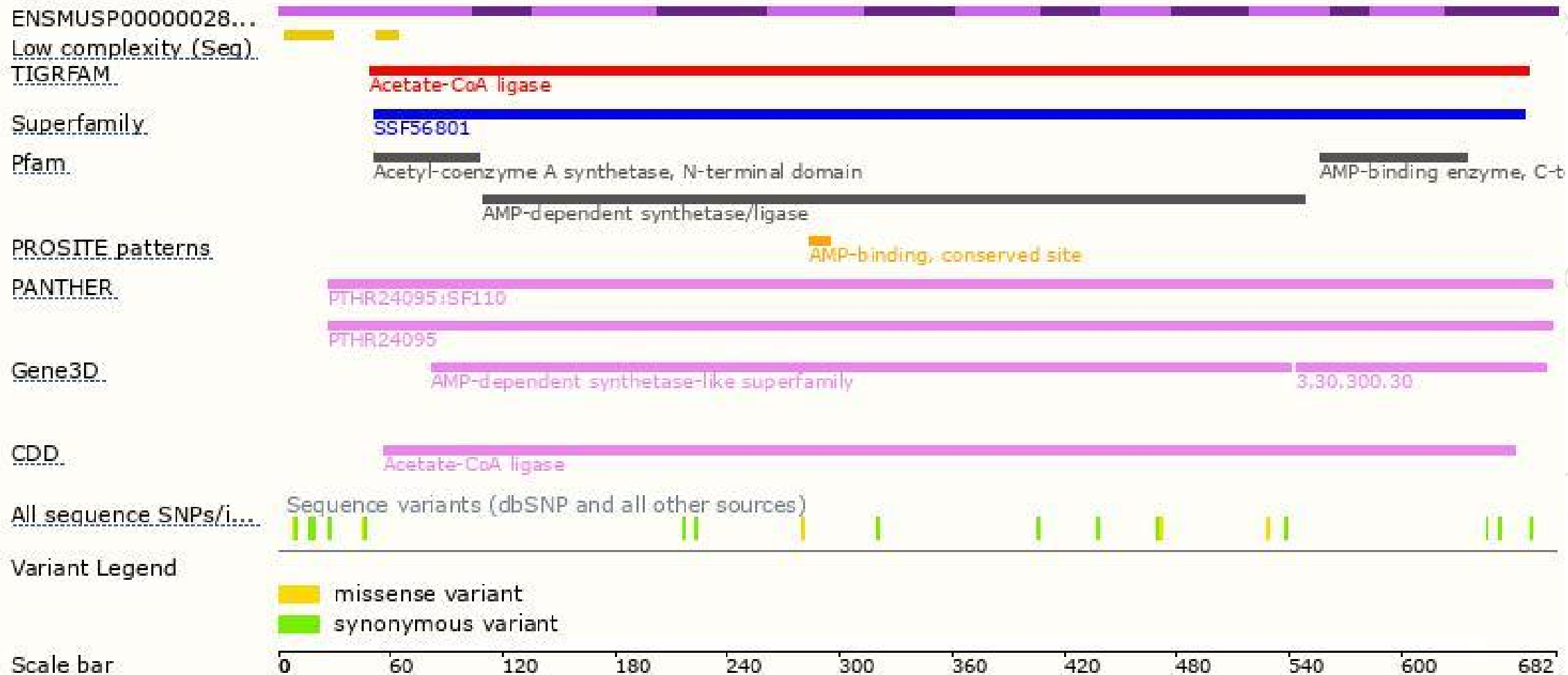


# Genomic location distribution

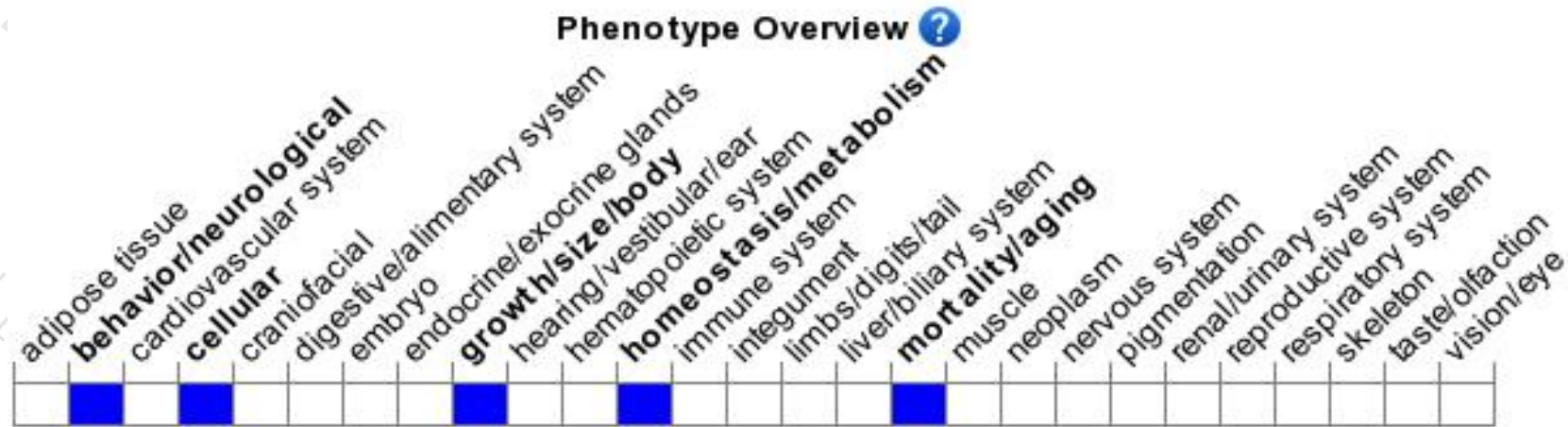




# Protein domain



# 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 with disruptions in this gene display abnormalities in acetate metabolism.

Ability to maintain body temperature under fasting conditions is reduced.

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

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