

Acs11 Cas9-KO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Acs11

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- 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

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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](#)

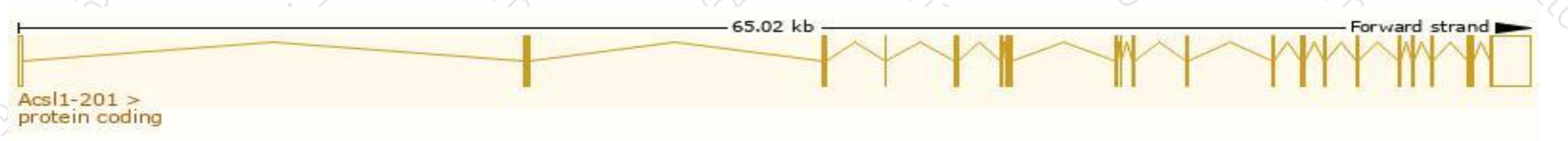
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

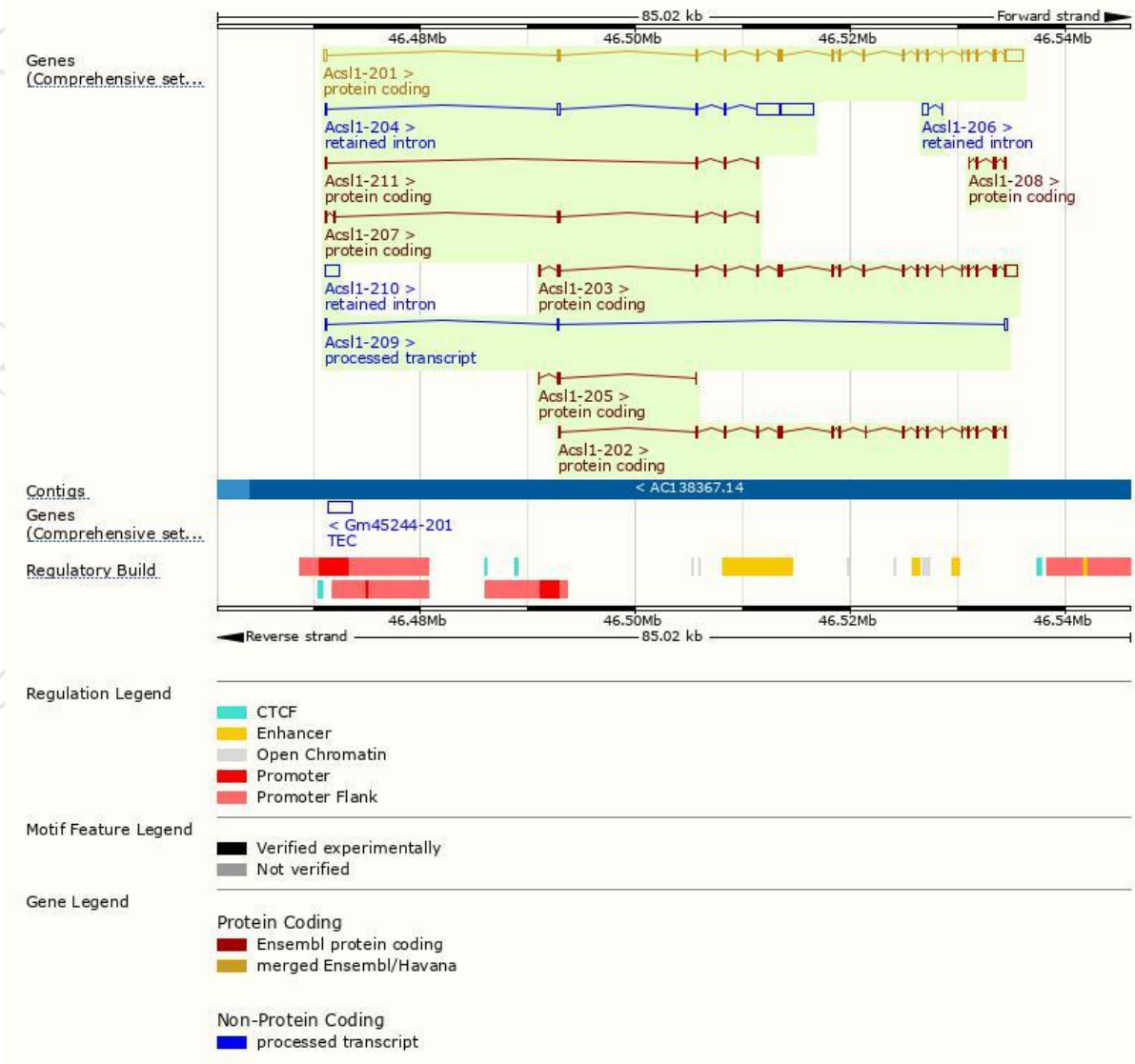
The gene has 11 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden)								Filter		
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags		
Acs11-201	ENSMUST00000034046.12	3897	699aa	Protein coding	CCDS22291	P41216	NM_007981 NP_032007	TSL:1	GENCODE basic	APPRIS P2
Acs11-203	ENSMUST00000110372.8	3429	699aa	Protein coding	CCDS22291	P41216	NM_001302163 NP_001289092	TSL:1	GENCODE basic	APPRIS P2
Acs11-202	ENSMUST00000110371.7	2100	699aa	Protein coding	-	D3Z041	-	TSL:5	GENCODE basic	APPRIS ALT1
Acs11-207	ENSMUST00000135955.7	673	136aa	Protein coding	-	D3Z457	-	CDS 3' incomplete	TSL:3	
Acs11-208	ENSMUST00000152423.1	441	95aa	Protein coding	-	F6WNZ2	-	CDS 5' incomplete	TSL:5	
Acs11-205	ENSMUST00000130563.1	368	86aa	Protein coding	-	D3YVF6	-	CDS 3' incomplete	TSL:2	
Acs11-211	ENSMUST00000211644.1	343	58aa	Protein coding	-	A0A1B0GRS8	-	CDS 3' incomplete	TSL:2	
Acs11-209	ENSMUST00000210929.1	474	No protein	Processed transcript	-	-	-	TSL:5		
Acs11-204	ENSMUST00000128746.2	5676	No protein	Retained intron	-	-	-	TSL:2		
Acs11-210	ENSMUST00000211289.1	1253	No protein	Retained intron	-	-	-	TSL:NA		
Acs11-206	ENSMUST00000133161.1	573	No protein	Retained intron	-	-	-	TSL:3		

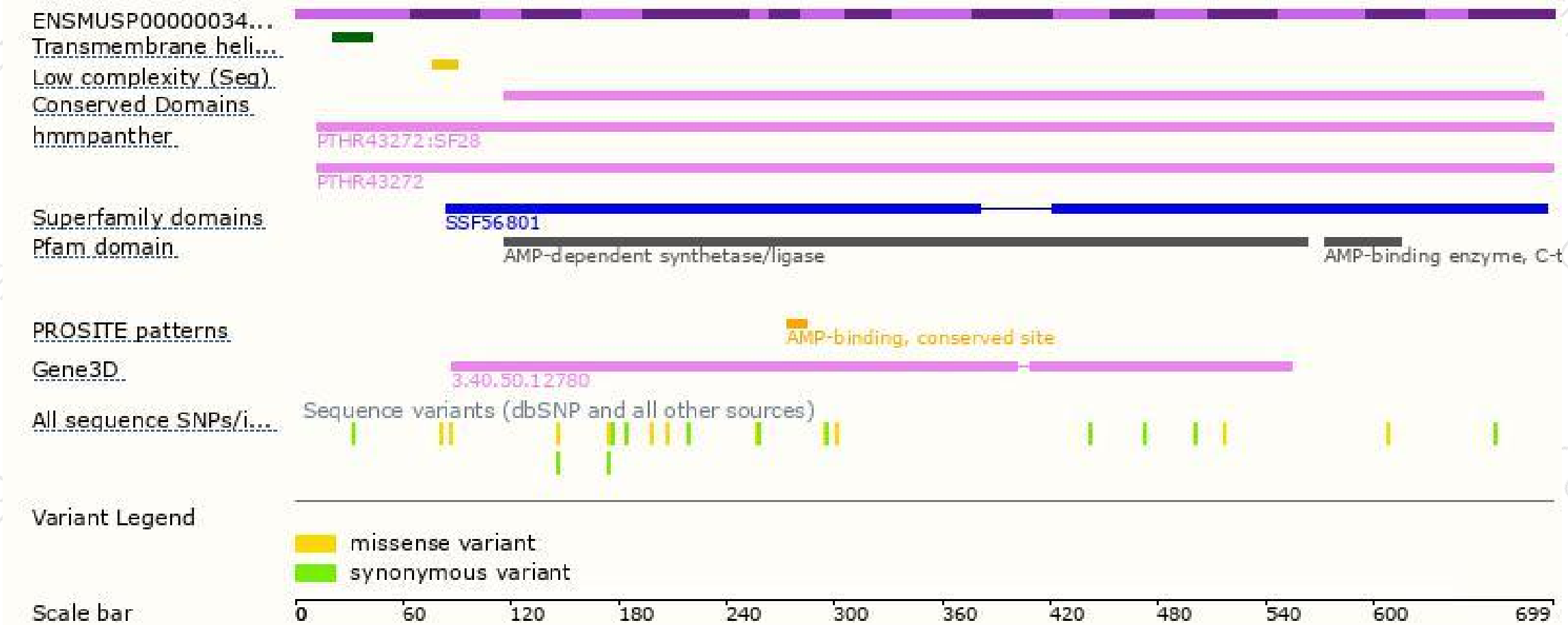
The strategy is based on the design of *Acs11-201* transcript,The transcription is shown below



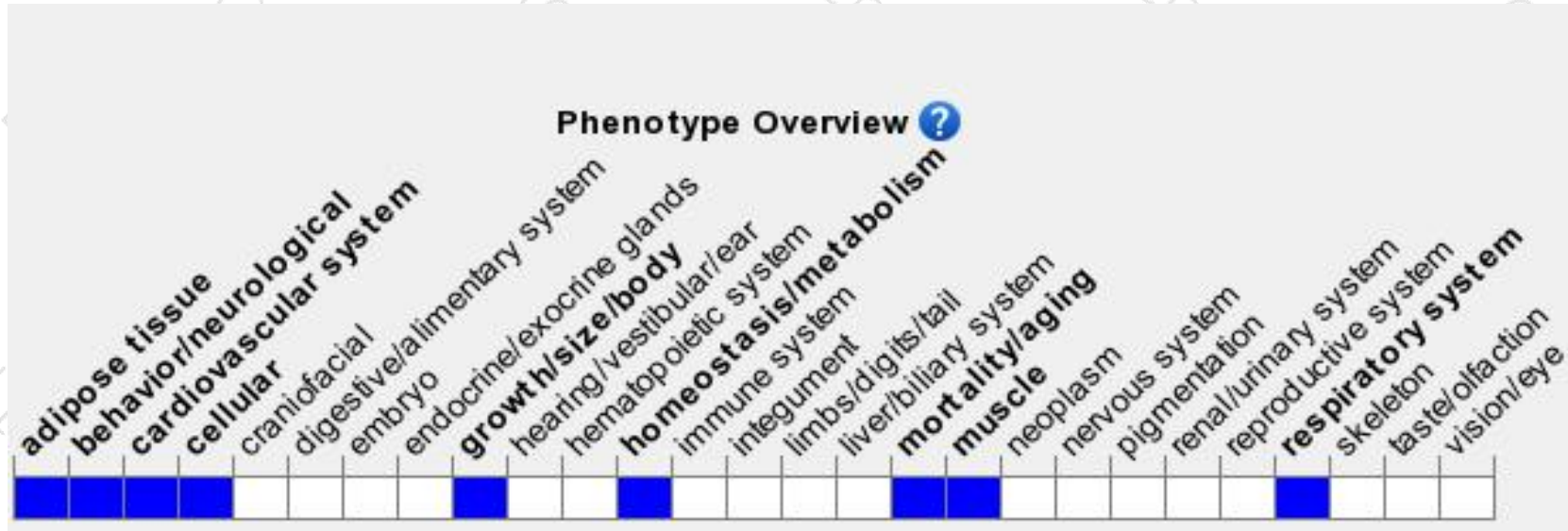
Genomic location distribution



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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