Electronic Supplementary Material (ESI) for Food & Function.

Table A1 Primers used in this study.

Primer names	Sequence (5′ to 3′)
PPARα-F	GACGCTGGGTCCTCTGGTT
PPARα-R	TCAGTCTTGGCTCGCCTCTA
PPARγ-F	GCCTCCCTGATGAATAAAGATG
PPARγ-R	CGACTGGGACTTTTCTGCTAAT
SREBP1-F	CCTGGAGCGAGCATTGAACT
SREBP1-R	CAGCGTCAGAACAGCTATTTAGC
CPT1-F	TCGTGGTGGTGGGTGTGATT
CPT1-R	AGCACCTTCAGCGAGTAGCG
ACC-1-F	TCTGCTCATGTTCCTTGCCC
ACC-1-R	GCTTCTTCTCTGTTTTCTCCCC
SCD1-F	TCGTCAGCACCTTCTTGAGAT
SCD1-R	GTGATGGTAGTTGTGGAAGCC
FAS-F	TACAATGGCACCCTGAACCT
FAS-R	TTCGCAAATACGCTCCATGG
β-Actin-F	CGTTGACATCCGTAAAGACCTC
β-Actin-R	TAGGAGCCAGGGCAGTAATCT

Table A2 Acyl content and DS of native and modified starch.

Sample	Starch: anhydride (m:v)	Temperature (°C)	PTSA (g)	Acyl (%)	DS[a]	DS[b]
HAMSA	1:4	70	0.15	9.70±0.22	0.40±0.10	0.47±0.06
HAMSP	1:6	95	0.45	13.13±0.19	0.43±0.15	0.48±0.07
HAMSB	1:6	105	0.45	14.27±0.21	0.38±0.17	0.41±0.07

[a] Determined by the hydrolysis method. [b] Determined by ^{1}H NMR method. Results were means ± SD (n = 3).

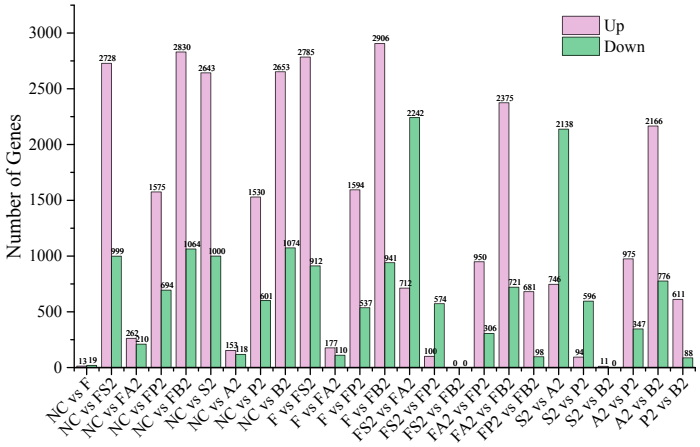

Figure A1. Statistical analysis of differentially expressed genes (DEGs) among treatment group. NC, normal control group; F, 200 μM FFA (M_{OA}: M_{PA} = 2: 1); FS2, 200 μM FFA + 10 mM SCFAs (M_{NaAc}: M_{NaPr}: M_{NaBu}=3:1:1); FA2, 200 μM FFA + 10 mM NaAc; FP2, 200 μM FFA + 5 mM NaPr; FB2, 200 μM FFA + 2.5 mM NaBu; S, 10 mM SCFAs (M_{NaAc}: M_{NaPr}: M_{NaBu}=3:1:1); A, 10 mM NaAc; P, 5 mM NaPr; B, 2.5 mM NaBu.

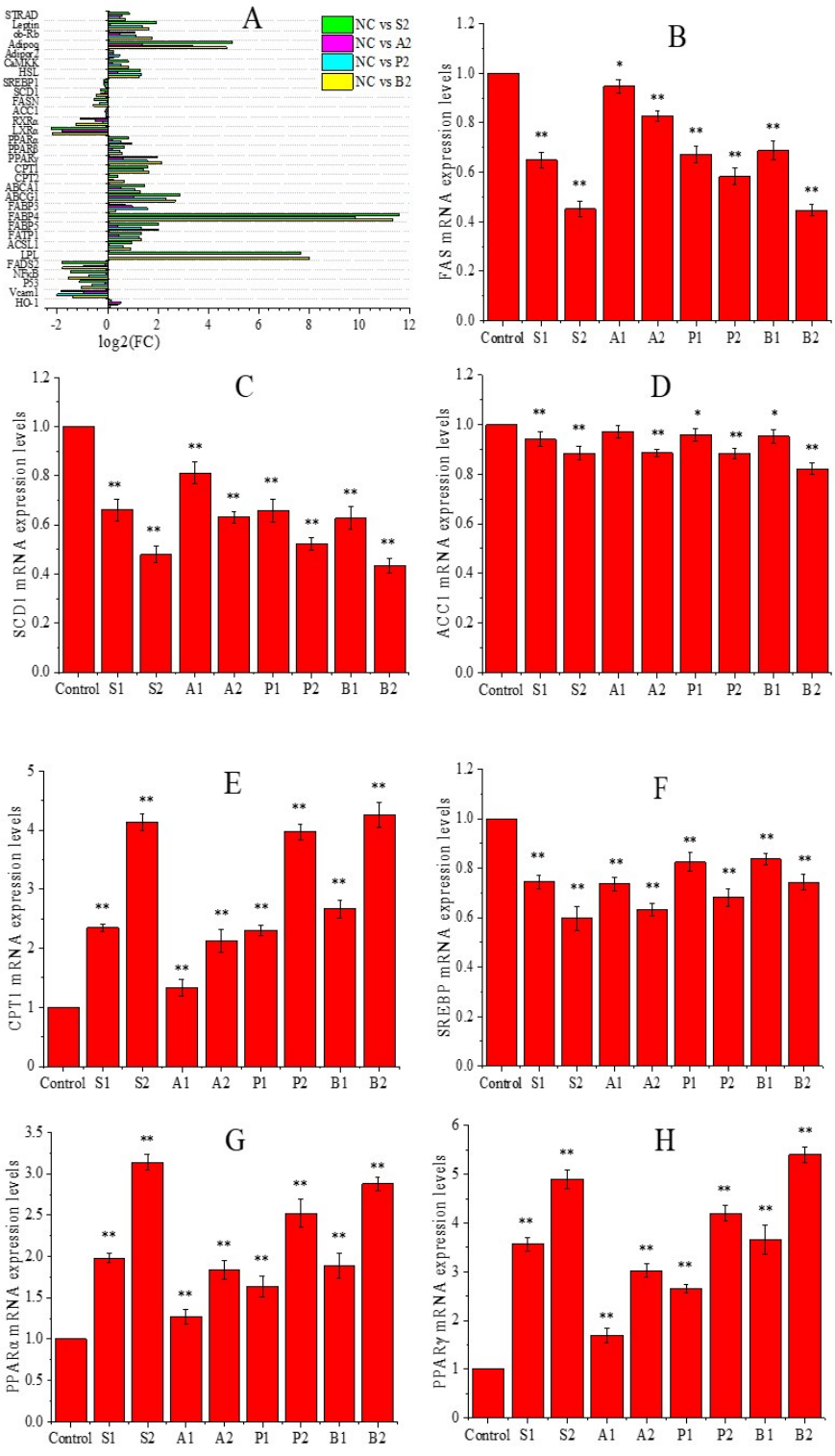

Figure A2. Validation of expression patterns of genes related to energy metabolism qRT-PCR. (A) Changes in transcript abundance based on a log2 (Fold Change, FC) values relative to control cells according to RNA-Seq. (B-H) Relative gene expression

levels determined by qRT-PCR from three biological replicates of each gene using the $2^{-\Delta\Delta CT}$ method. Data shown are the mean ± SD (error bars; n=3). NC, normal control group; S1, 5 mM SCFAs (M_{NaAc}: M_{NaPr}: M_{NaBu}=3:1:1); S2, 10 mM SCFAs (M_{NaAc}: M_{NaPr}: M_{NaBu}=3:1:1); A1, 5 mM NaAc; A2, 10 mM NaAc; P1, 2.5 mM NaPr; P2, 5 mM NaPr; B1, 1.25 mM NaBu; B2, 2.5 mM NaBu. *$P < 0.05$, **$P < 0.01$ SCFAs groups vs NC group.

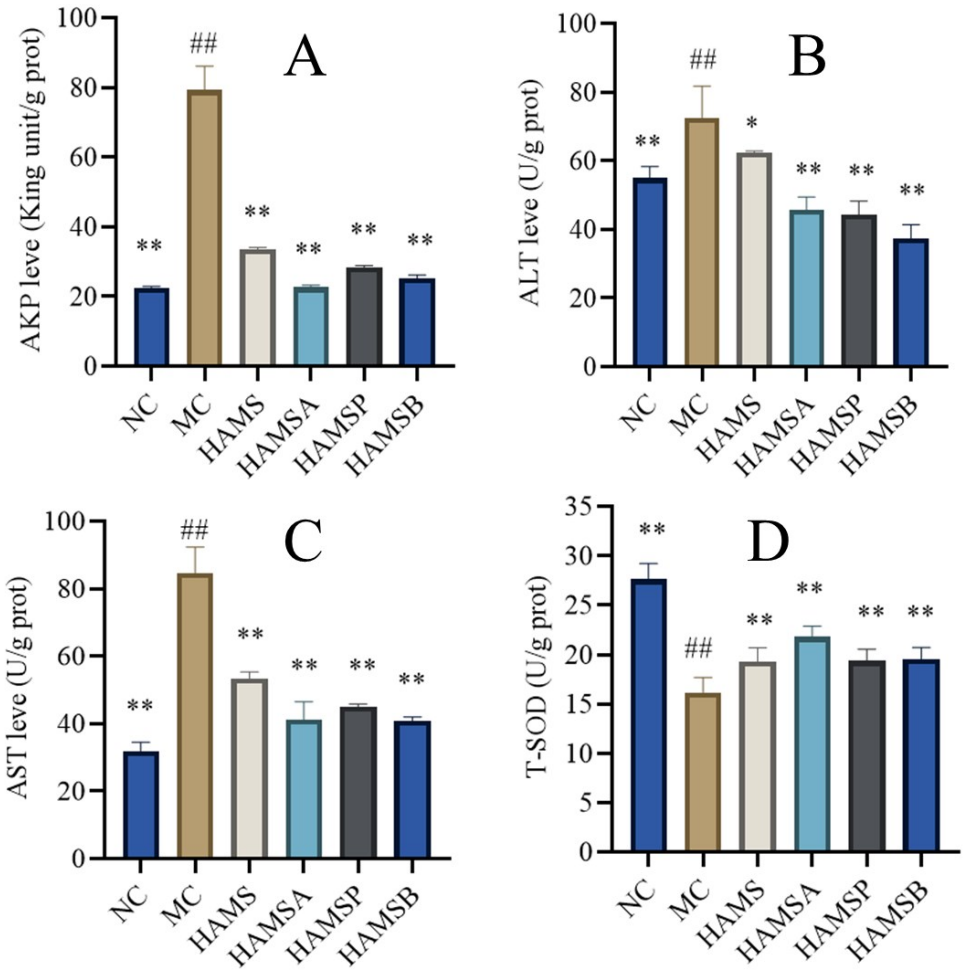

Figure A3. Liver parameters in animal model (*in vivo*, model 2). (NC, native control; MC, model group; HAMS, high-amylose maize starch; HAMSA, acetylated starch; HAMSP, propionylated starch; HAMSB, butylated starch). $^{\#}P < 0.05$, $^{\#\#}P < 0.01$, MC group vs NC group; $*P < 0.05$, $**P < 0.01$, treatment groups vs MC group.

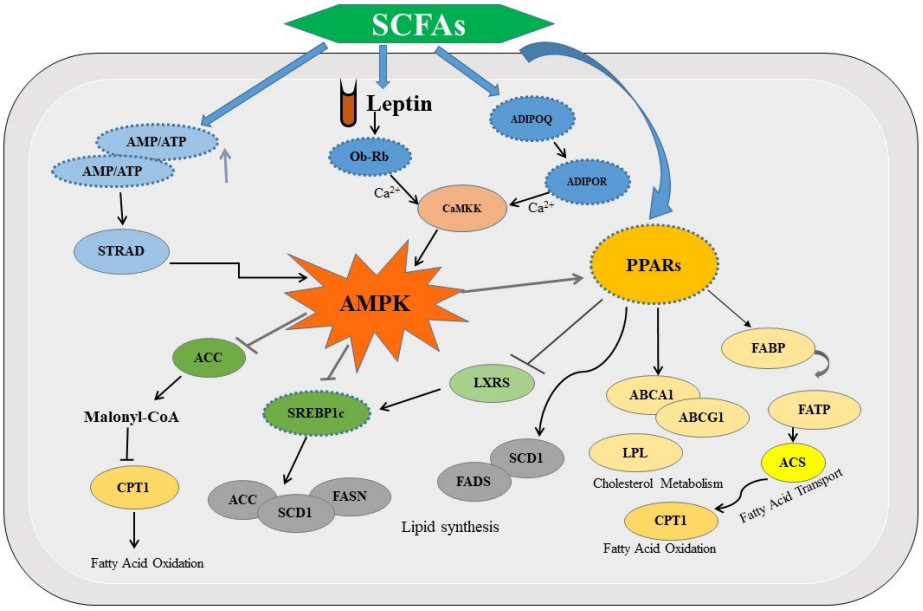

Figure A4. Cellular pathways which may be activated by SCFAs and affect fatty acid oxidation and lipid synthesis.