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Primer namesSequence (5' to 3')PPARα-FGACGCTGGGTCCTCTGGTTPPARα-RTCAGTCTTGGCTCGCCTCTAPPAR γ -FGCCTCCCTGATGAATAAAGATGPPAR γ -RCGACTGGGACTTTTCTGCTAATSREBP1-FCCTGGAGCGAGCATTGAACTSREBP1-RCAGCGTCAGAACAGCTATTAGCCPT1-FTCGTGGTGGTGGGTGGATTCPT1-RAGCACCTTCAGCGAGTAGCGACC-1-FTCTGCTCATGTTCCTTGCCCSCD1-FTCGTCAGGAACCTTCTTGAGATSCD1-RGTGATGGTAGTTGTGGAAGCCFAS-FTACAATGGCACCTTGAACCTFAS-RTTCGCCAAATACGCTCCATGGβ-Actin-FCGTTGACATCCGTAAAGACCTCβ-Actin-RTAGGAGCCAGGGCAGTAATCT					
PPARα-F GACGCTGGGTCCTCTGGTT PPARα-R TCAGTCTTGGCTCGCCTCA PPARγ-F GCCTCCCTGATGAATAAAGATG PPARγ-R CGACTGGGACTTTTCTGCTAAT SREBP1-F CCTGGAGCGAGCATTGAACT SREBP1-R CAGCGTCAGAACAGCTATTTAGC CPT1-F TCGTGGTGGTGGGTGTGATT CPT1-R AGCACCTTCAGCGAGTAGCG ACC-1-F TCTGCTCATGTTCCTTGCCC SCD1-F TCGTCAGCACCTTCTTGAGAT SCD1-R GTGATGGTAGTTGTGGAAGCC FAS-F TACAATGGCACCTGAACCT FAS-R TTCGCAAATACGCTCCATGG β-Actin-F CGTTGAGCATCCGTAAAGACCTC β-Actin-R TAGGAGCCAGGGCAGTAATCT	Primer names	Sequence (5' to 3')			
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 SCD1-F TCGTCAGCACCTTCTTGAGAT SCD1-R GTGATGGTAGTTGTGGAAGCC FAS-F TACAATGGCACCTGAACCT FAS-R TTCGCAAATACGCTCCATGG β-Actin-F CGTTGACATCCGTAAAGACCTC β-Actin-R TAGGAGCCAGGGCAGTAATCT	PPARα-F	GACGCTGGGTCCTCTGGTT			
PPARγ-F GCCTCCCTGATGAATAAAGATG PPARγ-R CGACTGGGACTTTTCTGCTAAT SREBP1-F CCTGGAGCGAGCATTGAACT SREBP1-R CAGCGTCAGAACAGCTATTTAGC CPT1-F TCGTGGTGGTGGTGTGATT CPT1-R AGCACCTTCAGCGAGTAGCG ACC-1-F TCTGCTCATGTTCCTTGCCC SCD1-F TCGTCAGCACCTTCTTGAGAT SCD1-R GTGATGGTAGTTGTGGAAGCC FAS-F TACAATGGCACCCTGAACCT FAS-R TTCGCAAATACGCTCCATGG β-Actin-F CGTTGACATCCGTAAGACCTC β-Actin-R TAGGAGCCAGGGCAGTAATCT	PPARa-R	TCAGTCTTGGCTCGCCTCTA			
РРАR ₇ -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 CGTTGACAGGGCAGTAATCT	PPAR _γ -F	GCCTCCCTGATGAATAAAGATG			
SREBP1-F CCTGGAGCGAGCATTGAACT SREBP1-R CAGCGTCAGAACAGCTATTTAGC CPT1-F TCGTGGTGGGTGGGTGTGATT CPT1-R AGCACCTTCAGCGAGTAGCG ACC-1-F TCTGCTCATGTTCCTTGCCC ACC-1-R GCTTCTTCTCTGTTTTCTCCCC SCD1-F TCGTCAGCACCTTCTGAGAT SCD1-R GTGATGGTAGTTGTGGAAGCC FAS-F TACAATGGCACCTGAACCT FAS-R TTCGCAAATACGCTCCATGG β-Actin-F CGTTGACATCCGTAAAGACCTC β-Actin-R TAGGAGCCAGGGCAGTAATCT	PPARy-R	CGACTGGGACTTTTCTGCTAAT			
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	SREBP1-F	CCTGGAGCGAGCATTGAACT			
CPT1-FTCGTGGTGGTGGGTGTGATTCPT1-RAGCACCTTCAGCGAGTAGCGACC-1-FTCTGCTCATGTTCCTTGCCCACC-1-RGCTTCTTCTCGTTTTCTCCCCSCD1-FTCGTCAGCACCTTCTTGAGATSCD1-RGTGATGGTAGTTGTGGAAGCCFAS-FTACAATGGCACCCTGAACCTFAS-RTTCGCAAATACGCTCCATGGβ-Actin-FCGTTGACATCCGTAAAGACCTCβ-Actin-RTAGGAGCCAGGGCAGTAATCT	SREBP1-R	CAGCGTCAGAACAGCTATTTAGC			
CPT1-RAGCACCTTCAGCGAGTAGCGACC-1-FTCTGCTCATGTTCCTTGCCCACC-1-RGCTTCTTCTGTTTTCTCCCCSCD1-FTCGTCAGCACCTTCTTGAGATSCD1-RGTGATGGTAGTTGTGGAAGCCFAS-FTACAATGGCACCCTGAACCTFAS-RTTCGCAAATACGCTCCATGGβ-Actin-FCGTTGACATCCGTAAAGACCTCβ-Actin-RTAGGAGCCAGGGCAGTAATCT	CPT1-F	TCGTGGTGGTGGGTGTGATT			
ACC-1-FTCTGCTCATGTTCCTTGCCCACC-1-RGCTTCTTCTCTGTTTTCTCCCCSCD1-FTCGTCAGCACCTTCTTGAGATSCD1-RGTGATGGTAGTTGTGGAAGCCFAS-FTACAATGGCACCCTGAACCTFAS-RTTCGCAAATACGCTCCATGGβ-Actin-FCGTTGACATCCGTAAAGACCTCβ-Actin-RTAGGAGCCAGGGCAGTAATCT	CPT1-R	AGCACCTTCAGCGAGTAGCG			
ACC-1-RGCTTCTTCTGTTTTCTCCCCSCD1-FTCGTCAGCACCTTCTTGAGATSCD1-RGTGATGGTAGTTGTGGAAGCCFAS-FTACAATGGCACCCTGAACCTFAS-RTTCGCAAATACGCTCCATGGβ-Actin-FCGTTGACATCCGTAAAGACCTCβ-Actin-RTAGGAGCCAGGGCAGTAATCT	ACC-1-F	TCTGCTCATGTTCCTTGCCC			
SCD1-FTCGTCAGCACCTTCTTGAGATSCD1-RGTGATGGTAGTTGTGGAAGCCFAS-FTACAATGGCACCCTGAACCTFAS-RTTCGCAAATACGCTCCATGGβ-Actin-FCGTTGACATCCGTAAAGACCTCβ-Actin-RTAGGAGCCAGGGCAGTAATCT	ACC-1-R	GCTTCTTCTCTGTTTTCTCCCC			
SCD1-RGTGATGGTAGTTGTGGAAGCCFAS-FTACAATGGCACCCTGAACCTFAS-RTTCGCAAATACGCTCCATGGβ-Actin-FCGTTGACATCCGTAAAGACCTCβ-Actin-RTAGGAGCCAGGGCAGTAATCT	SCD1-F	TCGTCAGCACCTTCTTGAGAT			
FAS-FTACAATGGCACCCTGAACCTFAS-RTTCGCAAATACGCTCCATGGβ-Actin-FCGTTGACATCCGTAAAGACCTCβ-Actin-RTAGGAGCCAGGGCAGTAATCT	SCD1-R	GTGATGGTAGTTGTGGAAGCC			
FAS-RTTCGCAAATACGCTCCATGGβ-Actin-FCGTTGACATCCGTAAAGACCTCβ-Actin-RTAGGAGCCAGGGCAGTAATCT	FAS-F	TACAATGGCACCCTGAACCT			
β-Actin-FCGTTGACATCCGTAAAGACCTCβ-Actin-RTAGGAGCCAGGGCAGTAATCT	FAS-R	TTCGCAAATACGCTCCATGG			
β-Actin-R TAGGAGCCAGGGCAGTAATCT	β-Actin-F	CGTTGACATCCGTAAAGACCTC			
	β-Actin-R	TAGGAGCCAGGGCAGTAATCT			

Table A1 Primers used in this study.

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Sample	Starch: anhydride	Temperature	PTSA	Acyl (%)	DS ^a	DS ^b
	(m:v)	(°C)	(g)			
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

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

^a Determined by the hydrolysis method. ^b Determined by ¹H NMR method. Results were means \pm SD (n = 3).



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