

Supporting Information

Dietary supplementation of methyl cedryl ether ameliorates adiposity in high-fat diet-fed mice

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Table S1. Primer sequences used for RT-qPCR.

Type	Gene Description	Sequences (5'→3')
	Peroxisome proliferator-activated receptor $\gamma 2$ (<i>PPAR$\gamma 2$</i>)	F: TTCGGAATCAGCTCTGTGGA R: CCATTGGGTCAGCTCTTGTG
	CCAAT/enhancer binding-protein α (<i>C/EBPα</i>)	F: TCAGCTTACAACAGGCCAGG R: ACACAAGGCTAATGGTCCCC
	Fatty acid synthase (<i>FAS</i>)	F: TTGCTGGCACTACAGAATGC R: AACAGCCTCAGAGCGACAAT
	Peroxisome proliferator-activated receptor gamma coactivator 1-alpha (<i>PGC-1α</i>)	F: TAAATCTGCGGGATGATGGA R: GTTTCGTTTCGACCTGCGTAA
	Uncoupling protein 1 (<i>UCP1</i>)	F: GGTTTGCACCACACTCCTG R: ACATGGACATCGCACAGCTT
Mouse	PR domain containing 16 (<i>PRDM16</i>)	F: CCACCAGCGAGGACTTCAC R: GGAGGACTCTCGTAGCTCGAA
	Cytochrome c (<i>Cytc</i>)	F: ACACTGTGGAAAAGGGAGGC R: GCACTGGTTAACCCAAGCAA
	Cytochrome c oxidase subunit 4 (<i>COX4</i>)	F: GTACCGCATCCAGTTTAACGA R: CCATACACATAGCTCTTCTCCCA
	Cell death activator CIDE-A (<i>Cidea</i>)	F: GGAATCTGCTGAGGTTTATG R: ATCCCACAGCCTATAACAGA
	3-hydroxy-3-methylglutaryl-Coenzyme synthase 1 (<i>Hmgcs1</i>)	A F: GCCGTGAACTGGGTCGAA R: GCATATATAGCAATGTCTCCTGCAA
	stearoyl-Coenzyme A desaturase 2 (<i>Scd2</i>)	F: AGTATTGCCACCCAGATGCT R: GTGGGGCACGAACCTTTACT

cytochrome P450 family 4 subfamily A	F: CCACTCATTCCCTGCCCTTC
polypeptide 12B (<i>Cyp4a12b</i>)	R: TCAGCTCATTTCATCGCAAAC
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acetyl-Coenzyme A acyltransferase 1B	F: ATGGGAATATTTCTTCCCGC
(<i>Acaa1b</i>)	R: ATTAAAGTGCTGTGACACAC
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solute carrier family 27 member 1 (<i>Slc27a1</i>)	F: AGCCTGGTCAAGTTCTGTTCTGGA
	R: AGAAGAGTCGATCATCCATGCCCT
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acyl-CoA synthetase long-chain family	F: CAGAGGAACTCAACTACTGGACC
member 6 (<i>Acs16</i>)	R: CCAATGTCTCCAGTGTGAAGCC
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acyl-CoA synthetase bubblegum family	F: ACTCGCAAACCAGCTCCTT
member 1 (<i>Acsbg1</i>)	R: CCGGGTTGTCCATAGTGCTT
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acyl-CoA synthetase bubblegum family	F: ATGCCTCCAACAGATCAGCC
member 2 (<i>Acsbg2</i>)	R: TGTTTTGGGCTCTGGGTGTT
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acyl-CoA synthetase bubblegum family	F: AACCCGTATCCCATCGAGGA
member 3 (<i>Acsbg3</i>)	R: CTTCGAAGCTTCCGACAGCA
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Glyceraldehyde-3-phosphate dehydrogenase	F: GTGATGGCATGGACTGTGGT
(<i>GAPDH</i>)	R: GGAGCCAAAAGGGTCATCAT

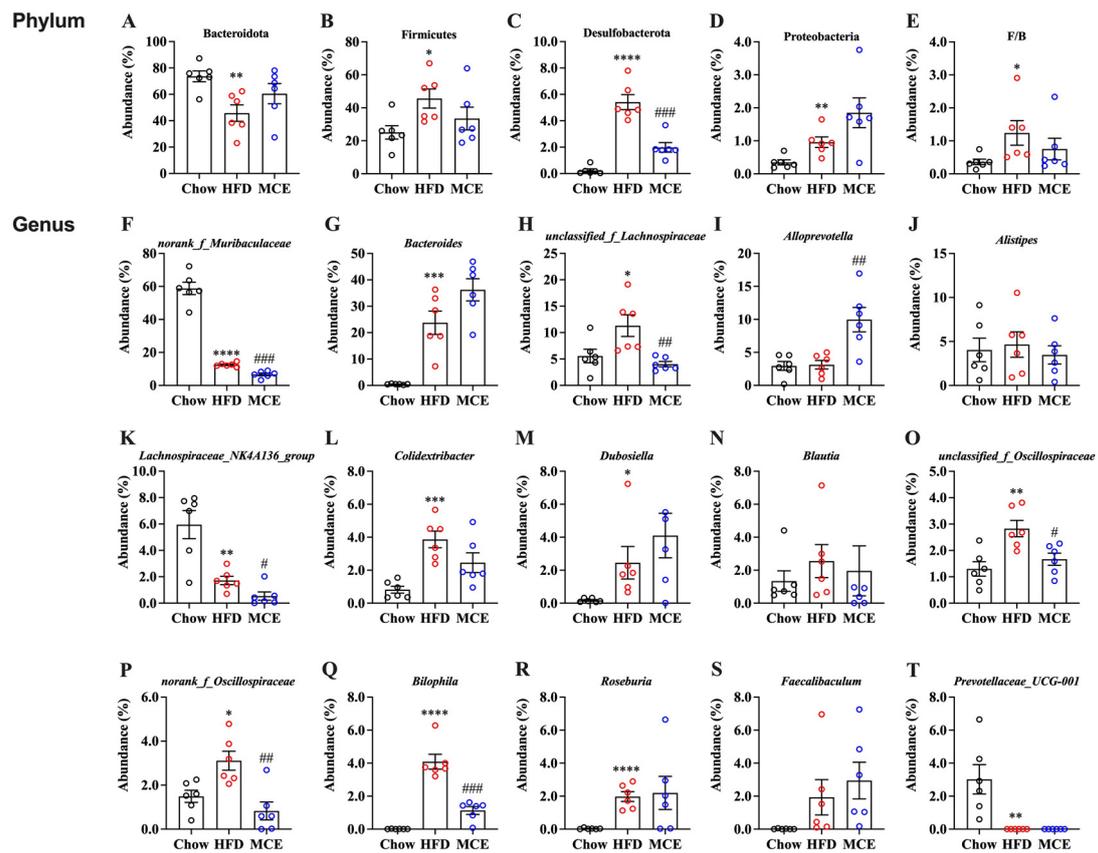


Figure S1. The relative abundance of gut microbiota at phylum (A-E) and genus (F-T) levels. * $p < 0.05$ versus chow group, ** $p < 0.01$ versus chow group, *** $p < 0.001$ versus chow group, **** $p < 0.0001$ versus chow group; # $p < 0.05$ versus HFD group, ## $p < 0.01$ versus HFD group, ### $p < 0.001$ versus HFD group.