

Table S1. Primers of RT-qPCR validation.

Gene name	Gene symbol	Primers	Primer sequences (5'-3')	TM/°C	Gene ID
<i>fatty acid synthase</i>	<i>FAS</i>	Forward	TCCTTCTTCAGCGTCTCT	53.0	Cluster-67591.17008
		Reverse	CCATACTTCTTCACTCTCACT		
<i>acyl-coenzyme A thioesterase</i>	<i>ACOT</i>	Forward	TCCACTGTCTGTCTTCAT	56.8	Cluster-67591.33303
		Reverse	CGTCAACCTCACCATTCC		
<i>acetyl CoA carboxylase</i>	<i>ACC</i>	Forward	TGGCAGCATTGGAGGTGTA	60.8	Cluster-67591.43403
		Reverse	GATGAGATGATGGCAGCAGAA		
<i>mitochondrial enoyl-[acyl-carrier protein] reductase</i>	<i>MECR</i>	Forward	GGCACTGGAGATGTTGTT	53.0	Cluster-67591.46559
		Reverse	CTTCTGTTACCACCACTGT		
<i>3-oxoacyl-[acyl-carrier-protein] synthase II</i>	<i>FabF</i>	Forward	GCTGGTATGGTAGTCTTGG	59.1	Cluster-67591.6543
		Reverse	GAGGTGCTGTGTAATGGAA		
<i>malonyl-CoA-acyl carrier protein transacylase</i>	<i>FabD</i>	Forward	GCATTGGTGTAGCAGGTT	63.0	Cluster-67591.23513
		Reverse	GTCTTGAATCTGGTCCGTAT		
<i>long-chain fatty acid CoA ligase</i>	<i>ACSL</i>	Forward	TGCGGATTACTCAGATGTG	53.0	Cluster-67591.28717
		Reverse	TGTAGATGCGGTCAAGGA		
<i>carnitine O-palmitoyltransferase 1</i>	<i>CPT1</i>	Forward	TTCCTTGGTGCTCTAACAG	56.8	Cluster-67591.38584
		Reverse	TGCCTTCTTCATCGTATCC		
<i>carnitine O-palmitoyltransferase 2</i>	<i>CPT2</i>	Forward	GTTGGAGACTGTAGCCTTC	59.3	Cluster-67591.35527
		Reverse	ACGGTGTGGTGGATATGA		
<i>enoyl-CoA hydratase</i>	<i>echA</i>	Forward	GGCTCTCAATGCTCTATGT	59.3	Cluster-67591.24041
		Reverse	CCTGCTGTGCTGTAATCA		
18s	18s	Forward	TATACGCTAGTGGAGCTGGAA	/	/
		Reverse	GGGGAGGTAGTGACGAAAAAT		