SUPPLEMENTARY DATA

Supplementary Table 1. mRNA Expressions of Key Lipid Metabolism Genes in Human Skeletal Muscle Tissue and Myotubes.

Skeletal Muscle Tissue			
Gene	Control	T2D	p-value
ATGL	1.35 ± 0.23	1.42 ± 0.21	0.8381
HSL	3.04 ± 0.59	3.54 ± 0.54	0.5515
DGAT1	1.52 ± 0.26	1.48 ± 0.23	0.9258
SCD1	0.02 ±0.01	0.03 ± 0.01	0.5615
PLIN5	3.88 ± 0.65	4.63 ± 0.57	0.4186
PGC1α	6.08 v 0.55	5.15 ± 0.51	0.2486
PPARδ	0.88 ± 0.10	0.83 ± 0.10	0.7169
CPT1β	4.11 ± 0.67	4.49 ± 0.61	0.6805
Myotubes			
Gene	Control	T2D	p-value
ATGL	0.75 ± 0.17	0.70 ± 0.17	0.8537
HSL	0.35 ± 0.07	0.28 ± 0.06	0.4988
DGAT1	0.90 ± 0.17	0.77 ± 0.16	0.5878
SCD1	1.03 ± 0.37	0.88 ± 0.37	0.7867
PLIN5	-	-	-
PGC1α	0.05 ± 0.04	0.03 ± 0.03	0.6978
PPARδ	1.14 ± 0.24	0.96 ± 0.23	0.6093
CPT1β	0.04 ± 0.01	0.04 ± 0.01	0.9021

Data are presented as mean ± SEM. N=6 per group. T2D, Type 2 Diabetes; ATGL, adipose triglyceride lipase; HSL, hormone sensitive lipase; DGAT1, diacylglycerol acyl-transferase 1. SCD1, stearoyl-CoA desaturase 1; PLIN5, perilipin 5; PGC-1α, peroxisome proliferator activated receptor coactivator-1 alpha; PPARδ, peroxisome proliferator activated receptor delta; CPT1β, carnitine palmitoyltransferase 1 beta. All data are normalized to an internal control gene, RPL26, ribosomal protein L26. "-" means that the mRNA expression was not detectable.

SUPPLEMENTARY DATA

Supplementary Table 2. Associations of PGC1α mRNA Expressions with Key Lipid Metabolism Endpoints in Human Skeletal Muscle Tissue and Myotubes.

mRNA	Lipid Metabolism Endpoint	*r*	p-value
PGC1α (myotubes)	PA incorporation into TAG (myotubes)	0.5818	0.0604
PGC1α (myotubes)	OA incorporation into TAG (myotubes)	0.6091	0.0467
PGC1α (myotubes)	DGAT activity (myotubes)	0.6573	0.0202
PGC1α (muscle tissue)	PLIN5 mRNA (muscle tissue)	0.7000	0.0165

Data are simple correlations among all 12 participants (Control and T2D). T2D, Type 2 Diabetes; PGC-1α, peroxisome proliferator activated receptor coactivator-1 α; DGAT1, diacylglycerol acyl-transferase 1. PLIN5, perlipin 5; All mRNA data are normalized to an internal control gene, RPL26, ribosomal protein L26.

SUPPLEMENTARY DATA

Supplementary Table 3. Oligonucleotide sequences for primer/probe sets used for qRT-PCR.

Gene	Accession number	Forward primer	Probe	Reverse primer
ATGL	NM_020376.2	CCACGGCGCTGGTCA	TTGGCACCAGCCTCACCCAGG	GGGCCTCTTTAGATACCTCAATGA
HSL	NM_005357.2	ACGCTGCATAAGGGATGCTT	AGTTCACGCCTGCCATCCGGC	CCTGTCTCGTTGCGTTTGTAGT
DGAT1	NM_012079	CGTGAGCTACCCGGACAATC	ACCTACCGCGATCTCTACTACTTCCTCTTCGC	AAAGTTGAGCTCGTAGCACAAGG
SCD1	NM_005063	TGGCATTCCAGAATGATGTCTATG	CGTGACCACCGTGCCCACCACA	GGAATTATGAGGATCAGCATGTGT
PLIN5	NM_001013706.2	GAGCCATGCTGTGGATGTTGTA	TGGATCACTTCCTGCCCATGACGG	CAGTGCCGCGAGCTCTTC
PGC1α	NM_013261.3	TGCTGAAGAGGGAAAGTGAGCGATTAGTTGA	CATGTAGAATTGGCAGGTGGAA	AGGTGAAAGTGTAATACTGTTGGTTGA
PPARδ	NM_006238.3	TCTACAATGCCTACCTGAAAAACTTC	ACATGACCAAAAAGAAGGCCCGCAG	GGCTTTGCCGGTGAGGAT
CPT1β	NM_152247.1	CCAGAGCAGCACCCCAAT	CATCTGCTACAGGGCCAAAGCCACCT	CTGCAATCATGTAGGAAACTCCATAG

For all gene expression assays the ribosomal protein L26 gene, RPL26, was used as the internal control. ATGL, adipose triglyceride lipase; HSL, hormone sensitive lipase; DGAT1, diacylglycerol acyl-transferase 1. SCD1, stearoyl-CoA desaturase 1; PLIN5, perlipin 5; PGC-1α, peroxisome proliferator activated receptor coactivator-1 alpha; PPARδ, peroxisome proliferator activated receptor delta; CPT1β, carnitine palmitoyltransferase 1 beta.

SUPPLEMENTARY DATA

Supplementary Figure 1. Correlation of the ratio ^{14}C-palmitate oxidation to CO_2:ASMs with (A) the VO_2max and (B) the fasting plasma glucose levels in obese individuals with T2D and BMI-matched controls.