

Supplementary Table S1

TaqMan assays for the selected genes validated with qRT-PCR.

Tissue	Gene	TaqMan assay
Adipose tissue		
	<i>ACADS</i>	Hs00916595_g1
	<i>ADIPOQ</i>	Hs00605917_m1
	<i>ATP5B</i>	Hs00969569_m1
	<i>ATP5H</i>	Hs01046889_gH
	<i>CD68</i>	Hs02836816_g1
	<i>COL5A1</i>	Hs00609140_m1
	<i>COL6A2</i>	Hs00242484_m1
	<i>COX5A</i>	Hs01561737_g1
	<i>FH</i>	Hs00895616_m1
	<i>HADH</i>	Hs00997450_m1
	<i>LAMA2</i>	Hs01124081_m1
	<i>NDUFB8</i>	Hs00428204_m1
	<i>PPARGC1A</i>	Hs01016719_m1
	<i>SDHD</i>	Hs00829723_g1
	<i>UQCRC2</i>	Hs00996395_m1
Reference gene	<i>ACTB</i>	Hs01060665_g1
Skeletal muscle		
	<i>ACADVL</i>	Hs00817723_g1
	<i>ACVR2B</i>	Hs00609603_m1
	<i>ADIPOR1</i>	Hs00360422_m1
	<i>ADIPOR2</i>	Hs00226105_m1
	<i>ATP5A1</i>	Hs00900735_m1
	<i>COX5B</i>	Hs00426948_m1
	<i>CPT1B</i>	Hs00992664_m1
	<i>CS</i>	Hs02574374_s1
	<i>ETFA</i>	Hs00164511_m1
	<i>FBXO32</i>	Hs01041408_m1
	<i>FOXO3</i>	Hs00818121_m1
	<i>HADH</i>	Hs00193428_m1
	<i>MEF2C</i>	Hs00231149_m1
	<i>MSTN</i>	Hs00976237_m1
	<i>MYF5</i>	Hs00271574_m1
	<i>MYF6</i>	Hs00231165_m1
	<i>MYH1</i>	Hs00428600_m1
	<i>MYH2</i>	Hs00430042_m1
	<i>MYH7</i>	Hs01110632_m1
	<i>MYOD1</i>	Hs00159528_m1

	<i>MYOG</i>	Hs01072232_m1
	<i>MYOZ1</i>	Hs00222007_m1
	<i>NDUFS1</i>	Hs00192297_m1
	<i>PDK4</i>	Hs01037712_m1
	<i>PGAM2</i>	Hs00165474_m1
	<i>PPARGC1A</i>	Hs01016719_m1
	<i>PPP3CA</i>	Hs00174223_m1
	<i>PPP3CB</i>	Hs00236113_m1
	<i>PRKAA2</i>	Hs00178903_m1
	<i>PRKAG3</i>	Hs00179660_m1
	<i>PSMA2</i>	Hs00746751_s1
	<i>PSMB3</i>	Hs00600803_m1
	<i>PSMB6</i>	Hs01572709_g1
	<i>PSMD1</i>	Hs00160631_m1
	<i>SDHA</i>	Hs00188166_m1
	<i>SMAD7</i>	Hs00998193_m1
	<i>TRIM63</i>	Hs00822397_m1
	<i>UQCRC1</i>	Hs00163415_m1
Reference gene	<i>IPO8</i>	Hs00183533_m1
Reference gene	<i>POLR2A</i>	Hs00172187_m1
Reference gene	<i>PPIA</i>	Hs00172187_m1

Supplementary Table S2

Anthropometric characteristics of males and females

	Obese controls	Type 2 diabetes	P-value
<i>Males (n)</i>	12	10	
BMI (kg/m ²)	30.5 ± 1.0	29.7 ± 1.4	0.66
Fat mass (kg)	29.9 ± 2.1	27.8 ± 2.7	0.55
Fat free mass (kg)	67.2 ± 2.5***	66.4 ± 2.2***	0.80
Percent fat mass (%)	30.7 ± 1.7***	28.9 ± 1.7***	0.47
Waist circumference (cm)	107 ± 3	109 ± 4	0.64
Hip circumference (cm)	106 ± 1	107 ± 3	0.84
Waist-hip ratio	1.01 ± 0.02	1.02 ± 0.02*	0.65
<i>Females (n)</i>	7	7	
BMI (kg/m ²)	30.6 ± 1.0	31.0 ± 1.8	0.85
Fat mass (kg)	34.0 ± 3.8	35.7 ± 3.6	0.76
Fat free mass (kg)	46.4 ± 1.6	47.4 ± 1.6	0.67
Percent fat mass (%)	41.6 ± 2.2	42.3 ± 1.9	0.82
Waist circumference (cm)	99 ± 4	97 ± 5	0.81
Hip circumference (cm)	105 ± 2	108 ± 8	0.77
Waist-hip ratio	0.94 ± 0.03	0.91 ± 0.04	0.68

Study participants were studied after an overnight fast. Data represent means ± SEM. *P<0.05, **P<0.01 and ***P<0.001 vs. females.

Supplementary Table S3

mRNA expression of genes involved in regulation of muscle mass and substrate metabolism

Gene	Obese controls	Type 2 diabetes	P-value
<i>FOXO3</i>	1.00 ± 0.09	0.77 ± 0.07	0.07
<i>MSTN</i>	1.00 ± 0.17	1.83 ± 0.20	0.005
<i>ACVR2B</i>	1.00 ± 0.06	1.19 ± 0.07	0.05
<i>SMAD7</i>	1.00 ± 0.08	0.95 ± 0.06	0.60
<i>MYOD1</i>	1.00 ± 0.09	0.78 ± 0.05	0.06
<i>MYF5</i>	1.00 ± 0.06	1.03 ± 0.08	0.73
<i>MYF6</i>	1.00 ± 0.08	1.08 ± 0.09	0.54
<i>MYOG</i>	1.00 ± 0.07	0.87 ± 0.05	0.12
<i>MYH1</i>	1.00 ± 0.33	1.82 ± 0.26	0.06
<i>MYH2</i>	1.00 ± 0.10	0.97 ± 0.07	0.82
<i>MYH7</i>	1.00 ± 0.11	0.96 ± 0.14	0.83
<i>MYOZ1</i>	1.00 ± 0.05	1.02 ± 0.03	0.72
<i>MEF2C</i>	1.00 ± 0.06	0.99 ± 0.04	0.87
<i>PPP3CA</i>	1.00 ± 0.04	1.26 ± 0.05	0.0004
<i>PPP3CB</i>	1.00 ± 0.04	1.09 ± 0.04	0.13
<i>NDUFS1</i>	1.00 ± 0.08	0.91 ± 0.04	0.32
<i>SDHA</i>	1.00 ± 0.07	0.92 ± 0.05	0.35
<i>UQCRC1</i>	1.00 ± 0.06	0.92 ± 0.04	0.25
<i>COX5B</i>	1.00 ± 0.08	0.93 ± 0.03	0.45
<i>ATP5A1</i>	1.00 ± 0.07	0.94 ± 0.04	0.50
<i>CS</i>	1.00 ± 0.08	1.06 ± 0.04	0.54
<i>CPT1B</i>	1.00 ± 0.09	0.95 ± 0.05	0.59
<i>ETFA</i>	1.00 ± 0.07	1.02 ± 0.03	0.77
<i>ACACDVL</i>	1.00 ± 0.09	0.96 ± 0.08	0.71
<i>HADH</i>	1.00 ± 0.05	1.13 ± 0.05	0.08
<i>PGAM2</i>	1.00 ± 0.07	1.00 ± 0.05	0.98
<i>ADIPOR1</i>	1.00 ± 0.04	0.98 ± 0.03	0.73
<i>ADIPOR2</i>	1.00 ± 0.06	1.10 ± 0.05	0.36
<i>PPKAA2</i>	1.00 ± 0.05	0.99 ± 0.05	0.90
<i>PRKAG3</i>	1.00 ± 0.14	1.39 ± 0.13	0.06
<i>PDK4</i>	1.00 ± 0.24	0.88 ± 0.27	0.76
<i>PPARGC1A</i>	1.00 ± 0.09	0.89 ± 0.05	0.28

Muscle transcript levels by qRT-PCR of genes involved in the regulation of muscle mass and substrate metabolism. Data represent means ± SEM.

Supplementary Table S4

Expression of pro-inflammatory adipokines and putative myokines

Affy ID	Gene Symbol	Protein Name	Fold change	P-value	FDR
<i>Pro-inflammatory adipokines</i>					
209496_at	<i>RARRES2</i>	Chemerin	-1.21	0.02	0.44
203381_s_at	<i>APOE</i>	Apolipoprotein E	1.14	0.31	0.86
216598_s_at	<i>CCL2</i>	MCP-1	-1.11	0.73	0.96
220570_at	<i>RETN</i>	Resistin	1.07	0.39	0.87
205207_at	<i>IL6</i>	Interleukin 6	-1.06	0.47	0.89
203980_at	<i>FABP4</i>	Fatty acid binding protein 4	-1.06	0.00	0.17
217739_s_at	<i>PBEF1</i>	Visfatin	1.02	0.81	0.97
219140_s_at	<i>RBP4</i>	Retinol binding protein 4	-1.01	0.81	0.97
207092_at	<i>LEP</i>	Leptin	1.01	0.94	0.99
205382_s_at	<i>CFD</i>	Complement factor D (adipsin)	-1.00	0.94	0.99
<i>Putative myokines</i>					
207145_at	<i>GDF8</i>	Growth differentiation factor 8 (myostatin)	1.66	0.03	0.25
209101_at	<i>CTGF</i>	Connective tissue growth factor	-1.28	0.30	0.62
207433_at	<i>IL10</i>	Interleukin 10	-1.11	0.15	0.47
206382_s	<i>BDNF</i>	Brain-derived neurotrophic factor	-1.07	0.61	0.82
221576_at	<i>GDF15</i>	Growth differentiation factor 15	-1.07	0.31	0.63
204421_s_at	<i>FGF2</i>	Fibroblast growth factor 2 (basic)	-1.06	0.46	0.72
208782_at	<i>FSTL1</i>	Follistatin-like 1	-1.06	0.58	0.80
221009_s_at	<i>ANGPTL4</i>	Angiopoietin-like 4	-1.06	0.34	0.65
205207_at	<i>IL6</i>	Interleukin 6	1.05	0.47	0.73
221433_at	<i>FGF21</i>	Fibroblast growth factor 21	-1.05	0.39	0.68
205266_at	<i>LIF</i>	Leukemia inhibitory factor	1.04	0.53	0.77
201893_x_at	<i>DCN</i>	Decorin	1.04	0.48	0.74
205992_s_at	<i>IL15</i>	Interleukin 15	1.04	0.50	0.75
200665_s_at	<i>SPARC</i>	Secreted protein, acidic, cysteine-rich (osteonectin)	1.03	0.83	0.93
216546_s_at	<i>CHI3L1</i>	Chitinase 3-like 1 (YKL40)	-1.01	0.93	0.97

The microarray data set was explored to identify possible changes in expression of pro-inflammatory adipokines in SAT and putative myokines in muscle of patients with T2D compared with overweight/obese controls. In this table the probe sets with the highest expression are shown. P-values are unadjusted. An FDR<0.1 is considered significant.