

Supplementary Table 3

**Changes in genes expression measured by RT-quantitative PCR in skeletal muscle and adipose tissue during the somatostatin control study.**

The fold changes in mRNA levels during the somatostatin control study were measured on tissue samples from 4 subjects for skeletal muscle and adipose tissue. RT-qPCR was performed as indicated under “research design and methods”. Values were corrected by the mRNA level of hypoxanthine phosphoribosyl transferase (HPRT) used as a house-keeping gene.

\*p<0.05 after vs. before hyperglycemic clamp or after vs. before somatostatin infusion, using the Student’s paired t test. ND: not detectable in a reliable manner using RT-qPCR.

Transcript Symbol	Unigene Cluster	Skeletal Muscle		Adipose Tissue	
		Hyperglycemic clamp	Somatostatin control study	Hyperglycemic clamp	Somatostatin control study
<b>AGTRL1</b>	Hs.438311	1.29 ± 0.10	-1.57 ± 0.05*	-1.33 ± 0.13*	-1.15 ± 0.16
<b>G0S2</b>	Hs.432132	2.01 ± 0.48*	-1.51 ± 0.19	1.12 ± 0.16	-1.08 ± 0.29
<b>GSTP1</b>	Hs.523836	-1.45 ± 0.08 *	-1.24 ± 0.24	-1.41 ± 0.08*	1.44 ± 0.34
<b>HK2</b>	Hs.591588	1.51 ± 0.20*	-1.19 ± 0.15	1.52 ± 0.24*	1.12 ± 0.32
<b>JAM2</b>	Hs.517227	-1.53 ± 0.17*	-1.41 ± 0.10	-1.02 ± 0.09	-1.36 ± 0.26
<b>MT1X</b>	Hs.374950	1.54 ± 0.13*	1.72 ± 0.35	1.53 ± 0.14*	1.36 ± 0.22
<b>MT2A</b>	Hs.534330	1.41 ± 0.14*	1.26 ± 0.14	1.37 ± 0.12*	1.20 ± 0.15
<b>MT1F</b>	Hs.513626	ND	ND	2.34 ± 0.46	1.07 ± 0.27
<b>PDK4</b>	Hs.8364	-4.09 ± 0.99*	5.90 ± 1.41*	-2.49 ± 0.36*	2.20 ± 0.49*
<b>PER1</b>	Hs.445534	-1.75 ± 0.20*	-1.15 ± 0.45	-1.55 ± 0.17*	1.01 ± 0.30
<b>TNFSF10</b>	Hs.478275	1.47 ± 0.21 *	1.15 ± 0.18	1.76 ± 0.23*	1.57 ± 0.33