

Figure S1.

Independent validation of microarray data from sedentary individuals (SED, n = 8, open circles) for exercise-responsiveness of 15 selected target genes in a second cohort of untrained individuals (SED-T, n = 10, filled circles) using qPCR. Box plots represent Log2 transformed fold changes in mRNA levels from *vastus lateralis* muscle at 3 hours (+3h) after intense cycling exercise in comparison to baseline levels at rest (+3h/rest).

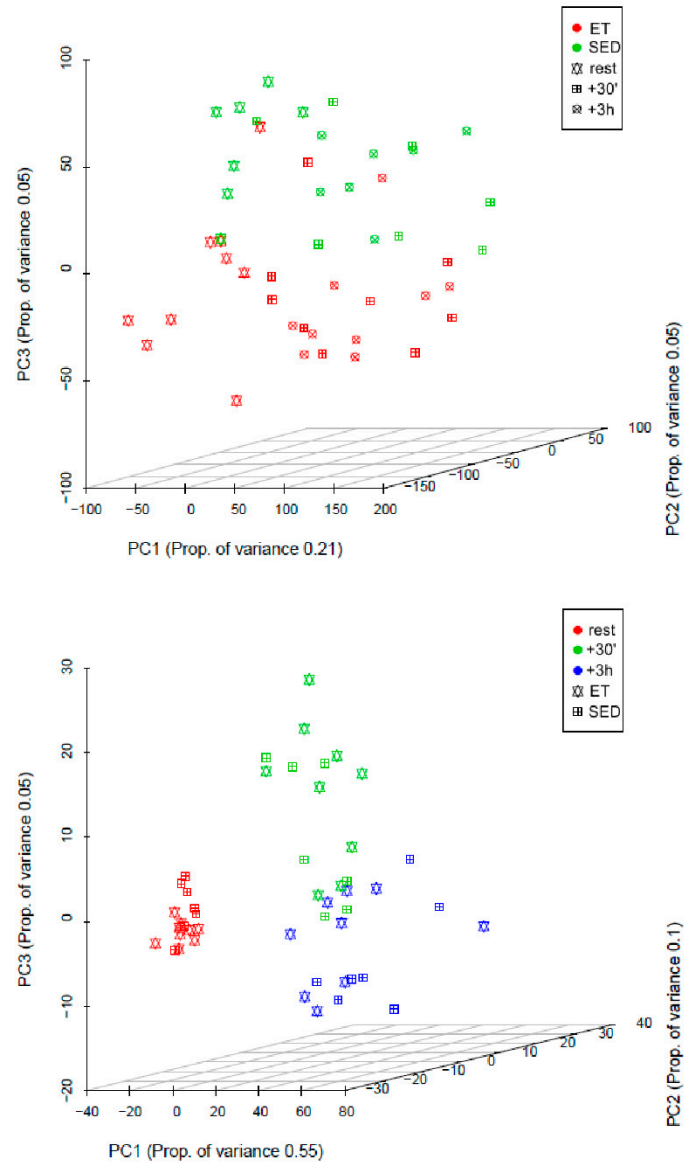


Figure S2.

Principal component analysis (PCA) scatter plots of gene expression profiles of *vastus lateralis* muscle samples from endurance-trained (ET) and sedentary (SED) individuals at baseline (rest), at 30 min (+30') and at 3 hours (+3h) after intense cycling exercise.

Table S2 (next page)

List of genes among differentially expressed genes at rest (fold difference ≥ 1.5 , $P < 0.05$) between endurance-trained (ET) and sedentary (SED) individuals in *vastus lateralis* muscle that were significantly affected by acute exercise in at least one group at any post-exercise time point (fold change ≥ 2 , $P < 0.05$). Mean fold differences in baseline expression levels (rest) are given in the comparison ET/SED with genes that showed relative higher expression levels in the ET group (ET \uparrow), and in the comparison SED/ET when baseline levels were higher in the SED group (SED \uparrow). Gene expression changes in response to acute exercise are given as mean fold changes compared to baseline expression at 30 min (+30') after completion of exercise, and after a recovery period of 3 hours (+3h). Positive fold change values indicate increased expression after exercise (\uparrow) while negative fold change values (\downarrow) indicate decreased expression in the respective group.

Gene symbol	Gene title	Baseline expression pattern			Exercise response pattern					
		Rest			+30'			+3h		
		Up-regulated in	Fold difference	P-value	Affected in	Fold change vs rest	P-value	Affected in	Fold change vs rest	P-value
<i>PFKFB2</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	ET↑	2.7	7.3E-05				ET↑ SED↑	2.0 3.5	1.4E-05 1.4E-03
<i>SLC38A1</i>	Sodium-coupled neutral amino acid transporter 1	ET↑	1.6	1.3E-02				ET↑ SED↑	2.6 2.8	1.3E-04 1.0E-03
<i>PPP1R1C</i>	Protein phosphatase 1, regulatory (inhibitor) subunit 1C	ET↑	1.7	4.5E-02	ET↓ SED↓	-2.3 -2.1	2.0E-03 9.6E-04	ET↓	-2.3	2.5E-03
<i>CEACAM1</i>	Carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	ET↑	1.5	4.3E-03				ET↑ SED↑	2.2 2.0	3.9E-05 4.3E-06
<i>CASP4</i>	Caspase 4, apoptosis-related cysteine peptidase	ET↑	1.5	8.1E-03	ET↑ SED↑	2.7 2.3	5.6E-04 1.3E-03	ET↑ SED↑	2.9 2.0	2.4E-04 4.4E-03
<i>PIM3</i>	Pim-3 oncogene	ET↑	1.6	3.1E-04				SED↑	2.5	2.0E-08
<i>BCAR3</i>	Breast cancer anti-estrogen resistance 3	ET↑	1.9	2.0E-02				SED↑	3.0	9.9E-04
<i>AQP7</i>	Aquaporin 7	ET↑	1.8	3.2E-03	SED↓	-2.1	2.6E-02			
<i>TNFSF10</i>	Tumor necrosis factor (ligand) superfamily, member 10	ET↑	1.5	1.1E-02	ET↓	-2.4	1.5E-07			
<i>CYP4V2</i>	Cytochrome P450, family 4, subfamily V, polypeptide 2	ET↑	2.1	1.8E-02	ET↓	-2.1	1.4E-02			
<i>PAQR9</i>	Progestin and adipoQ receptor family member IX	ET↑	1.8	3.3E-02	ET↓	-2.6	1.2E-03			
<i>FILIP1L</i>	Filamin A interacting protein 1-like	SED↑	1.6	8.5E-03	ET↓ SED↓	-2.4 -3.6	1.0E-02 1.3E-02	ET↓ SED↓	-2.4 -3.6	1.0E-02 1.3E-02
<i>MSTN</i>	Myostatin	SED↑	2.6	1.4E-03	SED↓	-2.9	4.2E-03	ET↓ SED↓	-2.0 -3.1	6.8E-03 2.5E-03
<i>DNAJB4</i>	DnaJ (Hsp40) homolog, subfamily B, member 4	SED↑	1.6	6.0E-04	ET↑ SED↑	2.1 2.0	5.6E-07 4.0E-04			
<i>RND3</i>	Rho family GTPase 3	SED↑	1.7	3.5E-02				ET↑ SED↑	2.3 2.1	2.6E-03 1.1E-04
<i>KY</i>	Kyphocoliosis peptidase	SED↑	1.6	5.0E-02	ET↓ SED↓	-2.0 -2.0	9.7E-07 1.7E-02	ET↓ SED↓	-2.3 -2.2	9.4E-08 1.4E-03
<i>PMP22</i>	Peripheral myelin protein 22	SED↑	1.5	2.7E-02				ET↑ SED↑	3.8 2.4	9.7E-08 9.4E-04
<i>DTNA</i>	Dystrobrevin, alpha	SED↑	1.6	1.3E-02	ET↑ SED↑	7.5 6.3	1.2E-03 3.8E-03	ET↑ SED↑	4.0 4.3	1.8E-02 1.7E-02
<i>MLF1</i>	Myeloid leukemia factor 1	SED↑	1.7	1.4E-04	SED↓	-2.2	2.3E-03			
<i>PLAGL2</i>	Pleiomorphic adenoma gene-like 2	SED↑	2.0	4.0E-05				SED↓	-2.4	5.9E-07
<i>SLC38A4</i>	Sodium-Coupled neutral amino acid transporter 4	SED↑	1.9	4.3E-04				SED↓	-2.1	4.6E-03
<i>GLRX</i>	Glutaredoxin (thioltransferase)	SED↑	1.9	4.0E-02	SED↑	2.0	3.5E-02			
<i>IRX3</i>	Iroquois homeobox 3	SED↑	2.3	8.6E-05	SED↓	-2.0	4.7E-03			
<i>ATP2B2</i>	ATPase, Ca++ transporting, plasma membrane 2	SED↑	2.2	2.1E-02	SED↓	-2.5	1.9E-02			
<i>LMOD1</i>	Leiomodin 1	SEDS↑	1.9	2.1E-02	SED↓	-2.4	8.5E-03	SED↓	-2.1	2.4E-02
<i>XPO4</i>	Exportin 4	SED↑	1.7	9.8E-03	SED↓	-2.1	1.1E-02			
<i>PRKAG3</i>	Protein kinase, AMP-activated, gamma 3 non-catalytic subunit	SED↑	2.2	2.8E-03	SED↓	-2.1	2.6E-02			
<i>ABRA</i>	Actin-binding Rho activating protein	SED↑	2.6	1.3E-06	ET↑	4.4	8.5E-07	ET↑	2.5	1.5E-05
<i>TSC22D2</i>	TSC22 domain family, member 2	SED↑	1.7	1.4E-05	ET↑	2.2	1.1E-06	ET↑	2.3	4.1E-07
<i>CHMP1B</i>	Chromatin modifying protein 1B	SED↑	1.7	4.4E-04	ET↑	2.3	1.8E-06	ET↑	2.3	1.1E-06
<i>GPD1</i>	Glycerol-3-phosphate dehydrogenase 1 (soluble)	SED↑	1.6	4.7E-02	ET↓	-2.1	3.8E-03			
<i>LITAF</i>	Lipopolysaccharide-induced TNF factor	SED↑	1.6	9.9E-03	ET↑	2.0	3.0E-04	ET↑	2.1	1.1E-04
<i>IL32</i>	Interleukin 32	SED↑	2.5	1.2E-02	ET↑	2.3	1.7E-02			
<i>PKNOX1</i>	PBX/knotted 1 homeobox 1	SED↑	1.5	1.0E-02	ET↑	2.0	3.5E-04			
<i>CHST3</i>	Carbohydrate (chondroitin 6) sulfotransferase 3	SED↑	1.7	5.0E-03	ET↑	2.1	2.7E-04			

Table S3. List of primers for qPCR analysis

Gene symbol	Gene name	Forward primer	Reverse primer	Amplicon length (bp)	Primer efficiency
ABRA	Actin Binding Rho Activating Protein	CCTTGCCCTCCAGGTAAAC	CCCTTTCAAGTTGCCCACTG	86	1.85
ACTN3	Actinin alpha 3	CGCAGGACATCAACACCAAG	CGGAGCCTCTCGTTTACCTG	106	1.90
B2M	Beta-2-Microglobulin	TTTCTGGCCTGGAGGCTATC	CGGATGGATGAAACCCAGAC	117	1.90
FBXO32	F-Box Protein 32	GACAAAGGGCAGCTGGATTG	TTATTGGCAGTGCACGGATG	149	1.90
GAPDH	Glyceraldehyde-3-Phosphate Dehydrogenase	TCAACAGCGACACCCACTCC	TGAGGTCCACCACCTGTTG	126	1.95
IL6	Interleukin 6	GCCAGAGCTGTGCAGATGAG	TGGGTCAGGGGTGTTATTG	90	1.85
IL6R	Interleukin 6 receptor	CAGCTGGGACTGTGCACTTG	AGCCTTTGTCGTAGGGATG	134	1.90
LDHA	Lactate Dehydrogenase A	GGAAAGGCTGGGAGTTCACC	TCCACTCCATACAGGCACACTG	85	1.90
LDHB	Lactate Dehydrogenase B	TCCAGATTATCCCGTGTC	CGGGCATTGAGGATACATGG	92	1.95
LPL	Lipoprotein Lipase	TTGGAGAAGCTATCCGCGTG	TCGTGGGAGCACTTCACTAGC	72	1.85
MSTN	Myostatin	ATGACGATTATCACGCTACAACG	TGGGTTTTCCATCCACTTGC	84	2.00
NR4A3	Nuclear receptor subfamily 4 group A member 3	CAAGCCTTAGCCTGCCTGTC	GTGGGCTCCAGAGCCTGTC	143	1.90
PPARGC1A	PPARG Coactivator 1 Alpha	TCCCACACAGTCGCAGTC	CCTTGGGGTCATTGGTGAC	91	1.90
RPL13A	Ribosomal Protein L13a	CTCAAGGTCGTGCTCTGAAG	GTGGCTGTCACTGCCTGGTAC	94	2.00
RPLP0	Ribosomal Protein Lateral Stalk Subunit P0	TCAACGGGTACAAACGAGTCC	CAGATGGATCAGCCAAGAAGG	96	1.95
TBP	TATA-Box Binding Protein	GATCAAACCCAGAATTGTTCTCC	AGCCATTACGTCGTCTTCCTG	143	1.90
TNFRSF12A	Tumor necrosis factor receptor superfamily member 12A	AGAGAAGTTCACCACCCCATATA	GGCAGAGACTGGCTCTAGAATG	141	1.95
TRIM63	Tripartite Motif Containing 63	GAGGATTCCCCTCGAGTGAC	CCAGGATGGCATACAACGTG	88	1.90
UCP3	Uncoupling Protein 3	TGCTGAGGTGGTGACCTACG	CAAAGTGGCAGGGGAAGTTG	83	1.95
VEGFA	Vascular Endothelial Growth Factor A	AAAACACAGACTCGCGTTGC	ATCTGGTTCCCGAAACCTG	126	1.90
ZFP36	Zinc finger protein 36	ACTTCAGCGCTCCCACTCTC	GTCCCTCCATGGTCGGATG	129	1.85