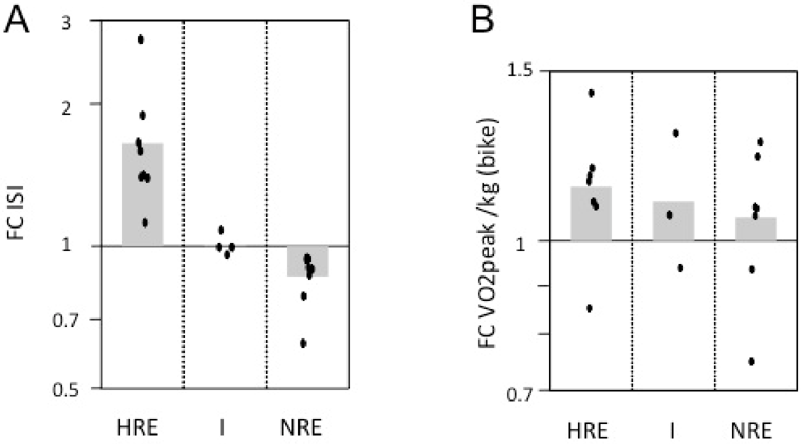
SUPPLEMENTARY DATA

Supplementary Figure S1
Individual fold changes in insulin sensitivity and VO_2peak

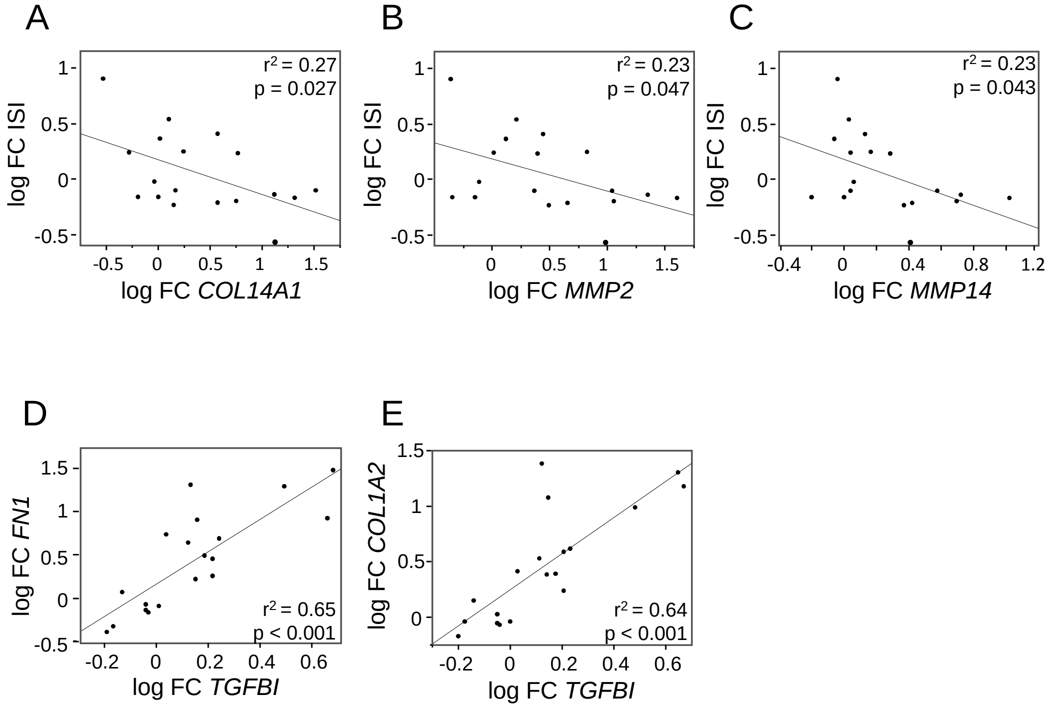
(**A, B**) Insulin sensitivity (ISI) was assessed by the OGTT-based surrogate marker Matsuda index and subjects were grouped into quintiles with 4 in each quintile on the basis of the fold change in ISI Matsuda index. The two upper quintiles with the highest fold change were classified as responders (HRE), the two lower quintiles as non-responders (NRE), and the intermediate quintile as intermediate responders (I). Shown are the individual fold changes (FC) in ISI and in VO_2peak (bike).



Supplementary Figure S2

Increased TGFβ target gene expression in muscle of ISI non-responders

(**A-C**) Correlation of log-transformed fold changes in ISI and fold changes (post-intervention vs. pre-intervention) in TGFβ target gene expression (transcriptome data of muscle biopsies; n=18). (**D**,**E**) Correlation of log-transformed fold changes (post intervention vs. pre-intervention) in *TGFBI* and *FN1* (**D**) and *COL1A2* (**E**) (transcriptome data of muscle biopsies; n=18).

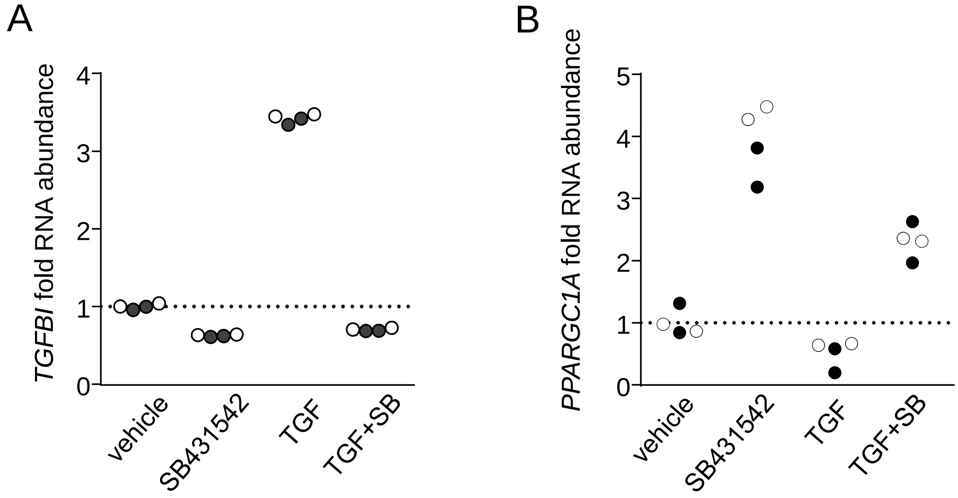


SUPPLEMENTARY DATA

Supplementary Figure S3

TGFβ1-dependent gene expression in myotubes obtained from HRE and NRE donors

Relative fold change of RNA abundance of *TGFBI* (A) and PPARGC1A (B) measured by qPCR in fully differentiated human skeletal muscle cells treated with 10µM SB 431524, 2ng/ml TGFβ1, or both (TGF+SB) for 24 h. Shown is the fold change compared with vehicle-treated cells of 4 different myotube cultures obtained from 2 HRE (black bowls) and 2 NRE donors (white balls); mean±SD is shown in Fig. 3.



SUPPLEMENTARY DATA

Supplementary Table S1. Participants' parameters pre and post intervention. Data represent means ±SD. Prior to statistical analysis, data were $\log_e$-transformed in order to approximate normal distribution; p: paired t-test, *available from 19 subjects; †available from 18 subjects; ‡ available from 17 subjects; f – female, m – male, CRP – C-reactive protein, ISI – Insulin sensitivity index, IAT – individual anaerobic threshold, RR – blood pressure.

	n=20 (13f, 7m)		
	pre	post	p
ISI OGTT ($\cdot 10^6$ Lkg^{-1}min^{-1})	8.3 ± 6.4	9.5 ± 7.8	0.1
IAT bike (W/kg)	1.1±0.3	1.3 ± 0.3	<0.0001
IAT treadmill (W/kg)	0.9±0.2	1.0 ± 0.3	<0.0001
VO$_2$peak bike (ml/min/kg)	22.9 ± 5.1*	25.4 ± 5.8†	0.047
VO$_2$peak treadmill (ml/min/kg)	26.3 ± 5.4	26.7 ± 5.3†	0.3
Age (years)	46.4 ± 11.0	46.4± 11.0	-
BMI (kg/m^2)	32.5 ± 4.7	32.2 ± 4.8	0.031
Total adipose tissue (kg)	35.4 ± 10.4*	34.6 ± 10.6*	0.023
Visceral adipose tissue (kg)	4.6 ± 2.8*	4.4 ± 2.8*	0.1
Lean Body Mass (kg)	59.8 ± 17*	59.5 ± 15.7‡	0.1
RR$_{sys}$ (mmHg)	136 ± 16	130 ± 11	0.09
RR$_{dia}$ (mmHg)	92 ± 10	88 ± 9	0.032
Heart rate (min^{-1})	76 ± 13	70 ± 9	0.020
Glucose$_0$ (mmol/L)	5.6 ± 0.5	5.7 ± 0.6	0.5
Glucose$_{120}$ (mmol/L)	6.5 ± 1.1	6.3 ± 1.1	0.4
Free fatty acids (µmol/L)	709 ± 539	552 ± 167	0.2
Triglycerides (mg/dL)	114 ± 36	98 ± 38	0.023
HDL cholesterol (mg/dL)	47 ± 11	47 ± 10	0.9
LDL cholesterol (mg/dL)	117 ± 28	111 ± 25	0.020
Leukocytes (µL^{-1})	6246 ± 1744	6043 ± 1673	0.4
CRP (mg/dL)	0.2 ± 0.2	0.4 ± 0.7	0.1

SUPPLEMENTARY DATA

Supplementary Table S2. Correlation of log-transformed fold changes (post-intervention vs. pre-intervention) in transcript abundance determined by microarray analysis and by qPCR. Data obtained by qPCR are related to transcript abundance of *TBP*.

transcript	r^2	p-value
PPARGC1A	0.74	<0.0001
PRKAA2	0.82	<0.0001
CPT1B	0.80	<0.0001
SLC2A4	0.70	<0.0001
CD68	0.69	<0.0001
TGFBI	0.57	0.0003
COL1A2	0.79	<0.0001

Supplementary Table S3. Comparison of the correlation of log-transformed fold changes in ISI and fold changes in transcript abundance determined by microarray analysis or by qPCR. Data obtained by qPCR are related to transcript abundance of *TBP*.

	Microarray data		qPCR data	
transcript	r^2	p-value	r^2	p-value
PPARGC1A	0.27	0.026	0.35	0.01
PRKAA2	0.24	0.039	0.22	0.047
CPT1B	0.57	0.0003	0.40	0.005
SLC2A4	0.42	0.004	0.22	0.048
CD68	0.34	0.01	0.21	0.059
TGFBI	0.29	0.02	0.12	0.15
COL1A2	0.23	0.044	0.15	0.11