1 Tables

Table 1. Participant characteristics.

	Experimental group		Control group	
-	Female	Male	Female	Male
n	6	5	4	4
Age (yrs)	23.4 (2.9)	25.7 (5.8)	24.1 (3.5)	25.5 (5.5)
Body mass, (kg)	64.0 (9.2)	77.5 (8.0)	63.7 (0.5)	76.0 (7.0)
Stature (cm)	167.8 (8.1)	177.2 (3.3)	166.0 (3.7)	181.8 (5.0)
Body mass index (kg m ⁻²)	22.7 (2.7)	24.7 (2.7)	23.2 (1.1)	23.1 (3.2)
Body fat (%)	30.8 (30.8)	25.1 (25.1)	30.3 (30.3)	17.9 (17.9)

Table 2. Primer sequences and average performance.

Symbol	Transcript name	Sequence	Mean Cq (SD) and efficiency	
rRNA47S ETS	450 mas allowed DNA	F: 5'-CTGTCGCTGGAGAGGTTGG-3'	27.3 (1.9), E = 1.84	
	45S pre-ribosomal RNA	R: 3'-GGACGCGCGAGAGAACAG-5'		
-DNA AFC ETC	-DNA 450 5T0 450 " 150"	F: 5'-GCCTTCTCTAGCGATCTGAGAG-3'	24.0 (2.2), E = 1.89	
rRNA45S ETS	45S pre-ribosomal RNA	R: 3'-CCATAACGGAGGCAGAGACA-5'		
rRNA45S ITS	45S pre-ribosomal RNA	F: 5'-TCCGAGACGCGACCTCAG-3'	12.2 (2.2), E = 2.14	
TRNA455115		R: 3'-TCGCCGTTACTGAGGGAATC-5'		
-DNAS OC	5 OC vib accord DNA	F: 5'-ACTCTTAGCGGTGGATCACTC-3'	15.7 (1.9), E = 1.96	
rRNA5.8S	5.8S ribosomal RNA	R: 3'-GTGTCGATGATCAATGTGTCCTG-5'		
"DNA 000	000 "! DNA	F: 5'-TGACGCGATGTGATTTCTGC-3'	10.7 (1.8), E = 2.07	
rRNA28S	28S ribosomal RNA	R: 3'-TAGATGACGAGGCATTTGGC-5'		
DVI 400	100 "	F: 5'-TGCATGGCCGTTCTTAGTTG-3'	40.0 (0.0) = 4.0	
rRNA18S	18S ribosomal RNA	R: 3'-AACGCCACTTGTCCCTCTAAG-5'	10.3 (2.9), E = 1.98	
D1450	50 "	F: 5'-TACGGCCATACCACCCTGAAC-3'	47.4 (0.0) 5000	
rRNA5S	5S ribosomal RNA	R: 3'-GGTCTCCCATCCAAGTACTAACC-5'	17.1 (2.2), E = 2.00	
PPLO	D"	F: 5'-AAGTTCCTGGTCCACAACG-3'		
RPL32	Ribosomal protein L32	R: 3'-CGGCACAGTAAGATTTGTTGC-5'	22.0 (1.6), E = 1.93	
DDOO	Ribosomal protein S6	F: 5'-TTGAAGTGGACGATGAACGC-3'	22.3 (1.7), E = 1.96	
RPS6		R: 3'-GGACCACATAACCCTTCCATTC-5'		
		F: 5'-CCGATTCAGGGAGGATCACC-3'		
UBTF [1,4]	Upstream bindning transcription factor	R: 3'-ACCTCCTTCGTAGTGGCATC-5'	28.4 (2.7), E = 1.87	
UDTE to at		F: 5'-CGGCCAGATGAGATCATGAGAG-3'	28.0 (1.8), E = 1.88	
UBTF [2,3]	Upstream bindning transcription factor	R: 3'-GGGTGGACTTGGTGATACCC-5'		
	Myosin heavy chain 7 (MHCslow)	F: 5'-AGGAGCTCACCTACCAGACG-3'	19.5 (2.3), E = 1.93	
MYH7		R: 3'-TGCAGCTTGTCTACCAGGTC-5'		
MYH2		F: 5'-CCAGGGTACGGGAGCTG-3'	18.0 (1.9), E = 1.99	
	Myosin heavy chain 2 (M	R: 3'-TCACTCGCCTCTCATGTTTG-5'		
MYH1		F: 5'-GGCCAGGGTTCGTGAACTT-3'	22.0 (2.5), E = 1.94	
	Myosin heavy chain 1 (M	R: 3'-TGCGTAGACCCTTGACAGC-5'		
Lambda		F: 5'-Proprietary-3'	22.2 (2.2) =	
	Lambda external reference	R: 3'-Proprietary-5'	22.2 (2.0), E = 1.98	

Table 3. Effect of UBF and rpS6 levels, sessions and de-training on RNA-levels.

Coefficient	Estimatea	SD	Lower 95% CI	Upper 95% CI
Intercept	5.91	0.06	5.80	6.03
UBF protein levels (SD-units)	0.06	0.02	0.02	0.10
Session 1-4 ^b	0.08	0.01	0.05	0.10
Session 4-8°	-0.06	0.02	-0.11	-0.02
Session 8-12 ^d	-0.02	0.03	-0.07	0.03
De-training	-0.19	0.07	-0.32	-0.06
Between Participant variation	0.13	0.04	0.06	0.23
Between Participant:Leg variation	0.03	0.03	0.00	0.10
Residual SD	0.22	0.01	0.19	0.24
Intercept	5.88	0.06	5.77	6.00
rpS6 protein levels (SD-units)	0.01	0.03	-0.04	0.07
Session 1-4 ^b	0.08	0.01	0.05	0.11
Session 4-8°	-0.06	0.03	-0.11	-0.01
Session 8-12 ^d	-0.02	0.03	-0.07	0.03
De-training	-0.21	0.07	-0.34	-0.07
Between Participant variation	0.13	0.05	0.06	0.24
Between Participant:Leg variation	0.03	0.02	0.00	0.09
Residual SD	0.22	0.01	0.20	0.25

^aThe dependent variable is total RNA levels (log); ^bSlope in response to session 1-4; ^cChange in slope in session 4-8; ^dChange in slope in session 8-12

Table 4. Total RNA as a predictor of muscle growth.

Coefficient	Estimate	SD	Lower 95% CI	Upper 95% CI
Intercept	-0.20	0.58	-1.32	0.98
Sex (Male)	0.95	0.59	-0.31	2.10
Mean Total RNA	-0.40	0.27	-0.93	0.13
Mean Total RNA increase per session	0.31	0.10	0.09	0.51
Between Participant variation	0.45	0.33	0.02	1.27
Between Participant:Leg variation	0.63	0.30	0.05	1.21
Residual SD	0.92	0.14	0.68	1.24

^aThe dependent variable is Δ Muscle thickness (mm)