

SUPPLEMENTARY

Heavy-load exercise in older adults activates vasculogenesis and has a stronger impact on muscle gene expression than in young adults

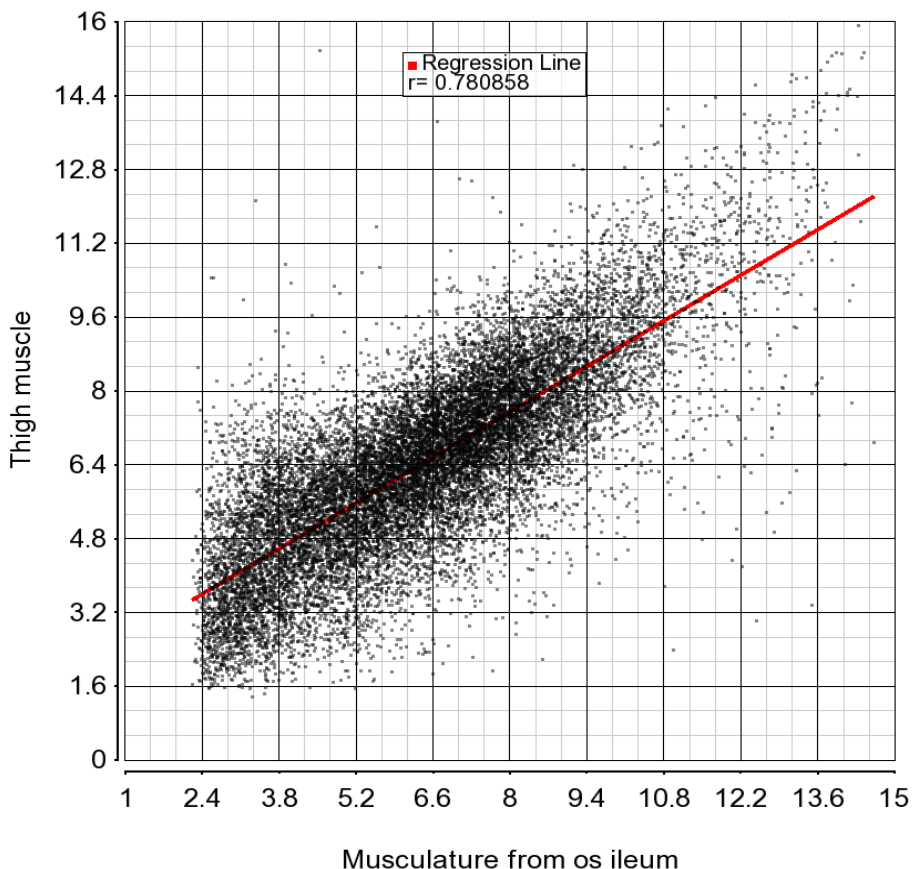


Figure S1. Comparison of transcript signal levels between os ileum–associated muscle and thigh muscle. Numbers on the axes represent \log_2 transformed signal levels. For technical reasons, it was possible to use 17,652 transcripts or 93.5% in further statistical analysis, which is presented in the scatterplot.

Gene symbol	Elderly	Young
COL4A1	Red	Dark Red
EDNRB	Red	Dark Red
SPARC	Red	Dark Red
COL1A1	Red	Dark Red
ENPP2	Red	Dark Red
COL1A2	Red	Dark Red
NQO1	Red	Dark Red
IGF1	Red	Dark Red
IGFBP5	Red	Dark Red
LOX	Red	Dark Red
JAM2	Red	Dark Red
SMOC2	Red	Dark Red
COL15A1	Red	Dark Red
PRCP	Red	Dark Red
THY1	Red	Dark Red
CAV1	Red	Dark Red
COL4A2	Red	Dark Red
TNFSF10	Red	Dark Red
KDR	Red	Dark Red
MMP2	Red	Dark Red
EDNRA	Red	Dark Red
HSPG2	Red	Dark Red
SNAI2	Red	Dark Red
IFI16	Red	Dark Red
F2R	Red	Dark Red
SEMA6A	Red	Dark Red
RHOJ	Red	Dark Red
FZD4	Red	Dark Red
CDH5	Red	Dark Red
CD34	Red	Dark Red
HEY1	Red	Dark Red
AKT3	Red	Dark Red
AHR	Red	Dark Red
PDGFRB	Red	Dark Red
F11R	Red	Dark Red
IGFBP7	Red	Dark Red
SULF2	Red	Dark Red
RECK	Red	Dark Red
SEMA5A	Red	Dark Red
HTRA1	Red	Dark Red
NOTCH4	Red	Dark Red
LRPAP1	Green	Dark Green
NQO2	Green	Dark Green
DYSF	Green	Dark Green
LRRFIP1	Green	Dark Green
QKI	Green	Dark Green
KCNMA1	Green	Dark Green
CAMK2A	Green	Dark Green
HIPK2	Green	Dark Green
PROX1	Green	Dark Green
CCR3	Green	Dark Green
TUBA4A	Green	Dark Green

Figure S2. Genes within the Diseases and Function category Vasculogenesis with increased (red) or reduced (green) expression end vs start of the training period in elderly as compared to young.

Gene Symbol		Oslo cohort			BSU cohort		
Gene Title		Fold-Change (End vs. Start)	p-value (End vs. Start)	Qvalue (End vs. Start)	Fold-Change (End vs. Start)	p-value (End vs. Start)	Qvalue (End vs. Start)
ABC1	ATP-binding cassette, sub-family G (WHITE), member 1	1.11	6.0E-04	4.0E-02	1.16	2.00E-02	8.14E-02
ACSS1	acyl-CoA synthetase short-chain family member 1	-1.12	2.8E-03	8.4E-02	-1.25	1.41E-02	6.91E-02
ACSS2	acyl-CoA synthetase short-chain family member 2	-1.12	2.3E-04	2.9E-02	-1.18	1.61E-04	8.02E-03
ACTN2	actinin, alpha 2	-1.09	1.7E-05	1.1E-02	-1.10	2.34E-03	2.92E-02
ADPRHL1	ADP-ribosylhydrolase like 1	-1.16	4.2E-05	1.4E-02	-1.18	4.25E-03	3.84E-02
AHR	aryl hydrocarbon receptor	1.11	1.8E-03	6.4E-02	1.37	1.08E-04	6.71E-03
AKT3	v-akt murine thymoma viral oncogene homolog 3	-1.12	2.8E-03	8.4E-02	1.23	2.24E-03	2.85E-02
ALPK3	alpha-kinase 3	-1.16	4.5E-04	3.6E-02	-1.31	6.68E-02	1.56E-02
ALYREF	Aly/REF export factor	-1.09	3.9E-04	3.5E-02	-1.21	2.32E-03	2.91E-02
ANK1	ankyrin 1, erythrocytic	-1.08	2.0E-03	6.8E-02	-1.25	5.13E-03	4.23E-02
ANKRD2	ankyrin repeat domain 2 (stretch responsive muscle)	-1.47	6.3E-04	4.0E-02	-1.82	6.65E-04	1.55E-02
ANXA11	annexin A11	-1.10	1.2E-03	5.4E-02	-1.14	6.56E-03	4.81E-02
AP1B1	adaptor-related protein complex 1, beta 1 subunit	-1.06	8.0E-04	4.4E-02	-1.12	1.05E-02	6.01E-02
APRT	adenine phosphoribosyltransferase	-1.08	4.3E-04	3.6E-02	-1.11	1.30E-02	6.65E-02
ASPN	asporin	1.17	1.0E-04	2.1E-02	1.92	2.25E-03	2.86E-02
AVPR1A	arginine vasopressin receptor 1A	1.14	5.7E-05	1.6E-02	1.76	1.15E-04	6.94E-03
B3GALT1	beta 1,3-galactosyltransferase-like	1.14	1.3E-03	5.7E-02	1.34	4.77E-04	1.34E-02
BACE2	beta-site APP-cleaving enzyme 2	1.08	2.1E-03	7.0E-02	1.38	3.29E-04	1.15E-02
BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	1.08	3.7E-03	9.5E-02	1.15	2.79E-02	9.49E-02
BOPI1	block of proliferation 1 /// microRNA 7112	-1.06	1.1E-03	5.2E-02	-1.22	9.31E-04	1.86E-02
C20orf166	chromosome 20 open reading frame 166	-1.21	5.4E-05	1.6E-02	-1.13	5.06E-03	4.21E-02
CAMK2A	calcium/calmodulin-dependent protein kinase II alpha	-1.14	6.4E-04	4.0E-02	-1.20	3.88E-03	3.67E-02
CAMK2B	calcium/calmodulin-dependent protein kinase II beta	-1.11	9.2E-05	1.9E-02	-1.23	5.12E-04	1.38E-02
CANP6	calpain 6	1.19	3.5E-03	9.3E-02	1.64	1.05E-03	1.98E-02
CARM1	coactivator-associated arginine methyltransferase 1	-1.07	3.7E-03	9.7E-02	-1.12	2.53E-02	9.04E-02
CASP4	caspase 4, apoptotic-related cysteine peptidase	1.14	1.5E-03	6.2E-02	1.38	1.18E-02	6.36E-02
CAV1	caveolin 1, caveolae protein, 22kDa	1.16	3.7E-04	3.5E-02	1.33	1.50E-05	2.74E-03
CCR3	chemokine (C-C motif) receptor 3	-1.25	2.4E-04	2.9E-02	-1.43	4.26E-03	3.84E-02
CD34	CD34 molecule	1.12	2.6E-03	8.0E-02	1.35	3.48E-06	1.51E-03
CD93	CD93 molecule	1.12	2.2E-03	7.2E-02	1.70	5.54E-08	1.77E-04
CD42EP4	CD42 effector protein (Rho GTPase binding) 4	-1.07	2.0E-03	6.8E-02	-1.18	1.10E-02	6.13E-02
CDH5	cadherin 5, type 2 (vascular endothelium)	1.12	1.7E-03	6.3E-02	1.58	9.52E-07	8.66E-04
CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	1.11	2.2E-03	7.1E-02	1.62	2.63E-05	3.57E-03
CEP57	centrosomal protein 57kDa	1.10	5.2E-04	3.8E-02	1.19	2.22E-02	8.52E-02
CHRD1L	chordin-like 1	1.19	1.2E-03	5.3E-02	1.39	1.45E-02	7.01E-02
CLEC14A	C-type lectin domain family 14, member A	1.08	2.0E-03	6.8E-02	1.29	2.06E-04	9.20E-03
CLEC2D	C-type lectin domain family 2, member D	1.10	1.4E-03	5.7E-02	1.42	1.43E-02	6.96E-02
CLTCL1	clathrin, heavy chain-like 1	-1.10	1.9E-03	6.6E-02	-1.24	6.31E-05	5.24E-03
CMIP	c-Maf inducing protein	1.09	1.8E-03	6.4E-02	1.27	2.61E-02	9.17E-02
CNNM4	cyclin M4	-1.18	5.8E-05	1.6E-02	-1.24	9.63E-05	6.37E-03
COL15A1	collagen, type XV, alpha 1	1.17	3.4E-05	1.2E-02	1.40	3.67E-04	1.20E-02
COL1A1	collagen, type I, alpha 1	1.33	3.6E-03	9.5E-02	1.94	5.61E-04	1.44E-02
COL1A2	collagen, type I, alpha 2	1.26	1.1E-03	5.1E-02	1.57	3.39E-04	1.16E-02
COL3A1	collagen, type III, alpha 1	1.35	6.2E-04	4.0E-02	1.69	3.30E-05	4.02E-03
COL4A1	collagen, type IV, alpha 1	1.18	6.3E-05	1.6E-02	2.45	5.72E-08	1.77E-04
COL4A2	collagen, type IV, alpha 2	1.16	2.0E-05	1.1E-02	2.31	6.02E-07	6.76E-04
COL5A2	collagen, type V, alpha 2	1.18	3.6E-03	9.4E-02	1.87	1.38E-03	2.22E-02
COL6A3	collagen, type VI, alpha 3	1.17	2.8E-03	8.4E-02	1.24	3.28E-03	3.43E-02
COLEC12	collectin sub-family member 12	1.18	2.2E-05	1.1E-02	1.30	2.62E-03	3.07E-02
CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	1.12	2.5E-03	7.8E-02	1.60	8.58E-05	6.06E-03
CTSK	cathepsin K	1.17	2.5E-03	7.8E-02	1.32	1.41E-02	6.91E-02
CTSO	cathepsin O	1.12	6.2E-04	4.0E-02	1.23	2.26E-02	8.60E-02
CYB5D2	cytochrome b5 domain containing 2	1.07	1.0E-03	5.0E-02	1.13	4.10E-03	3.77E-02
CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	-1.24	1.6E-05	1.1E-02	-1.67	6.94E-05	5.45E-03
DCAF15	DCB1 and CUL4 associated factor 15	-1.07	5.0E-04	3.8E-02	-1.22	6.26E-03	4.70E-02
DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1	1.13	3.3E-03	9.2E-02	1.29	3.74E-03	3.61E-02
DGKD	diacylglycerol kinase, delta 130kDa	-1.12	4.3E-04	3.6E-02	-1.18	1.43E-04	7.54E-03
DHCR24	24-dehydrocholesterol reductase	-1.19	2.3E-03	7.3E-02	-1.38	3.03E-04	1.10E-02
DHFR	dihydrofolate reductase	1.10	1.4E-03	5.9E-02	1.29	3.64E-04	1.20E-02
DHRS7B	dehydrogenase/reductase (SDR family) member 7B	-1.09	4.4E-04	3.6E-02	-1.19	1.29E-03	2.16E-02
DNAI85	DnaJ (Hsp40) homolog, subfamily B, member 5	-1.14	7.0E-04	4.1E-02	-1.21	2.54E-02	9.05E-02
DOCK1	dedicator of cytokinesis 1	1.09	4.3E-04	3.6E-02	1.48	9.55E-05	6.37E-03
DOCK10	dedicator of cytokinesis 10	1.14	1.7E-03	6.4E-02	1.79	2.03E-03	2.72E-02
DYSF	dysferlin	-1.09	7.0E-04	4.1E-02	-1.10	2.54E-02	9.05E-02
EBF3	early B-cell factor 3	1.08	2.9E-04	3.1E-02	1.31	2.16E-03	2.79E-02
ECM2	extracellular matrix protein 2, female organ and adipocyte specific	1.14	6.9E-04	4.1E-02	1.67	1.97E-03	2.68E-02
EDNRA	endothelin receptor type A	1.15	3.1E-03	8.8E-02	1.61	1.80E-04	8.62E-03
EDNRB	endothelin receptor type B	1.19	4.3E-04	3.6E-02	1.88	1.07E-06	8.93E-04
ELOF1	elongation factor 1 homolog (S. cerevisiae)	-1.09	3.7E-04	3.5E-02	-1.19	1.92E-03	2.64E-02
ENAM	enamelin	-1.23	4.2E-04	3.6E-02	-1.20	1.67E-02	7.47E-02
ENDOD1	endonuclease domain containing 1	-1.12	1.2E-03	5.4E-02	-1.17	2.90E-03	3.24E-02
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	1.27	5.0E-07	1.5E-03	1.36	8.60E-04	1.80E-02
EPHB1	EPH receptor B1	-1.17	9.1E-04	4.6E-02	-1.21	2.95E-02	9.71E-02
F11R	F11 receptor	1.11	5.2E-04	3.8E-02	1.31	2.65E-03	3.09E-02
F2R	coagulation factor II (thrombin) receptor	1.14	1.6E-04	2.6E-02	1.53	1.14E-05	2.59E-03
FAM78A	family with sequence similarity 78, member A	-1.15	3.1E-04	3.2E-02	-1.30	1.55E-03	2.36E-02
FBXW5	F-box and WD repeat domain containing 5	-1.10	2.4E-05	1.1E-02	-1.29	3.32E-03	3.45E-02
FLIPL1	filamin A interacting protein 1-like	1.11	1.2E-03	5.5E-02	1.26	2.02E-02	8.18E-02
FLNC	filamin C, gamma	-1.14	9.0E-04	4.6E-02	-1.20	4.70E-03	4.03E-02
FLRT3	fibronectin leucine rich transmembrane protein 3	-1.24	6.3E-04	4.0E-02	-1.26	1.02E-02	5.94E-02
FRMD6	FERM domain containing 6	1.12	1.6E-04	2.6E-02	1.51	2.15E-03	2.79E-02
FXYD6	FXYD domain containing ion transport regulator 6	1.08	7.4E-04	4.2E-02	1.24	1.87E-03	2.61E-02
FZD4	frizzled class receptor 4	1.13	1.0E-06	2.4E-03	1.35	2.13E-06	1.16E-03
FZD6	frizzled class receptor 6	1.13	8.8E-04	4.6E-02	1.58	1.15E-04	6.96E-03
GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	1.10	3.6E-03	9.5E-02	1.30	5.24E-03	4.29E-02
GBA2	glucosidase, beta (bile acid) 2	-1.14	5.0E-04	3.8E-02	-1.16	1.49E-02	7.07E-02
GNAI1	G Protein Subunit Alpha I1	1.12	1.9E-03	6.6E-02	1.51	3.22E-05	4.02E-03
GPR133	G protein-coupled receptor 133	-1.10	3.8E-04	3.5E-02	-1.28	2.88E-04	1.07E-02
GRIP2	glutamate receptor interacting protein 2	-1.12	1.7E-03	6.3E-02	-1.41	4.48E-03	3.93E-02
GSS	glutathione synthetase	-1.11	3.9E-05	1.4E-02	-1.24	9.63E-04	1.89E-02
GTZF2H4	general transcription factor IIH, polypeptide 4, 52kDa	-1.07	6.2E-04	4.0E-02	-1.11	1.06E-02	6.03E-02
GYS1	glycogen synthase 1 (muscle)	-1.10	7.0E-04	4.1E-02	-1.17	2.70E-02	9.31E-02
HDAC5	histone deacetylase 5	-1.13	2.0E-05	1.1E-02	-1.24	2.69E-04	1.03E-02
HEY1	hes-related family bHLH transcription factor with YRPW motif 1	1.12	1.1E-03	5.3E-02	1.26	7.22E-03	5.00E-02
HIBCH	3-hydroxyisobutyryl-CoA hydrolase	1.13	1.3E-03	5.7E-02	1.23	5.67E-04	1.45E-02
HIPK2	homeodomain interacting protein kinase 2	-1.14	1.8E-04	2.6E-02	-1.32	1.05E-02	6.01E-02
HIVEP3	human immunodeficiency virus type 1 enhancer binding protein 3	-1.08	2.0E-04	2.7E-02	-1.15	1.34E-02	6.75E-02
HOMER2	homolog 2 (Drosophila)	-1.14	3.9E-04	3.5E-02	-1.28	1.52E-02	7.14E-02
HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular)	-1.21	5.0E-05	1.6E-02	-1.29	7.10E-04	1.62E-02
HSPG2	heparan sulfate proteoglycan 2	1.15	4.4E-06	4.8E-03	1.38	7.78E-04	1.70E-02
HTRA1	HtrA serine peptidase 1	1.09	2.2E-03	7.1E-02	1.20	1.32E-02	6.71E-02
IFI16	interferon, gamma-inducible protein 16	1.14	3.6E-03	9.4E-02	1.45	1.61E-03	2.42E-02
IGF1	insulin-like growth factor 1 (somatomedin C)	1.20	5.5E-04	3.9E-02	1.71	6.44E-04	1.54E-02
IGF2	insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough	1.27	2.5E-06	3.4E-03	1.59	2.50E-04	9.98E-03
IGFBP5	insulin-like growth factor binding protein 5	1.18	9.0E-04	4.6E-02	1.19	2.58E-02	9.13E-02
IGFBP7	insulin-like growth factor binding protein 7	1.10	3.2E-03	8.9E-02	1.41	1.83E-04	8.64E-03
ITGB5	integrin, beta 5	1.06	3.5E-03	9.3E-02	1.17	2.97E-03	3.28E-02
ITPR1	inositol 1,4,5-trisphosphate receptor, type 1	1.11	1.7E-03	6.3E-02	1.22	7.06E-03	4.97E-02
JAM2	junctional adhesion molecule 2	1.18	5.1E-05	1.6E-02	1.39	1.44E-05	2.72E-03
JMJD1C	jumonji domain containing 1C	1.09	3.0E-03	8.8E-02	1.34	4.80E-03	4.07E-02
JPH2	junctophilin 2	-1.11	3.4E-04	3.4E-02	-1.11	2.93E-02	9.69E-02
JUND	jun D proto-oncogene	-1.12	5.5E-04	3.9E-02	-1.14	2.36E-02	8.75E-02
KCNMA1	Potassium Calcium-Activated Channel Subfamily M Alpha 1	-1.13	3.6E-03	9.5E-02	-1.37	6.47E-04	1.54E-02
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	1.16	9.7E-04	4.8E-02	1.51	2.49E-04	9.98E-03
KLHD2C	kelch domain containing 2	1.08	2.1E-03	7.1E-02	1.07	2.11E-02	8.31E-02
LAMA4	laminin, alpha 4	1.18	1.7E-04	2.6E-02	1.74	8.65E-06	2.23E-03
LAMB1	laminin, beta 1	1.16	4.3E-04	3.6E-02	1.68	1.61E-03	2.42E-02
LANCL1	LanC antibiotic synthetase component C-like 1 (bacterial)	1.09	7.5E-04	4.3E-02	1.15	2.78E-03	3.16E-02
LARGE	like-glycosyltransferase	-1.09	3.2E-04	3.3E-02	-1.17	2.24E-02	8.54E-02
LINC00312	long intergenic non-protein coding RNA 312	-1.22	1.2E-03	5.4E-02	-1.13	2.57E-02	9.11E-02
LOX	lysyl oxidase	1.18	3.0E-03	8.7E-02	3.02	5.47E-05	5.00E-03
LPIN1	lipin 1	1.11	5.8E-04	4.0E-02	1.09	1.26E-02	6.57E-02
LRPAP1	low density lipoprotein receptor-related protein associated protein 1	-1.06	2.1E-03	7.0E-02	-1.17	6.41E-04	1.54E-02
LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	-1.10	2.6E-04	3.0E-02	-1.16	2.38E-02	8.79E-02
LSM12	LSM12 homolog (S. cerevisiae)	-1.07	1.1E-03	5.2E-02	-1.36	3.14E-04	1.11E-02
LSMEM2	leucine-rich single-pass membrane protein 2	-1.08	7.4E-04	4.2E-02	-1.27	2.06E-02	8.22E-02
MAPK12	mitogen-activated protein kinase 12	-1.10	1.2E-03	5.3E-02	-1.36	5.08E-05	4.85E-03