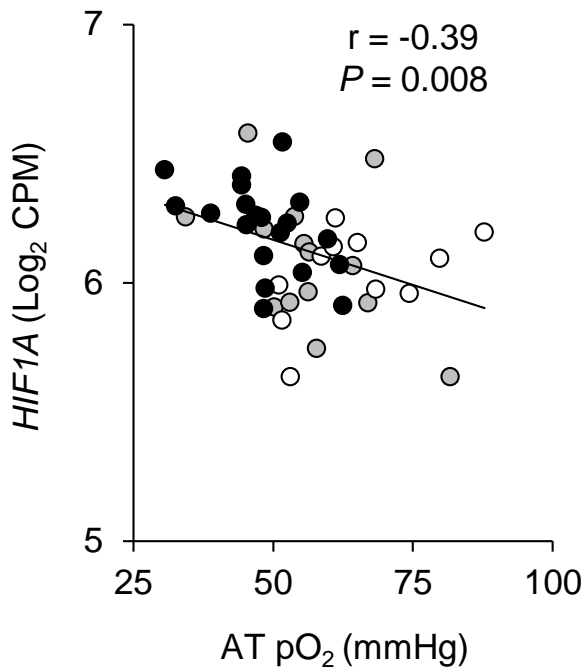


## Supplemental Data

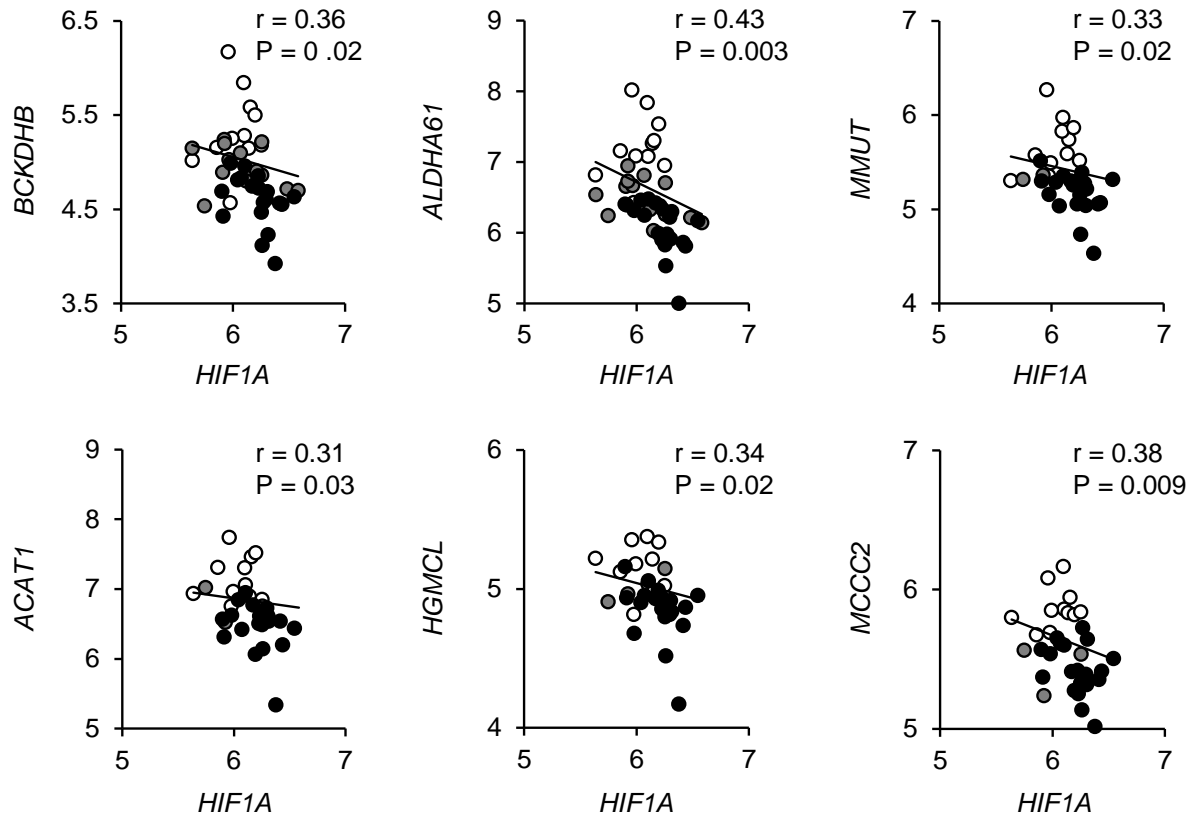
**Supplementary Table 1.** Genes included in the angiogenesis gene set that were negatively associated with AT pO<sub>2</sub>.

Gene	Function
DAB2 interacting protein (DAB2IP)	Angiogenesis
EPH receptor B2 (EPHB2)	Angiogenesis
Rho GTPase activating protein 22 (ARHGAP22)	Angiogenesis
Thy-1 cell surface antigen (THY1)	Angiogenesis
Cytochrome P450 family 1 subfamily B member 1 (CYP1B1)	Angiogenesis
Heme oxygenase 1 (HMOX1)	Angiogenesis
Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma (PIK3CG)	Angiogenesis
C-C motif chemokine ligand 2 (CCL2)	Inflammation
C-X-C motif chemokine ligand 8 (CXCL8)	Inflammation
C-X-C motif chemokine receptor 3 (CXCR3)	Inflammation
TNF alpha induced protein 2 (TNFAIP2)	Inflammation
TNF receptor superfamily member 12A (TNFRSF12A)	Inflammation
Interleukin 18 (IL18)	Inflammation
Collagen type VIII alpha 2 chain (COL8A2)	ECM
Connective tissue growth factor (CTGF)	ECM
Fibronectin 1 (FN1)	ECM
Integrin subunit alpha V (ITGAV)	ECM

Genes were significantly ( $P < 0.005$ ) negatively associated with adipose tissue (AT) oxygen partial pressure (pO<sub>2</sub>) by using Pearson's correlation. Abbreviations: ECM, extracellular matrix.



**Supplementary Figure 1. Adipose tissue oxygen tension is negatively associated with adipose tissue *HIF1A* expression.** Relationship between adipose tissue (AT) oxygen partial pressure (pO<sub>2</sub>) and AT *HIF1A* gene expression in metabolically-healthy lean (white circles; n=11), metabolically-healthy obese (grey circles; n=14) and metabolically-unhealthy obese (black circles; n=20) participants. Associations between AT pO<sub>2</sub> and AT *HIF1A* gene expression were determined by using Pearson's correlation coefficient.



**Supplementary Figure 2. Adipose tissue *HIF1A* gene expression is negatively associated with adipose tissue expression of genes involved in BCAA catabolism.** Relationship between adipose tissue (AT) *HIF1A* and expression of AT genes involved in regulating branched-chain amino acid (BCAA) catabolism in metabolically-healthy lean (white circles; n=11), metabolically-healthy obese (grey circles; n=14) and metabolically-unhealthy obese (black circles; n=20) participants. Gene expression values are log<sub>2</sub> counts per million reads. Associations between AT *HIF1A* and BCAA enzyme gene expression were determined by using Pearson's correlation coefficient.