

SUPPLEMENTARY TABLE S3. GO ANALYSIS OF GENES WITH 5 TIMES HIGHER EXPRESSION IN CD34⁺/CD206⁺ ATMs COMPARED TO CD34⁻/CD206⁺ ATMs IS SHOWN

<i>GO Term</i>	<i>Corrected P-value</i>
Extracellular matrix organization	2.07E-08
Extracellular structure organization	2.07E-08
Vasculature development	1.25E-07
Translation	2.50E-07
Blood vessel development	3.69E-07
Cardiovascular system development	6.17E-06
Circulatory system development	6.17E-06
Cell adhesion	2.60E-05
Biological adhesion	2.68E-05
Macromolecule biosynthetic process	4.01E-05
Anatomical structure morphogenesis	9.24E-05
Anatomical structure development	1.06E-04
System development	1.56E-04
Skeletal system development	2.64E-04
Regulation of cell migration	2.64E-04
Blood vessel morphogenesis	2.82E-04
Regulation of cell motility	3.64E-04
Biosynthetic process	3.78E-04
Cell migration	4.21E-04
Cellular macromolecule biosynthetic process	7.30E-04
Translational elongation	7.63E-04
Regulation of locomotion	0.001109251
Multicellular organismal development	0.001119221
Collagen fibril organization	0.001119221
Regulation of cellular component movement	0.001361031
Cellular biosynthetic process	0.001419218
Skeletal system morphogenesis	0.001419218
Developmental process	0.00156327
Angiogenesis	0.002708858
Collagen biosynthetic process	0.002761109
Regulation of cell growth	0.004425475
Negative regulation of cell proliferation	0.004425475
Cell motility	0.005208333
Localization of cell	0.005208333
Regulation of cell proliferation	0.006625843
Oxidation-reduction process	0.008819223

Corrected *P*-values for the selected ontologies are provided.
GO, gene ontology; ATMs, adipose tissue-resident macrophages.