

SUPPLEMENTARY TABLE S4. GO ANALYSIS OF GENES WITH 5 TIMES HIGHER EXPRESSION IN CD34<sup>+</sup>/CD206<sup>+</sup> ATMs COMPARED TO ASCs IS SHOWN

<i>GO Term</i>	<i>Corrected P-value</i>
Immune system process	∞
Immune response	∞
Response to stimulus	5.43E-35
Defense response	1.39E-34
Inflammatory response	7.20E-25
Response to wounding	7.27E-23
Signal transduction	7.03E-20
Cell communication	5.04E-19
Signaling	6.49E-19
Response to stress	7.62E-17
Cellular response to stimulus	4.16E-16
Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	5.08E-16
Regulation of immune system process	3.32E-14
Cell activation	6.80E-13
Positive regulation of immune system process	8.81E-12
Leukocyte activation	1.15E-11
Regulation of immune response	2.78E-11
Chemotaxis	3.22E-11
Taxis	3.22E-11
Regulation of response to stimulus	6.19E-11
Locomotion	1.42E-10
Response to external stimulus	5.71E-09
Positive regulation of immune response	1.92E-08
Antigen processing and presentation	2.02E-08
Response to other organism	5.02E-08
Myeloid leukocyte activation	5.04E-08
Regulation of cell activation	5.06E-08
Biological regulation	6.63E-08
Regulation of leukocyte activation	6.99E-08
Response to bacterium	1.36E-07
Response to biotic stimulus	1.42E-07
Regulation of biological process	1.48E-07
Immune effector process	1.57E-07
Leukocyte migration	6.88E-07
Regulation of lymphocyte differentiation	8.76E-07
Endocytosis	1.05E-06
Response to cytokine stimulus	1.34E-06
Leukocyte cell-cell adhesion	1.38E-06
Regulation of cellular process	2.35E-06
Leukocyte differentiation	2.83E-06
Regulation of lymphocyte activation	3.08E-06
Cell surface receptor signaling pathway	3.10E-06
Lymphocyte activation	3.27E-06
Hemopoietic or lymphoid organ development	3.84E-06
Phagocytosis	4.37E-06
Positive regulation of response to stimulus	4.37E-06
Response to chemical stimulus	4.67E-06
Hemopoiesis	4.69E-06
Regulation of T cell differentiation	5.55E-06
Positive regulation of lymphocyte differentiation	5.82E-06
Positive regulation of molecular function	7.53E-06
Cellular response to cytokine stimulus	7.64E-06
Cell adhesion	7.75E-06
Biological adhesion	8.01E-06

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SUPPLEMENTARY TABLE S4. (CONTINUED)

<i>GO Term</i>	<i>Corrected P-value</i>
T cell activation	8.01E-06
Immune response-regulating signaling pathway	1.11E-05
Immune system development	1.36E-05
Multiorganism process	1.63E-05
Regulation of signal transduction	1.97E-05
Positive regulation of T cell differentiation	2.30E-05
Cytokine-mediated signaling pathway	2.83E-05
Regulation of cytokine production	3.57E-05
Response to organic substance	3.57E-05
Regulation of molecular function	3.88E-05
Positive regulation of catalytic activity	3.99E-05
Positive regulation of hydrolase activity	4.51E-05
Activation of immune response	4.91E-05
Integrin-mediated signaling pathway	5.28E-05
Cellular defense response	6.45E-05
Regulation of hydrolase activity	6.62E-05
Positive regulation of cell activation	6.68E-05
Regulation of catalytic activity	7.27E-05
Regulation of defense response	7.27E-05
Cytokine secretion	7.27E-05
Regulation of immune effector process	8.18E-05
Regulation of T cell activation	1.10E-04
Cytokine production	1.26E-04
Lymphocyte differentiation	1.53E-04
Positive regulation of leukocyte activation	1.56E-04
Positive regulation of biological process	1.56E-04
Regulation of multicellular organismal process	1.62E-04
Regulation of signaling	1.64E-04
Regulation of developmental process	2.05E-04
Response to molecule of bacterial origin	2.40E-04
Humoral immune response	2.41E-04
Regulation of leukocyte mediated immunity	2.67E-04
Regulation of multicellular organismal development	2.67E-04
Defense response to bacterium	3.72E-04
Response to lipopolysaccharide	4.42E-04
Positive regulation of alpha-beta T cell activation	4.82E-04
Cellular component movement	5.25E-04
Positive regulation of defense response	5.82E-04
Intracellular signal transduction	5.82E-04
Neutrophil chemotaxis	6.40E-04
Positive regulation of alpha-beta T cell differentiation	6.40E-04
Immune response-activating signal transduction	6.49E-04
Regulation of cytokine biosynthetic process	9.36E-04
Regulation of response to stress	0.001009593
Positive regulation of T cell activation	0.001077212
Immune response-regulating cell surface receptor signaling pathway	0.001113145
Leukocyte chemotaxis	0.001120852
Cellular response to chemical stimulus	0.001575736
Regulation of cell communication	0.001782856
Regulation of interleukin-6 production	0.001805702

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SUPPLEMENTARY TABLE S4. (CONTINUED)

<i>GO Term</i>	<i>Corrected P-value</i>
Cell activation involved in immune response	0.001993049
Leukocyte activation involved in immune response	0.001993049
Receptor-mediated endocytosis	0.002200685
Positive regulation of developmental process	0.002200685
Cell chemotaxis	0.002200685
Positive regulation of cellular process	0.002291025
Vesicle-mediated transport	0.002429623
Regulation of alpha-beta T cell differentiation	0.002570316
Negative regulation of response to stimulus	0.002570316
Positive regulation of cytokine biosynthetic process	0.002740176
Regulation of programmed cell death	0.003240427
Regulation of localization	0.003245588
T cell differentiation	0.003421228
Regulation of cell death	0.003531571
Positive regulation of lymphocyte activation	0.003531571
Regulation of humoral immune response	0.003613442
Negative regulation of signal transduction	0.003613442
Regulation of GTP catabolic process	0.003891622
Purinergic nucleotide receptor signaling pathway	0.003891622
Regulation of GTPase activity	0.003891622
Icosanoid biosynthetic process	0.003891622
Positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	0.00430254
Regulation of inflammatory response	0.004514677
Regulation of alpha-beta T cell activation	0.004796446
Regulation of MAP kinase activity	0.004937568
Programmed cell death	0.005048261
Positive regulation of adaptive immune response	0.005361815
Positive regulation of cholesterol storage	0.005361815
Negative regulation of signaling	0.005361815
Regulation of homeostatic process	0.005361815
G-protein coupled purinergic nucleotide receptor signaling pathway	0.005361815
Regulation of gamma-delta T cell differentiation	0.005361815
Positive regulation of gamma-delta T cell differentiation	0.005361815
Regulation of gamma-delta T cell activation	0.005361815
Positive regulation of gamma-delta T cell activation	0.005361815
Chemokine-mediated signaling pathway	0.005361815

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SUPPLEMENTARY TABLE S4. (CONTINUED)

<i>GO Term</i>	<i>Corrected P-value</i>
Negative regulation of cell communication	0.005416574
Positive regulation of multicellular organismal process	0.005416574
Regulation of intracellular protein kinase cascade	0.006412205
Unsaturated fatty acid biosynthetic process	0.006811583
Regulation of innate immune response	0.006811583
Regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	0.006869566
Positive regulation of cytokine production	0.00708369
Apoptotic process	0.007268565
Regulation of apoptotic process	0.007500938
Elevation of cytosolic calcium ion concentration	0.007600843
Regulation of response to external stimulus	0.007642637
Regulation of adaptive immune response	0.007895952
Icosanoid metabolic process	0.007895952
Positive regulation of innate immune response	0.008009519
Negative regulation of immune system process	0.008068467
Positive regulation of cell communication	0.008068467
Positive regulation of signaling	0.008068467
Positive regulation of MAP kinase activity	0.008068467
Regulation of nitric oxide biosynthetic process	0.008068467
Regulation of catabolic process	0.008303124
Cell migration	0.008339778
Regulation of CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation	0.008655869
Positive regulation of CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation	0.008655869
Fc receptor signaling pathway	0.008655869
Positive regulation of GTPase activity	0.008655869
Regulation of biological quality	0.008798162
Purinergic receptor signaling pathway	0.009140613
Small molecule biosynthetic process	0.009377632
Regulation of nucleotide catabolic process	0.009520843
Regulation of purine nucleotide catabolic process	0.009520843

Corrected P-values for the selected ontologies are provided.