Macrophages_LYVE1 - IMM - Colon - ActiveCD_vs_Control negative regulation of protein processing — GO:0010955 — p: 2.38e—04 ***
Wnt signaling pathway — GO:0016055 — p: 2.01e—04 ***
regulation of canonical Wnt signaling pathway — GO:0060828 — p: 1.73e—04 ***
protein phosphorylation — GO:0006468 — p: 1.69e—04 ***
phosphorylation — GO:0016310 — p: 9.76e—05 ***
negative regulation of cell adhesion — GO:0007162 — p: 2.30e—04 ***
B cell activation — GO:0042113 — p: 3.23e—05 ***
negative regulation of cell activation — GO:0046631 — p: 1.73e—04 ***
lymphocyte activation involved in immune response — GO:0046631 — p: 1.73e—04 ***
lymphocyte activation involved in immune response — GO:0046632 — p: 2.35e—04 ***
negative regulation of leukocyte activation — GO:0046632 — p: 2.35e—04 ***
negative regulation of leukocyte activation — GO:0002695 — p: 1.11e—04 ***
B cell differentiation — GO:00036710 — p: 5.58e—05 ***
negative regulation of adaptive immune response — GO:0002820 — p: 1.11e—04 ***
negative regulation of adaptive immune response ba... — GO:0002823 — p: 6.22e—05 ***
peptide antigen assembly with MHC class II protein... — GO:0002503 — p: 5.00e—05 ***
peptide antigen assembly with MHC class II protein... — GO:0002399 — p: 5.00e—05 ***
antigen processing and presentation of peptide ant... — GO:0002495 — p: 1.15e—04 ***
generation of neurons — GO:0004969 — p: 2.07e—04 ***
positive regulation of cellular component organiza... — GO:0001309 — p: 1.44e—04 ***
cellular response to endogenous stimulus — GO:0011094 — p: 8.86e—05 ***
positive regulation of developmental process — GO:0003008 — p: 5.70e—05 ***
response to nitrogen compound — GO:0009725 — p: 6.49e—05 ***
hemopoiesis — GO:00048666 — p: 1.35e—04 ***
negrouse of compound — GO:00048666 — p: 1.35e—04 *** Up p: 2.38e-04 p: 2.01e-04 *** p: 1.73e-04 *** p: 1.69e-04 *** p: 9.76e-05 *** 1.85e-04 *** 1.73e-04 *** 1.44e-04 *** 5.36e-05 1.11e-04 *** -6.22e-05 *** -1.22e-05 *** -5.00e-05 *** -1.05e-05 *** -2.07e-04 *** -1.44e-04 *** 4 p: 1.44e-04 p: 1.55e-04 *** p: 8.86e-05 *** p: 5.70e-05 *** p: 3.06e-05 *** response to hormone — GO:0009725 - p: 6.49e-05 hemopoiesis — GO:0009725 - p: 6.49e-05 hemopoiesis — GO:0009725 - p: 1.80e-05 anatomical structure formation involved in morphog... — GO:0048646 - p: 6.26e-05 neuron development — GO:0048666 - p: 1.35e-04 response to peptide hormone — GO:0043434 - p: 2.39e-04 cell morphogenesis — GO:0003097 - p: 1.53e-04 positive regulation of intracellular signal transd... — GO:1902533 — p: 8.40e-05 positive regulation of response to external stimul... — GO:0032103 — p: 2.39e-04 regulation of immune response — GO:005776 — p: 2.72e-05 regulation of defense response — GO:0031347 — p: 4.07e-05 innate immune response — GO:0031347 — p: 4.07e-05 innate immune response — GO:0032101 — p: 1.87e-06 regulation of response to external stimulus — GO:0032101 — p: 1.87e-06 regulation of immune response — GO:0002253 — p: 4.46e-05 regulation of response to biotic stimulus — GO:0002833 — p: 2.30e-04 regulation of response to biotic stimulus — GO:0002833 — p: 2.30e-04 regulation of response to biotic stimulus — GO:0002833 — p: 2.46e-05 regulation of response to biotic stimulus — GO:0002833 — p: 2.49e-05 regulation of innate immune response — GO:0002831 — p: 5.14e-05 regulation of innate immune response — GO:0002831 — p: 6.56e-06 regulation of innate immune response — GO:0002831 — p: 6.56e-06 regulation of innate immune response — GO:0002831 — p: 1.96e-04 regulation of innate immune response — GO:0002838 — p: 5.19e-05 regulation of innate immune response — GO:0002888 — p: 5.19e-05 regulation of innate immune response — GO:0002888 — p: 5.19e-05 regulation of innate immune response — GO:0002888 — p: 5.19e-05 regulation of innate immune response — GO:0002889 — p: 1.96e-04 regulation of innate immune response — GO:0002889 — p: 1.96e-04 regulation of innate immune response — GO:0005889 — p: 1.96e-04 regulation of innate immune response — GO:0005889 — p: 1.96e-04 regulation of innate immune response — GO:0005889 — p: 1.96e-04 regulation of innate immune response — GO:0005889 — p: 1.96e-04 regulation of inn 6.26e-05 *** 1.35e-04 *** 2.39e-04 *** Gene Count 1.53e-04 1.8.40e-05 *** 1.2.39e-04 *** 1.72e-05 *** 1.72e-06 *** 100 200 5.14e-05 *** 2.30e-04 *** Cluster ficolin-1-rich granule membrane – GO:0101003 – p: 1.01e–03 **perinuclear endoplasmic reticulum – GO:0097038 – p: 9.00e–04 ***cell surface – GO:000986 – p: 7.92e–04 ***external side of plasma membrane – GO:0009897 – p: 1.02e–03 **early endosome – GO:0005769 – p: 6.64e–04 ***earry endosome – GC:0005/69 – p: 6.64e–04 ***methylosome – GO:0034709 – p: 6.33e–04 ***extracellular matrix – GO:0031012 – p: 4.49e–04 ***external encapsulating structure – GO:0030312 – p: 4.49e–04 ***PML body – GO:0016605 – p: 1.03e–04 ***perinuclear region of cytoplasm – GO:0048471 – p: 8.86e–05 ***MHC class II protein complex – GO:0042613 – p: 3.21e–05 ***transition metal ion binding – GO:0042613 – p: 3.21e–05 *** – lipid kinase activity – GO:0001727 – p: 2.50e–04 *** – phosphatidylinositol kinase activity – GO:0051742 – p: 1.80e–04 *** – ubiquitin–protein transferase inhibitor activity – GO:0055105 – p: 4.43e–05 *** – glutathione peroxidase activity – GO:0055105 – p: 4.72e–05 *** – glutathione peroxidase activity – GO:00043665 – p: 6.15e–05 *** – Sequence–specific DNA binding – GO:00043665 – p: 6.15e–05 *** – DNA-binding transcription regulatory region ... – GO:0000977 – p: 1.87e–04 *** – DNA-binding transcription factor activity, RNA pol... – GO:0000981 – p: 4.03e–04 *** – double–stranded DNA binding – GO:0003700 – p: 2.21e–04 *** – double–stranded DNA binding – GO:0003690 – p: 1.10e–05 *** – transcription regulatory region nucleic acid bindi... – GO:0001669 – p: 2.16e–05 *** – transcription cis–regulatory region binding – GO:000976 – p: 2.16e–05 *** – ATP hydrolysis activity – GO:016887 – p: 6.04e–05 *** – ATP hydrolysis activity – GO:0140657 – p: 3.25e–06 *** – ATP dependent activity – GO:0011067 – p: 3.25e–06 *** – GTPase binding – GO:0031267 – p: 8.13e–07 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine receptor activity – GO:0004896 – p: 1.91e–04 *** – cytokine rec 12 cytokine receptor activity protein serine/threonine kinase activity - GO:0004674 photein serificitified life kinase activity – GO:0004672
phosphotransferase activity, alcohol group as acce... – GO:0016773
histone kinase activity – GO:0035173
protein serine kinase activity – GO:0106310
histone H3 kinase activity – GO:0140996 histone H2AX kinase activity – GO:0140990
histone modifying activity – GO:0140993
histone H3T45 kinase activity – GO:0140857
histone H3T11 kinase activity – GO:0035402 histone H3T11 kinase activity – GO:0140637 histone H3T11 kinase activity – GO:0035402 histone H3T6 kinase activity – GO:035403 histone H2AT120 kinase activity – GO:1990244 8.63e-05 *** 7.84e-05 *** 7.84e-05 *** 7.84e-05 *** 7.84e-05 *** histone H2B kinase activity GO:0140998 histone H4 kinase activity histone H2A kinase activity histone H3S57 kinase activity – G0:0140855 histone H3S57 kinase activity – G0:0140853 histone H2BS36 kinase activity – G0:0140823 Rho–dependent protein serine/threonine kinase acti... – G0:0072371 histone H2AS121 kinase activity – G0:0072371 histone H3T3 kinase activity – G0:0072354 7.84e-05 7.84e-05 7.84e-05 histone H3T3 kinase activity – G0:0072354 – p: 7.84e-05 *
histone H2BS14 kinase activity – G0:0044025 – p: 7.84e-05 *
histone H2AS1 kinase activity – G0:0044024 – p: 7.84e-05 *
histone H4S1 kinase activity – G0:0044023 – p: 7.84e-05 *
histone H3S28 kinase activity – G0:0044022 – p: 7.84e-05 *
histone H2AXS139 kinase activity – G0:0035797 – p: 7.84e-05 *
histone H2AXS139 kinase activity – G0:0035175 – p: 7.84e-05 *
histone H3S10 kinase activity – G0:0004711 – p: 7.84e-05 *
ribosomal protein S6 kinase activity – G0:0004674 – p: 7.84e-05 *
eukaryotic translation initiation factor 2alpha ki... – G0:0004694 – p: 7.84e-05 *
DNA-dependent protein kinase activity – G0:0004676 – p: 7.84e-05 *
3-phosphoinositide-dependent protein kinase activity – G0:0004679 – p: 8.63e-05 *
phospholipid transporter activity – G0:0005548 – p: 2.55e-04 * - p: 7.84e-05 *** - p: 7.84e-05 ***

2.0

2.4

Absolute NES

1.6

2.0

2.4

GO Term