T_cells_Naive_CD4 - IMM - Colon - ActiveCD_vs_Control Up phosphorylation - GO:0016310 - p: 3.34e-05 *** protein phosphorylation - GO:0006468 - p: 3.23e-05 ** response to endogenous stimulus - GO:0009719 - p: 5.50e-06 *** positive regulation of developmental process - GO:0051094 - p: 2.05e-05 *** regulation of cell development - GO:0060284 - p: 5.42e-05 *** cell adhesion - GO:0007155 - p: 1.17e-05 ** epithelium development - GO:0060429 - p: 6.37e-05 *** regulation of multicellular organismal development - GO:2000026 - p: 2.67e-06 ** cellular response to endogenous stimulus - GO:0071495 - p: 2.77e-06 *** circulatory system development - GO:0072359 - p: 4.39e-06 *** regulation of cell adhesion - GO:0030155 - p: 4.25e-06 *** system process - GO:0003008 - p: 4.90e-07 *** regulation of anatomical structure morphogenesis - GO:0022603 - p: 5.47e-05 *** anatomical structure formation involved in morphog... - GO:0048646 - p: 2.94e-07 *** Gene Count enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 9.81e-08 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 7.50e-08 *** extrinsic component of membrane - GO:0019898 - p: 2.14e-03 ** neuron projection - GO:0043005 - p: 2.42e-03 ** axon - GO:0030424 - p: 1.39e-04 ** somatodendritic compartment - GO:0036477 - p: 2.22e-05 *** GO Term Cluster dendritic tree - GO:0097447 - p: 2.17e-04 *** dendrite - GO:0030425 - p: 2.17e-04 *** perinuclear region of cytoplasm - GO:0048471 - p: 1.53e-06 ** chromatin - GO:0000785 - p: 1.00e-10 *** histone binding - GO:0042393 - p: 4.40e-09 *** kinase activity - GO:0016301 - p: 1.75e-05 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 6.09e-07 *** histone modifying activity - GO:0140993 - p: 2.79e-08 *** protein kinase activity - GO:0004672 - p: 5.93e-08 *** histone kinase activity - GO:0035173 - p: 7.39e-08 *** histone H2AX kinase activity - GO:0141003 - p: 2.14e-07 *** histone H3 kinase activity - GO:0140996 - p: 1.09e-07 *** DNA-binding transcription factor activity - GO:0003700 - p: 1.05e-05 *** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 1.01e-05 ** RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 2.91e-06 *** double-stranded DNA binding - GO:0003690 - p: 2.25e-08 ** sequence-specific DNA binding - GO:0043565 - p: 6.65e-09 *** transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 3.03e-07 *** transcription cis-regulatory region binding - GO:0000976 - p: 3.03e-07 *** sequence-specific double-stranded DNA binding - GO:1990837 - p: 1.12e-08 ** chromatin binding - GO:0003682 - p: 1.00e-10 *** 1.3 1.4 1.5 1.6 Absolute NES