T_cells_Naive_CD4 - IMM - Colon - InactiveCD_vs_Control phosphorylation - GO:0016310 - p: 1.14e-06 *** protein phosphorylation - GO:0006468 - p: 1.05e-06 *** system process - GO:0003008 - p: 1.73e-08 ** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 1.05e-08 *** response to nitrogen compound - GO:1901698 - p: 1.41e-05 *** positive regulation of developmental process - GO:0051094 - p: 1.00e-06 *** regulation of multicellular organismal development - GO:2000026 - p: 2.31e-07 *** circulatory system development - GO:0072359 - p: 3.32e-06 ** tube morphogenesis - GO:0035239 - p: 1.63e-05 *** response to hormone - GO:0009725 - p: 1.48e-06 *** anatomical structure formation involved in morphog... - GO:0048646 - p: 2.22e-06 ** regulation of anatomical structure morphogenesis - GO:0022603 - p: 8.96e-06 *** cellular response to endogenous stimulus - GO:0071495 - p: 7.43e-09 *** cellular response to nitrogen compound - GO:1901699 - p: 3.91e-06 ** cellular response to hormone stimulus - GO:0032870 - p: 7.45e-07 *** enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 5.30e-08 ** Cluster animal organ morphogenesis - GO:0009887 - p: 9.33e-07 *** cellular response to peptide hormone stimulus - GO:0071375 - p: 4.12e-06 *** perinuclear region of cytoplasm - GO:0048471 - p: 6.09e-07 *** neuron projection - GO:0043005 - p: 1.98e-04 *** GO Term CC axon - GO:0030424 - p: 1.28e-04 ** somatodendritic compartment - GO:0036477 - p: 5.08e-06 *** transcription regulator complex - GO:0005667 - p: 3.49e-04 ** Gene Count kinase activity - GO:0016301 - p: 2.67e-09 *** histone modifying activity - GO:0140993 - p: 3.76e-10 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 1.00e-10 *** protein kinase activity - GO:0004672 - p: 1.93e-10 *** histone kinase activity - GO:0035173 - p: 1.46e-07 *** histone H3 kinase activity - GO:0140996 - p: 7.81e-08 *** histone H2AX kinase activity - GO:0141003 - p: 3.68e-08 *** cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 1.41e-06 *** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 9.33e-07 *** DNA-binding transcription factor activity - GO:0003700 - p: 3.16e-08 *** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 1.55e-07 *** RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 1.47e-08 *** double-stranded DNA binding - GO:0003690 - p: 1.00e-10 *** sequence-specific DNA binding - GO:0043565 - p: 1.00e-10 *** transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 2.46e-10 *** transcription cis-regulatory region binding - GO:0000976 - p: 2.46e-10 *** sequence-specific double-stranded DNA binding - GO:1990837 - p: 1.00e-10 ** chromatin binding - GO:0003682 - p: 1.00e-10 *** histone binding - GO:0042393 - p: 1.00e-10 *** 1.4 1.5 1.7 1.8 1.6 Absolute NES