T_cells_CD4_FOSB - IMM - Colon - InactiveCD_vs_Control nuclear transport - GO:0051169 - p: 1.10e-05 *** nucleocytoplasmic transport - GO:0006913 - p: 1.10e-05 *** circulatory system development - GO:0072359 - p: 1.01e-05 *** anatomical structure formation involved in morphog... - GO:0048646 - p: 1.38e-06 *** regulation of cell development - GO:0060284 - p: 2.87e-06 *** regulation of cell adhesion - GO:0030155 - p: 1.91e-06 *** regulation of anatomical structure morphogenesis - GO:0022603 - p: 5.77e-06 *** cellular response to hormone stimulus - GO:0032870 - p: 6.26e-06 ** cellular response to nitrogen compound - GO:1901699 - p: 2.67e-06 *** protein phosphorylation - GO:0006468 - p: 1.59e-07 *** peptidyl-amino acid modification - GO:0018193 - p: 2.98e-06 ** protein autophosphorylation - GO:0046777 - p: 5.92e-07 *** enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 6.76e-08 *** cell surface receptor protein serine/threonine kin... - GO:0007178 - p: 2.53e-06 ** Gene Count regulation of transmembrane receptor protein serin... - GO:0090092 - p: 9.68e-07 *** 100 neuron projection development - GO:0031175 - p: 7.80e-10 ** 200 neuron development - GO:0048666 - p: 1.00e-10 *** axon development - GO:0061564 - p: 1.38e-07 *** transcription regulator complex - GO:0005667 - p: 1.77e-05 ** perinuclear region of cytoplasm - GO:0048471 - p: 6.12e-06 *** Cluster GO Term plasma membrane region - GO:0098590 - p: 2.39e-04 *** glutamatergic synapse - GO:0098978 - p: 1.94e-04 *** neuron projection - GO:0043005 - p: 1.57e-07 *** axon - GO:0030424 - p: 7.88e-07 ** dendritic tree - GO:0097447 - p: 3.75e-07 *** dendrite - GO:0030425 - p: 3.75e-07 *** postsynapse - GO:0098794 - p: 1.36e-09 ** somatodendritic compartment - GO:0036477 - p: 1.28e-09 ** protein domain specific binding - GO:0019904 - p: 3.62e-05 ** chromatin binding - GO:0003682 - p: 1.00e-10 *** histone binding - GO:0042393 - p: 1.01e-07 *** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 1.19e-06 *** cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 1.87e-06 *** transcription factor binding - GO:0008134 - p: 1.65e-06 *** transferase activity, transferring phosphorus-cont... - GO:0016772 - p: 2.52e-07 ** kinase activity - GO:0016301 - p: 3.15e-09 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 2.42e-10 *** protein kinase activity - GO:0004672 - p: 1.00e-10 *** histone modifying activity - GO:0140993 - p: 1.00e-10 *** histone kinase activity - GO:0035173 - p: 1.49e-09 ** histone H3 kinase activity - GO:0140996 - p: 1.34e-09 *** histone H2AX kinase activity - GO:0141003 - p: 1.01e-09 *** 1.3 1.4 1.5 1.6 Absolute NES