B_cells - IMM - Colon - InactiveCD_vs_Control Up phosphorylation - GO:0016310 - p: 2.95e-08 ** protein phosphorylation - GO:0006468 - p: 5.82e-08 *** circulatory system development - GO:0072359 - p: 3.32e-06 ** regulation of protein localization - GO:0032880 - p: 3.79e-07 *** positive regulation of cell differentiation - GO:0045597 - p: 9.16e-07 *** regulation of cell adhesion - GO:0030155 - p: 3.63e-08 *** cell-cell adhesion - GO:0098609 - p: 4.30e-08 *** enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 4.10e-08 ** epithelium development - GO:0060429 - p: 1.62e-08 *** response to hormone - GO:0009725 - p: 4.92e-09 ** regulation of cell development - GO:0060284 - p: 2.83e-09 *** ΒP regulation of hemopoiesis - GO:1903706 - p: 3.08e-06 ** cellular response to nitrogen compound - GO:1901699 - p: 3.07e-07 *** regulation of anatomical structure morphogenesis - GO:0022603 - p: 4.25e-08 ** animal organ morphogenesis - GO:0009887 - p: 6.66e-08 *** cellular response to hormone stimulus - GO:0032870 - p: 6.27e-09 *** intracellular receptor signaling pathway - GO:0030522 - p: 1.07e-06 *** gland development - GO:0048732 - p: 1.33e-06 *** Cluster neuron differentiation - GO:0030182 - p: 1.00e-10 *** neuron development - GO:0048666 - p: 1.00e-10 *** neuron projection development - GO:0031175 - p: 4.55e-10 *** axon development - GO:0061564 - p: 1.84e-06 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 1.00e-10 ** anchoring junction - GO:0070161 - p: 6.09e-04 *** perinuclear region of cytoplasm - GO:0048471 - p: 1.20e-09 * neuron projection - GO:0043005 - p: 4.15e-08 *** glutamatergic synapse - GO:0098978 - p: 3.00e-05 ** Gene Count dendritic tree - GO:0097447 - p: 8.82e-06 *** dendrite - GO:0030425 - p: 8.82e-06 ** somatodendritic compartment - GO:0036477 - p: 1.57e-07 *** postsynapse - GO:0098794 - p: 1.49e-07 ** axon - GO:0030424 - p: 7.60e-08 *** transcription regulator complex - GO:0005667 - p: 1.63e-05 ** protein domain specific binding - GO:0019904 - p: 1.14e-06 *** chromatin binding - GO:0003682 - p: 1.00e-10 *** histone binding - GO:0042393 - p: 4.83e-08 *** cell adhesion molecule binding - GO:0050839 - p: 1.27e-06 *** transferase activity, transferring phosphorus-cont... - GO:0016772 - p: 2.98e-06 ** kinase activity - GO:0016301 - p: 2.32e-08 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 4.21e-09 ** histone modifying activity - GO:0140993 - p: 1.00e-10 *** protein kinase activity - GO:0004672 - p: 1.71e-09 *** histone kinase activity - GO:0035173 - p: 6.87e-08 *** histone H3 kinase activity - GO:0140996 - p: 3.52e-08 ** 4 histone H2AX kinase activity - GO:0141003 - p: 3.00e-08 *** 4 cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 3.54e-07 *** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 3.58e-07 *** transcription factor binding - GO:0008134 - p: 4.17e-07 *** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 1.39e-08 ***

1.4

Absolute NES

1.5

1.3

GO Term