Immune_Cycling_cells - IMM - Colon - InactiveCD_vs_Control intracellular receptor signaling pathway - GO:0030522 - p: 3.33e-07 ** peptidyl-amino acid modification - GO:0018193 - p: 4.72e-09 ** neuron projection development - GO:0031175 - p: 3.47e-08 *** neuron development - GO:0048666 - p: 3.63e-09 *** regulation of cell adhesion - GO:0030155 - p: 6.00e-07 *** epithelium development - GO:0060429 - p: 2.56e-07 *** tube development - GO:0035295 - p: 5.93e-08 *** regulation of cell migration - GO:0030334 - p: 3.89e-08 *** cellular response to nitrogen compound - GO:1901699 - p: 1.12e-06 *** animal organ morphogenesis - GO:0009887 - p: 1.43e-06 *** regulation of cell motility - GO:2000145 - p: 7.30e-09 *** ВР tube morphogenesis - GO:0035239 - p: 4.56e-07 *** anatomical structure formation involved in morphog... - GO:0048646 - p: 2.54e-09 *** positive regulation of cell motility - GO:2000147 - p: 6.43e-07 ** blood vessel development - GO:0001568 - p: 6.43e-07 *** positive regulation of locomotion - GO:0040017 - p: 3.71e-07 *** regulation of anatomical structure morphogenesis - GO:0022603 - p: 8.34e-08 *** enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 1.54e-09 *** Cluster vasculature development - GO:0001944 - p: 3.07e-07 *** circulatory system development - GO:0072359 - p: 9.62e-10 *** cell-substrate adhesion - GO:0031589 - p: 7.71e-07 ** cell surface receptor protein serine/threonine kin... - GO:0007178 - p: 1.36e-07 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 1.00e-10 ** receptor complex - GO:0043235 - p: 2.23e-04 *** perinuclear region of cytoplasm - GO:0048471 - p: 1.78e-08 glutamatergic synapse - GO:0098978 - p: 7.19e-04 *** neuron projection - GO:0043005 - p: 6.26e-06 *** somatodendritic compartment - GO:0036477 - p: 1.64e-04 *** dendritic tree - GO:0097447 - p: 1.01e-04 *** CC Gene Count dendrite - GO:0030425 - p: 6.26e-05 ** postsynapse - GO:0098794 - p: 3.49e-06 *** axon - GO:0030424 - p: 1.26e-06 *** plasma membrane region - GO:0098590 - p: 4.72e-04 *** anchoring junction - GO:0070161 - p: 1.62e-04 * transcription regulator complex - GO:0005667 - p: 1.27e-05 ** chromatin binding - GO:0003682 - p: 1.00e-10 *** histone binding - GO:0042393 - p: 5.37e-09 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 2.12e-06 ** protein kinase activity - GO:0004672 - p: 1.02e-06 *** histone modifying activity - GO:0140993 - p: 1.09e-09 *** histone H2AX kinase activity - GO:0141003 - p: 1.43e-06 *** histone kinase activity - GO:0035173 - p: 7.88e-07 *** histone H3 kinase activity - GO:0140996 - p: 1.22e-06 *** kinase binding - GO:0019900 - p: 1.42e-07 *** protein kinase binding - GO:0019901 - p: 2.61e-07 *** transcription factor binding - GO:0008134 - p: 3.96e-07 *** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 4.31e-10 *** cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 1.00e-10 *** RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 1.00e-10 *** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 1.00e-10 *** DNA-binding transcription factor activity - GO:0003700 - p: 1.00e-10 *** 1.3 1.4 1.6 Absolute NES