Macrophages_LYVE1 - IMM - Colon - InactiveCD_vs_Control epithelium development - GO:0060429 - p: 9.64e-05 ** regulation of cell adhesion - GO:0030155 - p: 8.52e-05 *** tube development - GO:0035295 - p: 4.57e-05 *** positive regulation of cell differentiation - GO:0045597 - p: 1.52e-05 *** anatomical structure formation involved in morphog... - GO:0048646 - p: 4.74e-06 *** animal organ morphogenesis - GO:0009887 - p: 6.04e-05 *** blood vessel development - GO:0001568 - p: 5.02e-05 *** circulatory system development - GO:0072359 - p: 1.51e-06 *** vasculature development - GO:0001944 - p: 6.81e-06 *** muscle cell proliferation - GO:0033002 - p: 1.05e-04 *** regulation of protein modification process - GO:0031399 - p: 1.91e-05 *** protein phosphorylation - GO:0006468 - p: 5.92e-07 *** regulation of protein localization - GO:0032880 - p: 9.42e-05 *** response to lipid - GO:0033993 - p: 9.53e-05 *** response to hormone - GO:0009725 - p: 4.30e-07 *** cellular response to hormone stimulus - GO:0032870 - p: 8.39e-07 *** response to peptide hormone - GO:0043434 - p: 9.38e-06 *** cellular response to peptide hormone stimulus - GO:0071375 - p: 5.02e-05 *** cellular response to nitrogen compound - GO:1901699 - p: 6.00e-07 *** Gene Count intracellular receptor signaling pathway - GO:0030522 - p: 7.99e-06 *** 3 cellular response to steroid hormone stimulus – GO:0071383 – p: 1.03e–04 *** 100 regulation of anatomical structure morphogenesis - GO:0022603 - p: 6.60e-05 *** 200 neuron projection development - GO:0031175 - p: 5.84e-06 *** neuron development - GO:0048666 - p: 1.02e-06 *** neuron differentiation - GO:0030182 - p: 3.10e-08 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 1.00e-10 *** membrane raft - GO:0045121 - p: 4.05e-03 * Cluster membrane microdomain - GO:0098857 - p: 2.98e-03 * perinuclear region of cytoplasm - GO:0048471 - p: 1.13e-05 *** somatodendritic compartment - GO:0036477 - p: 1.52e-03 ** postsynapse - GO:0098794 - p: 1.21e-03 ** neuron projection - GO:0043005 - p: 4.74e-05 *** dendritic tree - GO:0097447 - p: 1.28e-03 ** dendrite - GO:0030425 - p: 1.28e-03 ** glutamatergic synapse - GO:0098978 - p: 4.81e-04 *** axon - GO:0030424 - p: 2.14e-05 *** transcription regulator complex - GO:0005667 - p: 6.04e-05 transferase activity, transferring phosphorus-cont... - GO:0016772 - p: 5.83e-07 *** kinase activity - GO:0016301 - p: 2.84e-08 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 5.82e-10 *** protein kinase activity - GO:0004672 - p: 6.93e-10 *** histone modifying activity - GO:0140993 - p: 1.00e-10 *** histone kinase activity - GO:0035173 - p: 2.14e-08 *** histone H2AX kinase activity - GO:0141003 - p: 1.34e-08 *** histone H3 kinase activity - GO:0140996 - p: 1.27e-08 *** transcription factor binding - GO:0008134 - p: 3.97e-06 *** chromatin binding - GO:0003682 - p: 1.93e-08 *** cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 6.61e-10 *** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 6.37e-10 *** RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 1.44e-10 *** transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 1.00e-10 *** transcription cis-regulatory region binding - GO:0000976 - p: 1.00e-10 *** DNA-binding transcription factor activity - GO:0003700 - p: 1.00e-10 *** sequence-specific double-stranded DNA binding - GO:1990837 - p: 1.00e-10 ***

Absolute NES

1.5

1.6

GO Term

DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 1.00e-10 ***

1.3