Macrophages_CCL3_CCL4 - IMM - Colon - InactiveCD_vs_Control cell surface receptor protein serine/threonine kin... - GO:0007178 - p: 1.16e-05 ** regulation of transmembrane receptor protein serin... - GO:0090092 - p: 2.42e-06 ** neuron projection development - GO:0031175 - p: 2.73e-06 *** neuron development - GO:0048666 - p: 1.46e-07 *** regulation of cell migration - GO:0030334 - p: 1.63e-05 *** multicellular organismal-level homeostasis - GO:0048871 - p: 7.29e-06 ** regulation of cell development - GO:0060284 - p: 5.22e-06 *** regulation of anatomical structure morphogenesis - GO:0022603 - p: 1.08e-05 *** positive regulation of cell differentiation – GO:0045597 – p: 1.45e–06 *** animal organ morphogenesis - GO:0009887 - p: 1.52e-05 *** blood vessel morphogenesis - GO:0048514 - p: 1.47e-05 *** negative regulation of cell differentiation - GO:0045596 - p: 1.04e-05 *** response to hormone - GO:0009725 - p: 5.09e-08 ** cell surface receptor protein tyrosine kinase sign... - GO:0007169 - p: 8.41e-06 ** cellular response to nitrogen compound - GO:1901699 - p: 5.75e-07 *** response to peptide hormone - GO:0043434 - p: 8.82e-06 *** cellular response to hormone stimulus - GO:0032870 - p: 2.35e-07 *** Gene Count enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 1.25e-09 *** cellular response to peptide hormone stimulus - GO:0071375 - p: 5.29e-06 *** 100 regulation of phosphorus metabolic process - GO:0051174 - p: 3.70e-06 *** 200 regulation of phosphate metabolic process - GO:0019220 - p: 1.72e-06 ** positive regulation of protein modification proces... - GO:0031401 - p: 1.24e-05 *** regulation of protein phosphorylation - GO:0001932 - p: 2.98e-06 *** regulation of phosphorylation - GO:0042325 - p: 5.75e-07 *** peptidyl-amino acid modification - GO:0018193 - p: 8.03e-10 *** Cluster protein autophosphorylation - GO:0046777 - p: 1.61e-05 * receptor complex - GO:0043235 - p: 1.98e-03 ** perinuclear region of cytoplasm - GO:0048471 - p: 5.36e-04 ** RNA polymerase II transcription regulator complex – GO:0090575 – p: 2.13e–03 * transcription regulator complex - GO:0005667 - p: 2.65e-07 ** glutamatergic synapse - GO:0098978 - p: 8.11e-04 *** somatodendritic compartment - GO:0036477 - p: 2.19e-05 *** dendritic tree - GO:0097447 - p: 6.37e-05 *** dendrite - GO:0030425 - p: 6.37e-05 *** axon - GO:0030424 - p: 2.25e-05 *** postsynapse - GO:0098794 - p: 9.67e-07 ** chromatin binding - GO:0003682 - p: 1.00e-10 *** histone binding - GO:0042393 - p: 1.14e-08 ** transcription factor binding - GO:0008134 - p: 1.57e-08 *** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 1.00e-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 - GO:0003700 - p: 1.00e-10 *** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 1.00e-10 *** kinase activity - GO:0016301 - p: 7.24e-10 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 1.00e-10 *** protein kinase activity - GO:0004672 - p: 1.00e-10 *** histone kinase activity - GO:0035173 - p: 2.38e-09 *** histone modifying activity - GO:0140993 - p: 1.00e-10 *** histone H3 kinase activity - GO:0140996 - p: 6.45e-10 *** histone H2AX kinase activity - GO:0141003 - p: 1.81e-09 *** 1.4 1.5 1.6 1.3 Absolute NES

GO Term