Fibroblasts_SMOC2_PTGIS - STR - Colon - InactiveCD_vs_Control enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 1.44e-10 ** protein phosphorylation - GO:0006468 - p: 1.00e-10 *** regulation of cell migration - GO:0030334 - p: 4.10e-08 *** cell-cell adhesion - GO:0098609 - p: 6.24e-08 ** regulation of cell development - GO:0060284 - p: 1.78e-08 *** regulation of cell adhesion - GO:0030155 - p: 7.30e-09 *** positive regulation of cell differentiation - GO:0045597 - p: 9.94e-10 *** actin cytoskeleton organization - GO:0030036 - p: 3.82e-09 *** animal organ morphogenesis - GO:0009887 - p: 1.00e-10 *** tube morphogenesis - GO:0035239 - p: 1.00e-10 *** PΡ vasculature development - GO:0001944 - p: 1.00e-10 *** actin filament-based process - GO:0030029 - p: 1.00e-10 *** regulation of anatomical structure morphogenesis - GO:0022603 - p: 1.00e-10 *** blood vessel morphogenesis - GO:0048514 - p: 1.06e-09 *** morphogenesis of an epithelium - GO:0002009 - p: 2.30e-08 *** blood vessel development - GO:0001568 - p: 1.17e-10 *** tissue morphogenesis - GO:0048729 - p: 3.52e-10 *** Gene Count circulatory system process - GO:0003013 - p: 5.24e-09 ** cell fate commitment - GO:0045165 - p: 6.23e-10 *** neuron projection development - GO:0031175 - p: 1.00e-10 *** plasma membrane raft - GO:0044853 - p: 2.23e-04 *** caveola - GO:0005901 - p: 5.97e-04 *** receptor complex - GO:0043235 - p: 1.17e-04 *** transcription regulator complex - GO:0005667 - p: 2.74e-08 *** Cluster anchoring junction - GO:0070161 - p: 5.82e-08 *** plasma membrane region - GO:0098590 - p: 1.73e-08 *** S somatodendritic compartment - GO:0036477 - p: 1.02e-06 *** axon - GO:0030424 - p: 9.10e-06 *** glutamatergic synapse - GO:0098978 - p: 3.39e-06 *** dendritic tree - GO:0097447 - p: 8.39e-07 *** dendrite - GO:0030425 - p: 8.39e-07 *** postsynapse - GO:0098794 - p: 1.00e-10 *** chromatin binding - GO:0003682 - p: 1.00e-10 *** histone binding - GO:0042393 - p: 1.29e-06 *** RNA polymerase II cis–regulatory region sequence–s... – GO:0000978 – p: 9.36e–09 ** ** cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 2.51e-09 *** 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 binding - GO:0019900 - p: 1.91e-07 *** protein kinase binding - GO:0019901 - p: 1.34e-07 *** protein domain specific binding - GO:0019904 - p: 1.38e-09 *** transferase activity, transferring phosphorus-cont... - GO:0016772 - p: 1.63e-07 *** kinase activity - GO:0016301 - p: 3.60e-10 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 5.50e-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: 2.23e-10 *** histone H2AX kinase activity - GO:0141003 - p: 5.82e-10 *** histone H3 kinase activity - GO:0140996 - p: 2.26e-10 *** 1.4 1.5 1.6 1.7 1.8

Absolute NES

GO Term