Fibroblasts_SMOC2_PTGIS - STR - Colon - ActiveCD_vs_Control response to nitrogen compound - GO:1901698 - p: 4.47e-07 ** tube development - GO:0035295 - p: 9.49e-08 * enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 4.31e-07 *** regulation of response to external stimulus - GO:0032101 - p: 2.08e-07 *** tube morphogenesis - GO:0035239 - p: 4.98e-07 *** epithelium development - GO:0060429 - p: 2.90e-08 *** positive regulation of cell population proliferati... - GO:0008284 - p: 4.48e-07 *** anatomical structure formation involved in morphog... - GO:0048646 - p: 3.70e-09 *** regulation of defense response - GO:0031347 - p: 4.91e-07 ** circulatory system development - GO:0072359 - p: 1.55e-09 *** vasculature development - GO:0001944 - p: 3.74e-08 *** cell-cell adhesion - GO:0098609 - p: 2.08e-07 *** blood vessel development - GO:0001568 - p: 9.71e-08 *** regulation of anatomical structure morphogenesis - GO:0022603 - p: 2.30e-08 *** regulation of cell adhesion - GO:0030155 - p: 1.27e-10 *** positive regulation of cell adhesion - GO:0045785 - p: 5.30e-09 ** positive regulation of cell-cell adhesion - GO:0022409 - p: 2.46e-07 ** regulation of protein modification process - GO:0031399 - p: 8.23e-08 *** peptidyl-amino acid modification - GO:0018193 - p: 1.63e-08 *** Cluster phosphorylation - GO:0016310 - p: 1.00e-10 *** protein phosphorylation - GO:0006468 - p: 1.00e-10 ** perinuclear region of cytoplasm - GO:0048471 - p: 1.65e-03 ribonucleoprotein granule - GO:0035770 - p: 4.07e-04 ** cytoplasmic ribonucleoprotein granule - GO:0036464 - p: 1.76e-04 ** somatodendritic compartment - GO:0036477 - p: 1.17e-03 * GO Term neuron projection - GO:0043005 - p: 3.97e-06 *** axon - GO:0030424 - p: 4.38e-04 *** dendritic tree - GO:0097447 - p: 1.08e-04 *** dendrite - GO:0030425 - p: 1.08e-04 * Gene Count focal adhesion - GO:0005925 - p: 1.47e-04 ** cell-substrate junction - GO:0030055 - p: 1.14e-04 *** anchoring junction - GO:0070161 - p: 5.24e-07 ** RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 2.80e-06 *** double-stranded DNA binding - GO:0003690 - p: 4.09e-07 *** transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 3.79e-07 *** transcription cis-regulatory region binding - GO:0000976 - p: 3.79e-07 *** DNA-binding transcription factor activity - GO:0003700 - p: 1.46e-06 ** sequence-specific DNA binding - GO:0043565 - p: 2.61e-08 *** sequence-specific double-stranded DNA binding - GO:1990837 - p: 5.93e-08 *** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 4.82e-07 *** chromatin binding - GO:0003682 - p: 6.29e-07 *** transferase activity, transferring phosphorus-cont... - GO:0016772 - p: 2.74e-07 *** kinase binding - GO:0019900 - p: 2.61e-08 *** protein kinase binding - GO:0019901 - p: 2.02e-08 ** protein kinase regulator activity - GO:0019887 - p: 3.03e-06 *** kinase activity - GO:0016301 - p: 1.02e-09 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 2.34e-09 *** protein kinase activity - GO:0004672 - p: 1.00e-10 *** histone modifying activity - GO:0140993 - p: 1.00e-10 ** histone H3 kinase activity - GO:0140996 - p: 3.88e-10 *** histone kinase activity - GO:0035173 - p: 2.31e-10 *** histone H2AX kinase activity - GO:0141003 - p: 1.00e-10 *** 1.7 1.5 1.9 Absolute NES