Myofibroblasts\_HHIP\_NPNT - STR - Colon - ActiveCD\_vs\_Control chromatin organization - GO:0006325 - p: 9.00e-07 \* chromatin remodeling - GO:0006338 - p: 3.47e-07 \*\*\* intracellular signaling cassette - GO:0141124 - p: 8.72e-07 \*\*\* tissue development - GO:0009888 - p: 9.68e-08 \*\*\* positive regulation of developmental process - GO:0051094 - p: 2.84e-06 \*\*\* regulation of response to stress - GO:0080134 - p: 6.53e-07 \*\*\* regulation of cell differentiation - GO:0045595 - p: 5.13e-07 \*\*\* regulation of multicellular organismal development - GO:2000026 - p: 2.92e-06 \*\*\* regulation of cell population proliferation - GO:0042127 - p: 8.92e-08 \*\*\* regulation of response to external stimulus – GO:0032101 – p: 4.54e–06 \*\*\* positive regulation of gene expression - GO:0010628 - p: 1.35e-06 \*\*\* positive regulation of multicellular organismal pr... - GO:0051240 - p: 9.50e-09 \*\*\* animal organ morphogenesis - GO:0009887 - p: 1.17e-06 \*\*\* positive regulation of cell differentiation - GO:0045597 - p: 1.15e-06 \*\*\* ВР anatomical structure formation involved in morphog... - GO:0048646 - p: 2.80e-08 \*\*\* system process - GO:0003008 - p: 2.13e-09 \*\*\* regulation of cell adhesion - GO:0030155 - p: 7.35e-07 \*\*\* cell adhesion - GO:0007155 - p: 3.82e-09 \*\*\* tube development - GO:0035295 - p: 1.37e-08 \*\*\* tube morphogenesis - GO:0035239 - p: 2.62e-08 \*\*\* circulatory system development - GO:0072359 - p: 4.41e-10 \*\*\* blood vessel morphogenesis - GO:0048514 - p: 5.03e-07 \*\*\* regulation of anatomical structure morphogenesis - GO:0022603 - p: 7.51e-08 \*\*\* cell surface receptor protein tyrosine kinase sign... - GO:0007169 - p: 1.26e-06 \*\*\* vasculature development - GO:0001944 - p: 5.99e-09 \*\*\* Gene Count blood vessel development - GO:0001568 - p: 2.27e-08 \*\*\* positive regulation of cell population proliferati... - GO:0008284 - p: 6.36e-10 \*\*\* muscle cell proliferation - GO:0033002 - p: 3.90e-06 \*\*\* chromosome - GO:0005694 - p: 4.84e-04 \*\*\* chromatin - GO:0000785 - p: 3.28e-05 \*\*\* plasma membrane bounded cell projection – GO:0120025 – p: 9.10e–04 \*\*\* cell projection - GO:0042995 - p: 6.96e-04 \*\* neuron projection - GO:0043005 - p: 3.11e-03 \*\* anchoring junction - GO:0070161 - p: 4.46e-05 \*\*\* Cluster focal adhesion - GO:0005925 - p: 2.60e-04 \*\*\* cell-substrate junction - GO:0030055 - p: 6.99e-05 \*\*\* somatodendritic compartment - GO:0036477 - p: 4.75e-04 \*\*\* dendritic tree - GO:0097447 - p: 4.39e-04 \*\*\* dendrite - GO:0030425 - p: 4.39e-04 \*\* transcription regulator activity - GO:0140110 - p: 3.04e-04 \*\* DNA binding - GO:0003677 - p: 4.62e-06 \*\*\* transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 5.94e-04 \*\*\* transcription cis-regulatory region binding - GO:0000976 - p: 5.94e-04 \*\*\* sequence-specific DNA binding - GO:0043565 - p: 9.15e-05 \*\*\* chromatin binding - GO:0003682 - p: 8.74e-04 \*\*\* sequence-specific double-stranded DNA binding - GO:1990837 - p: 1.36e-04 \*\*\* double-stranded DNA binding - GO:0003690 - p: 9.84e-05 \*\*\* purine ribonucleoside triphosphate binding - GO:0035639 - p: 5.05e-04 \*\*\* ribonucleotide binding - GO:0032553 - p: 2.51e-04 \*\*\* purine ribonucleotide binding - GO:0032555 - p: 6.44e-04 \*\*\* adenyl nucleotide binding - GO:0030554 - p: 1.08e-04 \*\*\* carbohydrate derivative binding - GO:0097367 - p: 8.33e-07 \*\*\* ATP binding - GO:0005524 - p: 1.40e-05 \*\*\* adenyl ribonucleotide binding - GO:0032559 - p: 4.08e-06 \*\*\* histone H2AXY142 kinase activity - GO:0140801 - p: 5.01e-04 \*\*\* histone H3Y41 kinase activity - GO:0035401 - p: 5.01e-04 \*\*\* protein tyrosine kinase activity - GO:0004713 - p: 4.62e-04 \*\*\* histone modifying activity - GO:0140993 - p: 4.14e-07 \*\*\* histone H2AX kinase activity - GO:0141003 - p: 1.13e-05 \*\*\* histone H3 kinase activity - GO:0140996 - p: 9.23e-06 \*\*\* 2 histone kinase activity - GO:0035173 - p: 9.23e-06 \*\*\* signaling receptor binding - GO:0005102 - p: 5.94e-06 \*\*\* cell adhesion molecule binding - GO:0050839 - p: 2.21e-05 \*\* 1.4 2.0

Absolute NES

GO Term