NK-like_cells_ID3_ENTPD1 - IMM - Colon - ActiveCD_vs_Control protein localization to nucleus - GO:0034504 - p: 4.91e-05 *** regulation of response to stress - GO:0080134 - p: 4.80e-06 *** hemopoiesis - GO:0030097 - p: 3.51e-05 ** cell activation - GO:0001775 - p: 1.10e-06 *** regulation of multicellular organismal development - GO:2000026 - p: 3.11e-06 *** negative regulation of nucleobase-containing compo... - GO:0045934 - p: 9.36e-09 ** regulation of cell differentiation - GO:0045595 - p: 9.18e-08 *** cell adhesion - GO:0007155 - p: 6.26e-07 *** negative regulation of DNA-templated transcription - GO:0045892 - p: 3.83e-08 ** regulation of cell development - GO:0060284 - p: 3.11e-06 *** negative regulation of RNA biosynthetic process - GO:1902679 - p: 2.61e-08 *** negative regulation of RNA metabolic process – GO:0051253 – p: 7.43e–09 ** cell-cell adhesion - GO:0098609 - p: 3.70e-06 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 1.44e-07 *** regulation of cell adhesion - GO:0030155 - p: 1.65e-06 ** Gene Count positive regulation of transcription by RNA polyme... - GO:0045944 - p: 2.16e-09 *** animal organ morphogenesis - GO:0009887 - p: 1.91e-05 *** phosphorylation - GO:0016310 - p: 3.96e-05 *** chromatin organization - GO:0006325 - p: 1.00e-10 *** chromatin remodeling - GO:0006338 - p: 1.00e-10 ** GO Term plasma membrane bounded cell projection - GO:0120025 - p: 4.49e-04 *** Cluster cell projection - GO:0042995 - p: 2.14e-04 ** neuron projection - GO:0043005 - p: 5.36e-04 *** somatodendritic compartment - GO:0036477 - p: 7.83e-04 *** perinuclear region of cytoplasm - GO:0048471 - p: 6.04e-05 ** axon - GO:0030424 - p: 8.47e-04 *** transcription regulator complex - GO:0005667 - p: 1.08e-03 ** chromatin - GO:0000785 - p: 9.88e-09 ** histone binding - GO:0042393 - p: 7.57e-06 ** transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 1.12e-05 *** transcription cis-regulatory region binding - GO:0000976 - p: 1.12e-05 *** double-stranded DNA binding - GO:0003690 - p: 1.53e-06 ** sequence-specific double-stranded DNA binding - GO:1990837 - p: 6.67e-06 *** sequence-specific DNA binding - GO:0043565 - p: 3.49e-07 *** transcription regulator activity - GO:0140110 - p: 3.31e-09 *** chromatin binding - GO:0003682 - p: 4.27e-09 *** adenyl nucleotide binding - GO:0030554 - p: 4.79e-09 *** adenyl ribonucleotide binding - GO:0032559 - p: 4.23e-10 *** ATP binding - GO:0005524 - p: 1.00e-10 ** histone modifying activity - GO:0140993 - p: 3.33e-07 *** 1.3 1.4 1.5 1.6 Absolute NES