T_cells_CD4_IL17A - IMM - Colon - InactiveCD_vs_Control system process - GO:0003008 - p: 1.45e-06 ** regulation of response to stress - GO:0080134 - p: 2.72e-05 * positive regulation of multicellular organismal pr... - GO:0051240 - p: 2.28e-05 hemopoiesis - GO:0030097 - p: 1.72e-05 ** regulation of multicellular organismal development - GO:2000026 - p: 1.69e-05 *** cellular response to endogenous stimulus - GO:0071495 - p: 1.35e-05 *** response to endogenous stimulus - GO:0009719 - p: 1.00e-06 *** response to nitrogen compound - GO:1901698 - p: 3.63e-06 *** regulation of cell differentiation - GO:0045595 - p: 5.93e-08 ** positive regulation of developmental process - GO:0051094 - p: 2.01e-06 ** anatomical structure formation involved in morphog... - GO:0048646 - p: 1.17e-05 *** ВР positive regulation of transcription by RNA polyme... - GO:0045944 - p: 2.48e-09 *** negative regulation of nucleobase-containing compo... - GO:0045934 - p: 1.00e-10 *** negative regulation of RNA metabolic process - GO:0051253 - p: 1.00e-10 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 5.75e-09 *** negative regulation of RNA biosynthetic process - GO:1902679 - p: 1.00e-10 *** negative regulation of DNA-templated transcription - GO:0045892 - p: 1.00e-10 *** cellular response to nitrogen compound - GO:1901699 - p: 1.42e-07 *** protein phosphorylation - GO:0006468 - p: 1.72e-05 *** phosphorylation - GO:0016310 - p: 1.16e-05 *** Gene Count chromatin remodeling - GO:0006338 - p: 1.00e-10 *** 100 chromatin organization - GO:0006325 - p: 1.00e-10 ** plasma membrane bounded cell projection - GO:0120025 - p: 3.73e-05 ** cell projection - GO:0042995 - p: 1.29e-05 ** somatodendritic compartment - GO:0036477 - p: 7.46e-04 *** neuron projection - GO:0043005 - p: 9.98e-05 *** CC perinuclear region of cytoplasm - GO:0048471 - p: 3.51e-05 *** axon - GO:0030424 - p: 3.39e-04 *** Cluster transcription regulator complex - GO:0005667 - p: 4.81e-04 ** chromatin - GO:0000785 - p: 1.00e-10 * 0 histone binding - GO:0042393 - p: 2.65e-07 *** cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 7.16e-06 *** DNA-binding transcription factor activity - GO:0003700 - p: 2.84e-06 *** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 2.70e-06 *** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 2.67e-06 *** transcription regulator activity - GO:0140110 - p: 1.93e-10 *** RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 4.64e-07 *** double-stranded DNA binding - GO:0003690 - p: 8.51e-10 *** transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 3.70e-09 *** transcription cis-regulatory region binding - GO:0000976 - p: 3.70e-09 *** sequence-specific double-stranded DNA binding - GO:1990837 - p: 5.03e-10 *** sequence-specific DNA binding - GO:0043565 - p: 1.00e-10 ** chromatin binding - GO:0003682 - p: 2.82e-10 *** adenyl nucleotide binding - GO:0030554 - p: 3.60e-10 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 7.02e-06 *** protein kinase activity - GO:0004672 - p: 9.93e-06 *** ATP binding - GO:0005524 - p: 1.00e-10 *** adenyl ribonucleotide binding - GO:0032559 - p: 1.00e-10 *** histone modifying activity - GO:0140993 - p: 6.66e-08 ** histone H3 kinase activity - GO:0140996 - p: 3.23e-05 *** histone kinase activity - GO:0035173 - p: 3.23e-05 *** histone H2AX kinase activity - GO:0141003 - p: 2.14e-05 ***

1.4

Absolute NES

1.5

1.6

1.3

GO Term