T_cells_CD4_IL17A - IMM - Colon - ActiveCD_vs_Control anatomical structure morphogenesis - GO:0009653 - p: 3.34e-05 *** system process - GO:0003008 - p: 2.98e-06 *** response to other organism - GO:0051707 - p: 2.67e-05 *** response to external biotic stimulus - GO:0043207 - p: 2.67e-05 *** regulation of response to stress - GO:0080134 - p: 4.24e-05 *** response to oxygen-containing compound - GO:1901700 - p: 2.14e-05 *** response to cytokine - GO:0034097 - p: 5.08e-05 *** defense response to other organism - GO:0098542 - p: 6.88e-06 *** regulation of defense response - GO:0031347 - p: 4.29e-05 *** cell adhesion - GO:0007155 - p: 1.69e-05 *** lymphocyte activation - GO:0046649 - p: 2.49e-06 *** leukocyte activation - GO:0045321 - p: 8.81e-07 *** positive regulation of transcription by RNA polyme... - GO:0045944 - p: 9.67e-07 *** T cell activation - GO:0042110 - p: 2.44e-05 *** regulation of cell differentiation - GO:0045595 - p: 2.61e-07 *** regulation of cell adhesion - GO:0030155 - p: 2.11e-05 *** multicellular organismal-level homeostasis - GO:0048871 - p: 3.28e-05 *** negative regulation of nucleobase-containing compo... - GO:0045934 - p: 1.17e-08 *** cell activation - GO:0001775 - p: 1.15e-07 *** positive regulation of DNA-templated transcription - GO:0045893 - p: 2.19e-10 *** negative regulation of RNA metabolic process - GO:0051253 - p: 1.08e-08 *** positive regulation of RNA biosynthetic process - GO:1902680 - p: 4.00e-10 *** Cluster negative regulation of RNA biosynthetic process - GO:1902679 - p: 1.73e-08 *** negative regulation of DNA-templated transcription - GO:0045892 - p: 1.47e-08 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 2.65e-07 *** enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 1.84e-06 *** cell surface receptor protein tyrosine kinase sign... - GO:0007169 - p: 7.02e-06 *** cellular response to nitrogen compound - GO:1901699 - p: 6.67e-06 *** chromatin organization - GO:0006325 - p: 1.00e-10 *** chromatin remodeling - GO:0006338 - p: 1.00e-10 *** Gene Count cytoplasmic side of plasma membrane - GO:0009898 - p: 3.99e-04 ** cell projection - GO:0042995 - p: 8.01e-04 *** S perinuclear region of cytoplasm - GO:0048471 - p: 5.70e-05 *** chromatin - GO:0000785 - p: 1.21e-07 phosphatase binding - GO:0019902 - p: 2.40e-04 *** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 7.92e-04 *** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 4.49e-04 *** transcription regulator activity - GO:0140110 - p: 4.17e-07 *** RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 7.61e-05 *** double-stranded DNA binding - GO:0003690 - p: 1.36e-06 *** sequence-specific DNA binding - GO:0043565 - p: 2.56e-07 *** transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 1.74e-06 *** transcription cis-regulatory region binding - GO:0000976 - p: 1.74e-06 *** sequence-specific double-stranded DNA binding - GO:1990837 - p: 1.41e-06 *** chromatin binding - GO:0003682 - p: 6.77e-10 *** carbohydrate derivative binding - GO:0097367 - p: 3.17e-05 *** nucleotide binding - GO:0000166 - p: 9.10e-06 *** purine nucleotide binding - GO:0017076 - p: 1.63e-05 *** ribonucleotide binding - GO:0032553 - p: 9.52e-06 *** purine ribonucleotide binding - GO:0032555 - p: 2.56e-06 *** purine ribonucleoside triphosphate binding - GO:0035639 - p: 3.49e-06 *** adenyl nucleotide binding - GO:0030554 - p: 2.35e-07 *** adenyl ribonucleotide binding - GO:0032559 - p: 2.17e-08 *** ATP binding - GO:0005524 - p: 4.40e-09 *** histone H3 kinase activity - GO:0140996 - p: 3.26e-04 *** histone kinase activity - GO:0035173 - p: 3.26e-04 ***

1.4

Absolute NES

1.5

1.6

1.3

GO Term

histone H2AX kinase activity – GO:0141003 – p: 5.55e–04 ***
histone modifying activity – GO:0140993 – p: 5.75e–07 ***