T_cells_CD8_KLRG1 - IMM - Colon - InactiveCD_vs_Control system process - GO:0003008 - p: 4.18e-05 *** regulation of multicellular organismal development - GO:2000026 - p: 3.62e-05 *** response to nitrogen compound - GO:1901698 - p: 1.02e-04 *** regulation of cell differentiation - GO:0045595 - p: 1.24e-06 *** positive regulation of cell differentiation - GO:0045597 - p: 1.26e-04 *** anatomical structure morphogenesis - GO:0009653 - p: 7.29e-08 ** negative regulation of nucleobase-containing compo... - GO:0045934 - p: 5.51e-08 *** positive regulation of transcription by RNA polyme... - GO:0045944 - p: 1.04e-06 *** cellular response to endogenous stimulus - GO:0071495 - p: 5.29e-06 *** response to endogenous stimulus - GO:0009719 - p: 1.61e-07 ** 뭐 negative regulation of RNA metabolic process - GO:0051253 - p: 2.09e-08 *** negative regulation of RNA biosynthetic process - GO:1902679 - p: 2.74e-08 *** negative regulation of DNA-templated transcription - GO:0045892 - p: 2.27e-08 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 8.30e-07 *** cellular response to nitrogen compound - GO:1901699 - p: 3.73e-05 *** animal organ morphogenesis - GO:0009887 - p: 3.34e-05 *** phosphorylation - GO:0016310 - p: 1.63e-05 *** protein phosphorylation - GO:0006468 - p: 3.84e-06 *** chromatin organization - GO:0006325 - p: 1.00e-10 *** chromatin remodeling - GO:0006338 - p: 1.00e-10 *** Gene Count neuron projection - GO:0043005 - p: 9.85e-04 *** 100 plasma membrane bounded cell projection - GO:0120025 - p: 4.24e-05 ** cell projection - GO:0042995 - p: 2.95e-05 *** perinuclear region of cytoplasm - GO:0048471 - p: 3.35e-04 *** somatodendritic compartment - GO:0036477 - p: 8.56e-04 *** dendritic tree - GO:0097447 - p: 1.91e-03 * dendrite - GO:0030425 - p: 1.91e-03 ** axon - GO:0030424 - p: 1.85e-03 * Cluster transcription regulator complex - GO:0005667 - p: 7.84e-05 *** chromatin - GO:0000785 - p: 1.00e-10 ** histone binding - GO:0042393 - p: 9.33e-07 *** transcription regulator activity - GO:0140110 - p: 8.23e-08 *** sequence-specific DNA binding - GO:0043565 - p: 2.04e-08 *** transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 4.38e-07 *** transcription cis-regulatory region binding - GO:0000976 - p: 4.38e-07 *** DNA-binding transcription factor activity - GO:0003700 - p: 3.91e-06 *** RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 1.29e-06 *** double-stranded DNA binding - GO:0003690 - p: 7.81e-09 *** sequence-specific double-stranded DNA binding - GO:1990837 - p: 1.31e-08 *** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 1.31e-06 *** chromatin binding - GO:0003682 - p: 1.46e-10 *** ₹ purine nucleotide binding - GO:0017076 - p: 7.96e-07 *** ribonucleotide binding - GO:0032553 - p: 2.56e-07 *** purine ribonucleotide binding - GO:0032555 - p: 5.92e-07 ** purine ribonucleoside triphosphate binding - GO:0035639 - p: 1.72e-07 *** adenyl nucleotide binding - GO:0030554 - p: 1.00e-10 ** adenyl ribonucleotide binding - GO:0032559 - p: 1.00e-10 *** ATP binding - GO:0005524 - p: 1.00e-10 *** protein kinase activity - GO:0004672 - p: 4.17e-07 *** histone modifying activity - GO:0140993 - p: 9.75e-09 *** histone H3 kinase activity - GO:0140996 - p: 6.85e-07 *** histone kinase activity - GO:0035173 - p: 6.85e-07 ***

1.4

Absolute NES

1.6

GO Term

histone H2AX kinase activity - GO:0141003 - p: 3.16e-07 ***

1.3