Tregs - IMM - Colon - InactiveCD_vs_Control Up protein phosphorylation - GO:0006468 - p: 1.72e-06 * phosphorylation - GO:0016310 - p: 7.54e-07 *** system process - GO:0003008 - p: 2.14e-07 *** tissue development - GO:0009888 - p: 4.01e-05 *** response to endogenous stimulus - GO:0009719 - p: 1.19e-05 *** cellular response to endogenous stimulus - GO:0071495 - p: 6.04e-05 ** regulation of cell differentiation - GO:0045595 - p: 1.04e-05 ** positive regulation of developmental process - GO:0051094 - p: 4.63e-05 *** regulation of multicellular organismal development - GO:2000026 - p: 2.28e-05 *** response to abiotic stimulus - GO:0009628 - p: 6.33e-06 * cellular response to hormone stimulus - GO:0032870 - p: 1.55e-04 *** positive regulation of cell differentiation - GO:0045597 - p: 5.42e-05 ** anatomical structure formation involved in morphog... - GO:0048646 - p: 2.75e-05 ** animal organ morphogenesis - GO:0009887 - p: 7.05e-05 *** negative regulation of DNA-templated transcription - GO:0045892 - p: 1.56e-10 ** negative regulation of RNA biosynthetic process - GO:1902679 - p: 1.01e-10 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 6.78e-09 *** cellular response to nitrogen compound - GO:1901699 - p: 1.38e-06 ** cellular response to peptide hormone stimulus - GO:0071375 - p: 7.28e-05 *** positive regulation of transcription by RNA polyme... - GO:0045944 - p: 1.00e-10 ** Cluster neuron projection - GO:0043005 - p: 1.17e-03 ** perinuclear region of cytoplasm - GO:0048471 - p: 1.83e-05 ** axon - GO:0030424 - p: 9.48e-04 *** somatodendritic compartment - GO:0036477 - p: 1.80e-04 *** S dendritic tree - GO:0097447 - p: 6.00e-04 *** 2 dendrite - GO:0030425 - p: 6.00e-04 *** Gene Count transcription regulator complex - GO:0005667 - p: 3.44e-04 *** chromatin - GO:0000785 - p: 1.00e-10 ** kinase activity - GO:0016301 - p: 8.81e-07 *** phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 5.40e-08 *** protein kinase activity - GO:0004672 - p: 4.30e-07 *** adenyl nucleotide binding - GO:0030554 - p: 1.00e-10 *** histone modifying activity - GO:0140993 - p: 2.19e-09 *** adenyl ribonucleotide binding - GO:0032559 - p: 1.00e-10 *** ATP binding - GO:0005524 - p: 1.00e-10 *** histone kinase activity - GO:0035173 - p: 9.33e-07 *** histone H3 kinase activity - GO:0140996 - p: 1.81e-06 *** cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 2.94e-07 ** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 3.03e-07 *** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 1.19e-07 *** DNA-binding transcription factor activity - GO:0003700 - p: 9.18e-08 *** double-stranded DNA binding - GO:0003690 - p: 1.00e-10 *** sequence-specific DNA binding - GO:0043565 - p: 1.00e-10 *** transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 4.87e-10 *** transcription cis-regulatory region binding - GO:0000976 - p: 4.87e-10 *** sequence-specific double-stranded DNA binding - GO:1990837 - p: 1.13e-10 *** transcription regulator activity - GO:0140110 - p: 1.00e-10 *** RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 2.89e-09 *** histone binding - GO:0042393 - p: 7.54e-07 *** chromatin binding - GO:0003682 - p: 1.00e-10 *** 1.4 1.3 Absolute NES

GO Term