T\_cells\_CD8 - IMM - Colon - ActiveCD\_vs\_Control Up response to nitrogen compound - GO:1901698 - p: 3.12e-05 \*\*\* cellular response to nitrogen compound - GO:1901699 - p: 4.21e-05 \*\*\* system process - GO:0003008 - p: 1.47e-05 \*\*\* regulation of cell differentiation - GO:0045595 - p: 3.45e-05 \*\*\* anatomical structure morphogenesis - GO:0009653 - p: 3.24e-07 \*\*\* positive regulation of developmental process - GO:0051094 - p: 5.70e-06 \*\* negative regulation of nucleobase-containing compo... - GO:0045934 - p: 1.46e-10 \*\*\* negative regulation of transcription by RNA polyme... - GO:0000122 - p: 4.09e-07 \*\*\* negative regulation of RNA metabolic process - GO:0051253 - p: 1.32e-10 \*\*\* BP negative regulation of RNA biosynthetic process - GO:1902679 - p: 1.60e-09 \*\* negative regulation of DNA-templated transcription - GO:0045892 - p: 6.37e-10 \*\*\* positive regulation of transcription by RNA polyme... - GO:0045944 - p: 2.41e-09 \*\*\* positive regulation of DNA-templated transcription - GO:0045893 - p: 1.00e-10 \*\*\* positive regulation of RNA biosynthetic process - GO:1902680 - p: 1.00e-10 \*\*\* phosphorylation - GO:0016310 - p: 1.84e-06 \*\*\* protein phosphorylation - GO:0006468 - p: 7.54e-07 \*\*\* chromatin organization - GO:0006325 - p: 1.00e-10 \*\*\* chromatin remodeling - GO:0006338 - p: 1.00e-10 \*\*\* cytoplasmic side of plasma membrane - GO:0009898 - p: 1.79e-03 \* extrinsic component of plasma membrane - GO:0019897 - p: 2.77e-03 \* Gene Count plasma membrane bounded cell projection - GO:0120025 - p: 1.83e-04 \*\*\* cell projection - GO:0042995 - p: 9.76e-05 \*\* perinuclear region of cytoplasm - GO:0048471 - p: 3.90e-05 \*\*\* dendritic tree - GO:0097447 - p: 3.50e-03 \* dendrite - GO:0030425 - p: 3.50e-03 \* somatodendritic compartment - GO:0036477 - p: 1.36e-04 \*\* neuron projection - GO:0043005 - p: 8.55e-06 \*\*\* axon - GO:0030424 - p: 5.08e-05 \*\*\* Cluster chromosome - GO:0005694 - p: 2.48e-09 \*\*\* chromatin - GO:0000785 - p: 1.00e-10 \*\* transcription regulator activity - GO:0140110 - p: 5.11e-09 \*\*\* transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 2.53e-06 \*\*\* transcription cis-regulatory region binding - GO:0000976 - p: 2.53e-06 \*\*\* sequence-specific DNA binding - GO:0043565 - p: 8.20e-09 \*\*\* double-stranded DNA binding - GO:0003690 - p: 2.79e-08 \*\*\* sequence-specific double-stranded DNA binding - GO:1990837 - p: 1.49e-07 \*\*\* chromatin binding - GO:0003682 - p: 4.08e-10 \*\*\* histone binding - GO:0042393 - p: 4.91e-07 \*\*\* nucleotide binding - GO:0000166 - p: 1.81e-06 \*\*\* carbohydrate derivative binding - GO:0097367 - p: 1.62e-06 \*\*\* purine nucleotide binding - GO:0017076 - p: 2.35e-07 \*\*\* ₹ ribonucleotide binding - GO:0032553 - p: 9.91e-08 \*\*\* purine ribonucleotide binding - GO:0032555 - p: 9.49e-08 \*\*\* purine ribonucleoside triphosphate binding - GO:0035639 - p: 2.43e-08 \*\* adenyl nucleotide binding - GO:0030554 - p: 2.99e-09 \*\*\* adenyl ribonucleotide binding - GO:0032559 - p: 1.40e-10 \*\*\* ATP binding - GO:0005524 - p: 1.00e-10 \*\*\* histone modifying activity - GO:0140993 - p: 5.13e-09 \*\*\* phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 1.66e-08 \*\*\* protein kinase activity - GO:0004672 - p: 2.44e-09 \*\*\* histone H2AX kinase activity - GO:0141003 - p: 8.31e-09 \*\*\* histone H3 kinase activity - GO:0140996 - p: 7.44e-09 \*\*\*

1.6

Absolute NES

1.8

1

2.0

GO Term

histone kinase activity - GO:0035173 - p: 7.44e-09 \*\*\*

1.4