IgA_plasma_cell - IMM - Ileum - InactiveCD_vs_Control Up sprouting angiogenesis - GO:0002040 - p: 5.17e-04 *** response to heat - GO:0009408 - p: 4.81e-04 *** mitochondrial respiratory chain complex assembly - GO:0033108 - p: 3.53e-04 *** peptidyl-tyrosine phosphorylation - GO:0018108 - p: 5.45e-04 *** peptidyl-tyrosine modification - GO:0018212 - p: 3.31e-04 *** adaptive immune response - GO:0002250 - p: 2.35e-04 *** cytoskeleton organization - GO:0007010 - p: 1.82e-04 *** actin filament organization - GO:0007015 - p: 4.77e-04 *** T cell migration - GO:0072678 - p: 3.73e-04 *** 3 lymphocyte migration - GO:0072676 - p: 4.26e-05 *** mRNA metabolic process - GO:0016071 - p: 4.11e-04 *** negative regulation of gene expression - GO:0010629 - p: 2.63e-04 *** nucleobase-containing compound catabolic process - GO:0034655 - p: 2.10e-05 *** mRNA catabolic process - GO:0006402 - p: 7.54e-05 *** nucleic acid catabolic process - GO:0141188 - p: 3.44e-05 *** regulation of mRNA catabolic process - GO:0061013 - p: 2.42e-04 *** RNA catabolic process - GO:0006401 - p: 3.64e-05 *** regulation of mRNA processing - GO:0050684 - p: 1.81e-04 *** Gene Count regulation of mRNA metabolic process - GO:1903311 - p: 1.99e-06 *** tissue development - GO:0009888 - p: 4.94e-04 *** negative regulation of RNA metabolic process - GO:0051253 - p: 2.69e-04 *** negative regulation of signaling - GO:0023057 - p: 2.12e-04 *** negative regulation of cell communication - GO:0010648 - p: 2.14e-04 *** regulation of cell cycle - GO:0051726 - p: 2.70e-04 *** negative regulation of signal transduction - GO:0009968 - p: 1.02e-04 *** locomotion - GO:0040011 - p: 4.29e-04 *** negative regulation of multicellular organismal pr... - GO:0051241 - p: 5.58e-04 *** response to abiotic stimulus - GO:0009628 - p: 2.14e-04 *** Cluster regulation of cell motility - GO:2000145 - p: 4.94e-04 *** regulation of locomotion - GO:0040012 - p: 4.86e-04 *** regulation of cell migration - GO:0030334 - p: 4.83e-04 *** enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 3.92e-04 *** circulatory system development - GO:0072359 - p: 3.59e-04 *** regulation of multicellular organismal development – GO:2000026 – p: 5.25e-05 *** response to cytokine - GO:0034097 - p: 1.53e-04 *** regulation of cell development - GO:0060284 - p: 4.07e-04 *** response to peptide - GO:1901652 - p: 3.96e-05 *** cell adhesion - GO:0007155 - p: 3.12e-05 *** negative regulation of cell differentiation - GO:0045596 - p: 3.66e-04 *** cellular response to cytokine stimulus – GO:0071345 – p: 6.77e-05 *** negative regulation of developmental process – GO:0051093 – p: 1.19e–04 *** cellular response to lipid - GO:0071396 - p: 5.26e-04 *** cellular response to endogenous stimulus - GO:0071495 - p: 5.81e-06 *** response to lipid - GO:0033993 - p: 1.70e-05 *** positive regulation of programmed cell death - GO:0043068 - p: 8.43e-05 *** positive regulation of apoptotic process - GO:0043065 - p: 5.33e-05 *** response to hormone - GO:0009725 - p: 9.79e-06 *** response to endogenous stimulus - GO:0009719 - p: 7.64e-08 *** response to growth factor - GO:0070848 - p: 1.23e-05 *** cellular response to growth factor stimulus - GO:0071363 - p: 3.00e-05 *** immunoglobulin complex - GO:0019814 - p: 1.99e-04 *** CC chromatin - GO:0000785 - p: 1.50e-04 *** G-protein alpha-subunit binding - GO:0001965 - p: 5.66e-04 *** chloride channel activity - GO:0005254 - p: 4.95e-04 *** enzyme regulator activity - GO:0030234 - p: 4.07e-04 *** molecular function inhibitor activity - GO:0140678 - p: 1.43e-04 *** adenyl nucleotide binding - GO:0030554 - p: 4.08e-04 *** adenyl ribonucleotide binding - GO:0032559 - p: 1.80e-04 *** ATP binding - GO:0005524 - p: 1.33e-04 *** ribonucleoside triphosphate phosphatase activity - GO:0017111 - p: 5.88e-04 *** electron transfer activity - GO:0009055 - p: 3.72e-04 *** protein-containing complex binding - GO:0044877 - p: 5.11e-04 *** protein kinase binding - GO:0019901 - p: 6.16e-04 ***

1.8

2.0

Absolute NES

1.6

2.0

kinase binding - GO:0019900 - p: 1.56e-04 **