Macrophages\_CCL3\_CCL4 - IMM - Colon - ActiveCD\_vs\_Control response to interleukin-15 - GO:0070672 - p: 2.37e-04 \*\*\* protein autophosphorylation - GO:0046777 - p: 1.83e-05 \*\*\* negative regulation of transcription by RNA polyme... - GO:0000122 - p: 1.10e-05 \*\*\* cellular response to organic cyclic compound - GO:0071407 - p: 1.46e-04 \*\*\* enzyme-linked receptor protein signaling pathway - GO:0007167 - p: 7.71e-06 \*\*\* transmembrane receptor protein serine/threonine ki... - GO:0007178 - p: 4.04e-06 \*\*\* regulation of transmembrane receptor protein serin... - GO:0090092 - p: 4.46e-05 \*\*\* cellular response to cytokine stimulus - GO:0071345 - p: 2.26e-04 \*\*\* lymphocyte activation - GO:0046649 - p: 1.21e-04 \*\* regulation of cell adhesion - GO:0030155 - p: 2.17e-04 multicellular organismal-level homeostasis - GO:0048871 - p: 1.58e-04 \* regulation of cell development - GO:0060284 - p: 2.08e-05 \*\* mononuclear cell differentiation - GO:1903131 - p: 6.37e-05 \*\* positive regulation of cell differentiation - GO:0045597 - p: 5.70e-06 leukocyte differentiation - GO:0002521 - p: 3.63e-06 \*\*\* Gene Count cytokine-mediated signaling pathway - GO:0019221 - p: 2.42e-05 \*\* lymphocyte differentiation - GO:0030098 - p: 1.38e-05 \*\*\* T cell differentiation - GO:0030217 - p: 1.44e-04 \*\*\* lymphocyte activation involved in immune response – GO:0002285 – p: 3.79e–05 \*\*\* CD4-positive, alpha-beta T cell activation - GO:0035710 - p: 1.53e-04 \*\*\* epithelium development - GO:0060429 - p: 8.18e-05 \*\*\* tube development - GO:0035295 - p: 5.64e-05 GO Term Cluster anatomical structure formation involved in morphog... - GO:0048646 - p: 7.29e-06 neuron projection development - GO:0031175 - p: 1.86e-05 \*\* neuron development - GO:0048666 - p: 2.56e-06 3 regulation of anatomical structure morphogenesis - GO:0022603 - p: 5.56e-06 tissue morphogenesis - GO:0048729 - p: 2.44e-04 \*\*\* animal organ morphogenesis - GO:0009887 - p: 3.91e-06 \*\*\* chromatin organization - GO:0006325 - p: 2.22e-07 \*\*\* chromatin remodeling - GO:0006338 - p: 6.60e-07 \*\*\* 8 perinuclear region of cytoplasm - GO:0048471 - p: 8.40e-05 \*\*\* kinase activity - GO:0016301 - p: 2.28e-05 \*\* phosphotransferase activity, alcohol group as acce... - GO:0016773 - p: 1.41e-06 \*\* protein kinase activity - GO:0004672 - p: 7.45e-07 transcription factor binding - GO:0008134 - p: 2.67e-04 \*\* RNA polymerase II-specific DNA-binding transcripti... - GO:0061629 - p: 8.29e-04 \*\* cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 1.09e-06 \*\*\* RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 7.54e-07 \*\*\* RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 1.91e-07 \*\*\* DNA-binding transcription factor activity - GO:0003700 - p: 8.65e-08 \*\* DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 2.35e-07 \*\*\* histone binding - GO:0042393 - p: 2.57e-04 \*\*\* chromatin binding - GO:0003682 - p: 9.67e-07 \*\*\* histone modifying activity - GO:0140993 - p: 1.57e-06 \*\* 1.4 1.6 1.8 Absolute NES