L_cells - EPI - Ileum - InactiveCD_vs_Control Down Up monocarboxylic acid transport - GO:0015718 - p: 1.56e-04 * sensory perception of pain - GO:0019233 - p: 5.28e-05 *** 4 skeletal muscle cell differentiation - GO:0035914 - p: 2.65e-05 *** positive regulation of transcription by RNA polyme... - GO:0045944 - p: 1.73e-06 *** G protein-coupled receptor signaling pathway - GO:0007186 - p: 1.29e-06 lipid metabolic process - GO:0006629 - p: 1.46e-04 *** 뭐 glycerolipid metabolic process - GO:0046486 - p: 1.09e-05 ** protein-lipid complex assembly - GO:0065005 - p: 9.20e-05 ** triglyceride biosynthetic process - GO:0019432 - p: 6.55e-06 *** acylglycerol metabolic process - GO:0006639 - p: 5.18e-08 *** 0 neutral lipid metabolic process - GO:0006638 - p: 5.18e-08 ** 0 triglyceride metabolic process - GO:0006641 - p: 4.27e-10 ** cluster of actin-based cell projections - GO:0098862 - p: 4.84e-04 *** 8 brush border membrane - GO:0031526 - p: 1.86e-04 ** Gene Count င္ပ secretory vesicle - GO:0099503 - p: 6.11e-05 *** 100 secretory granule - GO:0030141 - p: 6.35e-05 *** chromatin - GO:0000785 - p: 1.71e-04 ** 1 protein heterodimerization activity - GO:0046982 - p: 8.31e-04 ** transcription regulator inhibitor activity - GO:0140416 - p: 9.44e-04 *** protein folding chaperone - GO:0044183 - p: 3.64e-04 *** ATP-dependent protein folding chaperone - GO:0140662 - p: 3.32e-04 *** Cluster guanyl ribonucleotide binding - GO:0032561 - p: 2.45e-04 *** GO Term guanyl nucleotide binding - GO:0019001 - p: 2.45e-04 *** GTP binding - GO:0005525 - p: 3.77e-04 *** solute:sodium symporter activity - GO:0015370 - p: 3.82e-04 *** transcription regulator activity - GO:0140110 - p: 1.04e-04 *** DNA-binding transcription factor activity - GO:0003700 - p: 4.39e-05 ** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 6.53e-05 ** double-stranded DNA binding - GO:0003690 - p: 3.54e-06 *** sequence-specific DNA binding - GO:0043565 - p: 8.78e-07 *** RNA polymerase II transcription regulatory region ... - GO:0000977 - p: 2.29e-06 ** cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 4.46e-06 *** transcription regulatory region nucleic acid bindi... - GO:0001067 - p: 1.10e-06 *** • 11 transcription cis-regulatory region binding - GO:0000976 - p: 1.10e-06 ** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 3.08e-06 *** sequence-specific double-stranded DNA binding - GO:1990837 - p: 3.39e-07 *** DNA-binding transcription activator activity, RNA ... - GO:0001228 - p: 6.20e-07 *** DNA-binding transcription activator activity - GO:0001216 - p: 6.20e-07 *** signaling receptor binding - GO:0005102 - p: 1.36e-04 *** molecular function activator activity - GO:0140677 - p: 8.06e-05 *** receptor ligand activity - GO:0048018 - p: 2.04e-04 *** signaling receptor activator activity - GO:0030546 - p: 2.31e-04 *** signaling receptor regulator activity - GO:0030545 - p: 1.84e-04 *** hormone activity - GO:0005179 - p: 3.46e-04 ** 2 G protein-coupled receptor binding - GO:0001664 - p: 2.16e-05 *** lipid transporter activity - GO:0005319 - p: 9.95e-04 *** lipid transfer activity - GO:0120013 - p: 9.06e-04 0 1.50 1.75 2.00 2.25 2.50 1.50 1.75 2.00 2.25 2.50 Absolute NES