IELs_ID3_ENTPD1 - IMM - Ileum - InactiveCD_vs_Control Up negative regulation of apoptotic signaling pathway – GO:2001234 – p: 1.05e–04 *** negative regulation of extrinsic apoptotic signali... – GO:2001237 – p: 1.39e–04 *** negative regulation of small molecule metabolic pr... - GO:0062014 - p: 5.68e-05 *** negative regulation of transcription by RNA polyme... - GO:0000122 - p: 5.47e-05 *** skeletal muscle cell differentiation - GO:0035914 - p: 2.61e-05 *** response to topologically incorrect protein - GO:0035966 - p: 1.95e-05 *** response to unfolded protein - GO:0006986 - p: 2.25e-05 *** regulation of heterotypic cell-cell adhesion – GO:0034114 – p: 1.07e-04 *** ΒP heterotypic cell-cell adhesion - GO:0034113 - p: 5.82e-06 *** 2 aerobic respiration - GO:0009060 - p: 1.06e-04 *** Gene Count oxidative phosphorylation - GO:0006119 - p: 1.12e-04 *** respiratory electron transport chain - GO:0022904 - p: 6.97e-05 *** proton motive force-driven mitochondrial ATP synth... - GO:0042776 - p: 1.80e-04 *** mitochondrial ATP synthesis coupled electron trans... - GO:0042775 - p: 5.62e-06 *** ATP synthesis coupled electron transport – GO:0042773 – p: 5.62e–06 ** aerobic electron transport chain - GO:0019646 - p: 1.79e-05 *** Cluster GO Term nuclear speck - GO:0016607 - p: 1.22e-04 *** transcription regulator complex - GO:0005667 - p: 2.58e-04 *** respiratory chain complex - GO:0098803 - p: 1.60e-05 *** respiratory chain complex I - GO:0045271 - p: 2.81e-04 *** NADH dehydrogenase complex - GO:0030964 - p: 2.81e-04 *** tumor necrosis factor receptor superfamily binding - GO:0032813 - p: 6.49e-04 *** cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p: 6.92e-04 *** RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p: 5.28e-04 *** DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p: 4.22e-04 *** monocarboxylic acid binding - GO:0033293 - p: 2.41e-04 *** fatty acid binding - GO:0005504 - p: 1.85e-04 *** ₹ transcription coregulator activity - GO:0003712 - p: 4.37e-04 *** transcription corepressor activity - GO:0003714 - p: 4.94e-04 *** proton transmembrane transporter activity - GO:0015078 - p: 4.48e-04 *** NADH dehydrogenase activity - GO:0003954 - p: 3.10e-04 *** electron transfer activity - GO:0009055 - p: 9.64e-06 ** oxidoreduction-driven active transmembrane transpo... - GO:0015453 - p: 2.28e-05 ** NADH dehydrogenase (ubiquinone) activity - GO:0008137 - p: 6.45e-05 *** 1.5 1.7 1.9 2.1 1.5 1.7 1.9 2.1 Absolute NES