T\_cells\_CD8\_KLRG1 - IMM - Ileum - InactiveCD\_vs\_Control Up mitochondrial translation - GO:0032543 - p: 1.59e-04 \*\*\* defense response to Gram-negative bacterium - GO:0050829 - p: 5.29e-05 \*\*\* 6 cellular response to hormone stimulus – GO:0032870 – p: 5.11e-05 \*\*\* cellular response to steroid hormone stimulus – GO:0071383 – p: 1.72e–04 \*\*\* nitric oxide biosynthetic process - GO:0006809 - p: 1.05e-04 \*\*\* regulation of nitric oxide metabolic process - GO:0080164 - p: 4.90e-05 \*\*\* regulation of nitric oxide biosynthetic process – GO:0045428 – p: 4.90e–05 \*\*\* ВР regulation of digestive system process - GO:0044058 - p: 1.94e-05 \*\*\* Gene Count chaperone-mediated protein folding - GO:0061077 - p: 1.72e-04 \*\*\* response to unfolded protein – GO:0006986 – p: 1.52e–05 \*\*\* response to topologically incorrect protein - GO:0035966 - p: 3.22e-06 \*\*\* negative regulation of inclusion body assembly - GO:0090084 - p: 6.71e-05 \*\*\* GO Term protein folding - GO:0006457 - p: 1.80e-07 \*\*\* Cluster 'de novo' protein folding - GO:0006458 - p: 7.45e-05 \*\*\* chaperone cofactor-dependent protein refolding - GO:0051085 - p: 4.50e-05 \*\*\* neuron projection - GO:0043005 - p: 1.69e-04 \*\*\* somatodendritic compartment - GO:0036477 - p: 1.11e-04 \*\*\* S dendritic tree - GO:0097447 - p: 1.57e-04 \*\*\* dendrite - GO:0030425 - p: 1.57e-04 \*\*\* neuronal cell body - GO:0043025 - p: 2.12e-04 \*\*\* transmembrane signaling receptor activity – GO:0004888 – p: 1.75e–04 \*\*\* immune receptor activity - GO:0140375 - p: 9.92e-06 \*\*\* protein-folding chaperone binding - GO:0051087 - p: 2.89e-04 \*\*\* unfolded protein binding - GO:0051082 - p: 4.38e-06 \*\*\* ATP-dependent protein folding chaperone - GO:0140662 - p: 1.05e-04 \*\*\* 0 1.6 1.8 2.0 2.2 1.6 1.8 2.0 2.2 Absolute NES