

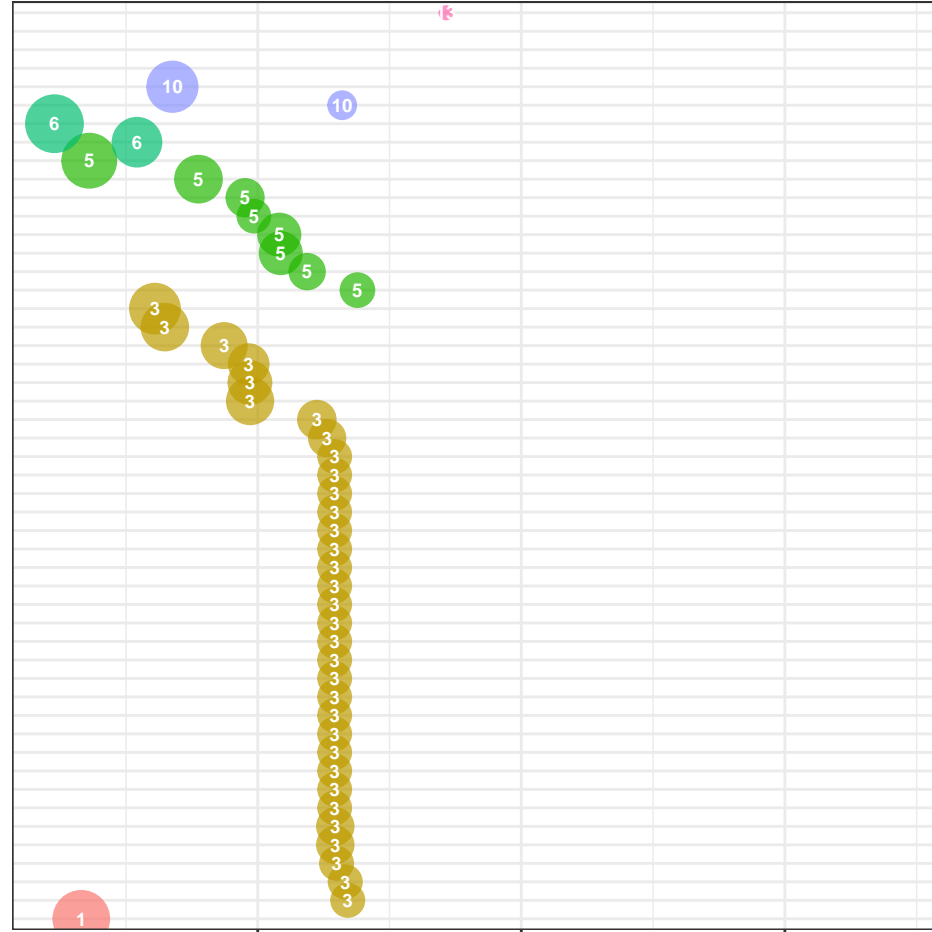
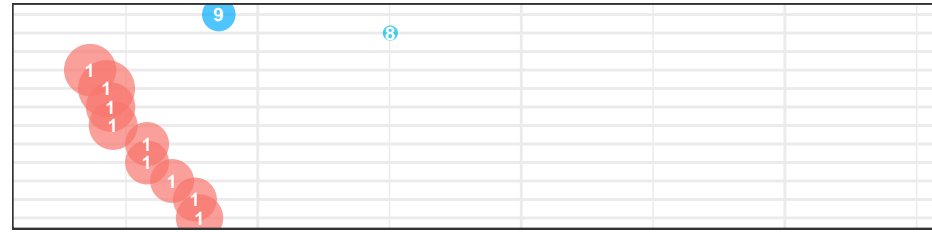
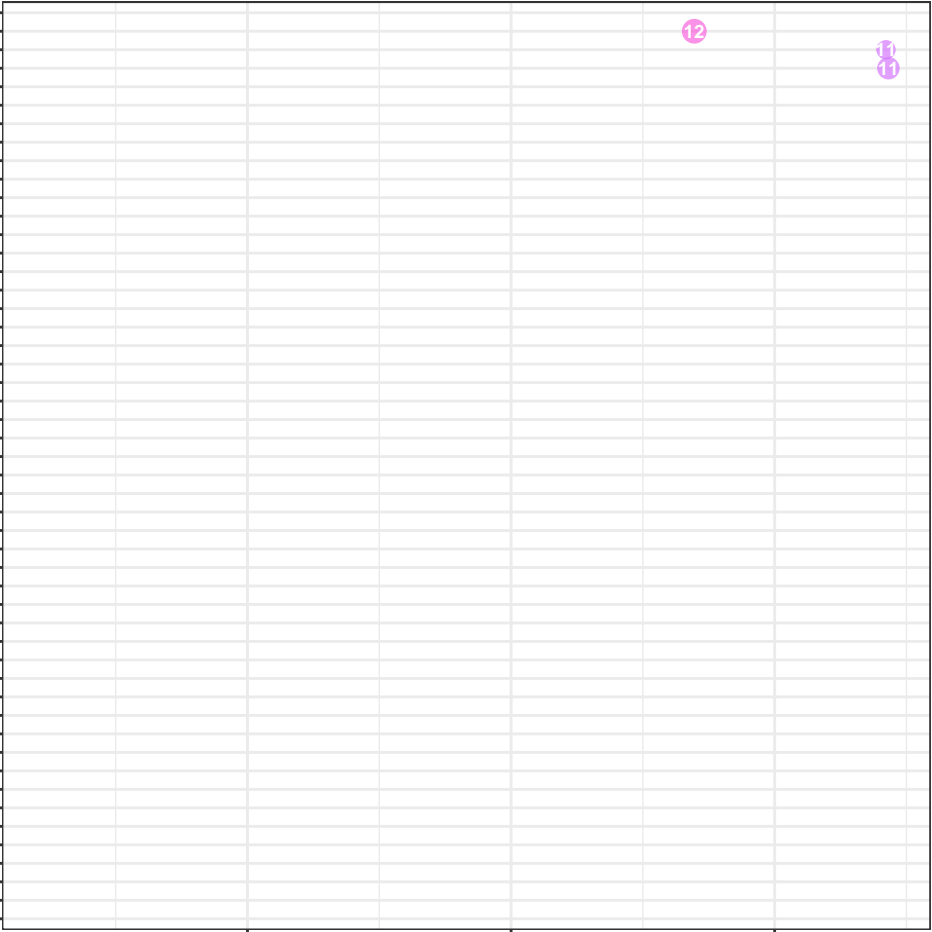
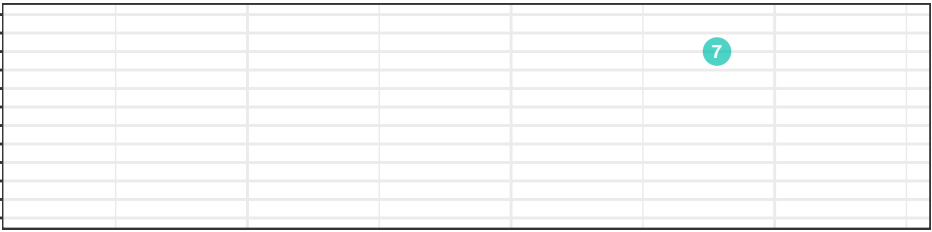
Lymphatics – STR – Ileum – InactiveCD\_vs\_Control

GO Term

|   |            |             |     |
|---|------------|-------------|-----|
| heterochromatin formation                             | GO:0031507 | p: 5.04e-05 | *** |
| regulation of small GTPase mediated signal transdu... | GO:0051056 | p: 3.81e-05 | *** |
| regulation of GTPase activity                         | GO:0043087 | p: 1.43e-05 | *** |
| mammary gland development                             | GO:0030879 | p: 4.98e-05 | *** |
| regulation of cell size                               | GO:0008361 | p: 6.88e-06 | *** |
| phosphorylation                                       | GO:0016310 | p: 1.55e-06 | *** |
| protein phosphorylation                               | GO:0006468 | p: 1.27e-06 | *** |
| response to nitrogen compound                         | GO:1901698 | p: 3.18e-06 | *** |
| vasculature development                               | GO:0001944 | p: 2.39e-05 | *** |
| circulatory system development                        | GO:0072359 | p: 9.33e-07 | *** |
| animal organ morphogenesis                            | GO:0009887 | p: 1.58e-05 | *** |
| positive regulation of developmental process          | GO:0051094 | p: 3.20e-07 | *** |
| anatomical structure formation involved in morphog... | GO:0048646 | p: 6.17e-07 | *** |
| enzyme-linked receptor protein signaling pathway      | GO:0007167 | p: 1.29e-06 | *** |
| blood vessel development                              | GO:0001568 | p: 6.39e-06 | *** |
| tube morphogenesis                                    | GO:0035239 | p: 2.80e-06 | *** |
| heart development                                     | GO:0007507 | p: 2.33e-05 | *** |
| head development                                      | GO:0060322 | p: 6.74e-06 | *** |
| blood vessel morphogenesis                            | GO:0048514 | p: 2.42e-06 | *** |
| brain development                                     | GO:0007420 | p: 8.68e-06 | *** |
| tube development                                      | GO:0035295 | p: 2.22e-08 | *** |
| response to peptide hormone                           | GO:0043434 | p: 1.08e-05 | *** |
| regulation of anatomical structure morphogenesis      | GO:0022603 | p: 2.18e-07 | *** |
| cellular response to nitrogen compound                | GO:1901699 | p: 9.67e-07 | *** |
| cell surface receptor protein tyrosine kinase sign... | GO:0007169 | p: 3.49e-07 | *** |
| sensory system development                            | GO:0048880 | p: 4.16e-05 | *** |
| developmental growth                                  | GO:0048589 | p: 1.55e-07 | *** |
| response to insulin                                   | GO:0032868 | p: 2.01e-05 | *** |
| multicellular organism growth                         | GO:0035264 | p: 7.38e-05 | *** |
| cellular response to insulin stimulus                 | GO:0032869 | p: 1.30e-05 | *** |
| insulin receptor signaling pathway                    | GO:0008286 | p: 7.23e-05 | *** |
| insulin-like growth factor receptor signaling path... | GO:0048009 | p: 3.11e-06 | *** |
| neuron differentiation                                | GO:0030182 | p: 1.99e-07 | *** |
| positive regulation of cellular component organiza... | GO:0051130 | p: 7.50e-08 | *** |
| neuron development                                    | GO:0048666 | p: 8.44e-08 | *** |
| actin cytoskeleton organization                       | GO:0030036 | p: 2.61e-07 | *** |
| actin filament-based process                          | GO:0030029 | p: 8.55e-08 | *** |
| cell morphogenesis                                    | GO:0000902 | p: 1.19e-07 | *** |
| regulation of neuron projection development           | GO:0010975 | p: 4.32e-05 | *** |
| neuron projection development                         | GO:0031175 | p: 5.88e-09 | *** |
| synapse organization                                  | GO:0050808 | p: 1.11e-05 | *** |
| cell projection morphogenesis                         | GO:0048858 | p: 2.69e-07 | *** |
| cell morphogenesis involved in neuron differentiat... | GO:0048667 | p: 3.49e-06 | *** |
| plasma membrane bounded cell projection morphogene... | GO:0120039 | p: 3.63e-07 | *** |
| neuron projection morphogenesis                       | GO:0048812 | p: 1.93e-07 | *** |
| cell junction assembly                                | GO:0034329 | p: 9.50e-07 | *** |
| cell junction organization                            | GO:0034330 | p: 5.74e-10 | *** |
| positive regulation of cell projection organizatio... | GO:0031346 | p: 8.18e-07 | *** |
| dendrite development                                  | GO:0016358 | p: 1.87e-06 | *** |
| dendrite morphogenesis                                | GO:0048813 | p: 1.46e-05 | *** |

|                                   |            |             |     |
|-----------------------------------|------------|-------------|-----|
| receptor complex                  | GO:0043235 | p: 1.04e-03 | **  |
| PRC1 complex                      | GO:0035102 | p: 4.16e-04 | *** |
| cytosolic large ribosomal subunit | GO:0022625 | p: 1.50e-06 | *** |
| plasma membrane region            | GO:0098590 | p: 5.36e-04 | *** |
| neuron projection                 | GO:0043005 | p: 6.71e-05 | *** |
| postsynapse                       | GO:0098794 | p: 7.01e-04 | *** |
| somatodendritic compartment       | GO:0036477 | p: 4.99e-04 | *** |
| dendritic tree                    | GO:0097447 | p: 3.40e-04 | *** |
| dendrite                          | GO:0030425 | p: 3.40e-04 | *** |
| cell-cell junction                | GO:0005911 | p: 9.54e-05 | *** |
| cell leading edge                 | GO:0031252 | p: 3.40e-05 | *** |
| actin cytoskeleton                | GO:0015629 | p: 1.09e-05 | *** |

|   |            |             |     |
|---|------------|-------------|-----|
| insulin-like growth factor binding                    | GO:0005520 | p: 1.63e-04 | *** |
| alcohol binding                                       | GO:0043178 | p: 5.93e-05 | *** |
| fatty acid binding                                    | GO:0005504 | p: 9.80e-06 | *** |
| monocarboxylic acid binding                           | GO:0033293 | p: 1.26e-05 | *** |
| protein domain specific binding                       | GO:0019904 | p: 1.87e-06 | *** |
| SH3 domain binding                                    | GO:0017124 | p: 7.36e-05 | *** |
| double-stranded DNA binding                           | GO:0003690 | p: 2.94e-04 | *** |
| chromatin binding                                     | GO:0003682 | p: 3.90e-05 | *** |
| molecular function activator activity                 | GO:0140677 | p: 1.69e-04 | *** |
| enzyme activator activity                             | GO:0008047 | p: 1.53e-06 | *** |
| GTPase binding  | GO:0051020 | p: 1.89e-05 | *** |
| guanyl-nucleotide exchange factor activity            | GO:0005085 | p: 1.89e-04 | *** |
| nucleoside-triphosphatase regulator activity          | GO:0060589 | p: 7.09e-08 | *** |
| GTPase regulator activity                             | GO:0030695 | p: 2.38e-08 | *** |
| small GTPase binding                                  | GO:0031267 | p: 3.57e-06 | *** |
| GTPase activator activity                             | GO:0005096 | p: 7.22e-07 | *** |
| transferase activity, transferring phosphorus-cont... | GO:0016772 | p: 6.19e-06 | *** |
| kinase activity                                       | GO:0016301 | p: 1.08e-05 | *** |
| phosphotransferase activity, alcohol group as acce... | GO:0016773 | p: 4.90e-07 | *** |
| protein serine/threonine kinase activity              | GO:0004674 | p: 2.36e-06 | *** |
| protein kinase activity                               | GO:0004672 | p: 5.16e-07 | *** |
| histone modifying activity                            | GO:0140993 | p: 2.04e-08 | *** |
| protein serine kinase activity                        | GO:0106310 | p: 1.85e-07 | *** |
| histone H2AX kinase activity                          | GO:0141003 | p: 3.54e-07 | *** |
| histone H2AT120 kinase activity                       | GO:1990244 | p: 2.44e-06 | *** |
| histone H2B kinase activity                           | GO:0140998 | p: 2.44e-06 | *** |
| histone H4 kinase activity                            | GO:0140997 | p: 2.44e-06 | *** |
| histone H2A kinase activity                           | GO:0140995 | p: 2.44e-06 | *** |
| histone H3S57 kinase activity                         | GO:0140855 | p: 2.44e-06 | *** |
| histone H2BS36 kinase activity                        | GO:0140823 | p: 2.44e-06 | *** |
| Rho-dependent protein serine/threonine kinase acti... | GO:0072518 | p: 2.44e-06 | *** |
| histone H2AS121 kinase activity                       | GO:0072371 | p: 2.44e-06 | *** |
| histone H3T3 kinase activity                          | GO:0072354 | p: 2.44e-06 | *** |
| histone H2BS14 kinase activity                        | GO:0044025 | p: 2.44e-06 | *** |
| histone H2AS1 kinase activity                         | GO:0044024 | p: 2.44e-06 | *** |
| histone H4S1 kinase activity                          | GO:0044023 | p: 2.44e-06 | *** |
| histone H3S28 kinase activity                         | GO:0044022 | p: 2.44e-06 | *** |
| histone H2AXS139 kinase activity                      | GO:0035979 | p: 2.44e-06 | *** |
| histone H3T6 kinase activity                          | GO:0035403 | p: 2.44e-06 | *** |
| histone H3S10 kinase activity                         | GO:0035175 | p: 2.44e-06 | *** |
| ribosomal protein S6 kinase activity                  | GO:0004711 | p: 2.44e-06 | *** |
| eukaryotic translation initiation factor 2alpha ki... | GO:0004694 | p: 2.44e-06 | *** |
| DNA-dependent protein kinase activity                 | GO:0004677 | p: 2.44e-06 | *** |
| 3-phosphoinositide-dependent protein kinase activi... | GO:0004676 | p: 2.44e-06 | *** |
| histone H3 kinase activity                            | GO:0140996 | p: 6.53e-07 | *** |
| histone kinase activity                               | GO:0035173 | p: 6.53e-07 | *** |
| AMP-activated protein kinase activity                 | GO:0004679 | p: 2.40e-06 | *** |
| histone H3T11 kinase activity                         | GO:0035402 | p: 1.75e-06 | *** |
| histone H3T45 kinase activity                         | GO:0140857 | p: 1.33e-06 | *** |
| cytoskeletal protein binding                          | GO:0008092 | p: 1.33e-04 | *** |

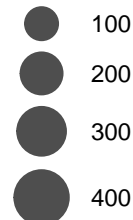


BP

CC

MF

Gene Count



Cluster



Absolute NES