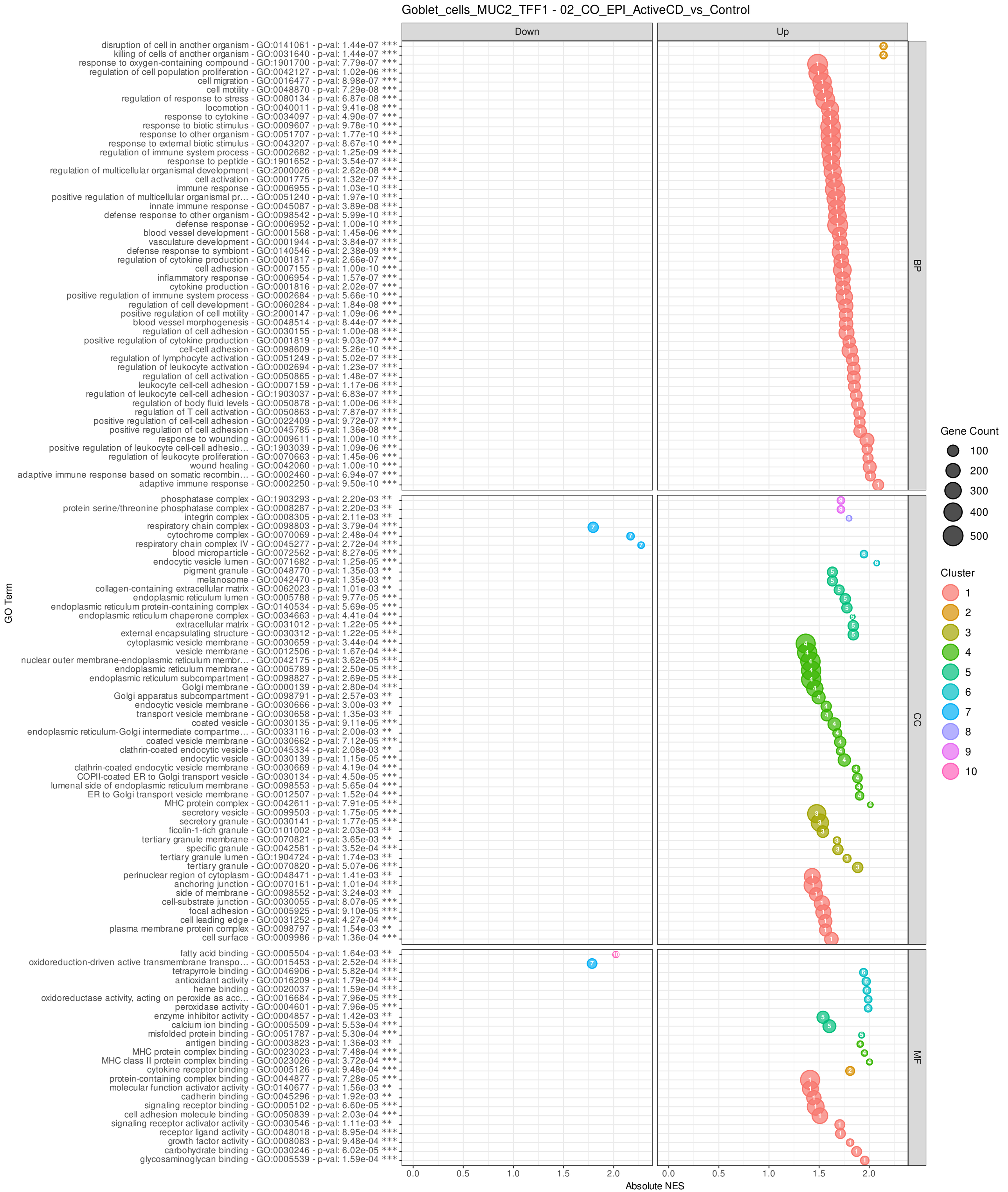
Goblet_cells_MUC2_TFF1 - 02_CO_EPI_ActiveCD_vs_Control
Down
Up
BP
CC
MF
GO Term
disruption of cell in another organism - GO:0141061 - p-val: 1.44e-07 ***
killing of cells of another organism - GO:0031640 - p-val: 1.44e-07 ***
response to oxygen-containing compound - GO:1901700 - p-val: 7.79e-07 ***
regulation of cell population proliferation - GO:0042127 - p-val: 1.02e-06 ***
cell migration - GO:0016477 - p-val: 8.98e-07 ***
cell motility - GO:0048870 - p-val: 7.29e-08 ***
regulation of response to stress - GO:0080134 - p-val: 6.87e-08 ***
locomotion - GO:0040011 - p-val: 9.41e-08 ***
response to cytokine - GO:0034097 - p-val: 4.90e-07 ***
response to biotic stimulus - GO:0009607 - p-val: 9.78e-10 ***
response to other organism - GO:0051707 - p-val: 1.77e-10 ***
response to external biotic stimulus - GO:0043207 - p-val: 8.67e-10 ***
regulation of immune system process - GO:0002682 - p-val: 1.25e-09 ***
response to peptide - GO:1901652 - p-val: 3.54e-07 ***
regulation of multicellular organismal development - GO:2000026 - p-val: 2.62e-08 ***
cell activation - GO:0001775 - p-val: 1.32e-07 ***
immune response - GO:0006955 - p-val: 1.03e-10 ***
positive regulation of multicellular organismal pr... - GO:0051240 - p-val: 1.97e-10 ***
innate immune response - GO:0045087 - p-val: 3.89e-08 ***
defense response to other organism - GO:0098542 - p-val: 5.99e-10 ***
defense response - GO:0006952 - p-val: 1.00e-10 ***
blood vessel development - GO:0001568 - p-val: 1.45e-06 ***
vasculature development - GO:0001944 - p-val: 3.84e-07 ***
defense response to symbiont - GO:0140546 - p-val: 2.38e-09 ***
regulation of cytokine production - GO:0001817 - p-val: 2.66e-07 ***
cell adhesion - GO:0007155 - p-val: 1.00e-10 ***
inflammatory response - GO:0006954 - p-val: 1.57e-07 ***
cytokine production - GO:0001816 - p-val: 2.02e-07 ***
positive regulation of immune system process - GO:0002684 - p-val: 5.66e-10 ***
regulation of cell development - GO:0060284 - p-val: 1.84e-08 ***
positive regulation of cell motility - GO:2000147 - p-val: 1.09e-06 ***
blood vessel morphogenesis - GO:0048514 - p-val: 8.44e-07 ***
regulation of cell adhesion - GO:0030155 - p-val: 1.00e-08 ***
positive regulation of cytokine production - GO:0001819 - p-val: 9.03e-07 ***
cell-cell adhesion - GO:0098609 - p-val: 5.26e-10 ***
regulation of lymphocyte activation - GO:0051249 - p-val: 5.02e-07 ***
regulation of leukocyte activation - GO:0002694 - p-val: 1.23e-07 ***
regulation of cell activation - GO:0050865 - p-val: 1.48e-07 ***
leukocyte cell-cell adhesion - GO:0007159 - p-val: 1.17e-06 ***
regulation of leukocyte cell-cell adhesion - GO:1903037 - p-val: 6.83e-07 ***
regulation of body fluid levels - GO:0050878 - p-val: 1.00e-06 ***
regulation of T cell activation - GO:0050863 - p-val: 7.87e-07 ***
positive regulation of cell-cell adhesion - GO:0022409 - p-val: 9.72e-07 ***
positive regulation of cell adhesion - GO:0045785 - p-val: 1.36e-08 ***
response to wounding - GO:0009611 - p-val: 1.00e-10 ***
positive regulation of leukocyte cell-cell adhesio... - GO:1903039 - p-val: 1.09e-06 ***
regulation of leukocyte proliferation - GO:0070663 - p-val: 1.45e-06 ***
wound healing - GO:0042060 - p-val: 1.00e-10 ***
adaptive immune response based on somatic recombin... - GO:0002460 - p-val: 6.94e-07 ***
adaptive immune response - GO:0002250 - p-val: 9.50e-10 ***
phosphatase complex - GO:1903293 - p-val: 2.20e-03 **
protein serine/threonine phosphatase complex - GO:0008287 - p-val: 2.20e-03 **
integrin complex - GO:0008305 - p-val: 2.11e-03 **
respiratory chain complex - GO:0098803 - p-val: 3.79e-04 ***
cytochrome complex - GO:0070069 - p-val: 2.48e-04 ***
respiratory chain complex IV - GO:0045277 - p-val: 2.72e-04 ***
blood microparticle - GO:0072562 - p-val: 8.27e-05 ***
endocytic vesicle lumen - GO:0071682 - p-val: 1.25e-05 ***
pigment granule - GO:0048770 - p-val: 1.35e-03 **
melanosome - GO:0042470 - p-val: 1.35e-03 **
collagen-containing extracellular matrix - GO:0062023 - p-val: 1.01e-03 **
endoplasmic reticulum lumen - GO:0005788 - p-val: 9.77e-05 ***
endoplasmic reticulum protein-containing complex - GO:0140534 - p-val: 5.69e-05 ***
endoplasmic reticulum chaperone complex - GO:0034663 - p-val: 4.41e-04 ***
extracellular matrix - GO:0031012 - p-val: 1.22e-05 ***
external encapsulating structure - GO:0030312 - p-val: 1.22e-05 ***
cytoplasmic vesicle membrane - GO:0030659 - p-val: 3.44e-04 ***
vesicle membrane - GO:0012506 - p-val: 1.67e-04 ***
nuclear outer membrane-endoplasmic reticulum membr... - GO:0042175 - p-val: 3.62e-05 ***
endoplasmic reticulum membrane - GO:0005789 - p-val: 2.50e-05 ***
endoplasmic reticulum subcompartment - GO:0098827 - p-val: 2.69e-05 ***
Golgi membrane - GO:0000139 - p-val: 2.80e-04 ***
Golgi apparatus subcompartment - GO:0098791 - p-val: 2.57e-03 **
endocytic vesicle membrane - GO:0030666 - p-val: 3.00e-03 **
transport vesicle membrane - GO:0030658 - p-val: 1.35e-03 **
coated vesicle - GO:0030135 - p-val: 9.11e-05 ***
endoplasmic reticulum-Golgi intermediate compartme... - GO:0033116 - p-val: 2.00e-03 **
coated vesicle membrane - GO:0030662 - p-val: 7.12e-05 ***
clathrin-coated endocytic vesicle - GO:0045334 - p-val: 2.08e-03 **
endocytic vesicle - GO:0030139 - p-val: 1.15e-05 ***
clathrin-coated endocytic vesicle membrane - GO:0030669 - p-val: 4.19e-04 ***
COPII-coated ER to Golgi transport vesicle - GO:0030134 - p-val: 4.50e-05 ***
lumenal side of endoplasmic reticulum membrane - GO:0098553 - p-val: 5.65e-04 ***
ER to Golgi transport vesicle membrane - GO:0012507 - p-val: 1.52e-04 ***
MHC protein complex - GO:0042611 - p-val: 7.91e-05 ***
secretory vesicle - GO:0099503 - p-val: 1.75e-05 ***
secretory granule - GO:0030141 - p-val: 1.77e-05 ***
ficolin-1-rich granule - GO:0101002 - p-val: 2.03e-03 **
tertiary granule membrane - GO:0070821 - p-val: 3.65e-03 **
specific granule - GO:0042581 - p-val: 3.52e-04 ***
tertiary granule lumen - GO:1904724 - p-val: 1.74e-03 **
tertiary granule - GO:0070820 - p-val: 5.07e-06 ***
perinuclear region of cytoplasm - GO:0048471 - p-val: 1.41e-03 **
anchoring junction - GO:0070161 - p-val: 1.01e-04 ***
side of membrane - GO:0098552 - p-val: 3.24e-03 **
cell-substrate junction - GO:0030055 - p-val: 8.07e-05 ***
focal adhesion - GO:0005925 - p-val: 9.10e-05 ***
cell leading edge - GO:0031252 - p-val: 4.27e-04 ***
plasma membrane protein complex - GO:0098797 - p-val: 1.54e-03 **
cell surface - GO:0009986 - p-val: 1.36e-04 ***
fatty acid binding - GO:0005504 - p-val: 1.64e-03 **
oxidoreduction-driven active transmembrane transpo... - GO:0015453 - p-val: 2.52e-04 ***
tetrapyrrole binding - GO:0046906 - p-val: 5.82e-04 ***
antioxidant activity - GO:0016209 - p-val: 1.79e-04 ***
heme binding - GO:0020037 - p-val: 1.59e-04 ***
oxidoreductase activity, acting on peroxide as acc... - GO:0016684 - p-val: 7.96e-05 ***
peroxidase activity - GO:0004601 - p-val: 7.96e-05 ***
enzyme inhibitor activity - GO:0004857 - p-val: 1.42e-03 **
calcium ion binding - GO:0005509 - p-val: 5.53e-04 ***
misfolded protein binding - GO:0051787 - p-val: 5.30e-04 ***
antigen binding - GO:0003823 - p-val: 1.36e-03 **
MHC protein complex binding - GO:0023023 - p-val: 7.48e-04 ***
MHC class II protein complex binding - GO:0023026 - p-val: 3.72e-04 ***
cytokine receptor binding - GO:0005126 - p-val: 9.48e-04 ***
protein-containing complex binding - GO:0044877 - p-val: 7.28e-05 ***
molecular function activator activity - GO:0140677 - p-val: 1.56e-03 **
cadherin binding - GO:0045296 - p-val: 1.92e-03 **
signaling receptor binding - GO:0005102 - p-val: 6.60e-05 ***
cell adhesion molecule binding - GO:0050839 - p-val: 2.03e-04 ***
signaling receptor activator activity - GO:0030546 - p-val: 1.11e-03 **
receptor ligand activity - GO:0048018 - p-val: 8.95e-04 ***
growth factor activity - GO:0008083 - p-val: 9.48e-04 ***
carbohydrate binding - GO:0030246 - p-val: 6.02e-05 ***
glycosaminoglycan binding - GO:0005539 - p-val: 1.59e-04 ***
0.0
0.5
1.0
1.5
2.0
Absolute NES
Gene Count
100
200
300
400
500
Cluster
1
2
3
4
5
6
7
8
9
10