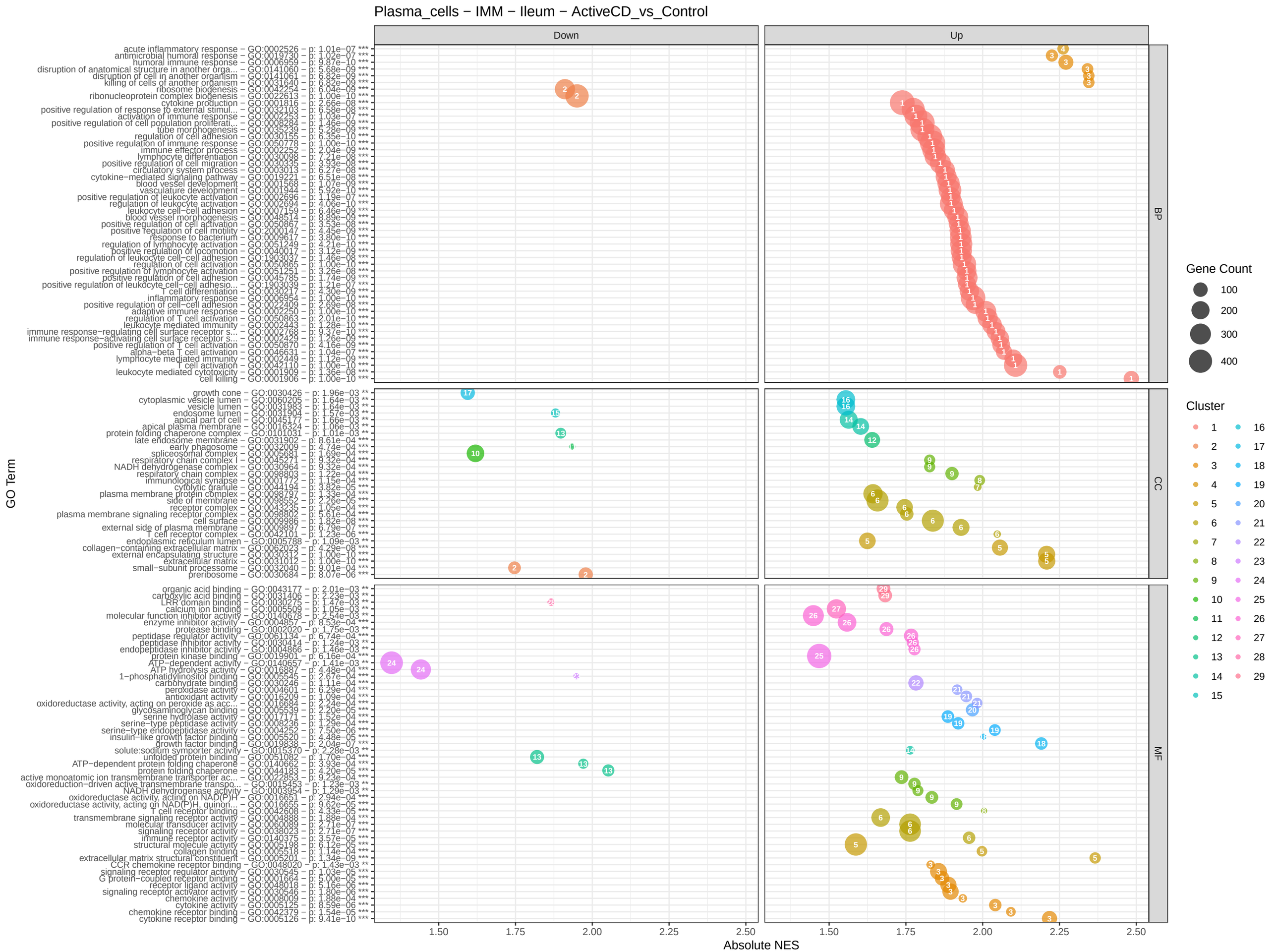
Plasma_cells − IMM − Ileum − ActiveCD_vs_Control
Down
Up
BP
CC
MF
GO Term
Absolute NES
1.50
1.75
2.00
2.25
2.50
Gene Count
100
200
300
400
Cluster
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
acute inflammatory response − GO:0002526 − p: 1.01e−07 ***
antimicrobial humoral response − GO:0019730 − p: 1.02e−07 ***
humoral immune response − GO:0006959 − p: 9.87e−10 ***
disruption of anatomical structure in another orga... − GO:0141060 − p: 5.68e−09 ***
disruption of cell in another organism − GO:0141061 − p: 6.82e−09 ***
killing of cells of another organism − GO:0031640 − p: 6.82e−09 ***
ribosome biogenesis − GO:0042254 − p: 6.04e−09 ***
ribonucleoprotein complex biogenesis − GO:0022613 − p: 1.00e−10 ***
cytokine production − GO:0001816 − p: 2.66e−08 ***
positive regulation of response to external stimul... − GO:0032103 − p: 6.58e−08 ***
activation of immune response − GO:0002253 − p: 1.03e−07 ***
positive regulation of cell population proliferati... − GO:0008284 − p: 1.46e−09 ***
tube morphogenesis − GO:0035239 − p: 5.28e−09 ***
regulation of cell adhesion − GO:0030155 − p: 6.35e−10 ***
positive regulation of immune response − GO:0050778 − p: 1.00e−10 ***
immune effector process − GO:0002252 − p: 2.04e−09 ***
lymphocyte differentiation − GO:0030098 − p: 7.21e−08 ***
positive regulation of cell migration − GO:0030335 − p: 3.93e−08 ***
circulatory system process − GO:0003013 − p: 6.27e−08 ***
cytokine−mediated signaling pathway − GO:0019221 − p: 6.51e−08 ***
blood vessel development − GO:0001568 − p: 1.07e−09 ***
vasculature development − GO:0001944 − p: 5.92e−10 ***
positive regulation of leukocyte activation − GO:0002696 − p: 1.19e−07 ***
regulation of leukocyte activation − GO:0002694 − p: 4.06e−10 ***
leukocyte cell−cell adhesion − GO:0007159 − p: 6.46e−09 ***
blood vessel morphogenesis − GO:0048514 − p: 8.89e−09 ***
positive regulation of cell activation − GO:0050867 − p: 3.53e−08 ***
positive regulation of cell motility − GO:2000147 − p: 4.45e−09 ***
response to bacterium − GO:0009617 − p: 3.80e−10 ***
regulation of lymphocyte activation − GO:0051249 − p: 4.21e−10 ***
positive regulation of locomotion − GO:0040017 − p: 3.12e−09 ***
regulation of leukocyte cell−cell adhesion − GO:1903037 − p: 1.46e−08 ***
regulation of cell activation − GO:0050865 − p: 1.00e−10 ***
positive regulation of lymphocyte activation − GO:0051251 − p: 3.26e−08 ***
positive regulation of cell adhesion − GO:0045785 − p: 1.74e−09 ***
positive regulation of leukocyte cell−cell adhesio... − GO:1903039 − p: 1.21e−07 ***
T cell differentiation − GO:0030217 − p: 4.30e−09 ***
inflammatory response − GO:0006954 − p: 1.00e−10 ***
positive regulation of cell−cell adhesion − GO:0022409 − p: 2.69e−08 ***
adaptive immune response − GO:0002250 − p: 1.00e−10 ***
regulation of T cell activation − GO:0050863 − p: 2.01e−10 ***
leukocyte mediated immunity − GO:0002443 − p: 1.28e−10 ***
immune response−regulating cell surface receptor s... − GO:0002768 − p: 9.37e−10 ***
immune response−activating cell surface receptor s... − GO:0002429 − p: 1.26e−09 ***
positive regulation of T cell activation − GO:0050870 − p: 4.16e−09 ***
alpha−beta T cell activation − GO:0046631 − p: 1.04e−07 ***
lymphocyte mediated immunity − GO:0002449 − p: 1.12e−09 ***
T cell activation − GO:0042110 − p: 1.00e−10 ***
leukocyte mediated cytotoxicity − GO:0001909 − p: 1.36e−08 ***
cell killing − GO:0001906 − p: 1.00e−10 ***
growth cone − GO:0030426 − p: 1.96e−03 **
cytoplasmic vesicle lumen − GO:0060205 − p: 1.64e−03 **
vesicle lumen − GO:0031983 − p: 1.64e−03 **
endosome lumen − GO:0031904 − p: 1.57e−03 **
apical part of cell − GO:0045177 − p: 1.66e−03 **
apical plasma membrane − GO:0016324 − p: 1.06e−03 **
protein folding chaperone complex − GO:0101031 − p: 1.01e−03 **
late endosome membrane − GO:0031902 − p: 8.61e−04 ***
early phagosome − GO:0032009 − p: 4.74e−04 ***
spliceosomal complex − GO:0005681 − p: 1.69e−04 ***
respiratory chain complex I − GO:0045271 − p: 9.32e−04 ***
NADH dehydrogenase complex − GO:0030964 − p: 9.32e−04 ***
respiratory chain complex − GO:0098803 − p: 1.22e−04 ***
immunological synapse − GO:0001772 − p: 1.15e−04 ***
cytolytic granule − GO:0044194 − p: 3.82e−05 ***
plasma membrane protein complex − GO:0098797 − p: 1.33e−04 ***
side of membrane − GO:0098552 − p: 2.26e−05 ***
receptor complex − GO:0043235 − p: 1.05e−04 ***
plasma membrane signaling receptor complex − GO:0098802 − p: 5.61e−04 ***
cell surface − GO:0009986 − p: 1.82e−08 ***
external side of plasma membrane − GO:0009897 − p: 6.79e−07 ***
T cell receptor complex − GO:0042101 − p: 1.23e−06 ***
endoplasmic reticulum lumen − GO:0005788 − p: 1.09e−03 **
collagen−containing extracellular matrix − GO:0062023 − p: 4.29e−08 ***
external encapsulating structure − GO:0030312 − p: 1.00e−10 ***
extracellular matrix − GO:0031012 − p: 1.00e−10 ***
small−subunit processome − GO:0032040 − p: 9.01e−04 ***
preribosome − GO:0030684 − p: 8.07e−06 ***
organic acid binding − GO:0043177 − p: 2.01e−03 **
carboxylic acid binding − GO:0031406 − p: 2.23e−03 **
LRR domain binding − GO:0030275 − p: 1.47e−03 **
calcium ion binding − GO:0005509 − p: 1.05e−03 **
molecular function inhibitor activity − GO:0140678 − p: 2.54e−03 **
enzyme inhibitor activity − GO:0004857 − p: 8.53e−04 ***
protease binding − GO:0002020 − p: 1.75e−03 **
peptidase regulator activity − GO:0061134 − p: 6.74e−04 ***
peptidase inhibitor activity − GO:0030414 − p: 1.24e−03 **
endopeptidase inhibitor activity − GO:0004866 − p: 1.46e−03 **
protein kinase binding − GO:0019901 − p: 6.16e−04 ***
ATP−dependent activity − GO:0140657 − p: 1.41e−03 **
ATP hydrolysis activity − GO:0016887 − p: 4.48e−04 ***
1−phosphatidylinositol binding − GO:0005545 − p: 2.67e−04 ***
carbohydrate binding − GO:0030246 − p: 1.11e−04 ***
peroxidase activity − GO:0004601 − p: 6.29e−04 ***
antioxidant activity − GO:0016209 − p: 1.09e−04 ***
oxidoreductase activity, acting on peroxide as acc... − GO:0016684 − p: 2.24e−04 ***
glycosaminoglycan binding − GO:0005539 − p: 2.20e−05 ***
serine hydrolase activity − GO:0017171 − p: 1.52e−04 ***
serine−type peptidase activity − GO:0008236 − p: 1.29e−04 ***
serine−type endopeptidase activity − GO:0004252 − p: 7.50e−06 ***
insulin−like growth factor binding − GO:0005520 − p: 4.48e−05 ***
growth factor binding − GO:0019838 − p: 2.04e−07 ***
solute:sodium symporter activity − GO:0015370 − p: 2.28e−03 **
unfolded protein binding − GO:0051082 − p: 1.70e−04 ***
ATP−dependent protein folding chaperone − GO:0140662 − p: 3.93e−04 ***
protein folding chaperone − GO:0044183 − p: 4.20e−05 ***
active monoatomic ion transmembrane transporter ac... − GO:0022853 − p: 9.23e−04 ***
oxidoreduction−driven active transmembrane transpo... − GO:0015453 − p: 1.23e−03 **
NADH dehydrogenase activity − GO:0003954 − p: 1.29e−03 **
oxidoreductase activity, acting on NAD(P)H − GO:0016651 − p: 2.94e−04 ***
oxidoreductase activity, acting on NAD(P)H, quinon... − GO:0016655 − p: 9.62e−05 ***
T cell receptor binding − GO:0042608 − p: 4.33e−05 ***
transmembrane signaling receptor activity − GO:0004888 − p: 1.88e−04 ***
molecular transducer activity − GO:0060089 − p: 2.71e−07 ***
signaling receptor activity − GO:0038023 − p: 2.71e−07 ***
immune receptor activity − GO:0140375 − p: 3.57e−05 ***
structural molecule activity − GO:0005198 − p: 6.12e−05 ***
collagen binding − GO:0005518 − p: 1.14e−04 ***
extracellular matrix structural constituent − GO:0005201 − p: 1.34e−09 ***
CCR chemokine receptor binding − GO:0048020 − p: 1.43e−03 **
signaling receptor regulator activity − GO:0030545 − p: 1.03e−05 ***
G protein−coupled receptor binding − GO:0001664 − p: 5.00e−05 ***
receptor ligand activity − GO:0048018 − p: 5.16e−06 ***
signaling receptor activator activity − GO:0030546 − p: 1.80e−06 ***
chemokine activity − GO:0008009 − p: 1.88e−04 ***
cytokine activity − GO:0005125 − p: 8.59e−06 ***
chemokine receptor binding − GO:0042379 − p: 1.54e−05 ***
cytokine receptor binding − GO:0005126 − p: 9.41e−10 ***