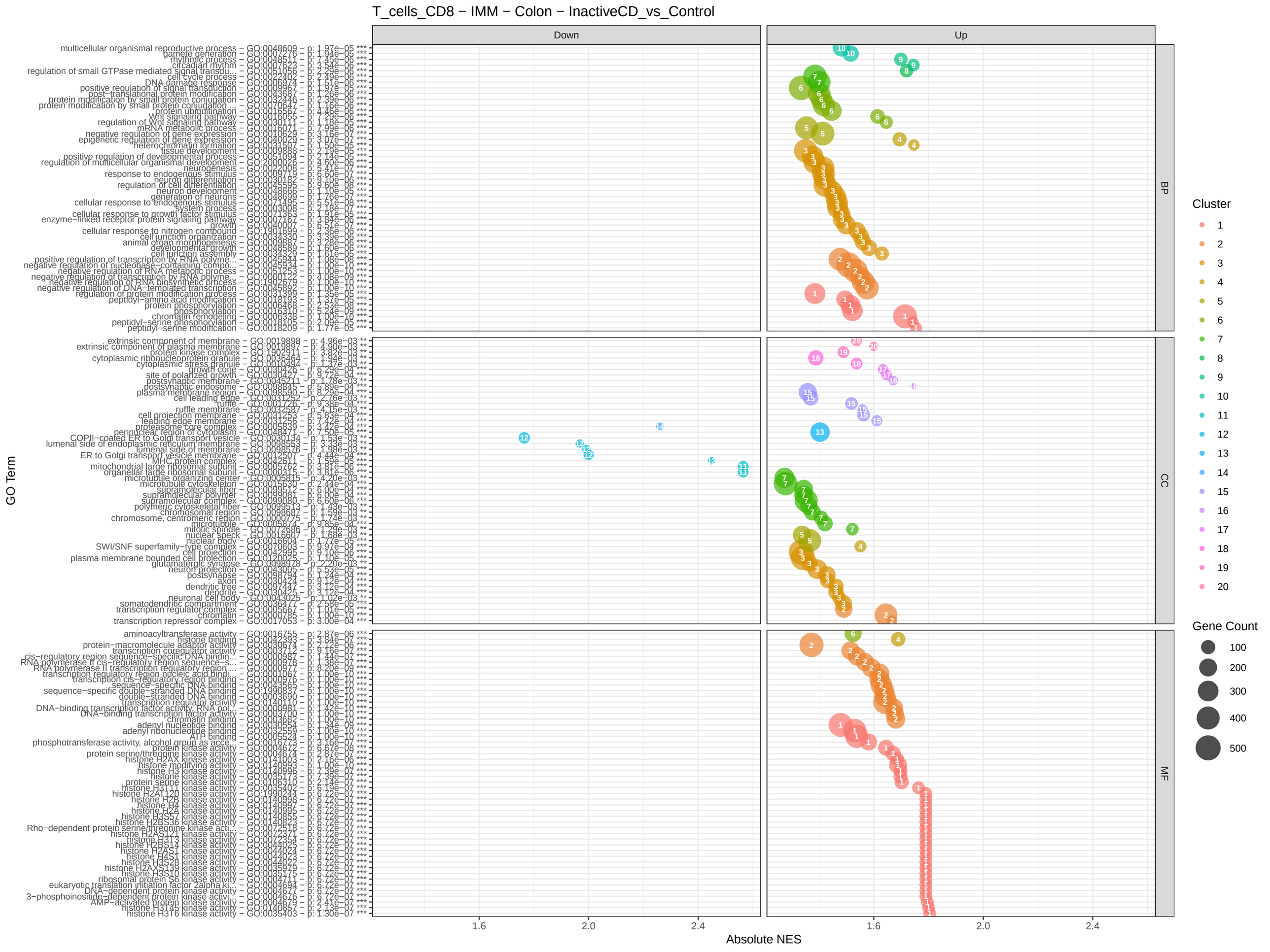
T_cells_CD8 − IMM − Colon − InactiveCD_vs_Control
Down
Up
BP
CC
MF
GO Term
multicellular organismal reproductive process − GO:0048609 − p: 1.97e−05 ***
gamete generation − GO:0007276 − p: 1.94e−05 ***
rhythmic process − GO:0048511 − p: 7.45e−06 ***
circadian rhythm − GO:0007623 − p: 3.54e−06 ***
regulation of small GTPase mediated signal transdu... − GO:0051056 − p: 2.29e−06 ***
cell cycle process − GO:0022402 − p: 2.49e−06 ***
DNA damage response − GO:0006974 − p: 1.51e−06 ***
positive regulation of signal transduction − GO:0009967 − p: 1.97e−05 ***
post−translational protein modification − GO:0043687 − p: 1.26e−06 ***
protein modification by small protein conjugation − GO:0032446 − p: 2.39e−06 ***
protein modification by small protein conjugation ... − GO:0070647 − p: 1.16e−06 ***
protein ubiquitination − GO:0016567 − p: 4.46e−06 ***
Wnt signaling pathway − GO:0016055 − p: 7.98e−06 ***
regulation of Wnt signaling pathway − GO:0030111 − p: 1.18e−05 ***
mRNA metabolic process − GO:0016071 − p: 7.99e−06 ***
negative regulation of gene expression − GO:0010629 − p: 3.16e−07 ***
epigenetic regulation of gene expression − GO:0040029 − p: 3.07e−07 ***
heterochromatin formation − GO:0031507 − p: 1.50e−05 ***
tissue development − GO:0009888 − p: 1.19e−05 ***
positive regulation of developmental process − GO:0051094 − p: 2.14e−05 ***
regulation of multicellular organismal development − GO:2000026 − p: 4.60e−06 ***
neurogenesis − GO:0022008 − p: 5.41e−07 ***
response to endogenous stimulus − GO:0009719 − p: 6.60e−07 ***
neuron differentiation − GO:0030182 − p: 9.10e−06 ***
regulation of cell differentiation − GO:0045595 − p: 9.60e−08 ***
neuron development − GO:0048666 − p: 1.10e−05 ***
generation of neurons − GO:0048699 − p: 1.76e−07 ***
cellular response to endogenous stimulus − GO:0071495 − p: 5.51e−08 ***
system process − GO:0003008 − p: 2.18e−07 ***
cellular response to growth factor stimulus − GO:0071363 − p: 1.91e−05 ***
enzyme−linked receptor protein signaling pathway − GO:0007167 − p: 3.84e−06 ***
growth − GO:0040007 − p: 6.51e−07 ***
cellular response to nitrogen compound − GO:1901699 − p: 2.36e−06 ***
cell junction organization − GO:0034330 − p: 3.39e−06 ***
animal organ morphogenesis − GO:0009887 − p: 3.28e−06 ***
developmental growth − GO:0048589 − p: 1.60e−06 ***
cell junction assembly − GO:0034329 − p: 1.61e−05 ***
positive regulation of transcription by RNA polyme... − GO:0045944 − p: 1.08e−08 ***
negative regulation of nucleobase−containing compo... − GO:0045934 − p: 1.00e−10 ***
negative regulation of RNA metabolic process − GO:0051253 − p: 1.00e−10 ***
negative regulation of transcription by RNA polyme... − GO:0000122 − p: 4.08e−09 ***
negative regulation of RNA biosynthetic process − GO:1903507 − p: 1.00e−10 ***
negative regulation of DNA−templated transcription − GO:0045892 − p: 1.00e−10 ***
regulation of protein modification process − GO:0031399 − p: 1.35e−05 ***
peptidyl−amino acid modification − GO:0018193 − p: 1.37e−05 ***
protein phosphorylation − GO:0006468 − p: 2.53e−08 ***
phosphorylation − GO:0016310 − p: 5.24e−08 ***
chromatin remodeling − GO:0006338 − p: 1.00e−10 ***
peptidyl−serine phosphorylation − GO:0018105 − p: 2.09e−05 ***
peptidyl−serine modification − GO:0018209 − p: 1.77e−05 ***
extrinsic component of membrane − GO:0019898 − p: 4.96e−03 **
extrinsic component of plasma membrane − GO:0019897 − p: 4.90e−03 **
protein kinase complex − GO:1902911 − p: 3.82e−03 **
cytoplasmic ribonucleoprotein granule − GO:0036464 − p: 1.94e−03 **
cytoplasmic stress granule − GO:0010494 − p: 1.37e−03 **
growth cone − GO:0030426 − p: 6.29e−04 ***
site of polarized growth − GO:0030427 − p: 9.72e−04 ***
postsynaptic membrane − GO:0045211 − p: 1.78e−03 **
postsynaptic endosome − GO:0098835 − p: 5.89e−04 ***
plasma membrane region − GO:0098590 − p: 8.28e−04 ***
cell leading edge − GO:0031252 − p: 2.76e−03 **
ruffle − GO:0001726 − p: 9.38e−04 ***
ruffle membrane − GO:0032587 − p: 4.15e−03 **
cell projection membrane − GO:0031253 − p: 5.83e−04 ***
leading edge membrane − GO:0031258 − p: 4.42e−04 ***
proteasome core complex − GO:0005839 − p: 3.42e−04 ***
perinuclear region of cytoplasm − GO:0048471 − p: 7.50e−05 ***
COPII−coated ER to Golgi transport vesicle − GO:0030134 − p: 1.53e−03 **
lumenal side of endoplasmic reticulum membrane − GO:0098553 − p: 3.33e−03 **
lumenal side of membrane − GO:0098576 − p: 1.98e−03 **
ER to Golgi transport vesicle membrane − GO:0012507 − p: 4.44e−04 ***
MHC protein complex − GO:0042611 − p: 1.59e−05 ***
mitochondrial large ribosomal subunit − GO:0005762 − p: 3.81e−06 ***
organellar large ribosomal subunit − GO:0000315 − p: 3.81e−06 ***
microtubule organizing center − GO:0005815 − p: 4.20e−03 **
microtubule cytoskeleton − GO:0015630 − p: 2.44e−04 ***
supramolecular fiber − GO:0099512 − p: 6.00e−04 ***
supramolecular polymer − GO:0099081 − p: 6.00e−04 ***
supramolecular complex − GO:0099080 − p: 6.60e−06 ***
polymeric cytoskeletal fiber − GO:0099513 − p: 1.43e−03 **
chromosomal region − GO:0098687 − p: 1.59e−03 **
chromosome, centromeric region − GO:0000775 − p: 1.74e−03 **
microtubule − GO:0005874 − p: 9.85e−04 ***
mitotic spindle − GO:0072686 − p: 1.29e−03 **
nuclear speck − GO:0016607 − p: 1.68e−03 **
nuclear body − GO:0016604 − p: 1.77e−05 ***
SWI/SNF superfamily−type complex − GO:0070603 − p: 9.97e−04 ***
cell projection − GO:0042995 − p: 9.10e−06 ***
plasma membrane bounded cell projection − GO:0120025 − p: 1.10e−05 ***
glutamatergic synapse − GO:0098978 − p: 2.20e−03 **
neuron projection − GO:0043005 − p: 5.53e−05 ***
postsynapse − GO:0098794 − p: 1.22e−04 ***
axon − GO:0030424 − p: 9.12e−04 ***
dendritic tree − GO:0097447 − p: 3.12e−04 ***
dendrite − GO:0030425 − p: 3.12e−04 ***
neuronal cell body − GO:0043025 − p: 1.02e−03 **
somatodendritic compartment − GO:0036477 − p: 2.58e−05 ***
transcription regulator complex − GO:0005667 − p: 1.01e−05 ***
chromatin − GO:0000785 − p: 1.00e−10 ***
transcription repressor complex − GO:0017053 − p: 3.00e−04 ***
aminoacyltransferase activity − GO:0016755 − p: 2.87e−06 ***
histone binding − GO:0042393 − p: 3.84e−07 ***
protein−macromolecule adaptor activity − GO:0030674 − p: 2.12e−06 ***
transcription coregulator activity − GO:0003712 − p: 9.16e−07 ***
cis−regulatory region sequence−specific DNA bindin... − GO:0000987 − p: 1.44e−07 ***
RNA polymerase II cis−regulatory region sequence−s... − GO:0000978 − p: 1.38e−07 ***
RNA polymerase II transcription regulatory region.... − GO:0000977 − p: 8.20e−09 ***
transcription regulatory region nucleic acid bindi... − GO:0001067 − p: 1.00e−10 ***
transcription cis−regulatory region binding − GO:0000976 − p: 1.00e−10 ***
sequence−specific DNA binding − GO:0043565 − p: 1.00e−10 ***
sequence−specific double−stranded DNA binding − GO:1990837 − p: 1.00e−10 ***
double−stranded DNA binding − GO:0003690 − p: 1.00e−10 ***
transcription regulator activity − GO:0140110 − p: 1.00e−10 ***
DNA−binding transcription factor activity, RNA pol... − GO:0000981 − p: 1.42e−10 ***
DNA−binding transcription factor activity − GO:0003700 − p: 1.00e−10 ***
chromatin binding − GO:0003682 − p: 1.00e−10 ***
adenyl nucleotide binding − GO:0030554 − p: 1.34e−09 ***
adenyl ribonucleotide binding − GO:0032559 − p: 1.00e−10 ***
ATP binding − GO:0005524 − p: 1.00e−10 ***
phosphotransferase activity, alcohol group as acce... − GO:0016773 − p: 3.16e−02 ***
protein kinase activity − GO:0004672 − p: 6.67e−08 ***
protein serine/threonine kinase activity − GO:0004674 − p: 3.87e−07 ***
histone H2AX kinase activity − GO:0141003 − p: 2.16e−06 ***
histone modifying activity − GO:0140993 − p: 1.00e−10 ***
histone H3 kinase activity − GO:0140996 − p: 7.39e−07 ***
histone kinase activity − GO:0035173 − p: 7.39e−07 ***
protein serine kinase activity − GO:0106310 − p: 2.12e−07 ***
histone H3T11 kinase activity − GO:0035402 − p: 6.19e−07 ***
histone H2AT120 kinase activity − GO:1990244 − p: 6.72e−07 ***
histone H2B kinase activity − GO:0140998 − p: 6.72e−07 ***
histone H4 kinase activity − GO:0140997 − p: 6.72e−07 ***
histone H2A kinase activity − GO:0140995 − p: 6.72e−07 ***
histone H3S57 kinase activity − GO:0140855 − p: 6.72e−07 ***
histone H2BS36 kinase activity − GO:0140853 − p: 6.72e−07 ***
Rho−dependent protein serine/threonine kinase acti... − GO:0072518 − p: 6.72e−07 ***
histone H2AS121 kinase activity − GO:0072371 − p: 6.72e−07 ***
histone H3T3 kinase activity − GO:0072354 − p: 6.72e−07 ***
histone H2BS14 kinase activity − GO:0044025 − p: 6.72e−07 ***
histone H2AS1 kinase activity − GO:0044024 − p: 6.72e−07 ***
histone H4S1 kinase activity − GO:0044023 − p: 6.72e−07 ***
histone H3S28 kinase activity − GO:0044022 − p: 6.72e−07 ***
histone H2AXS139 kinase activity − GO:0035979 − p: 6.72e−07 ***
histone H3S10 kinase activity − GO:0035175 − p: 6.72e−07 ***
ribosomal protein S6 kinase activity − GO:0004711 − p: 6.72e−07 ***
eukaryotic translation initiation factor 2alpha ki... − GO:0004694 − p: 6.72e−07 ***
DNA−dependent protein kinase activity − GO:0004677 − p: 6.72e−07 ***
3−phosphoinositide−dependent protein kinase activi... − GO:0004676 − p: 6.72e−07 ***
AMP−activated protein kinase activity − GO:0004679 − p: 2.41e−07 ***
histone H3T45 kinase activity − GO:0140867 − p: 2.13e−07 ***
histone H3T6 kinase activity − GO:0035403 − p: 1.30e−07 ***
1.6
2.0
2.4
Absolute NES
Cluster
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
Gene Count
100
200
300
400
500