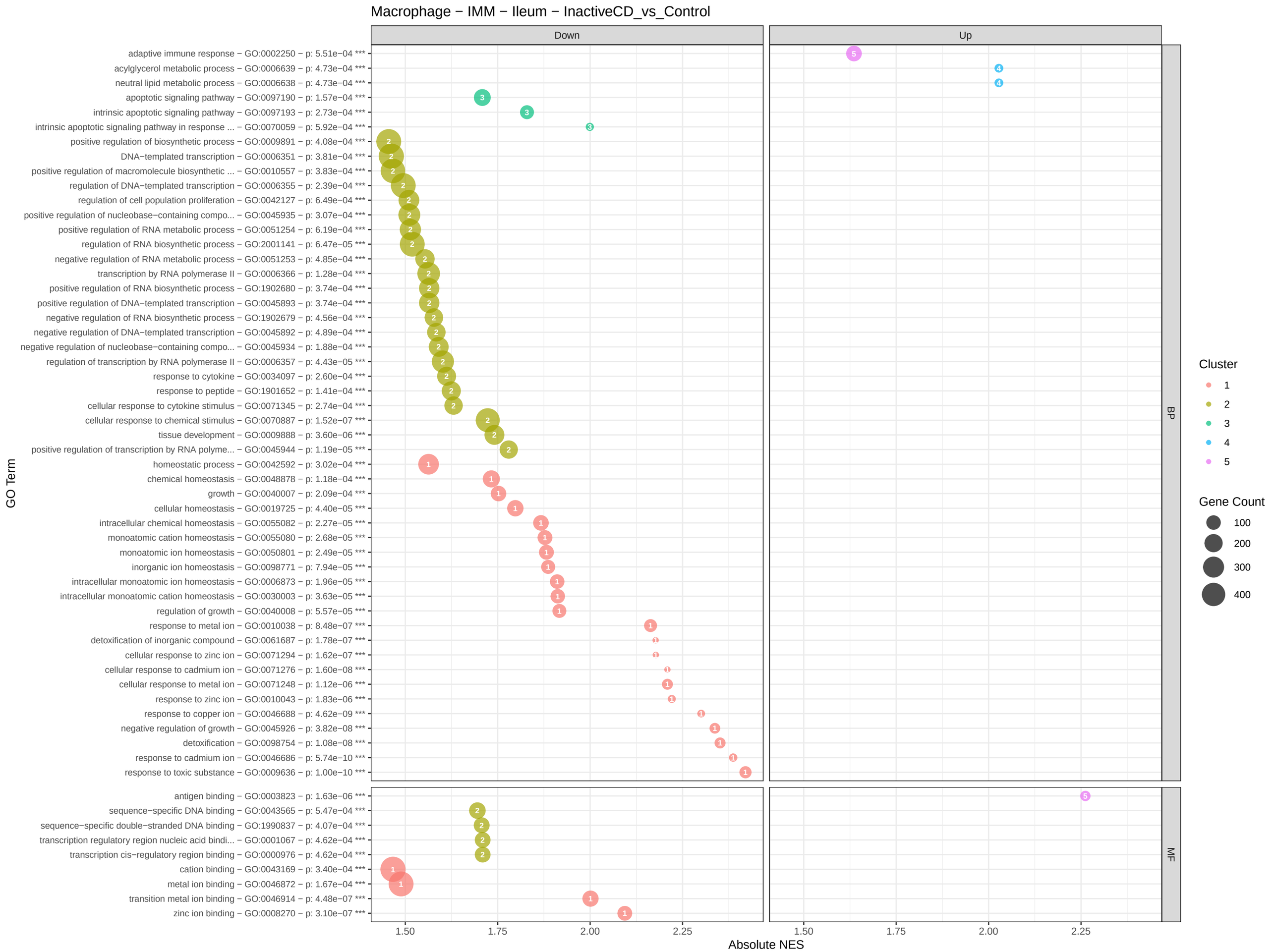
Macrophage − IMM − Ileum − InactiveCD_vs_Control
Down
Up
BP
MF
GO Term
adaptive immune response − GO:0002250 − p: 5.51e−04 ***
acylglycerol metabolic process − GO:0006639 − p: 4.73e−04 ***
neutral lipid metabolic process − GO:0006638 − p: 4.73e−04 ***
apoptotic signaling pathway − GO:0097190 − p: 1.57e−04 ***
intrinsic apoptotic signaling pathway − GO:0097193 − p: 2.73e−04 ***
intrinsic apoptotic signaling pathway in response ... − GO:0070059 − p: 5.92e−04 ***
positive regulation of biosynthetic process − GO:0009891 − p: 4.08e−04 ***
DNA−templated transcription − GO:0006351 − p: 3.81e−04 ***
positive regulation of macromolecule biosynthetic ... − GO:0010557 − p: 3.83e−04 ***
regulation of DNA−templated transcription − GO:0006355 − p: 2.39e−04 ***
regulation of cell population proliferation − GO:0042127 − p: 6.49e−04 ***
positive regulation of nucleobase−containing compo... − GO:0045935 − p: 3.07e−04 ***
positive regulation of RNA metabolic process − GO:0051254 − p: 6.19e−04 ***
regulation of RNA biosynthetic process − GO:2001141 − p: 6.47e−05 ***
negative regulation of RNA metabolic process − GO:0051253 − p: 4.85e−04 ***
transcription by RNA polymerase II − GO:0006366 − p: 1.28e−04 ***
positive regulation of RNA biosynthetic process − GO:1902680 − p: 3.74e−04 ***
positive regulation of DNA−templated transcription − GO:0045893 − p: 3.74e−04 ***
negative regulation of RNA biosynthetic process − GO:1902679 − p: 4.56e−04 ***
negative regulation of DNA−templated transcription − GO:0045892 − p: 4.89e−04 ***
negative regulation of nucleobase−containing compo... − GO:0045934 − p: 1.88e−04 ***
regulation of transcription by RNA polymerase II − GO:0006357 − p: 4.43e−05 ***
response to cytokine − GO:0034097 − p: 2.60e−04 ***
response to peptide − GO:1901652 − p: 1.41e−04 ***
cellular response to cytokine stimulus − GO:0071345 − p: 2.74e−04 ***
cellular response to chemical stimulus − GO:0070887 − p: 1.52e−07 ***
tissue development − GO:0009888 − p: 3.60e−06 ***
positive regulation of transcription by RNA polyme... − GO:0045944 − p: 1.19e−05 ***
homeostatic process − GO:0042592 − p: 3.02e−04 ***
chemical homeostasis − GO:0048878 − p: 1.18e−04 ***
growth − GO:0040007 − p: 2.09e−04 ***
cellular homeostasis − GO:0019725 − p: 4.40e−05 ***
intracellular chemical homeostasis − GO:0055082 − p: 2.27e−05 ***
monoatomic cation homeostasis − GO:0055080 − p: 2.68e−05 ***
monoatomic ion homeostasis − GO:0050801 − p: 2.49e−05 ***
inorganic ion homeostasis − GO:0098771 − p: 7.94e−05 ***
intracellular monoatomic ion homeostasis − GO:0006873 − p: 1.96e−05 ***
intracellular monoatomic cation homeostasis − GO:0030003 − p: 3.63e−05 ***
regulation of growth − GO:0040008 − p: 5.57e−05 ***
response to metal ion − GO:0010038 − p: 8.48e−07 ***
detoxification of inorganic compound − GO:0061687 − p: 1.78e−07 ***
cellular response to zinc ion − GO:0071294 − p: 1.62e−07 ***
cellular response to cadmium ion − GO:0071276 − p: 1.60e−08 ***
cellular response to metal ion − GO:0071248 − p: 1.12e−06 ***
response to zinc ion − GO:0010043 − p: 1.83e−06 ***
response to copper ion − GO:0046688 − p: 4.62e−09 ***
negative regulation of growth − GO:0045926 − p: 3.82e−08 ***
detoxification − GO:0098754 − p: 1.08e−08 ***
response to cadmium ion − GO:0046686 − p: 5.74e−10 ***
response to toxic substance − GO:0009636 − p: 1.00e−10 ***
antigen binding − GO:0003823 − p: 1.63e−06 ***
sequence−specific DNA binding − GO:0043565 − p: 5.47e−04 ***
sequence−specific double−stranded DNA binding − GO:1990837 − p: 4.07e−04 ***
transcription regulatory region nucleic acid bindi... − GO:0001067 − p: 4.62e−04 ***
transcription cis−regulatory region binding − GO:0000976 − p: 4.62e−04 ***
cation binding − GO:0043169 − p: 3.40e−04 ***
metal ion binding − GO:0046872 − p: 1.67e−04 ***
transition metal ion binding − GO:0046914 − p: 4.48e−07 ***
zinc ion binding − GO:0008270 − p: 3.10e−07 ***
1.50
1.75
2.00
2.25
Absolute NES
Cluster
1
2
3
4
5
Gene Count
100
200
300
400