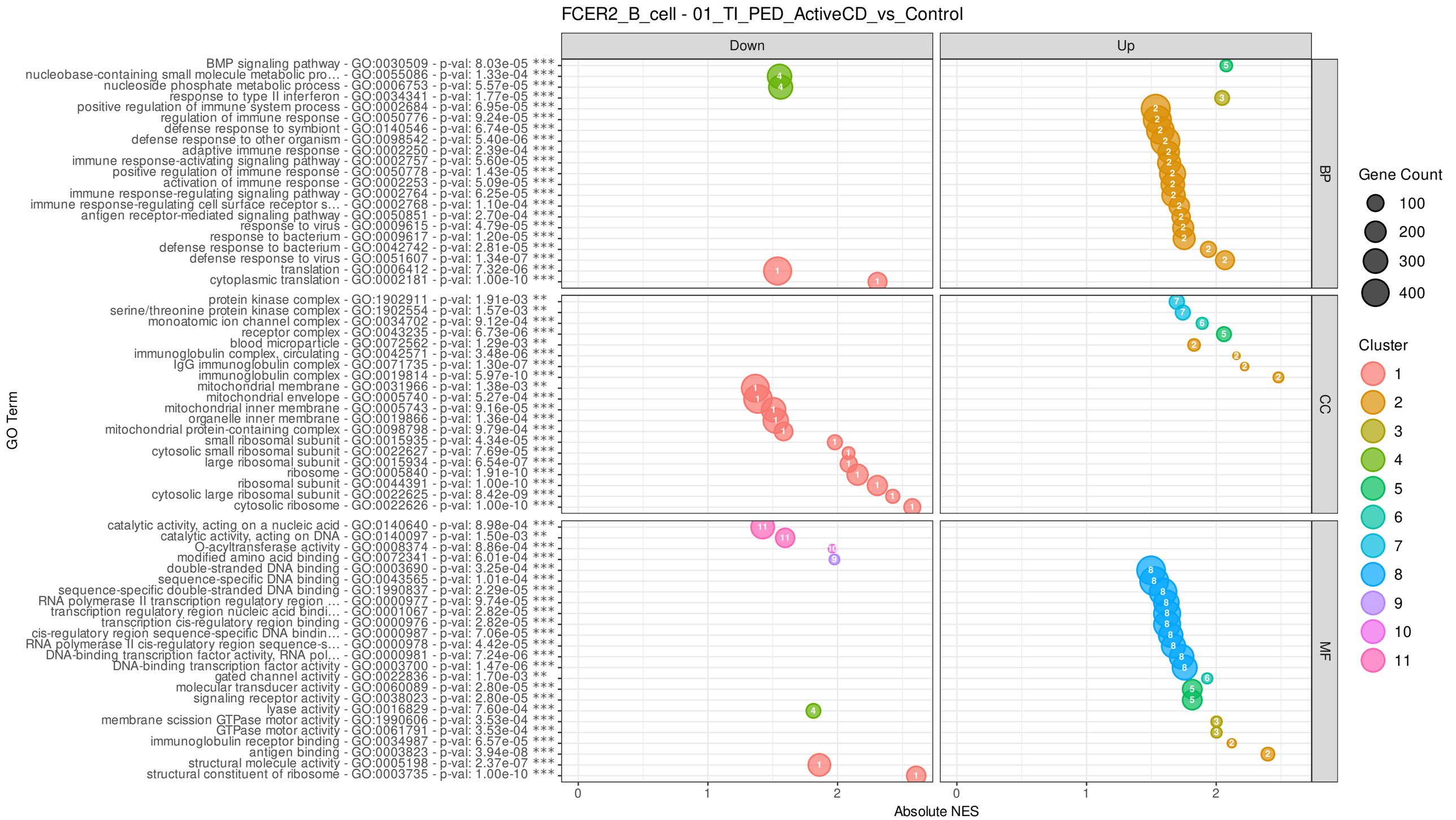
FCER2_B_cell - 01_TI_PED_ActiveCD_vs_Control
Down
Up
BP
CC
MF
GO Term
BMP signaling pathway - GO:0030509 - p-val: 8.03e-05 ***
nucleobase-containing small molecule metabolic pro... - GO:0055086 - p-val: 1.33e-04 ***
nucleoside phosphate metabolic process - GO:0006753 - p-val: 5.57e-05 ***
response to type II interferon - GO:0034341 - p-val: 1.77e-05 ***
positive regulation of immune system process - GO:0002684 - p-val: 6.95e-05 ***
regulation of immune response - GO:0050776 - p-val: 9.24e-05 ***
defense response to symbiont - GO:0140546 - p-val: 6.74e-05 ***
defense response to other organism - GO:0098542 - p-val: 5.40e-06 ***
adaptive immune response - GO:0002250 - p-val: 2.39e-04 ***
immune response-activating signaling pathway - GO:0002757 - p-val: 5.60e-05 ***
positive regulation of immune response - GO:0050778 - p-val: 1.43e-05 ***
activation of immune response - GO:0002253 - p-val: 5.09e-05 ***
immune response-regulating signaling pathway - GO:0002764 - p-val: 6.25e-05 ***
immune response-regulating cell surface receptor s... - GO:0002768 - p-val: 1.10e-04 ***
antigen receptor-mediated signaling pathway - GO:0050851 - p-val: 2.70e-04 ***
response to virus - GO:0009615 - p-val: 4.79e-05 ***
response to bacterium - GO:0009617 - p-val: 1.20e-05 ***
defense response to bacterium - GO:0042742 - p-val: 2.81e-05 ***
defense response to virus - GO:0051607 - p-val: 1.34e-07 ***
translation - GO:0006412 - p-val: 7.32e-06 ***
cytoplasmic translation - GO:0002181 - p-val: 1.00e-10 ***
protein kinase complex - GO:1902911 - p-val: 1.91e-03 **
serine/threonine protein kinase complex - GO:1902554 - p-val: 1.57e-03 **
monoatomic ion channel complex - GO:0034702 - p-val: 9.12e-04 ***
receptor complex - GO:0043235 - p-val: 6.73e-06 ***
blood microparticle - GO:0072562 - p-val: 1.29e-03 **
immunoglobulin complex, circulating - GO:0042571 - p-val: 3.48e-06 ***
IgG immunoglobulin complex - GO:0071735 - p-val: 1.30e-07 ***
immunoglobulin complex - GO:0019814 - p-val: 5.97e-10 ***
mitochondrial membrane - GO:0031966 - p-val: 1.38e-03 **
mitochondrial envelope - GO:0005740 - p-val: 5.27e-04 ***
mitochondrial inner membrane - GO:0005743 - p-val: 9.16e-05 ***
organelle inner membrane - GO:0019866 - p-val: 1.36e-04 ***
mitochondrial protein-containing complex - GO:0098798 - p-val: 9.79e-04 ***
small ribosomal subunit - GO:0015935 - p-val: 4.34e-05 ***
cytosolic small ribosomal subunit - GO:0022627 - p-val: 7.69e-05 ***
large ribosomal subunit - GO:0015934 - p-val: 6.54e-07 ***
ribosome - GO:0005840 - p-val: 1.91e-10 ***
ribosomal subunit - GO:0044391 - p-val: 1.00e-10 ***
cytosolic large ribosomal subunit - GO:0022625 - p-val: 8.42e-09 ***
cytosolic ribosome - GO:0022626 - p-val: 1.00e-10 ***
catalytic activity, acting on a nucleic acid - GO:0140640 - p-val: 8.98e-04 ***
catalytic activity, acting on DNA - GO:0140097 - p-val: 1.50e-03 **
O-acyltransferase activity - GO:0008374 - p-val: 8.86e-04 ***
modified amino acid binding - GO:0072341 - p-val: 6.01e-04 ***
double-stranded DNA binding - GO:0003690 - p-val: 3.25e-04 ***
sequence-specific DNA binding - GO:0043565 - p-val: 1.01e-04 ***
sequence-specific double-stranded DNA binding - GO:1990837 - p-val: 2.29e-05 ***
RNA polymerase II transcription regulatory region ... - GO:0000977 - p-val: 9.74e-05 ***
transcription regulatory region nucleic acid bindi... - GO:0001067 - p-val: 2.82e-05 ***
transcription cis-regulatory region binding - GO:0000976 - p-val: 2.82e-05 ***
cis-regulatory region sequence-specific DNA bindin... - GO:0000987 - p-val: 7.06e-05 ***
RNA polymerase II cis-regulatory region sequence-s... - GO:0000978 - p-val: 4.42e-05 ***
DNA-binding transcription factor activity, RNA pol... - GO:0000981 - p-val: 7.24e-06 ***
DNA-binding transcription factor activity - GO:0003700 - p-val: 1.47e-06 ***
gated channel activity - GO:0022836 - p-val: 1.70e-03 **
molecular transducer activity - GO:0060089 - p-val: 2.80e-05 ***
signaling receptor activity - GO:0038023 - p-val: 2.80e-05 ***
lyase activity - GO:0016829 - p-val: 7.60e-04 ***
membrane scission GTPase motor activity - GO:1990606 - p-val: 3.53e-04 ***
GTPase motor activity - GO:0061791 - p-val: 3.53e-04 ***
immunoglobulin receptor binding - GO:0034987 - p-val: 6.57e-05 ***
antigen binding - GO:0003823 - p-val: 3.94e-08 ***
structural molecule activity - GO:0005198 - p-val: 2.37e-07 ***
structural constituent of ribosome - GO:0003735 - p-val: 1.00e-10 ***
0
1
2
Absolute NES
Gene Count
100
200
300
400
Cluster
1
2
3
4
5
6
7
8
9
10
11