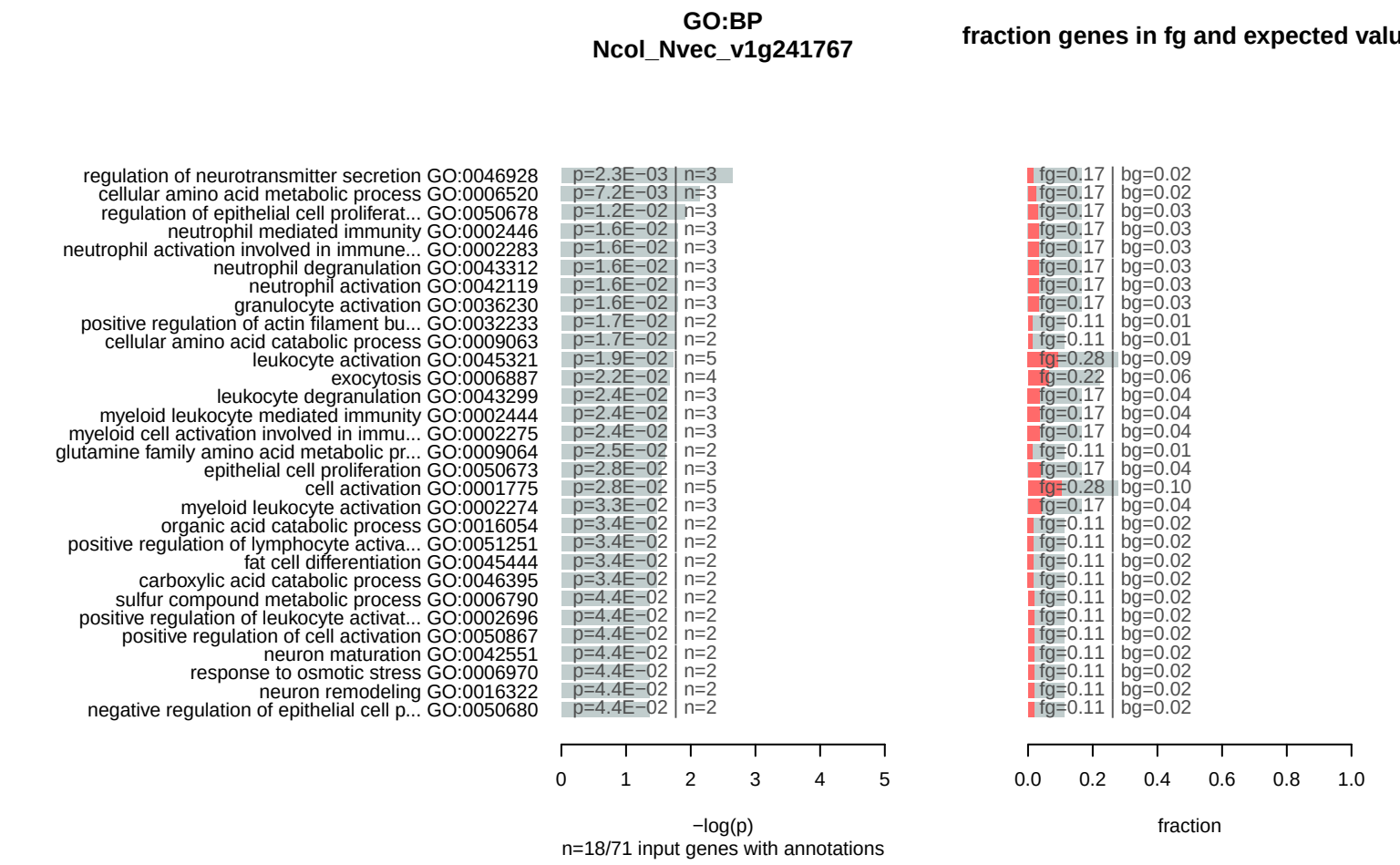
GO:BP
Ncol_Nvec_v1g241767
fraction genes in fg and expected valu
regulation of neurotransmitter secretion GO:0046928 p=2.3E−03 n=3 fg=0.17 bg=0.02
cellular amino acid metabolic process GO:0006520 p=7.2E−03 n=3 fg=0.17 bg=0.02
regulation of epithelial cell proliferat... GO:0050678 p=1.2E−02 n=3 fg=0.17 bg=0.03
neutrophil mediated immunity GO:0002446 p=1.6E−02 n=3 fg=0.17 bg=0.03
neutrophil activation involved in immune... GO:0002283 p=1.6E−02 n=3 fg=0.17 bg=0.03
neutrophil degranulation GO:0043312 p=1.6E−02 n=3 fg=0.17 bg=0.03
neutrophil activation GO:0042119 p=1.6E−02 n=3 fg=0.17 bg=0.03
granulocyte activation GO:0036230 p=1.6E−02 n=3 fg=0.17 bg=0.03
positive regulation of actin filament bu... GO:0032233 p=1.7E−02 n=2 fg=0.11 bg=0.01
cellular amino acid catabolic process GO:0009063 p=1.7E−02 n=2 fg=0.11 bg=0.01
leukocyte activation GO:0045321 p=1.9E−02 n=5 fg=0.28 bg=0.09
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myeloid leukocyte mediated immunity GO:0002444 p=2.4E−02 n=3 fg=0.17 bg=0.04
myeloid cell activation involved in immu... GO:0002275 p=2.4E−02 n=3 fg=0.17 bg=0.04
glutamine family amino acid metabolic pr... GO:0009064 p=2.5E−02 n=2 fg=0.11 bg=0.01
epithelial cell proliferation GO:0050673 p=2.8E−02 n=3 fg=0.17 bg=0.04
cell activation GO:0001775 p=2.8E−02 n=5 fg=0.28 bg=0.10
myeloid leukocyte activation GO:0002274 p=3.3E−02 n=3 fg=0.17 bg=0.04
organic acid catabolic process GO:0016054 p=3.4E−02 n=2 fg=0.11 bg=0.02
positive regulation of lymphocyte activa... GO:0051251 p=3.4E−02 n=2 fg=0.11 bg=0.02
fat cell differentiation GO:0045444 p=3.4E−02 n=2 fg=0.11 bg=0.02
carboxylic acid catabolic process GO:0046395 p=3.4E−02 n=2 fg=0.11 bg=0.02
sulfur compound metabolic process GO:0006790 p=4.4E−02 n=2 fg=0.11 bg=0.02
positive regulation of leukocyte activat... GO:0002696 p=4.4E−02 n=2 fg=0.11 bg=0.02
positive regulation of cell activation GO:0050867 p=4.4E−02 n=2 fg=0.11 bg=0.02
neuron maturation GO:0042551 p=4.4E−02 n=2 fg=0.11 bg=0.02
response to osmotic stress GO:0006970 p=4.4E−02 n=2 fg=0.11 bg=0.02
neuron remodeling GO:0016322 p=4.4E−02 n=2 fg=0.11 bg=0.02
negative regulation of epithelial cell p... GO:0050680 p=4.4E−02 n=2 fg=0.11 bg=0.02
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−log(p)
n=18/71 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_v1g241767
fraction genes in fg and expected valu
acetyltransferase activity GO:0016407 p=9.6E−04 n=3 fg=0.17 bg=0.01
cAMP response element binding GO:0035497 p=4.9E−02 n=1 fg=0.06 bg=0.00
amino acid kinase activity GO:0019202 p=4.9E−02 n=1 fg=0.06 bg=0.00
O−acyltransferase activity GO:0008374 p=4.9E−02 n=1 fg=0.06 bg=0.00
galactosylgalactosylxylosylprotein 3−bet... GO:0015018 p=4.9E−02 n=1 fg=0.06 bg=0.00
threonine−type peptidase activity GO:0070003 p=4.9E−02 n=1 fg=0.06 bg=0.00
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=4.9E−02 n=1 fg=0.06 bg=0.00
glutamate 5−kinase activity GO:0004349 p=4.9E−02 n=1 fg=0.06 bg=0.00
phosphatase regulator activity GO:0019208 p=4.9E−02 n=1 fg=0.06 bg=0.00
delta1−pyrroline−5−carboxylate synthetas... GO:0017084 p=4.9E−02 n=1 fg=0.06 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=4.9E−02 n=1 fg=0.06 bg=0.00
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gamma−glutamylcyclotransferase activity GO:0003839 p=4.9E−02 n=1 fg=0.06 bg=0.00
oxidoreductase activity, acting on the a... GO:0016903 p=4.9E−02 n=1 fg=0.06 bg=0.00
modified amino acid binding GO:0072341 p=4.9E−02 n=1 fg=0.06 bg=0.00
Notch binding GO:0005112 p=4.9E−02 n=1 fg=0.06 bg=0.00
phosphotransferase activity, carboxyl gr... GO:0016774 p=4.9E−02 n=1 fg=0.06 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=4.9E−02 n=1 fg=0.06 bg=0.00
protein phosphatase regulator activity GO:0019888 p=4.9E−02 n=1 fg=0.06 bg=0.00
cAMP response element binding protein bi... GO:0008140 p=4.9E−02 n=1 fg=0.06 bg=0.00
oxysterol binding GO:0008142 p=4.9E−02 n=1 fg=0.06 bg=0.00
protein phosphatase activator activity GO:0072542 p=4.9E−02 n=1 fg=0.06 bg=0.00
glutamate−5−semialdehyde dehydrogenase a... GO:0004350 p=4.9E−02 n=1 fg=0.06 bg=0.00
phosphatase activator activity GO:0019211 p=4.9E−02 n=1 fg=0.06 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=4.9E−02 n=1 fg=0.06 bg=0.00
phosphatidylinositol−4−phosphate binding GO:0070273 p=4.9E−02 n=1 fg=0.06 bg=0.00
phospholipase A2 activity GO:0004623 p=4.9E−02 n=1 fg=0.06 bg=0.00
beta−aspartyl−peptidase activity GO:0008798 p=4.9E−02 n=1 fg=0.06 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=4.9E−02 n=1 fg=0.06 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=4.9E−02 n=1 fg=0.06 bg=0.00
0 1 2 3 4 5
−log(p)
n=18/71 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_v1g241767
fraction genes in fg and expected valu
organelle envelope GO:0031967 p=4.2E−02 n=4 fg=0.20 bg=0.07
envelope GO:0031975 p=4.2E−02 n=4 fg=0.20 bg=0.07
azurophil granule GO:0042582 p=4.3E−02 n=2 fg=0.10 bg=0.02
primary lysosome GO:0005766 p=4.3E−02 n=2 fg=0.10 bg=0.02
anchored component of plasma membrane GO:0046658 p=5.0E−02 n=1 fg=0.05 bg=0.00
core−binding factor complex GO:0016513 p=5.0E−02 n=1 fg=0.05 bg=0.00
secretory granule GO:0030141 p=5.3E−02 n=3 fg=0.15 bg=0.04
secretory granule lumen GO:0034774 p=5.5E−02 n=2 fg=0.10 bg=0.02
cytoplasmic vesicle lumen GO:0060205 p=5.5E−02 n=2 fg=0.10 bg=0.02
vesicle lumen GO:0031983 p=5.5E−02 n=2 fg=0.10 bg=0.02
endoplasmic reticulum subcompartment GO:0098827 p=5.8E−02 n=4 fg=0.20 bg=0.08
secretory vesicle GO:0099503 p=7.8E−02 n=4 fg=0.20 bg=0.08
cortical endoplasmic reticulum GO:0032541 p=9.7E−02 n=1 fg=0.05 bg=0.01
site of double−strand break GO:0035861 p=9.7E−02 n=1 fg=0.05 bg=0.01
site of DNA damage GO:0090734 p=9.7E−02 n=1 fg=0.05 bg=0.01
intrinsic component of the cytoplasmic s... GO:0031235 p=9.7E−02 n=1 fg=0.05 bg=0.01
endoplasmic reticulum tubular network GO:0071782 p=9.7E−02 n=1 fg=0.05 bg=0.01
azurophil granule membrane GO:0035577 p=9.7E−02 n=1 fg=0.05 bg=0.01
Golgi lumen GO:0005796 p=9.7E−02 n=1 fg=0.05 bg=0.01
anchored component of membrane GO:0031225 p=9.7E−02 n=1 fg=0.05 bg=0.01
nuclear envelope GO:0005635 p=1.2E−01 n=2 fg=0.10 bg=0.03
endoplasmic reticulum GO:0005783 p=1.2E−01 n=6 fg=0.30 bg=0.18
organelle subcompartment GO:0031984 p=1.4E−01 n=5 fg=0.25 bg=0.14
dendrite membrane GO:0032590 p=1.4E−01 n=1 fg=0.05 bg=0.01
filopodium GO:0030175 p=1.4E−01 n=1 fg=0.05 bg=0.01
ficolin−1−rich granule lumen GO:1904813 p=1.4E−01 n=1 fg=0.05 bg=0.01
cis−Golgi network GO:0005801 p=1.4E−01 n=1 fg=0.05 bg=0.01
mitochondrial membrane GO:0031966 p=1.5E−01 n=2 fg=0.10 bg=0.03
endoplasmic reticulum membrane GO:0005789 p=1.5E−01 n=3 fg=0.15 bg=0.07
nuclear outer membrane−endoplasmic retic... GO:0042175 p=1.5E−01 n=3 fg=0.15 bg=0.07
0 1 2 3 4 5
−log(p)
n=20/71 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction