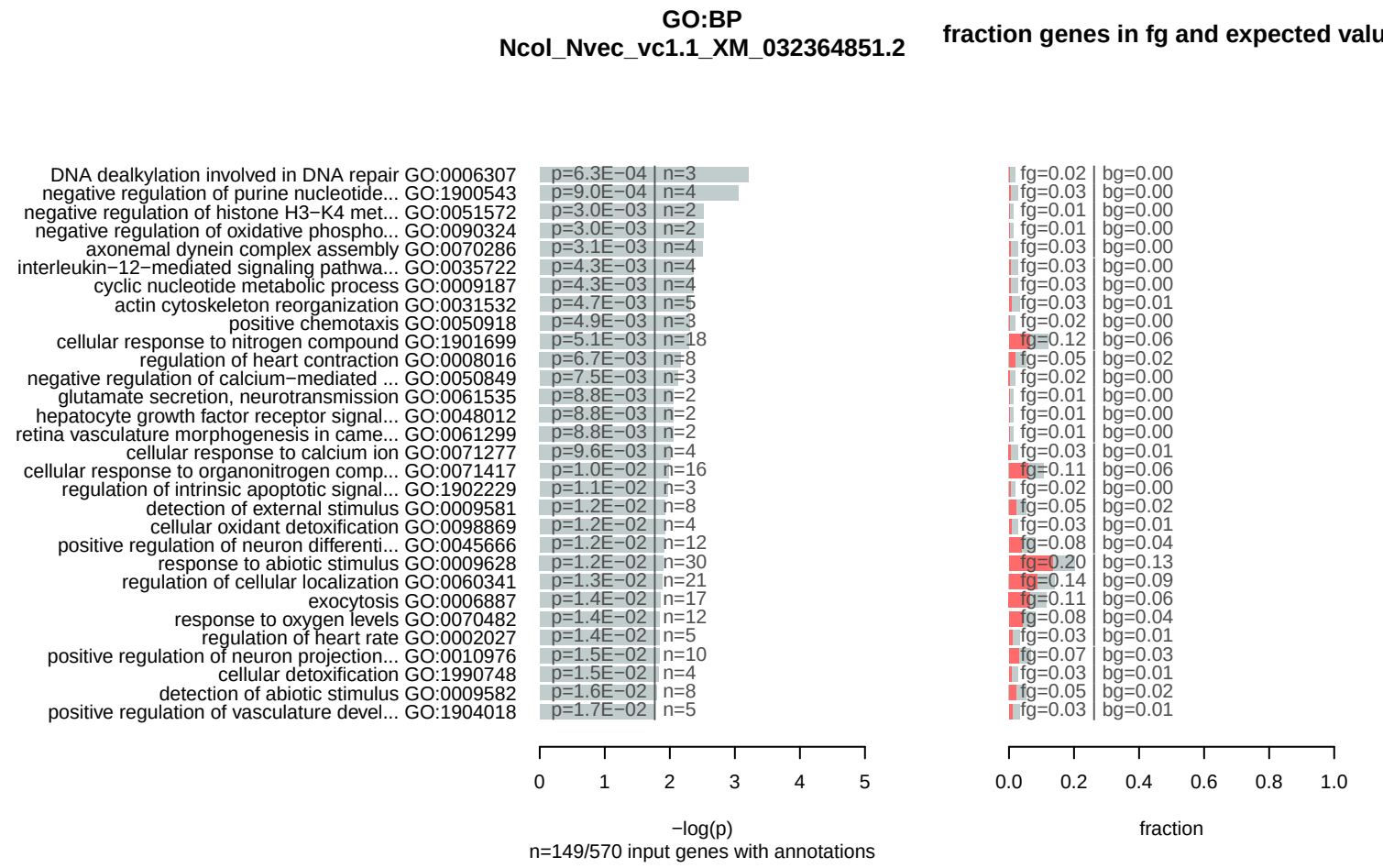
GO:BP
Ncol_Nvec_vc1.1_XM_032364851.2
fraction genes in fg and expected valu
DNA dealkylation involved in DNA repair GO:0006307 p=6.3E−04 n=3 fg=0.02 bg=0.00
negative regulation of purine nucleotide... GO:1900543 p=9.0E−04 n=4 fg=0.03 bg=0.00
negative regulation of histone H3−K4 met... GO:0051572 p=3.0E−03 n=2 fg=0.01 bg=0.00
negative regulation of oxidative phospho... GO:0090324 p=3.0E−03 n=2 fg=0.01 bg=0.00
axonemal dynein complex assembly GO:0070286 p=3.1E−03 n=4 fg=0.03 bg=0.00
interleukin−12−mediated signaling pathwa... GO:0035722 p=4.3E−03 n=4 fg=0.03 bg=0.00
cyclic nucleotide metabolic process GO:0009187 p=4.3E−03 n=4 fg=0.03 bg=0.00
actin cytoskeleton reorganization GO:0031532 p=4.7E−03 n=5 fg=0.03 bg=0.01
positive chemotaxis GO:0050918 p=4.9E−03 n=3 fg=0.02 bg=0.00
cellular response to nitrogen compound GO:1901699 p=5.1E−03 n=18 fg=0.12 bg=0.06
regulation of heart contraction GO:0008016 p=6.7E−03 n=8 fg=0.05 bg=0.02
negative regulation of calcium−mediated ... GO:0050849 p=7.5E−03 n=3 fg=0.02 bg=0.00
glutamate secretion, neurotransmission GO:0061535 p=8.8E−03 n=2 fg=0.01 bg=0.00
hepatocyte growth factor receptor signal... GO:0048012 p=8.8E−03 n=2 fg=0.01 bg=0.00
retina vasculature morphogenesis in came... GO:0061299 p=8.8E−03 n=2 fg=0.01 bg=0.00
cellular response to calcium ion GO:0071277 p=9.6E−03 n=4 fg=0.03 bg=0.01
cellular response to organonitrogen comp... GO:0071417 p=1.0E−02 n=16 fg=0.11 bg=0.06
regulation of intrinsic apoptotic signal... GO:1902229 p=1.1E−02 n=3 fg=0.02 bg=0.00
detection of external stimulus GO:0009581 p=1.2E−02 n=8 fg=0.05 bg=0.02
cellular oxidant detoxification GO:0098869 p=1.2E−02 n=4 fg=0.03 bg=0.01
positive regulation of neuron differenti... GO:0045666 p=1.2E−02 n=12 fg=0.08 bg=0.04
response to abiotic stimulus GO:0009628 p=1.2E−02 n=30 fg=0.20 bg=0.13
regulation of cellular localization GO:0060341 p=1.3E−02 n=21 fg=0.14 bg=0.09
exocytosis GO:0006887 p=1.4E−02 n=17 fg=0.11 bg=0.06
response to oxygen levels GO:0070482 p=1.4E−02 n=12 fg=0.08 bg=0.04
regulation of heart rate GO:0002027 p=1.4E−02 n=5 fg=0.03 bg=0.01
positive regulation of neuron projection... GO:0010976 p=1.5E−02 n=10 fg=0.07 bg=0.03
cellular detoxification GO:1990748 p=1.5E−02 n=4 fg=0.03 bg=0.01
detection of abiotic stimulus GO:0009582 p=1.6E−02 n=8 fg=0.05 bg=0.02
positive regulation of vasculature devel... GO:1904018 p=1.7E−02 n=5 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=149/570 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032364851.2
fraction genes in fg and expected valu
dynein heavy chain binding GO:0045504 p=1.2E−04 n=4 fg=0.03 bg=0.00
phosphatidylethanolamine binding GO:0008429 p=6.1E−04 n=3 fg=0.02 bg=0.00
calcium−dependent phospholipid binding GO:0005544 p=1.5E−03 n=3 fg=0.02 bg=0.00
high voltage−gated calcium channel activ... GO:0008331 p=2.9E−03 n=2 fg=0.02 bg=0.00
antioxidant activity GO:0016209 p=4.1E−03 n=4 fg=0.03 bg=0.01
ammonium ion binding GO:0070405 p=4.1E−03 n=4 fg=0.03 bg=0.01
MAP kinase kinase kinase activity GO:0004709 p=4.7E−03 n=3 fg=0.02 bg=0.00
phosphatidylcholine binding GO:0031210 p=4.7E−03 n=3 fg=0.02 bg=0.00
ion gated channel activity GO:0022839 p=9.7E−03 n=8 fg=0.06 bg=0.02
receptor ligand activity GO:0048018 p=1.4E−02 n=3 fg=0.02 bg=0.00
syntaxin−1 binding GO:0017075 p=1.6E−02 n=2 fg=0.02 bg=0.00
signaling receptor activator activity GO:0030546 p=1.9E−02 n=3 fg=0.02 bg=0.00
flavin adenine dinucleotide binding GO:0050660 p=2.4E−02 n=3 fg=0.02 bg=0.01
signaling receptor regulator activity GO:0030545 p=2.4E−02 n=3 fg=0.02 bg=0.01
mannosyltransferase activity GO:0000030 p=2.6E−02 n=2 fg=0.02 bg=0.00
chemoattractant activity GO:0042056 p=2.6E−02 n=2 fg=0.02 bg=0.00
dynein light chain binding GO:0045503 p=2.6E−02 n=2 fg=0.02 bg=0.00
calcium ion binding GO:0005509 p=2.7E−02 n=7 fg=0.05 bg=0.02
cytoskeletal motor activity GO:0003774 p=2.9E−02 n=4 fg=0.03 bg=0.01
oxidoreductase activity GO:0016491 p=3.2E−02 n=13 fg=0.10 bg=0.06
peroxidase activity GO:0004601 p=3.8E−02 n=2 fg=0.02 bg=0.00
cyclic−nucleotide phosphodiesterase acti... GO:0004112 p=3.8E−02 n=2 fg=0.02 bg=0.00
3',5'−cyclic−nucleotide phosphodiesteras... GO:0004114 p=3.8E−02 n=2 fg=0.02 bg=0.00
DNA−(apurinic or apyrimidinic site) endo... GO:0003906 p=3.8E−02 n=2 fg=0.02 bg=0.00
3',5'−cyclic−GMP phosphodiesterase activ... GO:0047555 p=3.8E−02 n=2 fg=0.02 bg=0.00
O−methyltransferase activity GO:0008171 p=3.8E−02 n=2 fg=0.02 bg=0.00
acyltransferase activity, transferring g... GO:0016747 p=4.3E−02 n=5 fg=0.04 bg=0.02
2−oxoglutarate−dependent dioxygenase act... GO:0016706 p=4.4E−02 n=3 fg=0.02 bg=0.01
transmitter−gated channel activity GO:0022835 p=5.2E−02 n=2 fg=0.02 bg=0.00
voltage−gated anion channel activity GO:0008308 p=5.2E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=129/570 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032364851.2
fraction genes in fg and expected valu
ficolin−1−rich granule membrane GO:0101003 p=5.1E−04 n=4 fg=0.03 bg=0.00
organelle membrane contact site GO:0044232 p=2.9E−03 n=3 fg=0.02 bg=0.00
hippocampal mossy fiber GO:0097457 p=3.0E−03 n=2 fg=0.01 bg=0.00
integral component of synaptic vesicle m... GO:0030285 p=4.2E−03 n=4 fg=0.03 bg=0.00
presynapse GO:0098793 p=4.7E−03 n=17 fg=0.11 bg=0.05
outer dynein arm GO:0036157 p=8.6E−03 n=2 fg=0.01 bg=0.00
side of membrane GO:0098552 p=9.8E−03 n=11 fg=0.07 bg=0.03
extrinsic component of plasma membrane GO:0019897 p=2.5E−02 n=5 fg=0.03 bg=0.01
extrinsic component of cytoplasmic side ... GO:0031234 p=2.5E−02 n=4 fg=0.03 bg=0.01
cytoplasmic side of plasma membrane GO:0009898 p=2.6E−02 n=7 fg=0.05 bg=0.02
Prp19 complex GO:0000974 p=2.7E−02 n=2 fg=0.01 bg=0.00
neuronal cell body GO:0043025 p=2.8E−02 n=15 fg=0.10 bg=0.06
apical plasma membrane GO:0016324 p=3.1E−02 n=10 fg=0.07 bg=0.03
presynaptic membrane GO:0042734 p=3.2E−02 n=5 fg=0.03 bg=0.01
presynaptic active zone GO:0048786 p=3.4E−02 n=4 fg=0.03 bg=0.01
cell surface GO:0009986 p=3.5E−02 n=10 fg=0.07 bg=0.04
synaptic membrane GO:0097060 p=3.7E−02 n=7 fg=0.05 bg=0.02
axon cytoplasm GO:1904115 p=3.9E−02 n=2 fg=0.01 bg=0.00
voltage−gated calcium channel complex GO:0005891 p=3.9E−02 n=2 fg=0.01 bg=0.00
perikaryon GO:0043204 p=3.9E−02 n=4 fg=0.03 bg=0.01
brush border GO:0005903 p=4.0E−02 n=5 fg=0.03 bg=0.01
somatodendritic compartment GO:0036477 p=4.4E−02 n=19 fg=0.13 bg=0.09
distal axon GO:0150034 p=4.7E−02 n=10 fg=0.07 bg=0.04
nuclear membrane GO:0031965 p=5.0E−02 n=7 fg=0.05 bg=0.02
cytoplasmic side of membrane GO:0098562 p=5.0E−02 n=7 fg=0.05 bg=0.02
phagocytic vesicle GO:0045335 p=5.1E−02 n=4 fg=0.03 bg=0.01
axon GO:0030424 p=5.2E−02 n=17 fg=0.11 bg=0.07
UBC13−UEV1A complex GO:0035370 p=5.5E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=5.5E−02 n=1 fg=0.01 bg=0.00
Shu complex GO:0097196 p=5.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=148/570 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction