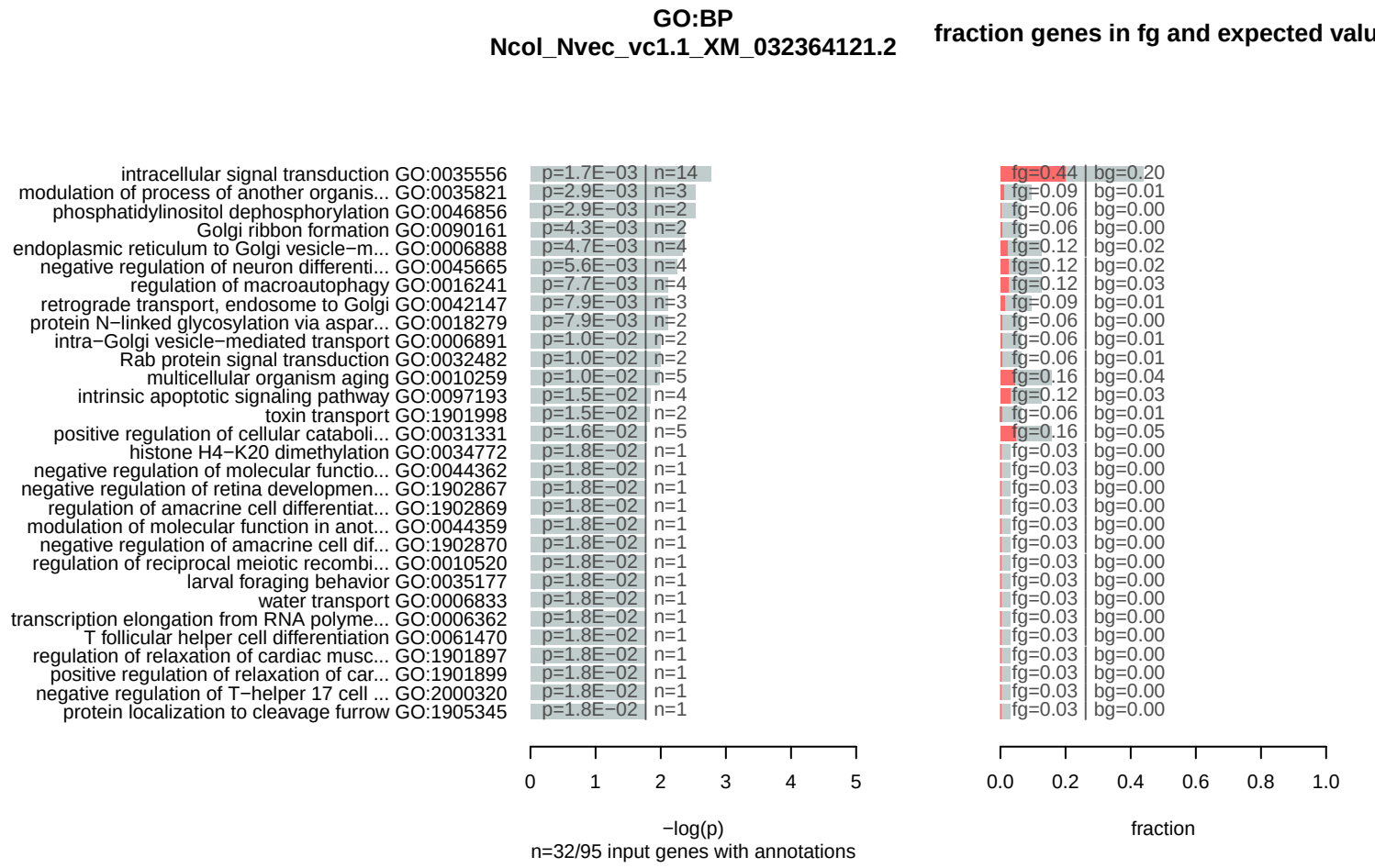
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fraction genes in fg and expected valu
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modulation of process of another organis... GO:0035821 p=2.9E−03 n=3 fg=0.09 bg=0.01
phosphatidylinositol dephosphorylation GO:0046856 p=2.9E−03 n=2 fg=0.06 bg=0.00
Golgi ribbon formation GO:0090161 p=4.3E−03 n=2 fg=0.06 bg=0.00
endoplasmic reticulum to Golgi vesicle−m... GO:0006888 p=4.7E−03 n=4 fg=0.12 bg=0.02
negative regulation of neuron differenti... GO:0045665 p=5.6E−03 n=4 fg=0.12 bg=0.02
regulation of macroautophagy GO:0016241 p=7.7E−03 n=4 fg=0.12 bg=0.03
retrograde transport, endosome to Golgi GO:0042147 p=7.9E−03 n=3 fg=0.09 bg=0.01
protein N−linked glycosylation via aspar... GO:0018279 p=7.9E−03 n=2 fg=0.06 bg=0.00
intra−Golgi vesicle−mediated transport GO:0006891 p=1.0E−02 n=2 fg=0.06 bg=0.01
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intrinsic apoptotic signaling pathway GO:0097193 p=1.5E−02 n=4 fg=0.12 bg=0.03
toxin transport GO:1901998 p=1.5E−02 n=2 fg=0.06 bg=0.01
positive regulation of cellular cataboli... GO:0031331 p=1.6E−02 n=5 fg=0.16 bg=0.05
histone H4−K20 dimethylation GO:0034772 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of molecular functio... GO:0044362 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of retina developmen... GO:1902867 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulation of amacrine cell differentiat... GO:1902869 p=1.8E−02 n=1 fg=0.03 bg=0.00
modulation of molecular function in anot... GO:0044359 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of amacrine cell dif... GO:1902870 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulation of reciprocal meiotic recombi... GO:0010520 p=1.8E−02 n=1 fg=0.03 bg=0.00
larval foraging behavior GO:0035177 p=1.8E−02 n=1 fg=0.03 bg=0.00
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transcription elongation from RNA polyme... GO:0006362 p=1.8E−02 n=1 fg=0.03 bg=0.00
T follicular helper cell differentiation GO:0061470 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulation of relaxation of cardiac musc... GO:1901897 p=1.8E−02 n=1 fg=0.03 bg=0.00
positive regulation of relaxation of car... GO:1901899 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of T−helper 17 cell ... GO:2000320 p=1.8E−02 n=1 fg=0.03 bg=0.00
protein localization to cleavage furrow GO:1905345 p=1.8E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=32/95 input genes with annotations
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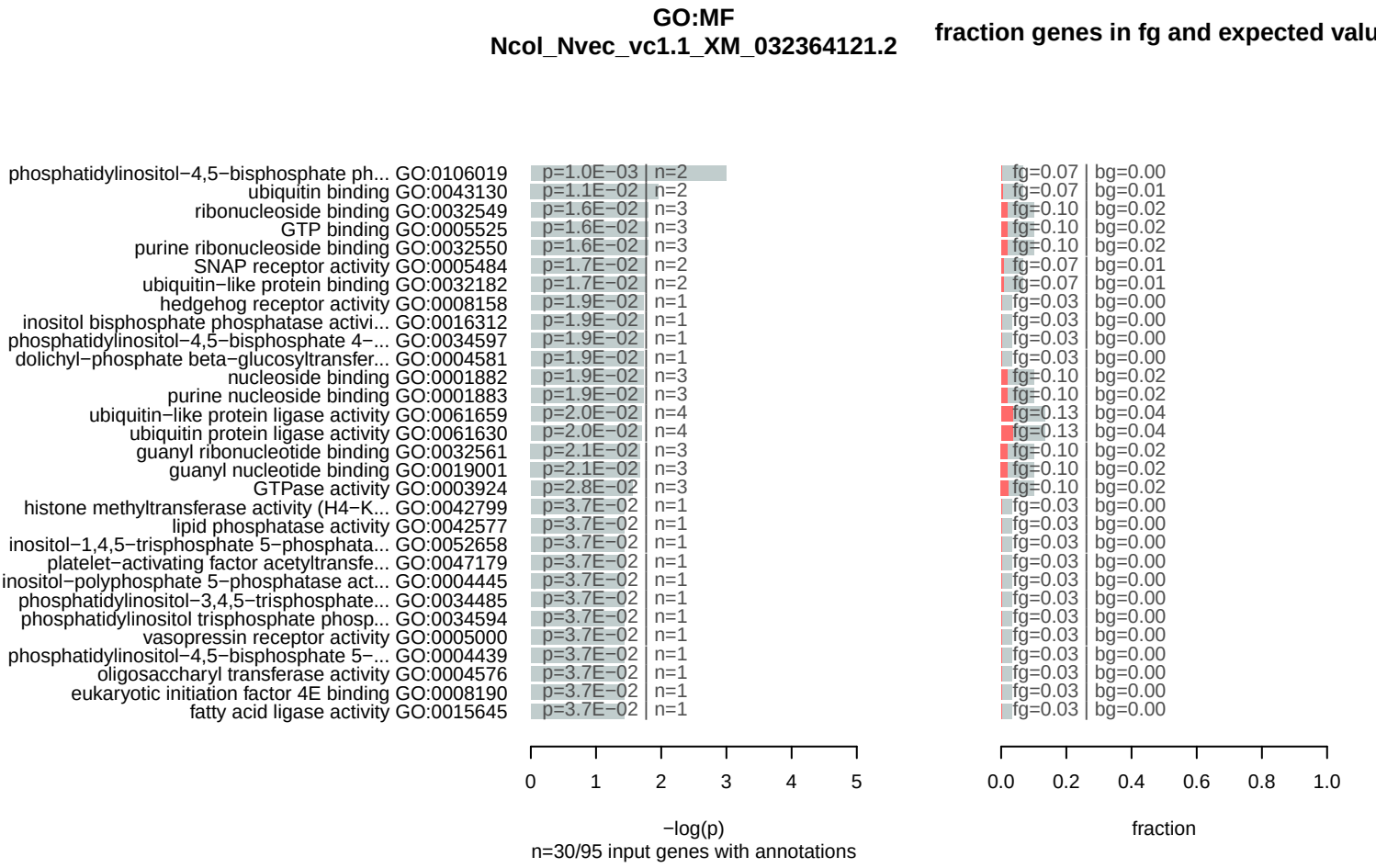
fraction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ubiquitin binding GO:0043130 p=1.1E−02 n=2 fg=0.07 bg=0.01
ribonucleoside binding GO:0032549 p=1.6E−02 n=3 fg=0.10 bg=0.02
GTP binding GO:0005525 p=1.6E−02 n=3 fg=0.10 bg=0.02
purine ribonucleoside binding GO:0032550 p=1.6E−02 n=3 fg=0.10 bg=0.02
SNAP receptor activity GO:0005484 p=1.7E−02 n=2 fg=0.07 bg=0.01
ubiquitin−like protein binding GO:0032182 p=1.7E−02 n=2 fg=0.07 bg=0.01
hedgehog receptor activity GO:0008158 p=1.9E−02 n=1 fg=0.03 bg=0.00
inositol bisphosphate phosphatase activi... GO:0016312 p=1.9E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−4,5−bisphosphate 4−... GO:0034597 p=1.9E−02 n=1 fg=0.03 bg=0.00
dolichyl−phosphate beta−glucosyltransfer... GO:0004581 p=1.9E−02 n=1 fg=0.03 bg=0.00
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purine nucleoside binding GO:0001883 p=1.9E−02 n=3 fg=0.10 bg=0.02
ubiquitin−like protein ligase activity GO:0061659 p=2.0E−02 n=4 fg=0.13 bg=0.04
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guanyl ribonucleotide binding GO:0032561 p=2.1E−02 n=3 fg=0.10 bg=0.02
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histone methyltransferase activity (H4−K... GO:0042799 p=3.7E−02 n=1 fg=0.03 bg=0.00
lipid phosphatase activity GO:0042577 p=3.7E−02 n=1 fg=0.03 bg=0.00
inositol−1,4,5−trisphosphate 5−phosphata... GO:0052658 p=3.7E−02 n=1 fg=0.03 bg=0.00
platelet−activating factor acetyltransfe... GO:0047179 p=3.7E−02 n=1 fg=0.03 bg=0.00
inositol−polyphosphate 5−phosphatase act... GO:0004445 p=3.7E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−3,4,5−trisphosphate... GO:0034485 p=3.7E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol trisphosphate phosp... GO:0034594 p=3.7E−02 n=1 fg=0.03 bg=0.00
vasopressin receptor activity GO:0005000 p=3.7E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol−4,5−bisphosphate 5−... GO:0004439 p=3.7E−02 n=1 fg=0.03 bg=0.00
oligosaccharyl transferase activity GO:0004576 p=3.7E−02 n=1 fg=0.03 bg=0.00
eukaryotic initiation factor 4E binding GO:0008190 p=3.7E−02 n=1 fg=0.03 bg=0.00
fatty acid ligase activity GO:0015645 p=3.7E−02 n=1 fg=0.03 bg=0.00
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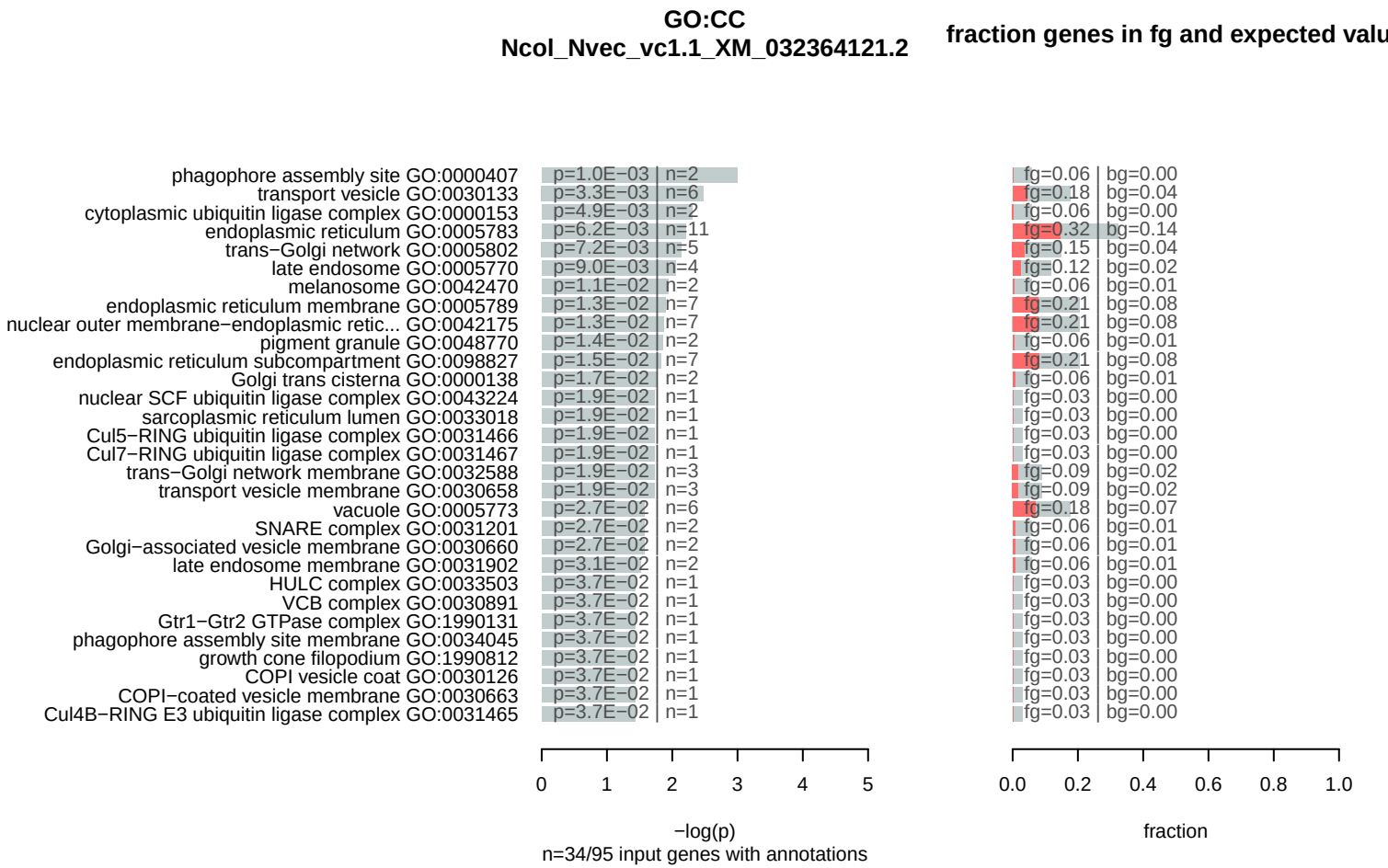
−log(p)
n=30/95 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction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Ncol_Nvec_vc1.1_XM_032364121.2
fraction genes in fg and expected valu
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transport vesicle GO:0030133 p=3.3E−03 n=6 fg=0.18 bg=0.04
cytoplasmic ubiquitin ligase complex GO:0000153 p=4.9E−03 n=2 fg=0.06 bg=0.00
endoplasmic reticulum GO:0005783 p=6.2E−03 n=11 fg=0.32 bg=0.14
trans−Golgi network GO:0005802 p=7.2E−03 n=5 fg=0.15 bg=0.04
late endosome GO:0005770 p=9.0E−03 n=4 fg=0.12 bg=0.02
melanosome GO:0042470 p=1.1E−02 n=2 fg=0.06 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=1.3E−02 n=7 fg=0.21 bg=0.08
nuclear outer membrane−endoplasmic retic... GO:0042175 p=1.3E−02 n=7 fg=0.21 bg=0.08
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endoplasmic reticulum subcompartment GO:0098827 p=1.5E−02 n=7 fg=0.21 bg=0.08
Golgi trans cisterna GO:0000138 p=1.7E−02 n=2 fg=0.06 bg=0.01
nuclear SCF ubiquitin ligase complex GO:0043224 p=1.9E−02 n=1 fg=0.03 bg=0.00
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Cul5−RING ubiquitin ligase complex GO:0031466 p=1.9E−02 n=1 fg=0.03 bg=0.00
Cul7−RING ubiquitin ligase complex GO:0031467 p=1.9E−02 n=1 fg=0.03 bg=0.00
trans−Golgi network membrane GO:0032588 p=1.9E−02 n=3 fg=0.09 bg=0.02
transport vesicle membrane GO:0030658 p=1.9E−02 n=3 fg=0.09 bg=0.02
vacuole GO:0005773 p=2.7E−02 n=6 fg=0.18 bg=0.07
SNARE complex GO:0031201 p=2.7E−02 n=2 fg=0.06 bg=0.01
Golgi−associated vesicle membrane GO:0030660 p=2.7E−02 n=2 fg=0.06 bg=0.01
late endosome membrane GO:0031902 p=3.1E−02 n=2 fg=0.06 bg=0.01
HULC complex GO:0033503 p=3.7E−02 n=1 fg=0.03 bg=0.00
VCB complex GO:0030891 p=3.7E−02 n=1 fg=0.03 bg=0.00
Gtr1−Gtr2 GTPase complex GO:1990131 p=3.7E−02 n=1 fg=0.03 bg=0.00
phagophore assembly site membrane GO:0034045 p=3.7E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=34/95 input genes with annotations
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fraction