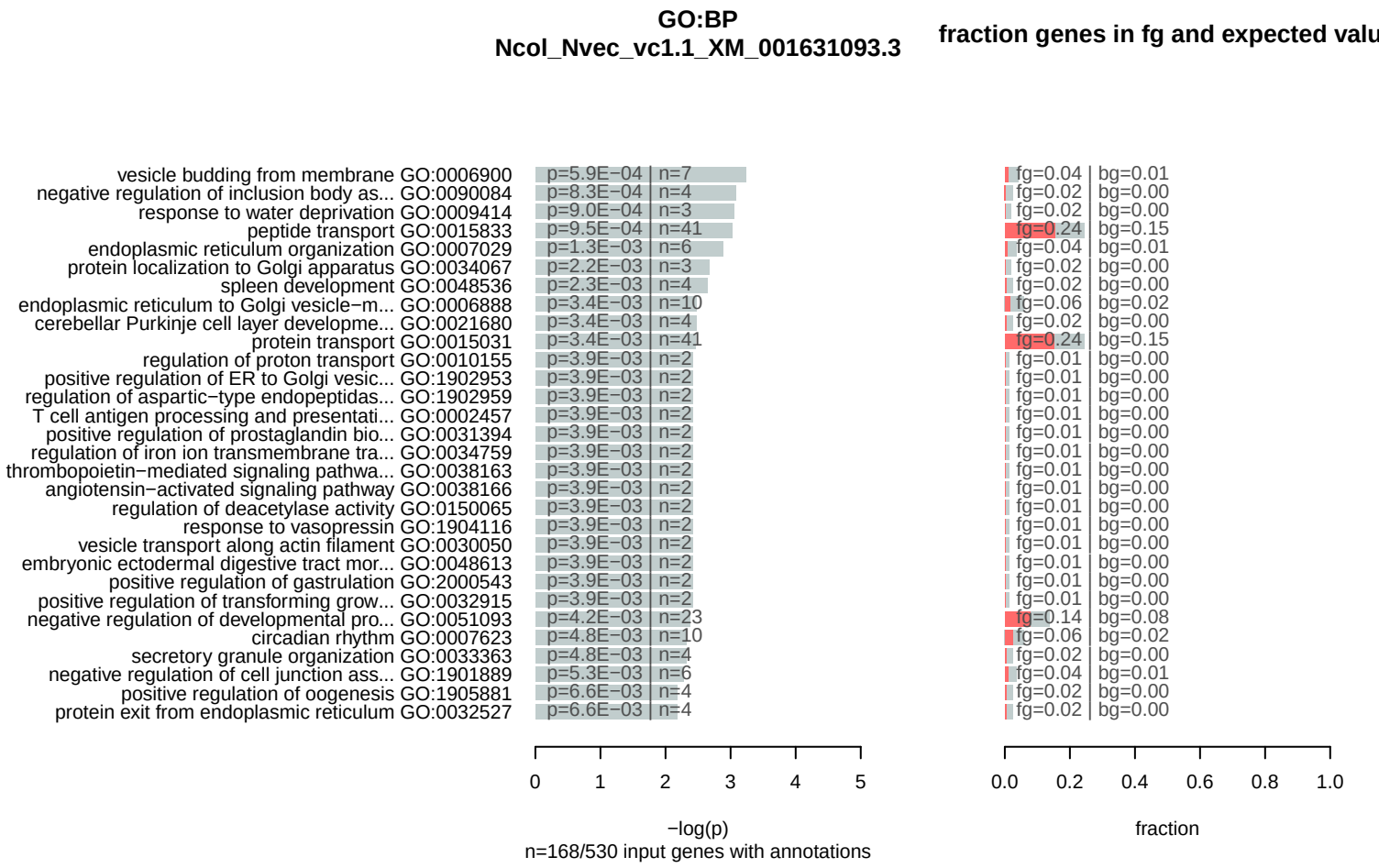
GO:BP
Ncol_Nvec_vc1.1_XM_001631093.3
fraction genes in fg and expected valu
vesicle budding from membrane GO:0006900 p=5.9E−04 n=7 fg=0.04 bg=0.01
negative regulation of inclusion body as... GO:0090084 p=8.3E−04 n=4 fg=0.02 bg=0.00
response to water deprivation GO:0009414 p=9.0E−04 n=3 fg=0.02 bg=0.00
peptide transport GO:0015833 p=9.5E−04 n=41 fg=0.24 bg=0.15
endoplasmic reticulum organization GO:0007029 p=1.3E−03 n=6 fg=0.04 bg=0.01
protein localization to Golgi apparatus GO:0034067 p=2.2E−03 n=3 fg=0.02 bg=0.00
spleen development GO:0048536 p=2.3E−03 n=4 fg=0.02 bg=0.00
endoplasmic reticulum to Golgi vesicle−m... GO:0006888 p=3.4E−03 n=10 fg=0.06 bg=0.02
cerebellar Purkinje cell layer developme... GO:0021680 p=3.4E−03 n=4 fg=0.02 bg=0.00
protein transport GO:0015031 p=3.4E−03 n=41 fg=0.24 bg=0.15
regulation of proton transport GO:0010155 p=3.9E−03 n=2 fg=0.01 bg=0.00
positive regulation of ER to Golgi vesic... GO:1902953 p=3.9E−03 n=2 fg=0.01 bg=0.00
regulation of aspartic−type endopeptidas... GO:1902959 p=3.9E−03 n=2 fg=0.01 bg=0.00
T cell antigen processing and presentati... GO:0002457 p=3.9E−03 n=2 fg=0.01 bg=0.00
positive regulation of prostaglandin bio... GO:0031394 p=3.9E−03 n=2 fg=0.01 bg=0.00
regulation of iron ion transmembrane tra... GO:0034759 p=3.9E−03 n=2 fg=0.01 bg=0.00
thrombopoietin−mediated signaling pathwa... GO:0038163 p=3.9E−03 n=2 fg=0.01 bg=0.00
angiotensin−activated signaling pathway GO:0038166 p=3.9E−03 n=2 fg=0.01 bg=0.00
regulation of deacetylase activity GO:0150065 p=3.9E−03 n=2 fg=0.01 bg=0.00
response to vasopressin GO:1904116 p=3.9E−03 n=2 fg=0.01 bg=0.00
vesicle transport along actin filament GO:0030050 p=3.9E−03 n=2 fg=0.01 bg=0.00
embryonic ectodermal digestive tract mor... GO:0048613 p=3.9E−03 n=2 fg=0.01 bg=0.00
positive regulation of gastrulation GO:2000543 p=3.9E−03 n=2 fg=0.01 bg=0.00
positive regulation of transforming grow... GO:0032915 p=3.9E−03 n=2 fg=0.01 bg=0.00
negative regulation of developmental pro... GO:0051093 p=4.2E−03 n=23 fg=0.14 bg=0.08
circadian rhythm GO:0007623 p=4.8E−03 n=10 fg=0.06 bg=0.02
secretory granule organization GO:0033363 p=4.8E−03 n=4 fg=0.02 bg=0.00
negative regulation of cell junction ass... GO:1901889 p=5.3E−03 n=6 fg=0.04 bg=0.01
positive regulation of oogenesis GO:1905881 p=6.6E−03 n=4 fg=0.02 bg=0.00
protein exit from endoplasmic reticulum GO:0032527 p=6.6E−03 n=4 fg=0.02 bg=0.00
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−log(p)
n=168/530 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001631093.3
fraction genes in fg and expected valu
small GTPase binding GO:0031267 p=5.6E−04 n=16 fg=0.11 bg=0.04
single−stranded DNA binding GO:0003697 p=7.2E−03 n=6 fg=0.04 bg=0.01
ribosome binding GO:0043022 p=8.5E−03 n=4 fg=0.03 bg=0.01
peptidase activator activity involved in... GO:0016505 p=1.1E−02 n=2 fg=0.01 bg=0.00
cysteine−type endopeptidase activator ac... GO:0008656 p=1.1E−02 n=2 fg=0.01 bg=0.00
triglyceride lipase activity GO:0004806 p=1.1E−02 n=2 fg=0.01 bg=0.00
low−density lipoprotein particle recepto... GO:0050750 p=1.5E−02 n=3 fg=0.02 bg=0.00
lipoprotein particle receptor binding GO:0070325 p=1.5E−02 n=3 fg=0.02 bg=0.00
proteasome binding GO:0070628 p=1.5E−02 n=3 fg=0.02 bg=0.00
transcription coregulator binding GO:0001221 p=1.5E−02 n=3 fg=0.02 bg=0.00
transporter activity GO:0005215 p=1.5E−02 n=23 fg=0.16 bg=0.10
transcription coactivator activity GO:0003713 p=1.8E−02 n=10 fg=0.07 bg=0.03
P−type transmembrane transporter activit... GO:0140358 p=2.0E−02 n=3 fg=0.02 bg=0.00
P−type ion transporter activity GO:0015662 p=2.0E−02 n=3 fg=0.02 bg=0.00
DNA−binding transcription factor activit... GO:0000981 p=2.1E−02 n=15 fg=0.10 bg=0.06
core promoter sequence−specific DNA bind... GO:0001046 p=2.1E−02 n=4 fg=0.03 bg=0.01
enzyme regulator activity GO:0030234 p=2.2E−02 n=21 fg=0.14 bg=0.09
ATPase−coupled transmembrane transporter... GO:0042626 p=2.2E−02 n=5 fg=0.03 bg=0.01
DNA−binding transcription factor activit... GO:0003700 p=2.5E−02 n=17 fg=0.12 bg=0.07
voltage−gated potassium channel activity GO:0005249 p=2.6E−02 n=3 fg=0.02 bg=0.00
transcription coactivator binding GO:0001223 p=3.3E−02 n=2 fg=0.01 bg=0.00
transcription regulator activity GO:0140110 p=3.5E−02 n=22 fg=0.15 bg=0.10
G protein−coupled receptor binding GO:0001664 p=3.7E−02 n=6 fg=0.04 bg=0.02
double−stranded DNA binding GO:0003690 p=4.3E−02 n=14 fg=0.10 bg=0.06
purine ribonucleoside triphosphate bindi... GO:0035639 p=4.6E−02 n=14 fg=0.10 bg=0.06
catalytic activity, acting on a glycopro... GO:0140103 p=4.8E−02 n=2 fg=0.01 bg=0.00
dynactin binding GO:0034452 p=4.8E−02 n=2 fg=0.01 bg=0.00
protein phosphatase 2B binding GO:0030346 p=4.8E−02 n=2 fg=0.01 bg=0.00
cysteine−type endopeptidase regulator ac... GO:0043028 p=4.8E−02 n=2 fg=0.01 bg=0.00
ubiquitin conjugating enzyme binding GO:0031624 p=5.1E−02 n=3 fg=0.02 bg=0.01
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−log(p)
n=146/530 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001631093.3
fraction genes in fg and expected valu
Golgi membrane GO:0000139 p=6.6E−04 n=19 fg=0.11 bg=0.05
cell body fiber GO:0070852 p=9.2E−04 n=3 fg=0.02 bg=0.00
Golgi apparatus subcompartment GO:0098791 p=2.7E−03 n=21 fg=0.12 bg=0.07
post−mRNA release spliceosomal complex GO:0071014 p=3.9E−03 n=2 fg=0.01 bg=0.00
autophagosome membrane GO:0000421 p=4.2E−03 n=3 fg=0.02 bg=0.00
FAR/SIN/STRIPAK complex GO:0090443 p=1.1E−02 n=2 fg=0.01 bg=0.00
actin cap GO:0030478 p=1.1E−02 n=2 fg=0.01 bg=0.00
phagocytic vesicle membrane GO:0030670 p=1.5E−02 n=3 fg=0.02 bg=0.00
trans−Golgi network transport vesicle GO:0030140 p=1.5E−02 n=3 fg=0.02 bg=0.00
cytoplasmic vesicle membrane GO:0030659 p=1.7E−02 n=19 fg=0.11 bg=0.07
phagocytic vesicle GO:0045335 p=2.0E−02 n=5 fg=0.03 bg=0.01
vesicle membrane GO:0012506 p=2.1E−02 n=19 fg=0.11 bg=0.07
endoplasmic reticulum−Golgi intermediate... GO:0033116 p=2.1E−02 n=3 fg=0.02 bg=0.00
basal dendrite GO:0097441 p=2.1E−02 n=2 fg=0.01 bg=0.00
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intracellular vesicle GO:0097708 p=2.3E−02 n=36 fg=0.21 bg=0.15
cytoplasmic vesicle GO:0031410 p=2.3E−02 n=36 fg=0.21 bg=0.15
Golgi stack GO:0005795 p=2.5E−02 n=7 fg=0.04 bg=0.02
transport vesicle GO:0030133 p=2.8E−02 n=11 fg=0.07 bg=0.03
endosome GO:0005768 p=2.9E−02 n=19 fg=0.11 bg=0.07
vesicle GO:0031982 p=3.2E−02 n=37 fg=0.22 bg=0.16
phagophore assembly site GO:0000407 p=3.4E−02 n=2 fg=0.01 bg=0.00
XY body GO:0001741 p=3.4E−02 n=2 fg=0.01 bg=0.00
microvillus GO:0005902 p=3.8E−02 n=4 fg=0.02 bg=0.01
Golgi−associated vesicle GO:0005798 p=4.0E−02 n=6 fg=0.04 bg=0.02
trans−Golgi network membrane GO:0032588 p=4.6E−02 n=5 fg=0.03 bg=0.01
endoplasmic reticulum−Golgi intermediate... GO:0005793 p=5.2E−02 n=4 fg=0.02 bg=0.01
Golgi cisterna GO:0031985 p=5.2E−02 n=5 fg=0.03 bg=0.01
fibrillar center GO:0001650 p=5.2E−02 n=5 fg=0.03 bg=0.01
endocytic vesicle membrane GO:0030666 p=5.9E−02 n=4 fg=0.02 bg=0.01
0 1 2 3 4 5
−log(p)
n=169/530 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction