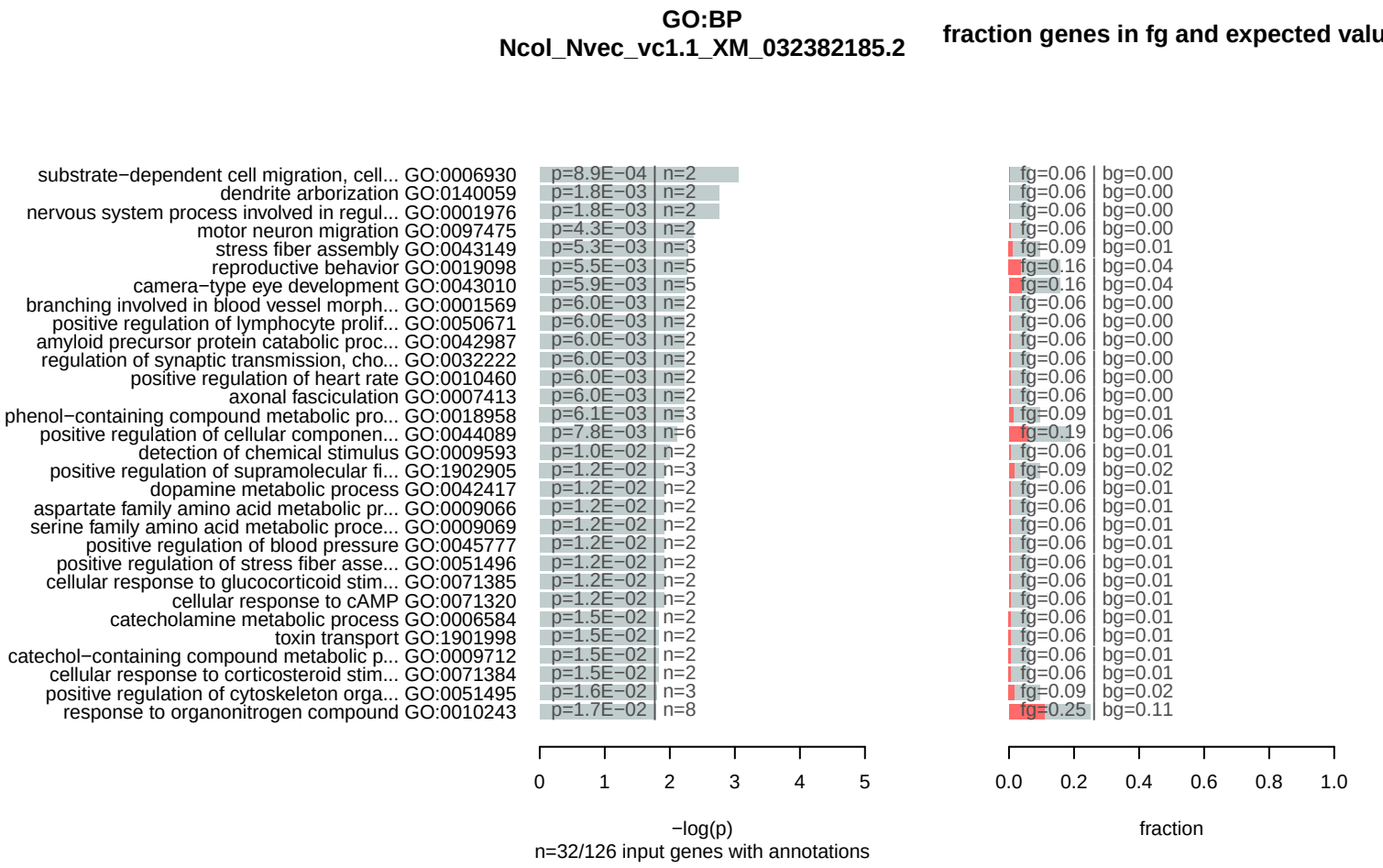
GO:BP
Ncol_Nvec_vc1.1_XM_032382185.2
fraction genes in fg and expected valu
substrate−dependent cell migration, cell... GO:0006930 p=8.9E−04 n=2 fg=0.06 bg=0.00
dendrite arborization GO:0140059 p=1.8E−03 n=2 fg=0.06 bg=0.00
nervous system process involved in regul... GO:0001976 p=1.8E−03 n=2 fg=0.06 bg=0.00
motor neuron migration GO:0097475 p=4.3E−03 n=2 fg=0.06 bg=0.00
stress fiber assembly GO:0043149 p=5.3E−03 n=3 fg=0.09 bg=0.01
reproductive behavior GO:0019098 p=5.5E−03 n=5 fg=0.16 bg=0.04
camera−type eye development GO:0043010 p=5.9E−03 n=5 fg=0.16 bg=0.04
branching involved in blood vessel morph... GO:0001569 p=6.0E−03 n=2 fg=0.06 bg=0.00
positive regulation of lymphocyte prolif... GO:0050671 p=6.0E−03 n=2 fg=0.06 bg=0.00
amyloid precursor protein catabolic proc... GO:0042987 p=6.0E−03 n=2 fg=0.06 bg=0.00
regulation of synaptic transmission, cho... GO:0032222 p=6.0E−03 n=2 fg=0.06 bg=0.00
positive regulation of heart rate GO:0010460 p=6.0E−03 n=2 fg=0.06 bg=0.00
axonal fasciculation GO:0007413 p=6.0E−03 n=2 fg=0.06 bg=0.00
phenol−containing compound metabolic pro... GO:0018958 p=6.1E−03 n=3 fg=0.09 bg=0.01
positive regulation of cellular componen... GO:0044089 p=7.8E−03 n=6 fg=0.19 bg=0.06
detection of chemical stimulus GO:0009593 p=1.0E−02 n=2 fg=0.06 bg=0.01
positive regulation of supramolecular fi... GO:1902905 p=1.2E−02 n=3 fg=0.09 bg=0.02
dopamine metabolic process GO:0042417 p=1.2E−02 n=2 fg=0.06 bg=0.01
aspartate family amino acid metabolic pr... GO:0009066 p=1.2E−02 n=2 fg=0.06 bg=0.01
serine family amino acid metabolic proce... GO:0009069 p=1.2E−02 n=2 fg=0.06 bg=0.01
positive regulation of blood pressure GO:0045777 p=1.2E−02 n=2 fg=0.06 bg=0.01
positive regulation of stress fiber asse... GO:0051496 p=1.2E−02 n=2 fg=0.06 bg=0.01
cellular response to glucocorticoid stim... GO:0071385 p=1.2E−02 n=2 fg=0.06 bg=0.01
cellular response to cAMP GO:0071320 p=1.2E−02 n=2 fg=0.06 bg=0.01
catecholamine metabolic process GO:0006584 p=1.5E−02 n=2 fg=0.06 bg=0.01
toxin transport GO:1901998 p=1.5E−02 n=2 fg=0.06 bg=0.01
catechol−containing compound metabolic p... GO:0009712 p=1.5E−02 n=2 fg=0.06 bg=0.01
cellular response to corticosteroid stim... GO:0071384 p=1.5E−02 n=2 fg=0.06 bg=0.01
positive regulation of cytoskeleton orga... GO:0051495 p=1.6E−02 n=3 fg=0.09 bg=0.02
response to organonitrogen compound GO:0010243 p=1.7E−02 n=8 fg=0.25 bg=0.11
0 1 2 3 4 5
−log(p)
n=32/126 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032382185.2
fraction genes in fg and expected valu
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=5.9E−03 n=2 fg=0.07 bg=0.00
E−box binding GO:0070888 p=1.0E−02 n=2 fg=0.07 bg=0.01
copper ion binding GO:0005507 p=1.0E−02 n=2 fg=0.07 bg=0.01
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=1.8E−02 n=1 fg=0.04 bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016812 p=1.8E−02 n=1 fg=0.04 bg=0.00
dynein light intermediate chain binding GO:0051959 p=1.8E−02 n=1 fg=0.04 bg=0.00
mannosyl−oligosaccharide mannosidase act... GO:0015924 p=1.8E−02 n=1 fg=0.04 bg=0.00
vascular endothelial growth factor bindi... GO:0038085 p=1.8E−02 n=1 fg=0.04 bg=0.00
alpha−1,6−mannosylglycoprotein 2−beta−N−... GO:0008455 p=1.8E−02 n=1 fg=0.04 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=1.8E−02 n=1 fg=0.04 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=1.8E−02 n=1 fg=0.04 bg=0.00
5−oxoprolinase (ATP−hydrolyzing) activit... GO:0017168 p=1.8E−02 n=1 fg=0.04 bg=0.00
semaphorin receptor activity GO:0017154 p=1.8E−02 n=1 fg=0.04 bg=0.00
mannosyl−oligosaccharide 1,2−alpha−manno... GO:0004571 p=1.8E−02 n=1 fg=0.04 bg=0.00
ammonium ion binding GO:0070405 p=1.8E−02 n=2 fg=0.07 bg=0.01
protein−disulfide reductase activity GO:0015035 p=3.3E−02 n=3 fg=0.11 bg=0.01
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=3.5E−02 n=1 fg=0.04 bg=0.00
neurotransmitter receptor activity invol... GO:0099529 p=3.5E−02 n=1 fg=0.04 bg=0.00
transmitter−gated ion channel activity i... GO:1904315 p=3.5E−02 n=1 fg=0.04 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=3.5E−02 n=1 fg=0.04 bg=0.00
acetylcholine receptor activity GO:0015464 p=3.5E−02 n=1 fg=0.04 bg=0.00
toxin transmembrane transporter activity GO:0019534 p=3.5E−02 n=1 fg=0.04 bg=0.00
substance P receptor activity GO:0016496 p=3.5E−02 n=1 fg=0.04 bg=0.00
substance K receptor activity GO:0016497 p=3.5E−02 n=1 fg=0.04 bg=0.00
metallochaperone activity GO:0016530 p=3.5E−02 n=1 fg=0.04 bg=0.00
copper chaperone activity GO:0016531 p=3.5E−02 n=1 fg=0.04 bg=0.00
superoxide dismutase copper chaperone ac... GO:0016532 p=3.5E−02 n=1 fg=0.04 bg=0.00
acetylcholine−gated cation−selective cha... GO:0022848 p=3.5E−02 n=1 fg=0.04 bg=0.00
acetylcholine binding GO:0042166 p=3.5E−02 n=1 fg=0.04 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=3.5E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=28/126 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032382185.2
fraction genes in fg and expected valu
receptor complex GO:0043235 p=1.8E−02 n=3 fg=0.09 bg=0.02
semaphorin receptor complex GO:0002116 p=1.8E−02 n=1 fg=0.03 bg=0.00
protein kinase CK2 complex GO:0005956 p=1.8E−02 n=1 fg=0.03 bg=0.00
neuron projection membrane GO:0032589 p=2.9E−02 n=2 fg=0.06 bg=0.01
cell surface GO:0009986 p=3.1E−02 n=4 fg=0.12 bg=0.04
anchored component of plasma membrane GO:0046658 p=3.6E−02 n=1 fg=0.03 bg=0.00
Gtr1−Gtr2 GTPase complex GO:1990131 p=3.6E−02 n=1 fg=0.03 bg=0.00
neurofilament GO:0005883 p=3.6E−02 n=1 fg=0.03 bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=3.6E−02 n=1 fg=0.03 bg=0.00
acetylcholine−gated channel complex GO:0005892 p=3.6E−02 n=1 fg=0.03 bg=0.00
cell body fiber GO:0070852 p=3.6E−02 n=1 fg=0.03 bg=0.00
sorting endosome GO:0097443 p=3.6E−02 n=1 fg=0.03 bg=0.00
external side of plasma membrane GO:0009897 p=3.7E−02 n=2 fg=0.06 bg=0.01
intrinsic component of plasma membrane GO:0031226 p=4.5E−02 n=6 fg=0.18 bg=0.08
exocytic vesicle membrane GO:0099501 p=5.0E−02 n=2 fg=0.06 bg=0.01
intermediate filament GO:0005882 p=5.4E−02 n=1 fg=0.03 bg=0.00
nuclear aryl hydrocarbon receptor comple... GO:0034753 p=5.4E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum exit site GO:0070971 p=5.4E−02 n=1 fg=0.03 bg=0.00
respiratory chain complex IV GO:0045277 p=5.4E−02 n=1 fg=0.03 bg=0.00
growth cone membrane GO:0032584 p=5.4E−02 n=1 fg=0.03 bg=0.00
mitochondrial respiratory chain complex ... GO:0005751 p=5.4E−02 n=1 fg=0.03 bg=0.00
perinuclear endoplasmic reticulum GO:0097038 p=5.4E−02 n=1 fg=0.03 bg=0.00
spot adherens junction GO:0005914 p=5.4E−02 n=1 fg=0.03 bg=0.00
mitochondrion GO:0005739 p=6.7E−02 n=8 fg=0.24 bg=0.14
aryl hydrocarbon receptor complex GO:0034751 p=7.1E−02 n=1 fg=0.03 bg=0.00
sperm head GO:0061827 p=7.1E−02 n=1 fg=0.03 bg=0.00
endoplasmic reticulum quality control co... GO:0044322 p=7.1E−02 n=1 fg=0.03 bg=0.00
zonula adherens GO:0005915 p=7.1E−02 n=1 fg=0.03 bg=0.00
leading edge membrane GO:0031256 p=7.5E−02 n=2 fg=0.06 bg=0.01
exocytic vesicle GO:0070382 p=7.6E−02 n=3 fg=0.09 bg=0.03
0 1 2 3 4 5
−log(p)
n=33/126 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction