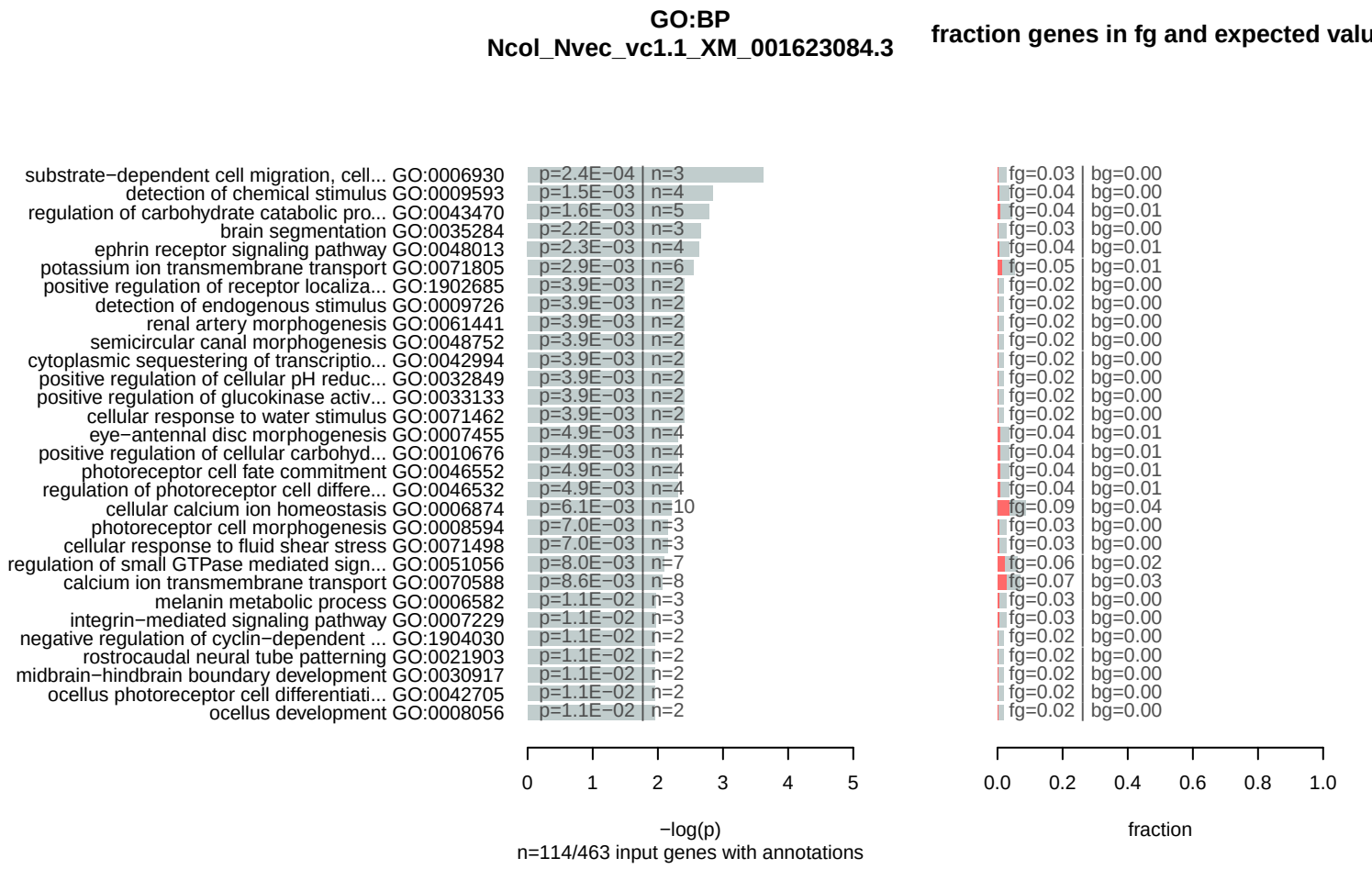
GO:BP
Ncol_Nvec_vc1.1_XM_001623084.3
fraction genes in fg and expected valu
substrate−dependent cell migration, cell... GO:0006930 p=2.4E−04 n=3 fg=0.03 bg=0.00
detection of chemical stimulus GO:0009593 p=1.5E−03 n=4 fg=0.04 bg=0.00
regulation of carbohydrate catabolic pro... GO:0043470 p=1.6E−03 n=5 fg=0.04 bg=0.01
brain segmentation GO:0035284 p=2.2E−03 n=3 fg=0.03 bg=0.00
ephrin receptor signaling pathway GO:0048013 p=2.3E−03 n=4 fg=0.04 bg=0.01
potassium ion transmembrane transport GO:0071805 p=2.9E−03 n=6 fg=0.05 bg=0.01
positive regulation of receptor localiza... GO:1902685 p=3.9E−03 n=2 fg=0.02 bg=0.00
detection of endogenous stimulus GO:0009726 p=3.9E−03 n=2 fg=0.02 bg=0.00
renal artery morphogenesis GO:0061441 p=3.9E−03 n=2 fg=0.02 bg=0.00
semicircular canal morphogenesis GO:0048752 p=3.9E−03 n=2 fg=0.02 bg=0.00
cytoplasmic sequestering of transcriptio... GO:0042994 p=3.9E−03 n=2 fg=0.02 bg=0.00
positive regulation of cellular pH reduc... GO:0032849 p=3.9E−03 n=2 fg=0.02 bg=0.00
positive regulation of glucokinase activ... GO:0033133 p=3.9E−03 n=2 fg=0.02 bg=0.00
cellular response to water stimulus GO:0071462 p=3.9E−03 n=2 fg=0.02 bg=0.00
eye−antennal disc morphogenesis GO:0007455 p=4.9E−03 n=4 fg=0.04 bg=0.01
positive regulation of cellular carbohyd... GO:0010676 p=4.9E−03 n=4 fg=0.04 bg=0.01
photoreceptor cell fate commitment GO:0046552 p=4.9E−03 n=4 fg=0.04 bg=0.01
regulation of photoreceptor cell differe... GO:0046532 p=4.9E−03 n=4 fg=0.04 bg=0.01
cellular calcium ion homeostasis GO:0006874 p=6.1E−03 n=10 fg=0.09 bg=0.04
photoreceptor cell morphogenesis GO:0008594 p=7.0E−03 n=3 fg=0.03 bg=0.00
cellular response to fluid shear stress GO:0071498 p=7.0E−03 n=3 fg=0.03 bg=0.00
regulation of small GTPase mediated sign... GO:0051056 p=8.0E−03 n=7 fg=0.06 bg=0.02
calcium ion transmembrane transport GO:0070588 p=8.6E−03 n=8 fg=0.07 bg=0.03
melanin metabolic process GO:0006582 p=1.1E−02 n=3 fg=0.03 bg=0.00
integrin−mediated signaling pathway GO:0007229 p=1.1E−02 n=3 fg=0.03 bg=0.00
negative regulation of cyclin−dependent ... GO:1904030 p=1.1E−02 n=2 fg=0.02 bg=0.00
rostrocaudal neural tube patterning GO:0021903 p=1.1E−02 n=2 fg=0.02 bg=0.00
midbrain−hindbrain boundary development GO:0030917 p=1.1E−02 n=2 fg=0.02 bg=0.00
ocellus photoreceptor cell differentiati... GO:0042705 p=1.1E−02 n=2 fg=0.02 bg=0.00
ocellus development GO:0008056 p=1.1E−02 n=2 fg=0.02 bg=0.00
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n=114/463 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
ephrin receptor binding GO:0046875 p=2.2E−03 n=3 fg=0.03 bg=0.00
voltage−gated potassium channel activity GO:0005249 p=2.3E−03 n=4 fg=0.04 bg=0.01
ion gated channel activity GO:0022839 p=3.6E−03 n=8 fg=0.08 bg=0.03
calcium−induced calcium release activity GO:0048763 p=3.9E−03 n=2 fg=0.02 bg=0.00
fructose−6−phosphate binding GO:0070095 p=3.9E−03 n=2 fg=0.02 bg=0.00
calcium, potassium:sodium antiporter act... GO:0008273 p=3.9E−03 n=2 fg=0.02 bg=0.00
cyclin−dependent protein serine/threonin... GO:0004861 p=3.9E−03 n=2 fg=0.02 bg=0.00
carbohydrate binding GO:0030246 p=4.9E−03 n=4 fg=0.04 bg=0.01
receptor tyrosine kinase binding GO:0030971 p=4.9E−03 n=4 fg=0.04 bg=0.01
signaling receptor complex adaptor activ... GO:0030159 p=7.0E−03 n=3 fg=0.03 bg=0.00
UDP−glucosyltransferase activity GO:0035251 p=1.1E−02 n=2 fg=0.02 bg=0.00
potassium ion binding GO:0030955 p=1.1E−02 n=2 fg=0.02 bg=0.00
sodium ion binding GO:0031402 p=1.1E−02 n=2 fg=0.02 bg=0.00
ion channel regulator activity GO:0099106 p=1.4E−02 n=5 fg=0.05 bg=0.02
ion channel inhibitor activity GO:0008200 p=1.5E−02 n=3 fg=0.03 bg=0.01
channel regulator activity GO:0016247 p=2.0E−02 n=5 fg=0.05 bg=0.02
channel inhibitor activity GO:0016248 p=2.1E−02 n=3 fg=0.03 bg=0.01
palmitoyl hydrolase activity GO:0098599 p=2.2E−02 n=2 fg=0.02 bg=0.00
palmitoyl−(protein) hydrolase activity GO:0008474 p=2.2E−02 n=2 fg=0.02 bg=0.00
voltage−gated sodium channel activity GO:0005248 p=2.2E−02 n=2 fg=0.02 bg=0.00
glucosyltransferase activity GO:0046527 p=2.2E−02 n=2 fg=0.02 bg=0.00
protein heterodimerization activity GO:0046982 p=2.5E−02 n=11 fg=0.11 bg=0.06
cysteine−type endopeptidase activity GO:0004197 p=2.7E−02 n=3 fg=0.03 bg=0.01
DNA−binding transcription factor activit... GO:0003700 p=2.8E−02 n=14 fg=0.14 bg=0.08
protein kinase inhibitor activity GO:0004860 p=3.3E−02 n=5 fg=0.05 bg=0.01
kinase inhibitor activity GO:0019210 p=3.3E−02 n=5 fg=0.05 bg=0.01
sodium channel activity GO:0005272 p=3.5E−02 n=2 fg=0.02 bg=0.00
monosaccharide binding GO:0048029 p=3.5E−02 n=2 fg=0.02 bg=0.00
alkali metal ion binding GO:0031420 p=3.5E−02 n=2 fg=0.02 bg=0.00
growth factor receptor binding GO:0070851 p=3.5E−02 n=3 fg=0.03 bg=0.01
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−log(p)
n=100/463 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001623084.3
fraction genes in fg and expected valu
secretory granule lumen GO:0034774 p=5.9E−03 n=7 fg=0.06 bg=0.02
intrinsic component of plasma membrane GO:0031226 p=8.0E−03 n=17 fg=0.15 bg=0.08
ficolin−1−rich granule lumen GO:1904813 p=8.2E−03 n=5 fg=0.04 bg=0.01
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azurophil granule GO:0042582 p=1.5E−02 n=5 fg=0.04 bg=0.01
primary lysosome GO:0005766 p=1.5E−02 n=5 fg=0.04 bg=0.01
intrinsic component of the cytoplasmic s... GO:0031235 p=2.2E−02 n=2 fg=0.02 bg=0.00
extracellular region GO:0005576 p=2.3E−02 n=14 fg=0.12 bg=0.07
ciliary base GO:0097546 p=2.8E−02 n=3 fg=0.03 bg=0.01
protein phosphatase type 1 complex GO:0000164 p=3.5E−02 n=2 fg=0.02 bg=0.00
sensory dendrite GO:0071683 p=3.5E−02 n=2 fg=0.02 bg=0.00
cation channel complex GO:0034703 p=3.9E−02 n=4 fg=0.04 bg=0.01
transport vesicle membrane GO:0030658 p=4.1E−02 n=5 fg=0.04 bg=0.02
integral component of plasma membrane GO:0005887 p=4.2E−02 n=14 fg=0.12 bg=0.08
supramolecular fiber GO:0099512 p=4.9E−02 n=10 fg=0.09 bg=0.05
supramolecular polymer GO:0099081 p=4.9E−02 n=10 fg=0.09 bg=0.05
ion channel complex GO:0034702 p=5.2E−02 n=4 fg=0.04 bg=0.01
azurophil granule lumen GO:0035578 p=5.3E−02 n=3 fg=0.03 bg=0.01
plasma membrane GO:0005886 p=5.5E−02 n=44 fg=0.39 bg=0.27
cell periphery GO:0071944 p=5.8E−02 n=46 fg=0.40 bg=0.29
katanin complex GO:0008352 p=6.3E−02 n=1 fg=0.01 bg=0.00
death−inducing signaling complex GO:0031264 p=6.3E−02 n=1 fg=0.01 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=6.3E−02 n=1 fg=0.01 bg=0.00
Sin3 complex GO:0016580 p=6.3E−02 n=1 fg=0.01 bg=0.00
FHF complex GO:0070695 p=6.3E−02 n=1 fg=0.01 bg=0.00
interleukin−5 receptor complex GO:0005895 p=6.3E−02 n=1 fg=0.01 bg=0.00
semaphorin receptor complex GO:0002116 p=6.3E−02 n=1 fg=0.01 bg=0.00
polycystin complex GO:0002133 p=6.3E−02 n=1 fg=0.01 bg=0.00
calcium channel complex GO:0034704 p=6.7E−02 n=2 fg=0.02 bg=0.00
ER to Golgi transport vesicle membrane GO:0012507 p=6.7E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=114/463 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction