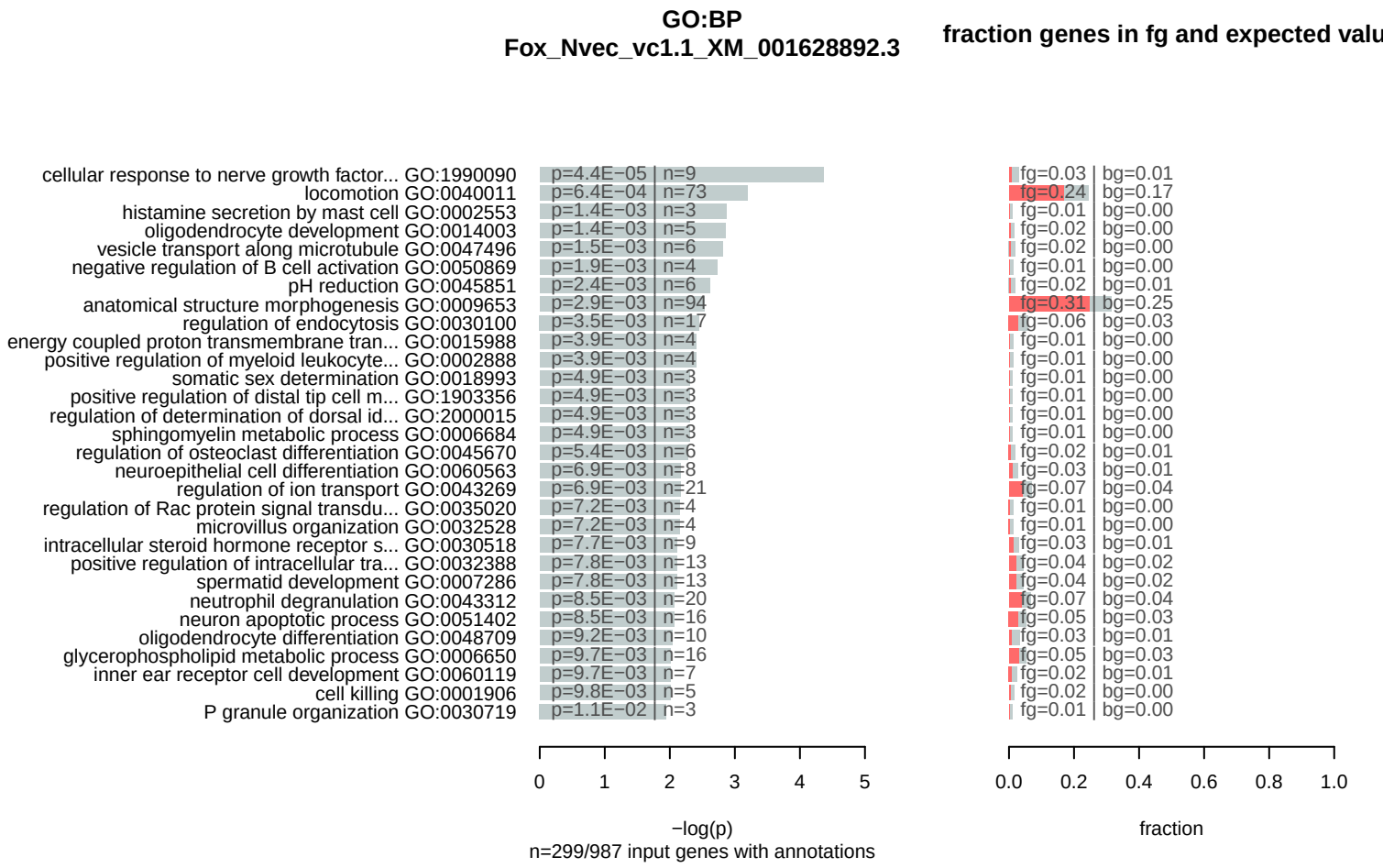
GO:BP
Fox_Nvec_vc1.1_XM_001628892.3
fraction genes in fg and expected valu
cellular response to nerve growth factor... GO:1990090 p=4.4E−05 n=9 fg=0.03 bg=0.01
locomotion GO:0040011 p=6.4E−04 n=73 fg=0.24 bg=0.17
histamine secretion by mast cell GO:0002553 p=1.4E−03 n=3 fg=0.01 bg=0.00
oligodendrocyte development GO:0014003 p=1.4E−03 n=5 fg=0.02 bg=0.00
vesicle transport along microtubule GO:0047496 p=1.5E−03 n=6 fg=0.02 bg=0.00
negative regulation of B cell activation GO:0050869 p=1.9E−03 n=4 fg=0.01 bg=0.00
pH reduction GO:0045851 p=2.4E−03 n=6 fg=0.02 bg=0.01
anatomical structure morphogenesis GO:0009653 p=2.9E−03 n=94 fg=0.31 bg=0.25
regulation of endocytosis GO:0030100 p=3.5E−03 n=17 fg=0.06 bg=0.03
energy coupled proton transmembrane tran... GO:0015988 p=3.9E−03 n=4 fg=0.01 bg=0.00
positive regulation of myeloid leukocyte... GO:0002888 p=3.9E−03 n=4 fg=0.01 bg=0.00
somatic sex determination GO:0018993 p=4.9E−03 n=3 fg=0.01 bg=0.00
positive regulation of distal tip cell m... GO:1903356 p=4.9E−03 n=3 fg=0.01 bg=0.00
regulation of determination of dorsal id... GO:2000015 p=4.9E−03 n=3 fg=0.01 bg=0.00
sphingomyelin metabolic process GO:0006684 p=4.9E−03 n=3 fg=0.01 bg=0.00
regulation of osteoclast differentiation GO:0045670 p=5.4E−03 n=6 fg=0.02 bg=0.01
neuroepithelial cell differentiation GO:0060563 p=6.9E−03 n=8 fg=0.03 bg=0.01
regulation of ion transport GO:0043269 p=6.9E−03 n=21 fg=0.07 bg=0.04
regulation of Rac protein signal transdu... GO:0035020 p=7.2E−03 n=4 fg=0.01 bg=0.00
microvillus organization GO:0032528 p=7.2E−03 n=4 fg=0.01 bg=0.00
intracellular steroid hormone receptor s... GO:0030518 p=7.7E−03 n=9 fg=0.03 bg=0.01
positive regulation of intracellular tra... GO:0032388 p=7.8E−03 n=13 fg=0.04 bg=0.02
spermatid development GO:0007286 p=7.8E−03 n=13 fg=0.04 bg=0.02
neutrophil degranulation GO:0043312 p=8.5E−03 n=20 fg=0.07 bg=0.04
neuron apoptotic process GO:0051402 p=8.5E−03 n=16 fg=0.05 bg=0.03
oligodendrocyte differentiation GO:0048709 p=9.2E−03 n=10 fg=0.03 bg=0.01
glycerophospholipid metabolic process GO:0006650 p=9.7E−03 n=16 fg=0.05 bg=0.03
inner ear receptor cell development GO:0060119 p=9.7E−03 n=7 fg=0.02 bg=0.01
cell killing GO:0001906 p=9.8E−03 n=5 fg=0.02 bg=0.00
P granule organization GO:0030719 p=1.1E−02 n=3 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=299/987 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001628892.3
fraction genes in fg and expected valu
spectrin binding GO:0030507 p=4.4E−03 n=4 fg=0.01 bg=0.00
phosphatidylinositol−4−phosphate binding GO:0070273 p=7.5E−03 n=5 fg=0.02 bg=0.01
guanyl−nucleotide exchange factor activi... GO:0005085 p=1.2E−02 n=10 fg=0.04 bg=0.02
gamma−butyrobetaine dioxygenase activity GO:0008336 p=1.3E−02 n=2 fg=0.01 bg=0.00
ligand−gated sodium channel activity GO:0015280 p=1.3E−02 n=2 fg=0.01 bg=0.00
oxysterol binding GO:0008142 p=1.3E−02 n=2 fg=0.01 bg=0.00
phospholipid transporter activity GO:0005548 p=1.6E−02 n=5 fg=0.02 bg=0.01
phosphoric diester hydrolase activity GO:0008081 p=2.0E−02 n=6 fg=0.02 bg=0.01
proteoglycan binding GO:0043394 p=2.2E−02 n=3 fg=0.01 bg=0.00
dynein intermediate chain binding GO:0045505 p=2.2E−02 n=3 fg=0.01 bg=0.00
ATPase−coupled ion transmembrane transpo... GO:0042625 p=2.8E−02 n=5 fg=0.02 bg=0.01
acylglycerol lipase activity GO:0047372 p=3.6E−02 n=2 fg=0.01 bg=0.00
neurexin family protein binding GO:0042043 p=3.6E−02 n=2 fg=0.01 bg=0.00
galactosidase activity GO:0015925 p=3.6E−02 n=2 fg=0.01 bg=0.00
insulin−like growth factor receptor bind... GO:0005159 p=3.6E−02 n=2 fg=0.01 bg=0.00
Arp2/3 complex binding GO:0071933 p=3.6E−02 n=2 fg=0.01 bg=0.00
phosphatidic acid binding GO:0070300 p=3.6E−02 n=3 fg=0.01 bg=0.00
transferase activity, transferring nitro... GO:0016769 p=3.6E−02 n=3 fg=0.01 bg=0.00
lipase activity GO:0016298 p=4.7E−02 n=6 fg=0.02 bg=0.01
microtubule motor activity GO:0003777 p=5.1E−02 n=4 fg=0.01 bg=0.01
calcium−dependent protein binding GO:0048306 p=5.1E−02 n=4 fg=0.01 bg=0.01
cysteine−type endopeptidase activity GO:0004197 p=6.6E−02 n=4 fg=0.01 bg=0.01
plus−end−directed microtubule motor acti... GO:0008574 p=6.7E−02 n=2 fg=0.01 bg=0.00
dynein light intermediate chain binding GO:0051959 p=6.7E−02 n=2 fg=0.01 bg=0.00
phosphatidylethanolamine binding GO:0008429 p=6.7E−02 n=2 fg=0.01 bg=0.00
WW domain binding GO:0050699 p=6.7E−02 n=2 fg=0.01 bg=0.00
5'−3' exonuclease activity GO:0008409 p=6.7E−02 n=2 fg=0.01 bg=0.00
syndecan binding GO:0045545 p=6.7E−02 n=2 fg=0.01 bg=0.00
nitric−oxide synthase regulator activity GO:0030235 p=6.7E−02 n=2 fg=0.01 bg=0.00
phospholipase C activity GO:0004629 p=6.7E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=270/987 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001628892.3
fraction genes in fg and expected valu
axon cytoplasm GO:1904115 p=2.0E−03 n=4 fg=0.01 bg=0.00
caveola GO:0005901 p=2.6E−03 n=8 fg=0.03 bg=0.01
platelet alpha granule GO:0031091 p=2.8E−03 n=5 fg=0.02 bg=0.00
apical dendrite GO:0097440 p=4.3E−03 n=4 fg=0.01 bg=0.00
azurophil granule GO:0042582 p=4.5E−03 n=9 fg=0.03 bg=0.01
phagocytic vesicle GO:0045335 p=6.2E−03 n=8 fg=0.03 bg=0.01
microvillus GO:0005902 p=6.4E−03 n=7 fg=0.02 bg=0.01
proton−transporting V−type ATPase comple... GO:0033176 p=7.8E−03 n=4 fg=0.01 bg=0.00
cytoplasmic dynein complex GO:0005868 p=7.8E−03 n=4 fg=0.01 bg=0.00
tertiary granule membrane GO:0070821 p=7.8E−03 n=4 fg=0.01 bg=0.00
extracellular exosome GO:0070062 p=1.1E−02 n=7 fg=0.02 bg=0.01
eukaryotic translation initiation factor... GO:0005851 p=1.2E−02 n=3 fg=0.01 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=1.3E−02 n=2 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.3E−02 n=2 fg=0.01 bg=0.00
azurophil granule membrane GO:0035577 p=1.3E−02 n=4 fg=0.01 bg=0.00
extracellular membrane−bounded organelle GO:0065010 p=1.4E−02 n=7 fg=0.02 bg=0.01
extracellular vesicle GO:1903561 p=1.4E−02 n=7 fg=0.02 bg=0.01
extracellular organelle GO:0043230 p=1.4E−02 n=7 fg=0.02 bg=0.01
cell periphery GO:0071944 p=1.5E−02 n=98 fg=0.32 bg=0.25
cytoplasmic side of plasma membrane GO:0009898 p=1.5E−02 n=12 fg=0.04 bg=0.02
extracellular region GO:0005576 p=1.6E−02 n=32 fg=0.10 bg=0.07
secretory granule membrane GO:0030667 p=1.8E−02 n=14 fg=0.05 bg=0.02
extrinsic component of plasma membrane GO:0019897 p=1.9E−02 n=8 fg=0.03 bg=0.01
cytoplasmic side of membrane GO:0098562 p=1.9E−02 n=13 fg=0.04 bg=0.02
extrinsic component of membrane GO:0019898 p=1.9E−02 n=13 fg=0.04 bg=0.02
plasma membrane proton−transporting V−ty... GO:0033181 p=2.2E−02 n=3 fg=0.01 bg=0.00
apical part of cell GO:0045177 p=3.2E−02 n=22 fg=0.07 bg=0.05
EARP complex GO:1990745 p=3.5E−02 n=2 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000221 p=3.5E−02 n=2 fg=0.01 bg=0.00
GARP complex GO:0000938 p=3.5E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=306/987 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction