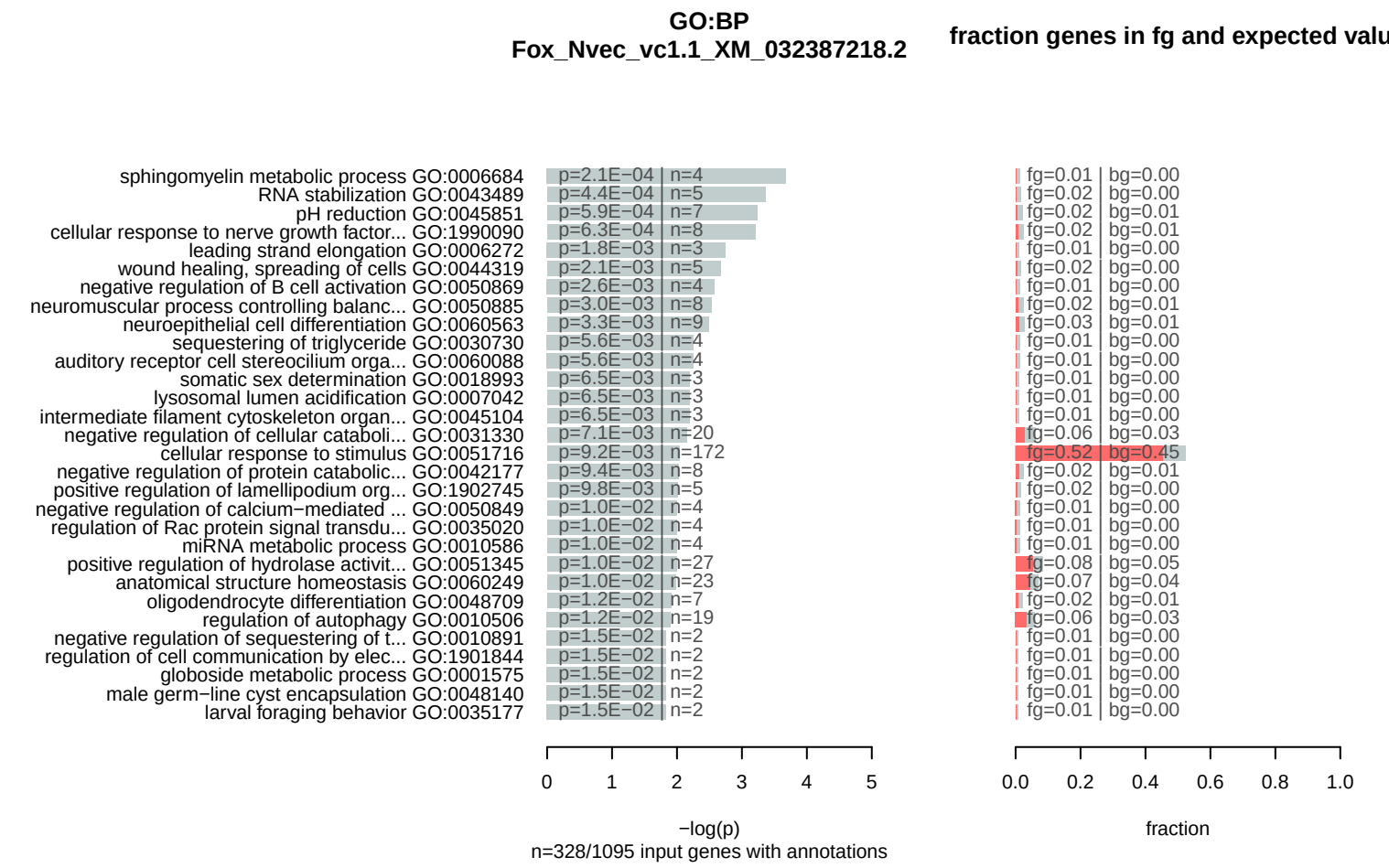
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fraction genes in fg and expected valu
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RNA stabilization GO:0043489 p=4.4E−04 n=5 fg=0.02 bg=0.00
pH reduction GO:0045851 p=5.9E−04 n=7 fg=0.02 bg=0.01
cellular response to nerve growth factor... GO:1990090 p=6.3E−04 n=8 fg=0.02 bg=0.01
leading strand elongation GO:0006272 p=1.8E−03 n=3 fg=0.01 bg=0.00
wound healing, spreading of cells GO:0044319 p=2.1E−03 n=5 fg=0.02 bg=0.00
negative regulation of B cell activation GO:0050869 p=2.6E−03 n=4 fg=0.01 bg=0.00
neuromuscular process controlling balanc... GO:0050885 p=3.0E−03 n=8 fg=0.02 bg=0.01
neuroepithelial cell differentiation GO:0060563 p=3.3E−03 n=9 fg=0.03 bg=0.01
sequestering of triglyceride GO:0030730 p=5.6E−03 n=4 fg=0.01 bg=0.00
auditory receptor cell stereocilium orga... GO:0060088 p=5.6E−03 n=4 fg=0.01 bg=0.00
somatic sex determination GO:0018993 p=6.5E−03 n=3 fg=0.01 bg=0.00
lysosomal lumen acidification GO:0007042 p=6.5E−03 n=3 fg=0.01 bg=0.00
intermediate filament cytoskeleton organ... GO:0045104 p=6.5E−03 n=3 fg=0.01 bg=0.00
negative regulation of cellular cataboli... GO:0031330 p=7.1E−03 n=20 fg=0.06 bg=0.03
cellular response to stimulus GO:0051716 p=9.2E−03 n=172 fg=0.52 bg=0.45
negative regulation of protein catabolic... GO:0042177 p=9.4E−03 n=8 fg=0.02 bg=0.01
positive regulation of lamellipodium org... GO:1902745 p=9.8E−03 n=5 fg=0.02 bg=0.00
negative regulation of calcium−mediated ... GO:0050849 p=1.0E−02 n=4 fg=0.01 bg=0.00
regulation of Rac protein signal transdu... GO:0035020 p=1.0E−02 n=4 fg=0.01 bg=0.00
miRNA metabolic process GO:0010586 p=1.0E−02 n=4 fg=0.01 bg=0.00
positive regulation of hydrolase activit... GO:0051345 p=1.0E−02 n=27 fg=0.08 bg=0.05
anatomical structure homeostasis GO:0060249 p=1.0E−02 n=23 fg=0.07 bg=0.04
oligodendrocyte differentiation GO:0048709 p=1.2E−02 n=7 fg=0.02 bg=0.01
regulation of autophagy GO:0010506 p=1.2E−02 n=19 fg=0.06 bg=0.03
negative regulation of sequestering of t... GO:0010891 p=1.5E−02 n=2 fg=0.01 bg=0.00
regulation of cell communication by elec... GO:1901844 p=1.5E−02 n=2 fg=0.01 bg=0.00
globoside metabolic process GO:0001575 p=1.5E−02 n=2 fg=0.01 bg=0.00
male germ−line cyst encapsulation GO:0048140 p=1.5E−02 n=2 fg=0.01 bg=0.00
larval foraging behavior GO:0035177 p=1.5E−02 n=2 fg=0.01 bg=0.00
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fraction
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Fox_Nvec_vc1.1_XM_032387218.2
fraction genes in fg and expected valu
miRNA binding GO:0035198 p=2.1E−03 n=3 fg=0.01 bg=0.00
GTPase regulator activity GO:0030695 p=8.8E−03 n=21 fg=0.07 bg=0.04
phosphoric diester hydrolase activity GO:0008081 p=9.7E−03 n=7 fg=0.02 bg=0.01
phosphatidylinositol−4−phosphate binding GO:0070273 p=1.3E−02 n=5 fg=0.02 bg=0.01
phospholipid binding GO:0005543 p=1.4E−02 n=19 fg=0.06 bg=0.04
ATP−dependent protein binding GO:0043008 p=1.7E−02 n=2 fg=0.01 bg=0.00
nucleotide diphosphatase activity GO:0004551 p=1.7E−02 n=2 fg=0.01 bg=0.00
gamma−butyrobetaine dioxygenase activity GO:0008336 p=1.7E−02 n=2 fg=0.01 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0016652 p=1.7E−02 n=2 fg=0.01 bg=0.00
bis(5'−nucleosyl)−tetraphosphatase activ... GO:0008796 p=1.7E−02 n=2 fg=0.01 bg=0.00
NAD(P)+ transhydrogenase activity GO:0008746 p=1.7E−02 n=2 fg=0.01 bg=0.00
heparan−alpha−glucosaminide N−acetyltran... GO:0015019 p=1.7E−02 n=2 fg=0.01 bg=0.00
calcium channel inhibitor activity GO:0019855 p=1.7E−02 n=2 fg=0.01 bg=0.00
bis(5'−nucleosyl)−tetraphosphatase (asym... GO:0004081 p=1.7E−02 n=2 fg=0.01 bg=0.00
sphingomyelin phosphodiesterase activity GO:0004767 p=1.7E−02 n=2 fg=0.01 bg=0.00
oxysterol binding GO:0008142 p=1.7E−02 n=2 fg=0.01 bg=0.00
double−stranded RNA binding GO:0003725 p=1.8E−02 n=5 fg=0.02 bg=0.01
5'−3' RNA polymerase activity GO:0034062 p=2.0E−02 n=4 fg=0.01 bg=0.00
RNA polymerase activity GO:0097747 p=2.0E−02 n=4 fg=0.01 bg=0.00
GTPase binding GO:0051020 p=2.1E−02 n=25 fg=0.08 bg=0.05
N−acyltransferase activity GO:0016410 p=2.6E−02 n=5 fg=0.02 bg=0.01
lipase activity GO:0016298 p=2.7E−02 n=7 fg=0.02 bg=0.01
BH domain binding GO:0051400 p=3.2E−02 n=3 fg=0.01 bg=0.00
dynein intermediate chain binding GO:0045505 p=3.2E−02 n=3 fg=0.01 bg=0.00
GTPase activator activity GO:0005096 p=3.4E−02 n=12 fg=0.04 bg=0.02
oxidoreductase activity, acting on NAD(P... GO:0016651 p=3.8E−02 n=8 fg=0.03 bg=0.01
lipid transporter activity GO:0005319 p=4.2E−02 n=7 fg=0.02 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=4.5E−02 n=5 fg=0.02 bg=0.01
galactosidase activity GO:0015925 p=4.6E−02 n=2 fg=0.01 bg=0.00
Arp2/3 complex binding GO:0071933 p=4.6E−02 n=2 fg=0.01 bg=0.00
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−log(p)
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0.0 0.2 0.4 0.6 0.8 1.0
fraction
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Fox_Nvec_vc1.1_XM_032387218.2
fraction genes in fg and expected valu
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lysosome GO:0005764 p=3.5E−03 n=25 fg=0.08 bg=0.04
vacuolar membrane GO:0005774 p=4.5E−03 n=17 fg=0.05 bg=0.03
dynein complex GO:0030286 p=5.9E−03 n=6 fg=0.02 bg=0.01
secretory vesicle GO:0099503 p=9.1E−03 n=34 fg=0.10 bg=0.07
phagocytic vesicle GO:0045335 p=9.4E−03 n=8 fg=0.02 bg=0.01
lysosomal membrane GO:0005765 p=1.0E−02 n=12 fg=0.04 bg=0.02
proton−transporting V−type ATPase comple... GO:0033176 p=1.0E−02 n=4 fg=0.01 bg=0.00
cytoplasmic dynein complex GO:0005868 p=1.0E−02 n=4 fg=0.01 bg=0.00
tertiary granule membrane GO:0070821 p=1.0E−02 n=4 fg=0.01 bg=0.00
nuclear speck GO:0016607 p=1.0E−02 n=18 fg=0.05 bg=0.03
apical part of cell GO:0045177 p=1.1E−02 n=25 fg=0.08 bg=0.05
cell−substrate junction GO:0030055 p=1.2E−02 n=8 fg=0.02 bg=0.01
synaptic vesicle GO:0008021 p=1.4E−02 n=13 fg=0.04 bg=0.02
Elg1 RFC−like complex GO:0031391 p=1.5E−02 n=2 fg=0.01 bg=0.00
Gtr1−Gtr2 GTPase complex GO:1990131 p=1.5E−02 n=2 fg=0.01 bg=0.00
stereocilium tip GO:0032426 p=1.5E−02 n=2 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.5E−02 n=2 fg=0.01 bg=0.00
cytoplasmic side of apical plasma membra... GO:0098592 p=1.5E−02 n=3 fg=0.01 bg=0.00
caveola GO:0005901 p=1.6E−02 n=7 fg=0.02 bg=0.01
actin−based cell projection GO:0098858 p=1.6E−02 n=12 fg=0.04 bg=0.02
MKS complex GO:0036038 p=1.6E−02 n=4 fg=0.01 bg=0.00
lytic vacuole membrane GO:0098852 p=2.2E−02 n=12 fg=0.04 bg=0.02
proton−transporting two−sector ATPase co... GO:0016469 p=2.5E−02 n=4 fg=0.01 bg=0.00
tertiary granule GO:0070820 p=2.5E−02 n=7 fg=0.02 bg=0.01
secretory granule GO:0030141 p=3.0E−02 n=25 fg=0.08 bg=0.05
apical plasma membrane GO:0016324 p=3.1E−02 n=18 fg=0.05 bg=0.03
cytoplasmic region GO:0099568 p=3.4E−02 n=27 fg=0.08 bg=0.05
microvillus GO:0005902 p=3.4E−02 n=6 fg=0.02 bg=0.01
recycling endosome membrane GO:0055038 p=3.5E−02 n=4 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=328/1095 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction