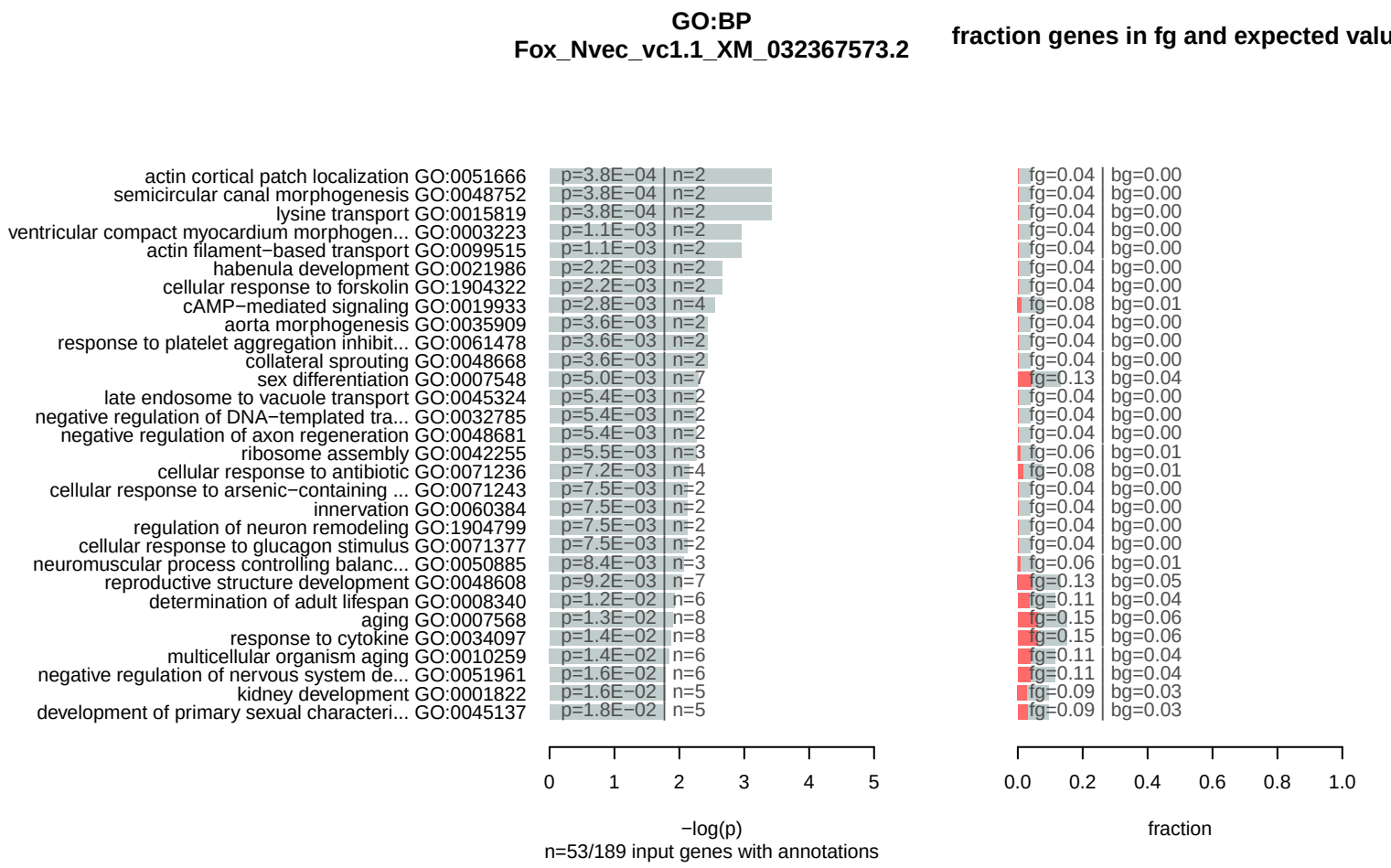
GO:BP
Fox_Nvec_vc1.1_XM_032367573.2
fraction genes in fg and expected valu
actin cortical patch localization GO:0051666 p=3.8E−04 n=2 fg=0.04 bg=0.00
semicircular canal morphogenesis GO:0048752 p=3.8E−04 n=2 fg=0.04 bg=0.00
lysine transport GO:0015819 p=3.8E−04 n=2 fg=0.04 bg=0.00
ventricular compact myocardium morphogen... GO:0003223 p=1.1E−03 n=2 fg=0.04 bg=0.00
actin filament−based transport GO:0099515 p=1.1E−03 n=2 fg=0.04 bg=0.00
habenula development GO:0021986 p=2.2E−03 n=2 fg=0.04 bg=0.00
cellular response to forskolin GO:1904322 p=2.2E−03 n=2 fg=0.04 bg=0.00
cAMP−mediated signaling GO:0019933 p=2.8E−03 n=4 fg=0.08 bg=0.01
aorta morphogenesis GO:0035909 p=3.6E−03 n=2 fg=0.04 bg=0.00
response to platelet aggregation inhibit... GO:0061478 p=3.6E−03 n=2 fg=0.04 bg=0.00
collateral sprouting GO:0048668 p=3.6E−03 n=2 fg=0.04 bg=0.00
sex differentiation GO:0007548 p=5.0E−03 n=7 fg=0.13 bg=0.04
late endosome to vacuole transport GO:0045324 p=5.4E−03 n=2 fg=0.04 bg=0.00
negative regulation of DNA−templated tra... GO:0032785 p=5.4E−03 n=2 fg=0.04 bg=0.00
negative regulation of axon regeneration GO:0048681 p=5.4E−03 n=2 fg=0.04 bg=0.00
ribosome assembly GO:0042255 p=5.5E−03 n=3 fg=0.06 bg=0.01
cellular response to antibiotic GO:0071236 p=7.2E−03 n=4 fg=0.08 bg=0.01
cellular response to arsenic−containing ... GO:0071243 p=7.5E−03 n=2 fg=0.04 bg=0.00
innervation GO:0060384 p=7.5E−03 n=2 fg=0.04 bg=0.00
regulation of neuron remodeling GO:1904799 p=7.5E−03 n=2 fg=0.04 bg=0.00
cellular response to glucagon stimulus GO:0071377 p=7.5E−03 n=2 fg=0.04 bg=0.00
neuromuscular process controlling balanc... GO:0050885 p=8.4E−03 n=3 fg=0.06 bg=0.01
reproductive structure development GO:0048608 p=9.2E−03 n=7 fg=0.13 bg=0.05
determination of adult lifespan GO:0008340 p=1.2E−02 n=6 fg=0.11 bg=0.04
aging GO:0007568 p=1.3E−02 n=8 fg=0.15 bg=0.06
response to cytokine GO:0034097 p=1.4E−02 n=8 fg=0.15 bg=0.06
multicellular organism aging GO:0010259 p=1.4E−02 n=6 fg=0.11 bg=0.04
negative regulation of nervous system de... GO:0051961 p=1.6E−02 n=6 fg=0.11 bg=0.04
kidney development GO:0001822 p=1.6E−02 n=5 fg=0.09 bg=0.03
development of primary sexual characteri... GO:0045137 p=1.8E−02 n=5 fg=0.09 bg=0.03
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−log(p)
n=53/189 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032367573.2
fraction genes in fg and expected valu
ankyrin binding GO:0030506 p=2.4E−03 n=2 fg=0.04 bg=0.00
nucleic acid binding GO:0003676 p=1.4E−02 n=17 fg=0.35 bg=0.21
heterocyclic compound binding GO:1901363 p=2.0E−02 n=21 fg=0.43 bg=0.28
promoter−specific chromatin binding GO:1990841 p=2.1E−02 n=2 fg=0.04 bg=0.00
ribonuclease III activity GO:0004525 p=2.1E−02 n=1 fg=0.02 bg=0.00
beta−endorphin binding GO:0031626 p=2.1E−02 n=1 fg=0.02 bg=0.00
uridine−diphosphatase activity GO:0045134 p=2.1E−02 n=1 fg=0.02 bg=0.00
histone pre−mRNA stem−loop binding GO:0071207 p=2.1E−02 n=1 fg=0.02 bg=0.00
nuclear progesterone receptor binding GO:0033142 p=2.1E−02 n=1 fg=0.02 bg=0.00
rRNA (cytosine−C5−)−methyltransferase ac... GO:0009383 p=2.1E−02 n=1 fg=0.02 bg=0.00
double−stranded RNA−specific ribonucleas... GO:0032296 p=2.1E−02 n=1 fg=0.02 bg=0.00
calcium− and calmodulin−responsive adeny... GO:0008294 p=2.1E−02 n=1 fg=0.02 bg=0.00
plus−end directed microfilament motor ac... GO:0060002 p=2.1E−02 n=1 fg=0.02 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=2.1E−02 n=1 fg=0.02 bg=0.00
DNA end binding GO:0045027 p=2.1E−02 n=1 fg=0.02 bg=0.00
JUN kinase activity GO:0004705 p=2.1E−02 n=1 fg=0.02 bg=0.00
insulin binding GO:0043559 p=2.1E−02 n=1 fg=0.02 bg=0.00
C−methyltransferase activity GO:0008169 p=2.1E−02 n=1 fg=0.02 bg=0.00
histone deacetylase regulator activity GO:0035033 p=2.1E−02 n=1 fg=0.02 bg=0.00
rRNA (cytosine) methyltransferase activi... GO:0016434 p=2.1E−02 n=1 fg=0.02 bg=0.00
SUMO polymer binding GO:0032184 p=2.1E−02 n=1 fg=0.02 bg=0.00
organic cyclic compound binding GO:0097159 p=2.4E−02 n=21 fg=0.43 bg=0.29
protein kinase C binding GO:0005080 p=2.4E−02 n=2 fg=0.04 bg=0.01
protein tyrosine phosphatase activity GO:0004725 p=2.8E−02 n=2 fg=0.04 bg=0.01
ubiquitin conjugating enzyme binding GO:0031624 p=3.3E−02 n=2 fg=0.04 bg=0.01
TBP−class protein binding GO:0017025 p=3.3E−02 n=2 fg=0.04 bg=0.01
ribosome binding GO:0043022 p=3.3E−02 n=2 fg=0.04 bg=0.01
sequence−specific DNA binding GO:0043565 p=3.5E−02 n=7 fg=0.14 bg=0.06
adenylate cyclase activity GO:0004016 p=4.1E−02 n=1 fg=0.02 bg=0.00
lipopolysaccharide binding GO:0001530 p=4.1E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=49/189 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032367573.2
fraction genes in fg and expected valu
fungal−type vacuole membrane GO:0000329 p=3.8E−03 n=2 fg=0.04 bg=0.00
cell tip GO:0051286 p=5.6E−03 n=2 fg=0.04 bg=0.00
fusome GO:0045169 p=1.3E−02 n=2 fg=0.04 bg=0.00
microprocessor complex GO:0070877 p=2.0E−02 n=1 fg=0.02 bg=0.00
spectrosome GO:0045170 p=2.0E−02 n=1 fg=0.02 bg=0.00
spectrin GO:0008091 p=2.0E−02 n=1 fg=0.02 bg=0.00
SUMO−targeted ubiquitin ligase complex GO:0033768 p=2.0E−02 n=1 fg=0.02 bg=0.00
ribonuclease III complex GO:1903095 p=2.0E−02 n=1 fg=0.02 bg=0.00
intrinsic component of autophagosome mem... GO:0097636 p=2.0E−02 n=1 fg=0.02 bg=0.00
integral component of autophagosome memb... GO:0097637 p=2.0E−02 n=1 fg=0.02 bg=0.00
histone pre−mRNA 3'end processing comple... GO:0071204 p=2.0E−02 n=1 fg=0.02 bg=0.00
PML body GO:0016605 p=2.7E−02 n=2 fg=0.04 bg=0.00
DNA replication preinitiation complex GO:0031261 p=4.0E−02 n=1 fg=0.02 bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=4.0E−02 n=1 fg=0.02 bg=0.00
NELF complex GO:0032021 p=4.0E−02 n=1 fg=0.02 bg=0.00
phenylalanine−tRNA ligase complex GO:0009328 p=4.0E−02 n=1 fg=0.02 bg=0.00
intrinsic component of vacuolar membrane GO:0031310 p=4.0E−02 n=1 fg=0.02 bg=0.00
GINS complex GO:0000811 p=4.0E−02 n=1 fg=0.02 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=4.0E−02 n=1 fg=0.02 bg=0.00
integral component of vacuolar membrane GO:0031166 p=4.0E−02 n=1 fg=0.02 bg=0.00
intracellular anatomical structure GO:0005622 p=4.6E−02 n=54 fg=1.00 bg=0.94
cell division site GO:0032153 p=5.4E−02 n=2 fg=0.04 bg=0.01
nuclear aryl hydrocarbon receptor comple... GO:0034753 p=5.9E−02 n=1 fg=0.02 bg=0.00
replication fork protection complex GO:0031298 p=5.9E−02 n=1 fg=0.02 bg=0.00
aryl hydrocarbon receptor complex GO:0034751 p=7.8E−02 n=1 fg=0.02 bg=0.00
guanylate cyclase complex, soluble GO:0008074 p=7.8E−02 n=1 fg=0.02 bg=0.00
basal dendrite GO:0097441 p=7.8E−02 n=1 fg=0.02 bg=0.00
endocytic vesicle membrane GO:0030666 p=8.2E−02 n=2 fg=0.04 bg=0.01
integral component of endoplasmic reticu... GO:0030176 p=9.2E−02 n=3 fg=0.06 bg=0.02
anchored component of plasma membrane GO:0046658 p=9.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=54/189 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction