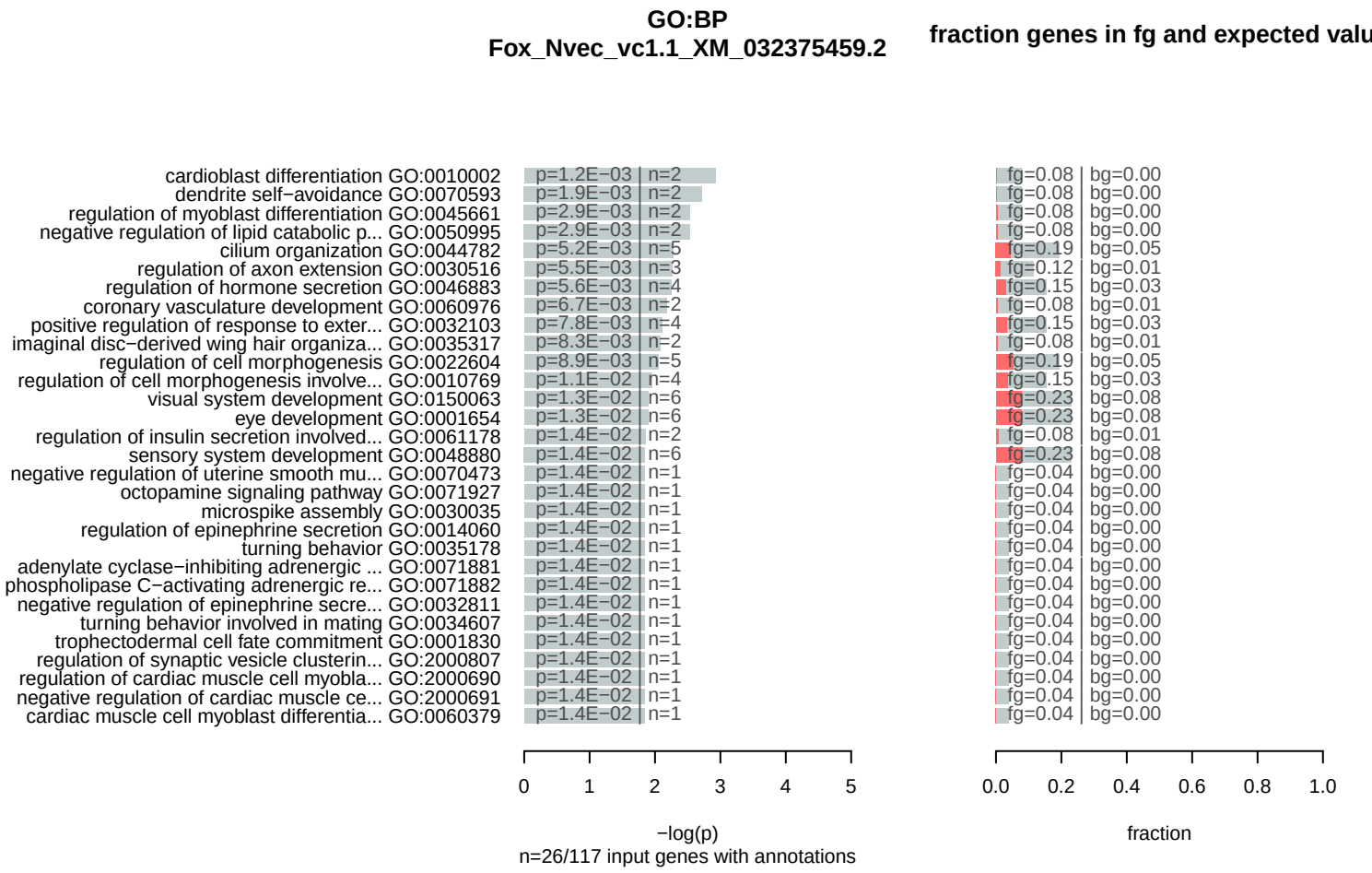
GO:BP
Fox_Nvec_vc1.1_XM_032375459.2
fraction genes in fg and expected valu
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dendrite self−avoidance GO:0070593 p=1.9E−03 n=2 fg=0.08 bg=0.00
regulation of myoblast differentiation GO:0045661 p=2.9E−03 n=2 fg=0.08 bg=0.00
negative regulation of lipid catabolic p... GO:0050995 p=2.9E−03 n=2 fg=0.08 bg=0.00
cilium organization GO:0044782 p=5.2E−03 n=5 fg=0.19 bg=0.05
regulation of axon extension GO:0030516 p=5.5E−03 n=3 fg=0.12 bg=0.01
regulation of hormone secretion GO:0046883 p=5.6E−03 n=4 fg=0.15 bg=0.03
coronary vasculature development GO:0060976 p=6.7E−03 n=2 fg=0.08 bg=0.01
positive regulation of response to exter... GO:0032103 p=7.8E−03 n=4 fg=0.15 bg=0.03
imaginal disc−derived wing hair organiza... GO:0035317 p=8.3E−03 n=2 fg=0.08 bg=0.01
regulation of cell morphogenesis GO:0022604 p=8.9E−03 n=5 fg=0.19 bg=0.05
regulation of cell morphogenesis involve... GO:0010769 p=1.1E−02 n=4 fg=0.15 bg=0.03
visual system development GO:0150063 p=1.3E−02 n=6 fg=0.23 bg=0.08
eye development GO:0001654 p=1.3E−02 n=6 fg=0.23 bg=0.08
regulation of insulin secretion involved... GO:0061178 p=1.4E−02 n=2 fg=0.08 bg=0.01
sensory system development GO:0048880 p=1.4E−02 n=6 fg=0.23 bg=0.08
negative regulation of uterine smooth mu... GO:0070473 p=1.4E−02 n=1 fg=0.04 bg=0.00
octopamine signaling pathway GO:0071927 p=1.4E−02 n=1 fg=0.04 bg=0.00
microspike assembly GO:0030035 p=1.4E−02 n=1 fg=0.04 bg=0.00
regulation of epinephrine secretion GO:0014060 p=1.4E−02 n=1 fg=0.04 bg=0.00
turning behavior GO:0035178 p=1.4E−02 n=1 fg=0.04 bg=0.00
adenylate cyclase−inhibiting adrenergic ... GO:0071881 p=1.4E−02 n=1 fg=0.04 bg=0.00
phospholipase C−activating adrenergic re... GO:0071882 p=1.4E−02 n=1 fg=0.04 bg=0.00
negative regulation of epinephrine secre... GO:0032811 p=1.4E−02 n=1 fg=0.04 bg=0.00
turning behavior involved in mating GO:0034607 p=1.4E−02 n=1 fg=0.04 bg=0.00
trophectodermal cell fate commitment GO:0001830 p=1.4E−02 n=1 fg=0.04 bg=0.00
regulation of synaptic vesicle clusterin... GO:2000807 p=1.4E−02 n=1 fg=0.04 bg=0.00
regulation of cardiac muscle cell myobla... GO:2000690 p=1.4E−02 n=1 fg=0.04 bg=0.00
negative regulation of cardiac muscle ce... GO:2000691 p=1.4E−02 n=1 fg=0.04 bg=0.00
cardiac muscle cell myoblast differentia... GO:0060379 p=1.4E−02 n=1 fg=0.04 bg=0.00
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−log(p)
n=26/117 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032375459.2
fraction genes in fg and expected valu
adrenergic receptor binding GO:0031690 p=3.0E−03 n=2 fg=0.10 bg=0.00
guanyl−nucleotide exchange factor activi... GO:0005085 p=7.3E−03 n=3 fg=0.15 bg=0.02
ubiquitin−like protein ligase binding GO:0044389 p=9.7E−03 n=4 fg=0.20 bg=0.04
SUMO binding GO:0032183 p=1.3E−02 n=1 fg=0.05 bg=0.00
nickel cation binding GO:0016151 p=1.3E−02 n=1 fg=0.05 bg=0.00
alpha−2C adrenergic receptor binding GO:0031696 p=1.3E−02 n=1 fg=0.05 bg=0.00
leptin receptor binding GO:1990460 p=1.3E−02 n=1 fg=0.05 bg=0.00
propionyl−CoA carboxylase activity GO:0004658 p=1.3E−02 n=1 fg=0.05 bg=0.00
CoA carboxylase activity GO:0016421 p=1.3E−02 n=1 fg=0.05 bg=0.00
transferrin receptor binding GO:1990459 p=1.3E−02 n=1 fg=0.05 bg=0.00
alpha−adrenergic receptor activity GO:0004936 p=1.3E−02 n=1 fg=0.05 bg=0.00
alpha2−adrenergic receptor activity GO:0004938 p=1.3E−02 n=1 fg=0.05 bg=0.00
octopamine receptor activity GO:0004989 p=2.5E−02 n=1 fg=0.05 bg=0.00
alpha−1B adrenergic receptor binding GO:0031692 p=2.5E−02 n=1 fg=0.05 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=2.5E−02 n=1 fg=0.05 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=2.5E−02 n=1 fg=0.05 bg=0.00
cAMP−dependent protein kinase regulator ... GO:0008603 p=2.5E−02 n=1 fg=0.05 bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=2.5E−02 n=1 fg=0.05 bg=0.00
norepinephrine binding GO:0051380 p=2.5E−02 n=1 fg=0.05 bg=0.00
adrenergic receptor activity GO:0004935 p=2.5E−02 n=1 fg=0.05 bg=0.00
ligase activity, forming carbon−carbon b... GO:0016885 p=2.5E−02 n=1 fg=0.05 bg=0.00
thioesterase binding GO:0031996 p=2.5E−02 n=1 fg=0.05 bg=0.00
signaling receptor binding GO:0005102 p=2.7E−02 n=7 fg=0.35 bg=0.10
fibroblast growth factor−activated recep... GO:0005007 p=3.7E−02 n=1 fg=0.05 bg=0.00
heterotrimeric G−protein binding GO:0032795 p=3.7E−02 n=1 fg=0.05 bg=0.00
carbonate dehydratase activity GO:0004089 p=3.7E−02 n=1 fg=0.05 bg=0.00
G protein−coupled neurotransmitter recep... GO:0099528 p=3.7E−02 n=1 fg=0.05 bg=0.00
beta−glucuronidase activity GO:0004566 p=3.7E−02 n=1 fg=0.05 bg=0.00
receptor−receptor interaction GO:0090722 p=3.7E−02 n=1 fg=0.05 bg=0.00
transmembrane signaling receptor activit... GO:0004888 p=4.0E−02 n=3 fg=0.15 bg=0.04
0 1 2 3 4 5
−log(p)
n=20/117 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032375459.2
fraction genes in fg and expected valu
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motile cilium GO:0031514 p=1.7E−02 n=3 fg=0.11 bg=0.02
activating signal cointegrator 1 complex GO:0099053 p=3.1E−02 n=1 fg=0.04 bg=0.00
microtubule organizing center GO:0005815 p=3.4E−02 n=5 fg=0.18 bg=0.07
cytoskeleton GO:0005856 p=3.5E−02 n=8 fg=0.29 bg=0.14
nucleotide−activated protein kinase comp... GO:0031588 p=4.6E−02 n=1 fg=0.04 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=4.6E−02 n=1 fg=0.04 bg=0.00
microtubule cytoskeleton GO:0015630 p=5.2E−02 n=6 fg=0.21 bg=0.10
germinal vesicle GO:0042585 p=6.1E−02 n=1 fg=0.04 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=6.1E−02 n=1 fg=0.04 bg=0.00
cytoplasmic dynein complex GO:0005868 p=6.1E−02 n=1 fg=0.04 bg=0.00
intrinsic component of plasma membrane GO:0031226 p=6.9E−02 n=5 fg=0.18 bg=0.08
cell junction GO:0030054 p=7.2E−02 n=7 fg=0.25 bg=0.13
female germ cell nucleus GO:0001674 p=7.5E−02 n=1 fg=0.04 bg=0.00
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receptor complex GO:0043235 p=8.2E−02 n=2 fg=0.07 bg=0.02
excitatory synapse GO:0060076 p=8.9E−02 n=1 fg=0.04 bg=0.00
cilium GO:0005929 p=9.5E−02 n=4 fg=0.14 bg=0.06
apicolateral plasma membrane GO:0016327 p=1.0E−01 n=1 fg=0.04 bg=0.00
dynein complex GO:0030286 p=1.0E−01 n=1 fg=0.04 bg=0.00
germ cell nucleus GO:0043073 p=1.2E−01 n=1 fg=0.04 bg=0.00
synapse GO:0045202 p=1.4E−01 n=5 fg=0.18 bg=0.10
cytoplasmic side of plasma membrane GO:0009898 p=1.4E−01 n=2 fg=0.07 bg=0.02
T−tubule GO:0030315 p=1.4E−01 n=1 fg=0.04 bg=0.01
integral component of plasma membrane GO:0005887 p=1.5E−01 n=4 fg=0.14 bg=0.08
lateral plasma membrane GO:0016328 p=1.6E−01 n=1 fg=0.04 bg=0.01
bicellular tight junction GO:0005923 p=1.6E−01 n=1 fg=0.04 bg=0.01
photoreceptor connecting cilium GO:0032391 p=1.6E−01 n=1 fg=0.04 bg=0.01
cytoplasmic side of membrane GO:0098562 p=1.6E−01 n=2 fg=0.07 bg=0.03
centrosome GO:0005813 p=1.7E−01 n=3 fg=0.11 bg=0.05
0 1 2 3 4 5
−log(p)
n=28/117 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction