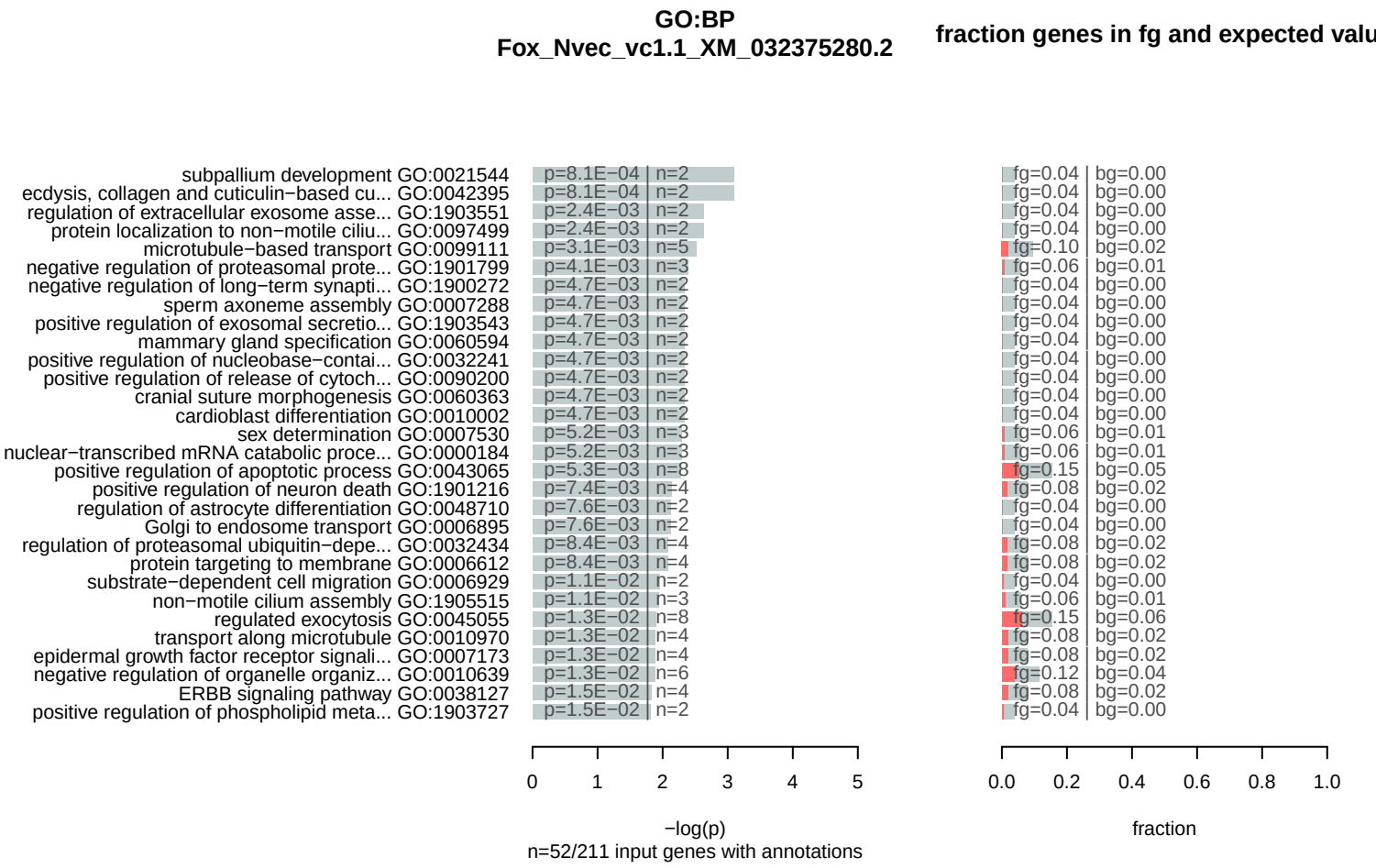
GO:BP
Fox_Nvec_vc1.1_XM_032375280.2
fraction genes in fg and expected valu
subpallium development GO:0021544 p=8.1E−04 n=2 fg=0.04 bg=0.00
ecdysis, collagen and cuticulin−based cu... GO:0042395 p=8.1E−04 n=2 fg=0.04 bg=0.00
regulation of extracellular exosome asse... GO:1903551 p=2.4E−03 n=2 fg=0.04 bg=0.00
protein localization to non−motile ciliu... GO:0097499 p=2.4E−03 n=2 fg=0.04 bg=0.00
microtubule−based transport GO:0099111 p=3.1E−03 n=5 fg=0.10 bg=0.02
negative regulation of proteasomal prote... GO:1901799 p=4.1E−03 n=3 fg=0.06 bg=0.01
negative regulation of long−term synapti... GO:1900272 p=4.7E−03 n=2 fg=0.04 bg=0.00
sperm axoneme assembly GO:0007288 p=4.7E−03 n=2 fg=0.04 bg=0.00
positive regulation of exosomal secretio... GO:1903543 p=4.7E−03 n=2 fg=0.04 bg=0.00
mammary gland specification GO:0060594 p=4.7E−03 n=2 fg=0.04 bg=0.00
positive regulation of nucleobase−contai... GO:0032241 p=4.7E−03 n=2 fg=0.04 bg=0.00
positive regulation of release of cytoch... GO:0090200 p=4.7E−03 n=2 fg=0.04 bg=0.00
cranial suture morphogenesis GO:0060363 p=4.7E−03 n=2 fg=0.04 bg=0.00
cardioblast differentiation GO:0010002 p=4.7E−03 n=2 fg=0.04 bg=0.00
sex determination GO:0007530 p=5.2E−03 n=3 fg=0.06 bg=0.01
nuclear−transcribed mRNA catabolic proce... GO:0000184 p=5.2E−03 n=3 fg=0.06 bg=0.01
positive regulation of apoptotic process GO:0043065 p=5.3E−03 n=8 fg=0.15 bg=0.05
positive regulation of neuron death GO:1901216 p=7.4E−03 n=4 fg=0.08 bg=0.02
regulation of astrocyte differentiation GO:0048710 p=7.6E−03 n=2 fg=0.04 bg=0.00
Golgi to endosome transport GO:0006895 p=7.6E−03 n=2 fg=0.04 bg=0.00
regulation of proteasomal ubiquitin−depe... GO:0032434 p=8.4E−03 n=4 fg=0.08 bg=0.02
protein targeting to membrane GO:0006612 p=8.4E−03 n=4 fg=0.08 bg=0.02
substrate−dependent cell migration GO:0006929 p=1.1E−02 n=2 fg=0.04 bg=0.00
non−motile cilium assembly GO:1905515 p=1.1E−02 n=3 fg=0.06 bg=0.01
regulated exocytosis GO:0045055 p=1.3E−02 n=8 fg=0.15 bg=0.06
transport along microtubule GO:0010970 p=1.3E−02 n=4 fg=0.08 bg=0.02
epidermal growth factor receptor signali... GO:0007173 p=1.3E−02 n=4 fg=0.08 bg=0.02
negative regulation of organelle organiz... GO:0010639 p=1.3E−02 n=6 fg=0.12 bg=0.04
ERBB signaling pathway GO:0038127 p=1.5E−02 n=4 fg=0.08 bg=0.02
positive regulation of phospholipid meta... GO:1903727 p=1.5E−02 n=2 fg=0.04 bg=0.00
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n=52/211 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032375280.2
fraction genes in fg and expected valu
ephrin receptor binding GO:0046875 p=8.1E−03 n=2 fg=0.04 bg=0.00
proteoglycan binding GO:0043394 p=8.1E−03 n=2 fg=0.04 bg=0.00
growth factor binding GO:0019838 p=8.6E−03 n=3 fg=0.06 bg=0.01
cell adhesion molecule binding GO:0050839 p=9.2E−03 n=4 fg=0.09 bg=0.02
guanyl−nucleotide exchange factor activi... GO:0005085 p=1.5E−02 n=4 fg=0.09 bg=0.02
tubulin binding GO:0015631 p=2.1E−02 n=5 fg=0.11 bg=0.03
frizzled binding GO:0005109 p=2.1E−02 n=2 fg=0.04 bg=0.01
hydro−lyase activity GO:0016836 p=2.1E−02 n=2 fg=0.04 bg=0.01
rRNA binding GO:0019843 p=2.1E−02 n=2 fg=0.04 bg=0.01
glycosaminoglycan binding GO:0005539 p=2.1E−02 n=2 fg=0.04 bg=0.01
peptide binding GO:0042277 p=2.6E−02 n=4 fg=0.09 bg=0.02
transmembrane receptor protein tyrosine ... GO:0004714 p=2.7E−02 n=2 fg=0.04 bg=0.01
ubiquitin binding GO:0043130 p=2.7E−02 n=2 fg=0.04 bg=0.01
ubiquitin−protein transferase inhibitor ... GO:0055105 p=2.9E−02 n=1 fg=0.02 bg=0.00
interleukin−5 receptor binding GO:0005137 p=2.9E−02 n=1 fg=0.02 bg=0.00
aminoacylase activity GO:0004046 p=2.9E−02 n=1 fg=0.02 bg=0.00
myosin VI binding GO:0070853 p=2.9E−02 n=1 fg=0.02 bg=0.00
myosin VI heavy chain binding GO:0070854 p=2.9E−02 n=1 fg=0.02 bg=0.00
neurotransmitter receptor regulator acti... GO:0099602 p=2.9E−02 n=1 fg=0.02 bg=0.00
calcitonin family binding GO:0097644 p=2.9E−02 n=1 fg=0.02 bg=0.00
amylin binding GO:0097645 p=2.9E−02 n=1 fg=0.02 bg=0.00
aspartate−tRNA ligase activity GO:0004815 p=2.9E−02 n=1 fg=0.02 bg=0.00
histone pre−mRNA stem−loop binding GO:0071207 p=2.9E−02 n=1 fg=0.02 bg=0.00
insulin−like growth factor II binding GO:0031995 p=2.9E−02 n=1 fg=0.02 bg=0.00
nickel cation binding GO:0016151 p=2.9E−02 n=1 fg=0.02 bg=0.00
insulin−like growth factor−activated rec... GO:0005010 p=2.9E−02 n=1 fg=0.02 bg=0.00
L−malate dehydrogenase activity GO:0030060 p=2.9E−02 n=1 fg=0.02 bg=0.00
retinoic acid binding GO:0001972 p=2.9E−02 n=1 fg=0.02 bg=0.00
ubiquitin ligase inhibitor activity GO:1990948 p=2.9E−02 n=1 fg=0.02 bg=0.00
kringle domain binding GO:0036143 p=2.9E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=47/211 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032375280.2
fraction genes in fg and expected valu
cilium GO:0005929 p=3.7E−03 n=9 fg=0.18 bg=0.06
cytosolic large ribosomal subunit GO:0022625 p=4.5E−03 n=2 fg=0.04 bg=0.00
extracellular region GO:0005576 p=7.2E−03 n=9 fg=0.18 bg=0.07
microtubule cytoskeleton GO:0015630 p=9.5E−03 n=11 fg=0.22 bg=0.10
nuclear envelope lumen GO:0005641 p=1.1E−02 n=2 fg=0.04 bg=0.00
secretory vesicle GO:0099503 p=1.3E−02 n=9 fg=0.18 bg=0.08
nuclear envelope GO:0005635 p=1.4E−02 n=6 fg=0.12 bg=0.04
ciliary tip GO:0097542 p=1.5E−02 n=2 fg=0.04 bg=0.00
secretory granule GO:0030141 p=1.7E−02 n=7 fg=0.14 bg=0.05
extracellular space GO:0005615 p=1.8E−02 n=5 fg=0.10 bg=0.03
transport vesicle GO:0030133 p=2.4E−02 n=6 fg=0.12 bg=0.04
trans−Golgi network transport vesicle GO:0030140 p=2.5E−02 n=2 fg=0.04 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=2.8E−02 n=1 fg=0.02 bg=0.00
lipoprotein particle GO:1990777 p=2.8E−02 n=1 fg=0.02 bg=0.00
interleukin−5 receptor complex GO:0005895 p=2.8E−02 n=1 fg=0.02 bg=0.00
keratin filament GO:0045095 p=2.8E−02 n=1 fg=0.02 bg=0.00
dendritic microtubule GO:1901588 p=2.8E−02 n=1 fg=0.02 bg=0.00
histone pre−mRNA 3'end processing comple... GO:0071204 p=2.8E−02 n=1 fg=0.02 bg=0.00
amyloid−beta complex GO:0106003 p=2.8E−02 n=1 fg=0.02 bg=0.00
ciliary transition fiber GO:0097539 p=2.8E−02 n=1 fg=0.02 bg=0.00
Swi5−Sfr1 complex GO:0032798 p=2.8E−02 n=1 fg=0.02 bg=0.00
desmosome GO:0030057 p=2.8E−02 n=1 fg=0.02 bg=0.00
DNA recombinase mediator complex GO:0033061 p=2.8E−02 n=1 fg=0.02 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=2.8E−02 n=1 fg=0.02 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=2.8E−02 n=1 fg=0.02 bg=0.00
high−density lipoprotein particle GO:0034364 p=2.8E−02 n=1 fg=0.02 bg=0.00
ESCRT−0 complex GO:0033565 p=2.8E−02 n=1 fg=0.02 bg=0.00
plasma lipoprotein particle GO:0034358 p=2.8E−02 n=1 fg=0.02 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=2.8E−02 n=1 fg=0.02 bg=0.00
Swi5−Swi2 complex GO:0034974 p=2.8E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=51/211 input genes with annotations
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fraction