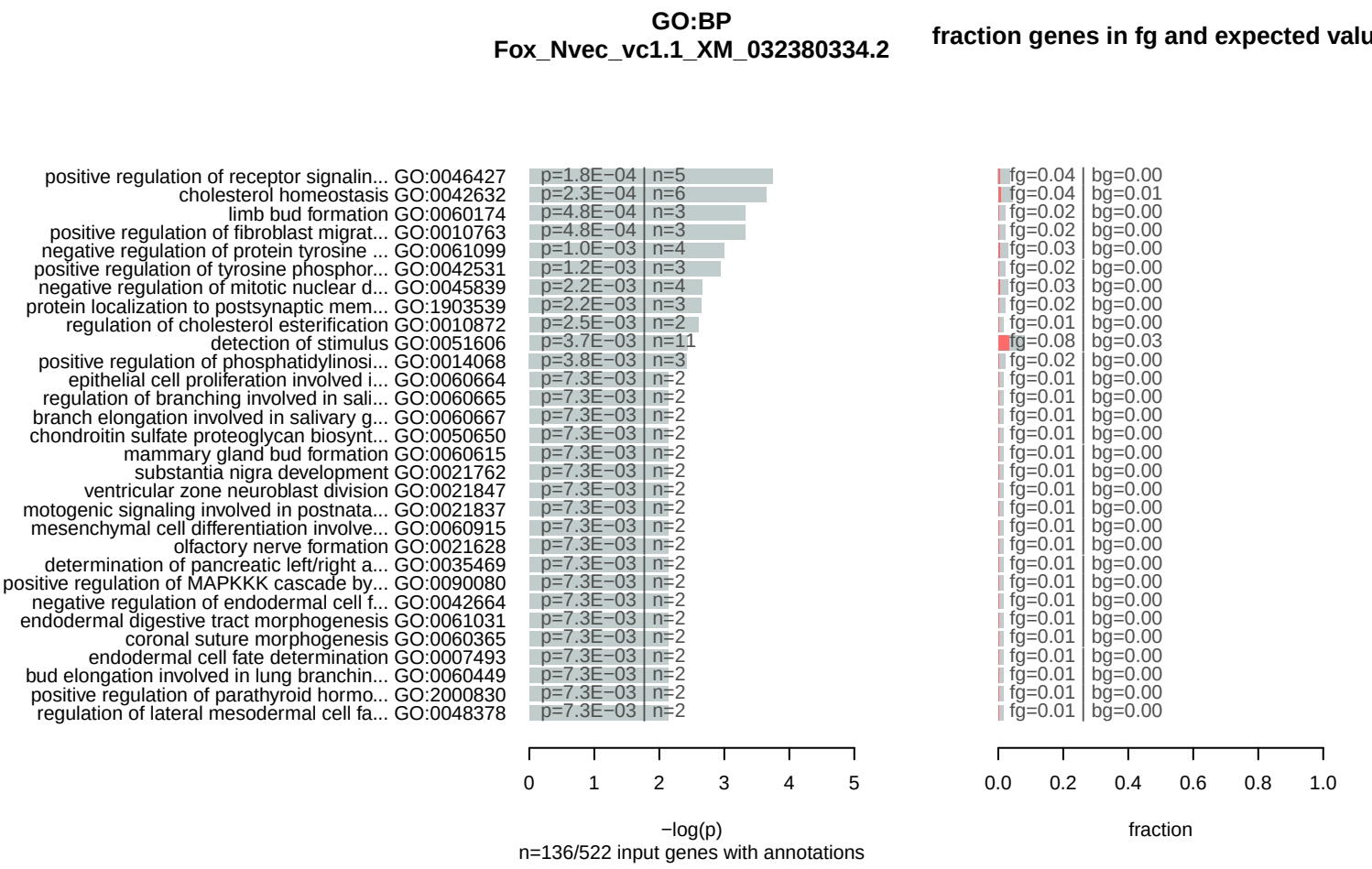
GO:BP
Fox_Nvec_vc1.1_XM_032380334.2
fraction genes in fg and expected valu
positive regulation of receptor signalin... GO:0046427 p=1.8E−04 n=5 fg=0.04 bg=0.00
cholesterol homeostasis GO:0042632 p=2.3E−04 n=6 fg=0.04 bg=0.01
limb bud formation GO:0060174 p=4.8E−04 n=3 fg=0.02 bg=0.00
positive regulation of fibroblast migrat... GO:0010763 p=4.8E−04 n=3 fg=0.02 bg=0.00
negative regulation of protein tyrosine ... GO:0061099 p=1.0E−03 n=4 fg=0.03 bg=0.00
positive regulation of tyrosine phosphor... GO:0042531 p=1.2E−03 n=3 fg=0.02 bg=0.00
negative regulation of mitotic nuclear d... GO:0045839 p=2.2E−03 n=4 fg=0.03 bg=0.00
protein localization to postsynaptic mem... GO:1903539 p=2.2E−03 n=3 fg=0.02 bg=0.00
regulation of cholesterol esterification GO:0010872 p=2.5E−03 n=2 fg=0.01 bg=0.00
detection of stimulus GO:0051606 p=3.7E−03 n=11 fg=0.08 bg=0.03
positive regulation of phosphatidylinosi... GO:0014068 p=3.8E−03 n=3 fg=0.02 bg=0.00
epithelial cell proliferation involved i... GO:0060664 p=7.3E−03 n=2 fg=0.01 bg=0.00
regulation of branching involved in sali... GO:0060665 p=7.3E−03 n=2 fg=0.01 bg=0.00
branch elongation involved in salivary g... GO:0060667 p=7.3E−03 n=2 fg=0.01 bg=0.00
chondroitin sulfate proteoglycan biosynt... GO:0050650 p=7.3E−03 n=2 fg=0.01 bg=0.00
mammary gland bud formation GO:0060615 p=7.3E−03 n=2 fg=0.01 bg=0.00
substantia nigra development GO:0021762 p=7.3E−03 n=2 fg=0.01 bg=0.00
ventricular zone neuroblast division GO:0021847 p=7.3E−03 n=2 fg=0.01 bg=0.00
motogenic signaling involved in postnata... GO:0021837 p=7.3E−03 n=2 fg=0.01 bg=0.00
mesenchymal cell differentiation involve... GO:0060915 p=7.3E−03 n=2 fg=0.01 bg=0.00
olfactory nerve formation GO:0021628 p=7.3E−03 n=2 fg=0.01 bg=0.00
determination of pancreatic left/right a... GO:0035469 p=7.3E−03 n=2 fg=0.01 bg=0.00
positive regulation of MAPKKK cascade by... GO:0090080 p=7.3E−03 n=2 fg=0.01 bg=0.00
negative regulation of endodermal cell f... GO:0042664 p=7.3E−03 n=2 fg=0.01 bg=0.00
endodermal digestive tract morphogenesis GO:0061031 p=7.3E−03 n=2 fg=0.01 bg=0.00
coronal suture morphogenesis GO:0060365 p=7.3E−03 n=2 fg=0.01 bg=0.00
endodermal cell fate determination GO:0007493 p=7.3E−03 n=2 fg=0.01 bg=0.00
bud elongation involved in lung branchin... GO:0060449 p=7.3E−03 n=2 fg=0.01 bg=0.00
positive regulation of parathyroid hormo... GO:2000830 p=7.3E−03 n=2 fg=0.01 bg=0.00
regulation of lateral mesodermal cell fa... GO:0048378 p=7.3E−03 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=136/522 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032380334.2
fraction genes in fg and expected valu
voltage−gated cation channel activity GO:0022843 p=3.6E−03 n=5 fg=0.04 bg=0.01
organic hydroxy compound transmembrane t... GO:1901618 p=7.0E−03 n=2 fg=0.02 bg=0.00
ATPase−coupled lipid transmembrane trans... GO:0034040 p=7.0E−03 n=2 fg=0.02 bg=0.00
metal ion transmembrane transporter acti... GO:0046873 p=7.3E−03 n=10 fg=0.09 bg=0.04
potassium channel activity GO:0005267 p=1.0E−02 n=4 fg=0.03 bg=0.01
beta−tubulin binding GO:0048487 p=1.1E−02 n=3 fg=0.03 bg=0.00
heparin binding GO:0008201 p=1.1E−02 n=3 fg=0.03 bg=0.00
fibroblast growth factor−activated recep... GO:0005007 p=1.4E−02 n=2 fg=0.02 bg=0.00
receptor−receptor interaction GO:0090722 p=1.4E−02 n=2 fg=0.02 bg=0.00
glycosaminoglycan binding GO:0005539 p=1.5E−02 n=3 fg=0.03 bg=0.00
voltage−gated potassium channel activity GO:0005249 p=1.5E−02 n=3 fg=0.03 bg=0.00
tubulin binding GO:0015631 p=1.5E−02 n=9 fg=0.08 bg=0.03
ion gated channel activity GO:0022839 p=1.9E−02 n=7 fg=0.06 bg=0.02
sequence−specific single stranded DNA bi... GO:0098847 p=2.2E−02 n=2 fg=0.02 bg=0.00
ABC−type transporter activity GO:0140359 p=2.2E−02 n=2 fg=0.02 bg=0.00
leak channel activity GO:0022840 p=2.2E−02 n=2 fg=0.02 bg=0.00
potassium ion leak channel activity GO:0022841 p=2.2E−02 n=2 fg=0.02 bg=0.00
narrow pore channel activity GO:0022842 p=2.2E−02 n=2 fg=0.02 bg=0.00
potassium ion transmembrane transporter ... GO:0015079 p=2.4E−02 n=4 fg=0.03 bg=0.01
phosphatidylinositol bisphosphate kinase... GO:0052813 p=3.2E−02 n=2 fg=0.02 bg=0.00
dynein heavy chain binding GO:0045504 p=3.2E−02 n=2 fg=0.02 bg=0.00
sodium channel activity GO:0005272 p=3.2E−02 n=2 fg=0.02 bg=0.00
rDNA binding GO:0000182 p=3.2E−02 n=2 fg=0.02 bg=0.00
phosphatidylinositol−4,5−bisphosphate 3−... GO:0046934 p=3.2E−02 n=2 fg=0.02 bg=0.00
glucuronosyltransferase activity GO:0015020 p=3.2E−02 n=2 fg=0.02 bg=0.00
1−phosphatidylinositol−3−kinase activity GO:0016303 p=4.3E−02 n=2 fg=0.02 bg=0.00
phosphatidylinositol 3−kinase activity GO:0035004 p=4.3E−02 n=2 fg=0.02 bg=0.00
phosphatidylinositol kinase activity GO:0052742 p=4.3E−02 n=2 fg=0.02 bg=0.00
guanyl−nucleotide exchange factor activi... GO:0005085 p=4.4E−02 n=5 fg=0.04 bg=0.02
protein kinase regulator activity GO:0019887 p=4.9E−02 n=5 fg=0.04 bg=0.02
0 1 2 3 4 5
−log(p)
n=117/522 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032380334.2
fraction genes in fg and expected valu
cation channel complex GO:0034703 p=1.6E−03 n=6 fg=0.04 bg=0.01
9+2 motile cilium GO:0097729 p=2.0E−03 n=7 fg=0.05 bg=0.01
excitatory synapse GO:0060076 p=4.0E−03 n=3 fg=0.02 bg=0.00
integral component of plasma membrane GO:0005887 p=6.4E−03 n=17 fg=0.12 bg=0.06
axoneme GO:0005930 p=6.8E−03 n=6 fg=0.04 bg=0.01
inner dynein arm GO:0036156 p=1.5E−02 n=2 fg=0.01 bg=0.00
central region of growth cone GO:0090724 p=1.5E−02 n=2 fg=0.01 bg=0.00
perinuclear region of cytoplasm GO:0048471 p=1.5E−02 n=16 fg=0.12 bg=0.06
endoplasmic reticulum GO:0005783 p=1.9E−02 n=27 fg=0.19 bg=0.13
transport vesicle GO:0030133 p=1.9E−02 n=10 fg=0.07 bg=0.03
endoplasmic reticulum membrane GO:0005789 p=2.2E−02 n=17 fg=0.12 bg=0.07
vesicle GO:0031982 p=2.3E−02 n=32 fg=0.23 bg=0.16
nuclear outer membrane−endoplasmic retic... GO:0042175 p=2.6E−02 n=17 fg=0.12 bg=0.07
endoplasmic reticulum subcompartment GO:0098827 p=2.8E−02 n=17 fg=0.12 bg=0.07
sperm flagellum GO:0036126 p=2.8E−02 n=5 fg=0.04 bg=0.01
cytoplasmic vesicle GO:0031410 p=3.1E−02 n=30 fg=0.22 bg=0.15
intracellular vesicle GO:0097708 p=3.1E−02 n=30 fg=0.22 bg=0.15
voltage−gated calcium channel complex GO:0005891 p=3.4E−02 n=2 fg=0.01 bg=0.00
dynein complex GO:0030286 p=3.8E−02 n=3 fg=0.02 bg=0.01
transport vesicle membrane GO:0030658 p=3.9E−02 n=5 fg=0.04 bg=0.01
growth cone GO:0030426 p=4.5E−02 n=6 fg=0.04 bg=0.02
axonemal dynein complex GO:0005858 p=4.7E−02 n=2 fg=0.01 bg=0.00
bub1−bub3 complex GO:1990298 p=5.1E−02 n=1 fg=0.01 bg=0.00
postsynaptic endosome GO:0098845 p=5.1E−02 n=1 fg=0.01 bg=0.00
Ragulator complex GO:0071986 p=5.1E−02 n=1 fg=0.01 bg=0.00
postsynaptic recycling endosome GO:0098837 p=5.1E−02 n=1 fg=0.01 bg=0.00
dendritic growth cone GO:0044294 p=5.1E−02 n=1 fg=0.01 bg=0.00
cyclin E1−CDK2 complex GO:0097134 p=5.1E−02 n=1 fg=0.01 bg=0.00
cyclin E2−CDK2 complex GO:0097135 p=5.1E−02 n=1 fg=0.01 bg=0.00
mitotic checkpoint complex GO:0033597 p=5.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=139/522 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction