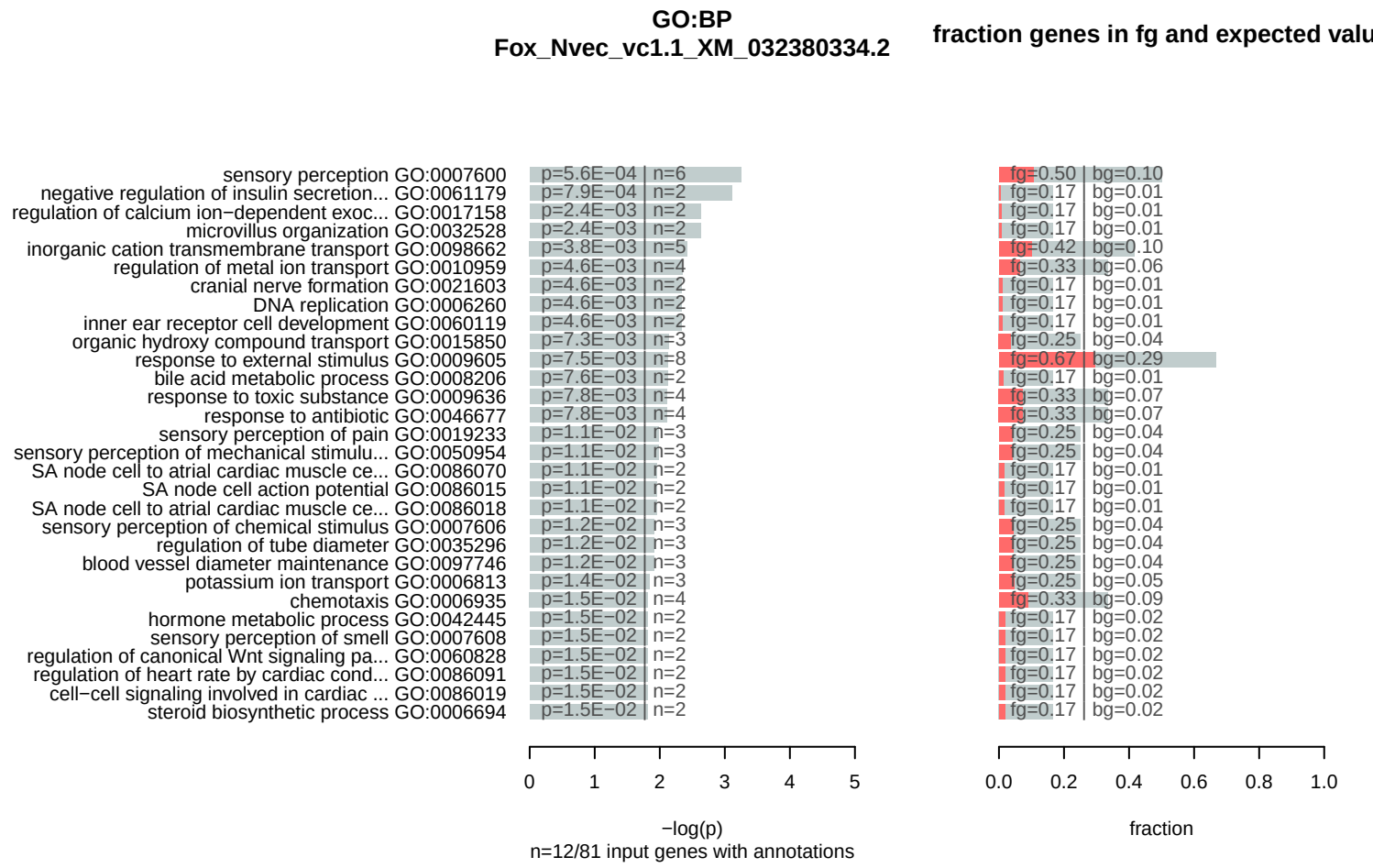
GO:BP
Fox_Nvec_vc1.1_XM_032380334.2
fraction genes in fg and expected valu
sensory perception GO:0007600 p=5.6E−04 n=6 fg=0.50 bg=0.10
negative regulation of insulin secretion... GO:0061179 p=7.9E−04 n=2 fg=0.17 bg=0.01
regulation of calcium ion−dependent exoc... GO:0017158 p=2.4E−03 n=2 fg=0.17 bg=0.01
microvillus organization GO:0032528 p=2.4E−03 n=2 fg=0.17 bg=0.01
inorganic cation transmembrane transport GO:0098662 p=3.8E−03 n=5 fg=0.42 bg=0.10
regulation of metal ion transport GO:0010959 p=4.6E−03 n=4 fg=0.33 bg=0.06
cranial nerve formation GO:0021603 p=4.6E−03 n=2 fg=0.17 bg=0.01
DNA replication GO:0006260 p=4.6E−03 n=2 fg=0.17 bg=0.01
inner ear receptor cell development GO:0060119 p=4.6E−03 n=2 fg=0.17 bg=0.01
organic hydroxy compound transport GO:0015850 p=7.3E−03 n=3 fg=0.25 bg=0.04
response to external stimulus GO:0009605 p=7.5E−03 n=8 fg=0.67 bg=0.29
bile acid metabolic process GO:0008206 p=7.6E−03 n=2 fg=0.17 bg=0.01
response to toxic substance GO:0009636 p=7.8E−03 n=4 fg=0.33 bg=0.07
response to antibiotic GO:0046677 p=7.8E−03 n=4 fg=0.33 bg=0.07
sensory perception of pain GO:0019233 p=1.1E−02 n=3 fg=0.25 bg=0.04
sensory perception of mechanical stimulu... GO:0050954 p=1.1E−02 n=3 fg=0.25 bg=0.04
SA node cell to atrial cardiac muscle ce... GO:0086070 p=1.1E−02 n=2 fg=0.17 bg=0.01
SA node cell action potential GO:0086015 p=1.1E−02 n=2 fg=0.17 bg=0.01
SA node cell to atrial cardiac muscle ce... GO:0086018 p=1.1E−02 n=2 fg=0.17 bg=0.01
sensory perception of chemical stimulus GO:0007606 p=1.2E−02 n=3 fg=0.25 bg=0.04
regulation of tube diameter GO:0035296 p=1.2E−02 n=3 fg=0.25 bg=0.04
blood vessel diameter maintenance GO:0097746 p=1.2E−02 n=3 fg=0.25 bg=0.04
potassium ion transport GO:0006813 p=1.4E−02 n=3 fg=0.25 bg=0.05
chemotaxis GO:0006935 p=1.5E−02 n=4 fg=0.33 bg=0.09
hormone metabolic process GO:0042445 p=1.5E−02 n=2 fg=0.17 bg=0.02
sensory perception of smell GO:0007608 p=1.5E−02 n=2 fg=0.17 bg=0.02
regulation of canonical Wnt signaling pa... GO:0060828 p=1.5E−02 n=2 fg=0.17 bg=0.02
regulation of heart rate by cardiac cond... GO:0086091 p=1.5E−02 n=2 fg=0.17 bg=0.02
cell−cell signaling involved in cardiac ... GO:0086019 p=1.5E−02 n=2 fg=0.17 bg=0.02
steroid biosynthetic process GO:0006694 p=1.5E−02 n=2 fg=0.17 bg=0.02
0 1 2 3 4 5
−log(p)
n=12/81 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
phosphoric ester hydrolase activity GO:0042578 p=1.4E−02 n=3 fg=0.25 bg=0.05
transmembrane transporter activity GO:0022857 p=1.8E−02 n=5 fg=0.42 bg=0.14
transporter activity GO:0005215 p=2.8E−02 n=5 fg=0.42 bg=0.16
calmodulin−activated dual specificity 3'... GO:0004117 p=3.3E−02 n=1 fg=0.08 bg=0.00
carbonate dehydratase activity GO:0004089 p=3.3E−02 n=1 fg=0.08 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=3.3E−02 n=1 fg=0.08 bg=0.00
phosphatidylinositol 3−kinase activity GO:0035004 p=3.3E−02 n=1 fg=0.08 bg=0.00
flippase activity GO:0140327 p=3.3E−02 n=1 fg=0.08 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=3.3E−02 n=1 fg=0.08 bg=0.00
carbon−oxygen lyase activity GO:0016835 p=3.3E−02 n=1 fg=0.08 bg=0.00
hydro−lyase activity GO:0016836 p=3.3E−02 n=1 fg=0.08 bg=0.00
voltage−gated calcium channel activity i... GO:0086056 p=3.3E−02 n=1 fg=0.08 bg=0.00
phosphatidylinositol bisphosphate kinase... GO:0052813 p=3.3E−02 n=1 fg=0.08 bg=0.00
voltage−gated calcium channel activity i... GO:0086059 p=3.3E−02 n=1 fg=0.08 bg=0.00
phosphatidylinositol−4,5−bisphosphate 3−... GO:0046934 p=3.3E−02 n=1 fg=0.08 bg=0.00
aminophospholipid flippase activity GO:0015247 p=3.3E−02 n=1 fg=0.08 bg=0.00
palmitoleyl hydrolase activity GO:1990699 p=3.3E−02 n=1 fg=0.08 bg=0.00
alpha−adrenergic receptor activity GO:0004936 p=3.3E−02 n=1 fg=0.08 bg=0.00
alpha2−adrenergic receptor activity GO:0004938 p=3.3E−02 n=1 fg=0.08 bg=0.00
thioesterase binding GO:0031996 p=3.3E−02 n=1 fg=0.08 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=3.3E−02 n=1 fg=0.08 bg=0.00
phosphatidylglycerol binding GO:1901611 p=3.3E−02 n=1 fg=0.08 bg=0.00
cardiolipin binding GO:1901612 p=3.3E−02 n=1 fg=0.08 bg=0.00
1−phosphatidylinositol−3−kinase activity GO:0016303 p=3.3E−02 n=1 fg=0.08 bg=0.00
phosphatidylinositol kinase activity GO:0052742 p=3.3E−02 n=1 fg=0.08 bg=0.00
organophosphate ester transmembrane tran... GO:0015605 p=3.3E−02 n=1 fg=0.08 bg=0.00
alpha−2C adrenergic receptor binding GO:0031696 p=3.3E−02 n=1 fg=0.08 bg=0.00
nickel cation binding GO:0016151 p=3.3E−02 n=1 fg=0.08 bg=0.00
phosphoric diester hydrolase activity GO:0008081 p=3.9E−02 n=2 fg=0.17 bg=0.03
scaffold protein binding GO:0097110 p=3.9E−02 n=2 fg=0.17 bg=0.03
0 1 2 3 4 5
−log(p)
n=12/81 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
integral component of plasma membrane GO:0005887 p=9.1E−03 n=6 fg=0.43 bg=0.15
perikaryon GO:0043204 p=2.8E−02 n=2 fg=0.14 bg=0.02
excitatory synapse GO:0060076 p=3.5E−02 n=1 fg=0.07 bg=0.00
receptor complex GO:0043235 p=4.3E−02 n=2 fg=0.14 bg=0.02
specific granule GO:0042581 p=6.9E−02 n=1 fg=0.07 bg=0.01
fusome GO:0045169 p=6.9E−02 n=1 fg=0.07 bg=0.01
phagocytic vesicle membrane GO:0030670 p=6.9E−02 n=1 fg=0.07 bg=0.01
specific granule membrane GO:0035579 p=6.9E−02 n=1 fg=0.07 bg=0.01
stereocilium GO:0032420 p=6.9E−02 n=1 fg=0.07 bg=0.01
stereocilium bundle GO:0032421 p=6.9E−02 n=1 fg=0.07 bg=0.01
endoplasmic reticulum GO:0005783 p=8.1E−02 n=5 fg=0.36 bg=0.18
cation channel complex GO:0034703 p=9.1E−02 n=2 fg=0.14 bg=0.04
perinuclear region of cytoplasm GO:0048471 p=9.1E−02 n=3 fg=0.21 bg=0.08
phagocytic vesicle GO:0045335 p=1.0E−01 n=1 fg=0.07 bg=0.01
rough endoplasmic reticulum GO:0005791 p=1.0E−01 n=1 fg=0.07 bg=0.01
tertiary granule GO:0070820 p=1.0E−01 n=1 fg=0.07 bg=0.01
tertiary granule membrane GO:0070821 p=1.0E−01 n=1 fg=0.07 bg=0.01
sensory dendrite GO:0071683 p=1.0E−01 n=1 fg=0.07 bg=0.01
transmembrane transporter complex GO:1902495 p=1.0E−01 n=2 fg=0.14 bg=0.04
ion channel complex GO:0034702 p=1.0E−01 n=2 fg=0.14 bg=0.04
transporter complex GO:1990351 p=1.0E−01 n=2 fg=0.14 bg=0.04
intrinsic component of organelle membran... GO:0031300 p=1.3E−01 n=2 fg=0.14 bg=0.04
integral component of organelle membrane GO:0031301 p=1.3E−01 n=2 fg=0.14 bg=0.04
acrosomal vesicle GO:0001669 p=1.3E−01 n=1 fg=0.07 bg=0.01
brush border membrane GO:0031526 p=1.3E−01 n=1 fg=0.07 bg=0.01
early endosome membrane GO:0031901 p=1.3E−01 n=1 fg=0.07 bg=0.01
plasma membrane region GO:0098590 p=1.3E−01 n=4 fg=0.29 bg=0.15
cell surface GO:0009986 p=1.4E−01 n=2 fg=0.14 bg=0.05
cytoplasmic vesicle membrane GO:0030659 p=1.5E−01 n=3 fg=0.21 bg=0.10
vesicle membrane GO:0012506 p=1.5E−01 n=3 fg=0.21 bg=0.10
0 1 2 3 4 5
−log(p)
n=14/81 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction