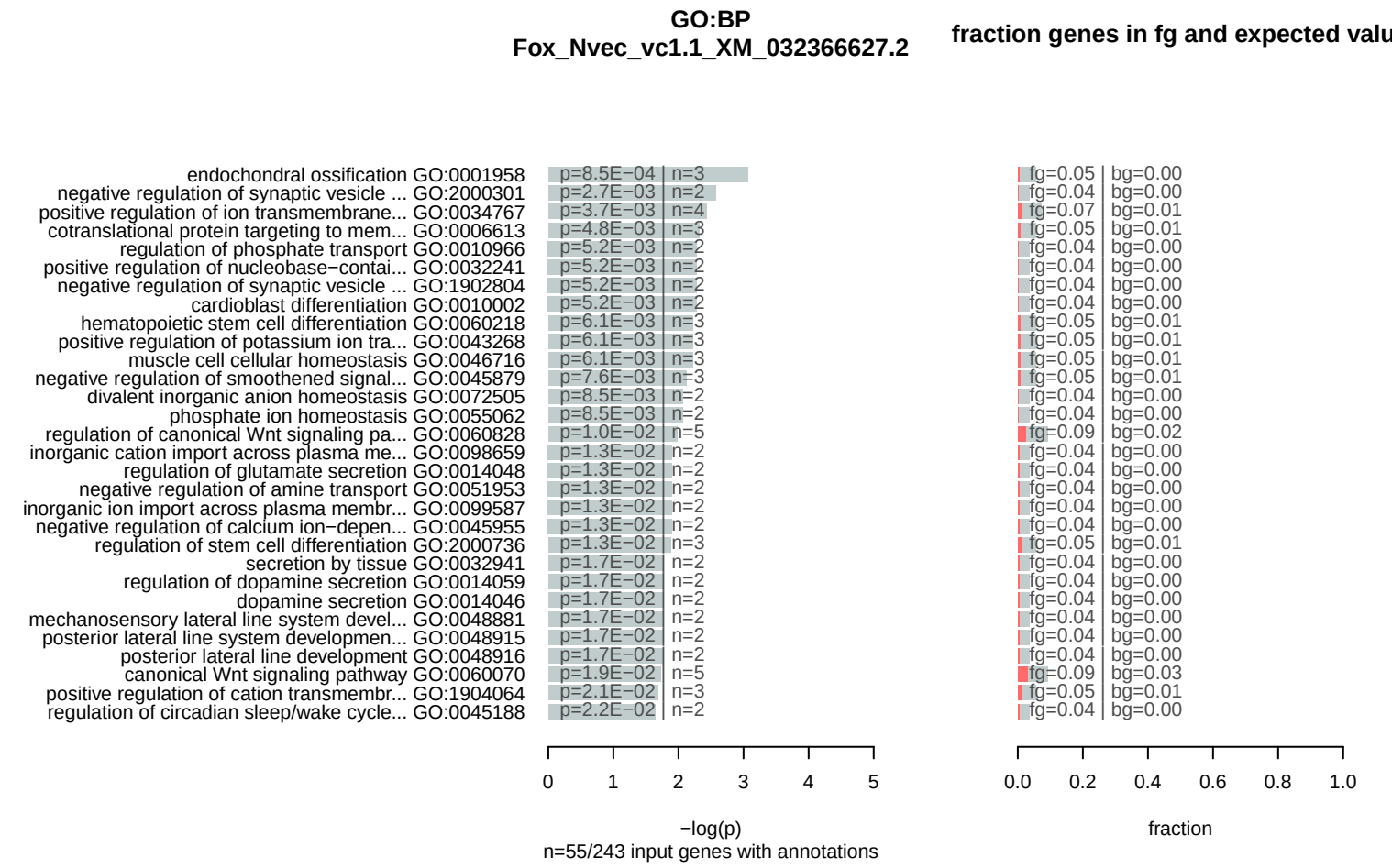
GO:BP
Fox_Nvec_vc1.1_XM_032366627.2
fraction genes in fg and expected valu
endochondral ossification GO:0001958 p=8.5E−04 n=3 fg=0.05 bg=0.00
negative regulation of synaptic vesicle ... GO:2000301 p=2.7E−03 n=2 fg=0.04 bg=0.00
positive regulation of ion transmembrane... GO:0034767 p=3.7E−03 n=4 fg=0.07 bg=0.01
cotranslational protein targeting to mem... GO:0006613 p=4.8E−03 n=3 fg=0.05 bg=0.01
regulation of phosphate transport GO:0010966 p=5.2E−03 n=2 fg=0.04 bg=0.00
positive regulation of nucleobase−contai... GO:0032241 p=5.2E−03 n=2 fg=0.04 bg=0.00
negative regulation of synaptic vesicle ... GO:1902804 p=5.2E−03 n=2 fg=0.04 bg=0.00
cardioblast differentiation GO:0010002 p=5.2E−03 n=2 fg=0.04 bg=0.00
hematopoietic stem cell differentiation GO:0060218 p=6.1E−03 n=3 fg=0.05 bg=0.01
positive regulation of potassium ion tra... GO:0043268 p=6.1E−03 n=3 fg=0.05 bg=0.01
muscle cell cellular homeostasis GO:0046716 p=6.1E−03 n=3 fg=0.05 bg=0.01
negative regulation of smoothened signal... GO:0045879 p=7.6E−03 n=3 fg=0.05 bg=0.01
divalent inorganic anion homeostasis GO:0072505 p=8.5E−03 n=2 fg=0.04 bg=0.00
phosphate ion homeostasis GO:0055062 p=8.5E−03 n=2 fg=0.04 bg=0.00
regulation of canonical Wnt signaling pa... GO:0060828 p=1.0E−02 n=5 fg=0.09 bg=0.02
inorganic cation import across plasma me... GO:0098659 p=1.3E−02 n=2 fg=0.04 bg=0.00
regulation of glutamate secretion GO:0014048 p=1.3E−02 n=2 fg=0.04 bg=0.00
negative regulation of amine transport GO:0051953 p=1.3E−02 n=2 fg=0.04 bg=0.00
inorganic ion import across plasma membr... GO:0099587 p=1.3E−02 n=2 fg=0.04 bg=0.00
negative regulation of calcium ion−depen... GO:0045955 p=1.3E−02 n=2 fg=0.04 bg=0.00
regulation of stem cell differentiation GO:2000736 p=1.3E−02 n=3 fg=0.05 bg=0.01
secretion by tissue GO:0032941 p=1.7E−02 n=2 fg=0.04 bg=0.00
regulation of dopamine secretion GO:0014059 p=1.7E−02 n=2 fg=0.04 bg=0.00
dopamine secretion GO:0014046 p=1.7E−02 n=2 fg=0.04 bg=0.00
mechanosensory lateral line system devel... GO:0048881 p=1.7E−02 n=2 fg=0.04 bg=0.00
posterior lateral line system developmen... GO:0048915 p=1.7E−02 n=2 fg=0.04 bg=0.00
posterior lateral line development GO:0048916 p=1.7E−02 n=2 fg=0.04 bg=0.00
canonical Wnt signaling pathway GO:0060070 p=1.9E−02 n=5 fg=0.09 bg=0.03
positive regulation of cation transmembr... GO:1904064 p=2.1E−02 n=3 fg=0.05 bg=0.01
regulation of circadian sleep/wake cycle... GO:0045188 p=2.2E−02 n=2 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=55/243 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032366627.2
fraction genes in fg and expected valu
phospholipase C activity GO:0004629 p=4.9E−03 n=2 fg=0.04 bg=0.00
ADP binding GO:0043531 p=2.1E−02 n=2 fg=0.04 bg=0.01
ion channel inhibitor activity GO:0008200 p=2.7E−02 n=2 fg=0.04 bg=0.01
phosphoglycerate kinase activity GO:0004618 p=2.9E−02 n=1 fg=0.02 bg=0.00
ribonuclease III activity GO:0004525 p=2.9E−02 n=1 fg=0.02 bg=0.00
lipopolysaccharide binding GO:0001530 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
sodium:phosphate symporter activity GO:0005436 p=2.9E−02 n=1 fg=0.02 bg=0.00
ATPase−coupled inorganic anion transmemb... GO:0043225 p=2.9E−02 n=1 fg=0.02 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=2.9E−02 n=1 fg=0.02 bg=0.00
palmitoleyl hydrolase activity GO:1990699 p=2.9E−02 n=1 fg=0.02 bg=0.00
phosphate ion binding GO:0042301 p=2.9E−02 n=1 fg=0.02 bg=0.00
double−stranded RNA−specific ribonucleas... GO:0032296 p=2.9E−02 n=1 fg=0.02 bg=0.00
DNA binding, bending GO:0008301 p=2.9E−02 n=1 fg=0.02 bg=0.00
phosphatidyl−N−methylethanolamine N−meth... GO:0000773 p=2.9E−02 n=1 fg=0.02 bg=0.00
non−sequence−specific DNA binding, bendi... GO:0044378 p=2.9E−02 n=1 fg=0.02 bg=0.00
phosphatidyl−N−dimethylethanolamine N−me... GO:0080101 p=2.9E−02 n=1 fg=0.02 bg=0.00
1−alkyl−2−acetylglycerophosphocholine es... GO:0003847 p=2.9E−02 n=1 fg=0.02 bg=0.00
channel inhibitor activity GO:0016248 p=3.3E−02 n=2 fg=0.04 bg=0.01
clathrin binding GO:0030276 p=4.7E−02 n=2 fg=0.04 bg=0.01
molecular function inhibitor activity GO:0140678 p=4.7E−02 n=2 fg=0.04 bg=0.01
protein heterodimerization activity GO:0046982 p=5.0E−02 n=6 fg=0.13 bg=0.06
metal ion binding GO:0046872 p=5.0E−02 n=9 fg=0.19 bg=0.10
nuclear vitamin D receptor binding GO:0042809 p=5.8E−02 n=1 fg=0.02 bg=0.00
G protein−coupled adenosine receptor act... GO:0001609 p=5.8E−02 n=1 fg=0.02 bg=0.00
chloride channel inhibitor activity GO:0019869 p=5.8E−02 n=1 fg=0.02 bg=0.00
phosphate ion transmembrane transporter ... GO:0015114 p=5.8E−02 n=1 fg=0.02 bg=0.00
primary miRNA binding GO:0070878 p=5.8E−02 n=1 fg=0.02 bg=0.00
phosphotransferase activity, carboxyl gr... GO:0016774 p=5.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=47/243 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032366627.2
fraction genes in fg and expected valu
exocytic vesicle membrane GO:0099501 p=2.2E−03 n=4 fg=0.08 bg=0.01
presynaptic active zone membrane GO:0048787 p=8.0E−03 n=2 fg=0.04 bg=0.00
excitatory synapse GO:0060076 p=1.2E−02 n=2 fg=0.04 bg=0.00
intrinsic component of postsynaptic memb... GO:0098936 p=1.6E−02 n=2 fg=0.04 bg=0.00
integral component of postsynaptic membr... GO:0099055 p=1.6E−02 n=2 fg=0.04 bg=0.00
integral component of presynaptic membra... GO:0099056 p=1.6E−02 n=2 fg=0.04 bg=0.00
intrinsic component of presynaptic membr... GO:0098889 p=1.6E−02 n=2 fg=0.04 bg=0.00
integral component of synaptic membrane GO:0099699 p=1.6E−02 n=2 fg=0.04 bg=0.00
intrinsic component of synaptic membrane GO:0099240 p=1.6E−02 n=2 fg=0.04 bg=0.00
synaptic vesicle membrane GO:0030672 p=1.7E−02 n=3 fg=0.06 bg=0.01
fusome GO:0045169 p=2.1E−02 n=2 fg=0.04 bg=0.00
preribosome GO:0030684 p=2.1E−02 n=2 fg=0.04 bg=0.00
dense core granule GO:0031045 p=2.9E−02 n=1 fg=0.02 bg=0.00
ribonuclease III complex GO:1903095 p=2.9E−02 n=1 fg=0.02 bg=0.00
microprocessor complex GO:0070877 p=2.9E−02 n=1 fg=0.02 bg=0.00
dense core granule membrane GO:0032127 p=2.9E−02 n=1 fg=0.02 bg=0.00
microvesicle GO:1990742 p=2.9E−02 n=1 fg=0.02 bg=0.00
ESCRT−0 complex GO:0033565 p=2.9E−02 n=1 fg=0.02 bg=0.00
dendritic microtubule GO:1901588 p=2.9E−02 n=1 fg=0.02 bg=0.00
asymmetric synapse GO:0032279 p=3.5E−02 n=4 fg=0.08 bg=0.02
neuron to neuron synapse GO:0098984 p=3.7E−02 n=4 fg=0.08 bg=0.02
integral component of synaptic vesicle m... GO:0030285 p=3.9E−02 n=2 fg=0.04 bg=0.01
integral component of plasma membrane GO:0005887 p=4.1E−02 n=8 fg=0.15 bg=0.08
intrinsic component of synaptic vesicle ... GO:0098563 p=4.6E−02 n=2 fg=0.04 bg=0.01
endocytic vesicle GO:0030139 p=4.6E−02 n=4 fg=0.08 bg=0.03
brush border membrane GO:0031526 p=5.3E−02 n=2 fg=0.04 bg=0.01
postsynaptic membrane GO:0045211 p=5.5E−02 n=3 fg=0.06 bg=0.02
preribosome, small subunit precursor GO:0030688 p=5.8E−02 n=1 fg=0.02 bg=0.00
histone locus body GO:0035363 p=5.8E−02 n=1 fg=0.02 bg=0.00
early phagosome GO:0032009 p=5.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=53/243 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction