GO:BP
Fox_Nvec_vc1.1_XM_001629605.3

fraction genes in fg and expected valu...

hair follicle morphogenesis GO:0031069	p=3.8E−04	n=4	fg=0.02 | bg=0.00
positive regulation of morphogenesis of ... GO:1905332	p=3.8E−04	n=4	fg=0.02 | bg=0.00
negative regulation of Ras protein signa... GO:0046580	p=4.3E−04	n=6	fg=0.04 | bg=0.01
regulation of morphogenesis of a branchi... GO:0060688	p=3.0E−03	n=4	fg=0.02 | bg=0.00
intra−Golgi vesicle−mediated transport GO:0006891	p=3.0E−03	n=4	fg=0.02 | bg=0.00
positive regulation of cell cycle G1/S p... GO:1902808	p=3.3E−03	n=5	fg=0.03 | bg=0.01
positive regulation of inclusion body as... GO:0090261	p=3.6E−03	n=2	fg=0.01 | bg=0.00
nucleoside transmembrane transport GO:1901642	p=3.6E−03	n=2	fg=0.01 | bg=0.00
regulation of iron ion transmembrane tra... GO:0034759	p=3.6E−03	n=2	fg=0.01 | bg=0.00
cellular response to copper ion GO:0071280	p=3.6E−03	n=2	fg=0.01 | bg=0.00
oviduct development GO:0060066	p=3.6E−03	n=2	fg=0.01 | bg=0.00
phagosome maturation involved in apoptot... GO:0090386	p=3.6E−03	n=2	fg=0.01 | bg=0.00
pyrimidine nucleoside transport GO:0015864	p=3.6E−03	n=2	fg=0.01 | bg=0.00
pyrimidine nucleobase transport GO:0015855	p=3.6E−03	n=2	fg=0.01 | bg=0.00
larval development GO:0002164	p=3.8E−03	n=17	fg=0.10 | bg=0.05
hindbrain development GO:0030902	p=3.9E−03	n=8	fg=0.05 | bg=0.02
positive regulation of epithelial cell d... GO:0030858	p=4.2E−03	n=4	fg=0.02 | bg=0.00
multicellular organismal movement GO:0050879	p=6.2E−03	n=3	fg=0.02 | bg=0.00
cellular response to estradiol stimulus GO:0071392	p=6.2E−03	n=3	fg=0.02 | bg=0.00
ventricular cardiac muscle tissue morpho... GO:0055010	p=6.2E−03	n=3	fg=0.02 | bg=0.00
negative regulation of DNA repair GO:0045738	p=6.2E−03	n=3	fg=0.02 | bg=0.00
positive regulation of mitotic cell cycl... GO:1901992	p=7.6E−03	n=6	fg=0.04 | bg=0.01
left/right axis specification GO:0070986	p=9.5E−03	n=3	fg=0.02 | bg=0.00
positive regulation of cell cycle G2/M p... GO:1902751	p=9.5E−03	n=3	fg=0.02 | bg=0.00
positive regulation of animal organ morp... GO:0110110	p=9.5E−03	n=3	fg=0.02 | bg=0.00
nephron epithelium morphogenesis GO:0072088	p=1.0E−02	n=5	fg=0.03 | bg=0.01
nephron tubule morphogenesis GO:0072078	p=1.0E−02	n=5	fg=0.03 | bg=0.01
regulation of nephron tubule epithelial ... GO:0072182	p=1.0E−02	n=2	fg=0.01 | bg=0.00
nephric duct morphogenesis GO:0072178	p=1.0E−02	n=2	fg=0.01 | bg=0.00
ventricular compact myocardium morphogen... GO:0003223	p=1.0E−02	n=2	fg=0.01 | bg=0.00

0 1 2 3 4 5
−log(p)
n=162/499 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:MF
Fox_Nvec_vc1.1_XM_001629605.3

fraction genes in fg and expected valu...

nucleoside transmembrane transporter act... GO:0005337	p=3.4E−03	n=2	fg=0.01 | bg=0.00
disordered domain specific binding GO:0097718	p=3.8E−03	n=4	fg=0.03 | bg=0.01
S100 protein binding GO:0044548	p=9.7E−03	n=2	fg=0.01 | bg=0.00
GTPase activator activity GO:0005096	p=1.0E−02	n=8	fg=0.06 | bg=0.02
oxidized DNA binding GO:0032356	p=1.9E−02	n=2	fg=0.01 | bg=0.00
oxidized purine DNA binding GO:0032357	p=1.9E−02	n=2	fg=0.01 | bg=0.00
hexosaminidase activity GO:0015929	p=1.9E−02	n=2	fg=0.01 | bg=0.00
chromatin DNA binding GO:0031490	p=2.1E−02	n=4	fg=0.03 | bg=0.01
GTPase regulator activity GO:0030695	p=2.1E−02	n=11	fg=0.08 | bg=0.04
phosphotransferase activity, alcohol gro... GO:0016773	p=2.2E−02	n=15	fg=0.11 | bg=0.06
promoter−specific chromatin binding GO:1990841	p=2.3E−02	n=3	fg=0.02 | bg=0.00
protein kinase A binding GO:0051018	p=2.3E−02	n=3	fg=0.02 | bg=0.00
transferase activity, transferring phosp... GO:0016772	p=2.7E−02	n=19	fg=0.14 | bg=0.09
mRNA binding GO:0003729	p=2.8E−02	n=9	fg=0.07 | bg=0.03
phospholipid binding GO:0005543	p=2.9E−02	n=10	fg=0.07 | bg=0.04
14−3−3 protein binding GO:0071889	p=3.0E−02	n=2	fg=0.01 | bg=0.00
protein kinase A regulatory subunit bind... GO:0034237	p=3.0E−02	n=2	fg=0.01 | bg=0.00
protein tyrosine kinase activity GO:0004713	p=3.0E−02	n=4	fg=0.03 | bg=0.01
RNA polymerase II−specific DNA−binding t... GO:0061629	p=3.2E−02	n=7	fg=0.05 | bg=0.02
hormone receptor binding GO:0051427	p=3.6E−02	n=6	fg=0.04 | bg=0.02
structural molecule activity GO:0005198	p=3.6E−02	n=12	fg=0.09 | bg=0.05
small GTPase binding GO:0031267	p=4.1E−02	n=11	fg=0.08 | bg=0.04
kinase activity GO:0016301	p=4.2E−02	n=15	fg=0.11 | bg=0.07
lipid transfer activity GO:0120013	p=4.3E−02	n=2	fg=0.01 | bg=0.00
snRNP binding GO:0070990	p=4.3E−02	n=2	fg=0.01 | bg=0.00
DNA−binding transcription factor binding GO:0140297	p=4.5E−02	n=7	fg=0.05 | bg=0.02
nucleoside−triphosphatase regulator acti... GO:0060589	p=5.2E−02	n=11	fg=0.08 | bg=0.05
metal ion transmembrane transporter acti... GO:0046873	p=5.2E−02	n=9	fg=0.07 | bg=0.04
protein self−association GO:0043621	p=5.3E−02	n=3	fg=0.02 | bg=0.01
protein kinase activity GO:0004672	p=5.3E−02	n=12	fg=0.09 | bg=0.05

0 1 2 3 4 5
−log(p)
n=138/499 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction

GO:CC
Fox_Nvec_vc1.1_XM_001629605.3

fraction genes in fg and expected valu...

collagen and cuticulin−based cuticle ext... GO:0060102	p=3.7E−03	n=2	fg=0.01 | bg=0.00
extrinsic component of cytoplasmic side ... GO:0031234	p=7.3E−03	n=5	fg=0.03 | bg=0.01
COPI vesicle coat GO:0030126	p=1.1E−02	n=2	fg=0.01 | bg=0.00
vesicle membrane GO:0012506	p=1.6E−02	n=19	fg=0.12 | bg=0.07
pseudopodium GO:0031143	p=2.1E−02	n=2	fg=0.01 | bg=0.00
COPI−coated vesicle membrane GO:0030663	p=2.1E−02	n=2	fg=0.01 | bg=0.00
microtubule organizing center GO:0005815	p=2.5E−02	n=18	fg=0.11 | bg=0.07
Golgi−associated vesicle membrane GO:0030660	p=2.5E−02	n=4	fg=0.02 | bg=0.01
cytoplasmic vesicle membrane GO:0030659	p=2.6E−02	n=18	fg=0.11 | bg=0.07
extrinsic component of membrane GO:0019898	p=3.3E−02	n=11	fg=0.07 | bg=0.02
bicellular tight junction GO:0005923	p=3.3E−02	n=3	fg=0.02 | bg=0.00
basolateral plasma membrane GO:0016323	p=3.3E−02	n=8	fg=0.05 | bg=0.02
basal plasma membrane GO:0009925	p=3.3E−02	n=8	fg=0.05 | bg=0.02
mRNA cleavage and polyadenylation specif... GO:0005847	p=3.3E−02	n=2	fg=0.01 | bg=0.00
mRNA cleavage factor complex GO:0005849	p=3.3E−02	n=2	fg=0.01 | bg=0.00
microvillus GO:0005902	p=3.6E−02	n=4	fg=0.02 | bg=0.01
ciliary basal body GO:0036064	p=4.0E−02	n=6	fg=0.04 | bg=0.02
PML body GO:0016605	p=4.1E−02	n=3	fg=0.02 | bg=0.00
rough endoplasmic reticulum GO:0005791	p=4.1E−02	n=4	fg=0.02 | bg=0.01
filopodium membrane GO:0031527	p=4.7E−02	n=2	fg=0.01 | bg=0.00
cell tip GO:0051286	p=4.7E−02	n=2	fg=0.01 | bg=0.00
rough endoplasmic reticulum membrane GO:0030867	p=4.7E−02	n=2	fg=0.01 | bg=0.00
endocytic vesicle GO:0030139	p=4.8E−02	n=7	fg=0.04 | bg=0.02
apical junction complex GO:0043296	p=5.5E−02	n=4	fg=0.02 | bg=0.01
protein kinase CK2 complex GO:0005956	p=6.1E−02	n=1	fg=0.01 | bg=0.00
nuclear pore inner ring GO:0044611	p=6.1E−02	n=1	fg=0.01 | bg=0.00
nuclear pore central transport channel GO:0044613	p=6.1E−02	n=1	fg=0.01 | bg=0.00
anchored component of external side of p... GO:0031362	p=6.1E−02	n=1	fg=0.01 | bg=0.00
microspike GO:0044393	p=6.1E−02	n=1	fg=0.01 | bg=0.00
catenin−TCF7L2 complex GO:0071664	p=6.1E−02	n=1	fg=0.01 | bg=0.00

0 1 2 3 4 5
−log(p)
n=165/499 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
fraction