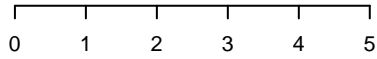


GO:BP  
Fox\_Nvec\_vc1.1\_XM\_048733302.1

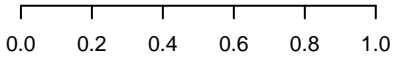
fraction genes in fg and expected value

negative regulation of MAP kinase activi...	GO:0043407	p=7.1E-04	n=6
endoplasmic reticulum organization	GO:0007029	p=9.5E-04	n=6
positive regulation of endocytosis	GO:0045807	p=1.7E-03	n=9
negative regulation of Ras protein signa...	GO:0046580	p=3.0E-03	n=5
positive regulation of hydrolase activit...	GO:0051345	p=3.1E-03	n=17
maintenance of Golgi location	GO:0051684	p=3.4E-03	n=2
terminal cell fate specification, open t...	GO:0035154	p=3.4E-03	n=2
positive regulation of R7 cell different...	GO:0045678	p=3.4E-03	n=2
syncytial blastoderm mitotic cell cycle	GO:0035186	p=3.4E-03	n=3
embryo development ending in birth or eg...	GO:0009792	p=3.6E-03	n=27
positive regulation of macroautophagy	GO:0016239	p=3.8E-03	n=5
calcium ion transmembrane import into cy...	GO:0097553	p=4.7E-03	n=6
positive regulation of purine nucleotide...	GO:1900544	p=5.3E-03	n=4
intestinal stem cell homeostasis	GO:0036335	p=7.1E-03	n=4
regulation of JNK cascade	GO:0046328	p=8.5E-03	n=8
lactate metabolic process	GO:0006089	p=8.9E-03	n=3
positive regulation of TOR signaling	GO:0032008	p=9.3E-03	n=4
secretion by cell	GO:0032940	p=9.5E-03	n=28
lymphocyte aggregation	GO:0071593	p=9.8E-03	n=2
positive regulation of endothelial cell ...	GO:2000353	p=9.8E-03	n=2
post-embryonic body morphogenesis	GO:0040032	p=9.8E-03	n=2
positive regulation of macrophage activa...	GO:0043032	p=9.8E-03	n=2
TORC2 signaling	GO:0038203	p=9.8E-03	n=2
regulation of JUN kinase activity	GO:0043506	p=1.1E-02	n=5
positive regulation of insulin secretion	GO:0032024	p=1.1E-02	n=5
cation transport	GO:0006812	p=1.1E-02	n=25
exocytosis	GO:0006887	p=1.2E-02	n=18
hemopoiesis	GO:0030097	p=1.3E-02	n=18
transferrin transport	GO:0033572	p=1.3E-02	n=3
positive regulation of receptor internal...	GO:0002092	p=1.3E-02	n=3



-log(p)  
n=158/502 input genes with annotations

fg=0.04	bg=0.01
fg=0.04	bg=0.01
fg=0.06	bg=0.02
fg=0.03	bg=0.01
fg=0.11	bg=0.05
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.00
fg=0.17	bg=0.10
fg=0.03	bg=0.01
fg=0.04	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.01
fg=0.05	bg=0.02
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.18	bg=0.11
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.16	bg=0.08
fg=0.11	bg=0.06
fg=0.11	bg=0.07
fg=0.02	bg=0.00
fg=0.02	bg=0.00

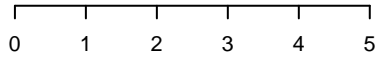


fraction

GO:MF  
Fox\_Nvec\_vc1.1\_XM\_048733302.1

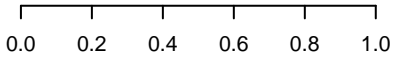
fraction genes in fg and expected value

myosin V binding	GO:0031489	p=3.1E-03	n=2
phosphotyrosine residue binding	GO:0001784	p=7.9E-03	n=3
ATPase-coupled cation transmembrane tran...	GO:0019829	p=8.0E-03	n=4
ATPase-coupled ion transmembrane transpo...	GO:0042625	p=1.0E-02	n=4
P-type ion transporter activity	GO:0015662	p=1.5E-02	n=3
P-type transmembrane transporter activit...	GO:0140358	p=1.5E-02	n=3
metal ion transmembrane transporter acti...	GO:0046873	p=1.7E-02	n=10
nucleotide-sugar transmembrane transport...	GO:0005338	p=1.7E-02	n=2
nitric-oxide synthase regulator activity	GO:0030235	p=1.7E-02	n=2
bHLH transcription factor binding	GO:0043425	p=1.7E-02	n=2
transmembrane transporter activity	GO:0022857	p=1.8E-02	n=21
passive transmembrane transporter activi...	GO:0022803	p=2.0E-02	n=10
channel activity	GO:0015267	p=2.0E-02	n=10
calcium activated cation channel activit...	GO:0005227	p=2.1E-02	n=3
inorganic cation transmembrane transport...	GO:0022890	p=2.1E-02	n=15
calcium ion transmembrane transporter ac...	GO:0015085	p=2.2E-02	n=6
nuclear receptor coactivator activity	GO:0030374	p=2.6E-02	n=3
nucleobase-containing compound transmemb...	GO:0015932	p=2.6E-02	n=3
proton transmembrane transporter activit...	GO:0015078	p=2.7E-02	n=4
P-type calcium transporter activity	GO:0005388	p=2.8E-02	n=2
transporter activity	GO:0005215	p=2.9E-02	n=23
cation transmembrane transporter activit...	GO:0008324	p=3.0E-02	n=15
glutamate receptor binding	GO:0035254	p=3.3E-02	n=3
SNAP receptor activity	GO:0005484	p=3.3E-02	n=3
cation channel activity	GO:0005261	p=3.4E-02	n=8
inorganic anion transmembrane transporte...	GO:0015103	p=3.5E-02	n=5
pyrophosphate hydrolysis-driven proton t...	GO:0009678	p=4.0E-02	n=2
ATPase activity, coupled to transmembran...	GO:0044769	p=4.0E-02	n=2
proton-transporting ATPase activity, rot...	GO:0046961	p=4.0E-02	n=2
bicarbonate transmembrane transporter ac...	GO:0015106	p=4.0E-02	n=2



-log(p)  
n=133/502 input genes with annotations

fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.08	bg=0.04
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.16	bg=0.08
fg=0.08	bg=0.04
fg=0.08	bg=0.04
fg=0.08	bg=0.04
fg=0.02	bg=0.00
fg=0.11	bg=0.05
fg=0.05	bg=0.02
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.17	bg=0.10
fg=0.11	bg=0.05
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.06	bg=0.03
fg=0.04	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00

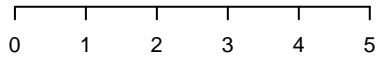


fraction

GO:CC  
Fox\_Nvec\_vc1.1\_XM\_048733302.1

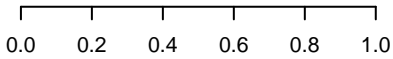
fraction genes in fg and expected value

plasma membrane	GO:0005886	p=1.9E-03	n=53
perinuclear region of cytoplasm	GO:0048471	p=2.2E-03	n=20
cytoplasmic vesicle membrane	GO:0030659	p=2.7E-03	n=22
collagen and cuticulin-based cuticle ext...	GO:0060102	p=3.4E-03	n=2
preribosome, small subunit precursor	GO:0030688	p=5.8E-03	n=3
endolysosome membrane	GO:0036020	p=9.8E-03	n=2
exocytic vesicle	GO:0070382	p=9.9E-03	n=9
synaptonemal structure	GO:009086	p=1.3E-02	n=3
synaptonemal complex	GO:0000795	p=1.3E-02	n=3
endocytic vesicle	GO:0030139	p=1.3E-02	n=8
clathrin-coated vesicle	GO:0030136	p=1.4E-02	n=6
synaptic vesicle	GO:0008021	p=1.5E-02	n=8
secretory granule	GO:0030141	p=1.6E-02	n=15
autophagosome	GO:0005776	p=2.4E-02	n=5
membrane protein complex	GO:0098796	p=2.6E-02	n=19
secretory granule membrane	GO:0030667	p=2.7E-02	n=7
ion channel complex	GO:0034702	p=2.8E-02	n=5
RNA polymerase II, core complex	GO:0005665	p=3.0E-02	n=2
late endosome membrane	GO:0031902	p=3.1E-02	n=4
integral component of synaptic vesicle m...	GO:0030285	p=3.6E-02	n=3
lysosomal membrane	GO:0005765	p=4.3E-02	n=8
vacuolar membrane	GO:0005774	p=4.3E-02	n=10
clathrin-coated endocytic vesicle membra...	GO:0030669	p=4.4E-02	n=2
intrinsic component of synaptic vesicle ...	GO:0098563	p=4.4E-02	n=3
secretory vesicle	GO:0099503	p=4.7E-02	n=21
endocytic vesicle membrane	GO:0030666	p=4.8E-02	n=4
lipid droplet	GO:0005811	p=4.8E-02	n=4
condensed nuclear chromosome	GO:0000794	p=5.5E-02	n=4
tertiary granule	GO:0070820	p=5.5E-02	n=4
nuclear pore central transport channel	GO:0044613	p=5.9E-02	n=1



-log(p)  
n=158/502 input genes with annotations

fg=0.34	bg=0.23
fg=0.13	bg=0.06
fg=0.14	bg=0.07
fg=0.01	bg=0.00
fg=0.02	bg=0.00
fg=0.01	bg=0.00
fg=0.06	bg=0.02
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.05	bg=0.02
fg=0.09	bg=0.05
fg=0.03	bg=0.01
fg=0.12	bg=0.08
fg=0.04	bg=0.02
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.05	bg=0.02
fg=0.06	bg=0.03
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.13	bg=0.07
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.01	bg=0.00



fraction