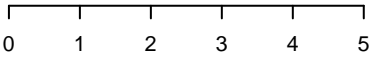


GO:BP  
Fox\_Nvec\_vc1.1\_XM\_048722445.1

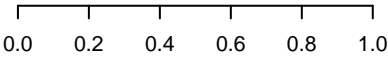
positive regulation of dendrite developm...	GO:1900006	p=9.8E-04	n=3
response to amphetamine	GO:0001975	p=1.4E-03	n=2
positive regulation of wound healing	GO:0090303	p=1.4E-03	n=2
positive regulation of protein localizat...	GO:1903078	p=2.5E-03	n=2
dendrite morphogenesis	GO:0048813	p=2.8E-03	n=4
response to bronchodilator	GO:0097366	p=3.2E-03	n=2
Rab protein signal transduction	GO:0032482	p=3.2E-03	n=2
regulation of ion transmembrane transpor...	GO:0032412	p=4.8E-03	n=3
tetrapyrrole metabolic process	GO:0033013	p=4.9E-03	n=2
positive regulation of dendritic spine d...	GO:0060999	p=4.9E-03	n=2
adenylate cyclase-activating G protein-c...	GO:0007189	p=4.9E-03	n=2
acute inflammatory response	GO:0002526	p=4.9E-03	n=2
positive regulation of signaling	GO:0023056	p=5.4E-03	n=7
positive regulation of cell communicatio...	GO:0010647	p=5.4E-03	n=7
intracellular signal transduction	GO:0035556	p=5.9E-03	n=10
cellular response to hormone stimulus	GO:0032870	p=5.9E-03	n=5
positive regulation of transcription fro...	GO:0036003	p=6.8E-03	n=2
cholesterol homeostasis	GO:0042632	p=6.8E-03	n=2
regulation of calcium ion transport	GO:0051924	p=6.9E-03	n=3
positive regulation of transferase activ...	GO:0051347	p=8.0E-03	n=4
positive regulation of neuron differenti...	GO:0045666	p=8.0E-03	n=4
cellular modified amino acid biosynthesi...	GO:0042398	p=9.1E-03	n=2
cell surface receptor signaling pathway	GO:0007166	p=9.1E-03	n=9
microspike assembly	GO:0030035	p=9.9E-03	n=1
proteasomal ubiquitin-independent protei...	GO:0010499	p=9.9E-03	n=1
positive regulation of cellular response...	GO:1905804	p=9.9E-03	n=1
lens fiber cell apoptotic process	GO:1990086	p=9.9E-03	n=1
progression of morphogenetic furrow invo...	GO:0007458	p=9.9E-03	n=1
protein localization to cleavage furrow	GO:1905345	p=9.9E-03	n=1
negative regulation of pancreatic juice ...	GO:0090188	p=9.9E-03	n=1



-log(p)  
n=18/77 input genes with annotations

fraction genes in fg and expected value

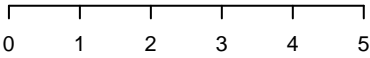
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fraction

GO:MF  
Fox\_Nvec\_vc1.1\_XM\_048722445.1

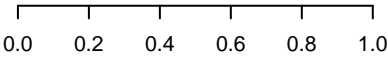
signaling receptor binding	GO:0005102	p=1.3E-03	n=7
transcription coregulator binding	GO:0001221	p=4.1E-03	n=2
calmodulin-dependent protein kinase acti...	GO:0004683	p=5.2E-03	n=2
GTPase activity	GO:0003924	p=6.9E-03	n=3
cobalamin binding	GO:0031419	p=1.1E-02	n=1
alpha-adrenergic receptor activity	GO:0004936	p=1.1E-02	n=1
alpha2-adrenergic receptor activity	GO:0004938	p=1.1E-02	n=1
methylmalonyl-CoA mutase activity	GO:0004494	p=1.1E-02	n=1
CD4 receptor binding	GO:0042609	p=1.1E-02	n=1
GMP binding	GO:0019002	p=1.1E-02	n=1
alpha-2C adrenergic receptor binding	GO:0031696	p=1.1E-02	n=1
actin filament binding	GO:0051015	p=1.2E-02	n=2
transcription regulator activity	GO:0140110	p=1.3E-02	n=6
transcription coregulator activity	GO:0003712	p=1.9E-02	n=4
octopamine receptor activity	GO:0004989	p=2.2E-02	n=1
chloride channel inhibitor activity	GO:0019869	p=2.2E-02	n=1
transcription corepressor binding	GO:0001222	p=2.2E-02	n=1
adrenergic receptor activity	GO:0004935	p=2.2E-02	n=1
norepinephrine binding	GO:0051380	p=2.2E-02	n=1
thioesterase binding	GO:0031996	p=2.2E-02	n=1
alpha-1B adrenergic receptor binding	GO:0031692	p=2.2E-02	n=1
small molecule binding	GO:0036094	p=2.7E-02	n=5
DNA-binding transcription activator acti...	GO:0001228	p=2.9E-02	n=3
DNA-binding transcription activator acti...	GO:0001216	p=2.9E-02	n=3
calcium-dependent protein serine/threoni...	GO:0009931	p=3.4E-02	n=1
D2 dopamine receptor binding	GO:0031749	p=3.4E-02	n=1
calcium-dependent protein kinase activit...	GO:0010857	p=3.4E-02	n=1
phosphorylase kinase activity	GO:0004689	p=3.4E-02	n=1
G protein-coupled neurotransmitter recep...	GO:0099528	p=3.4E-02	n=1
intramolecular transferase activity	GO:0016866	p=3.4E-02	n=1



-log(p)  
n=18/77 input genes with annotations

fraction genes in fg and expected value

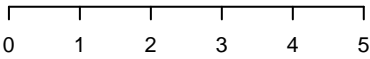
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fraction

GO:CC  
Fox\_Nvec\_vc1.1\_XM\_048722445.1

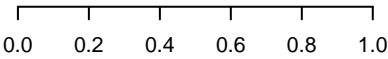
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dendritic spine neck	GO:0044326	p=1.0E-02	n=1
dendritic spine head	GO:0044327	p=1.0E-02	n=1
filopodium	GO:0030175	p=1.0E-02	n=2
ruffle	GO:0001726	p=1.3E-02	n=2
endoplasmic reticulum-Golgi intermediate...	GO:0005793	p=1.6E-02	n=2
phagophore assembly site membrane	GO:0034045	p=2.0E-02	n=1
phosphorylase kinase complex	GO:0005964	p=3.0E-02	n=1
growth cone lamellipodium	GO:1990761	p=3.0E-02	n=1
phagophore assembly site	GO:0000407	p=3.0E-02	n=1
Sin3-type complex	GO:0070822	p=3.0E-02	n=1
intrinsic component of the cytoplasmic s...	GO:0031235	p=3.9E-02	n=1
presynaptic periaxial zone	GO:0036062	p=3.9E-02	n=1
protein phosphatase type 1 complex	GO:0000164	p=4.9E-02	n=1
septin cytoskeleton	GO:0032156	p=4.9E-02	n=1
autolysosome	GO:0044754	p=4.9E-02	n=1
actin-based cell projection	GO:0098858	p=5.1E-02	n=2
intrinsic component of plasma membrane	GO:0031226	p=5.1E-02	n=4
adherens junction	GO:0005912	p=5.8E-02	n=2
growth cone	GO:0030426	p=6.1E-02	n=2
plasma membrane	GO:0005886	p=6.2E-02	n=9
site of polarized growth	GO:0030427	p=6.6E-02	n=2
cell junction	GO:0030054	p=6.6E-02	n=6
apicolateral plasma membrane	GO:0016327	p=6.8E-02	n=1
polytene chromosome puff	GO:0005703	p=6.8E-02	n=1
secondary lysosome	GO:0005767	p=6.8E-02	n=1
apical dendrite	GO:0097440	p=6.8E-02	n=1
presynapse	GO:0098793	p=7.1E-02	n=3
plasma membrane region	GO:0098590	p=7.4E-02	n=5
azurophil granule membrane	GO:0035577	p=7.7E-02	n=1



-log(p)  
n=18/77 input genes with annotations

fraction genes in fg and expected value

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fraction