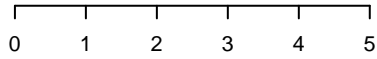


GO:BP  
Fox\_Nvec\_vc1.1\_XM\_032366627.2

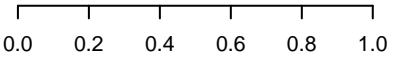
glutamate secretion	GO:0014047	p=3.9E−03	n=4
regulation of primitive erythrocyte diff...	GO:0010725	p=4.2E−03	n=2
positive regulation of cytolysis	GO:0045919	p=4.2E−03	n=2
GPI anchor release	GO:0006507	p=4.2E−03	n=2
positive regulation of megakaryocyte dif...	GO:0045654	p=4.2E−03	n=2
regulation of stem cell differentiation	GO:2000736	p=4.3E−03	n=6
positive regulation of nucleobase−contai...	GO:0032241	p=4.6E−03	n=3
regulation of membrane invagination	GO:1905153	p=5.6E−03	n=4
regulation of epithelial cell migration	GO:0010632	p=6.3E−03	n=8
regulation of extrinsic apoptotic signal...	GO:2001239	p=7.7E−03	n=4
negative regulation of neurotransmitter ...	GO:0046929	p=7.7E−03	n=3
zymogen activation	GO:0031638	p=7.7E−03	n=3
positive regulation of lipid metabolic p...	GO:0045834	p=8.3E−03	n=7
positive regulation of ion transmembrane...	GO:0034767	p=9.2E−03	n=6
protein deacylation	GO:0035601	p=9.4E−03	n=5
negative regulation of epithelial cell p...	GO:0050680	p=9.4E−03	n=5
cell fate determination	GO:0001709	p=1.1E−02	n=7
blood vessel endothelial cell migration	GO:0043534	p=1.1E−02	n=5
regulation of Rac protein signal transdu...	GO:0035020	p=1.2E−02	n=3
tube development	GO:0035295	p=1.2E−02	n=31
negative regulation of synaptic vesicle ...	GO:2000301	p=1.2E−02	n=2
mitochondrial unfolded protein response	GO:0034514	p=1.2E−02	n=2
activation of cysteine−type endopeptidas...	GO:0097202	p=1.2E−02	n=2
asparagine metabolic process	GO:0006528	p=1.2E−02	n=2
positive regulation of potassium ion tra...	GO:0043268	p=1.3E−02	n=4
myoblast fusion	GO:0007520	p=1.3E−02	n=4
histone deacetylation	GO:0016575	p=1.3E−02	n=4
embryo development ending in birth or eg...	GO:0009792	p=1.5E−02	n=27
protein deacetylation	GO:0006476	p=1.7E−02	n=4
imaginal disc−derived wing hair organiza...	GO:0035317	p=1.7E−02	n=4



−log(p)  
n=175/638 input genes with annotations

fraction genes in fg and expected value

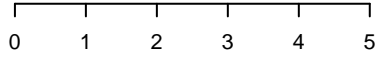
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fraction

GO:MF  
Fox\_Nvec\_vc1.1\_XM\_032366627.2

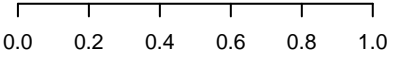
histone deacetylase activity	GO:0004407	p=2.8E−03	n=4
lipase activity	GO:0016298	p=3.7E−03	n=6
caspase binding	GO:0089720	p=1.2E−02	n=2
calcium−dependent cysteine−type endopept...	GO:0004198	p=2.4E−02	n=2
phospholipase C activity	GO:0004629	p=2.4E−02	n=2
bHLH transcription factor binding	GO:0043425	p=2.4E−02	n=2
solute:sodium symporter activity	GO:0015370	p=3.1E−02	n=3
AP−2 adaptor complex binding	GO:0035612	p=3.8E−02	n=2
histone H3−methyl−lysine−4 demethylase a...	GO:0032453	p=3.8E−02	n=2
phosphatidylinositol−5−phosphate binding	GO:0010314	p=3.8E−02	n=2
phospholipase activity	GO:0004620	p=3.8E−02	n=4
telomeric DNA binding	GO:0042162	p=4.0E−02	n=3
demethylase activity	GO:0032451	p=4.0E−02	n=3
cysteine−type endopeptidase activity	GO:0004197	p=6.0E−02	n=3
cytokine receptor binding	GO:0005126	p=6.0E−02	n=4
sodium ion transmembrane transporter act...	GO:0015081	p=6.0E−02	n=4
phospholipid binding	GO:0005543	p=6.0E−02	n=10
catalytic activity, acting on RNA	GO:0140098	p=6.1E−02	n=11
sodium:dicarboxylate symporter activity	GO:0017153	p=6.6E−02	n=1
CCR5 chemokine receptor binding	GO:0031730	p=6.6E−02	n=1
ribonuclease III activity	GO:0004525	p=6.6E−02	n=1
histone kinase activity (H3−T11 specific...	GO:0035402	p=6.6E−02	n=1
CCR chemokine receptor binding	GO:0048020	p=6.6E−02	n=1
glutamate:sodium symporter activity	GO:0015501	p=6.6E−02	n=1
open rectifier potassium channel activit...	GO:0005252	p=6.6E−02	n=1
oxidative DNA demethylase activity	GO:0035516	p=6.6E−02	n=1
amino acid:sodium symporter activity	GO:0005283	p=6.6E−02	n=1
purine−specific nucleoside:sodium sympor...	GO:0015390	p=6.6E−02	n=1
nucleobase:cation symporter activity	GO:0015391	p=6.6E−02	n=1
non−sequence−specific DNA binding, bendi...	GO:0044378	p=6.6E−02	n=1



−log(p)  
n=156/638 input genes with annotations

fraction genes in fg and expected value

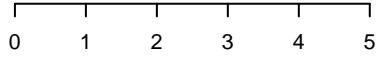
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fraction

GO:CC  
Fox\_Nvec\_vc1.1\_XM\_032366627.2

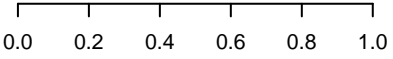
nuclear speck	GO:0016607	p=2.2E−02	n=11
phagocytic cup	GO:0001891	p=3.9E−02	n=2
microvillus	GO:0005902	p=4.7E−02	n=4
endonuclease complex	GO:1905348	p=5.5E−02	n=2
endoribonuclease complex	GO:1902555	p=5.5E−02	n=2
fibrillar center	GO:0001650	p=6.5E−02	n=5
presynaptic membrane	GO:0042734	p=6.5E−02	n=5
protein farnesyltransferase complex	GO:0005965	p=6.7E−02	n=1
ciliary cap	GO:0061822	p=6.7E−02	n=1
nuclear pore cytoplasmic filaments	GO:0044614	p=6.7E−02	n=1
cytoplasmic periphery of the nuclear por...	GO:1990723	p=6.7E−02	n=1
tRNA−intron endonuclease complex	GO:0000214	p=6.7E−02	n=1
nuclear RNA−directed RNA polymerase comp...	GO:0031380	p=6.7E−02	n=1
microvesicle	GO:1990742	p=6.7E−02	n=1
RNA−directed RNA polymerase complex	GO:0031379	p=6.7E−02	n=1
pinosome	GO:0044352	p=6.7E−02	n=1
macropinosome	GO:0044354	p=6.7E−02	n=1
tubular endosome	GO:0097422	p=6.7E−02	n=1
ribonuclease III complex	GO:1903095	p=6.7E−02	n=1
sperm individualization complex	GO:0070864	p=6.7E−02	n=1
investment cone	GO:0070865	p=6.7E−02	n=1
mRNA cap methyltransferase complex	GO:0031533	p=6.7E−02	n=1
hippocampal mossy fiber expansion	GO:1990026	p=6.7E−02	n=1
microprocessor complex	GO:0070877	p=6.7E−02	n=1
macropinocytic cup	GO:0070685	p=6.7E−02	n=1
micropyle	GO:0070825	p=6.7E−02	n=1
egg chorion	GO:0042600	p=6.7E−02	n=1
dense core granule membrane	GO:0032127	p=6.7E−02	n=1
dendritic microtubule	GO:1901588	p=6.7E−02	n=1
ESCRT−0 complex	GO:0033565	p=6.7E−02	n=1



−log(p)  
n=180/638 input genes with annotations

fraction genes in fg and expected value

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fraction