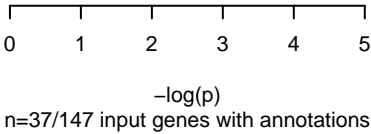


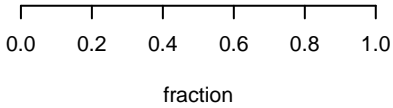
GO:BP  
Fox\_Nvec\_vc1.1\_XM\_001628279.3

fraction genes in fg and expected value

regulation of skeletal muscle tissue dev...	GO:0048641	p=1.2E-03	n=3
phospholipid transport	GO:0015914	p=2.4E-03	n=3
organic anion transport	GO:0015711	p=3.2E-03	n=6
intestinal absorption	GO:0050892	p=3.9E-03	n=2
regulation of T cell differentiation in ...	GO:0033081	p=3.9E-03	n=2
endocrine pancreas development	GO:0031018	p=5.8E-03	n=2
response to xenobiotic stimulus	GO:0009410	p=8.0E-03	n=5
cellular response to parathyroid hormone...	GO:0071374	p=8.0E-03	n=2
cellular response to glucagon stimulus	GO:0071377	p=8.0E-03	n=2
cellular response to fluid shear stress	GO:0071498	p=8.0E-03	n=2
positive regulation of canonical Wnt sig...	GO:0090263	p=8.1E-03	n=3
protein acetylation	GO:0006473	p=8.7E-03	n=4
regulation of striated muscle tissue dev...	GO:0016202	p=1.0E-02	n=3
imaginal disc growth	GO:0007446	p=1.1E-02	n=2
regulation of muscle organ development	GO:0048634	p=1.2E-02	n=3
learning or memory	GO:0007611	p=1.2E-02	n=6
phospholipid translocation	GO:0045332	p=1.3E-02	n=2
lipid translocation	GO:0034204	p=1.3E-02	n=2
detection of light stimulus	GO:0009583	p=1.6E-02	n=3
negative regulation of protein ubiquitin...	GO:0031397	p=1.6E-02	n=2
positive regulation of protein acetylati...	GO:1901985	p=1.6E-02	n=2
regulation of membrane lipid distributio...	GO:0097035	p=1.6E-02	n=2
cognition	GO:0050890	p=1.8E-02	n=6
plasma membrane bounded cell projection ...	GO:0120036	p=2.0E-02	n=12
follic acid transport	GO:0015884	p=2.0E-02	n=1
negative regulation of miRNA transcripti...	GO:1902894	p=2.0E-02	n=1
regulation of histone H2A K63-linked ubi...	GO:1901314	p=2.0E-02	n=1
negative regulation of histone H2A K63-l...	GO:1901315	p=2.0E-02	n=1
microspike assembly	GO:0030035	p=2.0E-02	n=1
neurofilament cytoskeleton organization	GO:0060052	p=2.0E-02	n=1



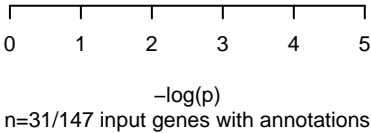
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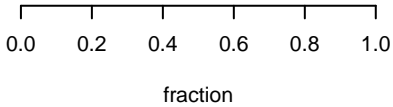
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Fox\_Nvec\_vc1.1\_XM\_001628279.3

fraction genes in fg and expected value

phospholipid transporter activity	GO:0005548	p=1.7E-03	n=3
magnesium ion binding	GO:0000287	p=4.0E-03	n=4
protein kinase binding	GO:0019901	p=6.6E-03	n=7
mevalonate kinase activity	GO:0004496	p=1.9E-02	n=1
phosphatidylcholine transporter activity	GO:0008525	p=1.9E-02	n=1
growth hormone-releasing hormone recepto...	GO:0016520	p=1.9E-02	n=1
follic acid transmembrane transporter act...	GO:0008517	p=1.9E-02	n=1
methotrexate transmembrane transporter a...	GO:0015350	p=1.9E-02	n=1
xenobiotic transmembrane transporter act...	GO:0042910	p=1.9E-02	n=1
pantetheine hydrolase activity	GO:0017159	p=1.9E-02	n=1
ATPase-coupled cation transmembrane tran...	GO:0019829	p=2.1E-02	n=2
receptor tyrosine kinase binding	GO:0030971	p=2.1E-02	n=2
ATPase-coupled ion transmembrane transpo...	GO:0042625	p=2.5E-02	n=2
protein tyrosine kinase binding	GO:1990782	p=2.9E-02	n=2
carbohydrate derivative binding	GO:0097367	p=3.2E-02	n=6
anion binding	GO:0043168	p=3.3E-02	n=8
hydrolase activity, acting on carbon-nit...	GO:0016811	p=3.7E-02	n=2
1-acylglycerophosphocholine O-acyltransf...	GO:0047184	p=3.9E-02	n=1
transcription corepressor binding	GO:0001222	p=3.9E-02	n=1
phosphatidylinositol transfer activity	GO:0008526	p=3.9E-02	n=1
GPI anchor binding	GO:0034235	p=3.9E-02	n=1
protein kinase A catalytic subunit bindi...	GO:0034236	p=3.9E-02	n=1
beta-2 adrenergic receptor binding	GO:0031698	p=3.9E-02	n=1
CoA-ligase activity	GO:0016405	p=3.9E-02	n=1
2-acylglycerol-3-phosphate O-acyltransfe...	GO:0047144	p=3.9E-02	n=1
cAMP-dependent protein kinase regulator ...	GO:0008603	p=3.9E-02	n=1
cAMP-dependent protein kinase inhibitor ...	GO:0004862	p=3.9E-02	n=1
1-alkylglycerophosphocholine O-acetyltra...	GO:0047192	p=3.9E-02	n=1
phosphatidic acid transfer activity	GO:1990050	p=3.9E-02	n=1
O-acetyltransferase activity	GO:0016413	p=3.9E-02	n=1



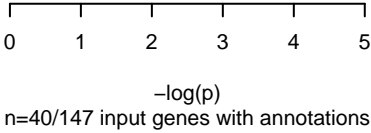
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GO:CC  
Fox\_Nvec\_vc1.1\_XM\_001628279.3

fraction genes in fg and expected value

fungal-type vacuole membrane	GO:0000329	p=2.8E-03	n=2
azurophil granule membrane	GO:0035577	p=1.2E-02	n=2
plus-end kinesin complex	GO:0005873	p=2.2E-02	n=1
RNA polymerase II transcription represso...	GO:0090571	p=2.2E-02	n=1
cell hair	GO:0070451	p=4.4E-02	n=1
cytoskeleton	GO:0005856	p=4.6E-02	n=10
secretory granule membrane	GO:0030667	p=5.0E-02	n=3
nucleotide-activated protein kinase comp...	GO:0031588	p=6.5E-02	n=1
subrhabdomeral cisterna	GO:0016029	p=6.5E-02	n=1
endoplasmic reticulum cisternal network	GO:0071781	p=6.5E-02	n=1
cAMP-dependent protein kinase complex	GO:0005952	p=6.5E-02	n=1
smooth endoplasmic reticulum cisterna	GO:0120082	p=6.5E-02	n=1
mitochondria-associated endoplasmic reti...	GO:0044233	p=6.5E-02	n=1
cell body	GO:0044297	p=7.7E-02	n=6
germinal vesicle	GO:0042585	p=8.6E-02	n=1
chromatoid body	GO:0033391	p=8.6E-02	n=1
cell tip	GO:0051286	p=8.6E-02	n=1
intrinsic component of the cytoplasmic s...	GO:0031235	p=8.6E-02	n=1
endoplasmic reticulum subcompartment	GO:0098827	p=9.3E-02	n=6
azurophil granule	GO:0042582	p=9.7E-02	n=2
primary lysosome	GO:0005766	p=9.7E-02	n=2
female germ cell nucleus	GO:0001674	p=1.1E-01	n=1
septin cytoskeleton	GO:0032156	p=1.1E-01	n=1
cell pole	GO:0060187	p=1.1E-01	n=1
microtubule organizing center	GO:0005815	p=1.2E-01	n=5
actin cytoskeleton	GO:0015629	p=1.2E-01	n=3
tertiary granule membrane	GO:0070821	p=1.3E-01	n=1
organelle membrane contact site	GO:0044232	p=1.3E-01	n=1
centrosome	GO:0005813	p=1.4E-01	n=4
plasma membrane bounded cell projection	GO:0120025	p=1.4E-01	n=11



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