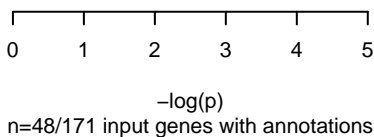


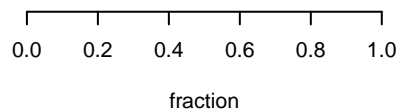
GO:BP
Fox_Nvec_vc1.1_XM_048733302.1

fraction genes in fg and expected value

positive regulation of endothelial cell ...	GO:2000353	p=6.9E-04	n=2
embryo development ending in birth or eg...	GO:0009792	p=1.0E-03	n=13
cellular response to glucocorticoid stim...	GO:0071385	p=1.8E-03	n=3
positive regulation of TOR signaling	GO:0032008	p=1.8E-03	n=3
neuroepithelial cell differentiation	GO:0060563	p=1.9E-03	n=4
tube development	GO:0035295	p=2.0E-03	n=14
cerebellar granular layer development	GO:0021681	p=2.0E-03	n=2
anatomical structure morphogenesis	GO:0009653	p=2.7E-03	n=24
R7 cell differentiation	GO:0045466	p=3.2E-03	n=3
aging	GO:0007568	p=3.5E-03	n=9
hematopoietic stem cell differentiation	GO:0060218	p=4.1E-03	n=3
cAMP-mediated signaling	GO:0019933	p=4.8E-03	n=4
positive regulation of gene expression	GO:0010628	p=5.7E-03	n=15
response to platelet aggregation inhibit...	GO:0061478	p=6.5E-03	n=2
cellular response to misfolded protein	GO:0071218	p=6.5E-03	n=2
protein quality control for misfolded or...	GO:0006515	p=6.5E-03	n=2
T cell differentiation	GO:0030217	p=9.0E-03	n=4
positive regulation of defense response	GO:0031349	p=9.0E-03	n=4
regulation of stem cell differentiation	GO:2000736	p=9.1E-03	n=3
release of sequestered calcium ion into ...	GO:0051209	p=9.1E-03	n=3
cellular response to pH	GO:0071467	p=9.6E-03	n=2
positive regulation of growth rate	GO:0040010	p=9.6E-03	n=2
nematode larval development	GO:0002119	p=9.7E-03	n=6
post-embryonic animal organ development	GO:0048569	p=1.0E-02	n=8
circulatory system development	GO:0072359	p=1.1E-02	n=9
heart morphogenesis	GO:0003007	p=1.1E-02	n=5
positive regulation of cellular componen...	GO:0051130	p=1.2E-02	n=12
neutral lipid biosynthetic process	GO:0046460	p=1.3E-02	n=2
acylglycerol biosynthetic process	GO:0046463	p=1.3E-02	n=2
regulation of R7 cell differentiation	GO:0045676	p=1.3E-02	n=2



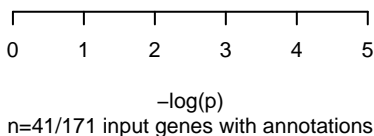
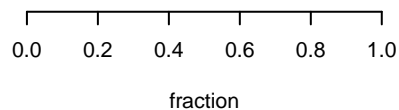
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GO:MF
Fox_Nvec_vc1.1_XM_048733302.1

fraction genes in fg and expected value

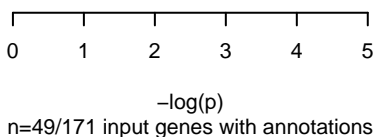
glutamate receptor binding	GO:0035254	p=2.3E-03	n=3
calcium-release channel activity	GO:0015278	p=6.2E-03	n=2
phosphotyrosine residue binding	GO:0001784	p=1.6E-02	n=2
P-type transmembrane transporter activit...	GO:0140358	p=1.6E-02	n=2
P-type ion transporter activity	GO:0015662	p=1.6E-02	n=2
E-box binding	GO:0070888	p=2.1E-02	n=2
protein phosphorylated amino acid bindin...	GO:0045309	p=2.6E-02	n=2
deubiquitinase activator activity	GO:0035800	p=2.6E-02	n=1
CXCR chemokine receptor binding	GO:0045236	p=2.6E-02	n=1
transmembrane receptor protein phosphata...	GO:0019198	p=2.6E-02	n=1
neurotrophin TRK receptor binding	GO:0005167	p=2.6E-02	n=1
neurotrophin TRKA receptor binding	GO:0005168	p=2.6E-02	n=1
transmembrane receptor protein tyrosine ...	GO:0005001	p=2.6E-02	n=1
phosphatidylinositol phospholipase C act...	GO:0004435	p=2.6E-02	n=1
intracellular sodium activated potassium...	GO:0005228	p=2.6E-02	n=1
intracellular phosphatidylinositol-3,5-b...	GO:0097682	p=2.6E-02	n=1
short-branched-chain-acyl-CoA dehydrogen...	GO:0016937	p=2.6E-02	n=1
protein heterodimerization activity	GO:0046982	p=2.8E-02	n=6
ATPase-coupled cation transmembrane tran...	GO:0019829	p=3.6E-02	n=2
ATPase-coupled ion transmembrane transpo...	GO:0042625	p=4.2E-02	n=2
kinesin binding	GO:0019894	p=4.8E-02	n=2
RNA polymerase II transcription regulato...	GO:0000977	p=4.9E-02	n=5
nuclear vitamin D receptor binding	GO:0042809	p=5.1E-02	n=1
peroxisome proliferator activated recept...	GO:0042975	p=5.1E-02	n=1
phosphatidylinositol-3,5-bisphosphate bi...	GO:0080025	p=5.1E-02	n=1
chemokine receptor binding	GO:0042379	p=5.1E-02	n=1
vitamin E binding	GO:0008431	p=5.1E-02	n=1
nitric-oxide synthase regulator activity	GO:0030235	p=5.1E-02	n=1
DNA ligase (ATP) activity	GO:0003910	p=5.1E-02	n=1
P-type proton-exporting transporter acti...	GO:0008553	p=5.1E-02	n=1

[illegible]

GO:CC
Fox_Nvec_vc1.1_XM_048733302.1

fraction genes in fg and expected value

transcription regulator complex	GO:0005667	p=8.2E-04	n=8
endolysosome membrane	GO:0036020	p=2.1E-03	n=2
extrinsic component of organelle membran...	GO:0031312	p=2.3E-02	n=2
mediator complex	GO:0016592	p=2.3E-02	n=2
apical cytoplasm	GO:0090651	p=2.7E-02	n=1
collagen and cuticulin-based cuticle ext...	GO:0060102	p=2.7E-02	n=1
SMN-Gemin2 complex	GO:0034718	p=2.7E-02	n=1
SMN-Sm protein complex	GO:0034719	p=2.7E-02	n=1
SMN complex	GO:0032797	p=2.7E-02	n=1
integral component of lysosomal membrane	GO:1905103	p=2.7E-02	n=1
Smd-containing SMN-Sm protein complex	GO:0034730	p=2.7E-02	n=1
cytoplasmic U snRNP body	GO:0071254	p=2.7E-02	n=1
TSC1-TSC2 complex	GO:0033596	p=2.7E-02	n=1
actin cortical patch	GO:0030479	p=2.7E-02	n=1
Gemini of coiled bodies	GO:0097504	p=2.7E-02	n=1
endocytic patch	GO:0061645	p=2.7E-02	n=1
PR-DUB complex	GO:0035517	p=2.7E-02	n=1
DNA ligase III-XRCC1 complex	GO:0070421	p=2.7E-02	n=1
nuclear protein-containing complex	GO:0140513	p=3.3E-02	n=10
integral component of synaptic vesicle m...	GO:0030285	p=3.4E-02	n=2
synaptic vesicle	GO:0008021	p=3.9E-02	n=4
intrinsic component of synaptic vesicle ...	GO:0098563	p=4.0E-02	n=2
nucleoplasm	GO:0005654	p=5.0E-02	n=19
peribosome, small subunit precursor	GO:0030688	p=5.3E-02	n=1
integral component of vacuolar membrane	GO:0031166	p=5.3E-02	n=1
NELF complex	GO:0032021	p=5.3E-02	n=1
intrinsic component of vacuolar membrane	GO:0031310	p=5.3E-02	n=1
extrinsic component of endoplasmic retic...	GO:0042406	p=5.3E-02	n=1
COP9 signalosome	GO:0008180	p=5.3E-02	n=1
cytosolic aryl hydrocarbon receptor comp...	GO:0034752	p=5.3E-02	n=1

[illegible]