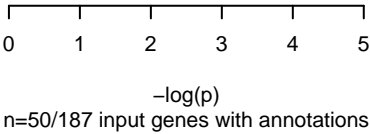


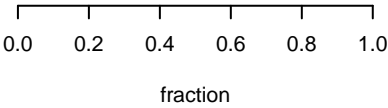
GO:BP
Fox_Nvec_vc1.1_XM_032365977.2

fraction genes in fg and expected value

positive regulation of cholesterol efflu...	GO:0010875	p=7.4E-04	n=2
regulation of cardioblast differentiatio...	GO:0051890	p=7.4E-04	n=2
right ventricular cardiac muscle tissue ...	GO:0003221	p=7.4E-04	n=2
ventricular trabecula myocardium morphog...	GO:0003222	p=7.4E-04	n=2
positive regulation of cholesterol biosy...	GO:0045542	p=2.2E-03	n=2
proximal/distal axis specification	GO:0009946	p=2.2E-03	n=2
negative regulation of synaptic vesicle ...	GO:2000301	p=2.2E-03	n=2
positive regulation of peroxisome prolif...	GO:0035360	p=2.2E-03	n=2
adult heart development	GO:0007512	p=2.2E-03	n=2
transcription by RNA polymerase III	GO:0006383	p=2.2E-03	n=2
cardiac myofibril assembly	GO:0055003	p=2.2E-03	n=2
positive regulation of cholesterol trans...	GO:0032376	p=2.2E-03	n=2
DNA duplex unwinding	GO:0032508	p=3.6E-03	n=3
neuroblast migration	GO:0097402	p=4.3E-03	n=2
negative regulation of synaptic vesicle ...	GO:1902804	p=4.3E-03	n=2
regulation of Rac protein signal transdu...	GO:0035020	p=4.3E-03	n=2
response to bacterium	GO:0009617	p=4.3E-03	n=7
negative regulation of Wnt signaling pat...	GO:0030178	p=5.6E-03	n=4
bicarbonate transport	GO:0015701	p=7.1E-03	n=2
behavior	GO:0007610	p=7.5E-03	n=14
negative regulation of calcium ion-depen...	GO:0045955	p=1.0E-02	n=2
response to amphetamine	GO:0001975	p=1.0E-02	n=2
sarcomere organization	GO:0045214	p=1.0E-02	n=2
regulation of defense response to bacter...	GO:1900424	p=1.0E-02	n=2
negative regulation of peptidyl-serine p...	GO:0033137	p=1.4E-02	n=2
response to amine	GO:0014075	p=1.4E-02	n=2
positive regulation of fibroblast prolif...	GO:0048146	p=1.4E-02	n=2
negative regulation of intracellular tra...	GO:0032387	p=1.6E-02	n=3
memory	GO:0007613	p=1.8E-02	n=5
regulation of neuronal synaptic plastici...	GO:0048168	p=1.9E-02	n=2



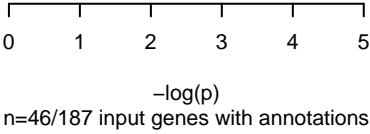
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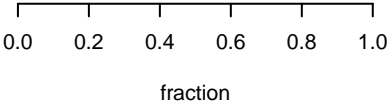
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Fox_Nvec_vc1.1_XM_032365977.2

fraction genes in fg and expected value

annealing activity	GO:0140666	p=8.2E-04	n=2
histone deacetylase binding	GO:0042826	p=1.4E-03	n=4
DNA helicase activity	GO:0003678	p=3.2E-03	n=3
hydrolase activity	GO:0016787	p=4.6E-03	n=17
RNA polymerase II cis-regulatory region ...	GO:0000978	p=5.0E-03	n=6
DNA-binding transcription activator acti...	GO:0001228	p=7.0E-03	n=6
phospholipid binding	GO:0005543	p=1.0E-02	n=6
beta-catenin binding	GO:0008013	p=1.1E-02	n=2
protein heterodimerization activity	GO:0046982	p=1.4E-02	n=7
nucleoside-triphosphatase activity	GO:0017111	p=1.6E-02	n=8
RNA polymerase II transcription regulato...	GO:0000977	p=1.8E-02	n=9
hydrolase activity, acting on acid anhyd...	GO:0016817	p=1.8E-02	n=8
hydrolase activity, acting on acid anhyd...	GO:0016818	p=1.8E-02	n=8
pyrophosphatase activity	GO:0016462	p=1.8E-02	n=8
ATP hydrolysis activity	GO:0016887	p=1.9E-02	n=6
methylation-dependent protein binding	GO:0140034	p=2.0E-02	n=2
methylated histone binding	GO:0035064	p=2.0E-02	n=2
ATPase-coupled transmembrane transporter...	GO:0042626	p=2.4E-02	n=3
exopeptidase activity	GO:0008238	p=2.6E-02	n=2
active transmembrane transporter activit...	GO:0022804	p=2.7E-02	n=5
DNA/DNA annealing activity	GO:1990814	p=2.9E-02	n=1
RNA strand-exchange activity	GO:0034057	p=2.9E-02	n=1
myosin VI binding	GO:0070853	p=2.9E-02	n=1
myosin VI heavy chain binding	GO:0070854	p=2.9E-02	n=1
ATPase-coupled inorganic anion transmemb...	GO:0043225	p=2.9E-02	n=1
protein N-acetylglucosaminyltransferase ...	GO:0016262	p=2.9E-02	n=1
serum response element binding	GO:0010736	p=2.9E-02	n=1
ABC-type sterol transporter activity	GO:0034041	p=2.9E-02	n=1
nickel cation binding	GO:0016151	p=2.9E-02	n=1
metalloaminopeptidase activity	GO:0070006	p=2.9E-02	n=1



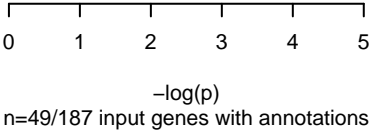
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GO:CC
Fox_Nvec_vc1.1_XM_032365977.2

fraction genes in fg and expected value

integral component of synaptic vesicle m...	GO:0030285	p=2.6E-03	n=3
presynaptic active zone membrane	GO:0048787	p=6.8E-03	n=2
apical dendrite	GO:0097440	p=1.4E-02	n=2
apicolateral plasma membrane	GO:0016327	p=1.4E-02	n=2
exocytic vesicle membrane	GO:0099501	p=2.1E-02	n=5
dense core granule	GO:0031045	p=2.7E-02	n=1
CA3 pyramidal cell dendrite	GO:0097442	p=2.7E-02	n=1
RNA polymerase III transcription regulat...	GO:0090576	p=2.7E-02	n=1
CHOP-C/EBP complex	GO:0036488	p=2.7E-02	n=1
dense core granule membrane	GO:0032127	p=2.7E-02	n=1
SMC loading complex	GO:0032116	p=2.7E-02	n=1
transcription factor TFIIIC complex	GO:0000127	p=2.7E-02	n=1
microvesicle	GO:1990742	p=2.7E-02	n=1
ESCRT-0 complex	GO:0033565	p=2.7E-02	n=1
dendritic microtubule	GO:1901588	p=2.7E-02	n=1
Scc2-Scc4 cohesin loading complex	GO:0090694	p=2.7E-02	n=1
eukaryotic translation initiation factor...	GO:0016281	p=2.7E-02	n=1
bleb	GO:0032059	p=2.7E-02	n=1
chromosome	GO:0005694	p=3.4E-02	n=8
endocytic vesicle	GO:0030139	p=3.6E-02	n=4
intrinsic component of plasma membrane	GO:0031226	p=3.9E-02	n=8
chromosomal region	GO:0098687	p=4.1E-02	n=4
brush border membrane	GO:0031526	p=4.6E-02	n=2
condensed chromosome	GO:0000793	p=4.9E-02	n=3
neuronal cell body	GO:0043025	p=5.1E-02	n=7
preribosome, small subunit precursor	GO:0030688	p=5.3E-02	n=1
striated muscle thin filament	GO:0005865	p=5.3E-02	n=1
myofilament	GO:0036379	p=5.3E-02	n=1
early phagosome	GO:0032009	p=5.3E-02	n=1
transcription regulator complex	GO:0005667	p=5.4E-02	n=5



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