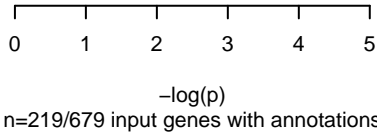


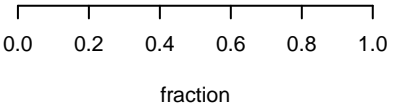
GO:BP  
Fox\_Nvec\_vc1.1\_XM\_032372114.2

negative regulation of smoothened signal...	GO:1901621	p=2.0E-03	n=3
negative regulation of embryonic develop...	GO:0045992	p=3.7E-03	n=5
organic substance catabolic process	GO:1901575	p=4.4E-03	n=56
protein targeting to membrane	GO:0006612	p=5.7E-03	n=10
amide transport	GO:0042886	p=5.8E-03	n=48
cellular catabolic process	GO:0044248	p=6.3E-03	n=59
nuclear export	GO:0051168	p=6.5E-03	n=12
photoreactive repair	GO:0000719	p=6.6E-03	n=5
nephric duct formation	GO:0072179	p=6.6E-03	n=2
negative regulation of viral transcripti...	GO:0032897	p=6.6E-03	n=2
phosphatidylcholine catabolic process	GO:0034638	p=6.6E-03	n=2
negative regulation of fat cell prolifer...	GO:0070345	p=6.6E-03	n=2
organelle disassembly	GO:1903008	p=7.0E-03	n=7
regulation of organelle assembly	GO:1902115	p=8.6E-03	n=11
peptide transport	GO:0015833	p=1.1E-02	n=46
protein K48-linked ubiquitination	GO:0070936	p=1.2E-02	n=5
secretory granule organization	GO:0033363	p=1.2E-02	n=4
protein K11-linked ubiquitination	GO:0070979	p=1.2E-02	n=4
leukocyte migration	GO:0050900	p=1.3E-02	n=8
microtubule cytoskeleton organization in...	GO:1902850	p=1.4E-02	n=11
centrosome separation	GO:0051299	p=1.7E-02	n=4
cellular macromolecule localization	GO:0070727	p=1.7E-02	n=55
cellular protein localization	GO:0034613	p=1.7E-02	n=54
small molecule catabolic process	GO:0044282	p=1.8E-02	n=14
neuron remodeling	GO:0016322	p=1.8E-02	n=6
neuron maturation	GO:0042551	p=1.8E-02	n=6
type 2 immune response	GO:0042092	p=1.9E-02	n=2
regulation of nephron tubule epithelial ...	GO:0072182	p=1.9E-02	n=2
negative regulation of interleukin-2 pro...	GO:0032703	p=1.9E-02	n=2
regulation of type 2 immune response	GO:0002828	p=1.9E-02	n=2



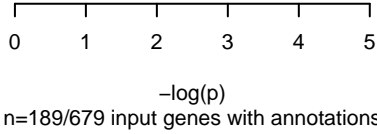
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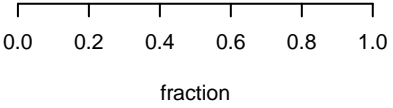
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Fox\_Nvec\_vc1.1\_XM\_032372114.2

GTPase activity	GO:0003924	p=3.7E-03	n=10
steroid dehydrogenase activity	GO:0016229	p=6.3E-03	n=2
calcium-independent phospholipase A2 act...	GO:0047499	p=6.3E-03	n=2
lipid phosphatase activity	GO:0042577	p=6.3E-03	n=2
ubiquitin-like protein binding	GO:0032182	p=7.6E-03	n=6
protein-macromolecule adaptor activity	GO:0030674	p=8.5E-03	n=11
GTPase binding	GO:0051020	p=1.2E-02	n=18
deoxyribodipyrimidine photo-lyase activi...	GO:0003904	p=1.8E-02	n=2
DNA photolyase activity	GO:0003913	p=1.8E-02	n=2
small GTPase binding	GO:0031267	p=1.9E-02	n=15
C2H2 zinc finger domain binding	GO:0070742	p=3.4E-02	n=2
4 iron, 4 sulfur cluster binding	GO:0051539	p=3.4E-02	n=2
poly-pyrimidine tract binding	GO:0008187	p=3.9E-02	n=3
GTPase activating protein binding	GO:0032794	p=3.9E-02	n=3
ubiquitin binding	GO:0043130	p=5.0E-02	n=4
general transcription initiation factor ...	GO:0140296	p=5.0E-02	n=4
JUN kinase binding	GO:0008432	p=5.4E-02	n=2
G-protein beta/gamma-subunit complex bin...	GO:0031683	p=5.4E-02	n=2
protein kinase A regulatory subunit bind...	GO:0034237	p=5.4E-02	n=2
G protein-coupled peptide receptor activ...	GO:0008528	p=6.4E-02	n=3
structural constituent of cytoskeleton	GO:0005200	p=6.4E-02	n=3
amide transmembrane transporter activity	GO:0042887	p=6.4E-02	n=3
ligase activity, forming carbon-oxygen b...	GO:0016875	p=6.4E-02	n=3
peptide receptor activity	GO:0001653	p=6.4E-02	n=3
aminoacyl-tRNA ligase activity	GO:0004812	p=6.4E-02	n=3
nuclear receptor coactivator activity	GO:0030374	p=6.4E-02	n=3
tRNA binding	GO:0000049	p=6.9E-02	n=4
phosphatidylinositol bisphosphate bindin...	GO:1902936	p=7.6E-02	n=5
nucleotide transmembrane transporter act...	GO:0015215	p=7.7E-02	n=2
gamma-tubulin binding	GO:0043015	p=7.7E-02	n=2



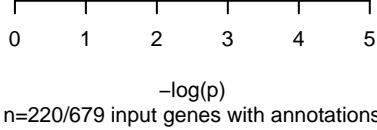
fraction genes in fg and expected value

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GO:CC  
Fox\_Nvec\_vc1.1\_XM\_032372114.2

Golgi medial cisterna	GO:0005797	p=5.2E-03	n=5
gamma-tubulin complex	GO:0000930	p=6.6E-03	n=2
mitotic spindle midzone	GO:1990023	p=8.9E-03	n=3
spindle pole	GO:0000922	p=1.3E-02	n=8
cis-Golgi network	GO:0005801	p=1.5E-02	n=5
Golgi-associated vesicle membrane	GO:0030660	p=1.5E-02	n=5
Golgi-associated vesicle	GO:0005798	p=1.5E-02	n=8
SAGA-type complex	GO:0070461	p=2.2E-02	n=3
COPII-coated ER to Golgi transport vesic...	GO:0030134	p=2.9E-02	n=4
nuclear pore	GO:0005643	p=2.9E-02	n=5
subapical complex	GO:0035003	p=3.5E-02	n=2
SAGA complex	GO:0000124	p=3.5E-02	n=2
COPI-coated vesicle membrane	GO:0030663	p=3.5E-02	n=2
nuclear envelope	GO:0005635	p=3.9E-02	n=16
cytoplasm	GO:0005737	p=4.0E-02	n=186
fibrillar center	GO:0001650	p=4.7E-02	n=6
Golgi membrane	GO:0000139	p=5.0E-02	n=17
cytosol	GO:0005829	p=5.4E-02	n=100
mitotic spindle pole	GO:0097431	p=5.4E-02	n=3
neuron projection cytoplasm	GO:0120111	p=5.4E-02	n=3
guanyl-nucleotide exchange factor comple...	GO:0032045	p=5.6E-02	n=2
nuclear proteasome complex	GO:0031595	p=5.6E-02	n=2
phagophore assembly site	GO:0000407	p=5.6E-02	n=2
Golgi cis cisterna	GO:0000137	p=5.6E-02	n=2
cytoplasmic side of apical plasma membra...	GO:0098592	p=5.6E-02	n=2
intrinsic component of mitochondrial mem...	GO:0098573	p=6.8E-02	n=3
polytene chromosome puff	GO:0005703	p=6.8E-02	n=3
integral component of mitochondrial memb...	GO:0032592	p=6.8E-02	n=3
Golgi trans cisterna	GO:0000138	p=6.8E-02	n=3
perinuclear region of cytoplasm	GO:0048471	p=6.9E-02	n=20



fraction genes in fg and expected value

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