GO:BP
Fox_Nvec_vc1.1_XM_001634845.3

fraction genes in fg and expected valu

Term	p-value	n	fg	bg
import across plasma membrane GO:0098739	p=6.3E−04	n=4	fg=0.04	bg=0.00
positive regulation of anion transmembra... GO:1903961	p=1.1E−03	n=2	fg=0.02	bg=0.00
negative regulation of activin receptor ... GO:0032926	p=3.2E−03	n=2	fg=0.02	bg=0.00
cellular response to growth factor stimu... GO:0071363	p=3.9E−03	n=11	fg=0.12	bg=0.05
rRNA modification GO:0000154	p=4.7E−03	n=3	fg=0.03	bg=0.00
cellular response to catecholamine stimu... GO:0071870	p=6.0E−03	n=4	fg=0.04	bg=0.01
negative regulation of protein kinase ac... GO:0044387	p=6.2E−03	n=2	fg=0.02	bg=0.00
aromatic amino acid transport GO:0015801	p=6.2E−03	n=2	fg=0.02	bg=0.00
negative regulation of phosphate metabol... GO:0045936	p=9.4E−03	n=12	fg=0.13	bg=0.05
proton transmembrane transport GO:1902600	p=9.5E−03	n=4	fg=0.04	bg=0.01
mitotic intra−S DNA damage checkpoint si... GO:0031573	p=1.0E−02	n=2	fg=0.02	bg=0.00
regulation of peptidyl−serine phosphoryl... GO:0033135	p=1.1E−02	n=4	fg=0.04	bg=0.01
import into cell GO:0098657	p=1.1E−02	n=10	fg=0.11	bg=0.05
L−alpha−amino acid transmembrane transpo... GO:1902475	p=1.2E−02	n=3	fg=0.03	bg=0.01
L−amino acid transport GO:0015807	p=1.2E−02	n=3	fg=0.03	bg=0.01
regulation of G protein−coupled receptor... GO:0008277	p=1.4E−02	n=4	fg=0.04	bg=0.01
positive regulation of peptidyl−serine p... GO:0033138	p=1.4E−02	n=3	fg=0.03	bg=0.01
negative regulation of protein modificat... GO:0031400	p=1.5E−02	n=12	fg=0.13	bg=0.05
positive regulation of epithelial cell a... GO:1904037	p=1.5E−02	n=2	fg=0.02	bg=0.00
negative regulation of extrinsic apoptot... GO:1902042	p=1.5E−02	n=2	fg=0.02	bg=0.00
export across plasma membrane GO:0140115	p=1.5E−02	n=2	fg=0.02	bg=0.00
positive regulation of oviposition GO:1901046	p=1.5E−02	n=2	fg=0.02	bg=0.00
sensory perception of pain GO:0019233	p=1.5E−02	n=5	fg=0.06	bg=0.02
amino acid transmembrane transport GO:0003333	p=1.7E−02	n=3	fg=0.03	bg=0.01
detection of stimulus involved in sensor... GO:0062149	p=1.7E−02	n=3	fg=0.03	bg=0.01
negative regulation of response to stimu... GO:0048585	p=1.8E−02	n=21	fg=0.24	bg=0.13
negative regulation of extrinsic apoptot... GO:2001237	p=2.0E−02	n=3	fg=0.03	bg=0.01
response to dopamine GO:1903350	p=2.0E−02	n=3	fg=0.03	bg=0.01
cellular response to dopamine GO:1903351	p=2.0E−02	n=3	fg=0.03	bg=0.01
natural killer cell mediated immunity GO:0002228	p=2.0E−02	n=2	fg=0.02	bg=0.00

−log(p)
n=89/263 input genes with annotations

fraction

GO:MF
Fox_Nvec_vc1.1_XM_001634845.3

fraction genes in fg and expected valu

Term	p-value	n	fg	bg
pre−mRNA 3'−splice site binding GO:0030628	p=3.0E−03	n=2	fg=0.03	bg=0.00
aromatic amino acid transmembrane transp... GO:0015173	p=5.8E−03	n=2	fg=0.03	bg=0.00
L−amino acid transmembrane transporter a... GO:0015179	p=9.0E−03	n=3	fg=0.04	bg=0.01
solute:proton symporter activity GO:0015295	p=9.5E−03	n=2	fg=0.03	bg=0.00
protein phosphatase inhibitor activity GO:0004864	p=9.5E−03	n=2	fg=0.03	bg=0.00
acetylcholine receptor binding GO:0033130	p=9.5E−03	n=2	fg=0.03	bg=0.00
aryl hydrocarbon receptor binding GO:0017162	p=1.4E−02	n=2	fg=0.03	bg=0.00
protein domain specific binding GO:0019904	p=2.0E−02	n=12	fg=0.16	bg=0.08
anion transmembrane transporter activity GO:0008509	p=2.0E−02	n=6	fg=0.08	bg=0.03
modified amino acid transmembrane transp... GO:0072349	p=2.5E−02	n=2	fg=0.03	bg=0.00
sphingomyelin phosphodiesterase D activi... GO:0050290	p=3.2E−02	n=1	fg=0.01	bg=0.00
ankyrin repeat binding GO:0071532	p=3.2E−02	n=1	fg=0.01	bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159	p=3.2E−02	n=1	fg=0.01	bg=0.00
platelet activating factor receptor bind... GO:0031859	p=3.2E−02	n=1	fg=0.01	bg=0.00
MDM2/MDM4 family protein binding GO:0097371	p=3.2E−02	n=1	fg=0.01	bg=0.00
amino acid:proton symporter activity GO:0005280	p=3.2E−02	n=1	fg=0.01	bg=0.00
cytoskeletal regulatory protein binding GO:0005519	p=3.2E−02	n=1	fg=0.01	bg=0.00
alpha−1A adrenergic receptor binding GO:0031691	p=3.2E−02	n=1	fg=0.01	bg=0.00
type 2A serotonin receptor binding GO:0031826	p=3.2E−02	n=1	fg=0.01	bg=0.00
protein serine/threonine phosphatase inh... GO:0004865	p=3.2E−02	n=1	fg=0.01	bg=0.00
double−stranded methylated DNA binding GO:0010385	p=3.2E−02	n=1	fg=0.01	bg=0.00
activin receptor activity, type I GO:0016361	p=3.2E−02	n=1	fg=0.01	bg=0.00
methotrexate transmembrane transporter a... GO:0015350	p=3.2E−02	n=1	fg=0.01	bg=0.00
G−protein gamma−subunit binding GO:0031682	p=3.2E−02	n=1	fg=0.01	bg=0.00
rRNA (guanosine−2'−O−)−methyltransferase... GO:0070039	p=3.2E−02	n=1	fg=0.01	bg=0.00
L−proline transmembrane transporter acti... GO:0015193	p=3.2E−02	n=1	fg=0.01	bg=0.00
L−tryptophan transmembrane transporter a... GO:0015196	p=3.2E−02	n=1	fg=0.01	bg=0.00
follicle−stimulating hormone receptor bi... GO:0031762	p=3.2E−02	n=1	fg=0.01	bg=0.00
transforming growth factor beta receptor... GO:0005025	p=3.2E−02	n=1	fg=0.01	bg=0.00
opsin binding GO:0002046	p=3.2E−02	n=1	fg=0.01	bg=0.00

−log(p)
n=76/263 input genes with annotations

fraction

GO:CC
Fox_Nvec_vc1.1_XM_001634845.3

fraction genes in fg and expected valu

Term	p-value	n	fg	bg
endomembrane system GO:0012505	p=4.3E−03	n=39	fg=0.44	bg=0.31
cortical cytoskeleton GO:0030863	p=5.8E−03	n=4	fg=0.05	bg=0.01
endocytic vesicle GO:0030139	p=8.1E−03	n=6	fg=0.07	bg=0.02
presynaptic periactive zone GO:0036062	p=9.9E−03	n=2	fg=0.02	bg=0.00
plasma membrane protein complex GO:0098797	p=1.2E−02	n=7	fg=0.08	bg=0.03
nuclear body GO:0016604	p=1.6E−02	n=11	fg=0.12	bg=0.06
brush border membrane GO:0031526	p=1.9E−02	n=3	fg=0.03	bg=0.01
supramolecular complex GO:0099080	p=2.1E−02	n=13	fg=0.15	bg=0.08
apical part of cell GO:0045177	p=2.4E−02	n=9	fg=0.10	bg=0.05
cortical actin cytoskeleton GO:0030864	p=2.5E−02	n=3	fg=0.03	bg=0.01
neuron spine GO:0044309	p=2.6E−02	n=5	fg=0.06	bg=0.02
dendritic spine GO:0043197	p=2.6E−02	n=5	fg=0.06	bg=0.02
vacuolar membrane GO:0005774	p=2.8E−02	n=6	fg=0.07	bg=0.03
plasma membrane GO:0005886	p=3.0E−02	n=30	fg=0.34	bg=0.23
apical plasma membrane GO:0016324	p=3.2E−02	n=7	fg=0.08	bg=0.03
centriolar satellite GO:0034451	p=3.3E−02	n=2	fg=0.02	bg=0.00
clathrin−coated pit GO:0005905	p=3.3E−02	n=2	fg=0.02	bg=0.00
anchored component of synaptic vesicle m... GO:0098993	p=3.3E−02	n=1	fg=0.01	bg=0.00
GTPase activator complex GO:1902773	p=3.3E−02	n=1	fg=0.01	bg=0.00
cytoskeleton of presynaptic active zone GO:0048788	p=3.3E−02	n=1	fg=0.01	bg=0.00
presynaptic active zone cytoplasmic comp... GO:0098831	p=3.3E−02	n=1	fg=0.01	bg=0.00
dense fibrillar component GO:0001651	p=3.3E−02	n=1	fg=0.01	bg=0.00
hemoglobin complex GO:0005833	p=3.3E−02	n=1	fg=0.01	bg=0.00
ESCRT−0 complex GO:0033565	p=3.3E−02	n=1	fg=0.01	bg=0.00
neuronal ribonucleoprotein granule GO:0071598	p=3.3E−02	n=1	fg=0.01	bg=0.00
checkpoint clamp complex GO:0030896	p=3.3E−02	n=1	fg=0.01	bg=0.00
varicosity GO:0043196	p=3.3E−02	n=1	fg=0.01	bg=0.00
myofibril GO:0030016	p=3.4E−02	n=5	fg=0.06	bg=0.02
Golgi apparatus GO:0005794	p=3.4E−02	n=16	fg=0.18	bg=0.11
supramolecular polymer GO:0099081	p=3.5E−02	n=9	fg=0.10	bg=0.05

−log(p)
n=88/263 input genes with annotations

fraction