GO:BP
Fox_Nvec_vc1.1_XM_032371996.2

fraction genes in fg and expected value

positive regulation of cellular response... GO:1905959	p=1.6E−03	n=2	fg=0.02	bg=0.00
histone dephosphorylation GO:0016576	p=4.5E−03	n=2	fg=0.02	bg=0.00
3'−UTR−mediated mRNA destabilization GO:0061158	p=4.5E−03	n=2	fg=0.02	bg=0.00
glucocorticoid receptor signaling pathwa... GO:0042921	p=4.5E−03	n=2	fg=0.02	bg=0.00
negative regulation of ubiquitin protein... GO:1904667	p=4.5E−03	n=2	fg=0.02	bg=0.00
endosome transport via multivesicular bo... GO:0032509	p=5.9E−03	n=3	fg=0.03	bg=0.00
carboxylic acid biosynthetic process GO:0046394	p=7.7E−03	n=9	fg=0.08	bg=0.03
nucleosome disassembly GO:0006337	p=8.9E−03	n=2	fg=0.02	bg=0.00
neuroblast differentiation GO:0014016	p=1.0E−02	n=3	fg=0.03	bg=0.00
neuron cellular homeostasis GO:0070050	p=1.0E−02	n=3	fg=0.03	bg=0.00
multivesicular body organization GO:0036257	p=1.3E−02	n=3	fg=0.03	bg=0.00
multivesicular body assembly GO:0036258	p=1.3E−02	n=3	fg=0.03	bg=0.00
L−serine metabolic process GO:0006563	p=1.4E−02	n=2	fg=0.02	bg=0.00
female germ−line stem cell population ma... GO:0036099	p=1.4E−02	n=2	fg=0.02	bg=0.00
neuroblast migration GO:0097402	p=1.4E−02	n=2	fg=0.02	bg=0.00
positive regulation of miRNA transcripti... GO:1902895	p=1.4E−02	n=2	fg=0.02	bg=0.00
alpha−amino acid biosynthetic process GO:1901607	p=1.5E−02	n=4	fg=0.04	bg=0.01
isoprenoid metabolic process GO:0006720	p=1.6E−02	n=3	fg=0.03	bg=0.01
transcription−coupled nucleotide−excisio... GO:0006283	p=1.8E−02	n=4	fg=0.04	bg=0.01
nucleotide−excision repair, DNA incision... GO:0006296	p=1.9E−02	n=3	fg=0.03	bg=0.01
endosome organization GO:0007032	p=2.0E−02	n=4	fg=0.04	bg=0.01
regulation of protein tyrosine kinase ac... GO:0061097	p=2.0E−02	n=4	fg=0.04	bg=0.01
peptidyl−serine dephosphorylation GO:0070262	p=2.1E−02	n=2	fg=0.02	bg=0.00
regulation of miRNA transcription GO:1902893	p=2.1E−02	n=2	fg=0.02	bg=0.00
cellular amino acid biosynthetic process GO:0008652	p=2.3E−02	n=4	fg=0.04	bg=0.01
nucleotide−excision repair, DNA incision GO:0033683	p=2.7E−02	n=3	fg=0.03	bg=0.01
miRNA transcription GO:0061614	p=2.9E−02	n=2	fg=0.02	bg=0.00
cellular modified amino acid metabolic p... GO:0006575	p=3.1E−02	n=5	fg=0.05	bg=0.02
female pregnancy GO:0007565	p=3.2E−02	n=4	fg=0.04	bg=0.01
DNA replication GO:0006260	p=3.3E−02	n=7	fg=0.07	bg=0.03

−log(p)

n=107/368 input genes with annotations

fraction

GO:MF
Fox_Nvec_vc1.1_XM_032371996.2

fraction genes in fg and expected valu

miRNA binding GO:0035198	p=4.7E−03	n=2	fg=0.02	bg=0.00
DNA topoisomerase binding GO:0044547	p=9.2E−03	n=2	fg=0.02	bg=0.00
S−adenosyl−L−methionine binding GO:1904047	p=1.5E−02	n=2	fg=0.02	bg=0.00
adiponectin binding GO:0055100	p=4.1E−02	n=1	fg=0.01	bg=0.00
nitrite reductase (NO−forming) activity GO:0050421	p=4.1E−02	n=1	fg=0.01	bg=0.00
DNA end binding GO:0045027	p=4.1E−02	n=1	fg=0.01	bg=0.00
TFIIF−class transcription factor complex... GO:0001096	p=4.1E−02	n=1	fg=0.01	bg=0.00
holo−[acyl−carrier−protein] synthase act... GO:0008897	p=4.1E−02	n=1	fg=0.01	bg=0.00
alpha−2C adrenergic receptor binding GO:0031696	p=4.1E−02	n=1	fg=0.01	bg=0.00
volume−sensitive chloride channel activi... GO:0072320	p=4.1E−02	n=1	fg=0.01	bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837	p=4.1E−02	n=1	fg=0.01	bg=0.00
3−oxo−5−alpha−steroid 4−dehydrogenase ac... GO:0003865	p=4.1E−02	n=1	fg=0.01	bg=0.00
uroporphyrinogen−III synthase activity GO:0004852	p=4.1E−02	n=1	fg=0.01	bg=0.00
cobalt ion binding GO:0050897	p=4.1E−02	n=1	fg=0.01	bg=0.00
chondroitin−glucuronate 5−epimerase acti... GO:0047757	p=4.1E−02	n=1	fg=0.01	bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946	p=4.1E−02	n=1	fg=0.01	bg=0.00
U5 snRNA binding GO:0030623	p=4.1E−02	n=1	fg=0.01	bg=0.00
steroid dehydrogenase activity, acting o... GO:0033765	p=4.1E−02	n=1	fg=0.01	bg=0.00
FAD transmembrane transporter activity GO:0015230	p=4.1E−02	n=1	fg=0.01	bg=0.00
arginine−tRNA ligase activity GO:0004814	p=4.1E−02	n=1	fg=0.01	bg=0.00
racemase and epimerase activity, acting ... GO:0016857	p=4.1E−02	n=1	fg=0.01	bg=0.00
RNA polymerase I general transcription i... GO:0001181	p=4.1E−02	n=1	fg=0.01	bg=0.00
adipokinetic hormone receptor activity GO:0097003	p=4.1E−02	n=1	fg=0.01	bg=0.00
nitrite reductase activity GO:0098809	p=4.1E−02	n=1	fg=0.01	bg=0.00
myosin phosphatase regulator activity GO:0017020	p=4.1E−02	n=1	fg=0.01	bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118	p=4.1E−02	n=1	fg=0.01	bg=0.00
oxidoreductase activity, acting on other... GO:0016661	p=4.1E−02	n=1	fg=0.01	bg=0.00
oxidoreductase activity, acting on other... GO:0016662	p=4.1E−02	n=1	fg=0.01	bg=0.00
alpha−adrenergic receptor activity GO:0004936	p=4.1E−02	n=1	fg=0.01	bg=0.00
alpha2−adrenergic receptor activity GO:0004938	p=4.1E−02	n=1	fg=0.01	bg=0.00

−log(p)

n=96/368 input genes with annotations

fraction

GO:CC
Fox_Nvec_vc1.1_XM_032371996.2

fraction genes in fg and expected valu

nuclear replisome GO:0043601	p=4.7E−03	n=3	fg=0.03	bg=0.00
DNA polymerase complex GO:0042575	p=1.1E−02	n=3	fg=0.03	bg=0.00
ESCRT complex GO:0036452	p=1.4E−02	n=3	fg=0.03	bg=0.00
transferase complex, transferring phosph... GO:0061695	p=1.5E−02	n=8	fg=0.07	bg=0.03
ESCRT III complex GO:0000815	p=2.2E−02	n=2	fg=0.02	bg=0.00
chaperone complex GO:0101031	p=3.1E−02	n=2	fg=0.02	bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0016471	p=3.1E−02	n=2	fg=0.02	bg=0.00
proton−transporting V−type ATPase comple... GO:0033176	p=4.0E−02	n=2	fg=0.02	bg=0.00
sodium channel complex GO:0034706	p=4.1E−02	n=1	fg=0.01	bg=0.00
endocytic patch GO:0061645	p=4.1E−02	n=1	fg=0.01	bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200	p=4.1E−02	n=1	fg=0.01	bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061202	p=4.1E−02	n=1	fg=0.01	bg=0.00
cyclin E1−CDK2 complex GO:0097134	p=4.1E−02	n=1	fg=0.01	bg=0.00
cyclin E2−CDK2 complex GO:0097135	p=4.1E−02	n=1	fg=0.01	bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066	p=4.1E−02	n=1	fg=0.01	bg=0.00
actin cortical patch GO:0030479	p=4.1E−02	n=1	fg=0.01	bg=0.00
FACT complex GO:0035101	p=4.1E−02	n=1	fg=0.01	bg=0.00
core TFIIH complex portion of holo TFIIH... GO:0000438	p=4.1E−02	n=1	fg=0.01	bg=0.00
clathrin−sculpted vesicle GO:0060198	p=4.1E−02	n=1	fg=0.01	bg=0.00
nuclear DNA−directed RNA polymerase comp... GO:0055029	p=4.2E−02	n=5	fg=0.05	bg=0.02
DNA−directed RNA polymerase complex GO:0000428	p=4.5E−02	n=5	fg=0.05	bg=0.02
SWI/SNF superfamily−type complex GO:0070603	p=4.6E−02	n=3	fg=0.03	bg=0.01
RNA polymerase complex GO:0030880	p=5.2E−02	n=5	fg=0.05	bg=0.02
P−body GO:0000932	p=5.2E−02	n=3	fg=0.03	bg=0.01
proton−transporting two−sector ATPase co... GO:0016469	p=6.1E−02	n=2	fg=0.02	bg=0.00
extrinsic component of mitochondrial inn... GO:0031314	p=8.1E−02	n=1	fg=0.01	bg=0.00
transcription preinitiation complex GO:0097550	p=8.1E−02	n=1	fg=0.01	bg=0.00
epsilon DNA polymerase complex GO:0008622	p=8.1E−02	n=1	fg=0.01	bg=0.00
hippocampal mossy fiber GO:0097457	p=8.1E−02	n=1	fg=0.01	bg=0.00
gamma−tubulin complex GO:0000930	p=8.1E−02	n=1	fg=0.01	bg=0.00

−log(p)

n=111/368 input genes with annotations

fraction