

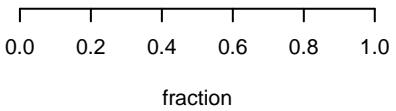
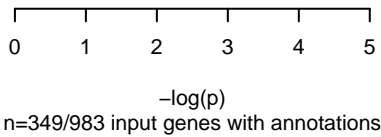
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032384912.2

fraction genes in fg and expected value

mRNA splicing, via spliceosome	GO:0000398
protein-containing complex localization	GO:0031503
mRNA polyadenylation	GO:0006378
RNA export from nucleus	GO:0006405
cellular response to increased oxygen le...	GO:0036295
cellular iron ion homeostasis	GO:0006879
regulation of protein catabolic process	GO:0042176
modulation of process of another organis...	GO:0035821
histone H3–K4 methylation	GO:0051568
protein export from nucleus	GO:0006611
modulation by host of symbiont transcrip...	GO:0052472
energy coupled proton transmembrane tran...	GO:0015988
modulation by host of viral transcriptio...	GO:0043921
modification-dependent macromolecule cat...	GO:0043632
cellular protein catabolic process	GO:0044257
microtubule-based transport	GO:0099111
endocytic recycling	GO:0032456
positive regulation of nucleocytoplasmic...	GO:0046824
regulation of mRNA polyadenylation	GO:1900363
positive regulation by host of viral tra...	GO:0043923
positive regulation of transcription of ...	GO:1901838
enteric nervous system development	GO:0048484
protein localization to postsynaptic mem...	GO:1903539
response to herbicide	GO:0009635
snRNA metabolic process	GO:0016073
exocytosis	GO:0006887
ncRNA 3'–end processing	GO:0043628
regulation of synaptic vesicle cycle	GO:0098693
modification-dependent protein catabolic...	GO:0019941
negative regulation of hydrolase activit...	GO:0051346

p=1.2E−05	n=26
p=3.2E−04	n=18
p=3.9E−04	n=12
p=9.9E−04	n=12
p=1.4E−03	n=4
p=1.5E−03	n=7
p=1.8E−03	n=26
p=1.8E−03	n=9
p=1.8E−03	n=9
p=3.3E−03	n=14
p=3.8E−03	n=5
p=3.8E−03	n=5
p=3.8E−03	n=5
p=3.8E−03	n=5
p=3.9E−03	n=34
p=4.2E−03	n=39
p=4.5E−03	n=14
p=4.9E−03	n=9
p=5.4E−03	n=7
p=5.7E−03	n=4
p=5.7E−03	n=4
p=7.1E−03	n=4
p=7.1E−03	n=3
p=7.1E−03	n=3
p=7.1E−03	n=3
p=7.1E−03	n=3
p=7.4E−03	n=9
p=8.4E−03	n=36
p=8.6E−03	n=5
p=9.1E−03	n=7
p=1.0E−02	n=32
p=1.1E−02	n=15

fg=0.07	bg=0.03
fg=0.05	bg=0.02
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.07	bg=0.04
fg=0.03	bg=0.01
fg=0.03	bg=0.01
fg=0.04	bg=0.02
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.10	bg=0.06
fg=0.11	bg=0.08
fg=0.04	bg=0.02
fg=0.03	bg=0.01
fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.10	bg=0.07
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.09	bg=0.06
fg=0.04	bg=0.02



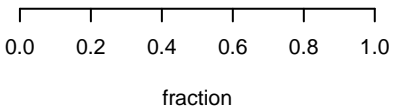
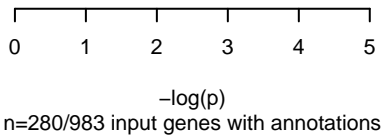
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032384912.2

fraction genes in fg and expected value

catalytic activity, acting on a nucleic ...	GO:0140640
ATP hydrolysis activity	GO:0016887
phosphatase inhibitor activity	GO:0019212
RNA binding	GO:0003723
small GTPase binding	GO:0031267
single-stranded RNA binding	GO:0003727
catalytic activity, acting on RNA	GO:0140098
ubiquitin-like protein ligase activity	GO:0061659
ubiquitin protein ligase activity	GO:0061630
helicase activity	GO:0004386
endonuclease activity, active with eithe...	GO:0016893
protein phosphatase inhibitor activity	GO:0004864
hydrolase activity, hydrolyzing O–glycos...	GO:0004553
ATP binding	GO:0005524
endoribonuclease activity	GO:0004521
polynucleotide adenyllyltransferase activ...	GO:0004652
transferase activity	GO:0016740
SMAD binding	GO:0046332
ATP-dependent activity, acting on RNA	GO:0008186
Tat protein binding	GO:0030957
ubiquitination-like modification–depende...	GO:0140035
ubiquitin-dependent protein binding	GO:0140036
ubiquitin-like protein transferase activ...	GO:0019787
microtubule motor activity	GO:0003777
poly(U) RNA binding	GO:0008266
pyrophosphate hydrolysis–driven proton t...	GO:0009678
ATPase activity, coupled to transmembran...	GO:0044769
R–SMAD binding	GO:0070412
proton-transporting ATPase activity, rot...	GO:0046961
nuclear localization sequence binding	GO:0008139

p=1.2E−03	n=26
p=1.4E−03	n=24
p=4.0E−03	n=4
p=4.6E−03	n=37
p=9.9E−03	n=24
p=1.1E−02	n=8
p=1.3E−02	n=16
p=1.5E−02	n=17
p=1.5E−02	n=17
p=1.5E−02	n=8
p=1.9E−02	n=3
p=1.9E−02	n=3
p=1.9E−02	n=7
p=2.1E−02	n=19
p=2.1E−02	n=4
p=2.1E−02	n=4
p=2.4E−02	n=69
p=2.4E−02	n=6
p=3.0E−02	n=5
p=3.1E−02	n=2
p=3.1E−02	n=2
p=3.1E−02	n=2
p=3.4E−02	n=24
p=3.6E−02	n=4
p=4.1E−02	n=3
p=4.1E−02	n=3
p=4.1E−02	n=3
p=4.1E−02	n=3
p=4.1E−02	n=3

fg=0.09	bg=0.05
fg=0.09	bg=0.05
fg=0.01	bg=0.00
fg=0.13	bg=0.09
fg=0.09	bg=0.05
fg=0.03	bg=0.01
fg=0.06	bg=0.03
fg=0.06	bg=0.04
fg=0.06	bg=0.04
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.07	bg=0.04
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.25	bg=0.20
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00



GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032384912.2

fraction genes in fg and expected value

catalytic step 2 spliceosome	GO:0071013
plasma membrane proton-transporting V–ty...	GO:0033181
nucleoplasm	GO:0005654
vacuolar proton-transporting V–type ATPa...	GO:0016471
intracellular non-membrane-bounded organ...	GO:0043232
nuclear protein-containing complex	GO:0140513
methyltransferase complex	GO:0034708
intracellular anatomical structure	GO:0005622
Prp19 complex	GO:0000974
intracellular membrane-bounded organelle	GO:0043231
recycling endosome	GO:0055037
photoreceptor connecting cilium	GO:0032391
ribonucleoprotein complex	GO:1990904
histone methyltransferase complex	GO:0035097
intracellular protein-containing complex	GO:0140535
spliceosomal complex	GO:0005681
Set1C/COMPASS complex	GO:0048188
peroxisomal matrix	GO:0005782
microbody lumen	GO:0031907
chromosome	GO:0005694
MLL1/2 complex	GO:0044665
precatalytic spliceosome	GO:0071011
nuclear membrane	GO:0031965
proton-transporting two-sector ATPase co...	GO:0033177
proton-transporting V–type ATPase, V0 do...	GO:0033179
GATOR2 complex	GO:0061700
U2-type catalytic step 2 spliceosome	GO:0071007
mRNA cleavage and polyadenylation specif...	GO:0005847
mRNA cleavage factor complex	GO:0005849
pre-snoRNP complex	GO:0070761

p=3.3E−04	n=8
p=1.1E−03	n=5
p=1.2E−03	n=115
p=3.3E−03	n=5
p=3.4E−03	n=124
p=3.6E−03	n=56
p=3.9E−03	n=9
p=4.6E−03	n=333
p=6.4E−03	n=3
p=7.6E−03	n=288
p=7.6E−03	n=14
p=8.0E−03	n=6
p=1.0E−02	n=39
p=1.8E−02	n=7
p=1.9E−02	n=39
p=1.9E−02	n=14
p=2.2E−02	n=3
p=2.2E−02	n=3
p=2.2E−02	n=3
p=2.4E−02	n=36
p=2.6E−02	n=4
p=2.6E−02	n=4
p=3.0E−02	n=12
p=3.5E−02	n=2
p=3.5E−02	n=2
p=3.5E−02	n=2
p=3.5E−02	n=2
p=3.5E−02	n=2
p=3.5E−02	n=2
p=3.5E−02	n=2
p=3.5E−02	n=2

fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.34	bg=0.27
fg=0.01	bg=0.00
fg=0.37	bg=0.30
fg=0.17	bg=0.11
fg=0.03	bg=0.01
fg=0.99	bg=0.94
fg=0.01	bg=0.00
fg=0.85	bg=0.78
fg=0.04	bg=0.02
fg=0.02	bg=0.01
fg=0.12	bg=0.07
fg=0.02	bg=0.01
fg=0.12	bg=0.09
fg=0.04	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.11	bg=0.08
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.04	bg=0.02
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00

