

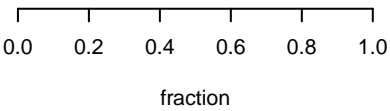
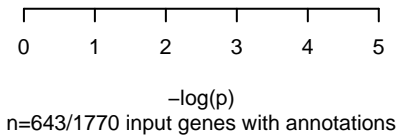
GO:BP
Elav_Nvec_vc1.1_XM_032387281.2

fraction genes in fg and expected value

mRNA splicing, via spliceosome	GO:0000398
mRNA polyadenylation	GO:0006378
negative regulation of DNA biosynthetic ...	GO:2000279
mitochondrial translational termination	GO:0070126
ncRNA processing	GO:0034470
microtubule-based transport	GO:0099111
cellular response to increased oxygen le...	GO:0036295
axoneme assembly	GO:0035082
RNA methylation	GO:0001510
biological process involved in interacti...	GO:0051702
mitochondrial translational elongation	GO:0070125
positive regulation of exocytosis	GO:0045921
tRNA metabolic process	GO:0006399
nuclear export	GO:0051168
energy coupled proton transmembrane tran...	GO:0015988
spliceosomal snRNP assembly	GO:0000387
protein export from nucleus	GO:0006611
modulation by host of viral process	GO:0044788
regulation of mRNA 3'-end processing	GO:0031440
NLS-bearing protein import into nucleus	GO:0006607
negative regulation of endothelial cell ...	GO:2000352
regulation of histone H3-K9 acetylation	GO:2000615
negative regulation of protein export fr...	GO:0046826
regulation of histone H3-K9 dimethylatio...	GO:1900109
spliceosomal tri-snRNP complex assembly	GO:0000244
negative regulation of telomere maintena...	GO:0032211
early endosome to recycling endosome tra...	GO:0061502
fatty-acyl-CoA biosynthetic process	GO:0046949
negative regulation of telomere maintena...	GO:1904357
histone H3-K9 dimethylation	GO:0036123

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p=5.6E-04	n=12
p=7.6E-04	n=5
p=7.7E-04	n=11
p=8.0E-04	n=42
p=3.0E-03	n=22
p=3.2E-03	n=4
p=4.8E-03	n=13
p=4.8E-03	n=13
p=6.0E-03	n=10
p=6.0E-03	n=10
p=6.6E-03	n=11
p=7.1E-03	n=21
p=8.5E-03	n=25
p=1.0E-02	n=5
p=1.1E-02	n=7
p=1.2E-02	n=23
p=1.3E-02	n=8
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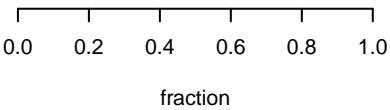
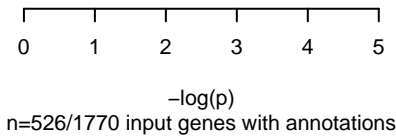
GO:MF
Elav_Nvec_vc1.1_XM_032387281.2

fraction genes in fg and expected value

catalytic activity, acting on a tRNA	GO:0140101
RNA methyltransferase activity	GO:0008173
phosphatase inhibitor activity	GO:0019212
small GTPase binding	GO:0031267
dipeptidase activity	GO:0016805
neurexin family protein binding	GO:0042043
NADH dehydrogenase activity	GO:0003954
structural constituent of ribosome	GO:0003735
GTPase binding	GO:0051020
tRNA methyltransferase activity	GO:0008175
ATPase activity, coupled to transmembran...	GO:0044769
nuclear localization sequence binding	GO:0008139
tRNA (guanine) methyltransferase activit...	GO:0016423
pyrophosphate hydrolysis-driven proton t...	GO:0009678
proton-transporting ATPase activity, rot...	GO:0046961
S-adenosylmethionine-dependent methyltra...	GO:0008757
ATP hydrolysis activity	GO:0016887
alpha-tubulin binding	GO:0043014
NAD(P)H dehydrogenase (quinone) activity	GO:0003955
NADH dehydrogenase (ubiquinone) activity	GO:0008137
NADH dehydrogenase (quinone) activity	GO:0050136
ubiquitin-like protein ligase activity	GO:0061659
ubiquitin protein ligase activity	GO:0061630
catalytic activity, acting on a nucleic ...	GO:0140640
isomerase activity	GO:0016853
SNARE binding	GO:0000149
xylosyltransferase activity	GO:0042285
UDP-xylosyltransferase activity	GO:0035252
palmitoyl hydrolase activity	GO:0098599
syndecan binding	GO:0045545

p=4.6E-04	n=16
p=5.7E-03	n=11
p=7.5E-03	n=5
p=1.1E-02	n=34
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p=1.1E-02	n=3
p=1.2E-02	n=7
p=1.7E-02	n=20
p=1.8E-02	n=39
p=1.9E-02	n=6
p=2.5E-02	n=4
p=2.5E-02	n=4
p=2.5E-02	n=4
p=2.5E-02	n=4
p=2.5E-02	n=4
p=2.5E-02	n=15
p=2.8E-02	n=33
p=3.0E-02	n=5
p=3.1E-02	n=6
p=3.1E-02	n=6
p=3.1E-02	n=6
p=3.4E-02	n=23
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p=3.4E-02	n=55
p=3.5E-02	n=14
p=3.5E-02	n=12
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GO:CC
Elav_Nvec_vc1.1_XM_032387281.2

fraction genes in fg and expected value

catalytic step 2 spliceosome	GO:0071013
Prp19 complex	GO:0000974
nucleoplasm	GO:0005654
intracellular non-membrane-bounded organ...	GO:0043232
plasma membrane proton-transporting V-ty...	GO:0033181
cytoplasm	GO:0005737
mitochondrial respiratory chain complex ...	GO:0005747
mitochondrial large ribosomal subunit	GO:0005762
axoneme	GO:0005930
methyltransferase complex	GO:0034708
nuclear protein-containing complex	GO:0140513
catalytic complex	GO:1902494
vacuolar proton-transporting V-type ATPa...	GO:0016471
organelle	GO:0043226
proton-transporting two-sector ATPase co...	GO:0033178
Cul4B-RING E3 ubiquitin ligase complex	GO:0031465
proton-transporting two-sector ATPase co...	GO:0033177
intracellular organelle	GO:0043229
chromosome	GO:0005694
membrane-bounded organelle	GO:0043227
U2-type spliceosomal complex	GO:0005684
trans-Golgi network	GO:0005802
intracellular protein-containing complex	GO:0140535
U12-type spliceosomal complex	GO:0005689
U2-type catalytic step 2 spliceosome	GO:0071007
protein-containing complex	GO:0032991
peptidase complex	GO:1905368
nucleolus	GO:0005730
polysome	GO:0005844
centriolar satellite	GO:0034451

p=2.3E-04	n=14
p=6.9E-04	n=5
p=1.1E-03	n=214
p=2.0E-03	n=248
p=3.3E-03	n=5
p=4.5E-03	n=529
p=4.5E-03	n=9
p=5.0E-03	n=7
p=5.8E-03	n=15
p=8.3E-03	n=14
p=8.9E-03	n=99
p=9.1E-03	n=124
p=9.4E-03	n=5
p=1.1E-02	n=568
p=1.2E-02	n=4
p=1.3E-02	n=3
p=1.3E-02	n=3
p=1.3E-02	n=560
p=1.5E-02	n=71
p=1.7E-02	n=537
p=1.8E-02	n=8
p=1.8E-02	n=25
p=1.9E-02	n=67
p=2.0E-02	n=5
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p=3.5E-02	n=10
p=3.7E-02	n=5

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