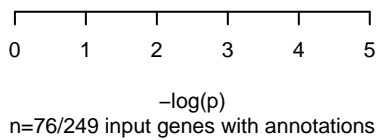


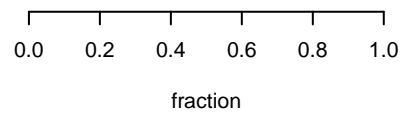
GO:BP
Elav_Nvec_vc1.1_XM_048724172.1

fraction genes in fg and expected value

mesodermal cell migration	GO:0008078	p=1.6E-03	n=3
regulation of transforming growth factor...	GO:0017015	p=1.6E-03	n=4
miRNA catabolic process	GO:0010587	p=2.3E-03	n=2
gastric acid secretion	GO:0001696	p=2.3E-03	n=2
regulation of growth hormone secretion	GO:0060123	p=2.3E-03	n=2
bile acid biosynthetic process	GO:0006699	p=3.0E-03	n=3
cell redox homeostasis	GO:0045454	p=4.5E-03	n=2
regulation of fibroblast apoptotic proce...	GO:2000269	p=4.5E-03	n=2
salivary gland boundary specification	GO:0007432	p=4.5E-03	n=2
response to other organism	GO:0051707	p=4.5E-03	n=13
negative regulation of translation	GO:0017148	p=6.5E-03	n=5
positive regulation of miRNA transcripti...	GO:1902895	p=7.4E-03	n=2
cystoblast division	GO:0007282	p=7.4E-03	n=2
renal filtration	GO:0097205	p=7.4E-03	n=2
regulation of mRNA stability	GO:0043488	p=8.1E-03	n=4
regulation of G protein-coupled receptor...	GO:0008277	p=8.1E-03	n=4
oocyte development	GO:0048599	p=8.4E-03	n=6
NADPH regeneration	GO:0006740	p=1.1E-02	n=2
secondary palate development	GO:0062009	p=1.1E-02	n=2
post-embryonic hemopoiesis	GO:0035166	p=1.3E-02	n=3
endoderm development	GO:0007492	p=1.3E-02	n=3
defense response	GO:0006952	p=1.4E-02	n=12
RNA stabilization	GO:0043489	p=1.5E-02	n=2
multicellular organismal movement	GO:0050879	p=1.5E-02	n=2
cellular macromolecule localization	GO:0070727	p=1.8E-02	n=21
positive regulation of muscle hypertroph...	GO:0014742	p=2.0E-02	n=2
positive regulation of cardiac muscle hy...	GO:0010613	p=2.0E-02	n=2
germ-line cyst formation	GO:0048134	p=2.0E-02	n=2
positive regulation of G protein-coupled...	GO:0045745	p=2.0E-02	n=2
positive regulation of sodium ion transp...	GO:0010765	p=2.0E-02	n=2



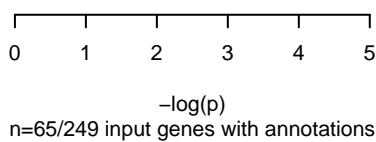
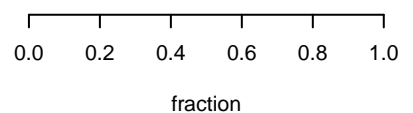
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GO:MF
Elav_Nvec_vc1.1_XM_048724172.1

fraction genes in fg and expected value

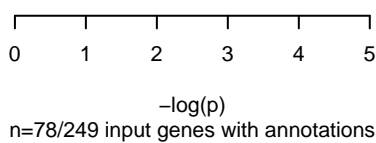
NAD binding	GO:0051287	p=1.5E-03	n=3
phosphatidylinositol binding	GO:0035091	p=1.5E-03	n=7
sodium channel regulator activity	GO:0017080	p=7.0E-03	n=2
DEAD/H-box RNA helicase binding	GO:0017151	p=1.4E-02	n=2
exoribonuclease activity, producing 5'-p...	GO:0016896	p=2.4E-02	n=2
3'-5'-exoribonuclease activity	GO:0000175	p=2.4E-02	n=2
5'-3' RNA polymerase activity	GO:0034062	p=2.4E-02	n=2
RNA polymerase activity	GO:0097747	p=2.4E-02	n=2
glycine N-choloyltransferase activity	GO:0047963	p=2.7E-02	n=1
NAD(P)+ transhydrogenase (AB-specific) a...	GO:0008750	p=2.7E-02	n=1
nucleoside:sodium symporter activity	GO:0005415	p=2.7E-02	n=1
medium-chain acyl-CoA hydrolase activity	GO:0052815	p=2.7E-02	n=1
long-chain acyl-CoA hydrolase activity	GO:0052816	p=2.7E-02	n=1
selenium binding	GO:0008430	p=2.7E-02	n=1
very long chain acyl-CoA hydrolase activ...	GO:0052817	p=2.7E-02	n=1
pyrimidine nucleobase transmembrane tran...	GO:0005350	p=2.7E-02	n=1
tumor necrosis factor-activated receptor...	GO:0005031	p=2.7E-02	n=1
death receptor activity	GO:0005035	p=2.7E-02	n=1
purine nucleoside transmembrane transpor...	GO:0015211	p=2.7E-02	n=1
calcitonin family receptor activity	GO:0097642	p=2.7E-02	n=1
macrophage migration inhibitory factor b...	GO:0035718	p=2.7E-02	n=1
ribokinase activity	GO:0004747	p=2.7E-02	n=1
insulin-like growth factor I binding	GO:0031994	p=2.7E-02	n=1
NAD(P)+ transhydrogenase (B-specific) ac...	GO:0003957	p=2.7E-02	n=1
dolichyl-phosphate beta-glucosyltransfer...	GO:0004581	p=2.7E-02	n=1
purine-specific nucleoside:sodium sympor...	GO:0015390	p=2.7E-02	n=1
nucleobase:cation symporter activity	GO:0015391	p=2.7E-02	n=1
calcitonin gene-related peptide receptor...	GO:0001635	p=2.7E-02	n=1
neurotrophin p75 receptor binding	GO:0005166	p=2.7E-02	n=1
cytochrome-b5 reductase activity, acting...	GO:0004128	p=2.7E-02	n=1

[illegible]

GO:CC
Elav_Nvec_vc1.1_XM_048724172.1

fraction genes in fg and expected value

eukaryotic translation initiation factor...	GO:0005852	p=4.4E-04	n=3
phagocytic cup	GO:0001891	p=7.8E-03	n=2
extrinsic component of endosome membrane	GO:0031313	p=1.1E-02	n=2
nuclear inner membrane	GO:0005637	p=2.1E-02	n=2
cytoplasmic ribonucleoprotein granule	GO:0036464	p=2.6E-02	n=5
integrin alpha3-beta1 complex	GO:0034667	p=2.9E-02	n=1
macropinocytic cup	GO:0070685	p=2.9E-02	n=1
Scc2-Scc4 cohesin loading complex	GO:0090694	p=2.9E-02	n=1
SMC loading complex	GO:0032116	p=2.9E-02	n=1
phagolysosome membrane	GO:0061474	p=2.9E-02	n=1
integrin alpha6-beta4 complex	GO:0034676	p=2.9E-02	n=1
integrin alpha7-beta1 complex	GO:0034677	p=2.9E-02	n=1
apical cytoplasm	GO:0090651	p=2.9E-02	n=1
cytophidium	GO:0097268	p=2.9E-02	n=1
Mon1-Ccz1 complex	GO:0035658	p=2.9E-02	n=1
phagolysosome	GO:0032010	p=2.9E-02	n=1
tubular endosome	GO:0097422	p=2.9E-02	n=1
nuclear RNA-directed RNA polymerase comp...	GO:0031380	p=2.9E-02	n=1
hemoglobin complex	GO:0005833	p=2.9E-02	n=1
RNA-directed RNA polymerase complex	GO:0031379	p=2.9E-02	n=1
alveolar lamellar body	GO:0097208	p=2.9E-02	n=1
ribonucleoprotein granule	GO:0035770	p=3.2E-02	n=5
supramolecular complex	GO:0099080	p=4.3E-02	n=11
extrinsic component of organelle membran...	GO:0031312	p=5.2E-02	n=2
SMAD protein complex	GO:0071141	p=5.7E-02	n=1
T cell receptor complex	GO:0042101	p=5.7E-02	n=1
exoribonuclease complex	GO:1905354	p=5.7E-02	n=1
cuticular plate	GO:0032437	p=5.7E-02	n=1
nuclear stress granule	GO:0097165	p=5.7E-02	n=1
DNA polymerase III complex	GO:0009360	p=5.7E-02	n=1

[illegible]