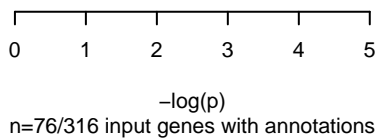


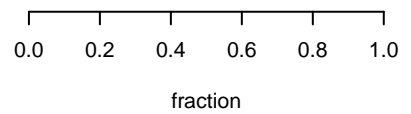
GO:BP
Elav_Nvec_vc1.1_XM_032362379.2

fraction genes in fg and expected value

cellular response to glucagon stimulus	GO:0071377	p=6.9E-04	n=3
positive regulation of mRNA processing	GO:0050685	p=6.9E-04	n=3
cellular response to antibiotic	GO:0071236	p=7.3E-04	n=6
positive regulation of transcription fro...	GO:0061419	p=7.8E-04	n=2
positive regulation of transcription fro...	GO:0061408	p=7.8E-04	n=2
regulation of Golgi organization	GO:1903358	p=2.3E-03	n=2
response to herbicide	GO:0009635	p=2.3E-03	n=2
regulation of cell maturation	GO:1903429	p=2.9E-03	n=4
energy derivation by oxidation of organi...	GO:0015980	p=3.8E-03	n=8
G protein-coupled adenosine receptor sig...	GO:0001973	p=4.5E-03	n=2
cellular response to forskolin	GO:1904322	p=4.5E-03	n=2
regulation of body fluid levels	GO:0050878	p=5.2E-03	n=7
angiogenesis	GO:0001525	p=6.1E-03	n=6
regulation of terminal button organizati...	GO:2000331	p=7.4E-03	n=2
regulation of transcription from RNA pol...	GO:0043619	p=7.4E-03	n=2
motor neuron apoptotic process	GO:0097049	p=7.4E-03	n=2
response to platelet aggregation inhibiti...	GO:0061478	p=7.4E-03	n=2
negative regulation of Rho protein signa...	GO:0035024	p=7.4E-03	n=2
positive regulation of reactive oxygen s...	GO:2000379	p=7.6E-03	n=3
cellular protein modification process	GO:0006464	p=8.7E-03	n=33
wound healing	GO:0042060	p=8.9E-03	n=8
cognition	GO:0050890	p=9.7E-03	n=9
cAMP-mediated signaling	GO:0019933	p=1.0E-02	n=4
regulation of superoxide metabolic proce...	GO:0090322	p=1.1E-02	n=2
negative regulation of cardiac muscle ce...	GO:0010667	p=1.1E-02	n=2
cellular response to dexamethasone stimu...	GO:0071549	p=1.1E-02	n=2
positive regulation of viral life cycle	GO:1903902	p=1.1E-02	n=3
cellular respiration	GO:0045333	p=1.1E-02	n=6
long-term memory	GO:0007616	p=1.3E-02	n=4
behavior	GO:0007610	p=1.4E-02	n=16



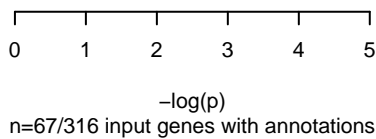
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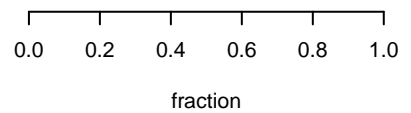
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Elav_Nvec_vc1.1_XM_032362379.2

fraction genes in fg and expected value

protein domain specific binding	GO:0019904	p=2.6E-03	n=13
actin monomer binding	GO:0003785	p=7.5E-03	n=2
phosphorus-oxygen lyase activity	GO:0016849	p=7.5E-03	n=2
cyclase activity	GO:0009975	p=1.1E-02	n=2
cholesterol binding	GO:0015485	p=1.5E-02	n=2
ubiquitin-ubiquitin ligase activity	GO:0034450	p=2.0E-02	n=2
sterol binding	GO:0032934	p=2.0E-02	n=2
carboxy-lyase activity	GO:0016831	p=2.0E-02	n=2
protein serine/threonine kinase inhibito...	GO:0030291	p=2.0E-02	n=2
active transmembrane transporter activi...	GO:0022804	p=2.4E-02	n=6
cyclin-dependent protein serine/threonin...	GO:0016538	p=2.5E-02	n=2
glycerone kinase activity	GO:0004371	p=2.8E-02	n=1
malate dehydrogenase (NADP+) activity	GO:0046554	p=2.8E-02	n=1
calcium- and calmodulin-responsive adeny...	GO:0008294	p=2.8E-02	n=1
peptide alpha-N-acetyltransferase activi...	GO:0004596	p=2.8E-02	n=1
inorganic phosphate transmembrane transp...	GO:0005315	p=2.8E-02	n=1
high-affinity inorganic phosphate:sodium...	GO:0005316	p=2.8E-02	n=1
peptide-serine-N-acetyltransferase activ...	GO:1990189	p=2.8E-02	n=1
volume-sensitive chloride channel activi...	GO:0072320	p=2.8E-02	n=1
cobalt ion binding	GO:0050897	p=2.8E-02	n=1
phosphatidylserine decarboxylase activi...	GO:0004609	p=2.8E-02	n=1
FAD-AMP lyase (cycling) activity	GO:0034012	p=2.8E-02	n=1
alpha-1,6-mannosylglycoprotein 2-beta-N-...	GO:0008455	p=2.8E-02	n=1
ABC-type sterol transporter activity	GO:0034041	p=2.8E-02	n=1
translation elongation factor binding	GO:0061770	p=2.8E-02	n=1
sodium:inorganic phosphate symporter act...	GO:0015319	p=2.8E-02	n=1
triokinase activity	GO:0050354	p=2.8E-02	n=1
histone deacetylase activity	GO:0004407	p=3.1E-02	n=2
GTP binding	GO:0005525	p=3.4E-02	n=4
histone deacetylase binding	GO:0042826	p=3.5E-02	n=3



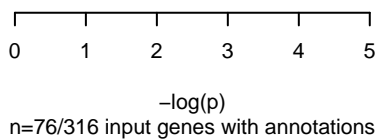
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GO:CC
Elav_Nvec_vc1.1_XM_032362379.2

fraction genes in fg and expected value

microvillus membrane	GO:0031528	p=1.5E-02	n=2
spindle pole	GO:0000922	p=2.5E-02	n=4
XPC complex	GO:0071942	p=2.8E-02	n=1
nucleotide-excision repair complex	GO:0000109	p=2.8E-02	n=1
plus-end kinesin complex	GO:0005873	p=2.8E-02	n=1
catalytic step 1 spliceosome	GO:0071012	p=2.8E-02	n=1
retromer, cargo-selective complex	GO:0030906	p=2.8E-02	n=1
U2-type catalytic step 1 spliceosome	GO:0071006	p=2.8E-02	n=1
sarcoplasmic reticulum lumen	GO:0033018	p=2.8E-02	n=1
protein kinase complex	GO:1902911	p=3.2E-02	n=3
mitotic spindle pole	GO:0097431	p=3.6E-02	n=2
nuclear body	GO:0016604	p=3.8E-02	n=9
plasma membrane region	GO:0098590	p=4.4E-02	n=11
apical plasma membrane	GO:0016324	p=4.7E-02	n=6
histone deacetylase complex	GO:0000118	p=5.0E-02	n=2
ribonucleoside-diphosphate reductase com...	GO:0005971	p=5.6E-02	n=1
Sin3 complex	GO:0016580	p=5.6E-02	n=1
integrin alpha9-beta1 complex	GO:0034679	p=5.6E-02	n=1
nuclear stress granule	GO:0097165	p=5.6E-02	n=1
cytoplasmic cyclin-dependent protein kin...	GO:0000308	p=5.6E-02	n=1
t-UTP complex	GO:0034455	p=5.6E-02	n=1
germ cell nucleus	GO:0043073	p=6.5E-02	n=2
apical part of cell	GO:0045177	p=7.0E-02	n=7
cytosol	GO:0005829	p=7.7E-02	n=37
Golgi apparatus	GO:0005794	p=8.0E-02	n=13
astral microtubule	GO:0000235	p=8.2E-02	n=1
FAR/SIN/STRIK complex	GO:0090443	p=8.2E-02	n=1
inhibitory synapse	GO:0060077	p=8.2E-02	n=1
prefoldin complex	GO:0016272	p=8.2E-02	n=1
PRC1 complex	GO:0035102	p=8.2E-02	n=1



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