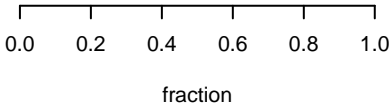
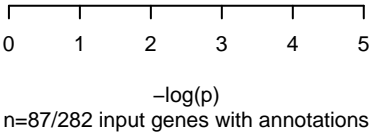


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001634160.3

fraction genes in fg and expected value

cellular response to glucose stimulus	GO:0071333	p=9.8E-04	n=6
carnitine biosynthetic process	GO:0045329	p=1.0E-03	n=2
energy coupled proton transmembrane tran...	GO:0015988	p=1.0E-03	n=3
cellular response to glucagon stimulus	GO:0071377	p=1.0E-03	n=3
nicotinamide nucleotide metabolic proces...	GO:0046496	p=1.1E-03	n=6
establishment of mitotic spindle orienta...	GO:0000132	p=2.2E-03	n=4
transferrin transport	GO:0033572	p=2.4E-03	n=3
adherens junction assembly	GO:0034333	p=2.4E-03	n=3
oocyte microtubule cytoskeleton organiza...	GO:0016325	p=2.4E-03	n=3
NAD metabolic process	GO:0019674	p=2.7E-03	n=4
establishment or maintenance of polarity...	GO:0016332	p=3.0E-03	n=2
NADH metabolic process	GO:0006734	p=5.8E-03	n=3
sperm capacitation	GO:0048240	p=5.9E-03	n=2
activation of phospholipase C activity	GO:0007202	p=5.9E-03	n=2
basal protein localization	GO:0045175	p=5.9E-03	n=2
N-terminal protein amino acid acetylatio...	GO:0006474	p=5.9E-03	n=2
proton-transporting two-sector ATPase co...	GO:0070071	p=5.9E-03	n=2
activation of protein kinase A activity	GO:0034199	p=5.9E-03	n=2
response to antipsychotic drug	GO:0097332	p=5.9E-03	n=2
response to clozapine	GO:0097338	p=5.9E-03	n=2
ecdysone-mediated induction of salivary ...	GO:0035072	p=5.9E-03	n=2
mitochondrial acetyl-CoA biosynthetic pr...	GO:0061732	p=5.9E-03	n=2
positive regulation of insulin secretion	GO:0032024	p=6.5E-03	n=4
energy derivation by oxidation of organi...	GO:0015980	p=8.6E-03	n=8
cellular response to cAMP	GO:0071320	p=9.1E-03	n=3
positive regulation of leukocyte mediate...	GO:0001912	p=9.6E-03	n=2
regulation of T cell differentiation in ...	GO:0033081	p=9.6E-03	n=2
innate immune response-activating signal...	GO:0002758	p=1.1E-02	n=3
alcohol biosynthetic process	GO:0046165	p=1.1E-02	n=4
embryonic morphogenesis	GO:0048598	p=1.2E-02	n=15

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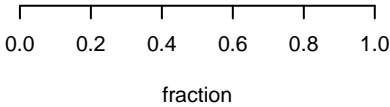
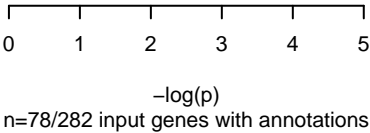


GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001634160.3

fraction genes in fg and expected value

gamma-butyrobetaine dioxygenase activity	GO:0008336	p=1.1E-03	n=2
protein-disulfide reductase (NAD(P)) act...	GO:0047134	p=2.5E-03	n=3
oxidoreductase activity, acting on NAD(P...	GO:0016651	p=3.0E-03	n=5
vinculin binding	GO:0017166	p=3.1E-03	n=2
ATPase-coupled ion transmembrane transpo...	GO:0042625	p=1.4E-02	n=3
proton-transporting ATPase activity, rot...	GO:0046961	p=1.5E-02	n=2
ATPase activity, coupled to transmembran...	GO:0044769	p=1.5E-02	n=2
pyrophosphate hydrolysis-driven proton t...	GO:0009678	p=1.5E-02	n=2
phosphatase regulator activity	GO:0019208	p=2.0E-02	n=3
phosphatase inhibitor activity	GO:0019212	p=2.0E-02	n=2
active ion transmembrane transporter act...	GO:0022853	p=2.3E-02	n=5
proton transmembrane transporter activit...	GO:0015078	p=3.0E-02	n=3
oxidoreductase activity, acting on a sul...	GO:0016668	p=3.2E-02	n=4
selenium binding	GO:0008430	p=3.3E-02	n=1
neuropilin binding	GO:0038191	p=3.3E-02	n=1
1-alkenylglycerophosphocholine O-acyltra...	GO:0047159	p=3.3E-02	n=1
myosin II binding	GO:0045159	p=3.3E-02	n=1
misfolded RNA binding	GO:0034336	p=3.3E-02	n=1
BH4 domain binding	GO:0051435	p=3.3E-02	n=1
Roundabout binding	GO:0048495	p=3.3E-02	n=1
tricarboxylate secondary active transmem...	GO:0005371	p=3.3E-02	n=1
nickel cation transmembrane transporter ...	GO:0015099	p=3.3E-02	n=1
glycogen binding	GO:2001069	p=3.3E-02	n=1
mitochondrial ribosome binding	GO:0097177	p=3.3E-02	n=1
[phosphorylase] phosphatase activity	GO:0050196	p=3.3E-02	n=1
neurotrophin TRK receptor binding	GO:0005167	p=3.3E-02	n=1
neurotrophin TRKA receptor binding	GO:0005168	p=3.3E-02	n=1
UDP-N-acetylglucosamine-dolichyl-phospha...	GO:0003975	p=3.3E-02	n=1
cobalt ion transmembrane transporter act...	GO:0015087	p=3.3E-02	n=1
netrin receptor activity	GO:0005042	p=3.3E-02	n=1

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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001634160.3

fraction genes in fg and expected value

vacuolar proton-transporting V-type ATPa...	GO:0016471	p=9.3E-04	n=3
mitochondrial tricarboxylic acid cycle e...	GO:0030062	p=2.8E-03	n=2
cAMP-dependent protein kinase complex	GO:0005952	p=2.8E-03	n=2
nucleotide-activated protein kinase comp...	GO:0031588	p=5.5E-03	n=2
RNA polymerase II, core complex	GO:0005665	p=9.0E-03	n=2
plasma membrane raft	GO:0044853	p=1.3E-02	n=4
plasma membrane proton-transporting V-ty...	GO:0033181	p=1.3E-02	n=2
germinal vesicle	GO:0042585	p=1.8E-02	n=2
apicolateral plasma membrane	GO:0016327	p=1.8E-02	n=2
female germ cell nucleus	GO:0001674	p=2.4E-02	n=2
apical plasma membrane	GO:0016324	p=2.5E-02	n=7
phagocytic vesicle membrane	GO:0030670	p=3.0E-02	n=2
axonal growth cone	GO:0044295	p=3.0E-02	n=2
integral component of organelle membran...	GO:0031301	p=3.1E-02	n=7
internode region of axon	GO:0033269	p=3.1E-02	n=1
isocitrate dehydrogenase complex (NAD+)	GO:0045242	p=3.1E-02	n=1
CAF-1 complex	GO:0033186	p=3.1E-02	n=1
Ric1-Rgp1 guanyl-nucleotide exchange fac...	GO:0034066	p=3.1E-02	n=1
mitochondrial isocitrate dehydrogenase c...	GO:0005962	p=3.1E-02	n=1
smooth septate junction	GO:0005920	p=3.1E-02	n=1
Schmidt-Lanterman incisure	GO:0043220	p=3.1E-02	n=1
oxoglutarate dehydrogenase complex	GO:0045252	p=3.1E-02	n=1
FACT complex	GO:0035101	p=3.1E-02	n=1
compact myelin	GO:0043218	p=3.1E-02	n=1
anterior cell cortex	GO:0061802	p=3.1E-02	n=1
acrosomal matrix	GO:0043159	p=3.1E-02	n=1
apical junction complex	GO:0043296	p=3.7E-02	n=3
intrinsic component of organelle membran...	GO:0031300	p=3.7E-02	n=7
plasma membrane region	GO:0098590	p=3.9E-02	n=12
microtubule cytoskeleton	GO:0015630	p=4.4E-02	n=14

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