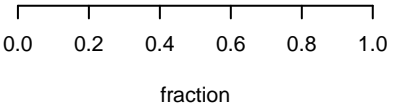
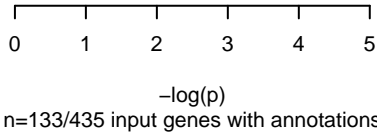


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001634132.3

fraction genes in fg and expected value

triglyceride biosynthetic process	GO:0019432	p=8.1E-04	n=4
canonical Wnt signaling pathway	GO:0060070	p=9.7E-04	n=11
regulation of biological quality	GO:0065008	p=1.5E-03	n=62
epithelial structure maintenance	GO:0010669	p=1.5E-03	n=3
negative regulation of angiogenesis	GO:0016525	p=1.5E-03	n=4
gluconeogenesis	GO:0006094	p=1.7E-03	n=6
liver development	GO:0001889	p=2.0E-03	n=7
nucleotide catabolic process	GO:0009166	p=2.0E-03	n=7
signal release	GO:0023061	p=2.5E-03	n=19
negative regulation of Rho protein signa...	GO:0035024	p=3.5E-03	n=3
positive regulation of cAMP-mediated sig...	GO:0043950	p=3.5E-03	n=3
response to acidic pH	GO:0010447	p=3.5E-03	n=3
G1/S transition of mitotic cell cycle	GO:0000082	p=3.5E-03	n=8
regulation of morphogenesis of an epithe...	GO:1905330	p=3.9E-03	n=7
heart development	GO:0007507	p=4.2E-03	n=16
cellular response to decreased oxygen le...	GO:0036294	p=4.2E-03	n=8
regulation of mitotic cell cycle phase t...	GO:1901990	p=4.3E-03	n=11
motor neuron axon guidance	GO:0008045	p=4.4E-03	n=5
negative regulation of sequestering of t...	GO:0010891	p=5.3E-03	n=2
nephric duct formation	GO:0072179	p=5.3E-03	n=2
negative regulation of Rac protein signa...	GO:0035021	p=5.3E-03	n=2
plasma membrane raft assembly	GO:0044854	p=5.3E-03	n=2
cellular response to leucine	GO:0071233	p=5.3E-03	n=2
positive regulation of rRNA processing	GO:2000234	p=5.3E-03	n=2
negative regulation of immunoglobulin pr...	GO:0002638	p=5.3E-03	n=2
canonical glycolysis	GO:0061621	p=5.3E-03	n=2
positive regulation of ribosome biogenes...	GO:0090070	p=5.3E-03	n=2
polarity specification of proximal/dista...	GO:0010085	p=5.3E-03	n=2
positive regulation of lipophagy	GO:1904504	p=5.3E-03	n=2
establishment of vesicle localization	GO:0051650	p=5.6E-03	n=12

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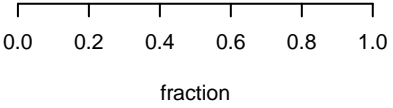
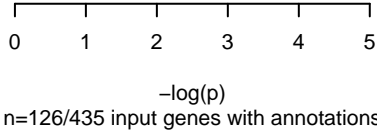


GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001634132.3

fraction genes in fg and expected value

carboxylic acid binding	GO:0031406	p=1.3E-03	n=6
signaling receptor binding	GO:0005102	p=1.6E-03	n=24
epinephrine binding	GO:0051379	p=4.3E-03	n=3
phospholipid binding	GO:0005543	p=4.3E-03	n=12
voltage-gated potassium channel activity	GO:0005249	p=5.4E-03	n=4
amino acid binding	GO:0016597	p=5.4E-03	n=4
telomerase RNA binding	GO:0070034	p=6.2E-03	n=2
GTPase regulator activity	GO:0030695	p=1.2E-02	n=12
outward rectifier potassium channel acti...	GO:0015271	p=1.3E-02	n=3
oxidoreductase activity, acting on a sul...	GO:0016668	p=1.3E-02	n=3
protein-disulfide reductase (NAD(P)) act...	GO:0047134	p=1.3E-02	n=3
nucleoside-triphosphatase regulator acti...	GO:0060589	p=1.4E-02	n=13
oxidoreductase activity, acting on the C...	GO:0016899	p=1.8E-02	n=2
inosine kinase activity	GO:0008906	p=1.8E-02	n=2
lactate dehydrogenase activity	GO:0004457	p=1.8E-02	n=2
receptor-receptor interaction	GO:0090722	p=1.8E-02	n=2
phosphoenolpyruvate carboxykinase activi...	GO:0004611	p=1.8E-02	n=2
phosphoenolpyruvate carboxykinase (GTP) ...	GO:0004613	p=1.8E-02	n=2
DNA binding domain binding	GO:0050692	p=1.8E-02	n=2
WW domain binding	GO:0050699	p=1.8E-02	n=2
kinesin binding	GO:0019894	p=2.0E-02	n=4
protein domain specific binding	GO:0019904	p=2.4E-02	n=19
phosphatidylinositol binding	GO:0035091	p=2.5E-02	n=8
oxidoreductase activity, acting on a sul...	GO:0016667	p=2.6E-02	n=4
sequence-specific DNA binding	GO:0043565	p=2.6E-02	n=15
DNA binding	GO:0003677	p=2.8E-02	n=22
protein-disulfide reductase activity	GO:0015035	p=2.9E-02	n=3
ion channel inhibitor activity	GO:0008200	p=2.9E-02	n=3
disordered domain specific binding	GO:0097718	p=2.9E-02	n=3
GTPase activator activity	GO:0005096	p=3.0E-02	n=7

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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001634132.3

fraction genes in fg and expected value

voltage-gated potassium channel complex	GO:0008076	p=2.9E-03	n=4
caveola	GO:0005901	p=5.1E-03	n=5
cell leading edge	GO:0031252	p=8.0E-03	n=11
lipid droplet	GO:0005811	p=1.1E-02	n=5
axon cytoplasm	GO:1904115	p=1.6E-02	n=2
beta-catenin-TCF complex	GO:1990907	p=1.6E-02	n=2
EARP complex	GO:1990745	p=1.6E-02	n=2
GARP complex	GO:0000938	p=1.6E-02	n=2
nuclear membrane	GO:0031965	p=1.8E-02	n=7
focal adhesion	GO:0005925	p=2.2E-02	n=4
mediator complex	GO:0016592	p=2.5E-02	n=3
adherens junction	GO:0005912	p=2.8E-02	n=7
subsynaptic reticulum	GO:0071212	p=3.1E-02	n=2
cytoplasmic dynein complex	GO:0005868	p=3.1E-02	n=2
spindle midzone	GO:0051233	p=3.1E-02	n=2
axon	GO:0030424	p=3.3E-02	n=17
type I terminal bouton	GO:0061174	p=3.4E-02	n=3
vesicle tethering complex	GO:0099023	p=3.5E-02	n=4
extrinsic component of membrane	GO:0019898	p=3.5E-02	n=7
Z disc	GO:0030018	p=3.6E-02	n=5
I band	GO:0031674	p=4.2E-02	n=5
cell-substrate junction	GO:0030055	p=4.2E-02	n=4
cell periphery	GO:0071944	p=4.2E-02	n=54
lamellipodium	GO:0030027	p=4.4E-02	n=6
intracellular canalculus	GO:0046691	p=4.9E-02	n=2
presynaptic active zone membrane	GO:0048787	p=4.9E-02	n=2
sperm fibrous sheath	GO:0035686	p=4.9E-02	n=2
juxtaparanode region of axon	GO:0044224	p=4.9E-02	n=2
messenger ribonucleoprotein complex	GO:1990124	p=4.9E-02	n=2
cytoplasmic region	GO:0099568	p=5.0E-02	n=12

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