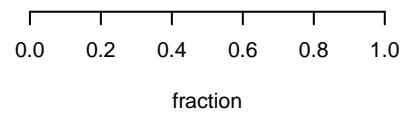
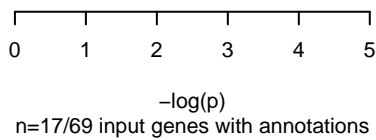


GO:BP
Elav_Nvec_vc1.1_XM_032363859.2

fraction genes in fg and expected value

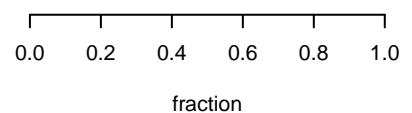
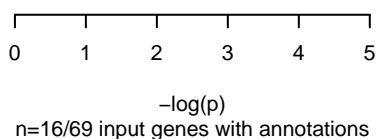
extracellular matrix disassembly	GO:0022617	p=9.4E-03	n=2	fg=0.12	bg=0.01
negative regulation of dephosphorylation	GO:0035305	p=2.2E-02	n=2	fg=0.12	bg=0.01
cell projection assembly	GO:0030031	p=2.9E-02	n=3	fg=0.18	bg=0.04
cell projection organization	GO:0030030	p=2.9E-02	n=7	fg=0.41	bg=0.19
dendrite morphogenesis	GO:0048813	p=3.8E-02	n=3	fg=0.18	bg=0.05
salivary gland morphogenesis	GO:0007435	p=4.0E-02	n=2	fg=0.12	bg=0.02
modulation by host of symbiont transcrip...	GO:0052472	p=4.2E-02	n=1	fg=0.06	bg=0.00
water transport	GO:0006833	p=4.2E-02	n=1	fg=0.06	bg=0.00
ruffle assembly	GO:0097178	p=4.2E-02	n=1	fg=0.06	bg=0.00
anterior Malpighian tubule development	GO:0061327	p=4.2E-02	n=1	fg=0.06	bg=0.00
hemocyte development	GO:0007516	p=4.2E-02	n=1	fg=0.06	bg=0.00
inositol phosphate catabolic process	GO:0071545	p=4.2E-02	n=1	fg=0.06	bg=0.00
establishment of protein localization to...	GO:0072666	p=4.2E-02	n=1	fg=0.06	bg=0.00
inositol phosphate dephosphorylation	GO:0046855	p=4.2E-02	n=1	fg=0.06	bg=0.00
negative regulation of viral process	GO:0048525	p=4.2E-02	n=1	fg=0.06	bg=0.00
TORC1 signaling	GO:0038202	p=4.2E-02	n=1	fg=0.06	bg=0.00
negative regulation of viral transcripti...	GO:0032897	p=4.2E-02	n=1	fg=0.06	bg=0.00
alcohol catabolic process	GO:0046164	p=4.2E-02	n=1	fg=0.06	bg=0.00
regulation of glycogen (starch) synthase...	GO:2000465	p=4.2E-02	n=1	fg=0.06	bg=0.00
negative regulation of glycogen (starch)...	GO:2000466	p=4.2E-02	n=1	fg=0.06	bg=0.00
fibrinolysis	GO:0042730	p=4.2E-02	n=1	fg=0.06	bg=0.00
phosphorylated carbohydrate dephosphoryl...	GO:0046838	p=4.2E-02	n=1	fg=0.06	bg=0.00
polyol catabolic process	GO:0046174	p=4.2E-02	n=1	fg=0.06	bg=0.00
negative regulation of single stranded v...	GO:0045869	p=4.2E-02	n=1	fg=0.06	bg=0.00
protein localization to lysosome	GO:0061462	p=4.2E-02	n=1	fg=0.06	bg=0.00
motor behavior	GO:0061744	p=4.2E-02	n=1	fg=0.06	bg=0.00
single stranded viral RNA replication vi...	GO:0039692	p=4.2E-02	n=1	fg=0.06	bg=0.00
secretion of lysosomal enzymes	GO:0033299	p=4.2E-02	n=1	fg=0.06	bg=0.00
lysosome organization	GO:0007040	p=4.2E-02	n=1	fg=0.06	bg=0.00
negative regulation of extracellular mat...	GO:1903054	p=4.2E-02	n=1	fg=0.06	bg=0.00



GO:MF
Elav_Nvec_vc1.1_XM_032363859.2

fraction genes in fg and expected value

metallopeptidase activity	GO:0008237	p=5.3E-03	n=2	fg=0.12	bg=0.01
guanyl-nucleotide exchange factor activi...	GO:0005085	p=3.4E-02	n=2	fg=0.12	bg=0.02
inositol bisphosphate phosphatase activi...	GO:0016312	p=4.4E-02	n=1	fg=0.06	bg=0.00
inositol 1,3,4,5 tetrakisphosphate bindi...	GO:0043533	p=4.4E-02	n=1	fg=0.06	bg=0.00
serine-type peptidase activity	GO:0008236	p=4.4E-02	n=1	fg=0.06	bg=0.00
1-phosphatidylinositol binding	GO:0005545	p=4.4E-02	n=1	fg=0.06	bg=0.00
dipeptidyl-peptidase activity	GO:0008239	p=4.4E-02	n=1	fg=0.06	bg=0.00
exogenous protein binding	GO:0140272	p=4.4E-02	n=1	fg=0.06	bg=0.00
inositol-1,4,5-trisphosphate 5-phosphata...	GO:0052658	p=4.4E-02	n=1	fg=0.06	bg=0.00
inositol-1,3,4,5-tetrakisphosphate 5-pho...	GO:0052659	p=4.4E-02	n=1	fg=0.06	bg=0.00
inositol trisphosphate phosphatase activ...	GO:0046030	p=4.4E-02	n=1	fg=0.06	bg=0.00
inositol tetrakisphosphate phosphatase a...	GO:0052743	p=4.4E-02	n=1	fg=0.06	bg=0.00
inositol-polyphosphate 5-phosphatase act...	GO:0004445	p=4.4E-02	n=1	fg=0.06	bg=0.00
lipid phosphatase activity	GO:0042577	p=4.4E-02	n=1	fg=0.06	bg=0.00
serine-type endopeptidase activity	GO:0004252	p=4.4E-02	n=1	fg=0.06	bg=0.00
N-acetylglucosamine-1-phosphodiester alp...	GO:0003944	p=4.4E-02	n=1	fg=0.06	bg=0.00
phosphatidylinositol-3,4,5-trisphosphate...	GO:0034485	p=4.4E-02	n=1	fg=0.06	bg=0.00
phosphatidylinositol-4,5-bisphosphate 5-...	GO:0004439	p=4.4E-02	n=1	fg=0.06	bg=0.00
protein N-terminus binding	GO:0047485	p=4.4E-02	n=1	fg=0.06	bg=0.00
small molecule sensor activity	GO:0140299	p=4.4E-02	n=1	fg=0.06	bg=0.00
metalloendopeptidase activity	GO:0004222	p=4.4E-02	n=1	fg=0.06	bg=0.00
phosphatidylinositol-4,5-bisphosphate ph...	GO:0106019	p=4.4E-02	n=1	fg=0.06	bg=0.00
aminopeptidase activity	GO:0004177	p=4.4E-02	n=1	fg=0.06	bg=0.00
phosphatidylinositol-3,4-bisphosphate bi...	GO:0043325	p=4.4E-02	n=1	fg=0.06	bg=0.00
virus receptor activity	GO:0001618	p=4.4E-02	n=1	fg=0.06	bg=0.00
oxygen binding	GO:0019825	p=4.4E-02	n=1	fg=0.06	bg=0.00
oxygen sensor activity	GO:0019826	p=4.4E-02	n=1	fg=0.06	bg=0.00
carbon monoxide binding	GO:0070025	p=4.4E-02	n=1	fg=0.06	bg=0.00
nitric oxide binding	GO:0070026	p=4.4E-02	n=1	fg=0.06	bg=0.00
hexosaminidase activity	GO:0015929	p=4.4E-02	n=1	fg=0.06	bg=0.00



GO:CC
Elav_Nvec_vc1.1_XM_032363859.2

fraction genes in fg and expected value

ruffle membrane	GO:0032587	p=9.6E-03	n=2	fg=0.12	bg=0.01
extrinsic component of membrane	GO:0019898	p=7.4E-02	n=2	fg=0.12	bg=0.03
muscle myosin complex	GO:0005859	p=8.3E-02	n=1	fg=0.06	bg=0.00
myosin II complex	GO:0016460	p=8.3E-02	n=1	fg=0.06	bg=0.00
unconventional myosin complex	GO:0016461	p=8.3E-02	n=1	fg=0.06	bg=0.00
myosin complex	GO:0016459	p=8.3E-02	n=1	fg=0.06	bg=0.00
intercellular canaliculus	GO:0046581	p=8.3E-02	n=1	fg=0.06	bg=0.00
myosin V complex	GO:0031475	p=8.3E-02	n=1	fg=0.06	bg=0.00
myosin VI complex	GO:0031476	p=8.3E-02	n=1	fg=0.06	bg=0.00
myosin VII complex	GO:0031477	p=8.3E-02	n=1	fg=0.06	bg=0.00
cytosol	GO:0005829	p=9.6E-02	n=9	fg=0.53	bg=0.35
extracellular space	GO:0005615	p=1.0E-01	n=2	fg=0.12	bg=0.03
ciliary transition zone	GO:0035869	p=1.2E-01	n=1	fg=0.06	bg=0.01
extrinsic component of cytoplasmic side ...	GO:0031234	p=1.6E-01	n=1	fg=0.06	bg=0.01
ciliary base	GO:0097546	p=1.6E-01	n=1	fg=0.06	bg=0.01
guanylate cyclase complex, soluble	GO:0008074	p=1.6E-01	n=1	fg=0.06	bg=0.01
cell surface	GO:0009986	p=1.9E-01	n=2	fg=0.12	bg=0.05
extrinsic component of plasma membrane	GO:0019897	p=2.0E-01	n=1	fg=0.06	bg=0.01
vacuolar lumen	GO:0005775	p=2.0E-01	n=1	fg=0.06	bg=0.01
azurophil granule lumen	GO:0035578	p=2.0E-01	n=1	fg=0.06	bg=0.01
brush border	GO:0005903	p=2.3E-01	n=1	fg=0.06	bg=0.01
cluster of actin-based cell projections	GO:0098862	p=2.6E-01	n=1	fg=0.06	bg=0.02
primary lysosome	GO:0005766	p=2.6E-01	n=1	fg=0.06	bg=0.02
azurophil granule	GO:0042582	p=2.6E-01	n=1	fg=0.06	bg=0.02
vesicle lumen	GO:0031983	p=2.9E-01	n=1	fg=0.06	bg=0.02
secretory granule lumen	GO:0034774	p=2.9E-01	n=1	fg=0.06	bg=0.02
cytoplasmic vesicle lumen	GO:0060205	p=2.9E-01	n=1	fg=0.06	bg=0.02
extracellular region	GO:0005576	p=3.0E-01	n=2	fg=0.12	bg=0.06
dendritic shaft	GO:0043198	p=3.2E-01	n=1	fg=0.06	bg=0.02
endocytic vesicle	GO:0030139	p=3.5E-01	n=1	fg=0.06	bg=0.02

