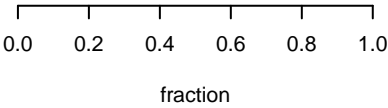
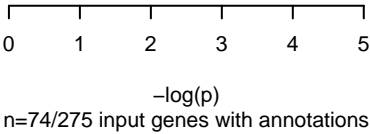


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001632824.3

fraction genes in fg and expected value

intermembrane lipid transfer	GO:0120009	p=1.6E-03	n=2
nephric duct formation	GO:0072179	p=1.6E-03	n=2
t-circle formation	GO:0090656	p=1.6E-03	n=2
ventral spinal cord development	GO:0021517	p=2.0E-03	n=3
cell differentiation in spinal cord	GO:0021515	p=3.1E-03	n=3
renal system development	GO:0072001	p=3.8E-03	n=10
regulation of nephron tubule epithelial ...	GO:0072182	p=4.8E-03	n=2
response to UV-C	GO:0010225	p=4.8E-03	n=2
lymphoid progenitor cell differentiation	GO:0002320	p=4.8E-03	n=2
somite rostral/caudal axis specification	GO:0032525	p=4.8E-03	n=2
positive regulation of cysteine-type end...	GO:2001269	p=4.8E-03	n=2
telomeric D-loop disassembly	GO:0061820	p=4.8E-03	n=2
ectoderm development	GO:0007398	p=6.4E-03	n=3
humoral immune response	GO:0006959	p=7.5E-03	n=4
neuroepithelial cell differentiation	GO:0060563	p=9.0E-03	n=4
uterus development	GO:0060065	p=9.3E-03	n=2
cardiac right ventricle morphogenesis	GO:0003215	p=9.3E-03	n=2
positive regulation of mesonephros devel...	GO:0061213	p=9.3E-03	n=2
epithelial cell migration, open tracheal...	GO:0007427	p=9.3E-03	n=2
embryonic epithelial tube formation	GO:0001838	p=9.6E-03	n=5
positive regulation of nucleobase-contai...	GO:0045935	p=9.6E-03	n=19
positive regulation of transcription, DN...	GO:0045893	p=1.1E-02	n=16
positive regulation of macromolecule bio...	GO:0010557	p=1.2E-02	n=18
regulation of actin filament bundle asse...	GO:0032231	p=1.3E-02	n=4
endoplasmic reticulum mannose trimming	GO:1904380	p=1.5E-02	n=2
cellular response to ethanol	GO:0071361	p=1.5E-02	n=2
isoprenoid metabolic process	GO:0006720	p=1.5E-02	n=2
T cell differentiation involved in immun...	GO:0002292	p=1.5E-02	n=2
positive regulation of nucleic acid-temp...	GO:1903508	p=1.6E-02	n=16
positive regulation of RNA biosynthetic ...	GO:1902680	p=1.6E-02	n=16

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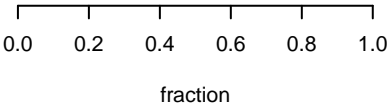
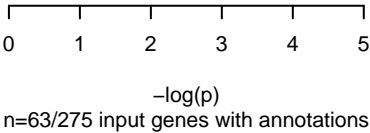


GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001632824.3

fraction genes in fg and expected value

E-box binding	GO:0070888	p=4.2E-03	n=3
nuclear receptor coactivator activity	GO:0030374	p=4.2E-03	n=3
lipid transfer activity	GO:0120013	p=1.4E-02	n=2
structural constituent of nuclear pore	GO:0017056	p=1.4E-02	n=2
telomeric DNA binding	GO:0042162	p=1.4E-02	n=2
manganese ion binding	GO:0030145	p=1.9E-02	n=3
HMG box domain binding	GO:0071837	p=2.1E-02	n=2
carboxy-lyase activity	GO:0016831	p=2.1E-02	n=2
DNA-binding transcription factor activit...	GO:0000981	p=2.2E-02	n=9
damaged DNA binding	GO:0003684	p=3.7E-02	n=2
transcription coactivator activity	GO:0003713	p=3.8E-02	n=8
four-way junction DNA binding	GO:0000400	p=4.0E-02	n=1
forked DNA-dependent helicase activity	GO:0061749	p=4.0E-02	n=1
fibroblast growth factor receptor bindin...	GO:0005104	p=4.0E-02	n=1
sphingomyelin phosphodiesterase D activi...	GO:0050290	p=4.0E-02	n=1
sphingolipid transfer activity	GO:0120016	p=4.0E-02	n=1
ceramide transfer activity	GO:0120017	p=4.0E-02	n=1
signal recognition particle binding	GO:0005047	p=4.0E-02	n=1
heparanase activity	GO:0030305	p=4.0E-02	n=1
G-protein beta-subunit binding	GO:0031681	p=4.0E-02	n=1
polynucleotide 5'-phosphatase activity	GO:0004651	p=4.0E-02	n=1
molybdopterin cofactor binding	GO:0043546	p=4.0E-02	n=1
7S RNA binding	GO:0008312	p=4.0E-02	n=1
polynucleotide phosphatase activity	GO:0098518	p=4.0E-02	n=1
BIR domain binding	GO:1990525	p=4.0E-02	n=1
8-hydroxy-2'-deoxyguanosine DNA binding	GO:1905773	p=4.0E-02	n=1
glycolipid transfer activity	GO:0017089	p=4.0E-02	n=1
mevalonate kinase activity	GO:0004496	p=4.0E-02	n=1
flap-structured DNA binding	GO:0070336	p=4.0E-02	n=1
3'-flap-structured DNA binding	GO:0070337	p=4.0E-02	n=1

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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001632824.3

fraction genes in fg and expected value

NuRD complex	GO:0016581	p=4.7E-03	n=2
intracellular membrane-bounded organelle	GO:0043231	p=5.3E-03	n=66
ruffle membrane	GO:0032587	p=6.2E-03	n=3
nucleus	GO:0005634	p=1.6E-02	n=45
Derlin-1 retrotranslocation complex	GO:0036513	p=2.2E-02	n=2
nuclear speck	GO:0016607	p=3.4E-02	n=6
lipid droplet	GO:0005811	p=3.8E-02	n=3
chromosome, telomeric region	GO:0000781	p=3.8E-02	n=2
signal recognition particle	GO:0048500	p=4.0E-02	n=1
signal recognition particle, endoplasmic...	GO:0005786	p=4.0E-02	n=1
SAM complex	GO:0001401	p=4.0E-02	n=1
mitochondrial outer membrane translocase...	GO:0005742	p=4.0E-02	n=1
TSC1-TSC2 complex	GO:0033596	p=4.0E-02	n=1
serine-type endopeptidase complex	GO:1905370	p=4.0E-02	n=1
serine-type peptidase complex	GO:1905286	p=4.0E-02	n=1
outer mitochondrial membrane protein com...	GO:0098799	p=4.0E-02	n=1
recycling endosome membrane	GO:0055038	p=4.8E-02	n=2
type I terminal bouton	GO:0061174	p=5.9E-02	n=2
mitochondrion	GO:0005739	p=5.9E-02	n=15
transcription regulator complex	GO:0005667	p=6.7E-02	n=8
endoplasmic reticulum protein-containing...	GO:0140534	p=7.7E-02	n=3
glycosylphosphatidylinositol-N-acetylglu...	GO:0000506	p=7.9E-02	n=1
Nebenkern	GO:0016006	p=7.9E-02	n=1
mitochondrial derivative	GO:0016007	p=7.9E-02	n=1
extrinsic component of membrane	GO:0019898	p=8.6E-02	n=4
nuclear body	GO:0016604	p=8.7E-02	n=8
transcription repressor complex	GO:0017053	p=9.4E-02	n=2
endoplasmic reticulum membrane	GO:0005789	p=1.0E-01	n=9
mitochondrial intermembrane space	GO:0005758	p=1.1E-01	n=2
extracellular matrix	GO:0031012	p=1.1E-01	n=2

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