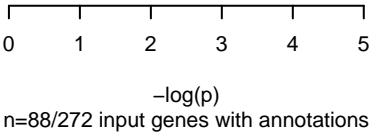


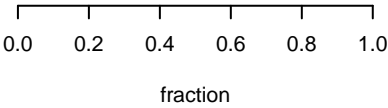
GO:BP
Elav_Nvec_vc1.1_XM_032370541.2

fraction genes in fg and expected value

| | | | |
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| regulation of chromatin binding | GO:0035561 | p=2.0E-03 | n=3 |
| surfactant homeostasis | GO:0043129 | p=2.3E-03 | n=2 |
| negative regulation of dendrite morphoge... | GO:0050774 | p=2.3E-03 | n=2 |
| negative regulation of oxidative stress... | GO:1903377 | p=2.3E-03 | n=2 |
| photoreceptor cell maintenance | GO:0045494 | p=2.6E-03 | n=4 |
| regulation of alternative mRNA splicing,... | GO:0000381 | p=2.6E-03 | n=4 |
| positive regulation of insulin secretion... | GO:0035774 | p=5.2E-03 | n=3 |
| regulation of cellular macromolecule bio... | GO:2000112 | p=6.2E-03 | n=33 |
| mRNA transcription by RNA polymerase II | GO:0042789 | p=6.8E-03 | n=2 |
| response to muscle activity | GO:0014850 | p=6.8E-03 | n=2 |
| regulation of mRNA export from nucleus | GO:0010793 | p=6.8E-03 | n=2 |
| negative regulation of miRNA-mediated ge... | GO:0060965 | p=6.8E-03 | n=2 |
| negative regulation of dendrite developm... | GO:2000171 | p=6.8E-03 | n=2 |
| B-1 B cell homeostasis | GO:0001922 | p=6.8E-03 | n=2 |
| connective tissue replacement | GO:0097709 | p=6.8E-03 | n=2 |
| regulation of cell cycle G1/S phase tran... | GO:1902806 | p=7.0E-03 | n=5 |
| negative regulation of synapse assembly | GO:0051964 | p=7.6E-03 | n=4 |
| courtship behavior | GO:0007619 | p=7.6E-03 | n=4 |
| positive regulation of transcription by ... | GO:0045944 | p=9.0E-03 | n=16 |
| positive regulation of cell cycle G1/S p... | GO:1902808 | p=1.0E-02 | n=3 |
| neural tube formation | GO:0001841 | p=1.1E-02 | n=5 |
| regulation of BMP signaling pathway | GO:0030510 | p=1.1E-02 | n=4 |
| dendritic spine maintenance | GO:0097062 | p=1.3E-02 | n=2 |
| antimicrobial peptide biosynthetic proce... | GO:0002777 | p=1.3E-02 | n=2 |
| regulation of antimicrobial peptide bios... | GO:0002805 | p=1.3E-02 | n=2 |
| norepinephrine metabolic process | GO:0042415 | p=1.3E-02 | n=2 |
| positive regulation of chromatin binding | GO:0035563 | p=1.3E-02 | n=2 |
| regulation of activin receptor signaling... | GO:0032925 | p=1.3E-02 | n=2 |
| negative regulation of reactive oxygen s... | GO:2000378 | p=1.4E-02 | n=3 |
| regulation of protein-containing complex... | GO:0043244 | p=1.6E-02 | n=4 |



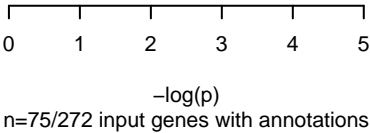
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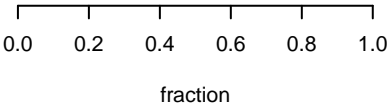
GO:MF
Elav_Nvec_vc1.1_XM_032370541.2

fraction genes in fg and expected value

| | | | |
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| DNA-binding transcription factor activit... | GO:0000981 | p=7.4E-05 | n=15 |
| core promoter sequence-specific DNA bind... | GO:0001046 | p=5.9E-04 | n=5 |
| transcription cis-regulatory region bind... | GO:0000976 | p=1.4E-03 | n=13 |
| RNA binding | GO:0003723 | p=1.7E-03 | n=15 |
| RNA polymerase II transcription regulato... | GO:0000977 | p=3.0E-03 | n=10 |
| mRNA regulatory element binding translat... | GO:0000900 | p=6.4E-03 | n=2 |
| G-quadruplex DNA binding | GO:0051880 | p=6.4E-03 | n=2 |
| single-stranded RNA binding | GO:0003727 | p=1.0E-02 | n=4 |
| cis-regulatory region sequence-specific ... | GO:0000987 | p=1.5E-02 | n=7 |
| RNA polymerase II cis-regulatory region ... | GO:0000978 | p=1.5E-02 | n=7 |
| DNA-binding transcription activator acti... | GO:0001228 | p=2.2E-02 | n=7 |
| DNA-binding transcription activator acti... | GO:0001216 | p=2.2E-02 | n=7 |
| voltage-gated channel activity | GO:0022832 | p=2.4E-02 | n=4 |
| voltage-gated ion channel activity | GO:0005244 | p=2.4E-02 | n=4 |
| mRNA binding | GO:0003729 | p=2.5E-02 | n=6 |
| potassium channel activity | GO:0005267 | p=2.5E-02 | n=3 |
| protein heterodimerization activity | GO:0046982 | p=2.6E-02 | n=9 |
| cyclin-dependent protein serine/threonin... | GO:0016538 | p=2.9E-02 | n=2 |
| Hsp90 protein binding | GO:0051879 | p=3.6E-02 | n=3 |
| single-stranded DNA binding | GO:0003697 | p=3.6E-02 | n=3 |
| transcription regulator activity | GO:0140110 | p=3.6E-02 | n=22 |
| RNA polymerase II core promoter sequence... | GO:0000979 | p=3.9E-02 | n=2 |
| endoribonuclease activity | GO:0004521 | p=3.9E-02 | n=2 |
| potassium ion transmembrane transporter ... | GO:0015079 | p=4.2E-02 | n=3 |
| K48-linked polyubiquitin modification-de... | GO:0036435 | p=4.7E-02 | n=1 |
| lipote synthase activity | GO:0016992 | p=4.7E-02 | n=1 |
| sphingomyelin phosphodiesterase D activi... | GO:0050290 | p=4.7E-02 | n=1 |
| pseudophosphatase activity | GO:0001691 | p=4.7E-02 | n=1 |
| 1-alkenylglycerophosphocholine O-acyltra... | GO:0047159 | p=4.7E-02 | n=1 |
| phosphatidylinositol 3-kinase catalytic ... | GO:0036313 | p=4.7E-02 | n=1 |



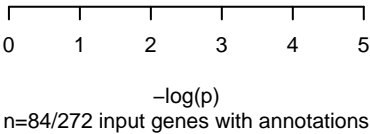
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GO:CC
Elav_Nvec_vc1.1_XM_032370541.2

fraction genes in fg and expected value

| | | | |
|---|------------|-----------|------|
| nuclear stress granule | GO:0097165 | p=2.1E-03 | n=2 |
| Lewy body | GO:0097413 | p=2.1E-03 | n=2 |
| voltage-gated potassium channel complex | GO:0008076 | p=6.6E-03 | n=3 |
| spindle pole | GO:0000922 | p=2.3E-02 | n=4 |
| centrosome | GO:0005813 | p=2.4E-02 | n=9 |
| Cajal body | GO:0015030 | p=2.8E-02 | n=2 |
| nuclear body | GO:0016604 | p=3.7E-02 | n=10 |
| integrin alpha3-beta1 complex | GO:0034667 | p=4.6E-02 | n=1 |
| katanin complex | GO:0008352 | p=4.6E-02 | n=1 |
| extrinsic component of mitochondrial inn... | GO:0031314 | p=4.6E-02 | n=1 |
| integrin alpha6-beta4 complex | GO:0034676 | p=4.6E-02 | n=1 |
| integrin alpha7-beta1 complex | GO:0034677 | p=4.6E-02 | n=1 |
| keratin filament | GO:0045095 | p=4.6E-02 | n=1 |
| ciliary transition fiber | GO:0097539 | p=4.6E-02 | n=1 |
| desmosome | GO:0030057 | p=4.6E-02 | n=1 |
| calcineurin complex | GO:0005955 | p=4.6E-02 | n=1 |
| lipid droplet | GO:0005811 | p=5.5E-02 | n=3 |
| cytoplasmic stress granule | GO:0010494 | p=7.5E-02 | n=2 |
| photoreceptor inner segment | GO:0001917 | p=8.9E-02 | n=2 |
| mRNA cleavage and polyadenylation specif... | GO:0005847 | p=9.1E-02 | n=1 |
| mRNA cleavage factor complex | GO:0005849 | p=9.1E-02 | n=1 |
| protein complex involved in cell adhesio... | GO:0098636 | p=9.1E-02 | n=1 |
| cytoplasmic cyclin-dependent protein kin... | GO:0000308 | p=9.1E-02 | n=1 |
| intrinsic component of nuclear inner mem... | GO:0031229 | p=9.1E-02 | n=1 |
| COPII vesicle coat | GO:0030127 | p=9.1E-02 | n=1 |
| integrin complex | GO:0008305 | p=9.1E-02 | n=1 |
| Parkin-FBXW7-Cul1 ubiquitin ligase compl... | GO:1990452 | p=9.1E-02 | n=1 |
| BBSome | GO:0034464 | p=9.1E-02 | n=1 |
| activating signal cointegrator 1 complex | GO:0099053 | p=9.1E-02 | n=1 |
| integral component of nuclear inner memb... | GO:0005639 | p=9.1E-02 | n=1 |



| | |
|---------|---------|
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