GO:BP
Elav_Nvec_vc1.1_XM_032365977.2

fraction genes in fg and expected valu...

Term	p-value	n	fg	bg
negative regulation of peptidyl−serine p... GO:0033137	p=2.7E−04	n=4	fg=0.04	bg=0.00
mitotic sister chromatid separation GO:0051306	p=5.1E−04	n=4	fg=0.04	bg=0.00
regulation of Rac protein signal transdu... GO:0035020	p=6.3E−04	n=3	fg=0.03	bg=0.00
stabilization of membrane potential GO:0030322	p=6.3E−04	n=3	fg=0.03	bg=0.00
chromosome organization involved in meio... GO:0070192	p=6.7E−04	n=6	fg=0.06	bg=0.01
forebrain development GO:0030900	p=9.4E−04	n=12	fg=0.12	bg=0.04
negative regulation of MAPK cascade GO:0043409	p=1.1E−03	n=7	fg=0.07	bg=0.02
regulation of cellular macromolecule bio... GO:2000112	p=1.3E−03	n=39	fg=0.39	bg=0.25
regulation of meiotic cell cycle process... GO:1903538	p=1.5E−03	n=3	fg=0.03	bg=0.00
phosphatidylinositol dephosphorylation GO:0046856	p=1.5E−03	n=3	fg=0.03	bg=0.00
cell fate determination GO:0001709	p=2.3E−03	n=6	fg=0.06	bg=0.01
negative regulation of protein serine/th... GO:0071901	p=2.3E−03	n=6	fg=0.06	bg=0.01
regulation of organelle organization GO:0033043	p=2.3E−03	n=24	fg=0.24	bg=0.12
response to mitochondrial depolarisation GO:0098780	p=2.9E−03	n=3	fg=0.03	bg=0.00
positive regulation of cholesterol efflu... GO:0010875	p=3.0E−03	n=2	fg=0.02	bg=0.00
actin filament network formation GO:0051639	p=3.0E−03	n=2	fg=0.02	bg=0.00
positive regulation of ribosome biogenes... GO:0090070	p=3.0E−03	n=2	fg=0.02	bg=0.00
positive regulation of rRNA processing GO:2000234	p=3.0E−03	n=2	fg=0.02	bg=0.00
negative regulation of protein targeting... GO:0090315	p=3.0E−03	n=2	fg=0.02	bg=0.00
positive regulation of megakaryocyte dif... GO:0045654	p=3.0E−03	n=2	fg=0.02	bg=0.00
canonical Wnt signaling pathway involved... GO:0061290	p=3.0E−03	n=2	fg=0.02	bg=0.00
regulation of primitive erythrocyte diff... GO:0010725	p=3.0E−03	n=2	fg=0.02	bg=0.00
negative regulation of Ras protein signa... GO:0046580	p=3.1E−03	n=4	fg=0.04	bg=0.01
synaptic transmission, GABAergic GO:0051932	p=4.2E−03	n=4	fg=0.04	bg=0.01
cellular response to organic cyclic comp... GO:0071407	p=4.3E−03	n=12	fg=0.12	bg=0.05
regulation of cellular localization GO:0060341	p=4.5E−03	n=20	fg=0.20	bg=0.10
negative regulation of tyrosine phosphor... GO:0042532	p=4.8E−03	n=3	fg=0.03	bg=0.00
regulation of oocyte maturation GO:1900193	p=4.8E−03	n=3	fg=0.03	bg=0.00
negative regulation of cell differentiat... GO:0045596	p=5.0E−03	n=13	fg=0.13	bg=0.06
regulation of GTPase activity GO:0043087	p=5.2E−03	n=9	fg=0.09	bg=0.03

−log(p)
n=100/334 input genes with annotations

fraction

GO:MF
Elav_Nvec_vc1.1_XM_032365977.2

fraction genes in fg and expected valu...

Term	p-value	n	fg	bg
potassium ion leak channel activity GO:0022841	p=1.5E−03	n=3	fg=0.03	bg=0.00
armadillo repeat domain binding GO:0070016	p=3.0E−03	n=2	fg=0.02	bg=0.00
RNA polymerase II cis−regulatory region ... GO:0000978	p=3.2E−03	n=9	fg=0.10	bg=0.04
ribosomal small subunit binding GO:0043024	p=8.7E−03	n=2	fg=0.02	bg=0.00
phosphatidylinositol−4,5−bisphosphate ph... GO:0106019	p=8.7E−03	n=2	fg=0.02	bg=0.00
nucleoside−triphosphatase activity GO:0017111	p=9.2E−03	n=13	fg=0.15	bg=0.07
translation factor activity, RNA binding GO:0008135	p=9.5E−03	n=4	fg=0.05	bg=0.01
transcription regulator activity GO:0140110	p=1.0E−02	n=18	fg=0.20	bg=0.12
protein domain specific binding GO:0019904	p=1.1E−02	n=17	fg=0.19	bg=0.09
transcription coactivator activity GO:0003713	p=1.4E−02	n=8	fg=0.09	bg=0.04
histone deacetylase binding GO:0042826	p=1.5E−02	n=4	fg=0.05	bg=0.01
histone acetyltransferase binding GO:0035035	p=1.5E−02	n=3	fg=0.03	bg=0.01
DNA−binding transcription activator acti... GO:0001228	p=1.7E−02	n=8	fg=0.09	bg=0.04
DNA−binding transcription activator acti... GO:0001216	p=1.7E−02	n=8	fg=0.09	bg=0.04
snRNA binding GO:0017069	p=1.7E−02	n=2	fg=0.02	bg=0.00
phosphatidylinositol phosphate 5−phospha... GO:0034595	p=1.7E−02	n=2	fg=0.02	bg=0.00
phosphatidylinositol phosphate 4−phospha... GO:0034596	p=1.7E−02	n=2	fg=0.02	bg=0.00
cAMP binding GO:0030552	p=1.7E−02	n=2	fg=0.02	bg=0.00
chromatin binding GO:0003682	p=1.9E−02	n=10	fg=0.11	bg=0.05
hormone receptor binding GO:0051427	p=1.9E−02	n=5	fg=0.06	bg=0.02
phosphatidylinositol−3,4,5−trisphosphate... GO:0005547	p=1.9E−02	n=3	fg=0.03	bg=0.01
translation initiation factor activity GO:0003743	p=1.9E−02	n=3	fg=0.03	bg=0.01
DNA−binding transcription factor activit... GO:0003700	p=2.3E−02	n=13	fg=0.15	bg=0.08
inositol phosphate phosphatase activity GO:0052745	p=2.7E−02	n=2	fg=0.02	bg=0.00
dynein complex binding GO:0070840	p=2.7E−02	n=2	fg=0.02	bg=0.00
AP−2 adaptor complex binding GO:0035612	p=2.7E−02	n=2	fg=0.02	bg=0.00
cyclic nucleotide binding GO:0030551	p=2.7E−02	n=2	fg=0.02	bg=0.00
phosphatidylinositol−3−phosphate binding GO:0032266	p=2.7E−02	n=2	fg=0.02	bg=0.00
telomeric DNA binding GO:0042162	p=2.7E−02	n=2	fg=0.02	bg=0.00
microtubule binding GO:0008017	p=2.8E−02	n=6	fg=0.07	bg=0.03

−log(p)
n=88/334 input genes with annotations

fraction

GO:CC
Elav_Nvec_vc1.1_XM_032365977.2

fraction genes in fg and expected valu...

Term	p-value	n	fg	bg
dendrite GO:0030425	p=1.3E−03	n=16	fg=0.16	bg=0.07
chromosome, centromeric region GO:0000775	p=3.3E−03	n=6	fg=0.06	bg=0.02
condensed chromosome GO:0000793	p=5.6E−03	n=6	fg=0.06	bg=0.02
intrinsic component of peroxisomal membr... GO:0031231	p=1.7E−02	n=2	fg=0.02	bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235	p=1.7E−02	n=2	fg=0.02	bg=0.00
integral component of peroxisomal membra... GO:0005779	p=1.7E−02	n=2	fg=0.02	bg=0.00
intrinsic component of plasma membrane GO:0031226	p=2.4E−02	n=14	fg=0.14	bg=0.08
polysome GO:0005844	p=2.4E−02	n=3	fg=0.03	bg=0.01
condensed chromosome, centromeric region GO:0000779	p=2.5E−02	n=4	fg=0.04	bg=0.01
zymogen granule GO:0042588	p=2.7E−02	n=2	fg=0.02	bg=0.00
cell body GO:0044297	p=3.2E−02	n=13	fg=0.13	bg=0.08
microbody membrane GO:0031903	p=3.8E−02	n=2	fg=0.02	bg=0.00
peroxisomal membrane GO:0005778	p=3.8E−02	n=2	fg=0.02	bg=0.00
axon GO:0030424	p=4.0E−02	n=13	fg=0.13	bg=0.08
neuronal cell body GO:0043025	p=4.0E−02	n=12	fg=0.12	bg=0.07
cell periphery GO:0071944	p=4.1E−02	n=37	fg=0.37	bg=0.29
apical dendrite GO:0097440	p=5.2E−02	n=2	fg=0.02	bg=0.00
kinetochore GO:0000776	p=5.3E−02	n=3	fg=0.03	bg=0.01
bleb GO:0032059	p=5.5E−02	n=1	fg=0.01	bg=0.00
dentate gyrus mossy fiber GO:0044302	p=5.5E−02	n=1	fg=0.01	bg=0.00
eukaryotic translation initiation factor... GO:0016281	p=5.5E−02	n=1	fg=0.01	bg=0.00
astral microtubule GO:0000235	p=5.5E−02	n=1	fg=0.01	bg=0.00
sarcoplasmic reticulum lumen GO:0033018	p=5.5E−02	n=1	fg=0.01	bg=0.00
integrin alpha3−beta1 complex GO:0034667	p=5.5E−02	n=1	fg=0.01	bg=0.00
clathrin−sculpted vesicle GO:0060198	p=5.5E−02	n=1	fg=0.01	bg=0.00
integrin alpha6−beta4 complex GO:0034676	p=5.5E−02	n=1	fg=0.01	bg=0.00
integrin alpha7−beta1 complex GO:0034677	p=5.5E−02	n=1	fg=0.01	bg=0.00
telomerase holoenzyme complex GO:0005697	p=5.5E−02	n=1	fg=0.01	bg=0.00
exosome (RNase complex) GO:0000178	p=5.5E−02	n=1	fg=0.01	bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200	p=5.5E−02	n=1	fg=0.01	bg=0.00

−log(p)
n=99/334 input genes with annotations

fraction