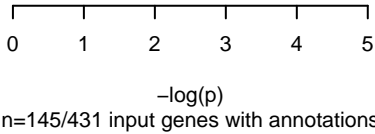


GO:BP
Elav_Nvec_vc1.1_XM_032370541.2

fraction genes in fg and expected value

T cell homeostasis	GO:0043029	p=1.3E−03	n=4
regulation of alternative mRNA splicing,....	GO:0000381	p=1.5E−03	n=5
regulation of ER to Golgi vesicle–mediat...	GO:0060628	p=2.7E−03	n=3
surfactant homeostasis	GO:0043129	p=2.9E−03	n=2
nodal signaling pathway	GO:0038092	p=2.9E−03	n=2
negative regulation of oxidative stress–...	GO:1903377	p=2.9E−03	n=2
regulation of transcriptional start site...	GO:0001178	p=2.9E−03	n=2
adult somatic muscle development	GO:0007527	p=2.9E−03	n=2
regulation of protein secretion	GO:0050708	p=3.2E−03	n=12
regulation of transcription by RNA polym...	GO:0006357	p=4.3E−03	n=35
regulation of chromatin binding	GO:0035561	p=4.5E−03	n=3
mRNA transcription	GO:0009299	p=4.5E−03	n=3
regulation of cilium assembly	GO:1902017	p=5.2E−03	n=5
regulation of mRNA 3′–end processing	GO:0031440	p=6.8E−03	n=4
regulation of peptide secretion	GO:0002791	p=8.0E−03	n=12
long–chain fatty acid catabolic process	GO:0042758	p=8.3E−03	n=2
negative regulation of miRNA–mediated ge...	GO:0060965	p=8.3E−03	n=2
B–1 B cell homeostasis	GO:0001922	p=8.3E−03	n=2
response to muscle activity	GO:0014850	p=8.3E−03	n=2
negative regulation of activin receptor ...	GO:0032926	p=8.3E−03	n=2
dopamine uptake	GO:0090494	p=8.3E−03	n=2
connective tissue replacement	GO:0097709	p=8.3E−03	n=2
negative regulation of dendrite morphoge...	GO:0050774	p=8.3E−03	n=2
regulation of mRNA export from nucleus	GO:0010793	p=8.3E−03	n=2
vesicle budding from membrane	GO:0006900	p=9.3E−03	n=5
primary neural tube formation	GO:0014020	p=9.6E−03	n=6
positive regulation of protein secretion	GO:0050714	p=1.0E−02	n=7
negative regulation of cell junction ass...	GO:1901889	p=1.3E−02	n=5
negative regulation of response to oxida...	GO:1902883	p=1.3E−02	n=4
photoreceptor cell maintenance	GO:0045494	p=1.3E−02	n=4

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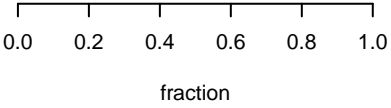
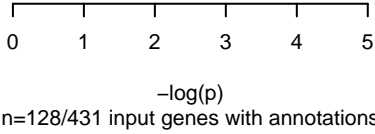


GO:MF
Elav_Nvec_vc1.1_XM_032370541.2

fraction genes in fg and expected value

DNA–binding transcription factor activit...	GO:0000981	p=1.1E−04	n=19
core promoter sequence–specific DNA bind...	GO:0001046	p=2.1E−03	n=5
mRNA binding	GO:0003729	p=6.1E−03	n=10
miRNA binding	GO:0035198	p=8.4E−03	n=2
G–quadruplex DNA binding	GO:0051880	p=8.4E−03	n=2
mRNA regulatory element binding translat...	GO:0000900	p=8.4E−03	n=2
single–stranded RNA binding	GO:0003727	p=1.3E−02	n=5
potassium channel activity	GO:0005267	p=1.4E−02	n=4
RNA polymerase II transcription regulato...	GO:0000977	p=1.6E−02	n=11
protein kinase B binding	GO:0043422	p=1.6E−02	n=2
double–stranded RNA binding	GO:0003725	p=3.0E−02	n=3
RNA methyltransferase activity	GO:0008173	p=3.2E−02	n=4
potassium ion transmembrane transporter ...	GO:0015079	p=3.2E−02	n=4
ubiquitin conjugating enzyme binding	GO:0031624	p=3.6E−02	n=3
phosphatidylinositol 3–kinase binding	GO:0043548	p=3.8E−02	n=2
O–methyltransferase activity	GO:0008171	p=3.8E−02	n=2
sequence–specific double–stranded DNA bi...	GO:1990837	p=4.0E−02	n=15
DNA–binding transcription activator acti...	GO:0001228	p=4.3E−02	n=8
DNA–binding transcription activator acti...	GO:0001216	p=4.3E−02	n=8
sequence–specific DNA binding	GO:0043565	p=4.6E−02	n=17
cis–regulatory region sequence–specific ...	GO:0000987	p=4.6E−02	n=8
RNA polymerase II cis–regulatory region ...	GO:0000978	p=4.6E−02	n=8
catalytic activity, acting on a rRNA	GO:0140102	p=5.1E−02	n=2
rRNA methyltransferase activity	GO:0008649	p=5.1E−02	n=2
mRNA 3′–UTR binding	GO:0003730	p=5.1E−02	n=3
transcription coregulator activity	GO:0003712	p=5.3E−02	n=11
transcription cis–regulatory region bind...	GO:0000976	p=5.4E−02	n=14
neuregulin binding	GO:0038132	p=5.4E−02	n=1
poly–ADP–D–ribose binding	GO:0072572	p=5.4E−02	n=1
phospholipase D activator activity	GO:1990583	p=5.4E−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=2.7E−03	n=2
Lewy body	GO:0097413	p=2.7E−03	n=2
voltage–gated potassium channel complex	GO:0008076	p=1.3E−02	n=3
potassium channel complex	GO:0034705	p=1.3E−02	n=3
proteasome core complex	GO:0005839	p=1.5E−02	n=2
Cajal body	GO:0015030	p=1.7E−02	n=3
cytoplasmic stress granule	GO:0010494	p=2.1E−02	n=3
phagocytic cup	GO:0001891	p=2.4E−02	n=2
nuclear pore	GO:0005643	p=2.4E−02	n=4
lipid droplet	GO:0005811	p=3.3E−02	n=4
cation channel complex	GO:0034703	p=4.3E−02	n=4
desmosome	GO:0030057	p=5.2E−02	n=1
bub1–bub3 complex	GO:1990298	p=5.2E−02	n=1
integrin alpha3–beta1 complex	GO:0034667	p=5.2E−02	n=1
integrin alpha6–beta4 complex	GO:0034676	p=5.2E−02	n=1
integrin alpha7–beta1 complex	GO:0034677	p=5.2E−02	n=1
mitotic checkpoint complex	GO:0033597	p=5.2E−02	n=1
keratin filament	GO:0045095	p=5.2E−02	n=1
proteasome core complex, beta–subunit co...	GO:0019774	p=5.2E−02	n=1
ion channel complex	GO:0034702	p=6.7E−02	n=4
centriole	GO:0005814	p=7.3E−02	n=4
centriolar satellite	GO:0034451	p=7.6E−02	n=2
nuclear body	GO:0016604	p=7.9E−02	n=13
endoplasmic reticulum membrane	GO:0005789	p=8.1E−02	n=15
microtubule organizing center	GO:0005815	p=8.2E−02	n=14
P–body	GO:0000932	p=9.2E−02	n=3
nuclear outer membrane–endoplasmic retic...	GO:0042175	p=9.3E−02	n=15
endoplasmic reticulum subcompartment	GO:0098827	p=9.6E−02	n=15
ciliary transition fiber	GO:0097539	p=1.0E−01	n=1
extrinsic component of mitochondrial inn...	GO:0031314	p=1.0E−01	n=1

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