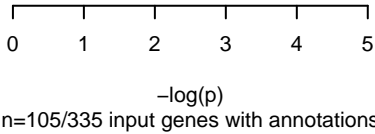


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_048728028.1

fraction genes in fg and expected value

forebrain development	GO:0030900	p=1.5E-03	n=12
response to iron ion	GO:0010039	p=1.7E-03	n=3
positive regulation of oxidoreductase ac...	GO:0051353	p=1.7E-03	n=3
blood vessel remodeling	GO:0001974	p=2.6E-03	n=4
negative regulation of vasoconstriction	GO:0045906	p=3.3E-03	n=3
positive regulation of autophagy of mito...	GO:1903599	p=3.3E-03	n=3
neural fold formation	GO:0001842	p=3.3E-03	n=2
elastin metabolic process	GO:0051541	p=3.3E-03	n=2
actin cortical patch localization	GO:0051666	p=3.3E-03	n=2
negative regulation of vascular associat...	GO:1904706	p=3.3E-03	n=2
negative regulation of engulfment of apo...	GO:1901075	p=3.3E-03	n=2
positive regulation of eye pigmentation	GO:0048075	p=3.3E-03	n=2
lysine transport	GO:0015819	p=3.3E-03	n=2
tryptophan metabolic process	GO:0006568	p=3.3E-03	n=2
protein maturation by copper ion transfe...	GO:0015680	p=3.3E-03	n=2
negative regulation of oxidative stress-...	GO:1903377	p=3.3E-03	n=2
transcriptional start site selection at ...	GO:0001174	p=3.3E-03	n=2
nucleotide-sugar biosynthetic process	GO:0009226	p=3.3E-03	n=2
regulation of ATP biosynthetic process	GO:2001169	p=3.7E-03	n=4
cardiac conduction	GO:0061337	p=4.6E-03	n=5
regulation of transporter activity	GO:0032409	p=5.1E-03	n=7
melanocyte differentiation	GO:0030318	p=5.6E-03	n=3
superoxide metabolic process	GO:0006801	p=5.6E-03	n=3
mitochondrion localization	GO:0051646	p=6.8E-03	n=4
regulation of reactive oxygen species bi...	GO:1903426	p=6.8E-03	n=4
learning	GO:0007612	p=6.8E-03	n=8
regulation of cellular macromolecule bio...	GO:2000112	p=6.8E-03	n=38
leukocyte differentiation	GO:0002521	p=7.9E-03	n=10
in utero embryonic development	GO:0001701	p=7.9E-03	n=9
regulation of transcription, DNA-templat...	GO:0006355	p=8.1E-03	n=35

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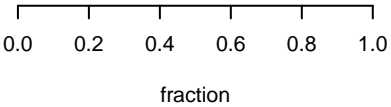
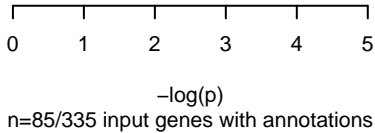


GO:MF  
Elav\_Nvec\_vc1.1\_XM\_048728028.1

fraction genes in fg and expected value

chaperone binding	GO:0051087	p=2.1E-04	n=7
histone acetyltransferase binding	GO:0035035	p=1.2E-03	n=4
ubiquitin protein ligase activity	GO:0061630	p=2.5E-03	n=9
superoxide dismutase copper chaperone ac...	GO:0016532	p=2.8E-03	n=2
signaling receptor binding	GO:0005102	p=4.7E-03	n=17
zinc ion binding	GO:0008270	p=5.7E-03	n=10
endoribonuclease activity, producing 5'-...	GO:0016891	p=8.2E-03	n=2
protein kinase binding	GO:0019901	p=9.1E-03	n=13
histone binding	GO:0042393	p=1.2E-02	n=5
nuclear thyroid hormone receptor binding	GO:0046966	p=1.6E-02	n=2
acetylcholine receptor binding	GO:0033130	p=1.6E-02	n=2
hormone receptor binding	GO:0051427	p=1.7E-02	n=5
solute:cation symporter activity	GO:0015294	p=1.8E-02	n=3
intramolecular oxidoreductase activity	GO:0016860	p=1.8E-02	n=3
symporter activity	GO:0015293	p=2.3E-02	n=3
TBP-class protein binding	GO:0017025	p=2.3E-02	n=3
intramolecular oxidoreductase activity, ...	GO:0016864	p=2.5E-02	n=2
protein disulfide isomerase activity	GO:0003756	p=2.5E-02	n=2
cis-regulatory region sequence-specific ...	GO:0000987	p=2.9E-02	n=7
RNA polymerase II cis-regulatory region ...	GO:0000978	p=2.9E-02	n=7
transcription coactivator activity	GO:0003713	p=3.4E-02	n=7
SMAD binding	GO:0046332	p=3.5E-02	n=3
general transcription initiation factor ...	GO:0140296	p=3.5E-02	n=3
lipoprotein particle receptor binding	GO:0070325	p=3.7E-02	n=2
beta-catenin binding	GO:0008013	p=3.7E-02	n=2
ubiquitin-specific protease binding	GO:1990381	p=3.7E-02	n=2
low-density lipoprotein particle recepto...	GO:0050750	p=3.7E-02	n=2
active ion transmembrane transporter act...	GO:0022853	p=3.9E-02	n=5
manganese ion binding	GO:0030145	p=4.2E-02	n=3
transcription cis-regulatory region bind...	GO:0000976	p=4.3E-02	n=9

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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_048728028.1

fraction genes in fg and expected value

growth cone filopodium	GO:1990812	p=3.1E-03	n=2
platelet alpha granule membrane	GO:0031092	p=3.1E-03	n=2
growth cone lamellipodium	GO:1990761	p=8.9E-03	n=2
dendritic shaft	GO:0043198	p=1.5E-02	n=4
pericentriolar material	GO:0000242	p=1.7E-02	n=2
fungal-type vacuole	GO:0000324	p=1.7E-02	n=2
fungal-type vacuole membrane	GO:0000329	p=1.7E-02	n=2
cell tip	GO:0051286	p=1.7E-02	n=2
aggresome	GO:0016235	p=1.7E-02	n=2
endoribonuclease complex	GO:1902555	p=1.7E-02	n=2
X chromosome	GO:0000805	p=1.7E-02	n=2
endonuclease complex	GO:1905348	p=1.7E-02	n=2
nuclear speck	GO:0016607	p=1.8E-02	n=8
intracellular protein-containing complex	GO:0140535	p=2.1E-02	n=15
neuron spine	GO:0044309	p=2.1E-02	n=6
dendritic spine	GO:0043197	p=2.1E-02	n=6
integral component of endoplasmic reticu...	GO:0030176	p=2.4E-02	n=6
intrinsic component of endoplasmic retic...	GO:0031227	p=2.4E-02	n=6
postsynapse	GO:0098794	p=2.5E-02	n=9
smooth endoplasmic reticulum	GO:0005790	p=2.6E-02	n=3
nucleus	GO:0005634	p=2.6E-02	n=58
endoplasmic reticulum	GO:0005783	p=2.7E-02	n=22
storage vacuole	GO:0000322	p=2.8E-02	n=2
cell pole	GO:0060187	p=2.8E-02	n=2
perinuclear region of cytoplasm	GO:0048471	p=2.8E-02	n=13
centrosome	GO:0005813	p=2.9E-02	n=10
asymmetric synapse	GO:0032279	p=2.9E-02	n=6
neuron to neuron synapse	GO:0098984	p=3.3E-02	n=6
membrane-bounded organelle	GO:0043227	p=3.4E-02	n=89
late endosome	GO:0005770	p=3.6E-02	n=6

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