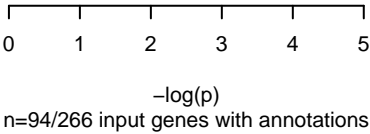


GO:BP
Elav_Nvec_vc1.1_XM_032374789.2

fraction genes in fg and expected value

mitotic cell cycle process	GO:1903047	p=3.1E-04	n=19
mating	GO:0007618	p=1.1E-03	n=7
male courtship behavior, veined wing gen...	GO:0045433	p=2.7E-03	n=2
aldosterone metabolic process	GO:0032341	p=2.7E-03	n=2
regulation of skeletal muscle fiber deve...	GO:0048742	p=2.7E-03	n=2
negative regulation of protein kinase ac...	GO:0044387	p=2.7E-03	n=2
synaptic vesicle priming	GO:0016082	p=4.0E-03	n=3
courtship behavior	GO:0007619	p=5.5E-03	n=6
mesodermal cell fate determination	GO:0007500	p=7.7E-03	n=2
positive regulation of nuclear cell cycl...	GO:0010571	p=7.7E-03	n=2
extracellular matrix assembly	GO:0085029	p=7.7E-03	n=2
protein heterotetramerization	GO:0051290	p=7.7E-03	n=2
sensory perception of pain	GO:0019233	p=9.1E-03	n=6
regulation of steroid metabolic process	GO:0019218	p=9.6E-03	n=4
mitotic cell cycle phase transition	GO:0044772	p=1.1E-02	n=10
male courtship behavior	GO:0008049	p=1.2E-02	n=5
ADP metabolic process	GO:0046031	p=1.2E-02	n=4
epidermis morphogenesis	GO:0048730	p=1.2E-02	n=3
regulation of mitotic cell cycle phase t...	GO:1901990	p=1.3E-02	n=8
positive regulation of hydrolase activit...	GO:0051345	p=1.4E-02	n=11
positive regulation of GTPase activity	GO:0043547	p=1.4E-02	n=7
regulation of ATP metabolic process	GO:1903578	p=1.4E-02	n=4
lipid homeostasis	GO:0055088	p=1.5E-02	n=5
labyrinthine layer morphogenesis	GO:0060713	p=1.5E-02	n=2
vascular associated smooth muscle contra...	GO:0014829	p=1.5E-02	n=2
maintenance of apical/basal cell polarit...	GO:0035090	p=1.5E-02	n=2
embryonic placenta morphogenesis	GO:0060669	p=1.5E-02	n=2
branching involved in labyrinthine layer...	GO:0060670	p=1.5E-02	n=2
regulation of extracellular matrix disas...	GO:0010715	p=1.5E-02	n=2
mitotic DNA replication	GO:1902969	p=1.5E-02	n=2

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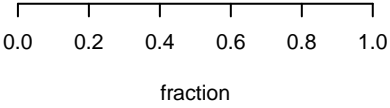
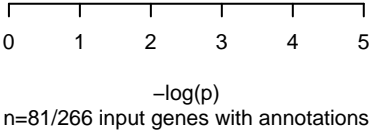


GO:MF
Elav_Nvec_vc1.1_XM_032374789.2

fraction genes in fg and expected value

low voltage-gated calcium channel activi...	GO:0008332	p=2.6E-03	n=2
GTPase regulator activity	GO:0030695	p=3.7E-03	n=10
deaminase activity	GO:0019239	p=7.4E-03	n=2
GTPase activator activity	GO:0005096	p=1.2E-02	n=6
carbohydrate kinase activity	GO:0019200	p=1.4E-02	n=2
hydrolase activity, acting on carbon-nit...	GO:0016814	p=1.4E-02	n=2
GTPase binding	GO:0051020	p=1.6E-02	n=11
helicase activity	GO:0004386	p=1.6E-02	n=4
AP-2 adaptor complex binding	GO:0035612	p=2.3E-02	n=2
small GTPase binding	GO:0031267	p=2.7E-02	n=9
potassium channel activity	GO:0005267	p=3.1E-02	n=3
potassium channel inhibitor activity	GO:0019870	p=3.4E-02	n=2
protein serine/threonine phosphatase act...	GO:0004722	p=3.7E-02	n=3
enzyme activator activity	GO:0008047	p=4.1E-02	n=8
ubiquitin-like protein transferase activ...	GO:0019787	p=4.8E-02	n=9
four-way junction DNA binding	GO:0000400	p=5.1E-02	n=1
voltage-gated calcium channel activity i...	GO:0086056	p=5.1E-02	n=1
voltage-gated calcium channel activity i...	GO:0086059	p=5.1E-02	n=1
myosin II binding	GO:0045159	p=5.1E-02	n=1
glyceraldehyde-3-phosphate dehydrogenase...	GO:0004365	p=5.1E-02	n=1
MDM2/MDM4 family protein binding	GO:0097371	p=5.1E-02	n=1
protein phosphatase 5 binding	GO:1990634	p=5.1E-02	n=1
5'-3' exodeoxyribonuclease activity	GO:0035312	p=5.1E-02	n=1
proteinase activated receptor binding	GO:0031871	p=5.1E-02	n=1
5'-3' exonuclease activity	GO:0008409	p=5.1E-02	n=1
D-xylose 1-dehydrogenase (NADP+) activit...	GO:0047837	p=5.1E-02	n=1
P-type divalent copper transporter activ...	GO:0043682	p=5.1E-02	n=1
cuprous ion binding	GO:1903136	p=5.1E-02	n=1
5' overhang single-stranded DNA endodeox...	GO:1990601	p=5.1E-02	n=1
flap-structured DNA binding	GO:0070336	p=5.1E-02	n=1

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GO:CC
Elav_Nvec_vc1.1_XM_032374789.2

fraction genes in fg and expected value

presynaptic active zone	GO:0048786	p=1.5E-03	n=5
U5 snRNP	GO:0005682	p=2.5E-03	n=2
myelin sheath	GO:0043209	p=3.6E-03	n=6
plasma membrane region	GO:0098590	p=1.2E-02	n=16
cytosol	GO:0005829	p=1.3E-02	n=46
basal part of cell	GO:0045178	p=1.8E-02	n=7
cation channel complex	GO:0034703	p=1.9E-02	n=4
replication fork	GO:0005657	p=2.3E-02	n=2
presynaptic active zone membrane	GO:0048787	p=2.3E-02	n=2
voltage-gated calcium channel complex	GO:0005891	p=2.3E-02	n=2
A band	GO:0031672	p=2.4E-02	n=3
actomyosin	GO:0042641	p=2.4E-02	n=3
ion channel complex	GO:0034702	p=2.5E-02	n=4
basal plasma membrane	GO:0009925	p=2.8E-02	n=6
basolateral plasma membrane	GO:0016323	p=2.8E-02	n=6
excitatory synapse	GO:0060076	p=3.3E-02	n=2
presynaptic membrane	GO:0042734	p=3.4E-02	n=4
centrosome	GO:0005813	p=3.8E-02	n=9
calcium channel complex	GO:0034704	p=4.5E-02	n=2
membrane raft	GO:0045121	p=4.7E-02	n=6
membrane microdomain	GO:0098857	p=4.7E-02	n=6
mitotic spindle	GO:0072686	p=5.0E-02	n=3
chromaffin granule	GO:0042583	p=5.0E-02	n=1
chromaffin granule membrane	GO:0042584	p=5.0E-02	n=1
RNA polymerase II transcription represso...	GO:0090571	p=5.0E-02	n=1
cortical microtubule	GO:0055028	p=5.0E-02	n=1
centrosomal corona	GO:0031592	p=5.0E-02	n=1
Flemming body	GO:0090543	p=5.0E-02	n=1
cortical microtubule cytoskeleton	GO:0030981	p=5.0E-02	n=1
cortical microtubule plus-end	GO:1903754	p=5.0E-02	n=1

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