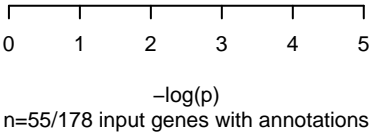


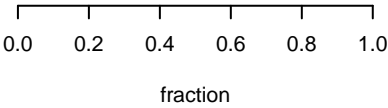
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Elav\_Nvec\_vc1.1\_XM\_032375459.2

fraction genes in fg and expected value

diacylglycerol metabolic process	GO:0046339	p=9.0E-04	n=2
regulation of mitotic cell cycle DNA rep...	GO:1903463	p=2.7E-03	n=2
regeneration	GO:0031099	p=3.5E-03	n=5
response to axon injury	GO:0048678	p=4.4E-03	n=4
ciliary basal body-plasma membrane docki...	GO:0097711	p=7.9E-03	n=4
neuron projection regeneration	GO:0031102	p=1.1E-02	n=3
axon regeneration	GO:0031103	p=1.1E-02	n=3
axonogenesis	GO:0007409	p=1.2E-02	n=9
animal organ maturation	GO:0048799	p=1.3E-02	n=2
peptidyl-threonine modification	GO:0018210	p=1.3E-02	n=3
response to leukemia inhibitory factor	GO:1990823	p=1.3E-02	n=3
cellular response to leukemia inhibitory...	GO:1990830	p=1.3E-02	n=3
regulation of mRNA splicing, via spliceo...	GO:0048024	p=1.3E-02	n=3
axon guidance	GO:0007411	p=1.3E-02	n=7
axon development	GO:0061564	p=1.6E-02	n=9
neuron projection guidance	GO:0097485	p=1.6E-02	n=7
negative regulation of cellular amide me...	GO:0034249	p=1.6E-02	n=4
positive regulation of neuron projection...	GO:0070572	p=1.7E-02	n=2
detection of light stimulus involved in ...	GO:0050962	p=1.7E-02	n=2
detection of light stimulus involved in ...	GO:0050908	p=1.7E-02	n=2
positive regulation of axon regeneration	GO:0048680	p=1.7E-02	n=2
chemotaxis	GO:0006935	p=1.9E-02	n=8
protein autophosphorylation	GO:0046777	p=2.2E-02	n=4
bile acid biosynthetic process	GO:0006699	p=2.2E-02	n=2
response to amyloid-beta	GO:1904645	p=2.2E-02	n=2
negative regulation of mitotic cell cycl...	GO:1901991	p=2.4E-02	n=3
taxi	GO:0042330	p=2.7E-02	n=8
macromolecule biosynthetic process	GO:0009059	p=2.7E-02	n=26
negative regulation of cellular macromol...	GO:2000113	p=2.8E-02	n=12
negative regulation of mRNA processing	GO:0050686	p=2.8E-02	n=2



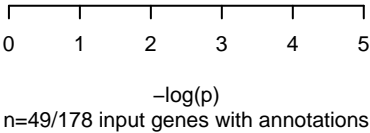
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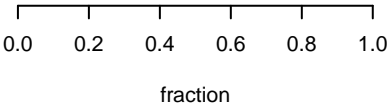
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fraction genes in fg and expected value

mRNA regulatory element binding translat...	GO:0000900	p=2.7E-03	n=2
tau-protein kinase activity	GO:0050321	p=5.4E-03	n=2
poly(U) RNA binding	GO:0008266	p=8.7E-03	n=2
protein tyrosine kinase activity	GO:0004713	p=1.4E-02	n=3
guanyl-nucleotide exchange factor activi...	GO:0005085	p=1.7E-02	n=4
ubiquitin-like protein ligase binding	GO:0044389	p=1.8E-02	n=6
voltage-gated calcium channel activity	GO:0005245	p=2.3E-02	n=2
transcription coregulator activity	GO:0003712	p=2.4E-02	n=7
calcium channel regulator activity	GO:0005246	p=2.9E-02	n=2
D-glucose transmembrane transporter acti...	GO:0055056	p=3.1E-02	n=1
L-alanine:2-oxoglutarate aminotransferas...	GO:0004021	p=3.1E-02	n=1
rRNA primary transcript binding	GO:0042134	p=3.1E-02	n=1
leptin receptor binding	GO:1990460	p=3.1E-02	n=1
sugar transmembrane transporter activity	GO:0051119	p=3.1E-02	n=1
transferrin receptor binding	GO:1990459	p=3.1E-02	n=1
carbohydrate:cation symporter activity	GO:0005402	p=3.1E-02	n=1
phosphatidylserine decarboxylase activit...	GO:0004609	p=3.1E-02	n=1
carbohydrate transmembrane transporter a...	GO:0015144	p=3.1E-02	n=1
monosaccharide transmembrane transporter...	GO:0015145	p=3.1E-02	n=1
hexose transmembrane transporter activit...	GO:0015149	p=3.1E-02	n=1
nickel cation binding	GO:0016151	p=3.1E-02	n=1
alanine-oxo-acid transaminase activity	GO:0047635	p=3.1E-02	n=1
polypeptide N-acetylgalactosaminyltransf...	GO:0004653	p=3.1E-02	n=1
SUMO binding	GO:0032183	p=3.1E-02	n=1
carbohydrate:proton symporter activity	GO:0005351	p=3.1E-02	n=1
glucose transmembrane transporter activi...	GO:0005355	p=3.1E-02	n=1
riboflavin transmembrane transporter act...	GO:0032217	p=3.1E-02	n=1
transcription coactivator activity	GO:0003713	p=3.2E-02	n=5
ribonucleoprotein complex binding	GO:0043021	p=3.9E-02	n=3
nucleoside-triphosphatase regulator acti...	GO:0060589	p=4.3E-02	n=6



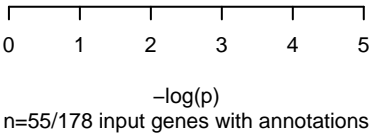
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032375459.2

fraction genes in fg and expected value

presynaptic active zone	GO:0048786	p=1.7E-03	n=4
nuclear body	GO:0016604	p=6.6E-03	n=9
voltage-gated calcium channel complex	GO:0005891	p=8.6E-03	n=2
transcription factor TFTC complex	GO:0033276	p=8.6E-03	n=2
excitatory synapse	GO:0060076	p=1.3E-02	n=2
vesicle coat	GO:0030120	p=1.7E-02	n=2
COPI-coated vesicle	GO:0030137	p=1.7E-02	n=2
membrane-bounded organelle	GO:0043227	p=2.8E-02	n=51
Ric1-Rgp1 guanyl-nucleotide exchange fac...	GO:0034066	p=3.0E-02	n=1
L-type voltage-gated calcium channel com...	GO:1990454	p=3.0E-02	n=1
chromaffin granule	GO:0042583	p=3.0E-02	n=1
chromaffin granule membrane	GO:0042584	p=3.0E-02	n=1
CHRA	GO:0008623	p=3.0E-02	n=1
ACF complex	GO:0016590	p=3.0E-02	n=1
T-tubule	GO:0030315	p=3.5E-02	n=2
nuclear speck	GO:0016607	p=3.5E-02	n=5
NURF complex	GO:0016589	p=6.0E-02	n=1
RNA polymerase II, core complex	GO:0005665	p=6.0E-02	n=1
COPI vesicle coat	GO:0030126	p=6.0E-02	n=1
COPII vesicle coat	GO:0030127	p=6.0E-02	n=1
gut granule	GO:0044840	p=6.0E-02	n=1
gut granule membrane	GO:0044841	p=6.0E-02	n=1
COPI-coated vesicle membrane	GO:0030663	p=6.0E-02	n=1
RSF complex	GO:0031213	p=6.0E-02	n=1
activating signal cointegrator 1 complex	GO:0099053	p=6.0E-02	n=1
coated vesicle	GO:0030135	p=6.3E-02	n=4
Golgi-associated vesicle membrane	GO:0030660	p=6.5E-02	n=2
intracellular membrane-bounded organelle	GO:0043231	p=6.6E-02	n=49
commitment complex	GO:0000243	p=8.8E-02	n=1
podosome	GO:0002102	p=8.8E-02	n=1



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