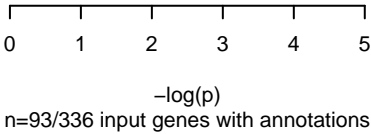


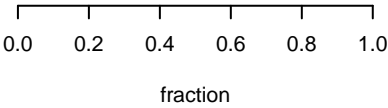
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Ncol_Nvec_vc1.1_XM_032385963.2

fraction genes in fg and expected value

negative regulation of MAP kinase activi...	GO:0043407	p=4.2E-03	n=4
regulation of reactive oxygen species bi...	GO:1903426	p=4.2E-03	n=4
negative regulation of synaptic transmis...	GO:0050805	p=4.2E-03	n=5
osteoblast differentiation	GO:0001649	p=5.5E-03	n=5
regulation of glucokinase activity	GO:0033131	p=6.7E-03	n=2
glycerolipid catabolic process	GO:0046503	p=6.9E-03	n=3
brain development	GO:0007420	p=8.5E-03	n=14
positive regulation of I-kappaB kinase/N...	GO:0043123	p=8.8E-03	n=3
larval locomotory behavior	GO:0008345	p=8.8E-03	n=3
positive regulation of ubiquitin-depende...	GO:2000060	p=8.9E-03	n=5
circadian behavior	GO:0048512	p=8.9E-03	n=5
regulation of small GTPase mediated sign...	GO:0051056	p=1.1E-02	n=6
unsaturated fatty acid metabolic process	GO:0033559	p=1.1E-02	n=3
negative regulation of Rac protein signa...	GO:0035021	p=1.1E-02	n=2
glycerophospholipid catabolic process	GO:0046475	p=1.1E-02	n=2
adherens junction maintenance	GO:0034334	p=1.1E-02	n=2
positive regulation of cell population p...	GO:0008284	p=1.3E-02	n=11
regulation of nitric oxide biosynthetic ...	GO:0045428	p=1.3E-02	n=3
nitric oxide biosynthetic process	GO:0006809	p=1.3E-02	n=3
icosanoid metabolic process	GO:0006690	p=1.3E-02	n=3
nitric oxide metabolic process	GO:0046209	p=1.3E-02	n=3
regulation of nitric oxide metabolic pro...	GO:0080164	p=1.3E-02	n=3
regulation of Ras protein signal transdu...	GO:0046578	p=1.3E-02	n=5
cellular response to inorganic substance	GO:0071241	p=1.5E-02	n=6
regulation of cell population proliferat...	GO:0042127	p=1.5E-02	n=18
reactive nitrogen species metabolic proc...	GO:2001057	p=1.6E-02	n=3
positive regulation of stem cell prolife...	GO:2000648	p=1.6E-02	n=3
positive regulation of cyclase activity	GO:0031281	p=1.6E-02	n=2
cellular response to manganese ion	GO:0071287	p=1.6E-02	n=2
cell-cell junction maintenance	GO:0045217	p=1.6E-02	n=2



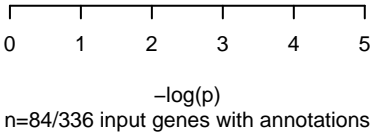
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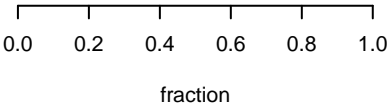
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Ncol_Nvec_vc1.1_XM_032385963.2

fraction genes in fg and expected value

actin monomer binding	GO:0003785	p=1.2E-02	n=2
kinesin binding	GO:0019894	p=2.0E-02	n=3
lysophospholipase activity	GO:0004622	p=2.3E-02	n=2
signaling adaptor activity	GO:0035591	p=2.4E-02	n=3
methyltransferase activity	GO:0008168	p=2.8E-02	n=5
cullin family protein binding	GO:0097602	p=3.0E-02	n=2
integrin binding	GO:0005178	p=3.2E-02	n=3
transferase activity, transferring one-c...	GO:0016741	p=3.2E-02	n=5
open rectifier potassium channel activit...	GO:0005252	p=3.5E-02	n=1
purine-specific nucleoside:sodium sympor...	GO:0015390	p=3.5E-02	n=1
nucleobase:cation symporter activity	GO:0015391	p=3.5E-02	n=1
misfolded RNA binding	GO:0034336	p=3.5E-02	n=1
cupric ion binding	GO:1903135	p=3.5E-02	n=1
pyrimidine nucleobase transmembrane tran...	GO:0005350	p=3.5E-02	n=1
ferrochelataase activity	GO:0004325	p=3.5E-02	n=1
RNA trimethylguanosine synthase activity	GO:0071164	p=3.5E-02	n=1
purine nucleoside transmembrane transpor...	GO:0015211	p=3.5E-02	n=1
F-box domain binding	GO:1990444	p=3.5E-02	n=1
MHC protein complex binding	GO:0023023	p=3.5E-02	n=1
MHC class Ib protein complex binding	GO:0023025	p=3.5E-02	n=1
MHC class Ib protein binding	GO:0023029	p=3.5E-02	n=1
histone deacetylase regulator activity	GO:0035033	p=3.5E-02	n=1
pyrimidine- and adenine-specific:sodium ...	GO:0015389	p=3.5E-02	n=1
S-methyl-5-thioadenosine phosphorylase a...	GO:0017061	p=3.5E-02	n=1
MHC class Ib protein binding, via antige...	GO:0023030	p=3.5E-02	n=1
ubiquitin activating enzyme activity	GO:0004839	p=3.5E-02	n=1
mannosyl-oligosaccharide mannosidase act...	GO:0015924	p=3.5E-02	n=1
phosphomannomutase activity	GO:0004615	p=3.5E-02	n=1
phosphoglycerate dehydrogenase activity	GO:0004617	p=3.5E-02	n=1
purine-nucleoside phosphorylase activity	GO:0004731	p=3.5E-02	n=1



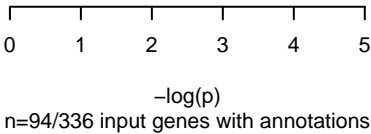
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GO:CC
Ncol_Nvec_vc1.1_XM_032385963.2

fraction genes in fg and expected value

postsynaptic density	GO:0014069	p=7.0E-03	n=6
intrinsic component of the cytoplasmic s...	GO:0031235	p=1.1E-02	n=2
neuronal cell body membrane	GO:0032809	p=1.9E-02	n=3
cell body membrane	GO:0044298	p=2.3E-02	n=3
presynapse	GO:0098793	p=2.4E-02	n=9
dendrite	GO:0030425	p=2.5E-02	n=11
dendritic tree	GO:0097447	p=2.6E-02	n=11
somatodendritic compartment	GO:0036477	p=2.7E-02	n=14
core-binding factor complex	GO:0016513	p=3.5E-02	n=1
NMDA selective glutamate receptor comple...	GO:0017146	p=3.5E-02	n=1
proteasome storage granule	GO:0034515	p=3.5E-02	n=1
smooth muscle contractile fiber	GO:0030485	p=3.5E-02	n=1
Ric1-Rgp1 guanyl-nucleotide exchange fac...	GO:0034066	p=3.5E-02	n=1
hippocampal mossy fiber expansion	GO:1990026	p=3.5E-02	n=1
varicosity	GO:0043196	p=3.5E-02	n=1
nuclear pore central transport channel	GO:0044613	p=3.5E-02	n=1
nuclear pore	GO:0005643	p=3.9E-02	n=3
cell cortex	GO:0005938	p=4.3E-02	n=7
synaptic vesicle	GO:0008021	p=4.3E-02	n=5
synaptic vesicle membrane	GO:0030672	p=4.4E-02	n=3
exocytic vesicle membrane	GO:0099501	p=4.9E-02	n=3
neuronal cell body	GO:0043025	p=5.1E-02	n=10
proteasome regulatory particle	GO:0005838	p=6.3E-02	n=2
proteasome accessory complex	GO:0022624	p=6.3E-02	n=2
exocytic vesicle	GO:0070382	p=6.6E-02	n=5
extrinsic component of Golgi membrane	GO:0090498	p=6.8E-02	n=1
6-phosphofructo-2-kinase/fructose-2,6-bi...	GO:0043540	p=6.8E-02	n=1
ionotropic glutamate receptor complex	GO:0008328	p=6.8E-02	n=1
cytoplasmic cyclin-dependent protein kin...	GO:0000308	p=6.8E-02	n=1
hippocampal mossy fiber	GO:0097457	p=6.8E-02	n=1



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