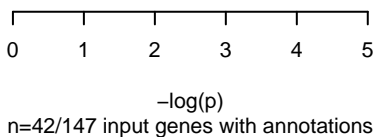
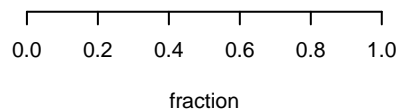


GO:BP  
Ncol\_Nvec\_vc1.1\_XM\_032384300.2

fraction genes in fg and expected value

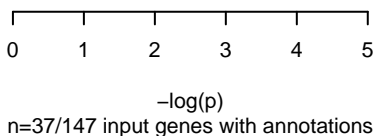
positive regulation of cholesterol biosy...	GO:0045542	p=1.5E-03	n=2
response to hermaphrodite contact	GO:0034606	p=3.0E-03	n=2
plasma lipoprotein particle organization	GO:0071827	p=3.0E-03	n=2
phospholipid transport	GO:0015914	p=3.5E-03	n=3
cellular response to angiotensin	GO:1904385	p=5.0E-03	n=2
negative regulation of lipid storage	GO:0010888	p=5.0E-03	n=2
extracellular structure organization	GO:0043062	p=6.2E-03	n=4
positive regulation of sodium ion transp...	GO:0010765	p=7.4E-03	n=2
positive regulation of exocytosis	GO:0045921	p=1.0E-02	n=3
exit from mitosis	GO:0010458	p=1.3E-02	n=2
cholesterol transport	GO:0030301	p=1.3E-02	n=2
regulation of lipid storage	GO:0010883	p=1.6E-02	n=4
positive regulation of cysteine-type end...	GO:0043280	p=1.7E-02	n=3
sterol transport	GO:0015918	p=2.1E-02	n=2
regulation of plasma lipoprotein particl...	GO:0097006	p=2.1E-02	n=2
positive regulation of apoptotic process	GO:0043065	p=2.2E-02	n=6
positive regulation of cysteine-type end...	GO:2001056	p=2.3E-02	n=3
positive regulation of acute inflammator...	GO:0002675	p=2.3E-02	n=1
positive regulation of microtubule bindi...	GO:1904528	p=2.3E-02	n=1
regulation of basement membrane organiza...	GO:0110011	p=2.3E-02	n=1
regulation of epithelial cell migration...	GO:2000274	p=2.3E-02	n=1
regulation of brain-derived neurotrophic...	GO:0031551	p=2.3E-02	n=1
negative regulation of brain-derived neu...	GO:0031552	p=2.3E-02	n=1
brain-derived neurotrophic factor recept...	GO:0031547	p=2.3E-02	n=1
regulation of brain-derived neurotrophic...	GO:0031548	p=2.3E-02	n=1
negative regulation of brain-derived neu...	GO:0031549	p=2.3E-02	n=1
regulation of late endosome to lysosome ...	GO:1902822	p=2.3E-02	n=1
positive regulation of late endosome to ...	GO:1902824	p=2.3E-02	n=1
protein-containing complex remodeling	GO:0034367	p=2.3E-02	n=1
protein-lipid complex remodeling	GO:0034368	p=2.3E-02	n=1

[illegible]

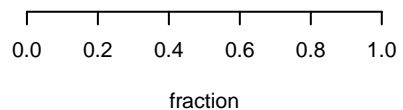
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fraction genes in fg and expected value

phospholipid transporter activity	GO:0005548	p=2.8E-03	n=3
protein disulfide isomerase activity	GO:0003756	p=5.0E-03	n=2
cholesterol binding	GO:0015485	p=7.4E-03	n=2
RNA polymerase II-specific DNA-binding t...	GO:0061629	p=1.0E-02	n=4
DNA-binding transcription factor binding	GO:0140297	p=1.3E-02	n=4
phospholipid binding	GO:0005543	p=1.6E-02	n=5
protein heterodimerization activity	GO:0046982	p=1.7E-02	n=6
dystroglycan binding	GO:0002162	p=2.3E-02	n=1
steroid dehydrogenase activity	GO:0016229	p=2.3E-02	n=1
TFIIF-class transcription factor complex...	GO:0001096	p=2.3E-02	n=1
translation elongation factor binding	GO:0061770	p=2.3E-02	n=1
N-acylneuraminate-9-phosphatase activity	GO:0050124	p=2.3E-02	n=1
lysine N-acetyltransferase activity, act...	GO:0004468	p=2.3E-02	n=1
kinetochore binding	GO:0043515	p=2.3E-02	n=1
steroid dehydrogenase activity, acting o...	GO:0033764	p=2.3E-02	n=1
glycerophosphoinositol glycerophosphodie...	GO:0047395	p=2.3E-02	n=1
phospholipase D activator activity	GO:1990583	p=2.3E-02	n=1
ABC-type sterol transporter activity	GO:0034041	p=2.3E-02	n=1
estradiol 17-beta-dehydrogenase activity	GO:0004303	p=2.3E-02	n=1
testosterone 17-beta-dehydrogenase (NADP...	GO:0047045	p=2.3E-02	n=1
glycerophosphodiester phosphodiesterase ...	GO:0008889	p=2.3E-02	n=1
RNA polymerase II transcription regulato...	GO:0000977	p=3.3E-02	n=5
identical protein binding	GO:0042802	p=3.5E-02	n=11
cis-regulatory region sequence-specific ...	GO:0000987	p=4.1E-02	n=4
RNA polymerase II cis-regulatory region ...	GO:0000978	p=4.1E-02	n=4
BH3 domain binding	GO:0051434	p=4.6E-02	n=1
Tat protein binding	GO:0030957	p=4.6E-02	n=1
nuclear retinoid X receptor binding	GO:0046965	p=4.6E-02	n=1
STAT family protein binding	GO:0097677	p=4.6E-02	n=1
toxin transmembrane transporter activity	GO:0019534	p=4.6E-02	n=1



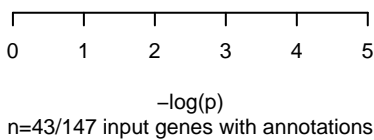
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GO:CC  
Ncol\_Nvec\_vc1.1\_XM\_032384300.2

fraction genes in fg and expected value

centrosomal corona	GO:0031592	p=2.4E-02	n=1
collagen and cuticulin-based cuticle ext...	GO:0060102	p=2.4E-02	n=1
cortical microtubule cytoskeleton	GO:0030981	p=2.4E-02	n=1
MutLalpha complex	GO:0032389	p=2.4E-02	n=1
neuronal ribonucleoprotein granule	GO:0071598	p=2.4E-02	n=1
cytoplasmic microtubule plus-end	GO:1904511	p=2.4E-02	n=1
protein kinase CK2 complex	GO:0005956	p=2.4E-02	n=1
cortical microtubule	GO:0055028	p=2.4E-02	n=1
ESCRT-0 complex	GO:0033565	p=2.4E-02	n=1
cortical microtubule plus-end	GO:1903754	p=2.4E-02	n=1
chromosome, centromeric region	GO:0000775	p=2.7E-02	n=3
myosin V complex	GO:0031475	p=4.7E-02	n=1
muscle myosin complex	GO:0005859	p=4.7E-02	n=1
Seh1-associated complex	GO:0035859	p=4.7E-02	n=1
myosin II complex	GO:0016460	p=4.7E-02	n=1
mismatch repair complex	GO:0032300	p=4.7E-02	n=1
COP1 vesicle coat	GO:0030126	p=4.7E-02	n=1
nuclear stress granule	GO:0097165	p=4.7E-02	n=1
GATOR2 complex	GO:0061700	p=4.7E-02	n=1
U2AF complex	GO:0089701	p=4.7E-02	n=1
COP1-coated vesicle membrane	GO:0030663	p=4.7E-02	n=1
kinetochore	GO:0000776	p=5.4E-02	n=2
heterochromatin	GO:0000792	p=6.0E-02	n=2
myosin VI complex	GO:0031476	p=7.0E-02	n=1
myosin VII complex	GO:0031477	p=7.0E-02	n=1
microtubule plus-end	GO:0035371	p=7.0E-02	n=1
Bcl-2 family protein complex	GO:0097136	p=7.0E-02	n=1
kinetochore microtubule	GO:0005828	p=7.0E-02	n=1
U2-type prespliceosome	GO:0071004	p=7.0E-02	n=1
commitment complex	GO:0000243	p=7.0E-02	n=1



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