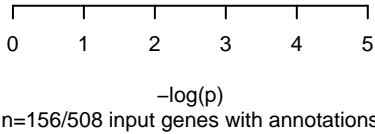


GO:BP
Ncol_Nvec_vc1.1_XM_032384420.2

fraction genes in fg and expected value

heart morphogenesis	GO:0003007	p=7.6E-04	n=11
negative regulation of angiogenesis	GO:0016525	p=1.1E-03	n=4
embryonic organ morphogenesis	GO:0048562	p=1.3E-03	n=13
response to hypoxia	GO:0001666	p=1.8E-03	n=13
cell surface receptor signaling pathway	GO:0007166	p=2.4E-03	n=42
negative regulation of intracellular est...	GO:0033147	p=3.3E-03	n=2
proximal/distal pattern formation, imagi...	GO:0007449	p=3.3E-03	n=2
negative regulation of sequestering of t...	GO:0010891	p=3.3E-03	n=2
cellular response to dexamethasone stimu...	GO:0071549	p=3.3E-03	n=3
neuroblast differentiation	GO:0014016	p=3.7E-03	n=4
cellular response to decreased oxygen le...	GO:0036294	p=5.4E-03	n=8
cellular response to ethanol	GO:0071361	p=5.6E-03	n=3
NADH regeneration	GO:0006735	p=5.6E-03	n=3
response to mitochondrial depolarisation	GO:0098780	p=5.6E-03	n=3
actin cytoskeleton reorganization	GO:0031532	p=5.8E-03	n=5
regulation of autophagy	GO:0010506	p=5.8E-03	n=12
hippocampus development	GO:0021766	p=6.3E-03	n=6
axon guidance	GO:0007411	p=6.5E-03	n=13
neural precursor cell proliferation	GO:0061351	p=6.7E-03	n=10
DNA methylation or demethylation	GO:0044728	p=7.1E-03	n=5
gland development	GO:0048732	p=7.6E-03	n=16
positive regulation of multicellular org...	GO:0051240	p=7.7E-03	n=31
forebrain regionalization	GO:0021871	p=8.5E-03	n=3
cellular response to catecholamine stimu...	GO:0071870	p=8.7E-03	n=5
eye development	GO:0001654	p=8.7E-03	n=19
positive regulation of stress fiber asse...	GO:0051496	p=8.9E-03	n=4
regulation of cAMP-mediated signaling	GO:0043949	p=8.9E-03	n=4
lactate biosynthetic process	GO:0019249	p=9.6E-03	n=2
regulation of transcription by glucose	GO:0046015	p=9.6E-03	n=2
glycerol catabolic process	GO:0019563	p=9.6E-03	n=2

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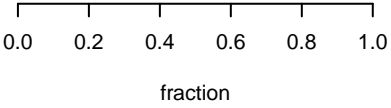
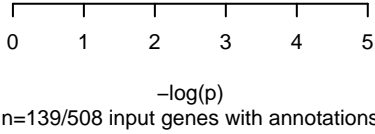


GO:MF
Ncol_Nvec_vc1.1_XM_032384420.2

fraction genes in fg and expected value

transferase activity, transferring alkyl...	GO:0016765	p=8.4E-04	n=5
phospholipase A2 activity	GO:0004623	p=3.5E-03	n=3
GDP binding	GO:0019003	p=5.4E-03	n=4
DNA-binding transcription factor activit...	GO:0000981	p=6.1E-03	n=16
oxidoreductase activity, acting on NAD(P...	GO:0016651	p=8.0E-03	n=6
triglyceride lipase activity	GO:0004806	p=9.9E-03	n=2
cAMP response element binding	GO:0035497	p=9.9E-03	n=2
oxidoreductase activity, acting on the C...	GO:0016899	p=9.9E-03	n=2
inosine kinase activity	GO:0008906	p=9.9E-03	n=2
phosphoenolpyruvate carboxykinase (GTP) ...	GO:0004613	p=9.9E-03	n=2
GTPase activator activity	GO:0005096	p=1.1E-02	n=8
ATPase-coupled ion transmembrane transpo...	GO:0042625	p=1.2E-02	n=4
phospholipid binding	GO:0005543	p=1.2E-02	n=11
protein-disulfide reductase (NAD(P)) act...	GO:0047134	p=1.3E-02	n=3
oxidoreductase activity, acting on a sul...	GO:0016668	p=1.7E-02	n=3
lactate dehydrogenase activity	GO:0004457	p=1.9E-02	n=2
DNA binding domain binding	GO:0050692	p=1.9E-02	n=2
GTPase regulator activity	GO:0030695	p=2.3E-02	n=11
protein-disulfide reductase activity	GO:0015035	p=2.9E-02	n=3
phosphatidylinositol-4-phosphate binding	GO:0070273	p=2.9E-02	n=3
phosphatidylinositol-5-phosphate binding	GO:0010314	p=3.0E-02	n=2
nucleoside diphosphate kinase activity	GO:0004550	p=3.0E-02	n=2
epinephrine binding	GO:0051379	p=3.0E-02	n=2
catecholamine binding	GO:1901338	p=3.0E-02	n=2
protein tyrosine phosphatase activity	GO:0004725	p=3.7E-02	n=3
primary active transmembrane transporter...	GO:0015399	p=4.1E-02	n=6
transcription coregulator activity	GO:0003712	p=4.3E-02	n=12
proteoglycan binding	GO:0043394	p=4.4E-02	n=2
BH domain binding	GO:0051400	p=4.4E-02	n=2
disulfide oxidoreductase activity	GO:0015036	p=4.5E-02	n=3

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GO:CC
Ncol_Nvec_vc1.1_XM_032384420.2

fraction genes in fg and expected value

collagen and cuticulin-based cuticle ext...	GO:0060102	p=3.3E-03	n=2
extrinsic component of organelle membran...	GO:0031312	p=5.0E-03	n=4
microtubule associated complex	GO:0005875	p=1.6E-02	n=7
NuRD complex	GO:0016581	p=1.8E-02	n=2
inner dynein arm	GO:0036156	p=1.8E-02	n=2
CHD-type complex	GO:0090545	p=1.8E-02	n=2
mitochondrial outer membrane	GO:0005741	p=1.9E-02	n=6
cis-Golgi network	GO:0005801	p=2.1E-02	n=4
organelle outer membrane	GO:0031968	p=2.2E-02	n=6
outer membrane	GO:0019867	p=2.2E-02	n=6
membrane	GO:0016020	p=2.4E-02	n=78
cell cortex region	GO:0099738	p=2.9E-02	n=4
TRAPP complex	GO:0030008	p=2.9E-02	n=2
platelet alpha granule lumen	GO:0031093	p=2.9E-02	n=2
cytoplasmic side of plasma membrane	GO:0009898	p=3.3E-02	n=7
histone deacetylase complex	GO:0000118	p=3.5E-02	n=3
cell periphery	GO:0071944	p=3.5E-02	n=51
cell projection	GO:0042995	p=3.6E-02	n=37
plasma membrane bounded cell projection ...	GO:0032838	p=4.1E-02	n=6
extrinsic component of endosome membrane	GO:0031313	p=4.2E-02	n=2
axon cytoplasm	GO:1904115	p=4.2E-02	n=2
heterotrimeric G-protein complex	GO:0005834	p=4.2E-02	n=2
GTPase complex	GO:1905360	p=4.2E-02	n=2
axoneme	GO:0005930	p=4.2E-02	n=5
endocytic vesicle membrane	GO:0030666	p=4.5E-02	n=4
cytoplasmic region	GO:0099568	p=4.5E-02	n=13
endosome	GO:0005768	p=4.7E-02	n=17
ciliary plasm	GO:0097014	p=4.7E-02	n=5
plasma membrane bounded cell projection	GO:0120025	p=5.1E-02	n=36
supramolecular polymer	GO:0099081	p=5.2E-02	n=13

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