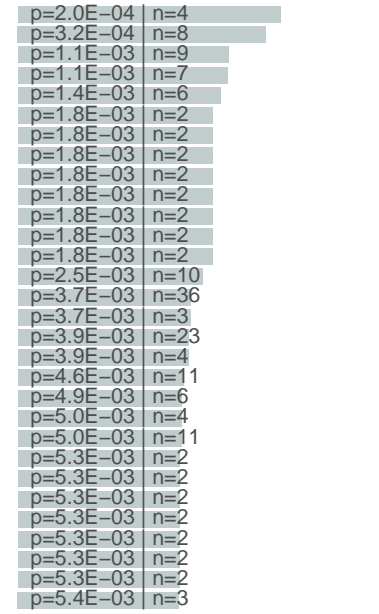


GO:BP
Ncol_Nvec_vc1.1_XM_048724012.1

regulation of intracellular estrogen rec...	GO:0033146
regulation of Ras protein signal transdu...	GO:0046578
neuron projection extension	GO:1990138
extracellular matrix organization	GO:0030198
positive regulation of cell–cell adhesio...	GO:0022409
positive regulation of myotube different...	GO:0010831
optic vesicle morphogenesis	GO:0003404
plasma membrane raft assembly	GO:0044854
mesectoderm development	GO:0048383
cellular response to exogenous dsRNA	GO:0071360
lens induction in camera–type eye	GO:0060235
positive regulation of myoblast fusion	GO:1901741
establishment or maintenance of cytoskel...	GO:0003380
positive regulation of neuron projection...	GO:0010976
regulation of localization	GO:0032879
activin receptor signaling pathway	GO:0032924
negative regulation of signal transducti...	GO:0009968
negative regulation of protein depolymer...	GO:1901880
axon guidance	GO:0007411
cell recognition	GO:0008037
negative regulation of mitochondrion org...	GO:0010823
positive regulation of neuron differenti...	GO:0045666
regulation of retina development in came...	GO:1902866
positive regulation of interferon–gamma ...	GO:0032729
vestibulocochlear nerve development	GO:0021562
post–embryonic body morphogenesis	GO:0040032
regulation of neural retina development	GO:0061074
microvillus assembly	GO:0030033
deoxyribonucleotide biosynthetic process	GO:0009263
actin filament depolymerization	GO:0030042



–log(p)
n=116/373 input genes with annotations

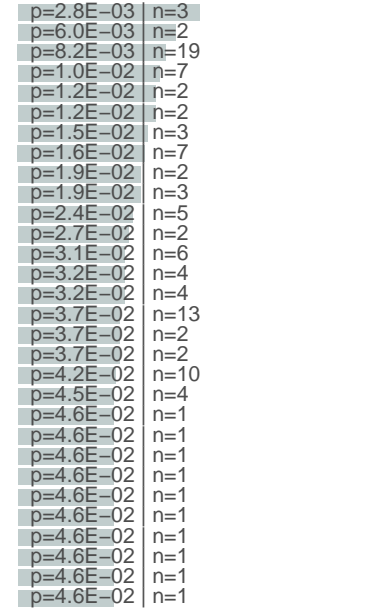
fraction genes in fg and expected value

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fraction

GO:MF
Ncol_Nvec_vc1.1_XM_048724012.1

phosphatidylcholine binding	GO:0031210
S100 protein binding	GO:0044548
signaling receptor binding	GO:0005102
enzyme inhibitor activity	GO:0004857
phosphatidylethanolamine binding	GO:0008429
ubiquitin–like modifier activating enzym...	GO:0008641
disordered domain specific binding	GO:0097718
microtubule binding	GO:0008017
glucosyltransferase activity	GO:0046527
ammonium ion binding	GO:0070405
transcription corepressor activity	GO:0003714
BH domain binding	GO:0051400
actin binding	GO:0003779
DNA–binding transcription repressor acti...	GO:0001227
DNA–binding transcription repressor acti...	GO:0001217
DNA–binding transcription factor activit...	GO:0003700
phosphatase inhibitor activity	GO:0019212
spectrin binding	GO:0030507
transcription coregulator activity	GO:0003712
hydrolase activity, acting on carbon–nit...	GO:0016810
neuregulin binding	GO:0038132
phosphatidylinositol phosphate kinase ac...	GO:0016307
1–phosphatidylinositol–4–phosphate 5–kin...	GO:0016308
1–phosphatidylinositol–5–phosphate 4–kin...	GO:0016309
oxidative DNA demethylase activity	GO:0035516
interleukin–6 receptor binding	GO:0005138
JUN kinase kinase activity	GO:0008545
MHC protein complex binding	GO:0023023
MHC class Ib protein complex binding	GO:0023025
MHC class Ib protein binding	GO:0023029



–log(p)
n=108/373 input genes with annotations

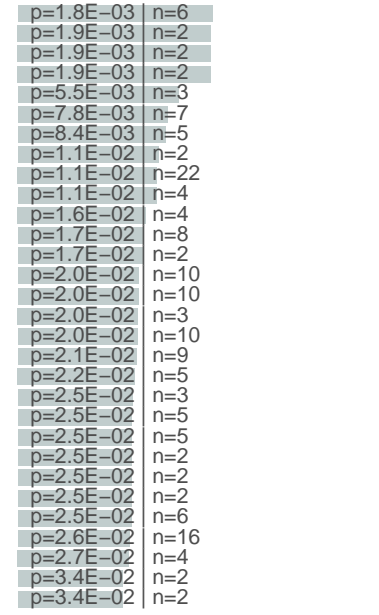
fraction genes in fg and expected value

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fg=0.01	bg=0.00

fraction

GO:CC
Ncol_Nvec_vc1.1_XM_048724012.1

extrinsic component of plasma membrane	GO:0019897
photoreceptor outer segment membrane	GO:0042622
uropod	GO:0001931
collagen and cuticulin–based cuticle ext...	GO:0060102
clathrin–coated pit	GO:0005905
cytoplasmic side of plasma membrane	GO:0009898
plasma membrane raft	GO:0044853
filamentous actin	GO:0031941
cell junction	GO:0030054
extrinsic component of cytoplasmic side ...	GO:0031234
caveola	GO:0005901
plasma membrane protein complex	GO:0098797
sensory dendrite	GO:0071683
anchoring junction	GO:0070161
cell–cell junction	GO:0005911
actin filament	GO:0005884
cell projection membrane	GO:0031253
cell leading edge	GO:0031252
mitochondrial outer membrane	GO:0005741
transcription elongation factor complex	GO:0008023
organelle outer membrane	GO:0031968
outer membrane	GO:0019867
heterotrimeric G–protein complex	GO:0005834
GTPase complex	GO:1905360
filopodium membrane	GO:0031527
lamellipodium	GO:0030027
synapse	GO:0045202
sarcolemma	GO:0042383
apicolateral plasma membrane	GO:0016327
microvillus membrane	GO:0031528



–log(p)
n=117/373 input genes with annotations

fraction genes in fg and expected value

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fraction