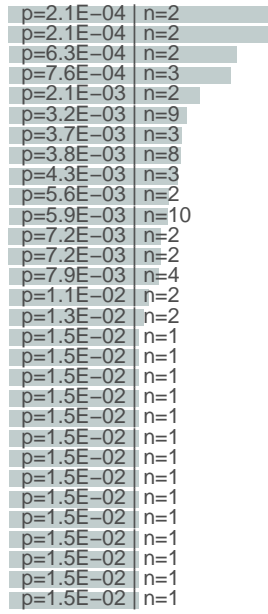


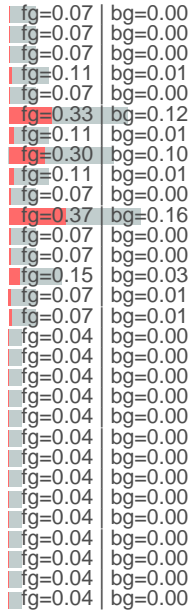
GO:BP
Fox_Nvec_vc1.1_XM_001637190.3

fraction genes in fg and expected value

| | |
|---|------------|
| establishment or maintenance of cytoskel... | GO:0003380 |
| mesectoderm development | GO:0048383 |
| regulation of myosin II filament organiz... | GO:0043519 |
| regulation of gastrulation | GO:0010470 |
| regulation of antimicrobial peptide prod... | GO:0002784 |
| negative regulation of cellular macromol... | GO:2000113 |
| G protein-coupled receptor signaling pat... | GO:0007187 |
| negative regulation of transcription, DN... | GO:0045892 |
| adenylate cyclase-modulating G protein-c... | GO:0007188 |
| convergent extension involved in gastrul... | GO:0060027 |
| negative regulation of gene expression | GO:0010629 |
| neuron cellular homeostasis | GO:0070050 |
| regulation of DNA-templated DNA replicat... | GO:0090329 |
| dorsal/ventral pattern formation | GO:0009953 |
| adenylate cyclase-activating G protein-c... | GO:0007189 |
| apoptotic process involved in developmen... | GO:1902742 |
| regulation of catecholamine uptake invol... | GO:0051940 |
| positive regulation of GTP cyclohydrolas... | GO:0043104 |
| regulation of mediator complex assembly | GO:2001176 |
| positive regulation of mediator complex ... | GO:2001178 |
| base-excision repair, DNA ligation | GO:0006288 |
| nodal signaling pathway | GO:0038092 |
| regulation of chorionic trophoblast cell... | GO:1901382 |
| granulosa cell apoptotic process | GO:1904700 |
| regulation of granulosa cell apoptotic p... | GO:1904708 |
| regulation of dopamine uptake involved i... | GO:0051584 |
| regulation of protein K48-linked deubiqu... | GO:1903093 |
| negative regulation of ubiquitin-protein... | GO:0051444 |
| dendrite development by retrograde exten... | GO:0003390 |
| amphid sensory organ dendrite retrograde... | GO:0003391 |



-log(p)
n=27/120 input genes with annotations

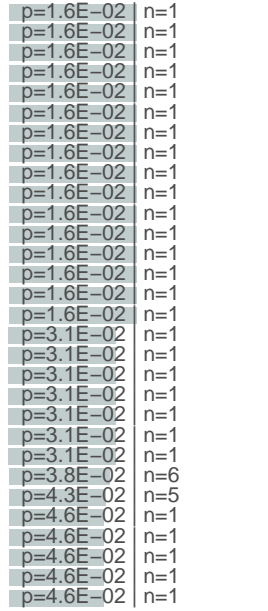


fraction

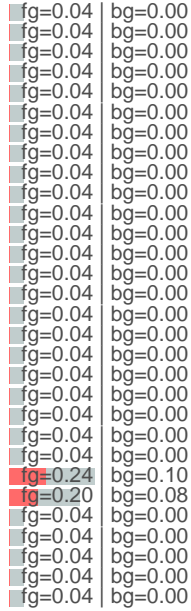
GO:MF
Fox_Nvec_vc1.1_XM_001637190.3

fraction genes in fg and expected value

| | |
|---|------------|
| ubiquitin ligase inhibitor activity | GO:1990948 |
| 5S rDNA binding | GO:0080084 |
| ATPase-coupled intramembrane lipid trans... | GO:0140326 |
| flippase activity | GO:0140327 |
| ubiquitin-like modifier activating enzym... | GO:0008641 |
| UFM1 activating enzyme activity | GO:0071566 |
| RNA polymerase III core binding | GO:0000994 |
| RNA polymerase III transcription regulat... | GO:0001016 |
| GABA receptor binding | GO:0050811 |
| aminophospholipid flippase activity | GO:0015247 |
| alkylglycerophosphoethanolamine phosphod... | GO:0047391 |
| D5 dopamine receptor binding | GO:0031752 |
| ubiquitin-protein transferase inhibitor ... | GO:0055105 |
| phosphatidylglycerol binding | GO:1901611 |
| cardiolipin binding | GO:1901612 |
| dynein light intermediate chain binding | GO:0051959 |
| DNA ligase activity | GO:0003909 |
| transcription corepressor binding | GO:0001222 |
| peroxisome proliferator activated recept... | GO:0042975 |
| nuclear retinoid X receptor binding | GO:0046965 |
| DNA ligase (ATP) activity | GO:0003910 |
| co-SMAD binding | GO:0070410 |
| 5S rRNA binding | GO:0008097 |
| signaling receptor binding | GO:0005102 |
| cytoskeletal protein binding | GO:0008092 |
| ankyrin binding | GO:0030506 |
| rDNA binding | GO:0000182 |
| nuclear retinoic acid receptor binding | GO:0042974 |
| ligase activity, forming phosphoric este... | GO:0016886 |
| ubiquitin-protein transferase regulator ... | GO:0055106 |



-log(p)
n=25/120 input genes with annotations

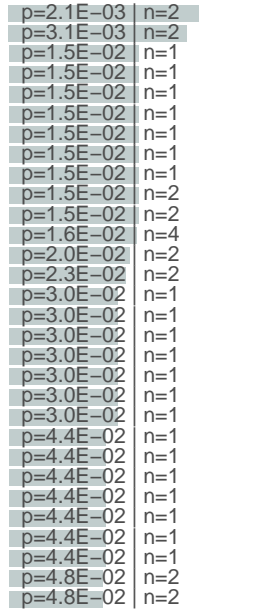


fraction

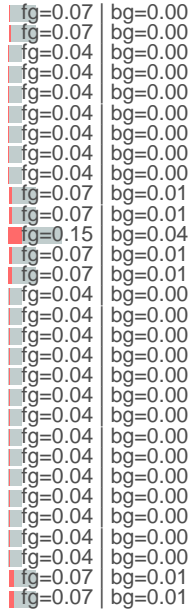
GO:CC
Fox_Nvec_vc1.1_XM_001637190.3

fraction genes in fg and expected value

| | |
|---|------------|
| sensory dendrite | GO:0071683 |
| heterotrimeric G-protein complex | GO:0005834 |
| spectrosome | GO:0045170 |
| spectrin | GO:0008091 |
| collagen and cuticulin-based cuticle ext... | GO:0060102 |
| endocytic patch | GO:0061645 |
| DNA ligase III-XRCC1 complex | GO:0070421 |
| actin cortical patch | GO:0030479 |
| molybdopterin synthase complex | GO:0019008 |
| brush border membrane | GO:0031526 |
| cortical actin cytoskeleton | GO:0030864 |
| cell projection membrane | GO:0031253 |
| cortical cytoskeleton | GO:0030863 |
| ciliary membrane | GO:0060170 |
| extrinsic component of endoplasmic retic... | GO:0042406 |
| NELF complex | GO:0032021 |
| cytoplasmic side of rough endoplasmic re... | GO:0098556 |
| photoreceptor outer segment membrane | GO:0042622 |
| RSF complex | GO:0031213 |
| cytoplasmic cyclin-dependent protein kin... | GO:0000308 |
| cis-Golgi network membrane | GO:0033106 |
| photoreceptor disc membrane | GO:0097381 |
| inhibitory synapse | GO:0060077 |
| aster | GO:0005818 |
| polysomal ribosome | GO:0042788 |
| spindle pole centrosome | GO:0031616 |
| ISWI-type complex | GO:0031010 |
| spot adherens junction | GO:0005914 |
| spindle pole | GO:0000922 |
| brush border | GO:0005903 |



-log(p)
n=27/120 input genes with annotations



fraction