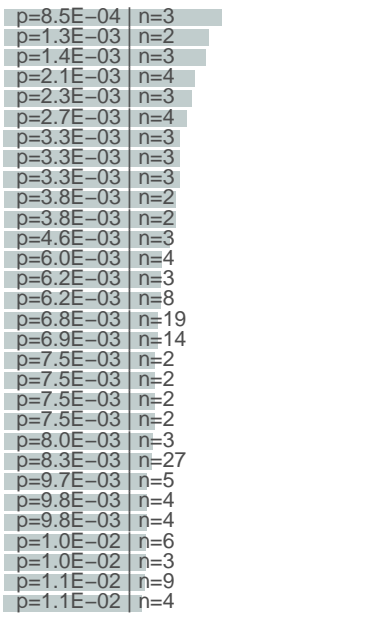


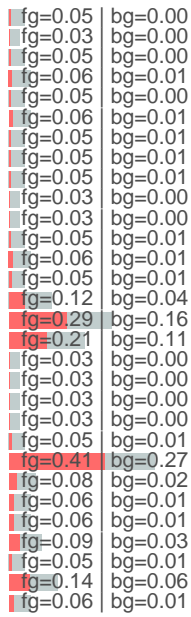
GO:BP
Fox_Nvec_vc1.1_XM_032378881.2

fraction genes in fg and expected value

| | |
|---|------------|
| positive regulation of transcription of ... | GO:0007221 |
| thrombopoietin-mediated signaling pathwa... | GO:0038163 |
| branching involved in blood vessel morph... | GO:0001569 |
| endoplasmic reticulum organization | GO:0007029 |
| protein N-linked glycosylation via aspar... | GO:0018279 |
| somatic stem cell population maintenance | GO:0035019 |
| spleen development | GO:0048536 |
| regulation of calcineurin-NFAT signaling... | GO:0070884 |
| proximal/distal pattern formation | GO:0009954 |
| positive regulation of glycoprotein meta... | GO:1903020 |
| entry of bacterium into host cell | GO:0035635 |
| epithelial cell differentiation involved... | GO:0035850 |
| kidney morphogenesis | GO:0060993 |
| adenylate cyclase-activating G protein-c... | GO:0007189 |
| negative regulation of nervous system de... | GO:0051961 |
| regulation of transport | GO:0051049 |
| chemical homeostasis | GO:0048878 |
| cellular response to forskolin | GO:1904322 |
| glomerulus morphogenesis | GO:0072102 |
| cellular response to vitamin D | GO:0071305 |
| triglyceride catabolic process | GO:0019433 |
| cyclic nucleotide metabolic process | GO:0009187 |
| establishment of localization in cell | GO:0051649 |
| spermatid development | GO:0007286 |
| cardiac ventricle development | GO:0003231 |
| cardiac chamber morphogenesis | GO:0003206 |
| negative regulation of cellular cataboli... | GO:0031330 |
| negative regulation of myeloid cell diff... | GO:0045638 |
| protein localization to membrane | GO:0072657 |
| cell-substrate adhesion | GO:0031589 |



–log(p)
n=66/221 input genes with annotations

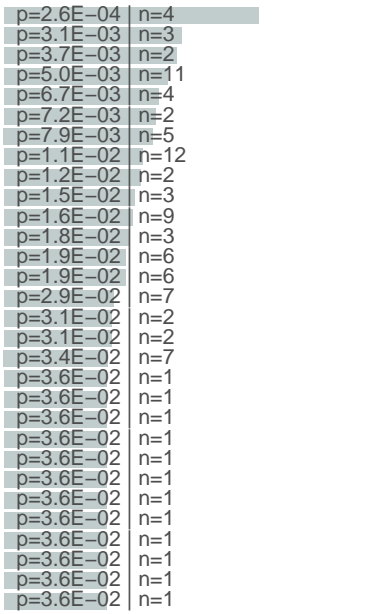


fraction

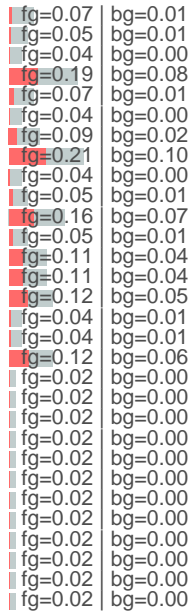
GO:MF
Fox_Nvec_vc1.1_XM_032378881.2

fraction genes in fg and expected value

| | |
|---|------------|
| ribosome binding | GO:0043022 |
| transcription coregulator binding | GO:0001221 |
| triglyceride lipase activity | GO:0004806 |
| DNA-binding transcription factor activit... | GO:0003700 |
| ATPase-coupled transmembrane transporter... | GO:0042626 |
| nitric-oxide synthase binding | GO:0050998 |
| active ion transmembrane transporter act... | GO:0022853 |
| signaling receptor binding | GO:0005102 |
| transcription coactivator binding | GO:0001223 |
| transmembrane transporter binding | GO:0044325 |
| inorganic molecular entity transmembrane... | GO:0015318 |
| phospholipase activity | GO:0004620 |
| DNA-binding transcription activator acti... | GO:0001228 |
| DNA-binding transcription activator acti... | GO:0001216 |
| inorganic cation transmembrane transport... | GO:0022890 |
| P-type transmembrane transporter activit... | GO:0140358 |
| P-type ion transporter activity | GO:0015662 |
| cation transmembrane transporter activit... | GO:0008324 |
| protein-membrane adaptor activity | GO:0043495 |
| L-proline transmembrane transporter acti... | GO:0015193 |
| L-tryptophan transmembrane transporter a... | GO:0015196 |
| amino acid:cation symporter activity | GO:0005416 |
| histone pre-mRNA stem-loop binding | GO:0071207 |
| calcium- and calmodulin-responsive adeny... | GO:0008294 |
| lysophosphatidic acid binding | GO:0035727 |
| ATP-dependent DNA/DNA annealing activity | GO:0036310 |
| histone methyltransferase binding | GO:1990226 |
| glycine transmembrane transporter activi... | GO:0015187 |
| mono-olein transacylation activity | GO:0051264 |
| diolein transacylation activity | GO:0051265 |



–log(p)
n=57/221 input genes with annotations

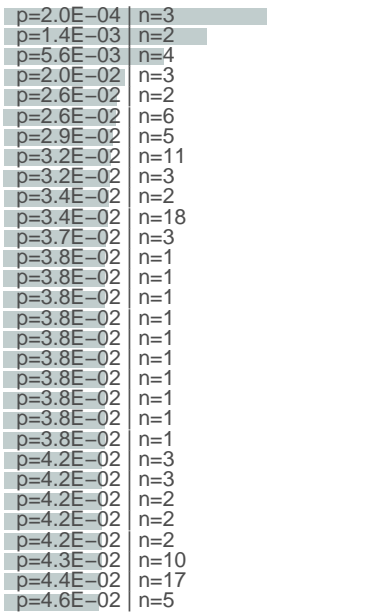


fraction

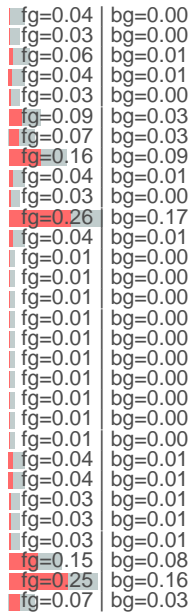
GO:CC
Fox_Nvec_vc1.1_XM_032378881.2

fraction genes in fg and expected value

| | |
|---|------------|
| microvillus membrane | GO:0031528 |
| oligosaccharyltransferase complex | GO:0008250 |
| exocytic vesicle membrane | GO:0099501 |
| caveola | GO:0005901 |
| intermediate filament cytoskeleton | GO:0045111 |
| vacuolar membrane | GO:0005774 |
| endocytic vesicle | GO:0030139 |
| endosome | GO:0005768 |
| synaptic vesicle membrane | GO:0030672 |
| cytoplasmic microtubule | GO:0005881 |
| intrinsic component of membrane | GO:0031224 |
| endoplasmic reticulum-Golgi intermediate... | GO:0005793 |
| fascia adherens | GO:0005916 |
| histone pre-mRNA 3'end processing comple... | GO:0071204 |
| catenin-TCF7L2 complex | GO:0071664 |
| Scrib-APC-beta-catenin complex | GO:0034750 |
| post-mRNA release spliceosomal complex | GO:0071014 |
| beta-catenin-TCF7L2 complex | GO:0070369 |
| DNA ligase III-XRCC1 complex | GO:0070421 |
| CA3 pyramidal cell dendrite | GO:0097442 |
| beta-catenin destruction complex | GO:0030877 |
| catenin complex | GO:0016342 |
| plasma membrane raft | GO:0044853 |
| endocytic vesicle membrane | GO:0030666 |
| melanosome | GO:0042470 |
| endoplasmic reticulum-Golgi intermediate... | GO:0033116 |
| phagocytic vesicle membrane | GO:0030670 |
| intrinsic component of plasma membrane | GO:0031226 |
| integral component of membrane | GO:0016021 |
| membrane raft | GO:0045121 |



–log(p)
n=68/221 input genes with annotations



fraction