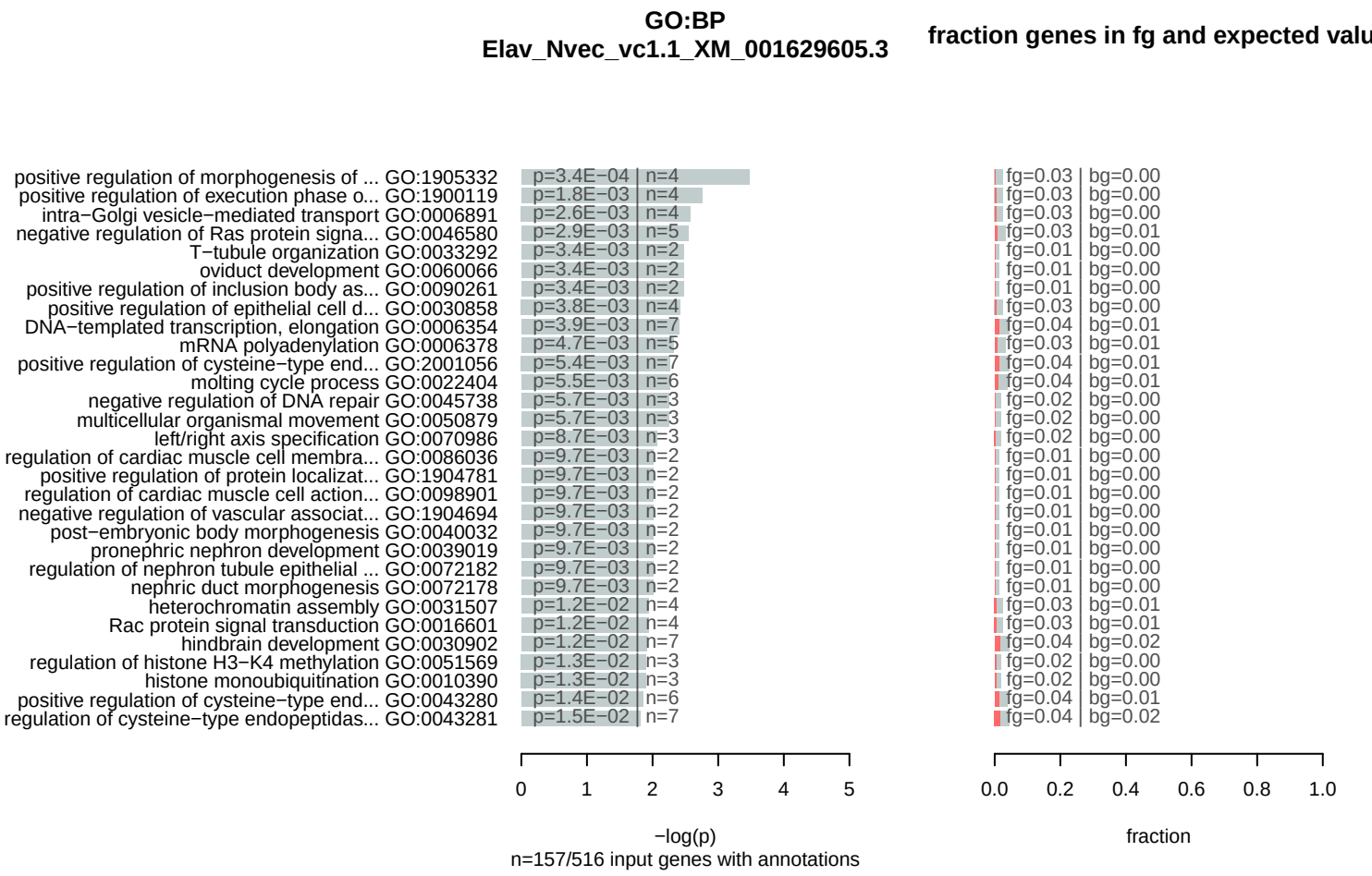
GO:BP
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fraction genes in fg and expected valu
positive regulation of morphogenesis of ... GO:1905332 p=3.4E−04 n=4 fg=0.03 bg=0.00
positive regulation of execution phase o... GO:1900119 p=1.8E−03 n=4 fg=0.03 bg=0.00
intra−Golgi vesicle−mediated transport GO:0006891 p=2.6E−03 n=4 fg=0.03 bg=0.00
negative regulation of Ras protein signa... GO:0046580 p=2.9E−03 n=5 fg=0.03 bg=0.01
T−tubule organization GO:0033292 p=3.4E−03 n=2 fg=0.01 bg=0.00
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positive regulation of inclusion body as... GO:0090261 p=3.4E−03 n=2 fg=0.01 bg=0.00
positive regulation of epithelial cell d... GO:0030858 p=3.8E−03 n=4 fg=0.03 bg=0.00
DNA−templated transcription, elongation GO:0006354 p=3.9E−03 n=7 fg=0.04 bg=0.01
mRNA polyadenylation GO:0006378 p=4.7E−03 n=5 fg=0.03 bg=0.01
positive regulation of cysteine−type end... GO:2001056 p=5.4E−03 n=7 fg=0.04 bg=0.01
molting cycle process GO:0022404 p=5.5E−03 n=6 fg=0.04 bg=0.01
negative regulation of DNA repair GO:0045738 p=5.7E−03 n=3 fg=0.02 bg=0.00
multicellular organismal movement GO:0050879 p=5.7E−03 n=3 fg=0.02 bg=0.00
left/right axis specification GO:0070986 p=8.7E−03 n=3 fg=0.02 bg=0.00
regulation of cardiac muscle cell membra... GO:0086036 p=9.7E−03 n=2 fg=0.01 bg=0.00
positive regulation of protein localizat... GO:1904781 p=9.7E−03 n=2 fg=0.01 bg=0.00
regulation of cardiac muscle cell action... GO:0098901 p=9.7E−03 n=2 fg=0.01 bg=0.00
negative regulation of vascular associat... GO:1904694 p=9.7E−03 n=2 fg=0.01 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=9.7E−03 n=2 fg=0.01 bg=0.00
pronephric nephron development GO:0039019 p=9.7E−03 n=2 fg=0.01 bg=0.00
regulation of nephron tubule epithelial ... GO:0072182 p=9.7E−03 n=2 fg=0.01 bg=0.00
nephric duct morphogenesis GO:0072178 p=9.7E−03 n=2 fg=0.01 bg=0.00
heterochromatin assembly GO:0031507 p=1.2E−02 n=4 fg=0.03 bg=0.01
Rac protein signal transduction GO:0016601 p=1.2E−02 n=4 fg=0.03 bg=0.01
hindbrain development GO:0030902 p=1.2E−02 n=7 fg=0.04 bg=0.02
regulation of histone H3−K4 methylation GO:0051569 p=1.3E−02 n=3 fg=0.02 bg=0.00
histone monoubiquitination GO:0010390 p=1.3E−02 n=3 fg=0.02 bg=0.00
positive regulation of cysteine−type end... GO:0043280 p=1.4E−02 n=6 fg=0.04 bg=0.01
regulation of cysteine−type endopeptidas... GO:0043281 p=1.5E−02 n=7 fg=0.04 bg=0.02
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−log(p)
n=157/516 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
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GTPase activator activity GO:0005096 p=7.9E−03 n=8 fg=0.06 bg=0.02
hexosaminidase activity GO:0015929 p=1.7E−02 n=2 fg=0.02 bg=0.00
chromatin DNA binding GO:0031490 p=1.9E−02 n=4 fg=0.03 bg=0.01
mRNA binding GO:0003729 p=2.1E−02 n=9 fg=0.07 bg=0.03
RNA polymerase II−specific DNA−binding t... GO:0061629 p=2.6E−02 n=7 fg=0.05 bg=0.02
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ubiquitin conjugating enzyme activity GO:0061631 p=3.2E−02 n=3 fg=0.02 bg=0.01
DNA−binding transcription factor binding GO:0140297 p=3.6E−02 n=7 fg=0.05 bg=0.02
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lipid transfer activity GO:0120013 p=4.0E−02 n=2 fg=0.02 bg=0.00
spectrin binding GO:0030507 p=5.4E+02 n=2 fg=0.02 bg=0.00
supercoiled DNA binding GO:0097100 p=5.6E+02 n=1 fg=0.01 bg=0.00
sphingolipid transfer activity GO:0120016 p=5.6E+02 n=1 fg=0.01 bg=0.00
ceramide transfer activity GO:0120017 p=5.6E+02 n=1 fg=0.01 bg=0.00
double−stranded methylated DNA binding GO:0010385 p=5.6E+02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0050664 p=5.6E+02 n=1 fg=0.01 bg=0.00
opsin binding GO:0002046 p=5.6E+02 n=1 fg=0.01 bg=0.00
URM1 activating enzyme activity GO:0042292 p=5.6E+02 n=1 fg=0.01 bg=0.00
sphingolipid transporter activity GO:0046624 p=5.6E+02 n=1 fg=0.01 bg=0.00
purine nucleoside transmembrane transpor... GO:0015211 p=5.6E+02 n=1 fg=0.01 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=5.6E+02 n=1 fg=0.01 bg=0.00
glutamate−ammonia ligase activity GO:0004356 p=5.6E+02 n=1 fg=0.01 bg=0.00
follicle−stimulating hormone receptor bi... GO:0031762 p=5.6E+02 n=1 fg=0.01 bg=0.00
alpha−N−acetylglucosaminidase activity GO:0004561 p=5.6E+02 n=1 fg=0.01 bg=0.00
ferrochelatase activity GO:0004325 p=5.6E+02 n=1 fg=0.01 bg=0.00
succinyl−CoA hydrolase activity GO:0004778 p=5.6E+02 n=1 fg=0.01 bg=0.00
lutropin−choriogonadotropic hormone rece... GO:0031775 p=5.6E+02 n=1 fg=0.01 bg=0.00
purine−specific nucleoside:sodium sympor... GO:0015390 p=5.6E+02 n=1 fg=0.01 bg=0.00
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−log(p)
n=132/516 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001629605.3
fraction genes in fg and expected valu
collagen and cuticulin−based cuticle ext... GO:0060102 p=3.4E−03 n=2 fg=0.01 bg=0.00
U2 snRNP GO:0005686 p=5.9E−03 n=3 fg=0.02 bg=0.00
extrinsic component of plasma membrane GO:0019897 p=8.2E−03 n=6 fg=0.04 bg=0.01
COPI vesicle coat GO:0030126 p=9.9E−03 n=2 fg=0.01 bg=0.00
mRNA cleavage and polyadenylation specif... GO:0005847 p=3.1E−02 n=2 fg=0.01 bg=0.00
mRNA cleavage factor complex GO:0005849 p=3.1E−02 n=2 fg=0.01 bg=0.00
extrinsic component of cytoplasmic side ... GO:0031234 p=3.2E−02 n=4 fg=0.03 bg=0.01
microtubule organizing center GO:0005815 p=3.4E−02 n=17 fg=0.11 bg=0.07
rough endoplasmic reticulum GO:0005791 p=3.7E−02 n=4 fg=0.03 bg=0.01
rough endoplasmic reticulum membrane GO:0030867 p=4.4E−02 n=2 fg=0.01 bg=0.00
nuclear outer membrane−endoplasmic retic... GO:0042175 p=4.5E−02 n=18 fg=0.11 bg=0.07
Golgi medial cisterna GO:0005797 p=5.4E+02 n=3 fg=0.02 bg=0.01
endopeptidase complex GO:1905369 p=5.6E+02 n=4 fg=0.03 bg=0.01
protein kinase CK2 complex GO:0005956 p=5.9E+02 n=1 fg=0.01 bg=0.00
nuclear pore inner ring GO:0044611 p=5.9E+02 n=1 fg=0.01 bg=0.00
nuclear pore central transport channel GO:0044613 p=5.9E+02 n=1 fg=0.01 bg=0.00
catenin−TCF7L2 complex GO:0071664 p=5.9E+02 n=1 fg=0.01 bg=0.00
Scrib−APC−beta−catenin complex GO:0034750 p=5.9E+02 n=1 fg=0.01 bg=0.00
fascia adherens GO:0005916 p=5.9E+02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200 p=5.9E+02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061202 p=5.9E+02 n=1 fg=0.01 bg=0.00
proteasome core complex, beta−subunit co... GO:0019774 p=5.9E+02 n=1 fg=0.01 bg=0.00
ribbon synapse GO:0097470 p=5.9E+02 n=1 fg=0.01 bg=0.00
pinosome GO:0044352 p=5.9E+02 n=1 fg=0.01 bg=0.00
macropinosome GO:0044354 p=5.9E+02 n=1 fg=0.01 bg=0.00
lumenal side of Golgi membrane GO:0098547 p=5.9E+02 n=1 fg=0.01 bg=0.00
platelet dense granule GO:0042827 p=5.9E+02 n=1 fg=0.01 bg=0.00
platelet dense tubular network GO:0031094 p=5.9E+02 n=1 fg=0.01 bg=0.00
platelet dense tubular network membrane GO:0031095 p=5.9E+02 n=1 fg=0.01 bg=0.00
clathrin−sculpted vesicle GO:0060198 p=5.9E+02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=159/516 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction