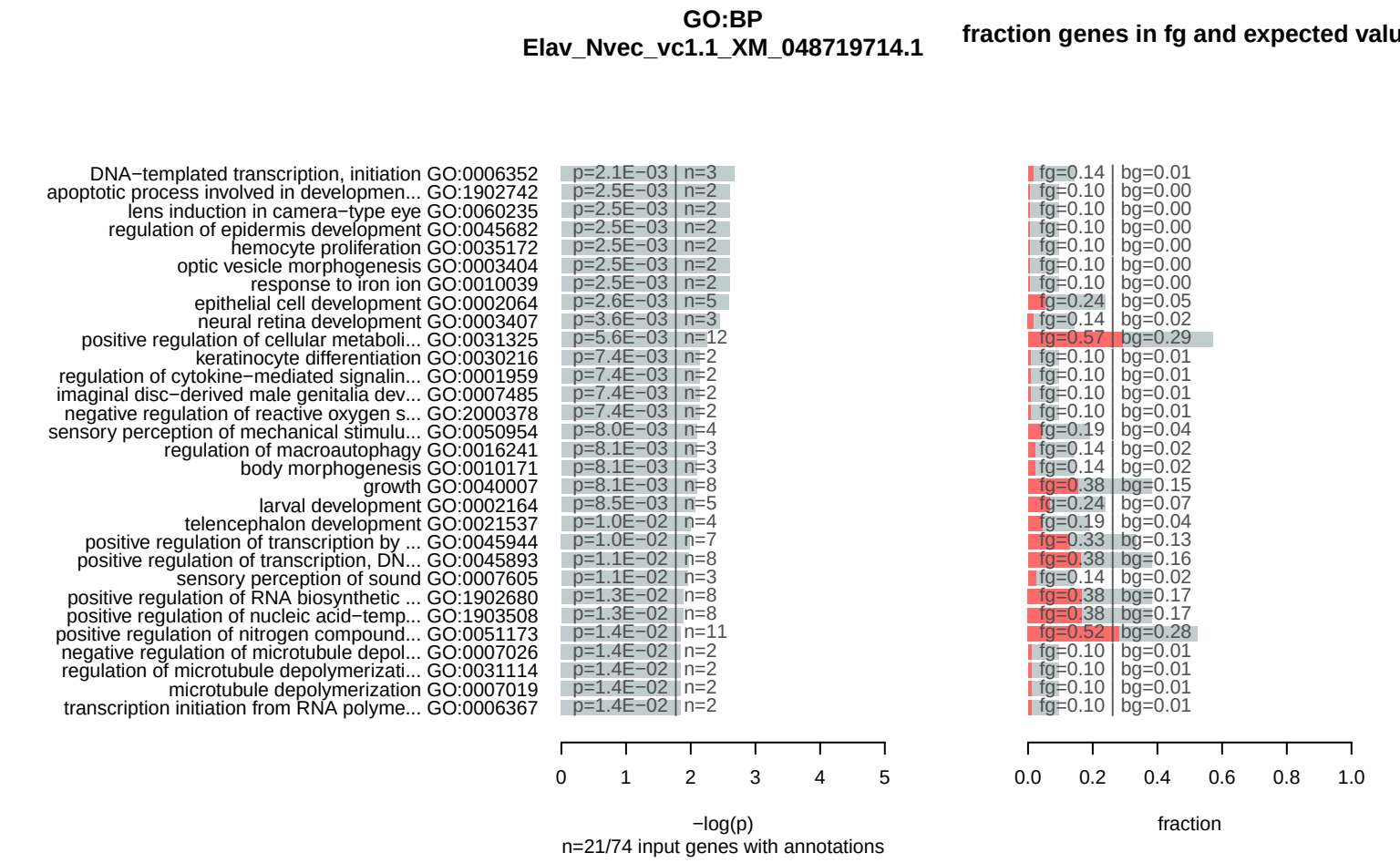
GO:BP
Elav_Nvec_vc1.1_XM_048719714.1
fraction genes in fg and expected valu
DNA−templated transcription, initiation GO:0006352 p=2.1E−03 n=3 fg=0.14 bg=0.01
apoptotic process involved in developmen... GO:1902742 p=2.5E−03 n=2 fg=0.10 bg=0.00
lens induction in camera−type eye GO:0060235 p=2.5E−03 n=2 fg=0.10 bg=0.00
regulation of epidermis development GO:0045682 p=2.5E−03 n=2 fg=0.10 bg=0.00
hemocyte proliferation GO:0035172 p=2.5E−03 n=2 fg=0.10 bg=0.00
optic vesicle morphogenesis GO:0003404 p=2.5E−03 n=2 fg=0.10 bg=0.00
response to iron ion GO:0010039 p=2.5E−03 n=2 fg=0.10 bg=0.00
epithelial cell development GO:0002064 p=2.6E−03 n=5 fg=0.24 bg=0.05
neural retina development GO:0003407 p=3.6E−03 n=3 fg=0.14 bg=0.02
positive regulation of cellular metaboli... GO:0031325 p=5.6E−03 n=12 fg=0.57 bg=0.29
keratinocyte differentiation GO:0030216 p=7.4E−03 n=2 fg=0.10 bg=0.01
regulation of cytokine−mediated signalin... GO:0001959 p=7.4E−03 n=2 fg=0.10 bg=0.01
imaginal disc−derived male genitalia dev... GO:0007485 p=7.4E−03 n=2 fg=0.10 bg=0.01
negative regulation of reactive oxygen s... GO:2000378 p=7.4E−03 n=2 fg=0.10 bg=0.01
sensory perception of mechanical stimulu... GO:0050954 p=8.0E−03 n=4 fg=0.19 bg=0.04
regulation of macroautophagy GO:0016241 p=8.1E−03 n=3 fg=0.14 bg=0.02
body morphogenesis GO:0010171 p=8.1E−03 n=3 fg=0.14 bg=0.02
growth GO:0040007 p=8.1E−03 n=8 fg=0.38 bg=0.15
larval development GO:0002164 p=8.5E−03 n=5 fg=0.24 bg=0.07
telencephalon development GO:0021537 p=1.0E−02 n=4 fg=0.19 bg=0.04
positive regulation of transcription by ... GO:0045944 p=1.0E−02 n=7 fg=0.33 bg=0.13
positive regulation of transcription, DN... GO:0045893 p=1.1E−02 n=8 fg=0.38 bg=0.16
sensory perception of sound GO:0007605 p=1.1E−02 n=3 fg=0.14 bg=0.02
positive regulation of RNA biosynthetic ... GO:1902680 p=1.3E−02 n=8 fg=0.38 bg=0.17
positive regulation of nucleic acid−temp... GO:1903508 p=1.3E−02 n=8 fg=0.38 bg=0.17
positive regulation of nitrogen compound... GO:0051173 p=1.4E−02 n=11 fg=0.52 bg=0.28
negative regulation of microtubule depol... GO:0007026 p=1.4E−02 n=2 fg=0.10 bg=0.01
regulation of microtubule depolymerizati... GO:0031114 p=1.4E−02 n=2 fg=0.10 bg=0.01
microtubule depolymerization GO:0007019 p=1.4E−02 n=2 fg=0.10 bg=0.01
transcription initiation from RNA polyme... GO:0006367 p=1.4E−02 n=2 fg=0.10 bg=0.01
0 1 2 3 4 5
−log(p)
n=21/74 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048719714.1
fraction genes in fg and expected valu
transcription factor binding GO:0008134 p=2.9E−03 n=6 fg=0.32 bg=0.09
nuclear receptor binding GO:0016922 p=1.5E−02 n=2 fg=0.11 bg=0.01
RNA polymerase II−specific DNA−binding t... GO:0061629 p=2.4E−02 n=2 fg=0.11 bg=0.01
signaling receptor binding GO:0005102 p=2.5E−02 n=6 fg=0.32 bg=0.13
calcium ion binding GO:0005509 p=2.5E−02 n=3 fg=0.16 bg=0.04
transcription coactivator activity GO:0003713 p=3.0E−02 n=3 fg=0.16 bg=0.04
transcription coregulator activity GO:0003712 p=3.3E−02 n=4 fg=0.21 bg=0.07
DNA−binding transcription factor binding GO:0140297 p=3.4E−02 n=2 fg=0.11 bg=0.02
ATPase−coupled ion transmembrane transpo... GO:0042625 p=3.4E−02 n=2 fg=0.11 bg=0.02
hormone receptor binding GO:0051427 p=3.4E−02 n=2 fg=0.11 bg=0.02
ATPase−coupled cation transmembrane tran... GO:0019829 p=3.4E−02 n=2 fg=0.11 bg=0.02
ATPase−coupled transmembrane transporter... GO:0042626 p=4.6E−02 n=2 fg=0.11 bg=0.02
primary active transmembrane transporter... GO:0015399 p=4.6E−02 n=2 fg=0.11 bg=0.02
aspartic−type peptidase activity GO:0070001 p=5.2E−02 n=1 fg=0.05 bg=0.00
proline−rich region binding GO:0070064 p=5.2E−02 n=1 fg=0.05 bg=0.00
aspartic endopeptidase activity, intrame... GO:0042500 p=5.2E−02 n=1 fg=0.05 bg=0.00
nitric−oxide synthase inhibitor activity GO:0036487 p=5.2E−02 n=1 fg=0.05 bg=0.00
aspartic−type endopeptidase activity GO:0004190 p=5.2E−02 n=1 fg=0.05 bg=0.00
1−phosphatidylinositol−3−phosphate 4−kin... GO:0052811 p=5.2E−02 n=1 fg=0.05 bg=0.00
nitric−oxide synthase binding GO:0050998 p=5.2E−02 n=1 fg=0.05 bg=0.00
ankyrin binding GO:0030506 p=5.2E−02 n=1 fg=0.05 bg=0.00
nitric−oxide synthase regulator activity GO:0030235 p=5.2E−02 n=1 fg=0.05 bg=0.00
calcium−dependent ATPase activity GO:0030899 p=5.2E−02 n=1 fg=0.05 bg=0.00
nuclear retinoic acid receptor binding GO:0042974 p=5.2E−02 n=1 fg=0.05 bg=0.00
nuclear retinoid X receptor binding GO:0046965 p=5.2E−02 n=1 fg=0.05 bg=0.00
nuclear thyroid hormone receptor binding GO:0046966 p=5.2E−02 n=1 fg=0.05 bg=0.00
tau protein binding GO:0048156 p=5.2E−02 n=1 fg=0.05 bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307 p=5.2E−02 n=1 fg=0.05 bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=5.2E−02 n=1 fg=0.05 bg=0.00
cytoskeletal anchor activity GO:0008093 p=5.2E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=19/74 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048719714.1
fraction genes in fg and expected valu
transcription elongation factor complex GO:0008023 p=2.6E−03 n=2 fg=0.10 bg=0.00
synaptic membrane GO:0097060 p=1.1E−02 n=4 fg=0.19 bg=0.04
I band GO:0031674 p=2.0E−02 n=3 fg=0.14 bg=0.03
presynaptic membrane GO:0042734 p=2.0E−02 n=3 fg=0.14 bg=0.03
transcription regulator complex GO:0005667 p=2.2E−02 n=4 fg=0.19 bg=0.05
cytoplasmic side of membrane GO:0098562 p=2.5E−02 n=3 fg=0.14 bg=0.03
sarcomere GO:0030017 p=3.1E−02 n=3 fg=0.14 bg=0.03
lysosomal membrane GO:0005765 p=3.4E−02 n=2 fg=0.10 bg=0.01
myofibril GO:0030016 p=3.7E−02 n=3 fg=0.14 bg=0.04
apical part of cell GO:0045177 p=4.4E−02 n=4 fg=0.19 bg=0.07
postsynaptic membrane GO:0045211 p=4.4E−02 n=3 fg=0.14 bg=0.04
nuclear outer membrane−endoplasmic retic... GO:0042175 p=4.9E−02 n=4 fg=0.19 bg=0.07
endoplasmic reticulum membrane GO:0005789 p=4.9E−02 n=4 fg=0.19 bg=0.07
side of membrane GO:0098552 p=5.2E−02 n=3 fg=0.14 bg=0.04
core−binding factor complex GO:0016513 p=5.2E−02 n=1 fg=0.05 bg=0.00
spectrosome GO:0045170 p=5.2E−02 n=1 fg=0.05 bg=0.00
growth cone lamellipodium GO:1990761 p=5.2E−02 n=1 fg=0.05 bg=0.00
postsynaptic specialization membrane GO:0099634 p=5.2E−02 n=1 fg=0.05 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000221 p=5.2E−02 n=1 fg=0.05 bg=0.00
proton−transporting V−type ATPase, V1 do... GO:0033180 p=5.2E−02 n=1 fg=0.05 bg=0.00
spectrin GO:0008091 p=5.2E−02 n=1 fg=0.05 bg=0.00
sperm principal piece GO:0097228 p=5.2E−02 n=1 fg=0.05 bg=0.00
proton−transporting two−sector ATPase co... GO:0033178 p=5.2E−02 n=1 fg=0.05 bg=0.00
NELF complex GO:0032021 p=5.2E−02 n=1 fg=0.05 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=5.2E−02 n=1 fg=0.05 bg=0.00
dendritic spine membrane GO:0032591 p=5.2E−02 n=1 fg=0.05 bg=0.00
presynaptic active zone membrane GO:0048787 p=5.2E−02 n=1 fg=0.05 bg=0.00
RSF complex GO:0031213 p=5.2E−02 n=1 fg=0.05 bg=0.00
postsynaptic density membrane GO:0098839 p=5.2E−02 n=1 fg=0.05 bg=0.00
growth cone filopodium GO:1990812 p=5.2E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=21/74 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction