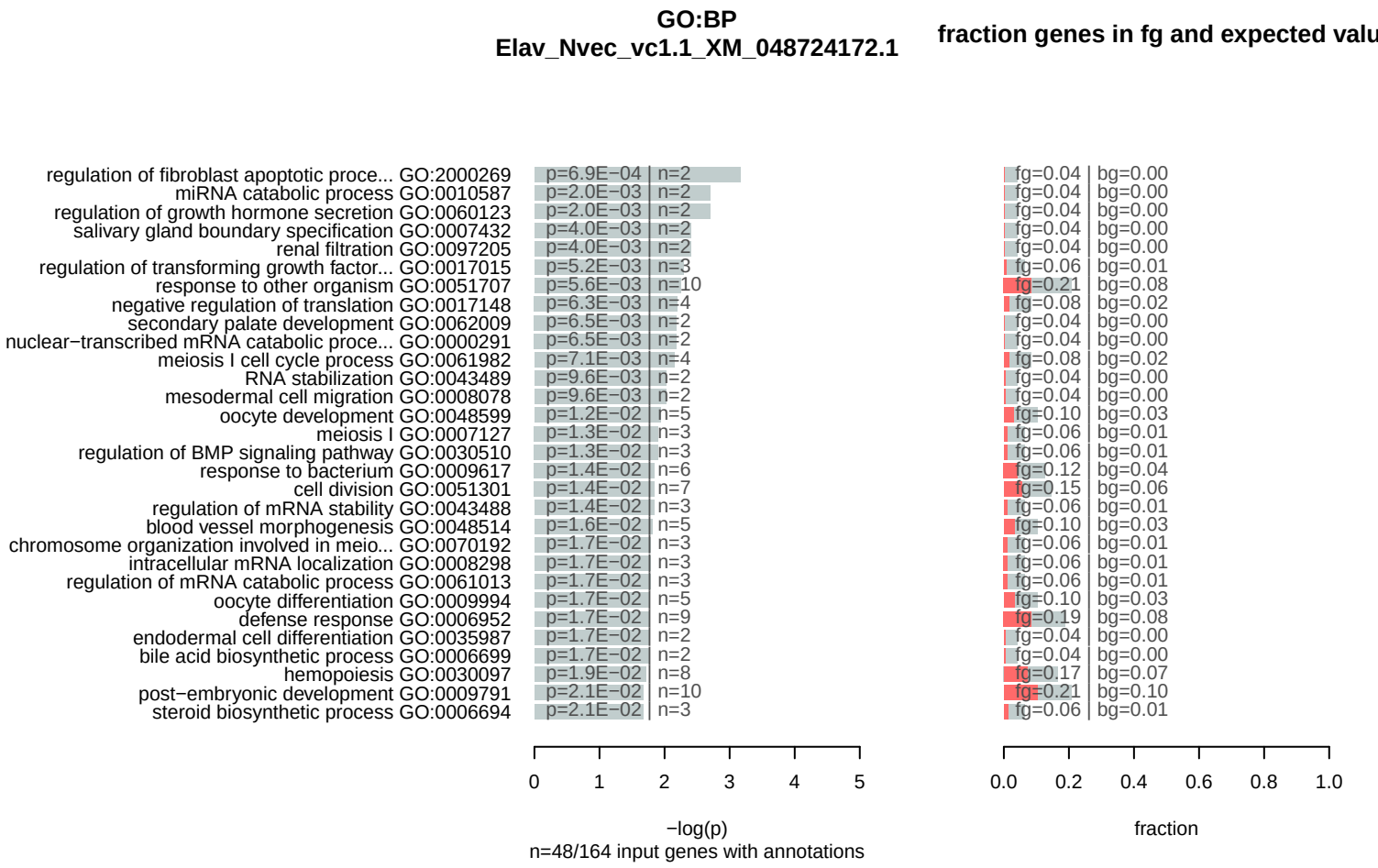
GO:BP
Elav_Nvec_vc1.1_XM_048724172.1
fraction genes in fg and expected valu
regulation of fibroblast apoptotic proce... GO:2000269 p=6.9E−04 n=2 fg=0.04 bg=0.00
miRNA catabolic process GO:0010587 p=2.0E−03 n=2 fg=0.04 bg=0.00
regulation of growth hormone secretion GO:0060123 p=2.0E−03 n=2 fg=0.04 bg=0.00
salivary gland boundary specification GO:0007432 p=4.0E−03 n=2 fg=0.04 bg=0.00
renal filtration GO:0097205 p=4.0E−03 n=2 fg=0.04 bg=0.00
regulation of transforming growth factor... GO:0017015 p=5.2E−03 n=3 fg=0.06 bg=0.01
response to other organism GO:0051707 p=5.6E−03 n=10 fg=0.21 bg=0.08
negative regulation of translation GO:0017148 p=6.3E−03 n=4 fg=0.08 bg=0.02
secondary palate development GO:0062009 p=6.5E−03 n=2 fg=0.04 bg=0.00
nuclear−transcribed mRNA catabolic proce... GO:0000291 p=6.5E−03 n=2 fg=0.04 bg=0.00
meiosis I cell cycle process GO:0061982 p=7.1E−03 n=4 fg=0.08 bg=0.02
RNA stabilization GO:0043489 p=9.6E−03 n=2 fg=0.04 bg=0.00
mesodermal cell migration GO:0008078 p=9.6E−03 n=2 fg=0.04 bg=0.00
oocyte development GO:0048599 p=1.2E−02 n=5 fg=0.10 bg=0.03
meiosis I GO:0007127 p=1.3E−02 n=3 fg=0.06 bg=0.01
regulation of BMP signaling pathway GO:0030510 p=1.3E−02 n=3 fg=0.06 bg=0.01
response to bacterium GO:0009617 p=1.4E−02 n=6 fg=0.12 bg=0.04
cell division GO:0051301 p=1.4E−02 n=7 fg=0.15 bg=0.06
regulation of mRNA stability GO:0043488 p=1.4E−02 n=3 fg=0.06 bg=0.01
blood vessel morphogenesis GO:0048514 p=1.6E−02 n=5 fg=0.10 bg=0.03
chromosome organization involved in meio... GO:0070192 p=1.7E−02 n=3 fg=0.06 bg=0.01
intracellular mRNA localization GO:0008298 p=1.7E−02 n=3 fg=0.06 bg=0.01
regulation of mRNA catabolic process GO:0061013 p=1.7E−02 n=3 fg=0.06 bg=0.01
oocyte differentiation GO:0009994 p=1.7E−02 n=5 fg=0.10 bg=0.03
defense response GO:0006952 p=1.7E−02 n=9 fg=0.19 bg=0.08
endodermal cell differentiation GO:0035987 p=1.7E−02 n=2 fg=0.04 bg=0.00
bile acid biosynthetic process GO:0006699 p=1.7E−02 n=2 fg=0.04 bg=0.00
hemopoiesis GO:0030097 p=1.9E−02 n=8 fg=0.17 bg=0.07
post−embryonic development GO:0009791 p=2.1E−02 n=10 fg=0.21 bg=0.10
steroid biosynthetic process GO:0006694 p=2.1E−02 n=3 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=48/164 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048724172.1
fraction genes in fg and expected valu
phosphatidylinositol binding GO:0035091 p=4.5E−03 n=5 fg=0.13 bg=0.03
anion binding GO:0043168 p=6.4E−03 n=11 fg=0.28 bg=0.13
organic cyclic compound binding GO:0097159 p=1.9E−02 n=17 fg=0.44 bg=0.27
alcohol binding GO:0043178 p=2.3E−02 n=2 fg=0.05 bg=0.01
ribokinase activity GO:0004747 p=2.5E−02 n=1 fg=0.03 bg=0.00
tumor necrosis factor−activated receptor... GO:0005031 p=2.5E−02 n=1 fg=0.03 bg=0.00
death receptor activity GO:0005035 p=2.5E−02 n=1 fg=0.03 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=2.5E−02 n=1 fg=0.03 bg=0.00
neuregulin binding GO:0038132 p=2.5E−02 n=1 fg=0.03 bg=0.00
thioredoxin−disulfide reductase activity GO:0004791 p=2.5E−02 n=1 fg=0.03 bg=0.00
insulin−like growth factor I binding GO:0031994 p=2.5E−02 n=1 fg=0.03 bg=0.00
fibronectin binding GO:0001968 p=2.5E−02 n=1 fg=0.03 bg=0.00
acid−sensing ion channel activity GO:0044736 p=2.5E−02 n=1 fg=0.03 bg=0.00
efflux transmembrane transporter activit... GO:0015562 p=2.5E−02 n=1 fg=0.03 bg=0.00
alpha−methylacyl−CoA racemase activity GO:0008111 p=2.5E−02 n=1 fg=0.03 bg=0.00
selenium binding GO:0008430 p=2.5E−02 n=1 fg=0.03 bg=0.00
neurotrophin p75 receptor binding GO:0005166 p=2.5E−02 n=1 fg=0.03 bg=0.00
small molecule binding GO:0036094 p=3.3E−02 n=8 fg=0.21 bg=0.10
heterocyclic compound binding GO:1901363 p=3.7E−02 n=16 fg=0.41 bg=0.27
ribonucleotide binding GO:0032553 p=4.2E−02 n=6 fg=0.15 bg=0.07
purine ribonucleotide binding GO:0032555 p=4.2E−02 n=6 fg=0.15 bg=0.07
purine nucleotide binding GO:0017076 p=4.8E−02 n=6 fg=0.15 bg=0.07
cis−regulatory region sequence−specific ... GO:0000987 p=4.8E−02 n=4 fg=0.10 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=4.8E−02 n=4 fg=0.10 bg=0.04
co−SMAD binding GO:0070410 p=4.8E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol transfer activity GO:0008526 p=4.8E−02 n=1 fg=0.03 bg=0.00
primary miRNA binding GO:0070878 p=4.8E−02 n=1 fg=0.03 bg=0.00
GDP−dissociation inhibitor activity GO:0005092 p=4.8E−02 n=1 fg=0.03 bg=0.00
insulin−like growth factor binding GO:0005520 p=4.8E−02 n=1 fg=0.03 bg=0.00
lamin binding GO:0005521 p=4.8E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=39/164 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048724172.1
fraction genes in fg and expected valu
cytoplasmic ribonucleoprotein granule GO:0036464 p=5.8E−03 n=5 fg=0.10 bg=0.02
nuclear inner membrane GO:0005637 p=1.4E−02 n=2 fg=0.04 bg=0.00
integrin alpha3−beta1 complex GO:0034667 p=2.7E−02 n=1 fg=0.02 bg=0.00
Scc2−Scc4 cohesin loading complex GO:0090694 p=2.7E−02 n=1 fg=0.02 bg=0.00
integrin alpha6−beta4 complex GO:0034676 p=2.7E−02 n=1 fg=0.02 bg=0.00
integrin alpha7−beta1 complex GO:0034677 p=2.7E−02 n=1 fg=0.02 bg=0.00
exoribonuclease complex GO:1905354 p=2.7E−02 n=1 fg=0.02 bg=0.00
apical cytoplasm GO:0090651 p=2.7E−02 n=1 fg=0.02 bg=0.00
nuclear RNA−directed RNA polymerase comp... GO:0031380 p=2.7E−02 n=1 fg=0.02 bg=0.00
RNA−directed RNA polymerase complex GO:0031379 p=2.7E−02 n=1 fg=0.02 bg=0.00
nuclear pore outer ring GO:0031080 p=2.7E−02 n=1 fg=0.02 bg=0.00
cuticular plate GO:0032437 p=2.7E−02 n=1 fg=0.02 bg=0.00
exosome (RNase complex) GO:0000178 p=2.7E−02 n=1 fg=0.02 bg=0.00
SMC loading complex GO:0032116 p=2.7E−02 n=1 fg=0.02 bg=0.00
Atg12−Atg5−Atg16 complex GO:0034274 p=5.3E−02 n=1 fg=0.02 bg=0.00
integrin complex GO:0008305 p=5.3E−02 n=1 fg=0.02 bg=0.00
integral component of nuclear inner memb... GO:0005639 p=5.3E−02 n=1 fg=0.02 bg=0.00
protein complex involved in cell adhesio... GO:0098636 p=5.3E−02 n=1 fg=0.02 bg=0.00
SMAD protein complex GO:0071141 p=5.3E−02 n=1 fg=0.02 bg=0.00
intrinsic component of nuclear inner mem... GO:0031229 p=5.3E−02 n=1 fg=0.02 bg=0.00
T cell receptor complex GO:0042101 p=5.3E−02 n=1 fg=0.02 bg=0.00
NSL complex GO:0044545 p=5.3E−02 n=1 fg=0.02 bg=0.00
filamentous actin GO:0031941 p=5.3E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=5.3E−02 n=1 fg=0.02 bg=0.00
cell body membrane GO:0044298 p=6.0E−02 n=2 fg=0.04 bg=0.01
plasma membrane signaling receptor compl... GO:0098802 p=6.0E−02 n=2 fg=0.04 bg=0.01
P−body GO:0000932 p=7.5E−02 n=2 fg=0.04 bg=0.01
phagocytic cup GO:0001891 p=7.9E−02 n=1 fg=0.02 bg=0.00
subrhabdomeral cisterna GO:0016029 p=7.9E−02 n=1 fg=0.02 bg=0.00
endoplasmic reticulum cisternal network GO:0071781 p=7.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=49/164 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction