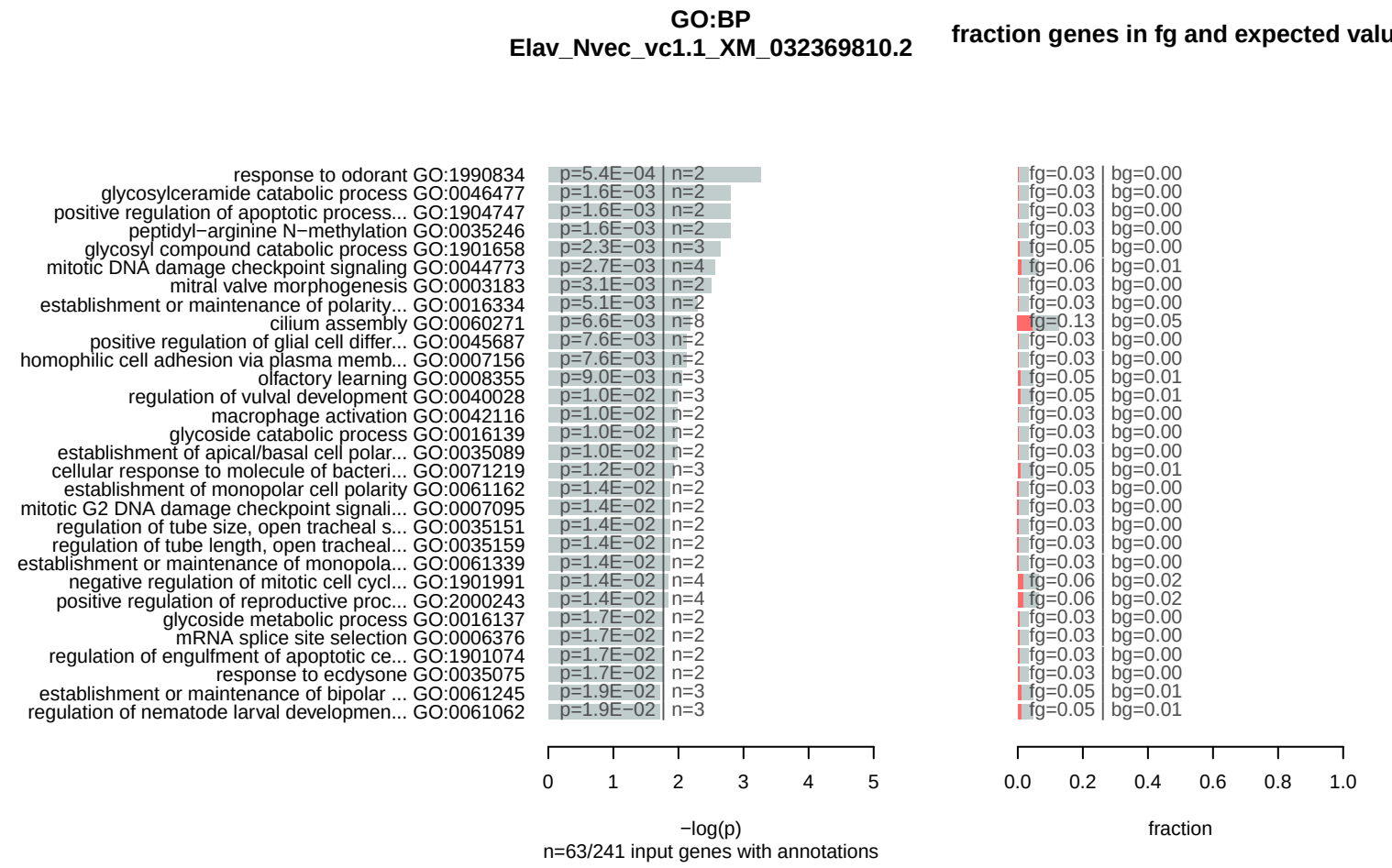
GO:BP
Elav_Nvec_vc1.1_XM_032369810.2
fraction genes in fg and expected valu
response to odorant GO:1990834 p=5.4E−04 n=2 fg=0.03 bg=0.00
glycosylceramide catabolic process GO:0046477 p=1.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of apoptotic process... GO:1904747 p=1.6E−03 n=2 fg=0.03 bg=0.00
peptidyl−arginine N−methylation GO:0035246 p=1.6E−03 n=2 fg=0.03 bg=0.00
glycosyl compound catabolic process GO:1901658 p=2.3E−03 n=3 fg=0.05 bg=0.00
mitotic DNA damage checkpoint signaling GO:0044773 p=2.7E−03 n=4 fg=0.06 bg=0.01
mitral valve morphogenesis GO:0003183 p=3.1E−03 n=2 fg=0.03 bg=0.00
establishment or maintenance of polarity... GO:0016334 p=5.1E−03 n=2 fg=0.03 bg=0.00
cilium assembly GO:0060271 p=6.6E−03 n=8 fg=0.13 bg=0.05
positive regulation of glial cell differ... GO:0045687 p=7.6E−03 n=2 fg=0.03 bg=0.00
homophilic cell adhesion via plasma memb... GO:0007156 p=7.6E−03 n=2 fg=0.03 bg=0.00
olfactory learning GO:0008355 p=9.0E−03 n=3 fg=0.05 bg=0.01
regulation of vulval development GO:0040028 p=1.0E−02 n=3 fg=0.05 bg=0.01
macrophage activation GO:0042116 p=1.0E−02 n=2 fg=0.03 bg=0.00
glycoside catabolic process GO:0016139 p=1.0E−02 n=2 fg=0.03 bg=0.00
establishment of apical/basal cell polar... GO:0035089 p=1.0E−02 n=2 fg=0.03 bg=0.00
cellular response to molecule of bacteri... GO:0071219 p=1.2E−02 n=3 fg=0.05 bg=0.01
establishment of monopolar cell polarity GO:0061162 p=1.4E−02 n=2 fg=0.03 bg=0.00
mitotic G2 DNA damage checkpoint signali... GO:0007095 p=1.4E−02 n=2 fg=0.03 bg=0.00
regulation of tube size, open tracheal s... GO:0035151 p=1.4E−02 n=2 fg=0.03 bg=0.00
regulation of tube length, open tracheal... GO:0035159 p=1.4E−02 n=2 fg=0.03 bg=0.00
establishment or maintenance of monopola... GO:0061339 p=1.4E−02 n=2 fg=0.03 bg=0.00
negative regulation of mitotic cell cycl... GO:1901991 p=1.4E−02 n=4 fg=0.06 bg=0.02
positive regulation of reproductive proc... GO:2000243 p=1.4E−02 n=4 fg=0.06 bg=0.02
glycoside metabolic process GO:0016137 p=1.7E−02 n=2 fg=0.03 bg=0.00
mRNA splice site selection GO:0006376 p=1.7E−02 n=2 fg=0.03 bg=0.00
regulation of engulfment of apoptotic ce... GO:1901074 p=1.7E−02 n=2 fg=0.03 bg=0.00
response to ecdysone GO:0035075 p=1.7E−02 n=2 fg=0.03 bg=0.00
establishment or maintenance of bipolar ... GO:0061245 p=1.9E−02 n=3 fg=0.05 bg=0.01
regulation of nematode larval developmen... GO:0061062 p=1.9E−02 n=3 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=63/241 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032369810.2
fraction genes in fg and expected valu
alpha−galactosidase activity GO:0004557 p=5.1E−04 n=2 fg=0.04 bg=0.00
alpha−N−acetylgalactosaminidase activity GO:0008456 p=5.1E−04 n=2 fg=0.04 bg=0.00
protein−arginine N−methyltransferase act... GO:0016274 p=1.5E−03 n=2 fg=0.04 bg=0.00
O−methyltransferase activity GO:0008171 p=7.2E−03 n=2 fg=0.04 bg=0.00
interleukin−5 receptor binding GO:0005137 p=2.3E−02 n=1 fg=0.02 bg=0.00
protein−arginine omega−N symmetric methy... GO:0035243 p=2.3E−02 n=1 fg=0.02 bg=0.00
growth hormone−releasing hormone recepto... GO:0016520 p=2.3E−02 n=1 fg=0.02 bg=0.00
light−activated ion channel activity GO:0010461 p=2.3E−02 n=1 fg=0.02 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=2.3E−02 n=1 fg=0.02 bg=0.00
rRNA (guanosine−2'−O−)−methyltransferase... GO:0070039 p=2.3E−02 n=1 fg=0.02 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=2.3E−02 n=1 fg=0.02 bg=0.00
oxygen sensor activity GO:0019826 p=2.3E−02 n=1 fg=0.02 bg=0.00
[myelin basic protein]−arginine N−methyl... GO:0016277 p=2.3E−02 n=1 fg=0.02 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulatory region RNA binding GO:0001069 p=2.3E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.3E−02 n=1 fg=0.02 bg=0.00
MDM2/MDM4 family protein binding GO:0097371 p=2.3E−02 n=1 fg=0.02 bg=0.00
guanyl nucleotide exchange factor inhibi... GO:1990624 p=2.3E−02 n=1 fg=0.02 bg=0.00
inositol oxygenase activity GO:0050113 p=2.3E−02 n=1 fg=0.02 bg=0.00
endoribonuclease activity, producing 3'−... GO:0016892 p=2.3E−02 n=1 fg=0.02 bg=0.00
small molecule sensor activity GO:0140299 p=2.3E−02 n=1 fg=0.02 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=2.3E−02 n=1 fg=0.02 bg=0.00
myosin II binding GO:0045159 p=2.3E−02 n=1 fg=0.02 bg=0.00
protein heterodimerization activity GO:0046982 p=3.2E−02 n=7 fg=0.13 bg=0.06
microtubule motor activity GO:0003777 p=3.4E−02 n=2 fg=0.04 bg=0.01
gamma−glutamylcyclotransferase activity GO:0003839 p=4.5E−02 n=1 fg=0.02 bg=0.00
protein−arginine omega−N monomethyltrans... GO:0035241 p=4.5E−02 n=1 fg=0.02 bg=0.00
mRNA CDS binding GO:1990715 p=4.5E−02 n=1 fg=0.02 bg=0.00
carbon monoxide binding GO:0070025 p=4.5E−02 n=1 fg=0.02 bg=0.00
nitric oxide binding GO:0070026 p=4.5E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=54/241 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032369810.2
fraction genes in fg and expected valu
perinuclear region of cytoplasm GO:0048471 p=4.3E−03 n=10 fg=0.17 bg=0.06
methylosome GO:0034709 p=4.7E−03 n=2 fg=0.03 bg=0.00
cytoplasmic ribonucleoprotein granule GO:0036464 p=9.1E−03 n=5 fg=0.08 bg=0.02
apicolateral plasma membrane GO:0016327 p=9.5E−03 n=2 fg=0.03 bg=0.00
membrane−bounded organelle GO:0043227 p=1.1E−02 n=55 fg=0.92 bg=0.80
smooth septate junction GO:0005920 p=2.2E−02 n=1 fg=0.02 bg=0.00
fungal biofilm matrix GO:0062040 p=2.2E−02 n=1 fg=0.02 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=2.2E−02 n=1 fg=0.02 bg=0.00
biofilm matrix GO:0062039 p=2.2E−02 n=1 fg=0.02 bg=0.00
interleukin−5 receptor complex GO:0005895 p=2.2E−02 n=1 fg=0.02 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=2.2E−02 n=1 fg=0.02 bg=0.00
rhabdomere membrane GO:0033583 p=2.2E−02 n=1 fg=0.02 bg=0.00
tRNA−intron endonuclease complex GO:0000214 p=2.2E−02 n=1 fg=0.02 bg=0.00
rhabdomere microvillus GO:0035996 p=2.2E−02 n=1 fg=0.02 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=2.2E−02 n=1 fg=0.02 bg=0.00
cytoplasmic stress granule GO:0010494 p=2.8E−02 n=2 fg=0.03 bg=0.00
multivesicular body GO:0005771 p=3.2E−02 n=2 fg=0.03 bg=0.00
presynaptic membrane GO:0042734 p=3.5E−02 n=3 fg=0.05 bg=0.01
microtubule cytoskeleton GO:0015630 p=3.8E−02 n=11 fg=0.18 bg=0.10
inclusion body GO:0016234 p=4.2E−02 n=2 fg=0.03 bg=0.01
growth cone filopodium GO:1990812 p=4.4E−02 n=1 fg=0.02 bg=0.00
Rb−E2F complex GO:0035189 p=4.4E−02 n=1 fg=0.02 bg=0.00
H zone GO:0031673 p=4.4E−02 n=1 fg=0.02 bg=0.00
radial spoke GO:0001534 p=4.4E−02 n=1 fg=0.02 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=4.4E−02 n=1 fg=0.02 bg=0.00
COPII vesicle coat GO:0030127 p=4.4E−02 n=1 fg=0.02 bg=0.00
U4 snRNP GO:0005687 p=4.4E−02 n=1 fg=0.02 bg=0.00
PTW/PP1 phosphatase complex GO:0072357 p=4.4E−02 n=1 fg=0.02 bg=0.00
epsilon DNA polymerase complex GO:0008622 p=4.4E−02 n=1 fg=0.02 bg=0.00
hippocampal mossy fiber GO:0097457 p=4.4E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=60/241 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction