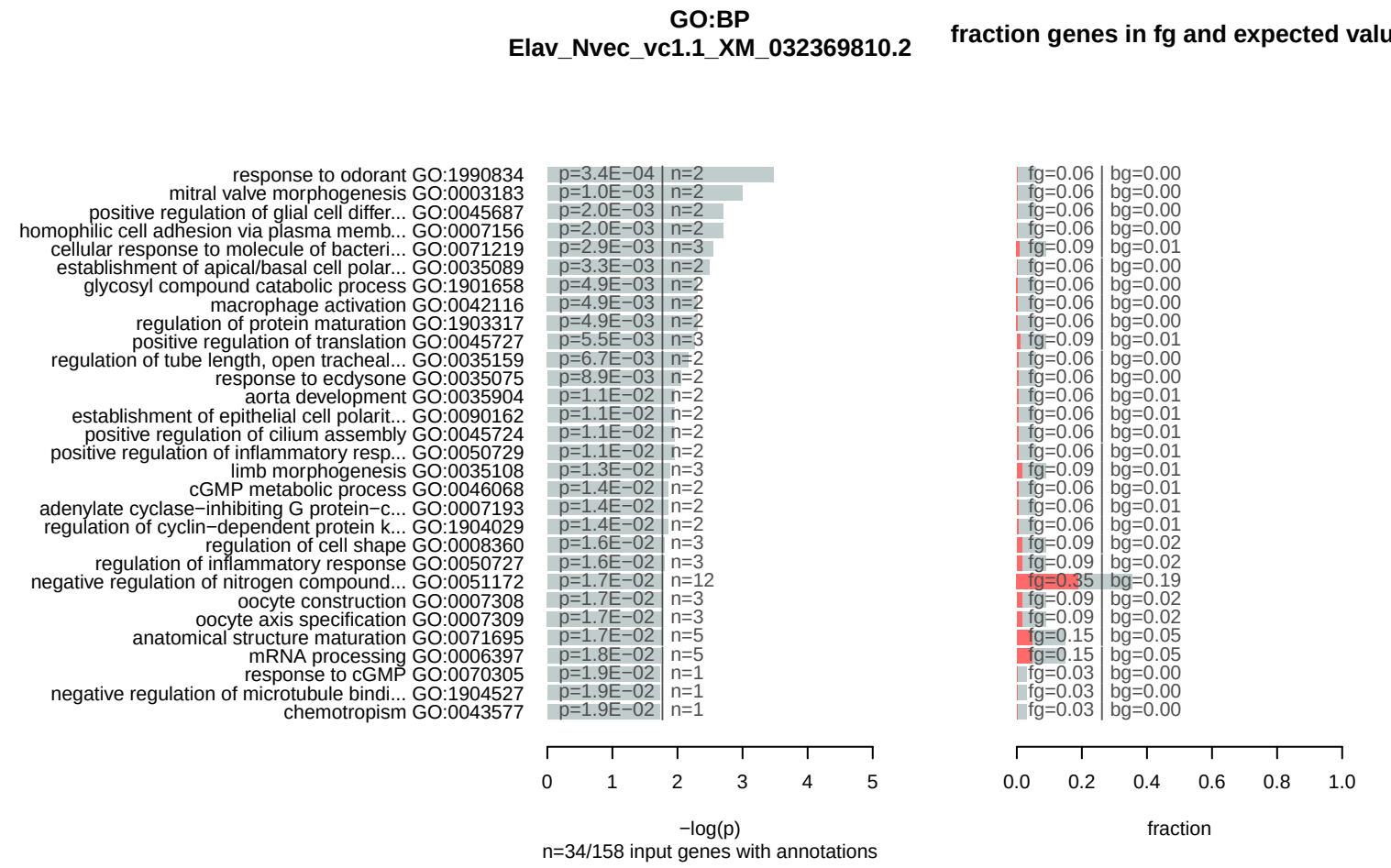
GO:BP
Elav_Nvec_vc1.1_XM_032369810.2
fraction genes in fg and expected valu
response to odorant GO:1990834 p=3.4E−04 n=2 fg=0.06 bg=0.00
mitral valve morphogenesis GO:0003183 p=1.0E−03 n=2 fg=0.06 bg=0.00
positive regulation of glial cell differ... GO:0045687 p=2.0E−03 n=2 fg=0.06 bg=0.00
homophilic cell adhesion via plasma memb... GO:0007156 p=2.0E−03 n=2 fg=0.06 bg=0.00
cellular response to molecule of bacteri... GO:0071219 p=2.9E−03 n=3 fg=0.09 bg=0.01
establishment of apical/basal cell polar... GO:0035089 p=3.3E−03 n=2 fg=0.06 bg=0.00
glycosyl compound catabolic process GO:1901658 p=4.9E−03 n=2 fg=0.06 bg=0.00
macrophage activation GO:0042116 p=4.9E−03 n=2 fg=0.06 bg=0.00
regulation of protein maturation GO:1903317 p=4.9E−03 n=2 fg=0.06 bg=0.00
positive regulation of translation GO:0045727 p=5.5E−03 n=3 fg=0.09 bg=0.01
regulation of tube length, open tracheal... GO:0035159 p=6.7E−03 n=2 fg=0.06 bg=0.00
response to ecdysone GO:0035075 p=8.9E−03 n=2 fg=0.06 bg=0.00
aorta development GO:0035904 p=1.1E−02 n=2 fg=0.06 bg=0.01
establishment of epithelial cell polarit... GO:0090162 p=1.1E−02 n=2 fg=0.06 bg=0.01
positive regulation of cilium assembly GO:0045724 p=1.1E−02 n=2 fg=0.06 bg=0.01
positive regulation of inflammatory resp... GO:0050729 p=1.1E−02 n=2 fg=0.06 bg=0.01
limb morphogenesis GO:0035108 p=1.3E−02 n=3 fg=0.09 bg=0.01
cGMP metabolic process GO:0046068 p=1.4E−02 n=2 fg=0.06 bg=0.01
adenylate cyclase−inhibiting G protein−c... GO:0007193 p=1.4E−02 n=2 fg=0.06 bg=0.01
regulation of cyclin−dependent protein k... GO:1904029 p=1.4E−02 n=2 fg=0.06 bg=0.01
regulation of cell shape GO:0008360 p=1.6E−02 n=3 fg=0.09 bg=0.02
regulation of inflammatory response GO:0050727 p=1.6E−02 n=3 fg=0.09 bg=0.02
negative regulation of nitrogen compound... GO:0051172 p=1.7E−02 n=12 fg=0.35 bg=0.19
oocyte construction GO:0007308 p=1.7E−02 n=3 fg=0.09 bg=0.02
oocyte axis specification GO:0007309 p=1.7E−02 n=3 fg=0.09 bg=0.02
anatomical structure maturation GO:0071695 p=1.7E−02 n=5 fg=0.15 bg=0.05
mRNA processing GO:0006397 p=1.8E−02 n=5 fg=0.15 bg=0.05
response to cGMP GO:0070305 p=1.9E−02 n=1 fg=0.03 bg=0.00
negative regulation of microtubule bindi... GO:1904527 p=1.9E−02 n=1 fg=0.03 bg=0.00
chemotropism GO:0043577 p=1.9E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=34/158 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032369810.2
fraction genes in fg and expected valu
myosin II binding GO:0045159 p=1.8E−02 n=1 fg=0.03 bg=0.00
fibroblast growth factor receptor bindin... GO:0005104 p=1.8E−02 n=1 fg=0.03 bg=0.00
arginine N−methyltransferase activity GO:0016273 p=1.8E−02 n=1 fg=0.03 bg=0.00
protein−arginine N−methyltransferase act... GO:0016274 p=1.8E−02 n=1 fg=0.03 bg=0.00
[myelin basic protein]−arginine N−methyl... GO:0016277 p=1.8E−02 n=1 fg=0.03 bg=0.00
endoribonuclease activity, producing 3′−... GO:0016892 p=1.8E−02 n=1 fg=0.03 bg=0.00
endonuclease activity, active with eithe... GO:0016894 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulatory region RNA binding GO:0001069 p=1.8E−02 n=1 fg=0.03 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=1.8E−02 n=1 fg=0.03 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=1.8E−02 n=1 fg=0.03 bg=0.00
protein−arginine omega−N monomethyltrans... GO:0035241 p=1.8E−02 n=1 fg=0.03 bg=0.00
protein−arginine omega−N symmetric methy... GO:0035243 p=1.8E−02 n=1 fg=0.03 bg=0.00
MDM2/MDM4 family protein binding GO:0097371 p=1.8E−02 n=1 fg=0.03 bg=0.00
alpha−galactosidase activity GO:0004557 p=1.8E−02 n=1 fg=0.03 bg=0.00
small molecule sensor activity GO:0140299 p=1.8E−02 n=1 fg=0.03 bg=0.00
histone−arginine N−methyltransferase act... GO:0008469 p=1.8E−02 n=1 fg=0.03 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=1.8E−02 n=1 fg=0.03 bg=0.00
alpha−N−acetylgalactosaminidase activity GO:0008456 p=1.8E−02 n=1 fg=0.03 bg=0.00
oxygen sensor activity GO:0019826 p=1.8E−02 n=1 fg=0.03 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=1.8E−02 n=1 fg=0.03 bg=0.00
histone methyltransferase activity (H4−R... GO:0044020 p=1.8E−02 n=1 fg=0.03 bg=0.00
growth hormone−releasing hormone recepto... GO:0016520 p=1.8E−02 n=1 fg=0.03 bg=0.00
GTPase activity GO:0003924 p=2.6E−02 n=3 fg=0.10 bg=0.02
gamma−glutamylcyclotransferase activity GO:0003839 p=3.6E−02 n=1 fg=0.03 bg=0.00
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=3.6E−02 n=1 fg=0.03 bg=0.00
magnesium ion transmembrane transporter ... GO:0015095 p=3.6E−02 n=1 fg=0.03 bg=0.00
LRR domain binding GO:0030275 p=3.6E−02 n=1 fg=0.03 bg=0.00
GAF domain binding GO:0036004 p=3.6E−02 n=1 fg=0.03 bg=0.00
galactosidase activity GO:0015925 p=3.6E−02 n=1 fg=0.03 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=3.6E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=29/158 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
apicolateral plasma membrane GO:0016327 p=5.7E−03 n=2 fg=0.06 bg=0.00
presynaptic membrane GO:0042734 p=8.1E−03 n=3 fg=0.10 bg=0.01
microtubule organizing center GO:0005815 p=1.4E−02 n=6 fg=0.19 bg=0.07
methylosome GO:0034709 p=1.7E−02 n=1 fg=0.03 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=1.7E−02 n=1 fg=0.03 bg=0.00
tRNA−intron endonuclease complex GO:0000214 p=1.7E−02 n=1 fg=0.03 bg=0.00
hippocampal mossy fiber GO:0097457 p=1.7E−02 n=1 fg=0.03 bg=0.00
H zone GO:0031673 p=1.7E−02 n=1 fg=0.03 bg=0.00
smooth septate junction GO:0005920 p=1.7E−02 n=1 fg=0.03 bg=0.00
nucleus GO:0005634 p=1.8E−02 n=21 fg=0.68 bg=0.48
centrosome GO:0005813 p=1.8E−02 n=5 fg=0.16 bg=0.05
neuronal cell body GO:0043025 p=1.8E−02 n=6 fg=0.19 bg=0.07
cell body GO:0044297 p=2.6E−02 n=6 fg=0.19 bg=0.08
somatodendritic compartment GO:0036477 p=2.9E−02 n=7 fg=0.23 bg=0.10
histone methyltransferase complex GO:0035097 p=2.9E−02 n=2 fg=0.06 bg=0.01
COPII vesicle coat GO:0030127 p=3.4E−02 n=1 fg=0.03 bg=0.00
glycosylphosphatidylinositol−N−acetylglu... GO:0000506 p=3.4E−02 n=1 fg=0.03 bg=0.00
growth cone filopodium GO:1990812 p=3.4E−02 n=1 fg=0.03 bg=0.00
PTW/PP1 phosphatase complex GO:0072357 p=3.4E−02 n=1 fg=0.03 bg=0.00
methyltransferase complex GO:0034708 p=4.1E−02 n=2 fg=0.06 bg=0.01
membrane−bounded organelle GO:0043227 p=4.3E−02 n=29 fg=0.94 bg=0.81
ribonucleoprotein granule GO:0035770 p=4.4E−02 n=3 fg=0.10 bg=0.03
growth cone lamellipodium GO:1990761 p=5.1E−02 n=1 fg=0.03 bg=0.00
myelin sheath abaxonal region GO:0035748 p=5.1E−02 n=1 fg=0.03 bg=0.00
intracellular membrane−bounded organelle GO:0043231 p=6.4E−02 n=28 fg=0.90 bg=0.78
endoribonuclease complex GO:1902555 p=6.7E−02 n=1 fg=0.03 bg=0.00
Golgi cis cisterna GO:0000137 p=6.7E−02 n=1 fg=0.03 bg=0.00
muscle cell postsynaptic specialization GO:0097482 p=6.7E−02 n=1 fg=0.03 bg=0.00
presynaptic periactive zone GO:0036062 p=6.7E−02 n=1 fg=0.03 bg=0.00
guanylate cyclase complex, soluble GO:0008074 p=6.7E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=31/158 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction