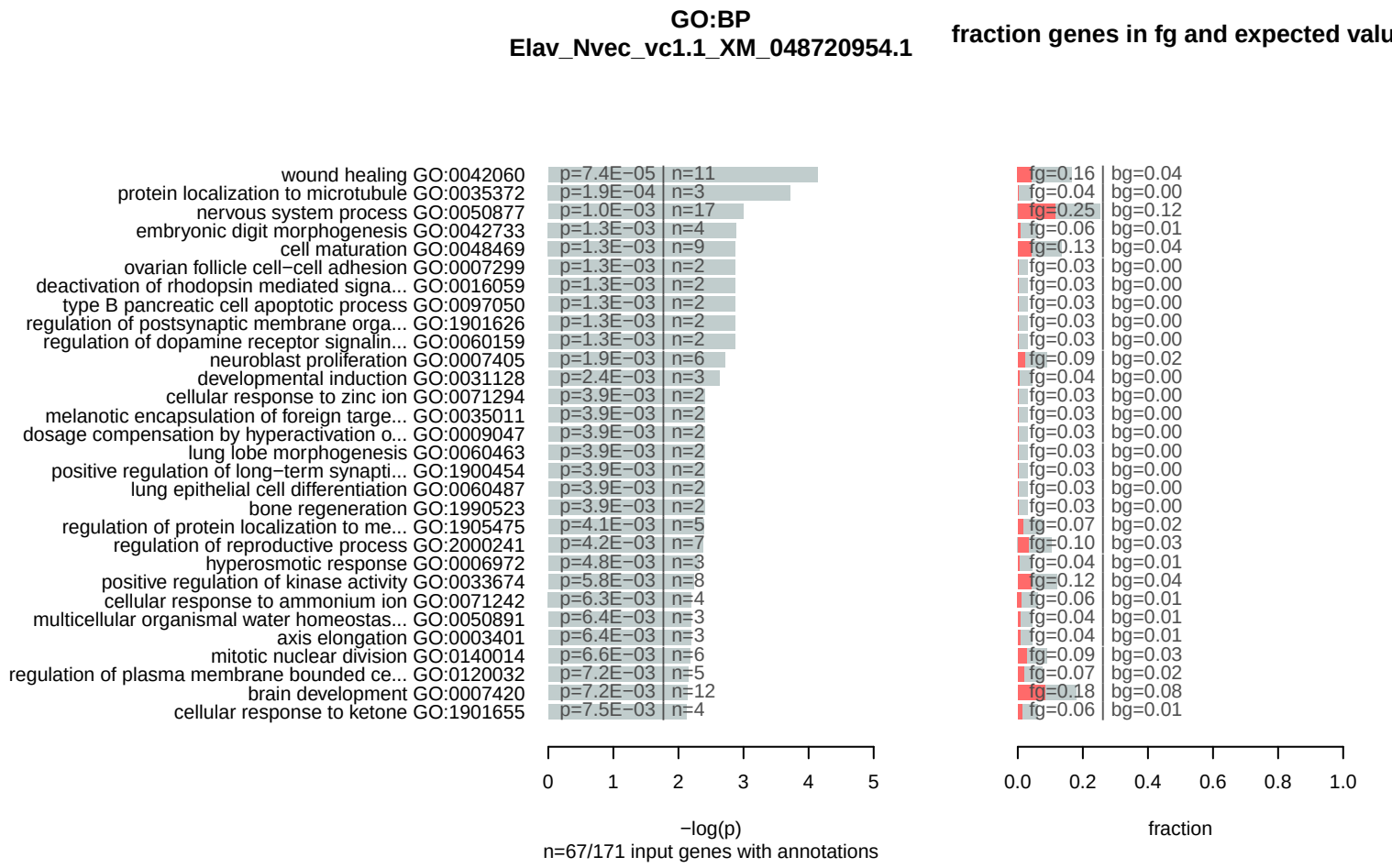
GO:BP
Elav_Nvec_vc1.1_XM_048720954.1
fraction genes in fg and expected valu
wound healing GO:0042060 p=7.4E−05 n=11 fg=0.16 bg=0.04
protein localization to microtubule GO:0035372 p=1.9E−04 n=3 fg=0.04 bg=0.00
nervous system process GO:0050877 p=1.0E−03 n=17 fg=0.25 bg=0.12
embryonic digit morphogenesis GO:0042733 p=1.3E−03 n=4 fg=0.06 bg=0.01
cell maturation GO:0048469 p=1.3E−03 n=9 fg=0.13 bg=0.04
ovarian follicle cell−cell adhesion GO:0007299 p=1.3E−03 n=2 fg=0.03 bg=0.00
deactivation of rhodopsin mediated signa... GO:0016059 p=1.3E−03 n=2 fg=0.03 bg=0.00
type B pancreatic cell apoptotic process GO:0097050 p=1.3E−03 n=2 fg=0.03 bg=0.00
regulation of postsynaptic membrane orga... GO:1901626 p=1.3E−03 n=2 fg=0.03 bg=0.00
regulation of dopamine receptor signalin... GO:0060159 p=1.3E−03 n=2 fg=0.03 bg=0.00
neuroblast proliferation GO:0007405 p=1.9E−03 n=6 fg=0.09 bg=0.02
developmental induction GO:0031128 p=2.4E−03 n=3 fg=0.04 bg=0.00
cellular response to zinc ion GO:0071294 p=3.9E−03 n=2 fg=0.03 bg=0.00
melanotic encapsulation of foreign targe... GO:0035011 p=3.9E−03 n=2 fg=0.03 bg=0.00
dosage compensation by hyperactivation o... GO:0009047 p=3.9E−03 n=2 fg=0.03 bg=0.00
lung lobe morphogenesis GO:0060463 p=3.9E−03 n=2 fg=0.03 bg=0.00
positive regulation of long−term synapti... GO:1900454 p=3.9E−03 n=2 fg=0.03 bg=0.00
lung epithelial cell differentiation GO:0060487 p=3.9E−03 n=2 fg=0.03 bg=0.00
bone regeneration GO:1990523 p=3.9E−03 n=2 fg=0.03 bg=0.00
regulation of protein localization to me... GO:1905475 p=4.1E−03 n=5 fg=0.07 bg=0.02
regulation of reproductive process GO:2000241 p=4.2E−03 n=7 fg=0.10 bg=0.03
hyperosmotic response GO:0006972 p=4.8E−03 n=3 fg=0.04 bg=0.01
positive regulation of kinase activity GO:0033674 p=5.8E−03 n=8 fg=0.12 bg=0.04
cellular response to ammonium ion GO:0071242 p=6.3E−03 n=4 fg=0.06 bg=0.01
multicellular organismal water homeostas... GO:0050891 p=6.4E−03 n=3 fg=0.04 bg=0.01
axis elongation GO:0003401 p=6.4E−03 n=3 fg=0.04 bg=0.01
mitotic nuclear division GO:0140014 p=6.6E−03 n=6 fg=0.09 bg=0.03
regulation of plasma membrane bounded ce... GO:0120032 p=7.2E−03 n=5 fg=0.07 bg=0.02
brain development GO:0007420 p=7.2E−03 n=12 fg=0.18 bg=0.08
cellular response to ketone GO:1901655 p=7.5E−03 n=4 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=67/171 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048720954.1
fraction genes in fg and expected valu
phosphatidic acid binding GO:0070300 p=7.5E−03 n=2 fg=0.03 bg=0.00
ubiquitin protein ligase binding GO:0031625 p=7.9E−03 n=7 fg=0.12 bg=0.04
dopamine receptor binding GO:0050780 p=1.8E−02 n=2 fg=0.03 bg=0.00
scaffold protein binding GO:0097110 p=1.8E−02 n=3 fg=0.05 bg=0.01
adrenergic receptor binding GO:0031690 p=2.4E−02 n=2 fg=0.03 bg=0.00
identical protein binding GO:0042802 p=2.5E−02 n=16 fg=0.28 bg=0.17
protein kinase activity GO:0004672 p=2.8E−02 n=7 fg=0.12 bg=0.05
histone deacetylase regulator activity GO:0035033 p=3.6E−02 n=1 fg=0.02 bg=0.00
arginine N−methyltransferase activity GO:0016273 p=3.6E−02 n=1 fg=0.02 bg=0.00
protein−arginine N−methyltransferase act... GO:0016274 p=3.6E−02 n=1 fg=0.02 bg=0.00
[myelin basic protein]−arginine N−methyl... GO:0016277 p=3.6E−02 n=1 fg=0.02 bg=0.00
lithium ion binding GO:0031403 p=3.6E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.6E−02 n=1 fg=0.02 bg=0.00
inositol monophosphate 3−phosphatase act... GO:0052832 p=3.6E−02 n=1 fg=0.02 bg=0.00
S100 protein binding GO:0044548 p=3.6E−02 n=1 fg=0.02 bg=0.00
rhodopsin kinase activity GO:0050254 p=3.6E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=3.6E−02 n=1 fg=0.02 bg=0.00
opioid receptor binding GO:0031628 p=3.6E−02 n=1 fg=0.02 bg=0.00
histone methyltransferase activity (H4−R... GO:0044020 p=3.6E−02 n=1 fg=0.02 bg=0.00
selenocystathionine beta−synthase activi... GO:0098605 p=3.6E−02 n=1 fg=0.02 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.6E−02 n=1 fg=0.02 bg=0.00
G protein−coupled receptor kinase activi... GO:0004703 p=3.6E−02 n=1 fg=0.02 bg=0.00
JUN kinase activity GO:0004705 p=3.6E−02 n=1 fg=0.02 bg=0.00
protein−arginine omega−N monomethyltrans... GO:0035241 p=3.6E−02 n=1 fg=0.02 bg=0.00
protein−arginine omega−N symmetric methy... GO:0035243 p=3.6E−02 n=1 fg=0.02 bg=0.00
beta−adrenergic receptor kinase activity GO:0047696 p=3.6E−02 n=1 fg=0.02 bg=0.00
delta−type opioid receptor binding GO:0031850 p=3.6E−02 n=1 fg=0.02 bg=0.00
kappa−type opioid receptor binding GO:0031851 p=3.6E−02 n=1 fg=0.02 bg=0.00
lysine N−acetyltransferase activity, act... GO:0004468 p=3.6E−02 n=1 fg=0.02 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=3.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=58/171 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048720954.1
fraction genes in fg and expected valu
cytoplasmic region GO:0099568 p=2.3E−03 n=10 fg=0.15 bg=0.05
chromocenter GO:0010369 p=8.0E−03 n=2 fg=0.03 bg=0.00
presynaptic periactive zone GO:0036062 p=8.0E−03 n=2 fg=0.03 bg=0.00
dendritic spine GO:0043197 p=1.5E−02 n=5 fg=0.07 bg=0.02
neuron spine GO:0044309 p=1.5E−02 n=5 fg=0.07 bg=0.02
plasma membrane bounded cell projection GO:0120025 p=1.6E−02 n=21 fg=0.31 bg=0.20
cell projection GO:0042995 p=1.7E−02 n=21 fg=0.31 bg=0.20
cell cortex GO:0005938 p=1.9E−02 n=7 fg=0.10 bg=0.04
intracellular non−membrane−bounded organ... GO:0043232 p=2.2E−02 n=30 fg=0.44 bg=0.30
non−membrane−bounded organelle GO:0043228 p=2.2E−02 n=30 fg=0.44 bg=0.30
perinuclear region of cytoplasm GO:0048471 p=2.3E−02 n=10 fg=0.15 bg=0.07
cytoskeleton GO:0005856 p=2.4E−02 n=16 fg=0.24 bg=0.14
endoplasmic reticulum tubular network GO:0071782 p=2.6E−02 n=2 fg=0.03 bg=0.00
dendritic shaft GO:0043198 p=2.8E−02 n=3 fg=0.04 bg=0.01
cell body GO:0044297 p=2.9E−02 n=10 fg=0.15 bg=0.08
microtubule cytoskeleton GO:0015630 p=3.2E−02 n=12 fg=0.18 bg=0.10
somatodendritic compartment GO:0036477 p=3.2E−02 n=12 fg=0.18 bg=0.10
nuclear chromosome GO:0000228 p=3.7E−02 n=6 fg=0.09 bg=0.04
internode region of axon GO:0033269 p=3.8E−02 n=1 fg=0.01 bg=0.00
MSL complex GO:0072487 p=3.8E−02 n=1 fg=0.01 bg=0.00
methylosome GO:0034709 p=3.8E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=3.8E−02 n=1 fg=0.01 bg=0.00
dosage compensation complex GO:0046536 p=3.8E−02 n=1 fg=0.01 bg=0.00
core−binding factor complex GO:0016513 p=3.8E−02 n=1 fg=0.01 bg=0.00
exoribonuclease complex GO:1905354 p=3.8E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=3.8E−02 n=1 fg=0.01 bg=0.00
exosome (RNase complex) GO:0000178 p=3.8E−02 n=1 fg=0.01 bg=0.00
X chromosome located dosage compensation... GO:0016456 p=3.8E−02 n=1 fg=0.01 bg=0.00
endoplasmic reticulum tubular network me... GO:0098826 p=3.8E−02 n=1 fg=0.01 bg=0.00
dendritic spine neck GO:0044326 p=3.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=68/171 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction