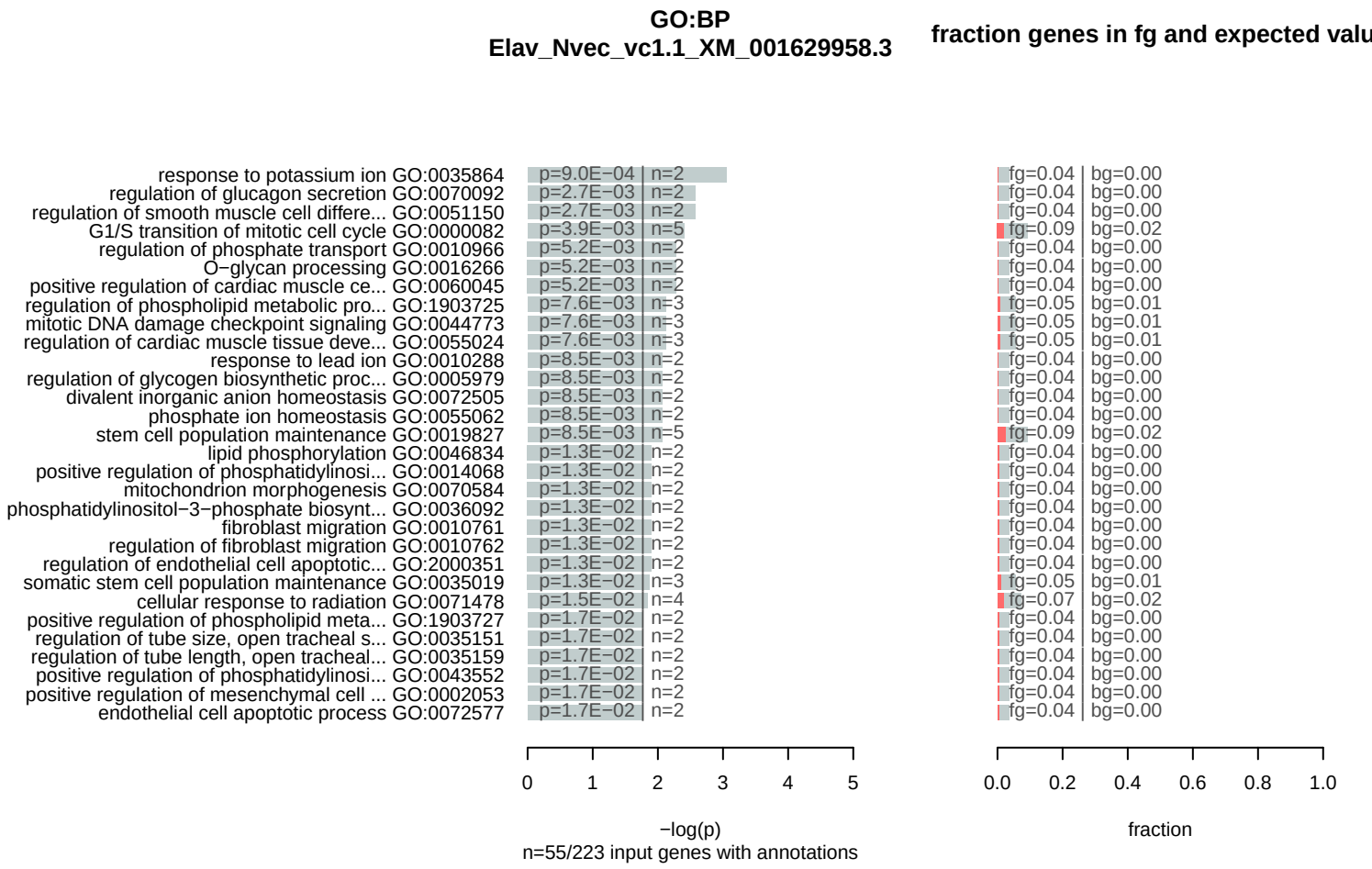
GO:BP
Elav_Nvec_vc1.1_XM_001629958.3
fraction genes in fg and expected valu
response to potassium ion GO:0035864 p=9.0E−04 n=2 fg=0.04 bg=0.00
regulation of glucagon secretion GO:0070092 p=2.7E−03 n=2 fg=0.04 bg=0.00
regulation of smooth muscle cell differe... GO:0051150 p=2.7E−03 n=2 fg=0.04 bg=0.00
G1/S transition of mitotic cell cycle GO:0000082 p=3.9E−03 n=5 fg=0.09 bg=0.02
regulation of phosphate transport GO:0010966 p=5.2E−03 n=2 fg=0.04 bg=0.00
O−glycan processing GO:0016266 p=5.2E−03 n=2 fg=0.04 bg=0.00
positive regulation of cardiac muscle ce... GO:0060045 p=5.2E−03 n=2 fg=0.04 bg=0.00
regulation of phospholipid metabolic pro... GO:1903725 p=7.6E−03 n=3 fg=0.05 bg=0.01
mitotic DNA damage checkpoint signaling GO:0044773 p=7.6E−03 n=3 fg=0.05 bg=0.01
regulation of cardiac muscle tissue deve... GO:0055024 p=7.6E−03 n=3 fg=0.05 bg=0.01
response to lead ion GO:0010288 p=8.5E−03 n=2 fg=0.04 bg=0.00
regulation of glycogen biosynthetic proc... GO:0005979 p=8.5E−03 n=2 fg=0.04 bg=0.00
divalent inorganic anion homeostasis GO:0072505 p=8.5E−03 n=2 fg=0.04 bg=0.00
phosphate ion homeostasis GO:0055062 p=8.5E−03 n=2 fg=0.04 bg=0.00
stem cell population maintenance GO:0019827 p=8.5E−03 n=5 fg=0.09 bg=0.02
lipid phosphorylation GO:0046834 p=1.3E−02 n=2 fg=0.04 bg=0.00
positive regulation of phosphatidylinosi... GO:0014068 p=1.3E−02 n=2 fg=0.04 bg=0.00
mitochondrion morphogenesis GO:0070584 p=1.3E−02 n=2 fg=0.04 bg=0.00
phosphatidylinositol−3−phosphate biosynt... GO:0036092 p=1.3E−02 n=2 fg=0.04 bg=0.00
fibroblast migration GO:0010761 p=1.3E−02 n=2 fg=0.04 bg=0.00
regulation of fibroblast migration GO:0010762 p=1.3E−02 n=2 fg=0.04 bg=0.00
regulation of endothelial cell apoptotic... GO:2000351 p=1.3E−02 n=2 fg=0.04 bg=0.00
somatic stem cell population maintenance GO:0035019 p=1.3E−02 n=3 fg=0.05 bg=0.01
cellular response to radiation GO:0071478 p=1.5E−02 n=4 fg=0.07 bg=0.02
positive regulation of phospholipid meta... GO:1903727 p=1.7E−02 n=2 fg=0.04 bg=0.00
regulation of tube size, open tracheal s... GO:0035151 p=1.7E−02 n=2 fg=0.04 bg=0.00
regulation of tube length, open tracheal... GO:0035159 p=1.7E−02 n=2 fg=0.04 bg=0.00
positive regulation of phosphatidylinosi... GO:0043552 p=1.7E−02 n=2 fg=0.04 bg=0.00
positive regulation of mesenchymal cell ... GO:0002053 p=1.7E−02 n=2 fg=0.04 bg=0.00
endothelial cell apoptotic process GO:0072577 p=1.7E−02 n=2 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=55/223 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001629958.3
fraction genes in fg and expected valu
sphingolipid binding GO:0046625 p=8.5E−04 n=2 fg=0.04 bg=0.00
UDP−xylosyltransferase activity GO:0035252 p=4.9E−03 n=2 fg=0.04 bg=0.00
lipid transfer activity GO:0120013 p=8.1E−03 n=2 fg=0.04 bg=0.00
1−phosphatidylinositol−3−kinase activity GO:0016303 p=8.1E−03 n=2 fg=0.04 bg=0.00
phosphatidylinositol−4,5−bisphosphate 3−... GO:0046934 p=8.1E−03 n=2 fg=0.04 bg=0.00
inorganic cation transmembrane transport... GO:0022890 p=1.1E−02 n=7 fg=0.15 bg=0.05
MAP kinase kinase kinase activity GO:0004709 p=1.2E−02 n=2 fg=0.04 bg=0.00
mitogen−activated protein kinase kinase ... GO:0031434 p=1.2E−02 n=2 fg=0.04 bg=0.00
cation transmembrane transporter activit... GO:0008324 p=1.3E−02 n=7 fg=0.15 bg=0.06
active ion transmembrane transporter act... GO:0022853 p=2.0E−02 n=4 fg=0.09 bg=0.02
P−type transmembrane transporter activit... GO:0140358 p=2.1E−02 n=2 fg=0.04 bg=0.01
P−type ion transporter activity GO:0015662 p=2.1E−02 n=2 fg=0.04 bg=0.01
metal ion transmembrane transporter acti... GO:0046873 p=2.6E−02 n=5 fg=0.11 bg=0.04
sphingolipid transfer activity GO:0120016 p=3.0E−02 n=1 fg=0.02 bg=0.00
ceramide transfer activity GO:0120017 p=3.0E−02 n=1 fg=0.02 bg=0.00
mismatch base pair DNA N−glycosylase act... GO:0000700 p=3.0E−02 n=1 fg=0.02 bg=0.00
sodium:phosphate symporter activity GO:0005436 p=3.0E−02 n=1 fg=0.02 bg=0.00
ATP−dependent protein binding GO:0043008 p=3.0E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086056 p=3.0E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086059 p=3.0E−02 n=1 fg=0.02 bg=0.00
fibroblast growth factor receptor bindin... GO:0005104 p=3.0E−02 n=1 fg=0.02 bg=0.00
ceramide binding GO:0097001 p=3.0E−02 n=1 fg=0.02 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=3.0E−02 n=1 fg=0.02 bg=0.00
phosphate ion binding GO:0042301 p=3.0E−02 n=1 fg=0.02 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=3.0E−02 n=1 fg=0.02 bg=0.00
JUN kinase kinase kinase activity GO:0004706 p=3.0E−02 n=1 fg=0.02 bg=0.00
pyrimidine−specific mismatch base pair D... GO:0008263 p=3.0E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.0E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=3.0E−02 n=1 fg=0.02 bg=0.00
adenylate cyclase activator activity GO:0010856 p=3.0E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=47/223 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001629958.3
fraction genes in fg and expected valu
secretory granule membrane GO:0030667 p=5.5E−03 n=5 fg=0.09 bg=0.02
terminal bouton GO:0043195 p=1.7E−02 n=4 fg=0.07 bg=0.02
nuclear body GO:0016604 p=2.3E−02 n=8 fg=0.14 bg=0.06
azurophil granule membrane GO:0035577 p=2.3E−02 n=2 fg=0.04 bg=0.00
integral component of organelle membrane GO:0031301 p=2.8E−02 n=6 fg=0.11 bg=0.04
intrinsic component of organelle membran... GO:0031300 p=3.1E−02 n=6 fg=0.11 bg=0.04
insulin receptor complex GO:0005899 p=3.1E−02 n=1 fg=0.02 bg=0.00
omegasome membrane GO:1903349 p=3.1E−02 n=1 fg=0.02 bg=0.00
omegasome GO:1990462 p=3.1E−02 n=1 fg=0.02 bg=0.00
clathrin−sculpted vesicle GO:0060198 p=3.1E−02 n=1 fg=0.02 bg=0.00
intrinsic component of omegasome membran... GO:0097630 p=3.1E−02 n=1 fg=0.02 bg=0.00
integral component of omegasome membrane GO:0097631 p=3.1E−02 n=1 fg=0.02 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200 p=3.1E−02 n=1 fg=0.02 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061202 p=3.1E−02 n=1 fg=0.02 bg=0.00
integral component of membrane GO:0016021 p=3.2E−02 n=15 fg=0.27 bg=0.16
intrinsic component of endoplasmic retic... GO:0031227 p=3.6E−02 n=4 fg=0.07 bg=0.02
integral component of endoplasmic reticu... GO:0030176 p=3.6E−02 n=4 fg=0.07 bg=0.02
type I terminal bouton GO:0061174 p=3.6E−02 n=2 fg=0.04 bg=0.01
nuclear speck GO:0016607 p=3.8E−02 n=5 fg=0.09 bg=0.03
lysosomal membrane GO:0005765 p=4.2E−02 n=4 fg=0.07 bg=0.02
intrinsic component of membrane GO:0031224 p=4.6E−02 n=15 fg=0.27 bg=0.17
lytic vacuole membrane GO:0098852 p=5.5E−02 n=4 fg=0.07 bg=0.03
axon terminus GO:0043679 p=5.5E−02 n=4 fg=0.07 bg=0.03
brush border membrane GO:0031526 p=5.9E−02 n=2 fg=0.04 bg=0.01
type Ib terminal bouton GO:0061176 p=6.1E−02 n=1 fg=0.02 bg=0.00
type Is terminal bouton GO:0061177 p=6.1E−02 n=1 fg=0.02 bg=0.00
ESC/E(Z) complex GO:0035098 p=6.1E−02 n=1 fg=0.02 bg=0.00
microtubule minus−end GO:0036449 p=6.1E−02 n=1 fg=0.02 bg=0.00
filamentous actin GO:0031941 p=6.1E−02 n=1 fg=0.02 bg=0.00
neuron projection terminus GO:0044306 p=6.2E−02 n=4 fg=0.07 bg=0.03
0 1 2 3 4 5
−log(p)
n=56/223 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction