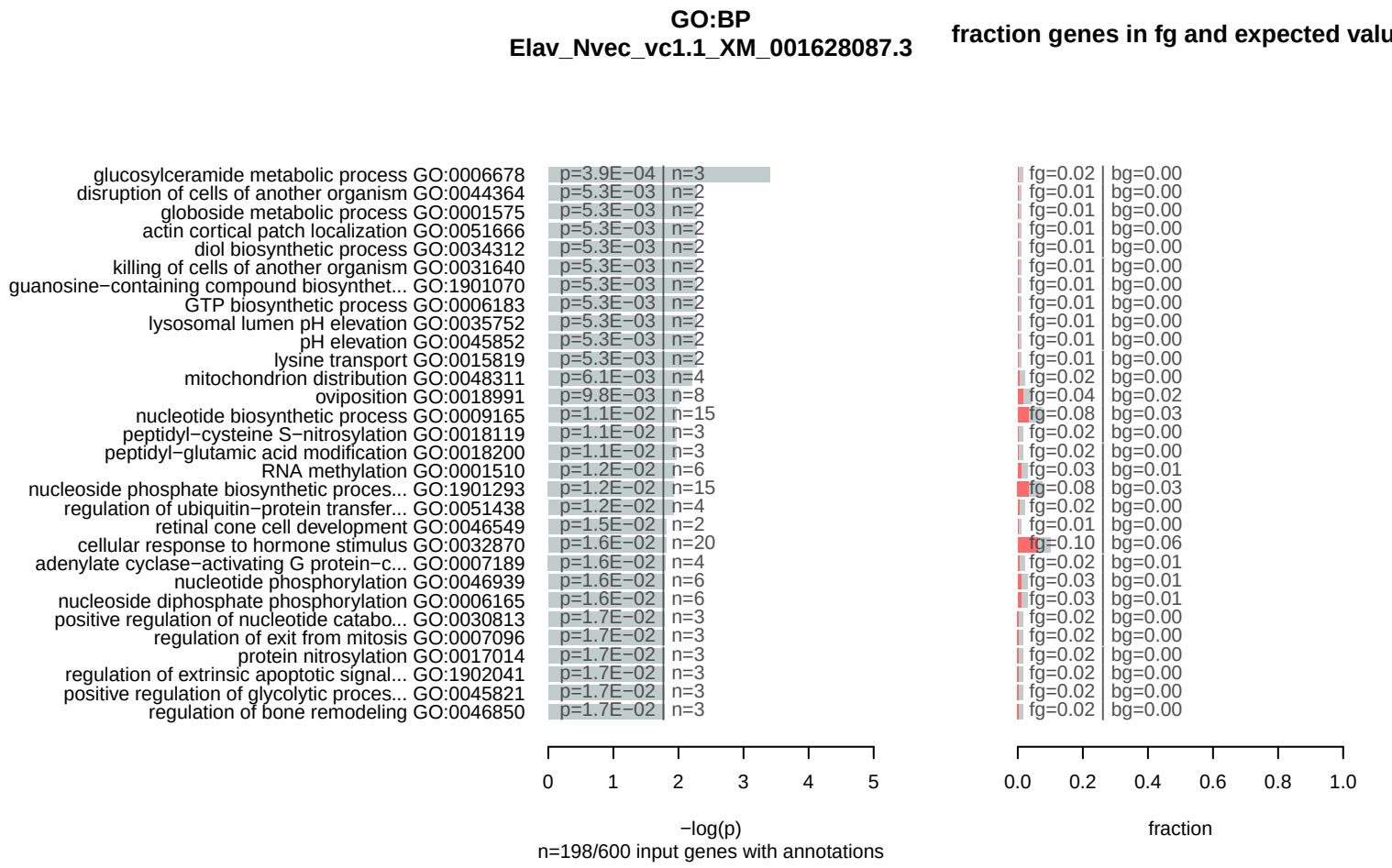
GO:BP
Elav_Nvec_vc1.1_XM_001628087.3
fraction genes in fg and expected valu
glucosylceramide metabolic process GO:0006678 p=3.9E−04 n=3 fg=0.02 bg=0.00
disruption of cells of another organism GO:0044364 p=5.3E−03 n=2 fg=0.01 bg=0.00
globoside metabolic process GO:0001575 p=5.3E−03 n=2 fg=0.01 bg=0.00
actin cortical patch localization GO:0051666 p=5.3E−03 n=2 fg=0.01 bg=0.00
diol biosynthetic process GO:0034312 p=5.3E−03 n=2 fg=0.01 bg=0.00
killing of cells of another organism GO:0031640 p=5.3E−03 n=2 fg=0.01 bg=0.00
guanosine−containing compound biosynthet... GO:1901070 p=5.3E−03 n=2 fg=0.01 bg=0.00
GTP biosynthetic process GO:0006183 p=5.3E−03 n=2 fg=0.01 bg=0.00
lysosomal lumen pH elevation GO:0035752 p=5.3E−03 n=2 fg=0.01 bg=0.00
pH elevation GO:0045852 p=5.3E−03 n=2 fg=0.01 bg=0.00
lysine transport GO:0015819 p=5.3E−03 n=2 fg=0.01 bg=0.00
mitochondrion distribution GO:0048311 p=6.1E−03 n=4 fg=0.02 bg=0.00
oviposition GO:0018991 p=9.8E−03 n=8 fg=0.04 bg=0.02
nucleotide biosynthetic process GO:0009165 p=1.1E−02 n=15 fg=0.08 bg=0.03
peptidyl−cysteine S−nitrosylation GO:0018119 p=1.1E−02 n=3 fg=0.02 bg=0.00
peptidyl−glutamic acid modification GO:0018200 p=1.1E−02 n=3 fg=0.02 bg=0.00
RNA methylation GO:0001510 p=1.2E−02 n=6 fg=0.03 bg=0.01
nucleoside phosphate biosynthetic proces... GO:1901293 p=1.2E−02 n=15 fg=0.08 bg=0.03
regulation of ubiquitin−protein transfer... GO:0051438 p=1.2E−02 n=4 fg=0.02 bg=0.00
retinal cone cell development GO:0046549 p=1.5E−02 n=2 fg=0.01 bg=0.00
cellular response to hormone stimulus GO:0032870 p=1.6E−02 n=20 fg=0.10 bg=0.06
adenylate cyclase−activating G protein−c... GO:0007189 p=1.6E−02 n=4 fg=0.02 bg=0.01
nucleotide phosphorylation GO:0046939 p=1.6E−02 n=6 fg=0.03 bg=0.01
nucleoside diphosphate phosphorylation GO:0006165 p=1.6E−02 n=6 fg=0.03 bg=0.01
positive regulation of nucleotide catabo... GO:0030813 p=1.7E−02 n=3 fg=0.02 bg=0.00
regulation of exit from mitosis GO:0007096 p=1.7E−02 n=3 fg=0.02 bg=0.00
protein nitrosylation GO:0017014 p=1.7E−02 n=3 fg=0.02 bg=0.00
regulation of extrinsic apoptotic signal... GO:1902041 p=1.7E−02 n=3 fg=0.02 bg=0.00
positive regulation of glycolytic proces... GO:0045821 p=1.7E−02 n=3 fg=0.02 bg=0.00
regulation of bone remodeling GO:0046850 p=1.7E−02 n=3 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=198/600 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001628087.3
fraction genes in fg and expected valu
ligand−gated sodium channel activity GO:0015280 p=5.2E−03 n=2 fg=0.01 bg=0.00
oxidoreductase activity, acting on CH−OH... GO:0016614 p=6.0E−03 n=6 fg=0.03 bg=0.01
organic cation transmembrane transporter... GO:0015101 p=6.4E−03 n=3 fg=0.02 bg=0.00
UDP−glycosyltransferase activity GO:0008194 p=1.1E−02 n=6 fg=0.03 bg=0.01
ether hydrolase activity GO:0016803 p=1.5E−02 n=2 fg=0.01 bg=0.00
epoxide hydrolase activity GO:0004301 p=1.5E−02 n=2 fg=0.01 bg=0.00
UDP−glucosyltransferase activity GO:0035251 p=1.5E−02 n=2 fg=0.01 bg=0.00
acid−amino acid ligase activity GO:0016881 p=1.6E−02 n=3 fg=0.02 bg=0.00
carboxy−lyase activity GO:0016831 p=1.6E−02 n=3 fg=0.02 bg=0.00
S−adenosylmethionine−dependent methyltra... GO:0008757 p=2.6E−02 n=7 fg=0.04 bg=0.02
tau protein binding GO:0048156 p=2.9E−02 n=2 fg=0.01 bg=0.00
RNA polymerase I transcription regulator... GO:0001163 p=2.9E−02 n=2 fg=0.01 bg=0.00
RNA polymerase I core promoter sequence−... GO:0001164 p=2.9E−02 n=2 fg=0.01 bg=0.00
hydrolase activity, acting on ether bond... GO:0016801 p=2.9E−02 n=2 fg=0.01 bg=0.00
glycosyltransferase activity GO:0016757 p=3.8E−02 n=8 fg=0.05 bg=0.02
lyase activity GO:0016829 p=4.1E−02 n=7 fg=0.04 bg=0.02
nucleoside diphosphate kinase activity GO:0004550 p=4.5E−02 n=2 fg=0.01 bg=0.00
glucosyltransferase activity GO:0046527 p=4.5E−02 n=2 fg=0.01 bg=0.00
nitric−oxide synthase binding GO:0050998 p=4.5E−02 n=2 fg=0.01 bg=0.00
deaminase activity GO:0019239 p=4.5E−02 n=2 fg=0.01 bg=0.00
oxidoreductase activity, acting on the C... GO:0016616 p=5.2E−02 n=4 fg=0.02 bg=0.01
methyltransferase activity GO:0008168 p=6.0E−02 n=7 fg=0.04 bg=0.02
glucuronosyltransferase activity GO:0015020 p=6.5E−02 n=2 fg=0.01 bg=0.00
DNA−(apurinic or apyrimidinic site) endo... GO:0003906 p=6.5E−02 n=2 fg=0.01 bg=0.00
proline−rich region binding GO:0070064 p=6.5E−02 n=2 fg=0.01 bg=0.00
tRNA (guanine) methyltransferase activit... GO:0016423 p=6.5E−02 n=2 fg=0.01 bg=0.00
guanyl−nucleotide exchange factor activi... GO:0005085 p=6.5E−02 n=6 fg=0.03 bg=0.02
hydrolase activity, acting on glycosyl b... GO:0016798 p=6.9E−02 n=5 fg=0.03 bg=0.01
transferase activity, transferring one−c... GO:0016741 p=7.2E−02 n=7 fg=0.04 bg=0.02
acid−sensing ion channel activity GO:0044736 p=7.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=172/600 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001628087.3
fraction genes in fg and expected valu
intrinsic component of endoplasmic retic... GO:0031227 p=7.1E−03 n=10 fg=0.05 bg=0.02
integral component of endoplasmic reticu... GO:0030176 p=1.5E−02 n=9 fg=0.05 bg=0.02
cyclin−dependent protein kinase holoenzy... GO:0000307 p=1.6E−02 n=3 fg=0.02 bg=0.00
filopodium GO:0030175 p=1.9E−02 n=5 fg=0.03 bg=0.01
dendritic spine membrane GO:0032591 p=2.9E−02 n=2 fg=0.01 bg=0.00
growth cone lamellipodium GO:1990761 p=2.9E−02 n=2 fg=0.01 bg=0.00
lytic vacuole membrane GO:0098852 p=3.6E−02 n=8 fg=0.04 bg=0.02
fungal−type vacuole GO:0000324 p=4.6E−02 n=2 fg=0.01 bg=0.00
fungal−type vacuole membrane GO:0000329 p=4.6E−02 n=2 fg=0.01 bg=0.00
mitochondrion GO:0005739 p=4.7E−02 n=36 fg=0.18 bg=0.14
nucleolus GO:0005730 p=5.1E−02 n=25 fg=0.13 bg=0.09
serine/threonine protein kinase complex GO:1902554 p=5.3E−02 n=4 fg=0.02 bg=0.01
lytic vacuole GO:0000323 p=6.4E−02 n=14 fg=0.07 bg=0.05
filopodium tip GO:0032433 p=6.5E−02 n=2 fg=0.01 bg=0.00
cell tip GO:0051286 p=6.5E−02 n=2 fg=0.01 bg=0.00
mitochondrial pyruvate dehydrogenase com... GO:0005967 p=7.3E−02 n=1 fg=0.01 bg=0.00
cytoplasmic side of dendritic spine plas... GO:1990780 p=7.3E−02 n=1 fg=0.01 bg=0.00
anchored component of external side of p... GO:0031362 p=7.3E−02 n=1 fg=0.01 bg=0.00
tRNA methyltransferase complex GO:0043527 p=7.3E−02 n=1 fg=0.01 bg=0.00
fungal biofilm matrix GO:0062040 p=7.3E−02 n=1 fg=0.01 bg=0.00
syntrophin complex GO:0016013 p=7.3E−02 n=1 fg=0.01 bg=0.00
biofilm matrix GO:0062039 p=7.3E−02 n=1 fg=0.01 bg=0.00
methionyl glutamyl tRNA synthetase compl... GO:0017102 p=7.3E−02 n=1 fg=0.01 bg=0.00
RNA polymerase I core factor complex GO:0070860 p=7.3E−02 n=1 fg=0.01 bg=0.00
dendritic spine head GO:0044327 p=7.3E−02 n=1 fg=0.01 bg=0.00
sperm individualization complex GO:0070864 p=7.3E−02 n=1 fg=0.01 bg=0.00
investment cone GO:0070865 p=7.3E−02 n=1 fg=0.01 bg=0.00
septin filament array GO:0032160 p=7.3E−02 n=1 fg=0.01 bg=0.00
DNA polymerase III, core complex GO:0044776 p=7.3E−02 n=1 fg=0.01 bg=0.00
RNA polymerase transcription factor SL1 ... GO:0005668 p=7.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=197/600 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction