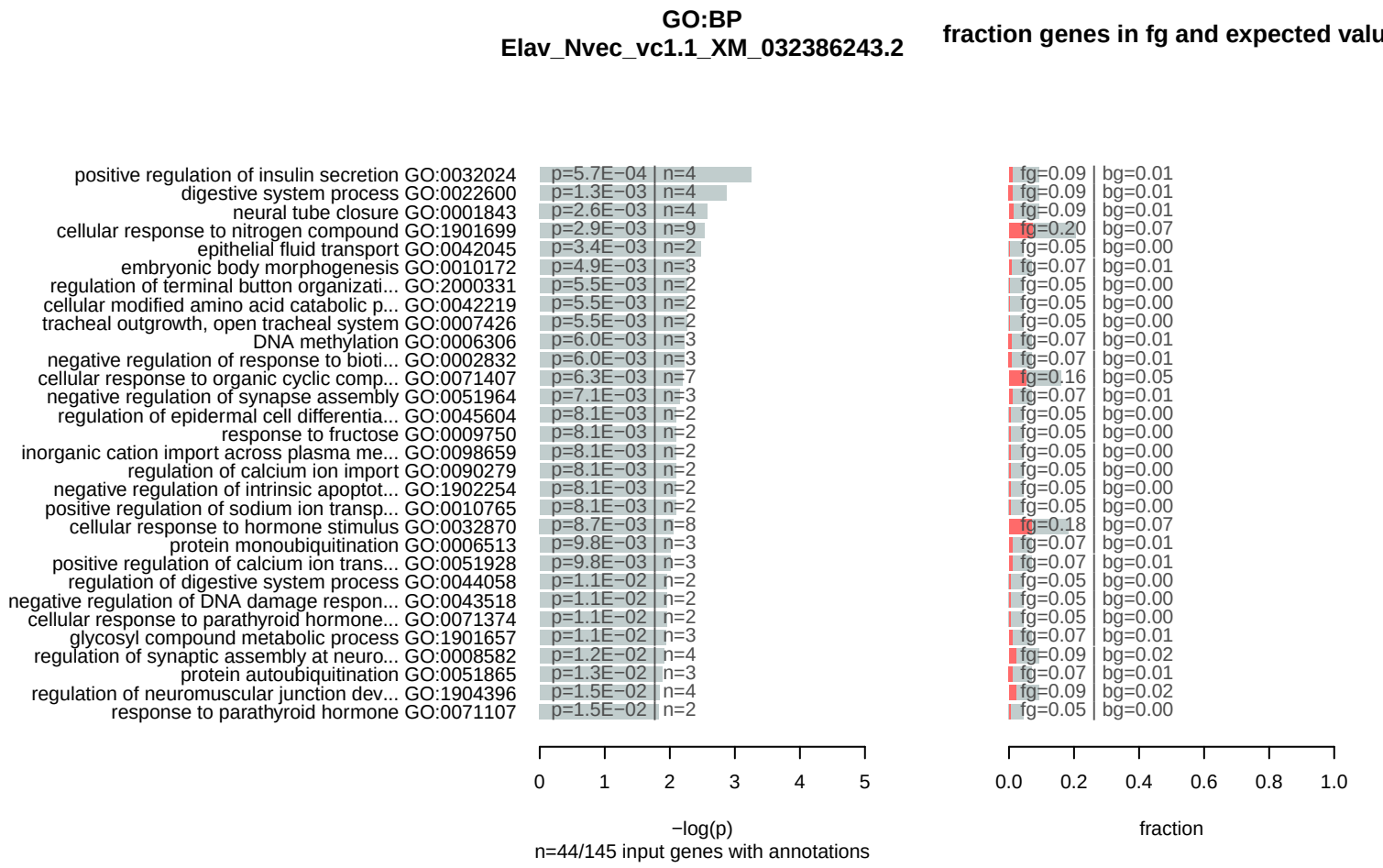
GO:BP
Elav_Nvec_vc1.1_XM_032386243.2
fraction genes in fg and expected valu
positive regulation of insulin secretion GO:0032024 p=5.7E−04 n=4 fg=0.09 bg=0.01
digestive system process GO:0022600 p=1.3E−03 n=4 fg=0.09 bg=0.01
neural tube closure GO:0001843 p=2.6E−03 n=4 fg=0.09 bg=0.01
cellular response to nitrogen compound GO:1901699 p=2.9E−03 n=9 fg=0.20 bg=0.07
epithelial fluid transport GO:0042045 p=3.4E−03 n=2 fg=0.05 bg=0.00
embryonic body morphogenesis GO:0010172 p=4.9E−03 n=3 fg=0.07 bg=0.01
regulation of terminal button organizati... GO:2000331 p=5.5E−03 n=2 fg=0.05 bg=0.00
cellular modified amino acid catabolic p... GO:0042219 p=5.5E−03 n=2 fg=0.05 bg=0.00
tracheal outgrowth, open tracheal system GO:0007426 p=5.5E−03 n=2 fg=0.05 bg=0.00
DNA methylation GO:0006306 p=6.0E−03 n=3 fg=0.07 bg=0.01
negative regulation of response to bioti... GO:0002832 p=6.0E−03 n=3 fg=0.07 bg=0.01
cellular response to organic cyclic comp... GO:0071407 p=6.3E−03 n=7 fg=0.16 bg=0.05
negative regulation of synapse assembly GO:0051964 p=7.1E−03 n=3 fg=0.07 bg=0.01
regulation of epidermal cell differentia... GO:0045604 p=8.1E−03 n=2 fg=0.05 bg=0.00
response to fructose GO:0009750 p=8.1E−03 n=2 fg=0.05 bg=0.00
inorganic cation import across plasma me... GO:0098659 p=8.1E−03 n=2 fg=0.05 bg=0.00
regulation of calcium ion import GO:0090279 p=8.1E−03 n=2 fg=0.05 bg=0.00
negative regulation of intrinsic apoptot... GO:1902254 p=8.1E−03 n=2 fg=0.05 bg=0.00
positive regulation of sodium ion transp... GO:0010765 p=8.1E−03 n=2 fg=0.05 bg=0.00
cellular response to hormone stimulus GO:0032870 p=8.7E−03 n=8 fg=0.18 bg=0.07
protein monoubiquitination GO:0006513 p=9.8E−03 n=3 fg=0.07 bg=0.01
positive regulation of calcium ion trans... GO:0051928 p=9.8E−03 n=3 fg=0.07 bg=0.01
regulation of digestive system process GO:0044058 p=1.1E−02 n=2 fg=0.05 bg=0.00
negative regulation of DNA damage respon... GO:0043518 p=1.1E−02 n=2 fg=0.05 bg=0.00
cellular response to parathyroid hormone... GO:0071374 p=1.1E−02 n=2 fg=0.05 bg=0.00
glycosyl compound metabolic process GO:1901657 p=1.1E−02 n=3 fg=0.07 bg=0.01
regulation of synaptic assembly at neuro... GO:0008582 p=1.2E−02 n=4 fg=0.09 bg=0.02
protein autoubiquitination GO:0051865 p=1.3E−02 n=3 fg=0.07 bg=0.01
regulation of neuromuscular junction dev... GO:1904396 p=1.5E−02 n=4 fg=0.09 bg=0.02
response to parathyroid hormone GO:0071107 p=1.5E−02 n=2 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=44/145 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032386243.2
fraction genes in fg and expected valu
insulin−like growth factor receptor bind... GO:0005159 p=1.7E−03 n=2 fg=0.05 bg=0.00
amidine−lyase activity GO:0016842 p=3.4E−03 n=2 fg=0.05 bg=0.00
ubiquitin−like protein ligase activity GO:0061659 p=1.1E−02 n=5 fg=0.13 bg=0.04
ubiquitin protein ligase activity GO:0061630 p=1.1E−02 n=5 fg=0.13 bg=0.04
phosphotransferase activity, phosphate g... GO:0016776 p=1.1E−02 n=2 fg=0.05 bg=0.00
nucleobase−containing compound kinase ac... GO:0019205 p=1.9E−02 n=2 fg=0.05 bg=0.01
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323 p=2.5E−02 n=1 fg=0.03 bg=0.00
sodium:phosphate symporter activity GO:0005436 p=2.5E−02 n=1 fg=0.03 bg=0.00
platelet activating factor receptor bind... GO:0031859 p=2.5E−02 n=1 fg=0.03 bg=0.00
follicle−stimulating hormone receptor bi... GO:0031762 p=2.5E−02 n=1 fg=0.03 bg=0.00
gamma−glutamylaminecyclotransferase acti... GO:0061929 p=2.5E−02 n=1 fg=0.03 bg=0.00
type 2A serotonin receptor binding GO:0031826 p=2.5E−02 n=1 fg=0.03 bg=0.00
opsin binding GO:0002046 p=2.5E−02 n=1 fg=0.03 bg=0.00
phosphate ion binding GO:0042301 p=2.5E−02 n=1 fg=0.03 bg=0.00
alpha−1A adrenergic receptor binding GO:0031691 p=2.5E−02 n=1 fg=0.03 bg=0.00
thiol oxidase activity GO:0016972 p=2.5E−02 n=1 fg=0.03 bg=0.00
V2 vasopressin receptor binding GO:0031896 p=2.5E−02 n=1 fg=0.03 bg=0.00
ubiquitin conjugating enzyme activity GO:0061631 p=2.8E−02 n=2 fg=0.05 bg=0.01
protein−macromolecule adaptor activity GO:0030674 p=2.9E−02 n=4 fg=0.10 bg=0.03
molecular adaptor activity GO:0060090 p=2.9E−02 n=4 fg=0.10 bg=0.03
ubiquitin−like protein conjugating enzym... GO:0061650 p=3.3E−02 n=2 fg=0.05 bg=0.01
transcription corepressor activity GO:0003714 p=3.8E−02 n=3 fg=0.08 bg=0.02
kinase activity GO:0016301 p=4.6E−02 n=6 fg=0.15 bg=0.07
cis−regulatory region sequence−specific ... GO:0000987 p=4.8E−02 n=4 fg=0.10 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=4.8E−02 n=4 fg=0.10 bg=0.04
gamma−glutamylcyclotransferase activity GO:0003839 p=4.8E−02 n=1 fg=0.03 bg=0.00
chloride channel inhibitor activity GO:0019869 p=4.8E−02 n=1 fg=0.03 bg=0.00
nuclear steroid receptor activity GO:0003707 p=4.8E−02 n=1 fg=0.03 bg=0.00
phosphate ion transmembrane transporter ... GO:0015114 p=4.8E−02 n=1 fg=0.03 bg=0.00
G protein−coupled serotonin receptor bin... GO:0031821 p=4.8E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=39/145 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032386243.2
fraction genes in fg and expected valu
NuRD complex GO:0016581 p=1.6E−03 n=2 fg=0.05 bg=0.00
nuclear lamina GO:0005652 p=1.6E−03 n=2 fg=0.05 bg=0.00
cytoplasmic vesicle membrane GO:0030659 p=1.9E−02 n=8 fg=0.19 bg=0.08
vesicle membrane GO:0012506 p=2.0E−02 n=8 fg=0.19 bg=0.08
type I terminal bouton GO:0061174 p=2.2E−02 n=2 fg=0.05 bg=0.01
basal plasma membrane GO:0009925 p=2.4E−02 n=4 fg=0.09 bg=0.03
basolateral plasma membrane GO:0016323 p=2.4E−02 n=4 fg=0.09 bg=0.03
apical cytoplasm GO:0090651 p=2.4E−02 n=1 fg=0.02 bg=0.00
podocyte foot GO:0098846 p=2.4E−02 n=1 fg=0.02 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=2.4E−02 n=1 fg=0.02 bg=0.00
mitochondrial alpha−ketoglutarate dehydr... GO:0005947 p=2.4E−02 n=1 fg=0.02 bg=0.00
transcription repressor complex GO:0017053 p=3.6E−02 n=2 fg=0.05 bg=0.01
basal part of cell GO:0045178 p=3.9E−02 n=4 fg=0.09 bg=0.03
terminal bouton GO:0043195 p=4.2E−02 n=3 fg=0.07 bg=0.02
anchoring junction GO:0070161 p=4.2E−02 n=5 fg=0.12 bg=0.05
cell−cell junction GO:0005911 p=4.2E−02 n=5 fg=0.12 bg=0.05
preribosome, small subunit precursor GO:0030688 p=4.7E−02 n=1 fg=0.02 bg=0.00
mitochondrial tricarboxylic acid cycle e... GO:0030062 p=4.7E−02 n=1 fg=0.02 bg=0.00
tricarboxylic acid cycle enzyme complex GO:0045239 p=4.7E−02 n=1 fg=0.02 bg=0.00
HULC complex GO:0033503 p=4.7E−02 n=1 fg=0.02 bg=0.00
platelet alpha granule membrane GO:0031092 p=4.7E−02 n=1 fg=0.02 bg=0.00
COPII vesicle coat GO:0030127 p=4.7E−02 n=1 fg=0.02 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=4.7E−02 n=1 fg=0.02 bg=0.00
cell periphery GO:0071944 p=4.7E−02 n=18 fg=0.42 bg=0.29
plasma membrane GO:0005886 p=5.1E−02 n=17 fg=0.40 bg=0.27
plasma membrane protein complex GO:0098797 p=5.7E−02 n=4 fg=0.09 bg=0.03
mitotic spindle GO:0072686 p=6.0E−02 n=2 fg=0.05 bg=0.01
cell−substrate junction GO:0030055 p=6.6E−02 n=2 fg=0.05 bg=0.01
adherens junction GO:0005912 p=6.7E−02 n=3 fg=0.07 bg=0.02
ubiquitin conjugating enzyme complex GO:0031371 p=7.0E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=43/145 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction