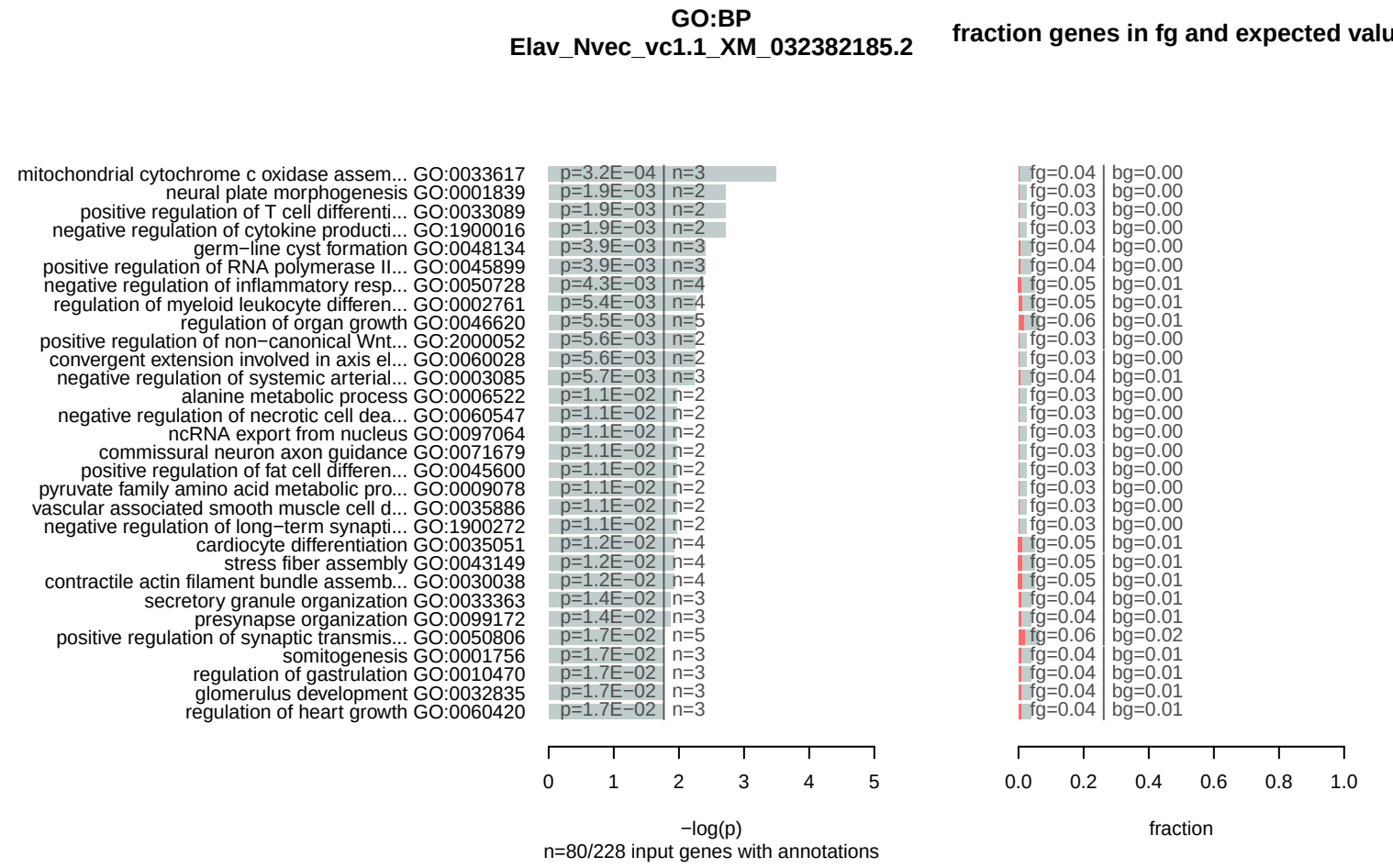
GO:BP
Elav_Nvec_vc1.1_XM_032382185.2
fraction genes in fg and expected valu
mitochondrial cytochrome c oxidase assem... GO:0033617 p=3.2E−04 n=3 fg=0.04 bg=0.00
neural plate morphogenesis GO:0001839 p=1.9E−03 n=2 fg=0.03 bg=0.00
positive regulation of T cell differenti... GO:0033089 p=1.9E−03 n=2 fg=0.03 bg=0.00
negative regulation of cytokine producti... GO:1900016 p=1.9E−03 n=2 fg=0.03 bg=0.00
germ−line cyst formation GO:0048134 p=3.9E−03 n=3 fg=0.04 bg=0.00
positive regulation of RNA polymerase II... GO:0045899 p=3.9E−03 n=3 fg=0.04 bg=0.00
negative regulation of inflammatory resp... GO:0050728 p=4.3E−03 n=4 fg=0.05 bg=0.01
regulation of myeloid leukocyte differen... GO:0002761 p=5.4E−03 n=4 fg=0.05 bg=0.01
regulation of organ growth GO:0046620 p=5.5E−03 n=5 fg=0.06 bg=0.01
positive regulation of non−canonical Wnt... GO:2000052 p=5.6E−03 n=2 fg=0.03 bg=0.00
convergent extension involved in axis el... GO:0060028 p=5.6E−03 n=2 fg=0.03 bg=0.00
negative regulation of systemic arterial... GO:0003085 p=5.7E−03 n=3 fg=0.04 bg=0.01
alanine metabolic process GO:0006522 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of necrotic cell dea... GO:0060547 p=1.1E−02 n=2 fg=0.03 bg=0.00
ncRNA export from nucleus GO:0097064 p=1.1E−02 n=2 fg=0.03 bg=0.00
commissural neuron axon guidance GO:0071679 p=1.1E−02 n=2 fg=0.03 bg=0.00
positive regulation of fat cell differen... GO:0045600 p=1.1E−02 n=2 fg=0.03 bg=0.00
pyruvate family amino acid metabolic pro... GO:0009078 p=1.1E−02 n=2 fg=0.03 bg=0.00
vascular associated smooth muscle cell d... GO:0035886 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of long−term synapti... GO:1900272 p=1.1E−02 n=2 fg=0.03 bg=0.00
cardiocyte differentiation GO:0035051 p=1.2E−02 n=4 fg=0.05 bg=0.01
stress fiber assembly GO:0043149 p=1.2E−02 n=4 fg=0.05 bg=0.01
contractile actin filament bundle assemb... GO:0030038 p=1.2E−02 n=4 fg=0.05 bg=0.01
secretory granule organization GO:0033363 p=1.4E−02 n=3 fg=0.04 bg=0.01
presynapse organization GO:0099172 p=1.4E−02 n=3 fg=0.04 bg=0.01
positive regulation of synaptic transmis... GO:0050806 p=1.7E−02 n=5 fg=0.06 bg=0.02
somitogenesis GO:0001756 p=1.7E−02 n=3 fg=0.04 bg=0.01
regulation of gastrulation GO:0010470 p=1.7E−02 n=3 fg=0.04 bg=0.01
glomerulus development GO:0032835 p=1.7E−02 n=3 fg=0.04 bg=0.01
regulation of heart growth GO:0060420 p=1.7E−02 n=3 fg=0.04 bg=0.01
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−log(p)
n=80/228 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032382185.2
fraction genes in fg and expected valu
protein−disulfide reductase activity GO:0015035 p=5.7E−03 n=3 fg=0.04 bg=0.01
oxidoreductase activity, acting on a hem... GO:0016675 p=1.1E−02 n=2 fg=0.03 bg=0.00
cytochrome−c oxidase activity GO:0004129 p=1.1E−02 n=2 fg=0.03 bg=0.00
carbohydrate binding GO:0030246 p=1.3E−02 n=3 fg=0.04 bg=0.01
G−protein beta/gamma−subunit complex bin... GO:0031683 p=1.8E−02 n=2 fg=0.03 bg=0.00
transcription coactivator binding GO:0001223 p=1.8E−02 n=2 fg=0.03 bg=0.00
myosin heavy chain binding GO:0032036 p=1.8E−02 n=2 fg=0.03 bg=0.00
protein tyrosine kinase binding GO:1990782 p=2.1E−02 n=3 fg=0.04 bg=0.01
chaperone binding GO:0051087 p=2.1E−02 n=4 fg=0.06 bg=0.02
signaling receptor binding GO:0005102 p=2.4E−02 n=13 fg=0.19 bg=0.10
unfolded protein binding GO:0051082 p=2.5E−02 n=4 fg=0.06 bg=0.02
actin filament binding GO:0051015 p=2.5E−02 n=3 fg=0.04 bg=0.01
dopamine receptor binding GO:0050780 p=2.5E−02 n=2 fg=0.03 bg=0.00
quaternary ammonium group binding GO:0050997 p=3.5E−02 n=2 fg=0.03 bg=0.00
phosphatidylcholine binding GO:0031210 p=3.5E−02 n=2 fg=0.03 bg=0.00
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=3.5E−02 n=2 fg=0.03 bg=0.00
oxidoreductase activity, acting on a sul... GO:0016668 p=3.5E−02 n=2 fg=0.03 bg=0.00
fibroblast growth factor receptor bindin... GO:0005104 p=4.4E−02 n=1 fg=0.01 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=4.4E−02 n=1 fg=0.01 bg=0.00
alanine−oxo−acid transaminase activity GO:0047635 p=4.4E−02 n=1 fg=0.01 bg=0.00
diacylglycerol binding GO:0019992 p=4.4E−02 n=1 fg=0.01 bg=0.00
deubiquitinase activator activity GO:0035800 p=4.4E−02 n=1 fg=0.01 bg=0.00
kinetochore binding GO:0043515 p=4.4E−02 n=1 fg=0.01 bg=0.00
prostaglandin−D synthase activity GO:0004667 p=4.4E−02 n=1 fg=0.01 bg=0.00
glucose−6−phosphate dehydrogenase activi... GO:0004345 p=4.4E−02 n=1 fg=0.01 bg=0.00
pantetheine hydrolase activity GO:0017159 p=4.4E−02 n=1 fg=0.01 bg=0.00
N6−methyladenosine−containing RNA bindin... GO:1990247 p=4.4E−02 n=1 fg=0.01 bg=0.00
prostaglandin−E synthase activity GO:0050220 p=4.4E−02 n=1 fg=0.01 bg=0.00
mannosyl−oligosaccharide mannosidase act... GO:0015924 p=4.4E−02 n=1 fg=0.01 bg=0.00
chitinase activity GO:0004568 p=4.4E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=70/228 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032382185.2
fraction genes in fg and expected valu
chaperone complex GO:0101031 p=5.8E−03 n=2 fg=0.02 bg=0.00
endoplasmic reticulum quality control co... GO:0044322 p=1.1E−02 n=2 fg=0.02 bg=0.00
presynaptic periactive zone GO:0036062 p=1.1E−02 n=2 fg=0.02 bg=0.00
protein serine/threonine phosphatase com... GO:0008287 p=2.7E−02 n=3 fg=0.04 bg=0.01
Golgi apparatus subcompartment GO:0098791 p=2.7E−02 n=12 fg=0.15 bg=0.08
recycling endosome GO:0055037 p=2.8E−02 n=5 fg=0.06 bg=0.02
growth cone GO:0030426 p=3.4E−02 n=5 fg=0.06 bg=0.02
phosphatase complex GO:1903293 p=3.7E−02 n=3 fg=0.04 bg=0.01
mitochondrion GO:0005739 p=3.8E−02 n=17 fg=0.21 bg=0.14
site of polarized growth GO:0030427 p=4.0E−02 n=5 fg=0.06 bg=0.02
presynaptic active zone GO:0048786 p=4.3E−02 n=3 fg=0.04 bg=0.01
cortical microtubule GO:0055028 p=4.5E−02 n=1 fg=0.01 bg=0.00
TSC1−TSC2 complex GO:0033596 p=4.5E−02 n=1 fg=0.01 bg=0.00
centrosomal corona GO:0031592 p=4.5E−02 n=1 fg=0.01 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=4.5E−02 n=1 fg=0.01 bg=0.00
cortical microtubule plus−end GO:1903754 p=4.5E−02 n=1 fg=0.01 bg=0.00
FANCM−MHF complex GO:0071821 p=4.5E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=4.5E−02 n=1 fg=0.01 bg=0.00
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dendritic spine neck GO:0044326 p=4.5E−02 n=1 fg=0.01 bg=0.00
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CURI complex GO:0032545 p=4.5E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=4.5E−02 n=1 fg=0.01 bg=0.00
PR−DUB complex GO:0035517 p=4.5E−02 n=1 fg=0.01 bg=0.00
cytoplasmic side of dendritic spine plas... GO:1990780 p=4.5E−02 n=1 fg=0.01 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=4.5E−02 n=1 fg=0.01 bg=0.00
azurophil granule membrane GO:0035577 p=4.6E−02 n=2 fg=0.02 bg=0.00
organelle envelope lumen GO:0031970 p=5.7E−02 n=3 fg=0.04 bg=0.01
stress fiber GO:0001725 p=5.8E−02 n=2 fg=0.02 bg=0.00
contractile actin filament bundle GO:0097517 p=5.8E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=81/228 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction