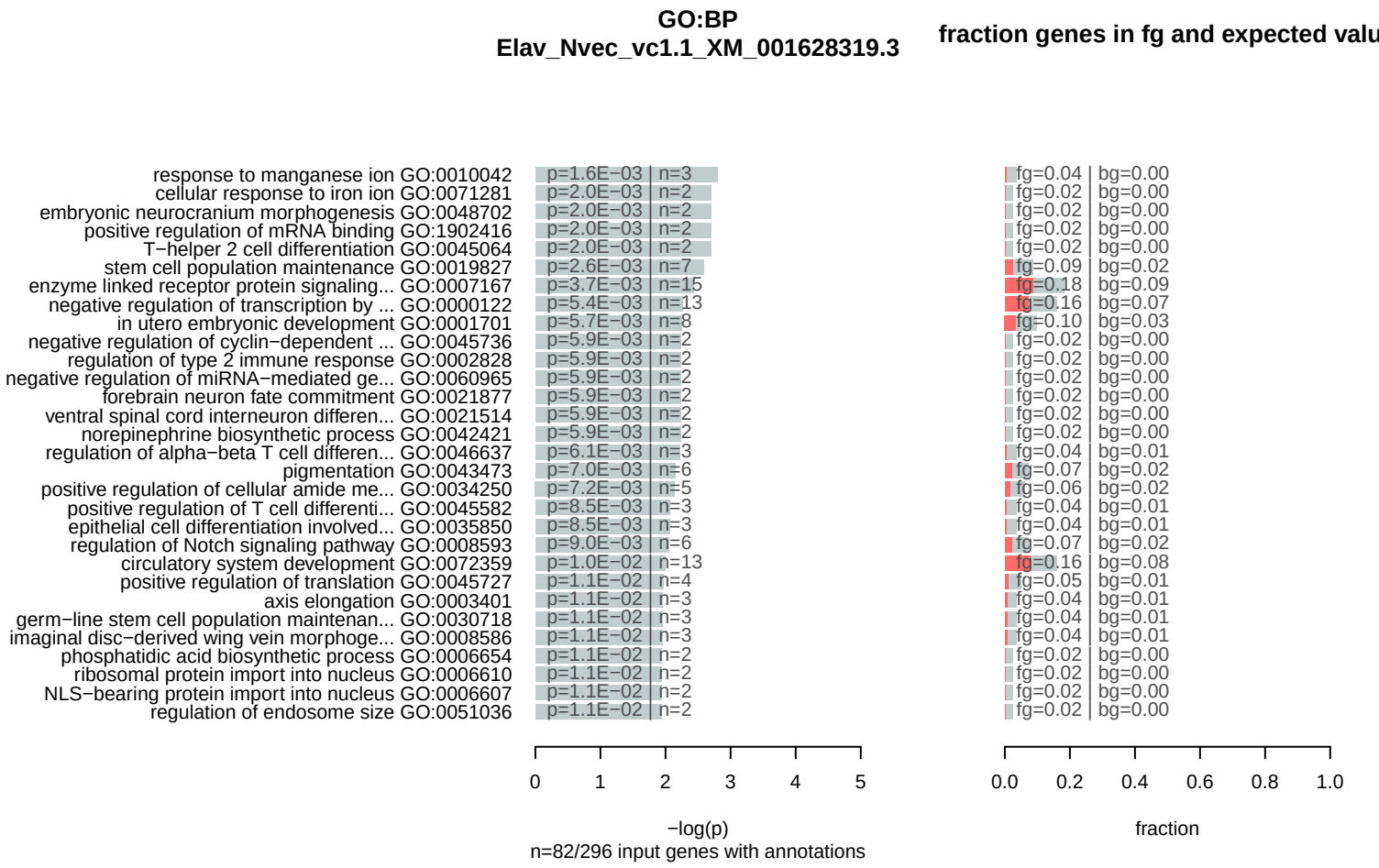
GO:BP
Elav_Nvec_vc1.1_XM_001628319.3
fraction genes in fg and expected valu
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cellular response to iron ion GO:0071281 p=2.0E−03 n=2 fg=0.02 bg=0.00
embryonic neurocranium morphogenesis GO:0048702 p=2.0E−03 n=2 fg=0.02 bg=0.00
positive regulation of mRNA binding GO:1902416 p=2.0E−03 n=2 fg=0.02 bg=0.00
T−helper 2 cell differentiation GO:0045064 p=2.0E−03 n=2 fg=0.02 bg=0.00
stem cell population maintenance GO:0019827 p=2.6E−03 n=7 fg=0.09 bg=0.02
enzyme linked receptor protein signaling... GO:0007167 p=3.7E−03 n=15 fg=0.18 bg=0.09
negative regulation of transcription by ... GO:0000122 p=5.4E−03 n=13 fg=0.16 bg=0.07
in utero embryonic development GO:0001701 p=5.7E−03 n=8 fg=0.10 bg=0.03
negative regulation of cyclin−dependent ... GO:0045736 p=5.9E−03 n=2 fg=0.02 bg=0.00
regulation of type 2 immune response GO:0002828 p=5.9E−03 n=2 fg=0.02 bg=0.00
negative regulation of miRNA−mediated ge... GO:0060965 p=5.9E−03 n=2 fg=0.02 bg=0.00
forebrain neuron fate commitment GO:0021877 p=5.9E−03 n=2 fg=0.02 bg=0.00
ventral spinal cord interneuron differen... GO:0021514 p=5.9E−03 n=2 fg=0.02 bg=0.00
norepinephrine biosynthetic process GO:0042421 p=5.9E−03 n=2 fg=0.02 bg=0.00
regulation of alpha−beta T cell differen... GO:0046637 p=6.1E−03 n=3 fg=0.04 bg=0.01
pigmentation GO:0043473 p=7.0E−03 n=6 fg=0.07 bg=0.02
positive regulation of cellular amide me... GO:0034250 p=7.2E−03 n=5 fg=0.06 bg=0.02
positive regulation of T cell differenti... GO:0045582 p=8.5E−03 n=3 fg=0.04 bg=0.01
epithelial cell differentiation involved... GO:0035850 p=8.5E−03 n=3 fg=0.04 bg=0.01
regulation of Notch signaling pathway GO:0008593 p=9.0E−03 n=6 fg=0.07 bg=0.02
circulatory system development GO:0072359 p=1.0E−02 n=13 fg=0.16 bg=0.08
positive regulation of translation GO:0045727 p=1.1E−02 n=4 fg=0.05 bg=0.01
axis elongation GO:0003401 p=1.1E−02 n=3 fg=0.04 bg=0.01
germ−line stem cell population maintenan... GO:0030718 p=1.1E−02 n=3 fg=0.04 bg=0.01
imaginal disc−derived wing vein morphoge... GO:0008586 p=1.1E−02 n=3 fg=0.04 bg=0.01
phosphatidic acid biosynthetic process GO:0006654 p=1.1E−02 n=2 fg=0.02 bg=0.00
ribosomal protein import into nucleus GO:0006610 p=1.1E−02 n=2 fg=0.02 bg=0.00
NLS−bearing protein import into nucleus GO:0006607 p=1.1E−02 n=2 fg=0.02 bg=0.00
regulation of endosome size GO:0051036 p=1.1E−02 n=2 fg=0.02 bg=0.00
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−log(p)
n=82/296 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001628319.3
fraction genes in fg and expected valu
calcium−dependent protein serine/threoni... GO:0004723 p=2.1E−03 n=2 fg=0.03 bg=0.00
DNA−binding transcription repressor acti... GO:0001227 p=2.2E−03 n=5 fg=0.07 bg=0.01
signal sequence binding GO:0005048 p=4.6E−03 n=3 fg=0.04 bg=0.01
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=6.2E−03 n=2 fg=0.03 bg=0.00
protein phosphatase activator activity GO:0072542 p=1.2E−02 n=2 fg=0.03 bg=0.00
oxidoreductase activity, acting on the C... GO:0016646 p=1.2E−02 n=2 fg=0.03 bg=0.00
phosphatase activator activity GO:0019211 p=1.2E−02 n=2 fg=0.03 bg=0.00
GTPase inhibitor activity GO:0005095 p=1.2E−02 n=2 fg=0.03 bg=0.00
nuclear localization sequence binding GO:0008139 p=1.9E−02 n=2 fg=0.03 bg=0.00
protein phosphatase regulator activity GO:0019888 p=2.0E−02 n=3 fg=0.04 bg=0.01
galactosyltransferase activity GO:0008378 p=2.8E−02 n=2 fg=0.03 bg=0.00
oxidoreductase activity, acting on the C... GO:0016645 p=2.8E−02 n=2 fg=0.03 bg=0.00
UDP−galactosyltransferase activity GO:0035250 p=2.8E−02 n=2 fg=0.03 bg=0.00
beta−1,3−galactosyltransferase activity GO:0048531 p=2.8E−02 n=2 fg=0.03 bg=0.00
UDP−galactose:beta−N−acetylglucosamine b... GO:0008499 p=2.8E−02 n=2 fg=0.03 bg=0.00
enzyme inhibitor activity GO:0004857 p=2.9E−02 n=5 fg=0.07 bg=0.02
phosphatase regulator activity GO:0019208 p=2.9E−02 n=3 fg=0.04 bg=0.01
core promoter sequence−specific DNA bind... GO:0001046 p=3.5E−02 n=3 fg=0.04 bg=0.01
cytokine receptor binding GO:0005126 p=3.5E−02 n=3 fg=0.04 bg=0.01
phosphatase binding GO:0019902 p=4.2E−02 n=5 fg=0.07 bg=0.03
protein phosphatase binding GO:0019903 p=4.2E−02 n=4 fg=0.05 bg=0.02
molecular function regulator activity GO:0098772 p=4.6E−02 n=14 fg=0.19 bg=0.12
type I transforming growth factor beta r... GO:0034713 p=4.6E−02 n=1 fg=0.01 bg=0.00
phosphofructokinase activity GO:0008443 p=4.6E−02 n=1 fg=0.01 bg=0.00
L−leucine transmembrane transporter acti... GO:0015190 p=4.6E−02 n=1 fg=0.01 bg=0.00
L−methionine transmembrane transporter a... GO:0015191 p=4.6E−02 n=1 fg=0.01 bg=0.00
cupric ion binding GO:1903135 p=4.6E−02 n=1 fg=0.01 bg=0.00
cuprous ion binding GO:1903136 p=4.6E−02 n=1 fg=0.01 bg=0.00
sphingolipid transfer activity GO:0120016 p=4.6E−02 n=1 fg=0.01 bg=0.00
ceramide transfer activity GO:0120017 p=4.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=74/296 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001628319.3
fraction genes in fg and expected valu
magnesium−dependent protein serine/threo... GO:0005963 p=2.8E−03 n=3 fg=0.04 bg=0.00
nucleoplasm GO:0005654 p=3.1E−03 n=34 fg=0.41 bg=0.27
protein phosphatase type 2A complex GO:0000159 p=1.9E−02 n=2 fg=0.02 bg=0.00
endoplasmic reticulum membrane GO:0005789 p=2.0E−02 n=12 fg=0.15 bg=0.08
nuclear outer membrane−endoplasmic retic... GO:0042175 p=2.2E−02 n=12 fg=0.15 bg=0.08
endoplasmic reticulum subcompartment GO:0098827 p=2.6E−02 n=12 fg=0.15 bg=0.08
I band GO:0031674 p=2.7E−02 n=4 fg=0.05 bg=0.01
apicolateral plasma membrane GO:0016327 p=3.7E−02 n=2 fg=0.02 bg=0.00
transverse filament GO:0000802 p=4.5E−02 n=1 fg=0.01 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=4.5E−02 n=1 fg=0.01 bg=0.00
spectrosome GO:0045170 p=4.5E−02 n=1 fg=0.01 bg=0.00
internode region of axon GO:0033269 p=4.5E−02 n=1 fg=0.01 bg=0.00
anterior cell cortex GO:0061802 p=4.5E−02 n=1 fg=0.01 bg=0.00
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Schmidt−Lanterman incisure GO:0043220 p=4.5E−02 n=1 fg=0.01 bg=0.00
nucleolar ribonuclease P complex GO:0005655 p=4.5E−02 n=1 fg=0.01 bg=0.00
AP−4 adaptor complex GO:0030124 p=4.5E−02 n=1 fg=0.01 bg=0.00
cuticular plate GO:0032437 p=4.5E−02 n=1 fg=0.01 bg=0.00
compact myelin GO:0043218 p=4.5E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200 p=4.5E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted vesicle GO:0060198 p=4.5E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061202 p=4.5E−02 n=1 fg=0.01 bg=0.00
ESCRT II complex GO:0000814 p=4.5E−02 n=1 fg=0.01 bg=0.00
sno(s)RNA−containing ribonucleoprotein c... GO:0005732 p=4.5E−02 n=1 fg=0.01 bg=0.00
calcineurin complex GO:0005955 p=4.5E−02 n=1 fg=0.01 bg=0.00
ribonuclease MRP complex GO:0000172 p=4.5E−02 n=1 fg=0.01 bg=0.00
azurophil granule membrane GO:0035577 p=4.8E−02 n=2 fg=0.02 bg=0.00
clathrin−coated vesicle GO:0030136 p=5.4E−02 n=4 fg=0.05 bg=0.02
endocytic vesicle GO:0030139 p=5.8E−02 n=5 fg=0.06 bg=0.03
trans−Golgi network transport vesicle GO:0030140 p=5.9E−02 n=2 fg=0.02 bg=0.01
0 1 2 3 4 5
−log(p)
n=82/296 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction