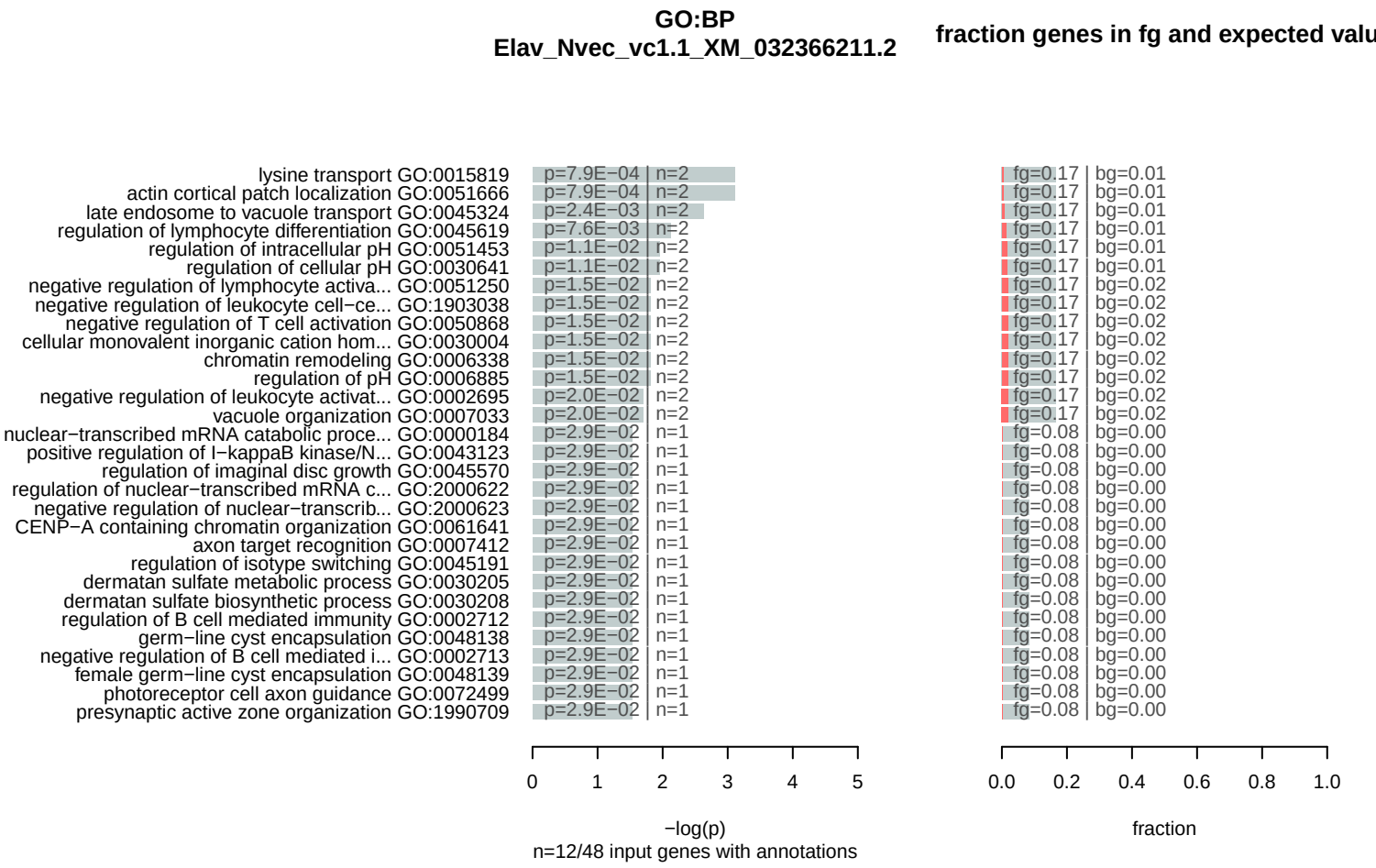
GO:BP
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fraction genes in fg and expected valu
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regulation of intracellular pH GO:0051453 p=1.1E−02 n=2 fg=0.17 bg=0.01
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negative regulation of lymphocyte activa... GO:0051250 p=1.5E−02 n=2 fg=0.17 bg=0.02
negative regulation of leukocyte cell−ce... GO:1903038 p=1.5E−02 n=2 fg=0.17 bg=0.02
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chromatin remodeling GO:0006338 p=1.5E−02 n=2 fg=0.17 bg=0.02
regulation of pH GO:0006885 p=1.5E−02 n=2 fg=0.17 bg=0.02
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vacuole organization GO:0007033 p=2.0E−02 n=2 fg=0.17 bg=0.02
nuclear−transcribed mRNA catabolic proce... GO:0000184 p=2.9E−02 n=1 fg=0.08 bg=0.00
positive regulation of I−kappaB kinase/N... GO:0043123 p=2.9E−02 n=1 fg=0.08 bg=0.00
regulation of imaginal disc growth GO:0045570 p=2.9E−02 n=1 fg=0.08 bg=0.00
regulation of nuclear−transcribed mRNA c... GO:2000622 p=2.9E−02 n=1 fg=0.08 bg=0.00
negative regulation of nuclear−transcrib... GO:2000623 p=2.9E−02 n=1 fg=0.08 bg=0.00
CENP−A containing chromatin organization GO:0061641 p=2.9E−02 n=1 fg=0.08 bg=0.00
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regulation of B cell mediated immunity GO:0002712 p=2.9E−02 n=1 fg=0.08 bg=0.00
germ−line cyst encapsulation GO:0048138 p=2.9E−02 n=1 fg=0.08 bg=0.00
negative regulation of B cell mediated i... GO:0002713 p=2.9E−02 n=1 fg=0.08 bg=0.00
female germ−line cyst encapsulation GO:0048139 p=2.9E−02 n=1 fg=0.08 bg=0.00
photoreceptor cell axon guidance GO:0072499 p=2.9E−02 n=1 fg=0.08 bg=0.00
presynaptic active zone organization GO:1990709 p=2.9E−02 n=1 fg=0.08 bg=0.00
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−log(p)
n=12/48 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032366211.2
fraction genes in fg and expected valu
phosphatidylinositol−4,5−bisphosphate bi... GO:0005546 p=9.6E−03 n=2 fg=0.20 bg=0.02
NADP binding GO:0050661 p=2.8E−02 n=1 fg=0.10 bg=0.00
ankyrin binding GO:0030506 p=2.8E−02 n=1 fg=0.10 bg=0.00
chondroitin−glucuronate 5−epimerase acti... GO:0047757 p=2.8E−02 n=1 fg=0.10 bg=0.00
racemase and epimerase activity GO:0016854 p=2.8E−02 n=1 fg=0.10 bg=0.00
racemase and epimerase activity, acting ... GO:0016857 p=2.8E−02 n=1 fg=0.10 bg=0.00
electron transfer activity GO:0009055 p=2.8E−02 n=1 fg=0.10 bg=0.00
1−phosphatidylinositol binding GO:0005545 p=2.8E−02 n=1 fg=0.10 bg=0.00
malic enzyme activity GO:0004470 p=2.8E−02 n=1 fg=0.10 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004471 p=2.8E−02 n=1 fg=0.10 bg=0.00
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WW domain binding GO:0050699 p=2.8E−02 n=1 fg=0.10 bg=0.00
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oxidoreductase activity, acting on CH−OH... GO:0016614 p=2.8E−02 n=1 fg=0.10 bg=0.00
malate dehydrogenase activity GO:0016615 p=2.8E−02 n=1 fg=0.10 bg=0.00
oxidoreductase activity, acting on the C... GO:0016616 p=2.8E−02 n=1 fg=0.10 bg=0.00
NAD binding GO:0051287 p=2.8E−02 n=1 fg=0.10 bg=0.00
inositol 1,3,4,5 tetrakisphosphate bindi... GO:0043533 p=2.8E−02 n=1 fg=0.10 bg=0.00
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transition metal ion binding GO:0046914 p=5.9E−02 n=2 fg=0.20 bg=0.04
small molecule binding GO:0036094 p=8.0E−02 n=3 fg=0.30 bg=0.11
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adenyl ribonucleotide binding GO:0032559 p=9.0E−02 n=2 fg=0.20 bg=0.05
adenyl nucleotide binding GO:0030554 p=9.9E−02 n=2 fg=0.20 bg=0.06
alcohol binding GO:0043178 p=1.1E−01 n=1 fg=0.10 bg=0.01
isomerase activity GO:0016853 p=1.1E−01 n=1 fg=0.10 bg=0.01
ribonucleotide binding GO:0032553 p=1.3E−01 n=2 fg=0.20 bg=0.06
purine ribonucleotide binding GO:0032555 p=1.3E−01 n=2 fg=0.20 bg=0.06
SNARE binding GO:0000149 p=1.3E−01 n=1 fg=0.10 bg=0.01
0 1 2 3 4 5
−log(p)
n=10/48 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032366211.2
fraction genes in fg and expected valu
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fungal−type vacuole membrane GO:0000329 p=2.4E−03 n=2 fg=0.17 bg=0.01
cell division site GO:0032153 p=7.8E−03 n=2 fg=0.17 bg=0.01
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integral component of organelle membrane GO:0031301 p=1.3E−02 n=3 fg=0.25 bg=0.05
chromosomal region GO:0098687 p=1.6E−02 n=2 fg=0.17 bg=0.02
intrinsic component of Golgi membrane GO:0031228 p=3.0E−02 n=1 fg=0.08 bg=0.00
vesicle tethering complex GO:0099023 p=3.0E−02 n=1 fg=0.08 bg=0.00
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chromocenter GO:0010369 p=3.0E−02 n=1 fg=0.08 bg=0.00
spectrosome GO:0045170 p=3.0E−02 n=1 fg=0.08 bg=0.00
spectrin GO:0008091 p=3.0E−02 n=1 fg=0.08 bg=0.00
intrinsic component of endoplasmic retic... GO:0031227 p=3.9E−02 n=2 fg=0.17 bg=0.03
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apicolateral plasma membrane GO:0016327 p=5.9E−02 n=1 fg=0.08 bg=0.01
M band GO:0031430 p=5.9E−02 n=1 fg=0.08 bg=0.01
cortical actin cytoskeleton GO:0030864 p=5.9E−02 n=1 fg=0.08 bg=0.01
ATPase complex GO:1904949 p=5.9E−02 n=1 fg=0.08 bg=0.01
fusome GO:0045169 p=5.9E−02 n=1 fg=0.08 bg=0.01
SWI/SNF superfamily−type complex GO:0070603 p=5.9E−02 n=1 fg=0.08 bg=0.01
polytene chromosome interband GO:0005705 p=5.9E−02 n=1 fg=0.08 bg=0.01
ubiquitin ligase complex GO:0000151 p=6.9E−02 n=2 fg=0.17 bg=0.04
organelle subcompartment GO:0031984 p=7.5E−02 n=4 fg=0.33 bg=0.14
cell cortex GO:0005938 p=8.7E−02 n=2 fg=0.17 bg=0.04
cortical cytoskeleton GO:0030863 p=8.7E−02 n=1 fg=0.08 bg=0.01
A band GO:0031672 p=8.7E−02 n=1 fg=0.08 bg=0.01
0 1 2 3 4 5
−log(p)
n=12/48 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction