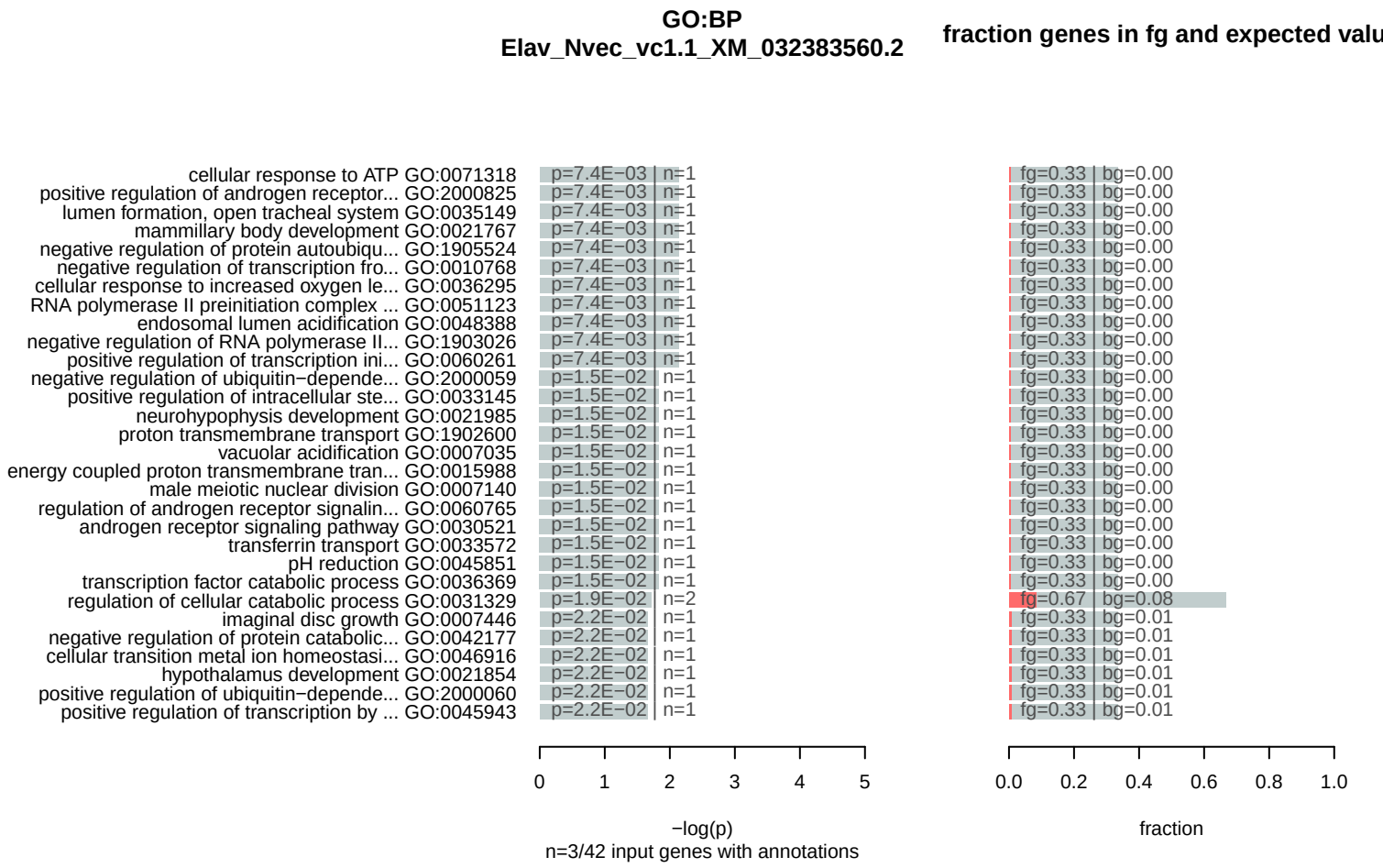
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fraction genes in fg and expected valu
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positive regulation of androgen receptor... GO:2000825 p=7.4E−03 n=1 fg=0.33 bg=0.00
lumen formation, open tracheal system GO:0035149 p=7.4E−03 n=1 fg=0.33 bg=0.00
mammillary body development GO:0021767 p=7.4E−03 n=1 fg=0.33 bg=0.00
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negative regulation of transcription fro... GO:0010768 p=7.4E−03 n=1 fg=0.33 bg=0.00
cellular response to increased oxygen le... GO:0036295 p=7.4E−03 n=1 fg=0.33 bg=0.00
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positive regulation of transcription ini... GO:0060261 p=7.4E−03 n=1 fg=0.33 bg=0.00
negative regulation of ubiquitin−depende... GO:2000059 p=1.5E−02 n=1 fg=0.33 bg=0.00
positive regulation of intracellular ste... GO:0033145 p=1.5E−02 n=1 fg=0.33 bg=0.00
neurohypophysis development GO:0021985 p=1.5E−02 n=1 fg=0.33 bg=0.00
proton transmembrane transport GO:1902600 p=1.5E−02 n=1 fg=0.33 bg=0.00
vacuolar acidification GO:0007035 p=1.5E−02 n=1 fg=0.33 bg=0.00
energy coupled proton transmembrane tran... GO:0015988 p=1.5E−02 n=1 fg=0.33 bg=0.00
male meiotic nuclear division GO:0007140 p=1.5E−02 n=1 fg=0.33 bg=0.00
regulation of androgen receptor signalin... GO:0060765 p=1.5E−02 n=1 fg=0.33 bg=0.00
androgen receptor signaling pathway GO:0030521 p=1.5E−02 n=1 fg=0.33 bg=0.00
transferrin transport GO:0033572 p=1.5E−02 n=1 fg=0.33 bg=0.00
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transcription factor catabolic process GO:0036369 p=1.5E−02 n=1 fg=0.33 bg=0.00
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imaginal disc growth GO:0007446 p=2.2E−02 n=1 fg=0.33 bg=0.01
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hypothalamus development GO:0021854 p=2.2E−02 n=1 fg=0.33 bg=0.01
positive regulation of ubiquitin−depende... GO:2000060 p=2.2E−02 n=1 fg=0.33 bg=0.01
positive regulation of transcription by ... GO:0045943 p=2.2E−02 n=1 fg=0.33 bg=0.01
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n=3/42 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032383560.2
fraction genes in fg and expected valu
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lysine−acetylated histone binding GO:0070577 p=8.2E−03 n=1 fg=0.33 bg=0.00
ATPase activity, coupled to transmembran... GO:0044769 p=1.6E−02 n=1 fg=0.33 bg=0.01
histone acetyltransferase activity GO:0004402 p=1.6E−02 n=1 fg=0.33 bg=0.01
proton−transporting ATPase activity, rot... GO:0046961 p=1.6E−02 n=1 fg=0.33 bg=0.01
proton transmembrane transporter activit... GO:0015078 p=1.6E−02 n=1 fg=0.33 bg=0.01
pyrophosphate hydrolysis−driven proton t... GO:0009678 p=1.6E−02 n=1 fg=0.33 bg=0.01
peptide−lysine−N−acetyltransferase activ... GO:0061733 p=1.6E−02 n=1 fg=0.33 bg=0.01
peptide N−acetyltransferase activity GO:0034212 p=1.6E−02 n=1 fg=0.33 bg=0.01
N−acyltransferase activity GO:0016410 p=2.5E−02 n=1 fg=0.33 bg=0.01
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RNA polymerase II−specific DNA−binding t... GO:0061629 p=4.1E−02 n=1 fg=0.33 bg=0.01
acetyltransferase activity GO:0016407 p=4.1E−02 n=1 fg=0.33 bg=0.01
ubiquitin−like protein conjugating enzym... GO:0061650 p=4.1E−02 n=1 fg=0.33 bg=0.01
ubiquitin conjugating enzyme activity GO:0061631 p=4.1E−02 n=1 fg=0.33 bg=0.01
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core promoter sequence−specific DNA bind... GO:0001046 p=4.9E−02 n=1 fg=0.33 bg=0.02
DNA−binding transcription factor binding GO:0140297 p=4.9E−02 n=1 fg=0.33 bg=0.02
ATPase−coupled ion transmembrane transpo... GO:0042625 p=4.9E−02 n=1 fg=0.33 bg=0.02
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DNA binding GO:0003677 p=5.1E−02 n=2 fg=0.67 bg=0.14
primary active transmembrane transporter... GO:0015399 p=5.7E−02 n=1 fg=0.33 bg=0.02
acyltransferase activity GO:0016746 p=5.7E−02 n=1 fg=0.33 bg=0.02
acyltransferase activity, transferring g... GO:0016747 p=5.7E−02 n=1 fg=0.33 bg=0.02
ATPase−coupled transmembrane transporter... GO:0042626 p=5.7E−02 n=1 fg=0.33 bg=0.02
DNA−binding transcription factor activit... GO:0003700 p=7.0E−02 n=2 fg=0.67 bg=0.16
nucleic acid binding GO:0003676 p=8.6E−02 n=2 fg=0.67 bg=0.18
active ion transmembrane transporter act... GO:0022853 p=8.8E−02 n=1 fg=0.33 bg=0.03
0 1 2 3 4 5
−log(p)
n=3/42 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032383560.2
fraction genes in fg and expected valu
vacuolar proton−transporting V−type ATPa... GO:0000221 p=5.0E−03 n=1 fg=0.50 bg=0.00
pronucleus GO:0045120 p=5.0E−03 n=1 fg=0.50 bg=0.00
transcription factor TFIID complex GO:0005669 p=5.0E−03 n=1 fg=0.50 bg=0.00
MLL1 complex GO:0071339 p=9.9E−03 n=1 fg=0.50 bg=0.01
plasma membrane proton−transporting V−ty... GO:0033181 p=9.9E−03 n=1 fg=0.50 bg=0.01
microvillus GO:0005902 p=1.5E−02 n=1 fg=0.50 bg=0.01
lysosomal membrane GO:0005765 p=3.0E−02 n=1 fg=0.50 bg=0.01
myelin sheath GO:0043209 p=3.0E−02 n=1 fg=0.50 bg=0.01
actin−based cell projection GO:0098858 p=4.0E−02 n=1 fg=0.50 bg=0.02
lytic vacuole membrane GO:0098852 p=4.4E−02 n=1 fg=0.50 bg=0.02
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chromatin GO:0000785 p=9.7E−02 n=1 fg=0.50 bg=0.05
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plasma membrane region GO:0098590 p=2.7E−01 n=1 fg=0.50 bg=0.14
plasma membrane bounded cell projection GO:0120025 p=4.2E−01 n=1 fg=0.50 bg=0.24
cell projection GO:0042995 p=4.2E−01 n=1 fg=0.50 bg=0.24
intracellular non−membrane−bounded organ... GO:0043232 p=4.7E−01 n=1 fg=0.50 bg=0.27
non−membrane−bounded organelle GO:0043228 p=4.7E−01 n=1 fg=0.50 bg=0.27
cytosol GO:0005829 p=5.8E−01 n=1 fg=0.50 bg=0.35
protein−containing complex GO:0032991 p=1.0E+00 n=2 fg=1.00 bg=0.34
organelle lumen GO:0043233 p=1.0E+00 n=1 fg=0.50 bg=0.32
transferase complex, transferring phosph... GO:0061695 p=1.0E+00 n=1 fg=0.50 bg=0.01
RNA polymerase complex GO:0030880 p=1.0E+00 n=1 fg=0.50 bg=0.01
RNA polymerase II, holoenzyme GO:0016591 p=1.0E+00 n=1 fg=0.50 bg=0.01
intracellular organelle lumen GO:0070013 p=1.0E+00 n=1 fg=0.50 bg=0.32
catalytic complex GO:1902494 p=1.0E+00 n=1 fg=0.50 bg=0.09
0 1 2 3 4 5
−log(p)
n=2/42 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction