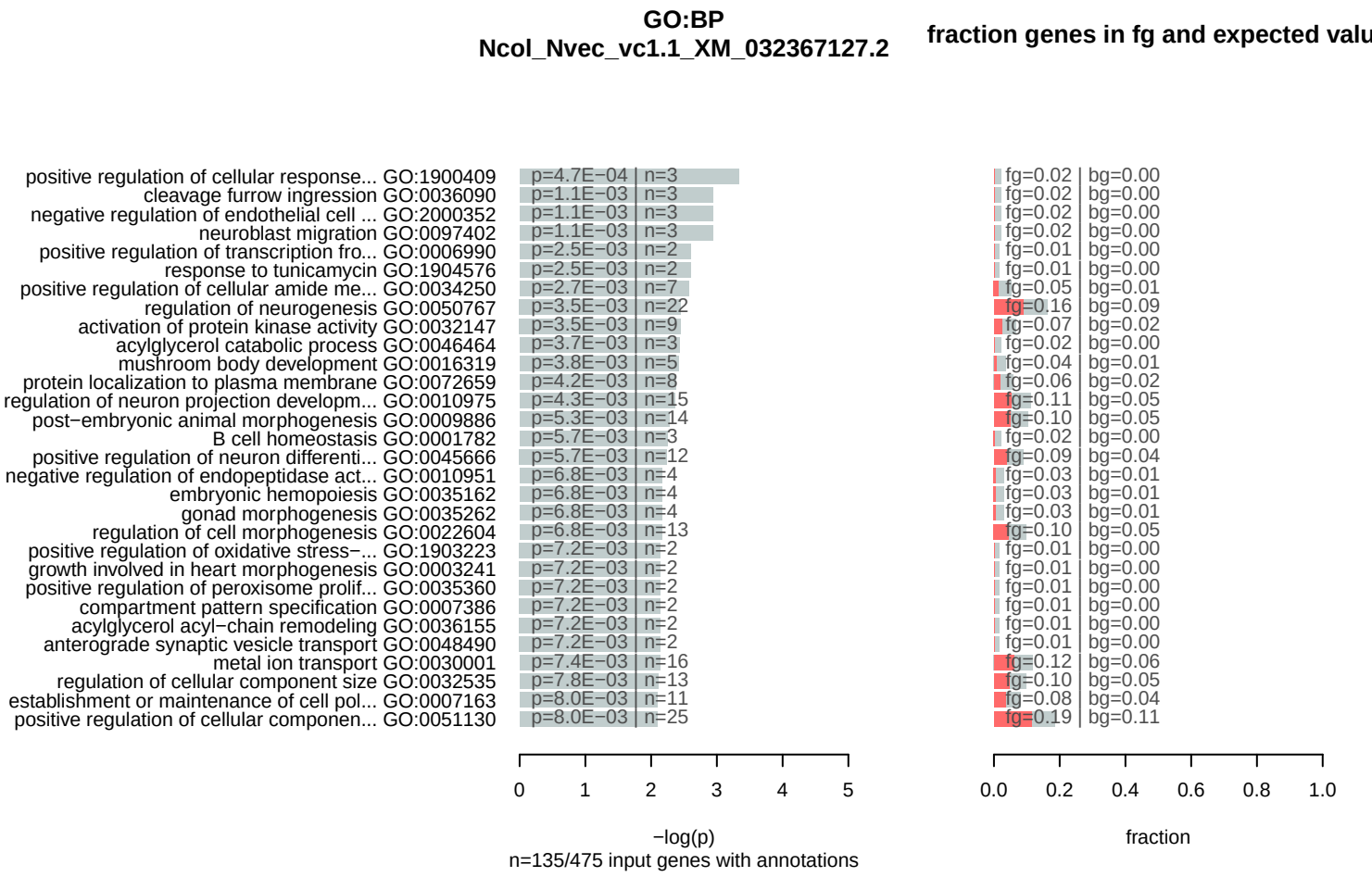
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Ncol_Nvec_vc1.1_XM_032367127.2
fraction genes in fg and expected valu
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cleavage furrow ingression GO:0036090 p=1.1E−03 n=3 fg=0.02 bg=0.00
negative regulation of endothelial cell ... GO:2000352 p=1.1E−03 n=3 fg=0.02 bg=0.00
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positive regulation of transcription fro... GO:0006990 p=2.5E−03 n=2 fg=0.01 bg=0.00
response to tunicamycin GO:1904576 p=2.5E−03 n=2 fg=0.01 bg=0.00
positive regulation of cellular amide me... GO:0034250 p=2.7E−03 n=7 fg=0.05 bg=0.01
regulation of neurogenesis GO:0050767 p=3.5E−03 n=22 fg=0.16 bg=0.09
activation of protein kinase activity GO:0032147 p=3.5E−03 n=9 fg=0.07 bg=0.02
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protein localization to plasma membrane GO:0072659 p=4.2E−03 n=8 fg=0.06 bg=0.02
regulation of neuron projection developm... GO:0010975 p=4.3E−03 n=15 fg=0.11 bg=0.05
post−embryonic animal morphogenesis GO:0009886 p=5.3E−03 n=14 fg=0.10 bg=0.05
B cell homeostasis GO:0001782 p=5.7E−03 n=3 fg=0.02 bg=0.00
positive regulation of neuron differenti... GO:0045666 p=5.7E−03 n=12 fg=0.09 bg=0.04
negative regulation of endopeptidase act... GO:0010951 p=6.8E−03 n=4 fg=0.03 bg=0.01
embryonic hemopoiesis GO:0035162 p=6.8E−03 n=4 fg=0.03 bg=0.01
gonad morphogenesis GO:0035262 p=6.8E−03 n=4 fg=0.03 bg=0.01
regulation of cell morphogenesis GO:0022604 p=6.8E−03 n=13 fg=0.10 bg=0.05
positive regulation of oxidative stress−... GO:1903223 p=7.2E−03 n=2 fg=0.01 bg=0.00
growth involved in heart morphogenesis GO:0003241 p=7.2E−03 n=2 fg=0.01 bg=0.00
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compartment pattern specification GO:0007386 p=7.2E−03 n=2 fg=0.01 bg=0.00
acylglycerol acyl−chain remodeling GO:0036155 p=7.2E−03 n=2 fg=0.01 bg=0.00
anterograde synaptic vesicle transport GO:0048490 p=7.2E−03 n=2 fg=0.01 bg=0.00
metal ion transport GO:0030001 p=7.4E−03 n=16 fg=0.12 bg=0.06
regulation of cellular component size GO:0032535 p=7.8E−03 n=13 fg=0.10 bg=0.05
establishment or maintenance of cell pol... GO:0007163 p=8.0E−03 n=11 fg=0.08 bg=0.04
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n=135/475 input genes with annotations
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fraction
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fraction genes in fg and expected valu
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ion channel regulator activity GO:0099106 p=4.8E−03 n=6 fg=0.05 bg=0.01
mRNA 3'−UTR binding GO:0003730 p=5.9E−03 n=4 fg=0.04 bg=0.01
triglyceride lipase activity GO:0004806 p=6.7E−03 n=2 fg=0.02 bg=0.00
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demethylase activity GO:0032451 p=1.7E−02 n=3 fg=0.03 bg=0.01
transcription regulator activity GO:0140110 p=1.9E−02 n=19 fg=0.17 bg=0.10
gated channel activity GO:0022836 p=1.9E−02 n=7 fg=0.06 bg=0.02
acetylcholine receptor binding GO:0033130 p=2.1E−02 n=2 fg=0.02 bg=0.00
arrestin family protein binding GO:1990763 p=2.1E−02 n=2 fg=0.02 bg=0.00
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protein domain specific binding GO:0019904 p=2.3E−02 n=16 fg=0.14 bg=0.08
DNA binding GO:0003677 p=2.4E−02 n=21 fg=0.18 bg=0.12
DNA−binding transcription factor activit... GO:0003700 p=2.7E−02 n=14 fg=0.12 bg=0.07
peptidase regulator activity GO:0061134 p=2.7E−02 n=3 fg=0.03 bg=0.01
calcium channel regulator activity GO:0005246 p=2.7E−02 n=3 fg=0.03 bg=0.01
mitogen−activated protein kinase kinase ... GO:0031434 p=3.0E−02 n=2 fg=0.02 bg=0.00
peptidase activator activity GO:0016504 p=4.1E−02 n=2 fg=0.02 bg=0.00
calcium−release channel activity GO:0015278 p=4.1E−02 n=2 fg=0.02 bg=0.00
insulin receptor binding GO:0005158 p=4.1E−02 n=2 fg=0.02 bg=0.00
ATPase binding GO:0051117 p=4.3E−02 n=4 fg=0.04 bg=0.01
enzyme inhibitor activity GO:0004857 p=4.3E−02 n=6 fg=0.05 bg=0.02
RNA polymerase II transcription regulato... GO:0000977 p=4.6E−02 n=9 fg=0.08 bg=0.04
ligand−gated channel activity GO:0022834 p=4.8E−02 n=4 fg=0.04 bg=0.01
ligand−gated ion channel activity GO:0015276 p=4.8E−02 n=4 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=114/475 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
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fraction genes in fg and expected valu
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COPII−coated ER to Golgi transport vesic... GO:0030134 p=6.0E−03 n=4 fg=0.03 bg=0.01
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transcription regulator complex GO:0005667 p=1.3E−02 n=11 fg=0.08 bg=0.04
subsynaptic reticulum GO:0071212 p=1.5E−02 n=2 fg=0.01 bg=0.00
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dendrite GO:0030425 p=2.0E−02 n=15 fg=0.11 bg=0.06
type I terminal bouton GO:0061174 p=2.1E−02 n=3 fg=0.02 bg=0.00
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endosome to plasma membrane transport ve... GO:0070381 p=5.2E−02 n=1 fg=0.01 bg=0.00
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amyloid−beta complex GO:0106003 p=5.2E−02 n=1 fg=0.01 bg=0.00
AP−3 adaptor complex GO:0030123 p=5.2E−02 n=1 fg=0.01 bg=0.00
histone pre−mRNA 3'end processing comple... GO:0071204 p=5.2E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=5.2E−02 n=1 fg=0.01 bg=0.00
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cyclin A1−CDK2 complex GO:0097123 p=5.2E−02 n=1 fg=0.01 bg=0.00
cyclin A2−CDK2 complex GO:0097124 p=5.2E−02 n=1 fg=0.01 bg=0.00
condensin complex GO:0000796 p=5.2E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=5.2E−02 n=1 fg=0.01 bg=0.00
steroid hormone aporeceptor complex GO:0005831 p=5.2E−02 n=1 fg=0.01 bg=0.00
ectoplasm GO:0043265 p=5.2E−02 n=1 fg=0.01 bg=0.00
single−stranded DNA−dependent ATP−depend... GO:0017117 p=5.2E−02 n=1 fg=0.01 bg=0.00
Sec61 translocon complex GO:0005784 p=5.2E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=140/475 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction