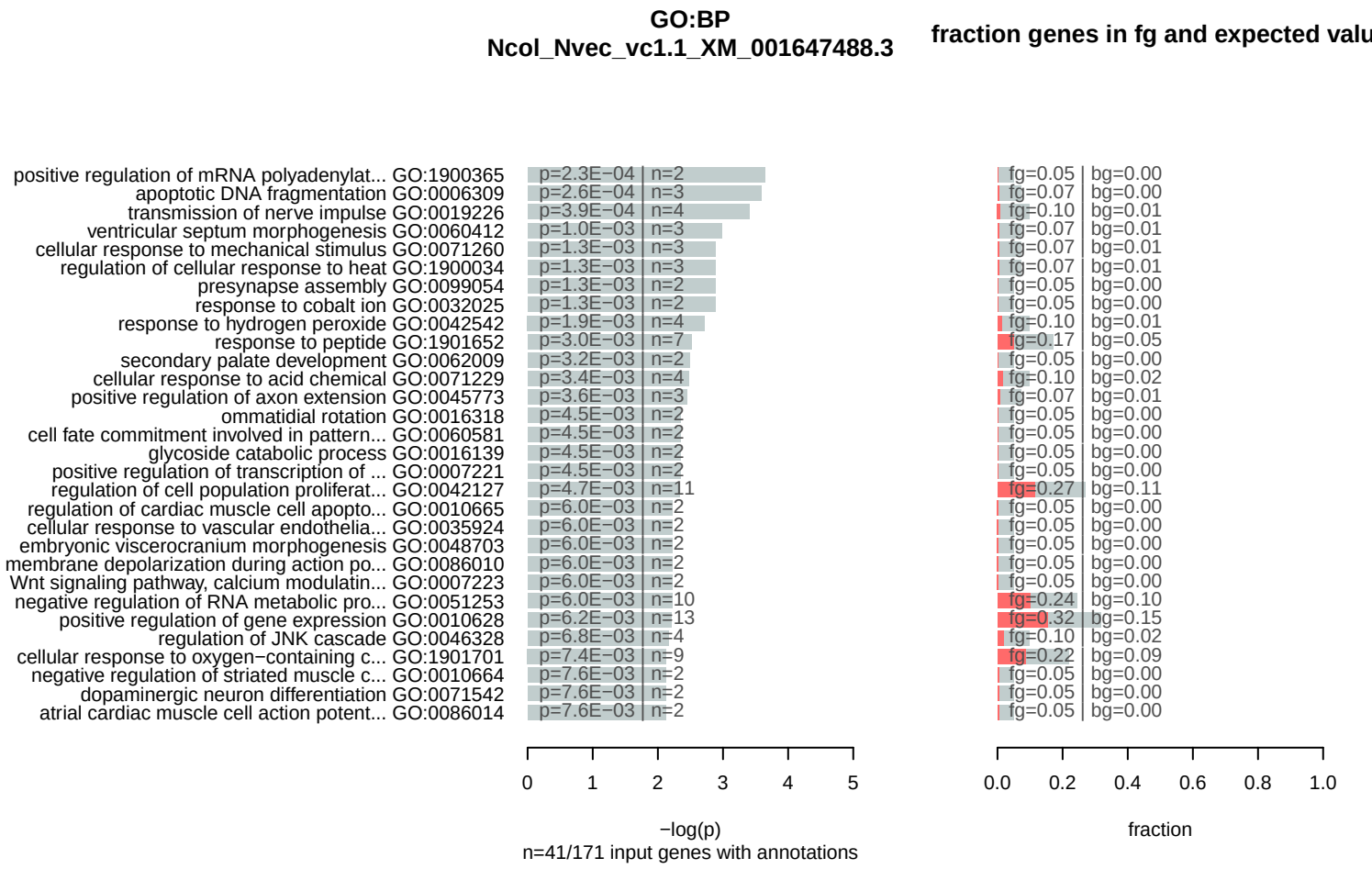
GO:BP
Ncol_Nvec_vc1.1_XM_001647488.3
fraction genes in fg and expected valu
positive regulation of mRNA polyadenylat... GO:1900365 p=2.3E−04 n=2 fg=0.05 bg=0.00
apoptotic DNA fragmentation GO:0006309 p=2.6E−04 n=3 fg=0.07 bg=0.00
transmission of nerve impulse GO:0019226 p=3.9E−04 n=4 fg=0.10 bg=0.01
ventricular septum morphogenesis GO:0060412 p=1.0E−03 n=3 fg=0.07 bg=0.01
cellular response to mechanical stimulus GO:0071260 p=1.3E−03 n=3 fg=0.07 bg=0.01
regulation of cellular response to heat GO:1900034 p=1.3E−03 n=3 fg=0.07 bg=0.01
presynapse assembly GO:0099054 p=1.3E−03 n=2 fg=0.05 bg=0.00
response to cobalt ion GO:0032025 p=1.3E−03 n=2 fg=0.05 bg=0.00
response to hydrogen peroxide GO:0042542 p=1.9E−03 n=4 fg=0.10 bg=0.01
response to peptide GO:1901652 p=3.0E−03 n=7 fg=0.17 bg=0.05
secondary palate development GO:0062009 p=3.2E−03 n=2 fg=0.05 bg=0.00
cellular response to acid chemical GO:0071229 p=3.4E−03 n=4 fg=0.10 bg=0.02
positive regulation of axon extension GO:0045773 p=3.6E−03 n=3 fg=0.07 bg=0.01
ommatidial rotation GO:0016318 p=4.5E−03 n=2 fg=0.05 bg=0.00
cell fate commitment involved in pattern... GO:0060581 p=4.5E−03 n=2 fg=0.05 bg=0.00
glycoside catabolic process GO:0016139 p=4.5E−03 n=2 fg=0.05 bg=0.00
positive regulation of transcription of ... GO:0007221 p=4.5E−03 n=2 fg=0.05 bg=0.00
regulation of cell population proliferat... GO:0042127 p=4.7E−03 n=11 fg=0.27 bg=0.11
regulation of cardiac muscle cell apopto... GO:0010665 p=6.0E−03 n=2 fg=0.05 bg=0.00
cellular response to vascular endothelia... GO:0035924 p=6.0E−03 n=2 fg=0.05 bg=0.00
embryonic viscerocranium morphogenesis GO:0048703 p=6.0E−03 n=2 fg=0.05 bg=0.00
membrane depolarization during action po... GO:0086010 p=6.0E−03 n=2 fg=0.05 bg=0.00
Wnt signaling pathway, calcium modulatin... GO:0007223 p=6.0E−03 n=2 fg=0.05 bg=0.00
negative regulation of RNA metabolic pro... GO:0051253 p=6.0E−03 n=10 fg=0.24 bg=0.10
positive regulation of gene expression GO:0010628 p=6.2E−03 n=13 fg=0.32 bg=0.15
regulation of JNK cascade GO:0046328 p=6.8E−03 n=4 fg=0.10 bg=0.02
cellular response to oxygen−containing c... GO:1901701 p=7.4E−03 n=9 fg=0.22 bg=0.09
negative regulation of striated muscle c... GO:0010664 p=7.6E−03 n=2 fg=0.05 bg=0.00
dopaminergic neuron differentiation GO:0071542 p=7.6E−03 n=2 fg=0.05 bg=0.00
atrial cardiac muscle cell action potent... GO:0086014 p=7.6E−03 n=2 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=41/171 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001647488.3
fraction genes in fg and expected valu
voltage−gated cation channel activity GO:0022843 p=3.4E−04 n=4 fg=0.11 bg=0.01
pre−mRNA binding GO:0036002 p=8.4E−03 n=2 fg=0.05 bg=0.00
frizzled binding GO:0005109 p=1.0E−02 n=2 fg=0.05 bg=0.00
voltage−gated calcium channel activity GO:0005245 p=1.0E−02 n=2 fg=0.05 bg=0.00
ion gated channel activity GO:0022839 p=1.1E−02 n=4 fg=0.11 bg=0.02
protein kinase C binding GO:0005080 p=1.5E−02 n=2 fg=0.05 bg=0.01
estradiol 17−beta−dehydrogenase activity GO:0004303 p=1.6E−02 n=1 fg=0.03 bg=0.00
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323 p=1.6E−02 n=1 fg=0.03 bg=0.00
aminomethyltransferase activity GO:0004047 p=1.6E−02 n=1 fg=0.03 bg=0.00
histone pre−mRNA stem−loop binding GO:0071207 p=1.6E−02 n=1 fg=0.03 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=1.6E−02 n=1 fg=0.03 bg=0.00
phospholipase A2 activator activity GO:0016005 p=1.6E−02 n=1 fg=0.03 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004486 p=1.6E−02 n=1 fg=0.03 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004487 p=1.6E−02 n=1 fg=0.03 bg=0.00
methylenetetrahydrofolate dehydrogenase ... GO:0004488 p=1.6E−02 n=1 fg=0.03 bg=0.00
methenyltetrahydrofolate cyclohydrolase ... GO:0004477 p=1.6E−02 n=1 fg=0.03 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=1.6E−02 n=1 fg=0.03 bg=0.00
formate−tetrahydrofolate ligase activity GO:0004329 p=1.6E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=1.6E−02 n=1 fg=0.03 bg=0.00
V1A vasopressin receptor binding GO:0031894 p=1.6E−02 n=1 fg=0.03 bg=0.00
steroid dehydrogenase activity, acting o... GO:0033764 p=1.6E−02 n=1 fg=0.03 bg=0.00
protein homodimerization activity GO:0042803 p=2.6E−02 n=8 fg=0.21 bg=0.10
G protein−coupled receptor binding GO:0001664 p=2.7E−02 n=3 fg=0.08 bg=0.02
mRNA binding GO:0003729 p=3.0E−02 n=4 fg=0.11 bg=0.03
transmembrane signaling receptor activit... GO:0004888 p=3.2E−02 n=4 fg=0.11 bg=0.03
STAT family protein binding GO:0097677 p=3.2E−02 n=1 fg=0.03 bg=0.00
chloride ion binding GO:0031404 p=3.2E−02 n=1 fg=0.03 bg=0.00
nicotinate transmembrane transporter act... GO:0090416 p=3.2E−02 n=1 fg=0.03 bg=0.00
beta−glucosidase activity GO:0008422 p=3.2E−02 n=1 fg=0.03 bg=0.00
urate transmembrane transporter activity GO:0015143 p=3.2E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=38/171 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001647488.3
fraction genes in fg and expected valu
death−inducing signaling complex GO:0031264 p=1.6E−02 n=1 fg=0.02 bg=0.00
histone pre−mRNA 3'end processing comple... GO:0071204 p=1.6E−02 n=1 fg=0.02 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=1.6E−02 n=1 fg=0.02 bg=0.00
paraspeckles GO:0042382 p=1.6E−02 n=1 fg=0.02 bg=0.00
NLS−dependent protein nuclear import com... GO:0042564 p=1.6E−02 n=1 fg=0.02 bg=0.00
euchromatin GO:0000791 p=2.2E−02 n=2 fg=0.05 bg=0.01
Wnt signalosome GO:1990909 p=3.1E−02 n=1 fg=0.02 bg=0.00
glycine cleavage complex GO:0005960 p=3.1E−02 n=1 fg=0.02 bg=0.00
Lsm1−7−Pat1 complex GO:1990726 p=3.1E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=3.1E−02 n=1 fg=0.02 bg=0.00
nucleocytoplasmic transport complex GO:0031074 p=3.1E−02 n=1 fg=0.02 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=3.1E−02 n=1 fg=0.02 bg=0.00
mitochondrial alpha−ketoglutarate dehydr... GO:0005947 p=3.1E−02 n=1 fg=0.02 bg=0.00
nuclear body GO:0016604 p=3.9E−02 n=6 fg=0.14 bg=0.06
nuclear speck GO:0016607 p=4.0E−02 n=4 fg=0.10 bg=0.03
RNA N6−methyladenosine methyltransferase... GO:0036396 p=4.6E−02 n=1 fg=0.02 bg=0.00
mitochondrial crista GO:0030061 p=4.6E−02 n=1 fg=0.02 bg=0.00
mitochondrial tricarboxylic acid cycle e... GO:0030062 p=4.6E−02 n=1 fg=0.02 bg=0.00
tricarboxylic acid cycle enzyme complex GO:0045239 p=4.6E−02 n=1 fg=0.02 bg=0.00
RSC−type complex GO:0016586 p=4.6E−02 n=1 fg=0.02 bg=0.00
mRNA editing complex GO:0045293 p=4.6E−02 n=1 fg=0.02 bg=0.00
mRNA cap binding complex GO:0005845 p=4.6E−02 n=1 fg=0.02 bg=0.00
integral component of plasma membrane GO:0005887 p=4.9E−02 n=6 fg=0.14 bg=0.06
heterochromatin GO:0000792 p=5.3E−02 n=2 fg=0.05 bg=0.01
Sm−like protein family complex GO:0120114 p=5.7E−02 n=2 fg=0.05 bg=0.01
cation channel complex GO:0034703 p=6.1E−02 n=2 fg=0.05 bg=0.01
RNA cap binding complex GO:0034518 p=6.1E−02 n=1 fg=0.02 bg=0.00
intrinsic component of mitochondrial out... GO:0031306 p=6.1E−02 n=1 fg=0.02 bg=0.00
integral component of mitochondrial oute... GO:0031307 p=6.1E−02 n=1 fg=0.02 bg=0.00
npBAF complex GO:0071564 p=6.1E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=42/171 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction