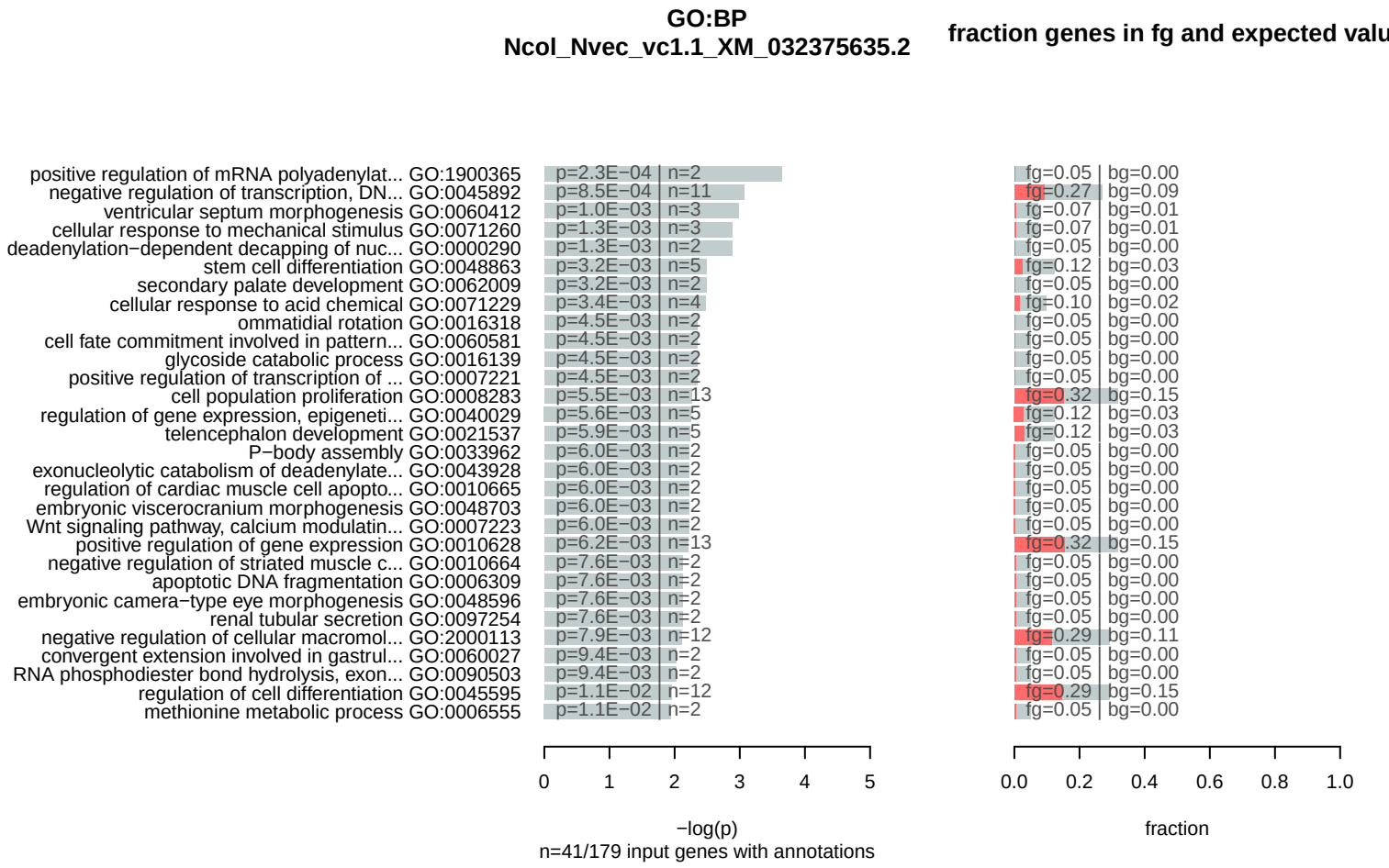
GO:BP
Ncol_Nvec_vc1.1_XM_032375635.2
fraction genes in fg and expected valu
positive regulation of mRNA polyadenylat... GO:1900365 p=2.3E−04 n=2 fg=0.05 bg=0.00
negative regulation of transcription, DN... GO:0045892 p=8.5E−04 n=11 fg=0.27 bg=0.09
ventricular septum morphogenesis GO:0060412 p=1.0E−03 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
deadenylation−dependent decapping of nuc... GO:0000290 p=1.3E−03 n=2 fg=0.05 bg=0.00
stem cell differentiation GO:0048863 p=3.2E−03 n=5 fg=0.12 bg=0.03
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
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
cell population proliferation GO:0008283 p=5.5E−03 n=13 fg=0.32 bg=0.15
regulation of gene expression, epigeneti... GO:0040029 p=5.6E−03 n=5 fg=0.12 bg=0.03
telencephalon development GO:0021537 p=5.9E−03 n=5 fg=0.12 bg=0.03
P−body assembly GO:0033962 p=6.0E−03 n=2 fg=0.05 bg=0.00
exonucleolytic catabolism of deadenylate... GO:0043928 p=6.0E−03 n=2 fg=0.05 bg=0.00
regulation of cardiac muscle cell apopto... GO:0010665 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
Wnt signaling pathway, calcium modulatin... GO:0007223 p=6.0E−03 n=2 fg=0.05 bg=0.00
positive regulation of gene expression GO:0010628 p=6.2E−03 n=13 fg=0.32 bg=0.15
negative regulation of striated muscle c... GO:0010664 p=7.6E−03 n=2 fg=0.05 bg=0.00
apoptotic DNA fragmentation GO:0006309 p=7.6E−03 n=2 fg=0.05 bg=0.00
embryonic camera−type eye morphogenesis GO:0048596 p=7.6E−03 n=2 fg=0.05 bg=0.00
renal tubular secretion GO:0097254 p=7.6E−03 n=2 fg=0.05 bg=0.00
negative regulation of cellular macromol... GO:2000113 p=7.9E−03 n=12 fg=0.29 bg=0.11
convergent extension involved in gastrul... GO:0060027 p=9.4E−03 n=2 fg=0.05 bg=0.00
RNA phosphodiester bond hydrolysis, exon... GO:0090503 p=9.4E−03 n=2 fg=0.05 bg=0.00
regulation of cell differentiation GO:0045595 p=1.1E−02 n=12 fg=0.29 bg=0.15
methionine metabolic process GO:0006555 p=1.1E−02 n=2 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=41/179 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032375635.2
fraction genes in fg and expected valu
NAD(P)+ transhydrogenase activity GO:0008746 p=2.6E−04 n=2 fg=0.05 bg=0.00
G protein−coupled receptor binding GO:0001664 p=4.1E−03 n=4 fg=0.10 bg=0.02
pre−mRNA binding GO:0036002 p=8.8E−03 n=2 fg=0.05 bg=0.00
3'−5'−exoribonuclease activity GO:0000175 p=8.8E−03 n=2 fg=0.05 bg=0.00
frizzled binding GO:0005109 p=1.1E−02 n=2 fg=0.05 bg=0.00
protein kinase C binding GO:0005080 p=1.6E−02 n=2 fg=0.05 bg=0.01
aminomethyltransferase activity GO:0004047 p=1.6E−02 n=1 fg=0.03 bg=0.00
NAD(P)+ transhydrogenase (B−specific) ac... GO:0003957 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
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
NAD(P)+ transhydrogenase (AB−specific) a... GO:0008750 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
protein homodimerization activity GO:0042803 p=3.0E−02 n=8 fg=0.21 bg=0.10
STAT family protein binding GO:0097677 p=3.3E−02 n=1 fg=0.03 bg=0.00
chloride ion binding GO:0031404 p=3.3E−02 n=1 fg=0.03 bg=0.00
nicotinate transmembrane transporter act... GO:0090416 p=3.3E−02 n=1 fg=0.03 bg=0.00
beta−glucosidase activity GO:0008422 p=3.3E−02 n=1 fg=0.03 bg=0.00
transcription corepressor binding GO:0001222 p=3.3E−02 n=1 fg=0.03 bg=0.00
urate transmembrane transporter activity GO:0015143 p=3.3E−02 n=1 fg=0.03 bg=0.00
U2 snRNP binding GO:1990447 p=3.3E−02 n=1 fg=0.03 bg=0.00
methionine adenosyltransferase activity GO:0004478 p=3.3E−02 n=1 fg=0.03 bg=0.00
sodium−independent organic anion transme... GO:0015347 p=3.3E−02 n=1 fg=0.03 bg=0.00
vasopressin receptor activity GO:0005000 p=3.3E−02 n=1 fg=0.03 bg=0.00
selenomethionine adenosyltransferase act... GO:0098601 p=3.3E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=39/179 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032375635.2
fraction genes in fg and expected valu
nuclear body GO:0016604 p=1.4E−02 n=7 fg=0.16 bg=0.06
histone pre−mRNA 3'end processing comple... GO:0071204 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cell part GO:0033643 p=1.6E−02 n=1 fg=0.02 bg=0.00
host intracellular part GO:0033646 p=1.6E−02 n=1 fg=0.02 bg=0.00
host intracellular organelle GO:0033647 p=1.6E−02 n=1 fg=0.02 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=1.6E−02 n=1 fg=0.02 bg=0.00
host intracellular region GO:0043656 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cell GO:0043657 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cell nuclear part GO:0044094 p=1.6E−02 n=1 fg=0.02 bg=0.00
other organism part GO:0044217 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cell nucleus GO:0042025 p=1.6E−02 n=1 fg=0.02 bg=0.00
host cellular component GO:0018995 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
host cell PML body GO:0075341 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
cytoplasmic microtubule GO:0005881 p=1.7E−02 n=2 fg=0.05 bg=0.00
supramolecular complex GO:0099080 p=1.8E−02 n=8 fg=0.19 bg=0.08
euchromatin GO:0000791 p=2.3E−02 n=2 fg=0.05 bg=0.01
CCR4−NOT core complex GO:0030015 p=3.2E−02 n=1 fg=0.02 bg=0.00
Wnt signalosome GO:1990909 p=3.2E−02 n=1 fg=0.02 bg=0.00
glycine cleavage complex GO:0005960 p=3.2E−02 n=1 fg=0.02 bg=0.00
Lsm1−7−Pat1 complex GO:1990726 p=3.2E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=3.2E−02 n=1 fg=0.02 bg=0.00
nucleocytoplasmic transport complex GO:0031074 p=3.2E−02 n=1 fg=0.02 bg=0.00
spindle microtubule GO:0005876 p=3.9E−02 n=2 fg=0.05 bg=0.01
microtubule GO:0005874 p=4.2E−02 n=3 fg=0.07 bg=0.02
nuclear speck GO:0016607 p=4.3E−02 n=4 fg=0.09 bg=0.03
P−body GO:0000932 p=4.3E−02 n=2 fg=0.05 bg=0.01
RNA N6−methyladenosine methyltransferase... GO:0036396 p=4.7E−02 n=1 fg=0.02 bg=0.00
RSC−type complex GO:0016586 p=4.7E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=43/179 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction