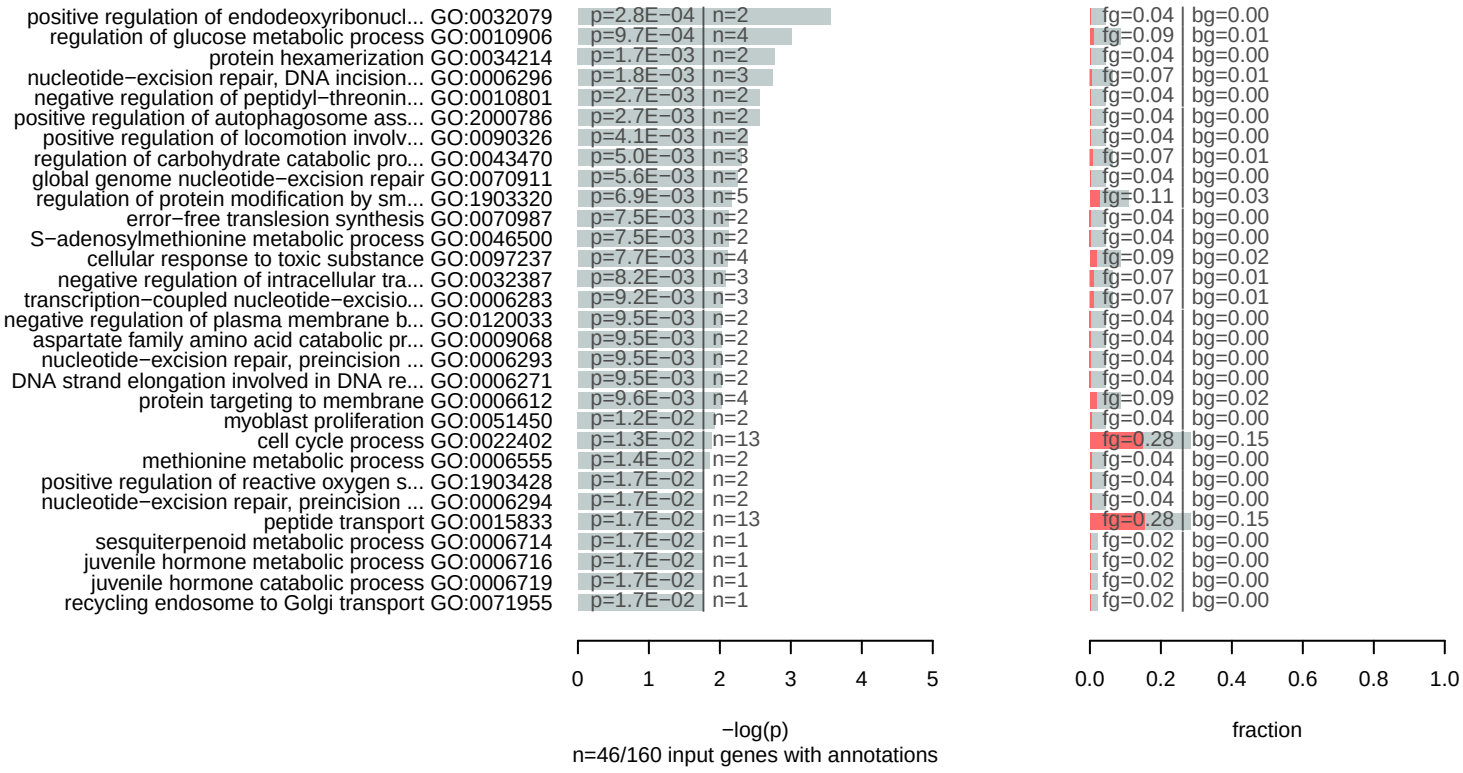
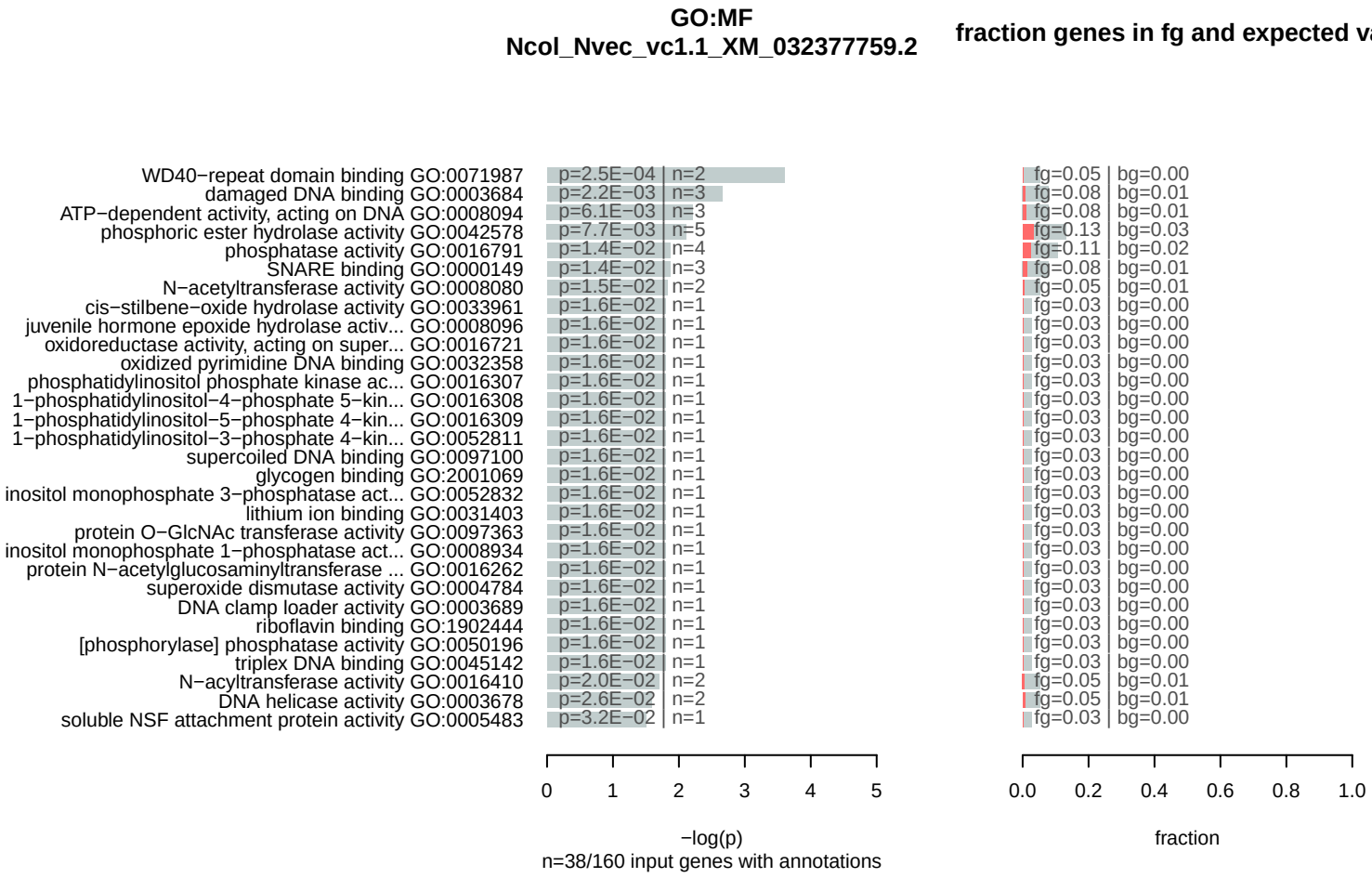

GO:BP
Ncol_Nvec_vc1.1_XM_032377759.2
fraction genes in fg and expected valu
positive regulation of endodeoxyribonucl... GO:0032079 p=2.8E−04 n=2 fg=0.04 bg=0.00
regulation of glucose metabolic process GO:0010906 p=9.7E−04 n=4 fg=0.09 bg=0.01
protein hexamerization GO:0034214 p=1.7E−03 n=2 fg=0.04 bg=0.00
nucleotide−excision repair, DNA incision... GO:0006296 p=1.8E−03 n=3 fg=0.07 bg=0.01
negative regulation of peptidyl−threonin... GO:0010801 p=2.7E−03 n=2 fg=0.04 bg=0.00
positive regulation of autophagosome ass... GO:2000786 p=2.7E−03 n=2 fg=0.04 bg=0.00
positive regulation of locomotion involv... GO:0090326 p=4.1E−03 n=2 fg=0.04 bg=0.00
regulation of carbohydrate catabolic pro... GO:0043470 p=5.0E−03 n=3 fg=0.07 bg=0.01
global genome nucleotide−excision repair GO:0070911 p=5.6E−03 n=2 fg=0.04 bg=0.00
regulation of protein modification by sm... GO:1903320 p=6.9E−03 n=5 fg=0.11 bg=0.03
error−free translesion synthesis GO:0070987 p=7.5E−03 n=2 fg=0.04 bg=0.00
S−adenosylmethionine metabolic process GO:0046500 p=7.5E−03 n=2 fg=0.04 bg=0.00
cellular response to toxic substance GO:0097237 p=7.7E−03 n=4 fg=0.09 bg=0.02
negative regulation of intracellular tra... GO:0032387 p=8.2E−03 n=3 fg=0.07 bg=0.01
transcription−coupled nucleotide−excisio... GO:0006283 p=9.2E−03 n=3 fg=0.07 bg=0.01
negative regulation of plasma membrane b... GO:0120033 p=9.5E−03 n=2 fg=0.04 bg=0.00
aspartate family amino acid catabolic pr... GO:0009068 p=9.5E−03 n=2 fg=0.04 bg=0.00
nucleotide−excision repair, preincision ... GO:0006293 p=9.5E−03 n=2 fg=0.04 bg=0.00
DNA strand elongation involved in DNA re... GO:0006271 p=9.5E−03 n=2 fg=0.04 bg=0.00
protein targeting to membrane GO:0006612 p=9.6E−03 n=4 fg=0.09 bg=0.02
myoblast proliferation GO:0051450 p=1.2E−02 n=2 fg=0.04 bg=0.00
cell cycle process GO:0022402 p=1.3E−02 n=13 fg=0.28 bg=0.15
methionine metabolic process GO:0006555 p=1.4E−02 n=2 fg=0.04 bg=0.00
positive regulation of reactive oxygen s... GO:1903428 p=1.7E−02 n=2 fg=0.04 bg=0.00
nucleotide−excision repair, preincision ... GO:0006294 p=1.7E−02 n=2 fg=0.04 bg=0.00
peptide transport GO:0015833 p=1.7E−02 n=13 fg=0.28 bg=0.15
sesquiterpenoid metabolic process GO:0006714 p=1.7E−02 n=1 fg=0.02 bg=0.00
juvenile hormone metabolic process GO:0006716 p=1.7E−02 n=1 fg=0.02 bg=0.00
juvenile hormone catabolic process GO:0006719 p=1.7E−02 n=1 fg=0.02 bg=0.00
recycling endosome to Golgi transport GO:0071955 p=1.7E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=46/160 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction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fraction genes in fg and expected valu
WD40−repeat domain binding GO:0071987 p=2.5E−04 n=2 fg=0.05 bg=0.00
damaged DNA binding GO:0003684 p=2.2E−03 n=3 fg=0.08 bg=0.01
ATP−dependent activity, acting on DNA GO:0008094 p=6.1E−03 n=3 fg=0.08 bg=0.01
phosphoric ester hydrolase activity GO:0042578 p=7.7E−03 n=5 fg=0.13 bg=0.03
phosphatase activity GO:0016791 p=1.4E−02 n=4 fg=0.11 bg=0.02
SNARE binding GO:0000149 p=1.4E−02 n=3 fg=0.08 bg=0.01
N−acetyltransferase activity GO:0008080 p=1.5E−02 n=2 fg=0.05 bg=0.01
cis−stilbene−oxide hydrolase activity GO:0033961 p=1.6E−02 n=1 fg=0.03 bg=0.00
juvenile hormone epoxide hydrolase activ... GO:0008096 p=1.6E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on super... GO:0016721 p=1.6E−02 n=1 fg=0.03 bg=0.00
oxidized pyrimidine DNA binding GO:0032358 p=1.6E−02 n=1 fg=0.03 bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307 p=1.6E−02 n=1 fg=0.03 bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=1.6E−02 n=1 fg=0.03 bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309 p=1.6E−02 n=1 fg=0.03 bg=0.00
1−phosphatidylinositol−3−phosphate 4−kin... GO:0052811 p=1.6E−02 n=1 fg=0.03 bg=0.00
supercoiled DNA binding GO:0097100 p=1.6E−02 n=1 fg=0.03 bg=0.00
glycogen binding GO:2001069 p=1.6E−02 n=1 fg=0.03 bg=0.00
inositol monophosphate 3−phosphatase act... GO:0052832 p=1.6E−02 n=1 fg=0.03 bg=0.00
lithium ion binding GO:0031403 p=1.6E−02 n=1 fg=0.03 bg=0.00
protein O−GlcNAc transferase activity GO:0097363 p=1.6E−02 n=1 fg=0.03 bg=0.00
inositol monophosphate 1−phosphatase act... GO:0008934 p=1.6E−02 n=1 fg=0.03 bg=0.00
protein N−acetylglucosaminyltransferase ... GO:0016262 p=1.6E−02 n=1 fg=0.03 bg=0.00
superoxide dismutase activity GO:0004784 p=1.6E−02 n=1 fg=0.03 bg=0.00
DNA clamp loader activity GO:0003689 p=1.6E−02 n=1 fg=0.03 bg=0.00
riboflavin binding GO:1902444 p=1.6E−02 n=1 fg=0.03 bg=0.00
[phosphorylase] phosphatase activity GO:0050196 p=1.6E−02 n=1 fg=0.03 bg=0.00
triplex DNA binding GO:0045142 p=1.6E−02 n=1 fg=0.03 bg=0.00
N−acyltransferase activity GO:0016410 p=2.0E−02 n=2 fg=0.05 bg=0.01
DNA helicase activity GO:0003678 p=2.6E−02 n=2 fg=0.05 bg=0.01
soluble NSF attachment protein activity GO:0005483 p=3.2E−02 n=1 fg=0.03 bg=0.00
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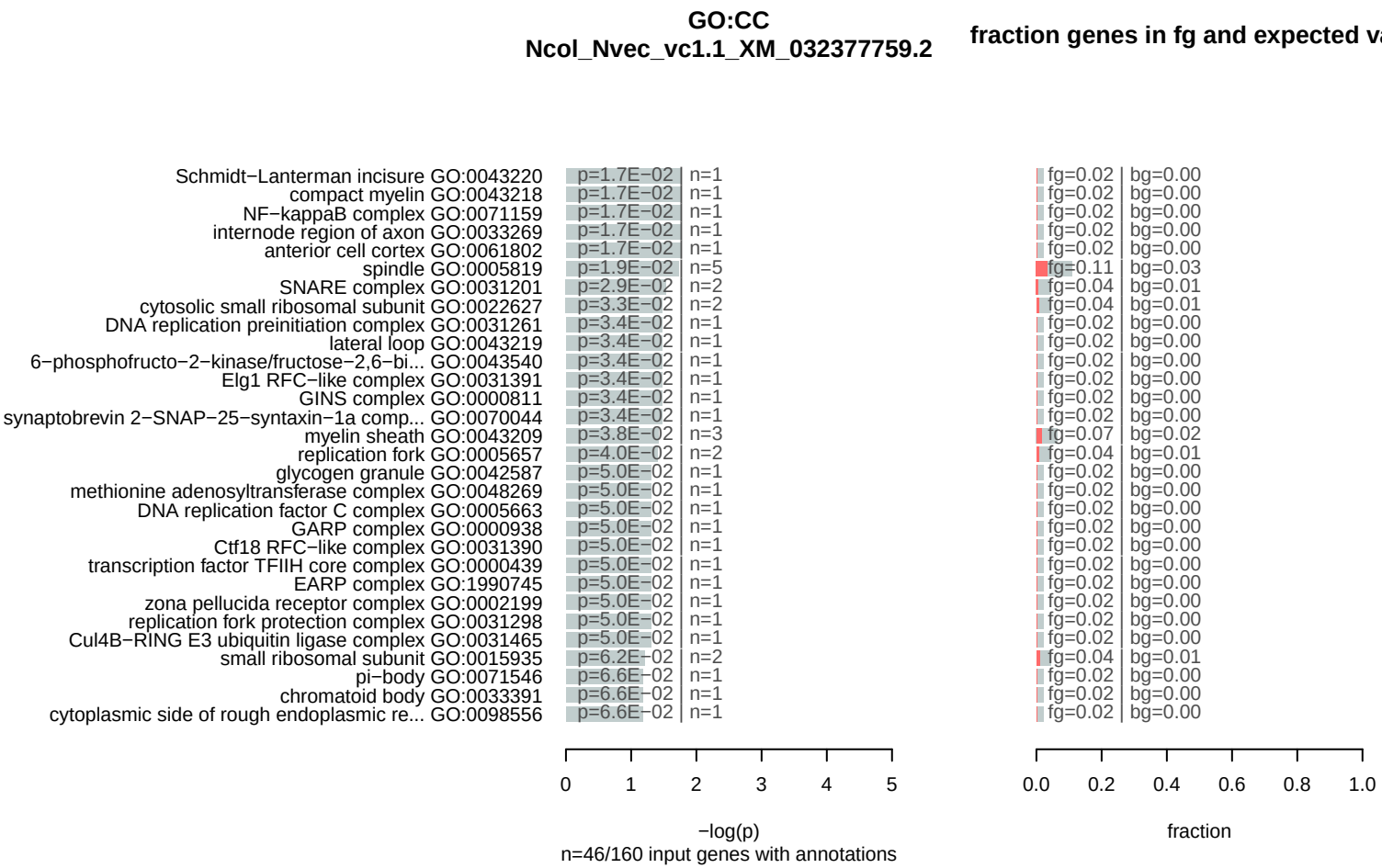
−log(p)
n=38/160 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Ncol_Nvec_vc1.1_XM_032377759.2
fraction genes in fg and expected valu
Schmidt−Lanterman incisure GO:0043220 p=1.7E−02 n=1 fg=0.02 bg=0.00
compact myelin GO:0043218 p=1.7E−02 n=1 fg=0.02 bg=0.00
NF−kappaB complex GO:0071159 p=1.7E−02 n=1 fg=0.02 bg=0.00
internode region of axon GO:0033269 p=1.7E−02 n=1 fg=0.02 bg=0.00
anterior cell cortex GO:0061802 p=1.7E−02 n=1 fg=0.02 bg=0.00
spindle GO:0005819 p=1.9E−02 n=5 fg=0.11 bg=0.03
SNARE complex GO:0031201 p=2.9E−02 n=2 fg=0.04 bg=0.01
cytosolic small ribosomal subunit GO:0022627 p=3.3E−02 n=2 fg=0.04 bg=0.01
DNA replication preinitiation complex GO:0031261 p=3.4E−02 n=1 fg=0.02 bg=0.00
lateral loop GO:0043219 p=3.4E−02 n=1 fg=0.02 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=3.4E−02 n=1 fg=0.02 bg=0.00
Elg1 RFC−like complex GO:0031391 p=3.4E−02 n=1 fg=0.02 bg=0.00
GINS complex GO:0000811 p=3.4E−02 n=1 fg=0.02 bg=0.00
synaptobrevin 2−SNAP−25−syntaxin−1a comp... GO:0070044 p=3.4E−02 n=1 fg=0.02 bg=0.00
myelin sheath GO:0043209 p=3.8E−02 n=3 fg=0.07 bg=0.02
replication fork GO:0005657 p=4.0E−02 n=2 fg=0.04 bg=0.01
glycogen granule GO:0042587 p=5.0E−02 n=1 fg=0.02 bg=0.00
methionine adenosyltransferase complex GO:0048269 p=5.0E−02 n=1 fg=0.02 bg=0.00
DNA replication factor C complex GO:0005663 p=5.0E−02 n=1 fg=0.02 bg=0.00
GARP complex GO:0000938 p=5.0E−02 n=1 fg=0.02 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=5.0E−02 n=1 fg=0.02 bg=0.00
transcription factor TFIIH core complex GO:0000439 p=5.0E−02 n=1 fg=0.02 bg=0.00
EARP complex GO:1990745 p=5.0E−02 n=1 fg=0.02 bg=0.00
zona pellucida receptor complex GO:0002199 p=5.0E−02 n=1 fg=0.02 bg=0.00
replication fork protection complex GO:0031298 p=5.0E−02 n=1 fg=0.02 bg=0.00
Cul4B−RING E3 ubiquitin ligase complex GO:0031465 p=5.0E−02 n=1 fg=0.02 bg=0.00
small ribosomal subunit GO:0015935 p=6.2E−02 n=2 fg=0.04 bg=0.01
pi−body GO:0071546 p=6.6E−02 n=1 fg=0.02 bg=0.00
chromatoid body GO:0033391 p=6.6E−02 n=1 fg=0.02 bg=0.00
cytoplasmic side of rough endoplasmic re... GO:0098556 p=6.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=46/160 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction