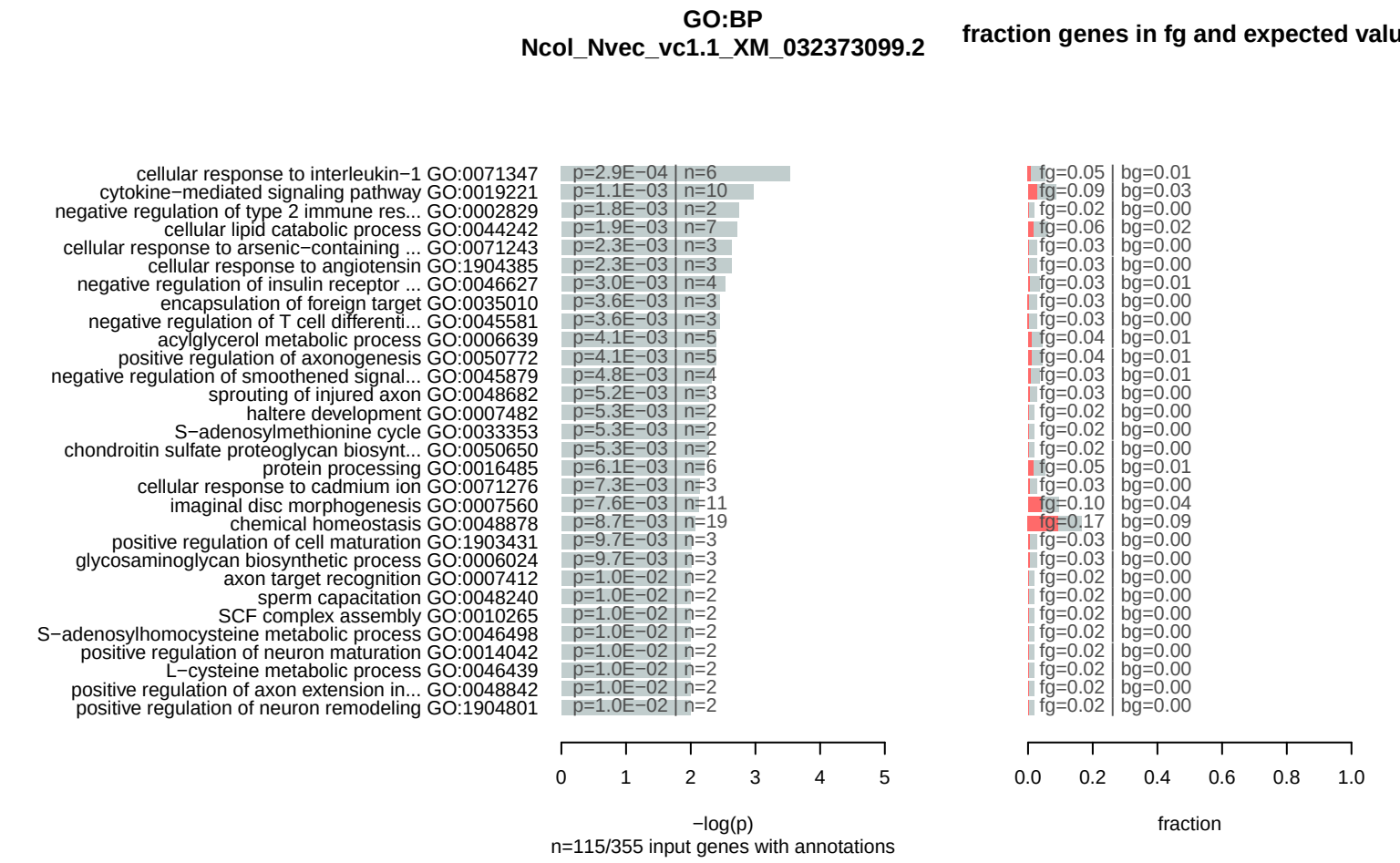
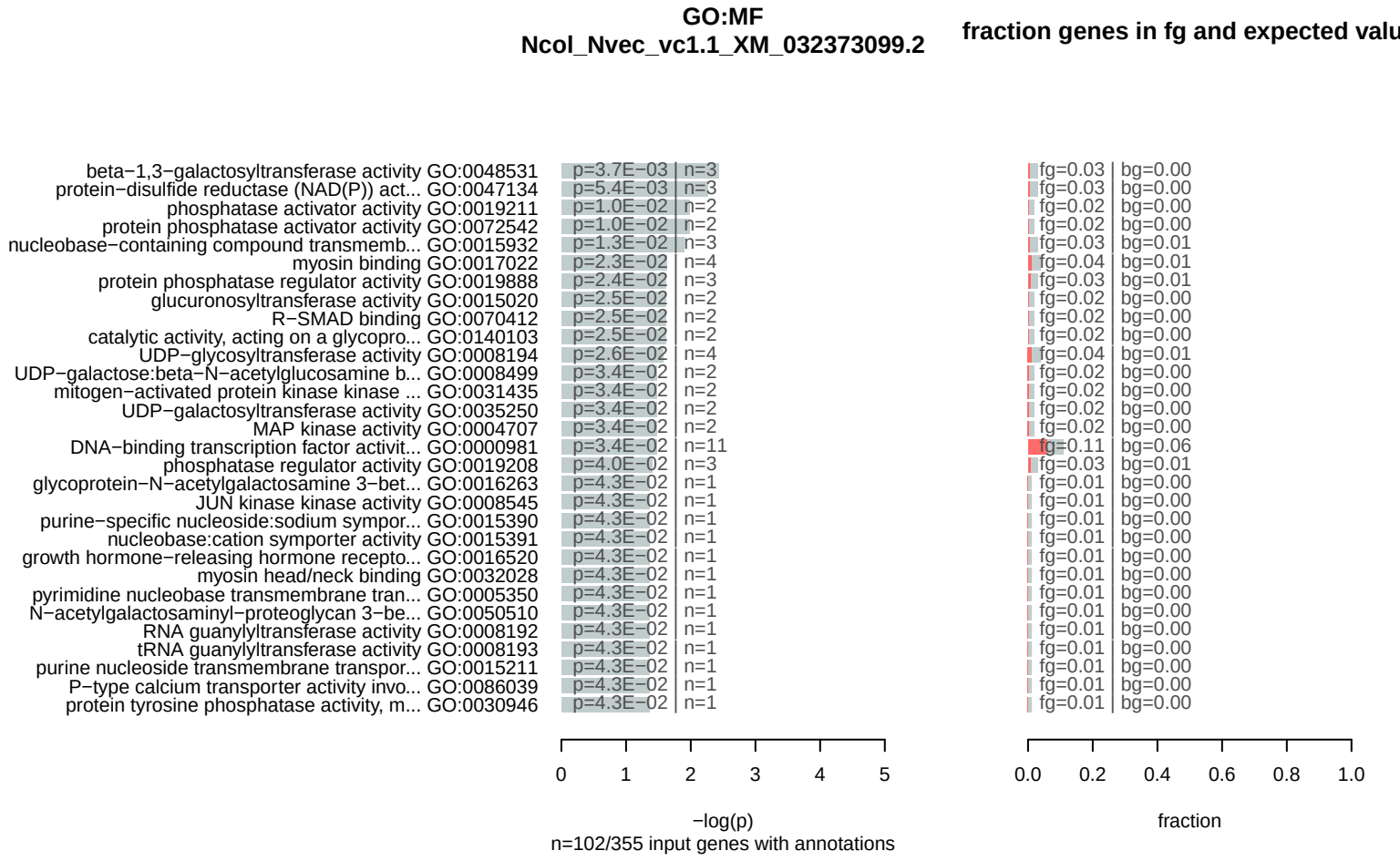
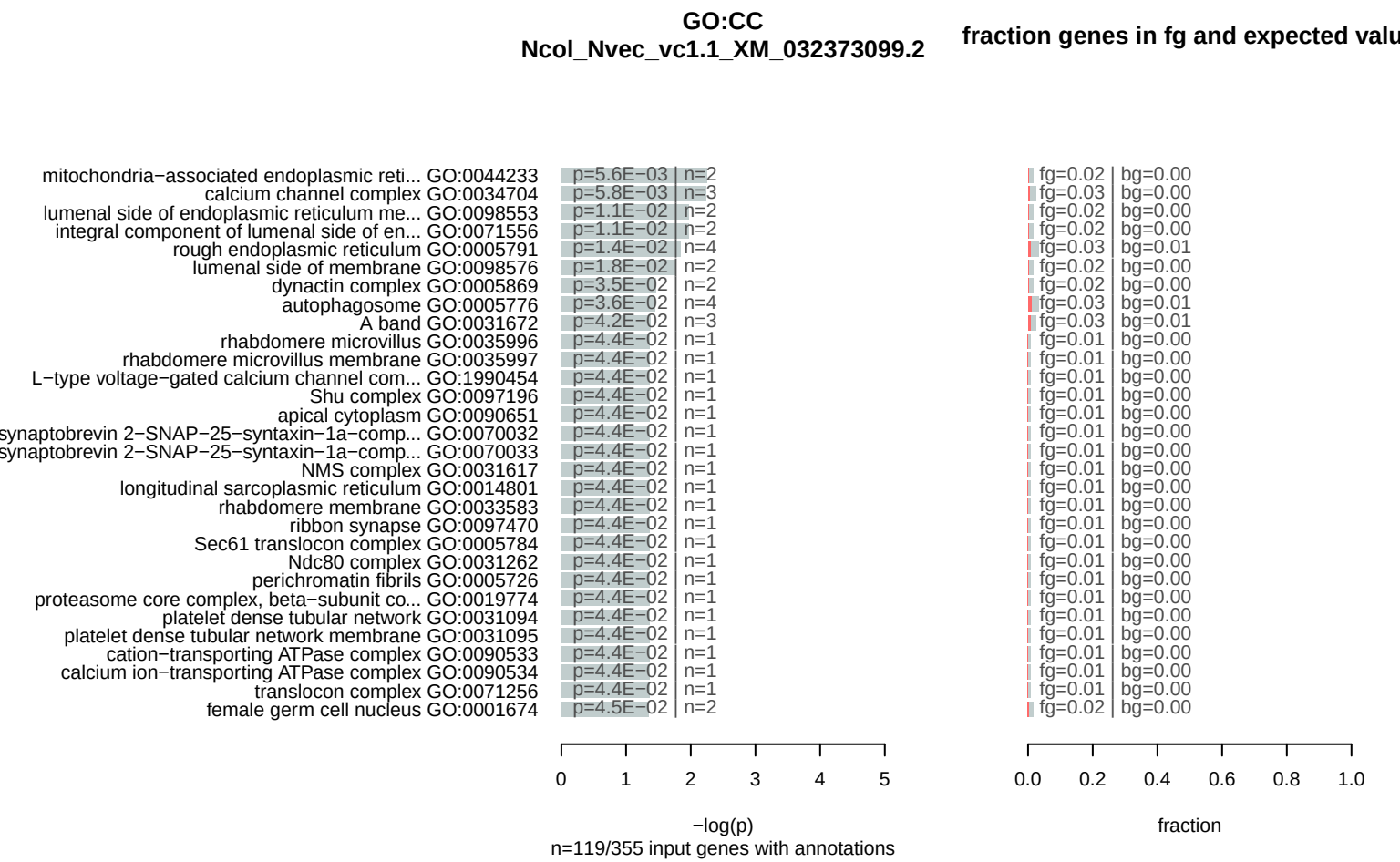

GO:BP
Ncol_Nvec_vc1.1_XM_032373099.2
fraction genes in fg and expected valu
cellular response to interleukin−1 GO:0071347 p=2.9E−04 n=6 fg=0.05 bg=0.01
cytokine−mediated signaling pathway GO:0019221 p=1.1E−03 n=10 fg=0.09 bg=0.03
negative regulation of type 2 immune res... GO:0002829 p=1.8E−03 n=2 fg=0.02 bg=0.00
cellular lipid catabolic process GO:0044242 p=1.9E−03 n=7 fg=0.06 bg=0.02
cellular response to arsenic−containing ... GO:0071243 p=2.3E−03 n=3 fg=0.03 bg=0.00
cellular response to angiotensin GO:1904385 p=2.3E−03 n=3 fg=0.03 bg=0.00
negative regulation of insulin receptor ... GO:0046627 p=3.0E−03 n=4 fg=0.03 bg=0.01
encapsulation of foreign target GO:0035010 p=3.6E−03 n=3 fg=0.03 bg=0.00
negative regulation of T cell differenti... GO:0045581 p=3.6E−03 n=3 fg=0.03 bg=0.00
acylglycerol metabolic process GO:0006639 p=4.1E−03 n=5 fg=0.04 bg=0.01
positive regulation of axonogenesis GO:0050772 p=4.1E−03 n=5 fg=0.04 bg=0.01
negative regulation of smoothened signal... GO:0045879 p=4.8E−03 n=4 fg=0.03 bg=0.01
sprouting of injured axon GO:0048682 p=5.2E−03 n=3 fg=0.03 bg=0.00
haltere development GO:0007482 p=5.3E−03 n=2 fg=0.02 bg=0.00
S−adenosylmethionine cycle GO:0033353 p=5.3E−03 n=2 fg=0.02 bg=0.00
chondroitin sulfate proteoglycan biosynt... GO:0050650 p=5.3E−03 n=2 fg=0.02 bg=0.00
protein processing GO:0016485 p=6.1E−03 n=6 fg=0.05 bg=0.01
cellular response to cadmium ion GO:0071276 p=7.3E−03 n=3 fg=0.03 bg=0.00
imaginal disc morphogenesis GO:0007560 p=7.6E−03 n=11 fg=0.10 bg=0.04
chemical homeostasis GO:0048878 p=8.7E−03 n=19 fg=0.17 bg=0.09
positive regulation of cell maturation GO:1903431 p=9.7E−03 n=3 fg=0.03 bg=0.00
glycosaminoglycan biosynthetic process GO:0006024 p=9.7E−03 n=3 fg=0.03 bg=0.00
axon target recognition GO:0007412 p=1.0E−02 n=2 fg=0.02 bg=0.00
sperm capacitation GO:0048240 p=1.0E−02 n=2 fg=0.02 bg=0.00
SCF complex assembly GO:0010265 p=1.0E−02 n=2 fg=0.02 bg=0.00
S−adenosylhomocysteine metabolic process GO:0046498 p=1.0E−02 n=2 fg=0.02 bg=0.00
positive regulation of neuron maturation GO:0014042 p=1.0E−02 n=2 fg=0.02 bg=0.00
L−cysteine metabolic process GO:0046439 p=1.0E−02 n=2 fg=0.02 bg=0.00
positive regulation of axon extension in... GO:0048842 p=1.0E−02 n=2 fg=0.02 bg=0.00
positive regulation of neuron remodeling GO:1904801 p=1.0E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=115/355 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
Ncol_Nvec_vc1.1_XM_032373099.2
fraction genes in fg and expected valu
beta−1,3−galactosyltransferase activity GO:0048531 p=3.7E−03 n=3 fg=0.03 bg=0.00
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=5.4E−03 n=3 fg=0.03 bg=0.00
phosphatase activator activity GO:0019211 p=1.0E−02 n=2 fg=0.02 bg=0.00
protein phosphatase activator activity GO:0072542 p=1.0E−02 n=2 fg=0.02 bg=0.00
nucleobase−containing compound transmemb... GO:0015932 p=1.3E−02 n=3 fg=0.03 bg=0.01
myosin binding GO:0017022 p=2.3E−02 n=4 fg=0.04 bg=0.01
protein phosphatase regulator activity GO:0019888 p=2.4E−02 n=3 fg=0.03 bg=0.01
glucuronosyltransferase activity GO:0015020 p=2.5E−02 n=2 fg=0.02 bg=0.00
R−SMAD binding GO:0070412 p=2.5E−02 n=2 fg=0.02 bg=0.00
catalytic activity, acting on a glycopro... GO:0140103 p=2.5E−02 n=2 fg=0.02 bg=0.00
UDP−glycosyltransferase activity GO:0008194 p=2.6E−02 n=4 fg=0.04 bg=0.01
UDP−galactose:beta−N−acetylglucosamine b... GO:0008499 p=3.4E−02 n=2 fg=0.02 bg=0.00
mitogen−activated protein kinase kinase ... GO:0031435 p=3.4E−02 n=2 fg=0.02 bg=0.00
UDP−galactosyltransferase activity GO:0035250 p=3.4E−02 n=2 fg=0.02 bg=0.00
MAP kinase activity GO:0004707 p=3.4E−02 n=2 fg=0.02 bg=0.00
DNA−binding transcription factor activit... GO:0000981 p=3.4E−02 n=11 fg=0.11 bg=0.06
phosphatase regulator activity GO:0019208 p=4.0E−02 n=3 fg=0.03 bg=0.01
glycoprotein−N−acetylgalactosamine 3−bet... GO:0016263 p=4.3E−02 n=1 fg=0.01 bg=0.00
JUN kinase kinase activity GO:0008545 p=4.3E−02 n=1 fg=0.01 bg=0.00
purine−specific nucleoside:sodium sympor... GO:0015390 p=4.3E−02 n=1 fg=0.01 bg=0.00
nucleobase:cation symporter activity GO:0015391 p=4.3E−02 n=1 fg=0.01 bg=0.00
growth hormone−releasing hormone recepto... GO:0016520 p=4.3E−02 n=1 fg=0.01 bg=0.00
myosin head/neck binding GO:0032028 p=4.3E−02 n=1 fg=0.01 bg=0.00
pyrimidine nucleobase transmembrane tran... GO:0005350 p=4.3E−02 n=1 fg=0.01 bg=0.00
N−acetylgalactosaminyl−proteoglycan 3−be... GO:0050510 p=4.3E−02 n=1 fg=0.01 bg=0.00
RNA guanylyltransferase activity GO:0008192 p=4.3E−02 n=1 fg=0.01 bg=0.00
tRNA guanylyltransferase activity GO:0008193 p=4.3E−02 n=1 fg=0.01 bg=0.00
purine nucleoside transmembrane transpor... GO:0015211 p=4.3E−02 n=1 fg=0.01 bg=0.00
P−type calcium transporter activity invo... GO:0086039 p=4.3E−02 n=1 fg=0.01 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=4.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=102/355 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Ncol_Nvec_vc1.1_XM_032373099.2
fraction genes in fg and expected valu
mitochondria−associated endoplasmic reti... GO:0044233 p=5.6E−03 n=2 fg=0.02 bg=0.00
calcium channel complex GO:0034704 p=5.8E−03 n=3 fg=0.03 bg=0.00
lumenal side of endoplasmic reticulum me... GO:0098553 p=1.1E−02 n=2 fg=0.02 bg=0.00
integral component of lumenal side of en... GO:0071556 p=1.1E−02 n=2 fg=0.02 bg=0.00
rough endoplasmic reticulum GO:0005791 p=1.4E−02 n=4 fg=0.03 bg=0.01
lumenal side of membrane GO:0098576 p=1.8E−02 n=2 fg=0.02 bg=0.00
dynactin complex GO:0005869 p=3.5E−02 n=2 fg=0.02 bg=0.00
autophagosome GO:0005776 p=3.6E−02 n=4 fg=0.03 bg=0.01
A band GO:0031672 p=4.2E−02 n=3 fg=0.03 bg=0.01
rhabdomere microvillus GO:0035996 p=4.4E−02 n=1 fg=0.01 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=4.4E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=4.4E−02 n=1 fg=0.01 bg=0.00
Shu complex GO:0097196 p=4.4E−02 n=1 fg=0.01 bg=0.00
apical cytoplasm GO:0090651 p=4.4E−02 n=1 fg=0.01 bg=0.00
synaptobrevin 2−SNAP−25−syntaxin−1a−comp... GO:0070032 p=4.4E−02 n=1 fg=0.01 bg=0.00
synaptobrevin 2−SNAP−25−syntaxin−1a−comp... GO:0070033 p=4.4E−02 n=1 fg=0.01 bg=0.00
NMS complex GO:0031617 p=4.4E−02 n=1 fg=0.01 bg=0.00
longitudinal sarcoplasmic reticulum GO:0014801 p=4.4E−02 n=1 fg=0.01 bg=0.00
rhabdomere membrane GO:0033583 p=4.4E−02 n=1 fg=0.01 bg=0.00
ribbon synapse GO:0097470 p=4.4E−02 n=1 fg=0.01 bg=0.00
Sec61 translocon complex GO:0005784 p=4.4E−02 n=1 fg=0.01 bg=0.00
Ndc80 complex GO:0031262 p=4.4E−02 n=1 fg=0.01 bg=0.00
perichromatin fibrils GO:0005726 p=4.4E−02 n=1 fg=0.01 bg=0.00
proteasome core complex, beta−subunit co... GO:0019774 p=4.4E−02 n=1 fg=0.01 bg=0.00
platelet dense tubular network GO:0031094 p=4.4E−02 n=1 fg=0.01 bg=0.00
platelet dense tubular network membrane GO:0031095 p=4.4E−02 n=1 fg=0.01 bg=0.00
cation−transporting ATPase complex GO:0090533 p=4.4E−02 n=1 fg=0.01 bg=0.00
calcium ion−transporting ATPase complex GO:0090534 p=4.4E−02 n=1 fg=0.01 bg=0.00
translocon complex GO:0071256 p=4.4E−02 n=1 fg=0.01 bg=0.00
female germ cell nucleus GO:0001674 p=4.5E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=119/355 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction