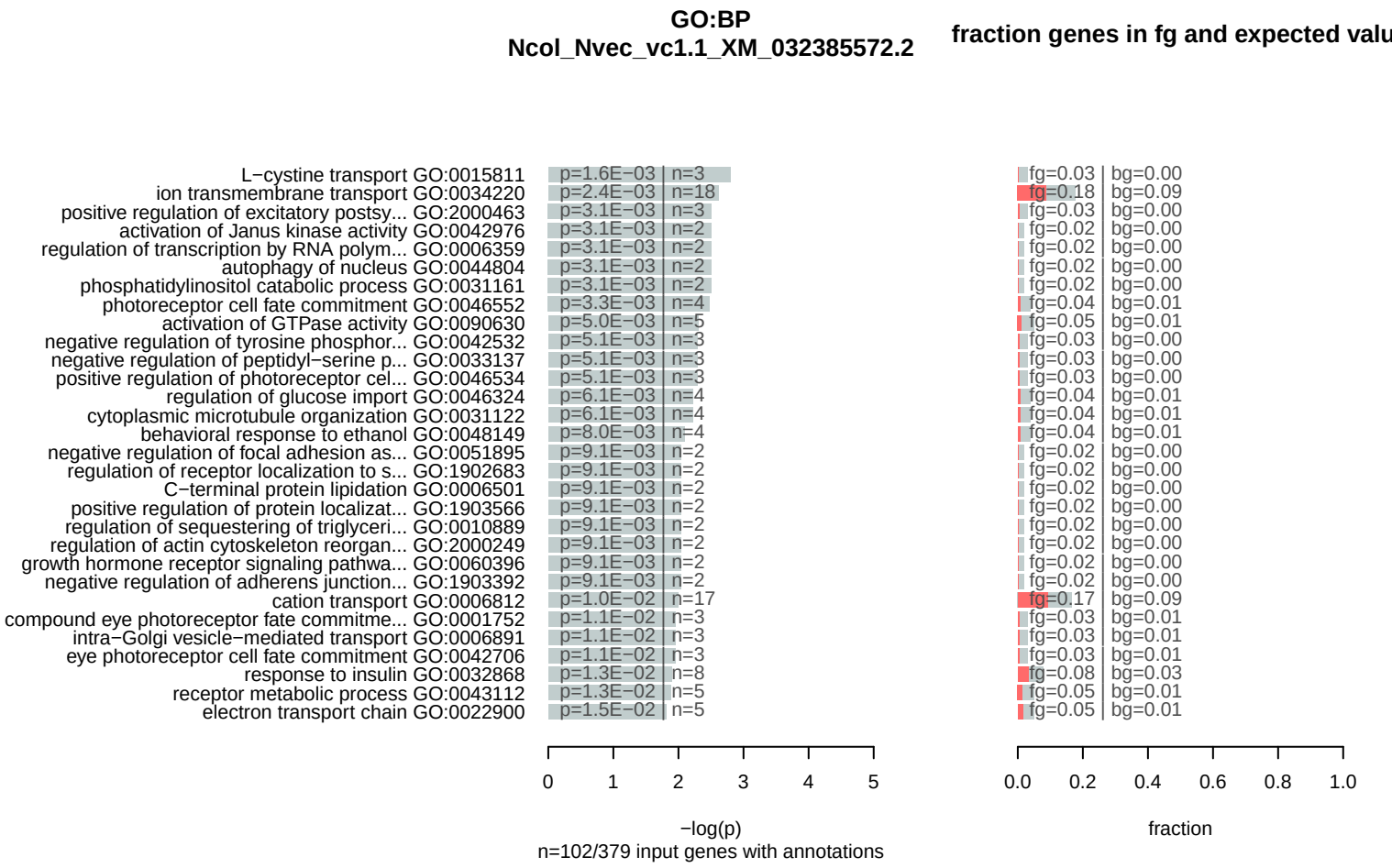
GO:BP
Ncol_Nvec_vc1.1_XM_032385572.2
fraction genes in fg and expected valu
L−cystine transport GO:0015811 p=1.6E−03 n=3 fg=0.03 bg=0.00
ion transmembrane transport GO:0034220 p=2.4E−03 n=18 fg=0.18 bg=0.09
positive regulation of excitatory postsy... GO:2000463 p=3.1E−03 n=3 fg=0.03 bg=0.00
activation of Janus kinase activity GO:0042976 p=3.1E−03 n=2 fg=0.02 bg=0.00
regulation of transcription by RNA polym... GO:0006359 p=3.1E−03 n=2 fg=0.02 bg=0.00
autophagy of nucleus GO:0044804 p=3.1E−03 n=2 fg=0.02 bg=0.00
phosphatidylinositol catabolic process GO:0031161 p=3.1E−03 n=2 fg=0.02 bg=0.00
photoreceptor cell fate commitment GO:0046552 p=3.3E−03 n=4 fg=0.04 bg=0.01
activation of GTPase activity GO:0090630 p=5.0E−03 n=5 fg=0.05 bg=0.01
negative regulation of tyrosine phosphor... GO:0042532 p=5.1E−03 n=3 fg=0.03 bg=0.00
negative regulation of peptidyl−serine p... GO:0033137 p=5.1E−03 n=3 fg=0.03 bg=0.00
positive regulation of photoreceptor cel... GO:0046534 p=5.1E−03 n=3 fg=0.03 bg=0.00
regulation of glucose import GO:0046324 p=6.1E−03 n=4 fg=0.04 bg=0.01
cytoplasmic microtubule organization GO:0031122 p=6.1E−03 n=4 fg=0.04 bg=0.01
behavioral response to ethanol GO:0048149 p=8.0E−03 n=4 fg=0.04 bg=0.01
negative regulation of focal adhesion as... GO:0051895 p=9.1E−03 n=2 fg=0.02 bg=0.00
regulation of receptor localization to s... GO:1902683 p=9.1E−03 n=2 fg=0.02 bg=0.00
C−terminal protein lipidation GO:0006501 p=9.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of protein localizat... GO:1903566 p=9.1E−03 n=2 fg=0.02 bg=0.00
regulation of sequestering of triglyceri... GO:0010889 p=9.1E−03 n=2 fg=0.02 bg=0.00
regulation of actin cytoskeleton reorgan... GO:2000249 p=9.1E−03 n=2 fg=0.02 bg=0.00
growth hormone receptor signaling pathwa... GO:0060396 p=9.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of adherens junction... GO:1903392 p=9.1E−03 n=2 fg=0.02 bg=0.00
cation transport GO:0006812 p=1.0E−02 n=17 fg=0.17 bg=0.09
compound eye photoreceptor fate commitme... GO:0001752 p=1.1E−02 n=3 fg=0.03 bg=0.01
intra−Golgi vesicle−mediated transport GO:0006891 p=1.1E−02 n=3 fg=0.03 bg=0.01
eye photoreceptor cell fate commitment GO:0042706 p=1.1E−02 n=3 fg=0.03 bg=0.01
response to insulin GO:0032868 p=1.3E−02 n=8 fg=0.08 bg=0.03
receptor metabolic process GO:0043112 p=1.3E−02 n=5 fg=0.05 bg=0.01
electron transport chain GO:0022900 p=1.5E−02 n=5 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=102/379 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032385572.2
fraction genes in fg and expected valu
peptide antigen binding GO:0042605 p=1.5E−03 n=3 fg=0.03 bg=0.00
L−cystine transmembrane transporter acti... GO:0015184 p=1.5E−03 n=3 fg=0.03 bg=0.00
neutral amino acid transmembrane transpo... GO:0015175 p=7.2E−03 n=3 fg=0.03 bg=0.01
fatty−acyl−CoA binding GO:0000062 p=8.5E−03 n=2 fg=0.02 bg=0.00
molecular carrier activity GO:0140104 p=8.5E−03 n=2 fg=0.02 bg=0.00
active transmembrane transporter activit... GO:0022804 p=1.4E−02 n=8 fg=0.09 bg=0.04
inorganic molecular entity transmembrane... GO:0015318 p=1.6E−02 n=12 fg=0.14 bg=0.07
oxidoreductase activity, acting on the C... GO:0016616 p=1.9E−02 n=3 fg=0.03 bg=0.01
electron transfer activity GO:0009055 p=2.4E−02 n=4 fg=0.05 bg=0.01
phosphatidylserine binding GO:0001786 p=2.6E−02 n=2 fg=0.02 bg=0.00
antiporter activity GO:0015297 p=3.0E−02 n=3 fg=0.03 bg=0.01
sequence−specific DNA binding GO:0043565 p=3.7E−02 n=11 fg=0.13 bg=0.07
secondary active transmembrane transport... GO:0015291 p=3.8E−02 n=4 fg=0.05 bg=0.02
histone methyltransferase activity GO:0042054 p=3.8E−02 n=2 fg=0.02 bg=0.00
oxidoreductase activity, acting on CH−OH... GO:0016614 p=4.4E−02 n=3 fg=0.03 bg=0.01
excitatory extracellular ligand−gated io... GO:0005231 p=5.2E−02 n=2 fg=0.02 bg=0.00
cis−trans isomerase activity GO:0016859 p=5.2E−02 n=2 fg=0.02 bg=0.00
peptidyl−prolyl cis−trans isomerase acti... GO:0003755 p=5.2E−02 n=2 fg=0.02 bg=0.00
transporter activity GO:0005215 p=5.3E−02 n=17 fg=0.20 bg=0.11
5S rDNA binding GO:0080084 p=5.5E−02 n=1 fg=0.01 bg=0.00
beta−adrenergic receptor kinase activity GO:0047696 p=5.5E−02 n=1 fg=0.01 bg=0.00
ABC−type vitamin B12 transporter activit... GO:0015420 p=5.5E−02 n=1 fg=0.01 bg=0.00
delta−type opioid receptor binding GO:0031850 p=5.5E−02 n=1 fg=0.01 bg=0.00
kappa−type opioid receptor binding GO:0031851 p=5.5E−02 n=1 fg=0.01 bg=0.00
poly(A)−specific ribonuclease activity GO:0004535 p=5.5E−02 n=1 fg=0.01 bg=0.00
carbohydrate:cation symporter activity GO:0005402 p=5.5E−02 n=1 fg=0.01 bg=0.00
RNA polymerase III core binding GO:0000994 p=5.5E−02 n=1 fg=0.01 bg=0.00
rhodopsin kinase activity GO:0050254 p=5.5E−02 n=1 fg=0.01 bg=0.00
carbohydrate:proton symporter activity GO:0005351 p=5.5E−02 n=1 fg=0.01 bg=0.00
glucose transmembrane transporter activi... GO:0005355 p=5.5E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=87/379 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032385572.2
fraction genes in fg and expected valu
Golgi transport complex GO:0017119 p=3.0E−03 n=2 fg=0.02 bg=0.00
phagocytic vesicle membrane GO:0030670 p=1.0E−02 n=3 fg=0.03 bg=0.00
mitochondrial protein−containing complex GO:0098798 p=1.3E−02 n=6 fg=0.06 bg=0.02
cortical endoplasmic reticulum GO:0032541 p=1.7E−02 n=2 fg=0.02 bg=0.00
oxidoreductase complex GO:1990204 p=2.1E−02 n=4 fg=0.04 bg=0.01
mitochondrial matrix GO:0005759 p=2.2E−02 n=9 fg=0.09 bg=0.04
smooth endoplasmic reticulum GO:0005790 p=2.4E−02 n=3 fg=0.03 bg=0.01
brush border membrane GO:0031526 p=3.0E−02 n=3 fg=0.03 bg=0.01
apical plasma membrane GO:0016324 p=3.9E−02 n=8 fg=0.08 bg=0.04
endocytic vesicle GO:0030139 p=4.0E−02 n=6 fg=0.06 bg=0.03
organellar ribosome GO:0000313 p=5.2E−02 n=2 fg=0.02 bg=0.00
mitochondrial ribosome GO:0005761 p=5.2E−02 n=2 fg=0.02 bg=0.00
endoplasmic reticulum tubular network GO:0071782 p=5.2E−02 n=2 fg=0.02 bg=0.00
transmembrane transporter complex GO:1902495 p=5.3E−02 n=5 fg=0.05 bg=0.02
early endosome membrane GO:0031901 p=5.3E−02 n=3 fg=0.03 bg=0.01
polar microtubule GO:0005827 p=5.5E−02 n=1 fg=0.01 bg=0.00
isocitrate dehydrogenase complex (NAD+) GO:0045242 p=5.5E−02 n=1 fg=0.01 bg=0.00
cortical microtubule GO:0055028 p=5.5E−02 n=1 fg=0.01 bg=0.00
signal recognition particle, endoplasmic... GO:0005786 p=5.5E−02 n=1 fg=0.01 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=5.5E−02 n=1 fg=0.01 bg=0.00
centrosomal corona GO:0031592 p=5.5E−02 n=1 fg=0.01 bg=0.00
Sin3 complex GO:0016580 p=5.5E−02 n=1 fg=0.01 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=5.5E−02 n=1 fg=0.01 bg=0.00
cortical microtubule plus−end GO:1903754 p=5.5E−02 n=1 fg=0.01 bg=0.00
gamma−tubulin small complex GO:0008275 p=5.5E−02 n=1 fg=0.01 bg=0.00
NMDA selective glutamate receptor comple... GO:0017146 p=5.5E−02 n=1 fg=0.01 bg=0.00
signal recognition particle GO:0048500 p=5.5E−02 n=1 fg=0.01 bg=0.00
equatorial microtubule organizing center GO:0000923 p=5.5E−02 n=1 fg=0.01 bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0005962 p=5.5E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=5.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=99/379 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction