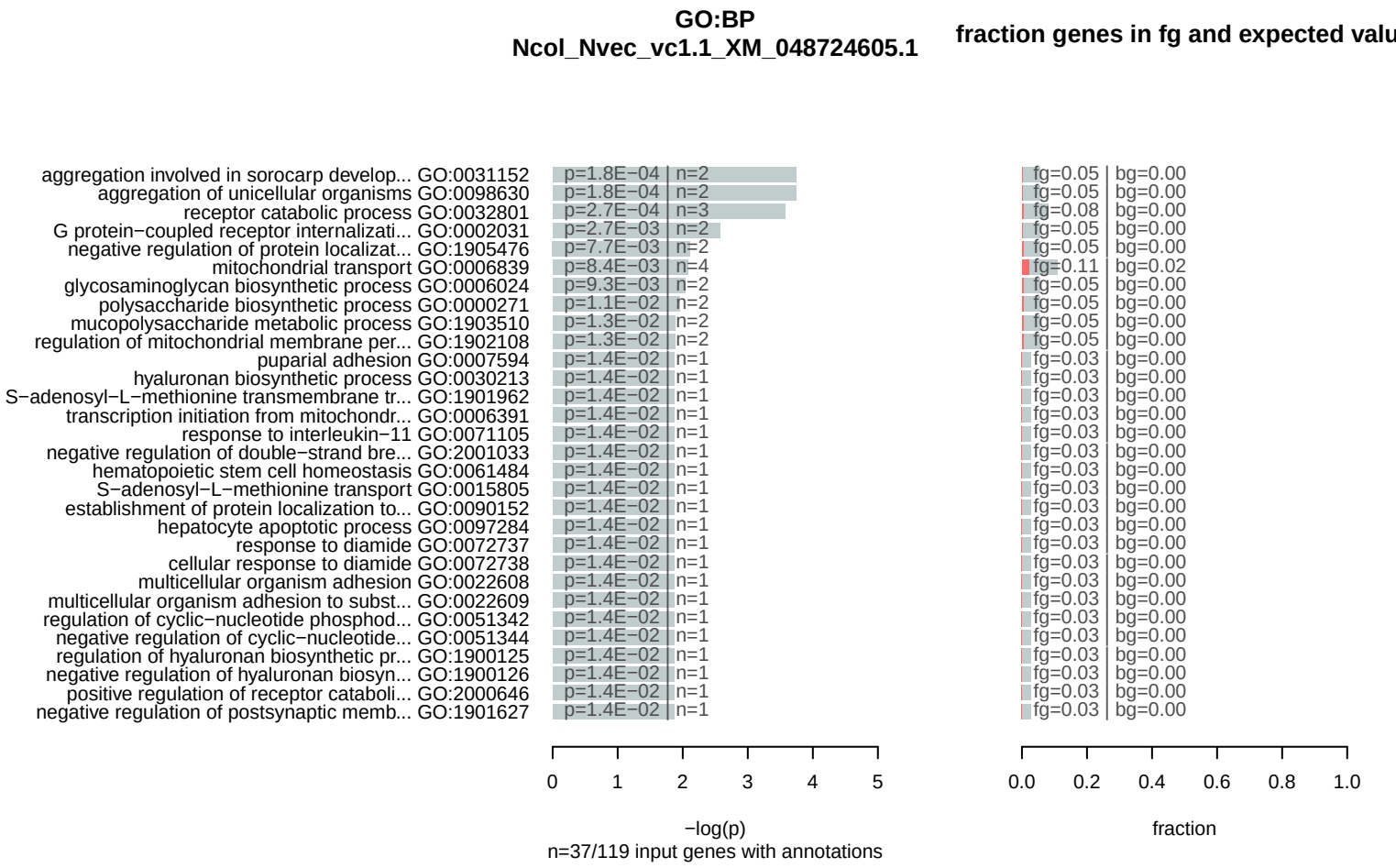
GO:BP
Ncol_Nvec_vc1.1_XM_048724605.1
fraction genes in fg and expected valu
aggregation involved in sorocarp develop... GO:0031152 p=1.8E−04 n=2 fg=0.05 bg=0.00
aggregation of unicellular organisms GO:0098630 p=1.8E−04 n=2 fg=0.05 bg=0.00
receptor catabolic process GO:0032801 p=2.7E−04 n=3 fg=0.08 bg=0.00
G protein−coupled receptor internalizati... GO:0002031 p=2.7E−03 n=2 fg=0.05 bg=0.00
negative regulation of protein localizat... GO:1905476 p=7.7E−03 n=2 fg=0.05 bg=0.00
mitochondrial transport GO:0006839 p=8.4E−03 n=4 fg=0.11 bg=0.02
glycosaminoglycan biosynthetic process GO:0006024 p=9.3E−03 n=2 fg=0.05 bg=0.00
polysaccharide biosynthetic process GO:0000271 p=1.1E−02 n=2 fg=0.05 bg=0.00
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regulation of mitochondrial membrane per... GO:1902108 p=1.3E−02 n=2 fg=0.05 bg=0.00
puparial adhesion GO:0007594 p=1.4E−02 n=1 fg=0.03 bg=0.00
hyaluronan biosynthetic process GO:0030213 p=1.4E−02 n=1 fg=0.03 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:1901962 p=1.4E−02 n=1 fg=0.03 bg=0.00
transcription initiation from mitochondr... GO:0006391 p=1.4E−02 n=1 fg=0.03 bg=0.00
response to interleukin−11 GO:0071105 p=1.4E−02 n=1 fg=0.03 bg=0.00
negative regulation of double−strand bre... GO:2001033 p=1.4E−02 n=1 fg=0.03 bg=0.00
hematopoietic stem cell homeostasis GO:0061484 p=1.4E−02 n=1 fg=0.03 bg=0.00
S−adenosyl−L−methionine transport GO:0015805 p=1.4E−02 n=1 fg=0.03 bg=0.00
establishment of protein localization to... GO:0090152 p=1.4E−02 n=1 fg=0.03 bg=0.00
hepatocyte apoptotic process GO:0097284 p=1.4E−02 n=1 fg=0.03 bg=0.00
response to diamide GO:0072737 p=1.4E−02 n=1 fg=0.03 bg=0.00
cellular response to diamide GO:0072738 p=1.4E−02 n=1 fg=0.03 bg=0.00
multicellular organism adhesion GO:0022608 p=1.4E−02 n=1 fg=0.03 bg=0.00
multicellular organism adhesion to subst... GO:0022609 p=1.4E−02 n=1 fg=0.03 bg=0.00
regulation of cyclic−nucleotide phosphod... GO:0051342 p=1.4E−02 n=1 fg=0.03 bg=0.00
negative regulation of cyclic−nucleotide... GO:0051344 p=1.4E−02 n=1 fg=0.03 bg=0.00
regulation of hyaluronan biosynthetic pr... GO:1900125 p=1.4E−02 n=1 fg=0.03 bg=0.00
negative regulation of hyaluronan biosyn... GO:1900126 p=1.4E−02 n=1 fg=0.03 bg=0.00
positive regulation of receptor cataboli... GO:2000646 p=1.4E−02 n=1 fg=0.03 bg=0.00
negative regulation of postsynaptic memb... GO:1901627 p=1.4E−02 n=1 fg=0.03 bg=0.00
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n=37/119 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
arrestin family protein binding GO:1990763 p=1.4E−03 n=2 fg=0.07 bg=0.00
lyase activity GO:0016829 p=1.9E−03 n=4 fg=0.14 bg=0.02
polyubiquitin modification−dependent pro... GO:0031593 p=8.9E−03 n=2 fg=0.07 bg=0.01
heparan sulfate 2−O−sulfotransferase act... GO:0004394 p=1.2E−02 n=1 fg=0.03 bg=0.00
heparan sulfate sulfotransferase activit... GO:0034483 p=1.2E−02 n=1 fg=0.03 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:0000095 p=1.2E−02 n=1 fg=0.03 bg=0.00
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farnesylated protein binding GO:0001918 p=1.2E−02 n=1 fg=0.03 bg=0.00
LEM domain binding GO:0097726 p=1.2E−02 n=1 fg=0.03 bg=0.00
clathrin light chain binding GO:0032051 p=1.2E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=1.2E−02 n=1 fg=0.03 bg=0.00
CXCR chemokine receptor binding GO:0045236 p=1.2E−02 n=1 fg=0.03 bg=0.00
carbon−carbon lyase activity GO:0016830 p=1.6E−02 n=2 fg=0.07 bg=0.01
3'−5'−exodeoxyribonuclease activity GO:0008296 p=2.4E−02 n=1 fg=0.03 bg=0.00
gamma−glutamylcyclotransferase activity GO:0003839 p=2.4E−02 n=1 fg=0.03 bg=0.00
chemokine receptor binding GO:0042379 p=2.4E−02 n=1 fg=0.03 bg=0.00
mismatch repair complex binding GO:0032404 p=2.4E−02 n=1 fg=0.03 bg=0.00
MutLalpha complex binding GO:0032405 p=2.4E−02 n=1 fg=0.03 bg=0.00
MutSalpha complex binding GO:0032407 p=2.4E−02 n=1 fg=0.03 bg=0.00
GAF domain binding GO:0036004 p=2.4E−02 n=1 fg=0.03 bg=0.00
thiamine pyrophosphate binding GO:0030976 p=2.4E−02 n=1 fg=0.03 bg=0.00
cystathionine beta−synthase activity GO:0004122 p=2.4E−02 n=1 fg=0.03 bg=0.00
cysteine synthase activity GO:0004124 p=2.4E−02 n=1 fg=0.03 bg=0.00
STAT family protein binding GO:0097677 p=2.4E−02 n=1 fg=0.03 bg=0.00
vitamin binding GO:0019842 p=2.9E−02 n=2 fg=0.07 bg=0.01
protein N−terminus binding GO:0047485 p=3.4E−02 n=2 fg=0.07 bg=0.01
Wnt−activated receptor activity GO:0042813 p=3.6E−02 n=1 fg=0.03 bg=0.00
deoxyribodipyrimidine photo−lyase activi... GO:0003904 p=3.6E−02 n=1 fg=0.03 bg=0.00
pre−mRNA 3'−splice site binding GO:0030628 p=3.6E−02 n=1 fg=0.03 bg=0.00
RNA polymerase II intronic transcription... GO:0001162 p=3.6E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=29/119 input genes with annotations
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fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048724605.1
fraction genes in fg and expected valu
sperm connecting piece GO:0097224 p=1.2E−02 n=1 fg=0.03 bg=0.00
mitochondrial DNA−directed RNA polymeras... GO:0034245 p=1.2E−02 n=1 fg=0.03 bg=0.00
clathrin complex GO:0071439 p=2.4E−02 n=1 fg=0.03 bg=0.00
Seh1−associated complex GO:0035859 p=2.4E−02 n=1 fg=0.03 bg=0.00
nuclear stress granule GO:0097165 p=2.4E−02 n=1 fg=0.03 bg=0.00
U2AF complex GO:0089701 p=2.4E−02 n=1 fg=0.03 bg=0.00
GATOR2 complex GO:0061700 p=2.4E−02 n=1 fg=0.03 bg=0.00
ESCRT I complex GO:0000813 p=2.4E−02 n=1 fg=0.03 bg=0.00
sorting endosome GO:0097443 p=2.4E−02 n=1 fg=0.03 bg=0.00
endolysosome membrane GO:0036020 p=3.5E−02 n=1 fg=0.03 bg=0.00
mitotic spindle microtubule GO:1990498 p=3.5E−02 n=1 fg=0.03 bg=0.00
endolysosome GO:0036019 p=3.5E−02 n=1 fg=0.03 bg=0.00
aryl hydrocarbon receptor complex GO:0034751 p=4.7E−02 n=1 fg=0.03 bg=0.00
trans−Golgi network GO:0005802 p=5.2E−02 n=3 fg=0.09 bg=0.03
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Golgi apparatus GO:0005794 p=6.1E−02 n=7 fg=0.22 bg=0.11
filopodium membrane GO:0031527 p=6.9E−02 n=1 fg=0.03 bg=0.00
clathrin−coated endocytic vesicle membra... GO:0030669 p=6.9E−02 n=1 fg=0.03 bg=0.00
mitotic spindle GO:0072686 p=7.3E−02 n=2 fg=0.06 bg=0.01
condensed chromosome, centromeric region GO:0000779 p=7.3E−02 n=2 fg=0.06 bg=0.01
proteasome regulatory particle, base sub... GO:0008540 p=8.0E−02 n=1 fg=0.03 bg=0.00
aggresome GO:0016235 p=9.1E−02 n=1 fg=0.03 bg=0.00
Myb complex GO:0031523 p=9.1E−02 n=1 fg=0.03 bg=0.00
cytosol GO:0005829 p=9.3E−02 n=17 fg=0.53 bg=0.40
spliceosomal complex GO:0005681 p=9.5E−02 n=2 fg=0.06 bg=0.02
microbody lumen GO:0031907 p=1.0E−01 n=1 fg=0.03 bg=0.00
clathrin−coated pit GO:0005905 p=1.0E−01 n=1 fg=0.03 bg=0.00
clathrin coat GO:0030118 p=1.0E−01 n=1 fg=0.03 bg=0.00
mitochondrial nucleoid GO:0042645 p=1.0E−01 n=1 fg=0.03 bg=0.00
clathrin−coated endocytic vesicle GO:0045334 p=1.0E−01 n=1 fg=0.03 bg=0.00
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−log(p)
n=32/119 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction