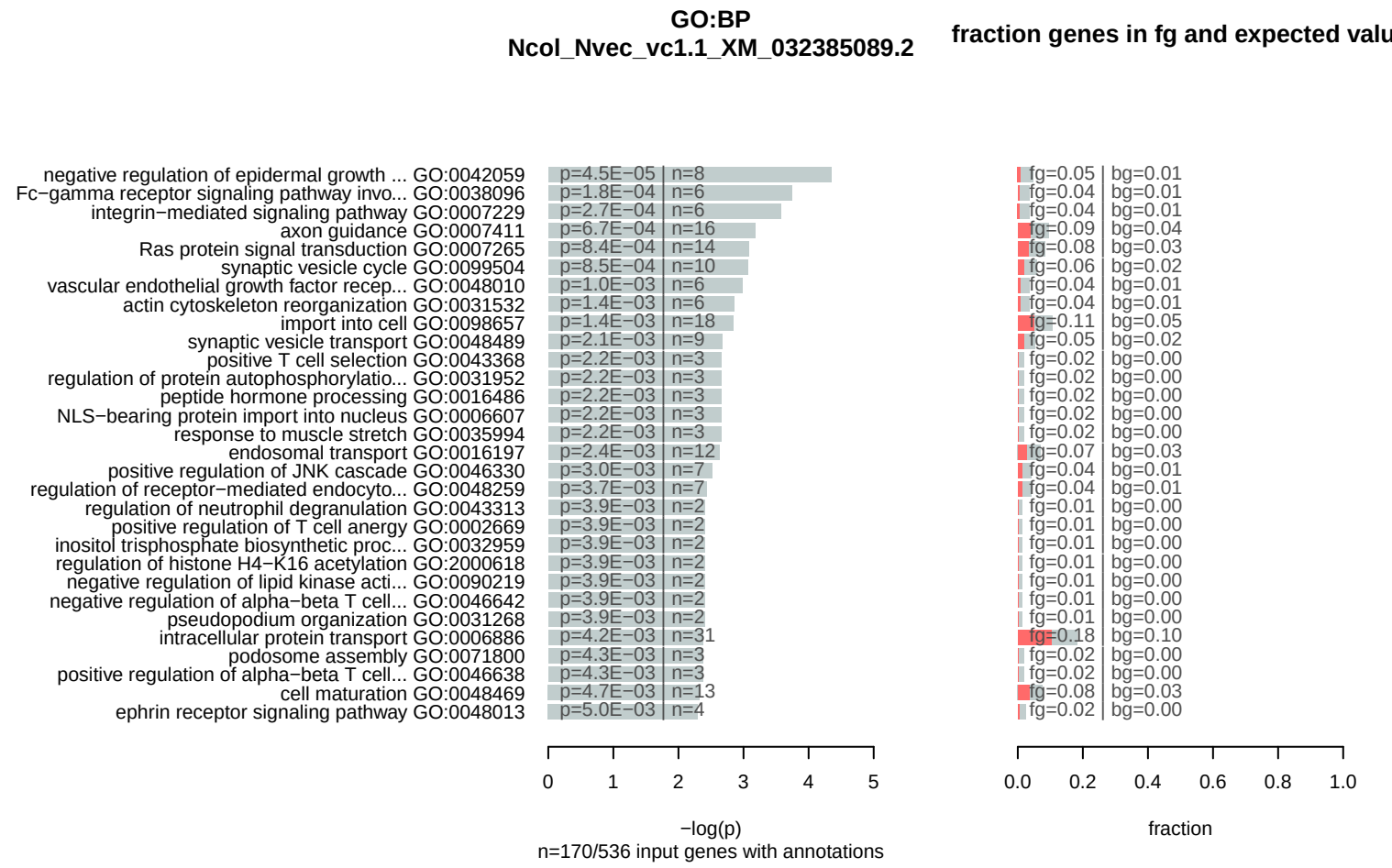
GO:BP
Ncol_Nvec_vc1.1_XM_032385089.2
fraction genes in fg and expected valu
negative regulation of epidermal growth ... GO:0042059 p=4.5E−05 n=8 fg=0.05 bg=0.01
Fc−gamma receptor signaling pathway invo... GO:0038096 p=1.8E−04 n=6 fg=0.04 bg=0.01
integrin−mediated signaling pathway GO:0007229 p=2.7E−04 n=6 fg=0.04 bg=0.01
axon guidance GO:0007411 p=6.7E−04 n=16 fg=0.09 bg=0.04
Ras protein signal transduction GO:0007265 p=8.4E−04 n=14 fg=0.08 bg=0.03
synaptic vesicle cycle GO:0099504 p=8.5E−04 n=10 fg=0.06 bg=0.02
vascular endothelial growth factor recep... GO:0048010 p=1.0E−03 n=6 fg=0.04 bg=0.01
actin cytoskeleton reorganization GO:0031532 p=1.4E−03 n=6 fg=0.04 bg=0.01
import into cell GO:0098657 p=1.4E−03 n=18 fg=0.11 bg=0.05
synaptic vesicle transport GO:0048489 p=2.1E−03 n=9 fg=0.05 bg=0.02
positive T cell selection GO:0043368 p=2.2E−03 n=3 fg=0.02 bg=0.00
regulation of protein autophosphorylatio... GO:0031952 p=2.2E−03 n=3 fg=0.02 bg=0.00
peptide hormone processing GO:0016486 p=2.2E−03 n=3 fg=0.02 bg=0.00
NLS−bearing protein import into nucleus GO:0006607 p=2.2E−03 n=3 fg=0.02 bg=0.00
response to muscle stretch GO:0035994 p=2.2E−03 n=3 fg=0.02 bg=0.00
endosomal transport GO:0016197 p=2.4E−03 n=12 fg=0.07 bg=0.03
positive regulation of JNK cascade GO:0046330 p=3.0E−03 n=7 fg=0.04 bg=0.01
regulation of receptor−mediated endocyto... GO:0048259 p=3.7E−03 n=7 fg=0.04 bg=0.01
regulation of neutrophil degranulation GO:0043313 p=3.9E−03 n=2 fg=0.01 bg=0.00
positive regulation of T cell anergy GO:0002669 p=3.9E−03 n=2 fg=0.01 bg=0.00
inositol trisphosphate biosynthetic proc... GO:0032959 p=3.9E−03 n=2 fg=0.01 bg=0.00
regulation of histone H4−K16 acetylation GO:2000618 p=3.9E−03 n=2 fg=0.01 bg=0.00
negative regulation of lipid kinase acti... GO:0090219 p=3.9E−03 n=2 fg=0.01 bg=0.00
negative regulation of alpha−beta T cell... GO:0046642 p=3.9E−03 n=2 fg=0.01 bg=0.00
pseudopodium organization GO:0031268 p=3.9E−03 n=2 fg=0.01 bg=0.00
intracellular protein transport GO:0006886 p=4.2E−03 n=31 fg=0.18 bg=0.10
podosome assembly GO:0071800 p=4.3E−03 n=3 fg=0.02 bg=0.00
positive regulation of alpha−beta T cell... GO:0046638 p=4.3E−03 n=3 fg=0.02 bg=0.00
cell maturation GO:0048469 p=4.7E−03 n=13 fg=0.08 bg=0.03
ephrin receptor signaling pathway GO:0048013 p=5.0E−03 n=4 fg=0.02 bg=0.00
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−log(p)
n=170/536 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032385089.2
fraction genes in fg and expected valu
phosphotyrosine residue binding GO:0001784 p=1.0E−03 n=4 fg=0.03 bg=0.00
signaling receptor complex adaptor activ... GO:0030159 p=1.8E−03 n=4 fg=0.03 bg=0.00
amide transmembrane transporter activity GO:0042887 p=5.9E−03 n=4 fg=0.03 bg=0.01
SH2 domain binding GO:0042169 p=5.9E−03 n=4 fg=0.03 bg=0.01
non−membrane spanning protein tyrosine k... GO:0004715 p=8.1E−03 n=3 fg=0.02 bg=0.00
phosphatidylcholine binding GO:0031210 p=8.1E−03 n=3 fg=0.02 bg=0.00
protein binding GO:0005515 p=8.6E−03 n=108 fg=0.69 bg=0.59
pyrimidine nucleotide−sugar transmembran... GO:0015165 p=1.2E−02 n=2 fg=0.01 bg=0.00
signaling adaptor activity GO:0035591 p=1.7E−02 n=7 fg=0.04 bg=0.01
peptide transmembrane transporter activi... GO:1904680 p=1.8E−02 n=3 fg=0.02 bg=0.00
protein−macromolecule adaptor activity GO:0030674 p=1.8E−02 n=12 fg=0.08 bg=0.03
molecular adaptor activity GO:0060090 p=1.8E−02 n=12 fg=0.08 bg=0.03
small GTPase binding GO:0031267 p=2.0E−02 n=13 fg=0.08 bg=0.04
nucleotide−sugar transmembrane transport... GO:0005338 p=2.4E−02 n=2 fg=0.01 bg=0.00
RNA polymerase I transcription regulator... GO:0001163 p=2.4E−02 n=2 fg=0.01 bg=0.00
RNA polymerase I core promoter sequence−... GO:0001164 p=2.4E−02 n=2 fg=0.01 bg=0.00
phosphatidylethanolamine binding GO:0008429 p=2.4E−02 n=2 fg=0.01 bg=0.00
RNA stem−loop binding GO:0035613 p=2.4E−02 n=2 fg=0.01 bg=0.00
sequence−specific mRNA binding GO:1990825 p=2.4E−02 n=2 fg=0.01 bg=0.00
RNA cap binding GO:0000339 p=2.4E−02 n=2 fg=0.01 bg=0.00
enzyme activator activity GO:0008047 p=2.6E−02 n=13 fg=0.08 bg=0.05
enzyme binding GO:0019899 p=2.6E−02 n=45 fg=0.29 bg=0.22
phosphatase regulator activity GO:0019208 p=2.7E−02 n=4 fg=0.03 bg=0.01
ephrin receptor binding GO:0046875 p=3.8E−02 n=2 fg=0.01 bg=0.00
phosphatidylinositol−3,4−bisphosphate bi... GO:0043325 p=3.8E−02 n=2 fg=0.01 bg=0.00
calcium−dependent phospholipid binding GO:0005544 p=3.8E−02 n=2 fg=0.01 bg=0.00
JUN kinase binding GO:0008432 p=3.8E−02 n=2 fg=0.01 bg=0.00
GTP−dependent protein binding GO:0030742 p=3.8E−02 n=2 fg=0.01 bg=0.00
macromolecule transmembrane transporter ... GO:0022884 p=3.8E−02 n=2 fg=0.01 bg=0.00
protein transmembrane transporter activi... GO:0008320 p=3.8E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=156/536 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032385089.2
fraction genes in fg and expected valu
cleavage furrow GO:0032154 p=1.0E−04 n=6 fg=0.04 bg=0.01
axon terminus GO:0043679 p=5.6E−04 n=11 fg=0.07 bg=0.02
extrinsic component of cytoplasmic side ... GO:0031234 p=1.3E−03 n=6 fg=0.04 bg=0.01
podosome GO:0002102 p=2.1E−03 n=3 fg=0.02 bg=0.00
stress fiber GO:0001725 p=2.2E−03 n=4 fg=0.02 bg=0.00
organelle membrane contact site GO:0044232 p=4.0E−03 n=3 fg=0.02 bg=0.00
early endosome GO:0005769 p=4.8E−03 n=12 fg=0.07 bg=0.03
cytoplasmic vesicle GO:0031410 p=5.8E−03 n=43 fg=0.26 bg=0.15
P−body GO:0000932 p=7.7E−03 n=5 fg=0.03 bg=0.01
septin ring GO:0005940 p=1.1E−02 n=2 fg=0.01 bg=0.00
sperm annulus GO:0097227 p=1.1E−02 n=2 fg=0.01 bg=0.00
septin complex GO:0031105 p=1.1E−02 n=2 fg=0.01 bg=0.00
type Ib terminal bouton GO:0061176 p=1.1E−02 n=2 fg=0.01 bg=0.00
type Is terminal bouton GO:0061177 p=1.1E−02 n=2 fg=0.01 bg=0.00
mRNA cap binding complex GO:0005845 p=1.1E−02 n=2 fg=0.01 bg=0.00
terminal bouton GO:0043195 p=1.1E−02 n=7 fg=0.04 bg=0.02
focal adhesion GO:0005925 p=1.2E−02 n=5 fg=0.03 bg=0.01
cell leading edge GO:0031252 p=1.4E−02 n=12 fg=0.07 bg=0.04
RNA cap binding complex GO:0034518 p=2.1E−02 n=2 fg=0.01 bg=0.00
alpha DNA polymerase:primase complex GO:0005658 p=2.1E−02 n=2 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0071541 p=2.1E−02 n=2 fg=0.01 bg=0.00
pre−snoRNP complex GO:0070761 p=2.1E−02 n=2 fg=0.01 bg=0.00
coated vesicle GO:0030135 p=2.2E−02 n=8 fg=0.05 bg=0.02
cell−substrate junction GO:0030055 p=2.3E−02 n=5 fg=0.03 bg=0.01
transport vesicle membrane GO:0030658 p=2.4E−02 n=6 fg=0.04 bg=0.01
late endosome GO:0005770 p=2.4E−02 n=8 fg=0.05 bg=0.02
recycling endosome membrane GO:0055038 p=2.7E−02 n=3 fg=0.02 bg=0.00
ruffle GO:0001726 p=3.0E−02 n=5 fg=0.03 bg=0.01
protein−containing complex GO:0032991 p=3.1E−02 n=83 fg=0.50 bg=0.42
protein phosphatase type 2A complex GO:0000159 p=3.4E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=167/536 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction