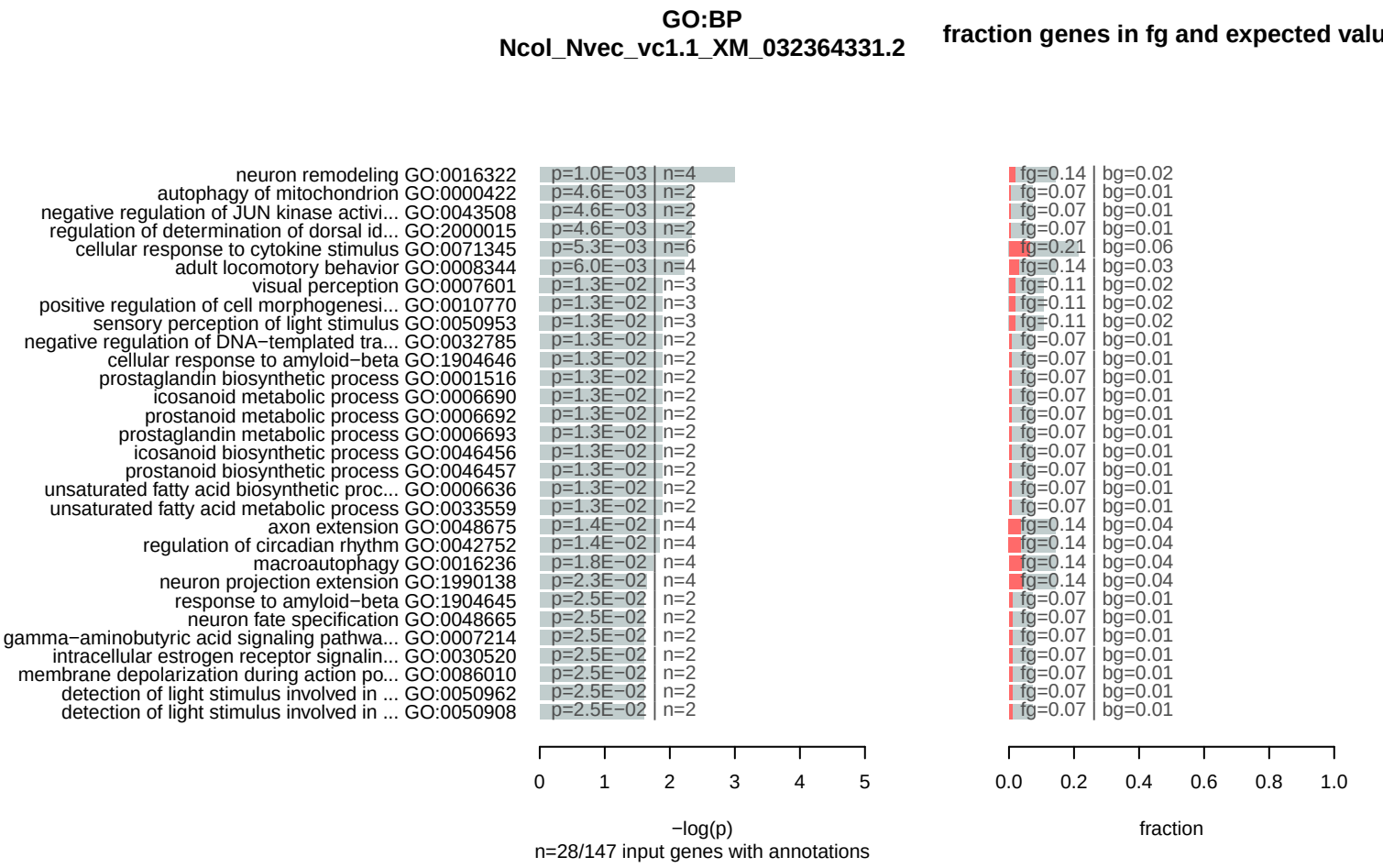
GO:BP
Ncol_Nvec_vc1.1_XM_032364331.2
fraction genes in fg and expected valu
neuron remodeling GO:0016322 p=1.0E−03 n=4 fg=0.14 bg=0.02
autophagy of mitochondrion GO:0000422 p=4.6E−03 n=2 fg=0.07 bg=0.01
negative regulation of JUN kinase activi... GO:0043508 p=4.6E−03 n=2 fg=0.07 bg=0.01
regulation of determination of dorsal id... GO:2000015 p=4.6E−03 n=2 fg=0.07 bg=0.01
cellular response to cytokine stimulus GO:0071345 p=5.3E−03 n=6 fg=0.21 bg=0.06
adult locomotory behavior GO:0008344 p=6.0E−03 n=4 fg=0.14 bg=0.03
visual perception GO:0007601 p=1.3E−02 n=3 fg=0.11 bg=0.02
positive regulation of cell morphogenesi... GO:0010770 p=1.3E−02 n=3 fg=0.11 bg=0.02
sensory perception of light stimulus GO:0050953 p=1.3E−02 n=3 fg=0.11 bg=0.02
negative regulation of DNA−templated tra... GO:0032785 p=1.3E−02 n=2 fg=0.07 bg=0.01
cellular response to amyloid−beta GO:1904646 p=1.3E−02 n=2 fg=0.07 bg=0.01
prostaglandin biosynthetic process GO:0001516 p=1.3E−02 n=2 fg=0.07 bg=0.01
icosanoid metabolic process GO:0006690 p=1.3E−02 n=2 fg=0.07 bg=0.01
prostanoid metabolic process GO:0006692 p=1.3E−02 n=2 fg=0.07 bg=0.01
prostaglandin metabolic process GO:0006693 p=1.3E−02 n=2 fg=0.07 bg=0.01
icosanoid biosynthetic process GO:0046456 p=1.3E−02 n=2 fg=0.07 bg=0.01
prostanoid biosynthetic process GO:0046457 p=1.3E−02 n=2 fg=0.07 bg=0.01
unsaturated fatty acid biosynthetic proc... GO:0006636 p=1.3E−02 n=2 fg=0.07 bg=0.01
unsaturated fatty acid metabolic process GO:0033559 p=1.3E−02 n=2 fg=0.07 bg=0.01
axon extension GO:0048675 p=1.4E−02 n=4 fg=0.14 bg=0.04
regulation of circadian rhythm GO:0042752 p=1.4E−02 n=4 fg=0.14 bg=0.04
macroautophagy GO:0016236 p=1.8E−02 n=4 fg=0.14 bg=0.04
neuron projection extension GO:1990138 p=2.3E−02 n=4 fg=0.14 bg=0.04
response to amyloid−beta GO:1904645 p=2.5E−02 n=2 fg=0.07 bg=0.01
neuron fate specification GO:0048665 p=2.5E−02 n=2 fg=0.07 bg=0.01
gamma−aminobutyric acid signaling pathwa... GO:0007214 p=2.5E−02 n=2 fg=0.07 bg=0.01
intracellular estrogen receptor signalin... GO:0030520 p=2.5E−02 n=2 fg=0.07 bg=0.01
membrane depolarization during action po... GO:0086010 p=2.5E−02 n=2 fg=0.07 bg=0.01
detection of light stimulus involved in ... GO:0050962 p=2.5E−02 n=2 fg=0.07 bg=0.01
detection of light stimulus involved in ... GO:0050908 p=2.5E−02 n=2 fg=0.07 bg=0.01
0 1 2 3 4 5
−log(p)
n=28/147 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032364331.2
fraction genes in fg and expected valu
high voltage−gated calcium channel activ... GO:0008331 p=3.8E−03 n=2 fg=0.09 bg=0.01
ion gated channel activity GO:0022839 p=2.0E−02 n=5 fg=0.22 bg=0.07
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=6.3E+02 n=1 fg=0.04 bg=0.00
oxidoreductase activity, acting on perox... GO:0016684 p=6.3E+02 n=1 fg=0.04 bg=0.00
5−oxoprolinase (ATP−hydrolyzing) activit... GO:0017168 p=6.3E+02 n=1 fg=0.04 bg=0.00
exoribonuclease activity, producing 5'−p... GO:0016896 p=6.3E+02 n=1 fg=0.04 bg=0.00
gamma−glutamylaminecyclotransferase acti... GO:0061929 p=6.3E+02 n=1 fg=0.04 bg=0.00
dipeptidase activity GO:0016805 p=6.3E+02 n=1 fg=0.04 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=6.3E+02 n=1 fg=0.04 bg=0.00
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=6.3E+02 n=1 fg=0.04 bg=0.00
oxidoreductase activity, acting on the C... GO:0016627 p=6.3E+02 n=1 fg=0.04 bg=0.00
oxidoreductase activity, acting on the C... GO:0016628 p=6.3E+02 n=1 fg=0.04 bg=0.00
carboxypeptidase activity GO:0004180 p=6.3E+02 n=1 fg=0.04 bg=0.00
peptidase activator activity GO:0016504 p=6.3E+02 n=1 fg=0.04 bg=0.00
peptidase activator activity involved in... GO:0016505 p=6.3E+02 n=1 fg=0.04 bg=0.00
cysteine−type endopeptidase activator ac... GO:0008656 p=6.3E+02 n=1 fg=0.04 bg=0.00
3'−5' exonuclease activity GO:0008408 p=6.3E+02 n=1 fg=0.04 bg=0.00
peroxidase activity GO:0004601 p=6.3E+02 n=1 fg=0.04 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=6.3E+02 n=1 fg=0.04 bg=0.00
acylglycerol O−acyltransferase activity GO:0016411 p=6.3E+02 n=1 fg=0.04 bg=0.00
O−acetyltransferase activity GO:0016413 p=6.3E+02 n=1 fg=0.04 bg=0.00
O−acyltransferase activity GO:0008374 p=6.3E+02 n=1 fg=0.04 bg=0.00
thromboxane−A synthase activity GO:0004796 p=6.3E+02 n=1 fg=0.04 bg=0.00
JUN kinase activity GO:0004705 p=6.3E+02 n=1 fg=0.04 bg=0.00
MAP kinase activity GO:0004707 p=6.3E+02 n=1 fg=0.04 bg=0.00
histone deacetylase regulator activity GO:0035033 p=6.3E+02 n=1 fg=0.04 bg=0.00
12−hydroxyheptadecatrienoic acid synthas... GO:0036134 p=6.3E+02 n=1 fg=0.04 bg=0.00
dephospho−CoA kinase activity GO:0004140 p=6.3E+02 n=1 fg=0.04 bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016812 p=6.3E+02 n=1 fg=0.04 bg=0.00
exonuclease activity GO:0004527 p=6.3E+02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=23/147 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032364331.2
fraction genes in fg and expected valu
voltage−gated calcium channel complex GO:0005891 p=3.6E−02 n=2 fg=0.08 bg=0.01
postsynapse GO:0098794 p=4.5E−02 n=5 fg=0.19 bg=0.08
presynapse GO:0098793 p=5.7E+02 n=5 fg=0.19 bg=0.08
core−binding factor complex GO:0016513 p=6.5E+02 n=1 fg=0.04 bg=0.00
intrinsic component of mitochondrial out... GO:0031306 p=6.5E+02 n=1 fg=0.04 bg=0.00
integral component of mitochondrial oute... GO:0031307 p=6.5E+02 n=1 fg=0.04 bg=0.00
neuron projection cytoplasm GO:0120111 p=6.5E+02 n=1 fg=0.04 bg=0.00
chromosome, telomeric region GO:0000781 p=6.5E+02 n=1 fg=0.04 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=6.5E+02 n=1 fg=0.04 bg=0.00
integral component of mitochondrial memb... GO:0032592 p=6.5E+02 n=1 fg=0.04 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=6.5E+02 n=1 fg=0.04 bg=0.00
intrinsic component of mitochondrial mem... GO:0098573 p=6.5E+02 n=1 fg=0.04 bg=0.00
septin collar GO:0032173 p=6.5E+02 n=1 fg=0.04 bg=0.00
podosome GO:0002102 p=6.5E+02 n=1 fg=0.04 bg=0.00
dendrite cytoplasm GO:0032839 p=6.5E+02 n=1 fg=0.04 bg=0.00
cation channel complex GO:0034703 p=6.5E+02 n=3 fg=0.12 bg=0.04
calcium channel complex GO:0034704 p=6.9E−02 n=2 fg=0.08 bg=0.02
ion channel complex GO:0034702 p=7.7E−02 n=3 fg=0.12 bg=0.04
transporter complex GO:1990351 p=7.7E−02 n=3 fg=0.12 bg=0.04
transmembrane transporter complex GO:1902495 p=7.7E−02 n=3 fg=0.12 bg=0.04
synapse GO:0045202 p=8.1E−02 n=7 fg=0.27 bg=0.15
RNA polymerase II transcription regulato... GO:0090575 p=8.9E−02 n=2 fg=0.08 bg=0.02
presynaptic active zone GO:0048786 p=8.9E−02 n=2 fg=0.08 bg=0.02
perikaryon GO:0043204 p=8.9E−02 n=2 fg=0.08 bg=0.02
nuclear speck GO:0016607 p=8.9E−02 n=2 fg=0.08 bg=0.02
sarcoplasmic reticulum GO:0016529 p=1.2E−01 n=1 fg=0.04 bg=0.01
site of DNA damage GO:0090734 p=1.2E−01 n=1 fg=0.04 bg=0.01
contractile actin filament bundle GO:0097517 p=1.2E−01 n=1 fg=0.04 bg=0.01
sperm annulus GO:0097227 p=1.2E−01 n=1 fg=0.04 bg=0.01
site of double−strand break GO:0035861 p=1.2E−01 n=1 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=26/147 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction