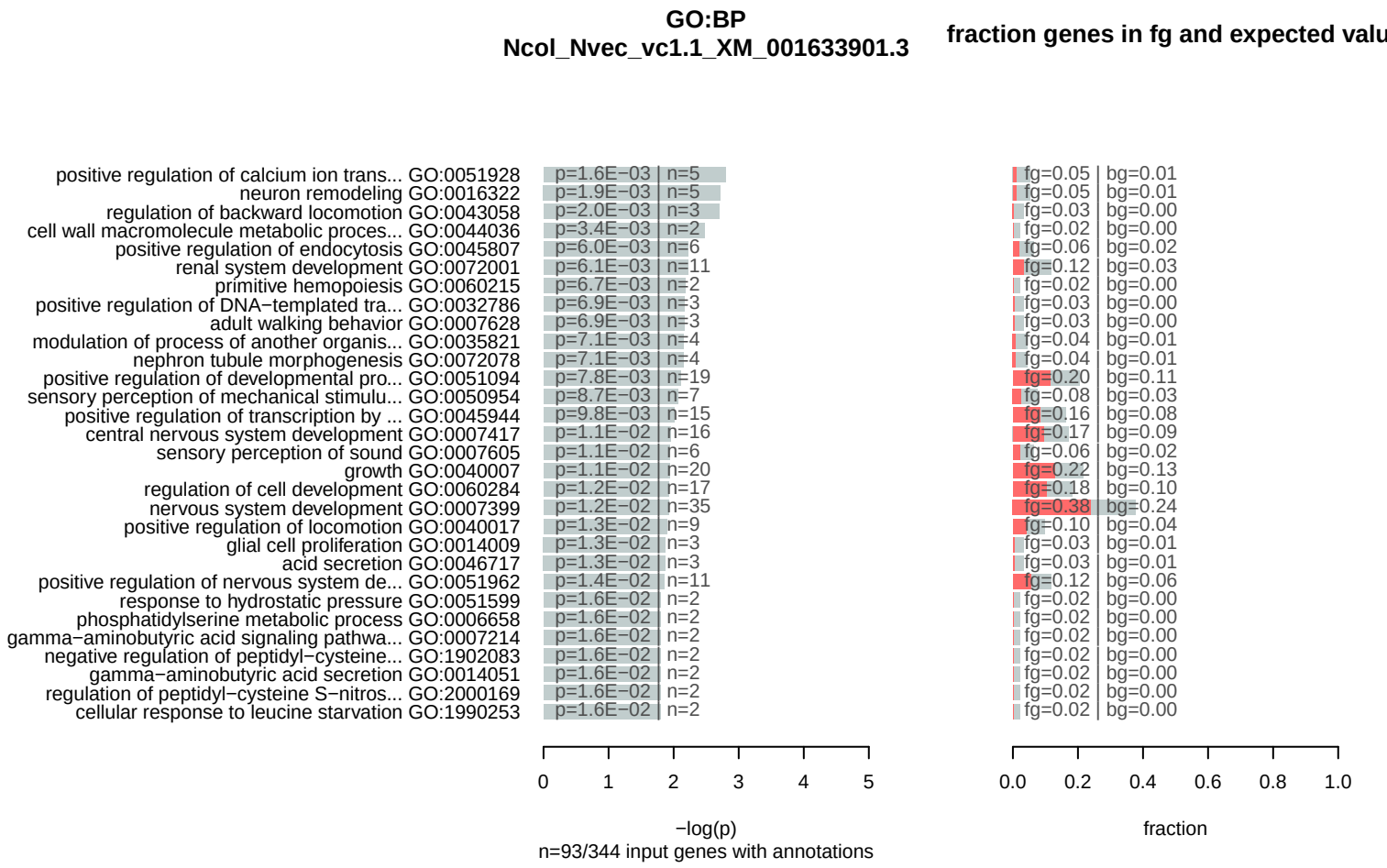
GO:BP
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fraction genes in fg and expected valu
positive regulation of calcium ion trans... GO:0051928 p=1.6E−03 n=5 fg=0.05 bg=0.01
neuron remodeling GO:0016322 p=1.9E−03 n=5 fg=0.05 bg=0.01
regulation of backward locomotion GO:0043058 p=2.0E−03 n=3 fg=0.03 bg=0.00
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positive regulation of endocytosis GO:0045807 p=6.0E−03 n=6 fg=0.06 bg=0.02
renal system development GO:0072001 p=6.1E−03 n=11 fg=0.12 bg=0.03
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positive regulation of developmental pro... GO:0051094 p=7.8E−03 n=19 fg=0.20 bg=0.11
sensory perception of mechanical stimulu... GO:0050954 p=8.7E−03 n=7 fg=0.08 bg=0.03
positive regulation of transcription by ... GO:0045944 p=9.8E−03 n=15 fg=0.16 bg=0.08
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sensory perception of sound GO:0007605 p=1.1E−02 n=6 fg=0.06 bg=0.02
growth GO:0040007 p=1.1E−02 n=20 fg=0.22 bg=0.13
regulation of cell development GO:0060284 p=1.2E−02 n=17 fg=0.18 bg=0.10
nervous system development GO:0007399 p=1.2E−02 n=35 fg=0.38 bg=0.24
positive regulation of locomotion GO:0040017 p=1.3E−02 n=9 fg=0.10 bg=0.04
glial cell proliferation GO:0014009 p=1.3E−02 n=3 fg=0.03 bg=0.01
acid secretion GO:0046717 p=1.3E−02 n=3 fg=0.03 bg=0.01
positive regulation of nervous system de... GO:0051962 p=1.4E−02 n=11 fg=0.12 bg=0.06
response to hydrostatic pressure GO:0051599 p=1.6E−02 n=2 fg=0.02 bg=0.00
phosphatidylserine metabolic process GO:0006658 p=1.6E−02 n=2 fg=0.02 bg=0.00
gamma−aminobutyric acid signaling pathwa... GO:0007214 p=1.6E−02 n=2 fg=0.02 bg=0.00
negative regulation of peptidyl−cysteine... GO:1902083 p=1.6E−02 n=2 fg=0.02 bg=0.00
gamma−aminobutyric acid secretion GO:0014051 p=1.6E−02 n=2 fg=0.02 bg=0.00
regulation of peptidyl−cysteine S−nitros... GO:2000169 p=1.6E−02 n=2 fg=0.02 bg=0.00
cellular response to leucine starvation GO:1990253 p=1.6E−02 n=2 fg=0.02 bg=0.00
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001633901.3
fraction genes in fg and expected valu
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cell adhesion molecule binding GO:0050839 p=3.5E−03 n=6 fg=0.07 bg=0.02
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actin monomer binding GO:0003785 p=1.1E−02 n=2 fg=0.02 bg=0.00
myosin light chain binding GO:0032027 p=1.1E−02 n=2 fg=0.02 bg=0.00
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phosphoprotein binding GO:0051219 p=3.0E−02 n=3 fg=0.04 bg=0.01
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succinyl−CoA hydrolase activity GO:0004778 p=3.5E−02 n=1 fg=0.01 bg=0.00
ribokinase activity GO:0004747 p=3.5E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.5E−02 n=1 fg=0.01 bg=0.00
MRF binding GO:0043426 p=3.5E−02 n=1 fg=0.01 bg=0.00
very long−chain fatty acid−CoA ligase ac... GO:0031957 p=3.5E−02 n=1 fg=0.01 bg=0.00
intramolecular oxidoreductase activity, ... GO:0016861 p=3.5E−02 n=1 fg=0.01 bg=0.00
BIR domain binding GO:1990525 p=3.5E−02 n=1 fg=0.01 bg=0.00
phosphoribosylaminoimidazolecarboxamide ... GO:0004643 p=3.5E−02 n=1 fg=0.01 bg=0.00
neurotrophin TRK receptor binding GO:0005167 p=3.5E−02 n=1 fg=0.01 bg=0.00
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TFIIF−class transcription factor complex... GO:0001096 p=3.5E−02 n=1 fg=0.01 bg=0.00
histone H3−methyl−lysine−9 demethylase a... GO:0032454 p=3.5E−02 n=1 fg=0.01 bg=0.00
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telomeric repeat−containing RNA binding GO:0061752 p=3.5E−02 n=1 fg=0.01 bg=0.00
mannose−6−phosphate isomerase activity GO:0004476 p=3.5E−02 n=1 fg=0.01 bg=0.00
hydroxymethylglutaryl−CoA hydrolase acti... GO:0047994 p=3.5E−02 n=1 fg=0.01 bg=0.00
aspartate−tRNA ligase activity GO:0004815 p=3.5E−02 n=1 fg=0.01 bg=0.00
hydroxymethyl−, formyl− and related tran... GO:0016742 p=3.5E−02 n=1 fg=0.01 bg=0.00
aminoacyl−tRNA hydrolase activity GO:0004045 p=3.5E−02 n=1 fg=0.01 bg=0.00
aminoacylase activity GO:0004046 p=3.5E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=82/344 input genes with annotations
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fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001633901.3
fraction genes in fg and expected valu
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cell projection GO:0042995 p=8.1E−03 n=26 fg=0.29 bg=0.18
plasma membrane bounded cell projection GO:0120025 p=1.5E−02 n=25 fg=0.27 bg=0.18
voltage−gated calcium channel complex GO:0005891 p=1.5E−02 n=2 fg=0.02 bg=0.00
presynapse GO:0098793 p=2.0E−02 n=9 fg=0.10 bg=0.05
DNA repair complex GO:1990391 p=2.8E−02 n=2 fg=0.02 bg=0.00
synapse GO:0045202 p=3.2E−02 n=13 fg=0.14 bg=0.08
transporter complex GO:1990351 p=3.4E−02 n=5 fg=0.05 bg=0.02
kinesin II complex GO:0016939 p=3.4E−02 n=1 fg=0.01 bg=0.00
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female germline ring canal outer rim GO:0035182 p=3.4E−02 n=1 fg=0.01 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=3.4E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=3.4E−02 n=1 fg=0.01 bg=0.00
smooth muscle contractile fiber GO:0030485 p=3.4E−02 n=1 fg=0.01 bg=0.00
XPC complex GO:0071942 p=3.4E−02 n=1 fg=0.01 bg=0.00
nucleotide−excision repair complex GO:0000109 p=3.4E−02 n=1 fg=0.01 bg=0.00
micropyle GO:0070825 p=3.4E−02 n=1 fg=0.01 bg=0.00
sperm connecting piece GO:0097224 p=3.4E−02 n=1 fg=0.01 bg=0.00
egg chorion GO:0042600 p=3.4E−02 n=1 fg=0.01 bg=0.00
hippocampal mossy fiber expansion GO:1990026 p=3.4E−02 n=1 fg=0.01 bg=0.00
varicosity GO:0043196 p=3.4E−02 n=1 fg=0.01 bg=0.00
trans−Golgi network transport vesicle GO:0030140 p=3.5E−02 n=2 fg=0.02 bg=0.00
calcium channel complex GO:0034704 p=3.5E−02 n=2 fg=0.02 bg=0.00
synaptic vesicle GO:0008021 p=3.8E−02 n=5 fg=0.05 bg=0.02
presynaptic active zone GO:0048786 p=4.0E−02 n=3 fg=0.03 bg=0.01
neuron projection cytoplasm GO:0120111 p=5.1E−02 n=2 fg=0.02 bg=0.00
exocytic vesicle GO:0070382 p=5.9E−02 n=5 fg=0.05 bg=0.02
Golgi trans cisterna GO:0000138 p=5.9E−02 n=2 fg=0.02 bg=0.00
external encapsulating structure GO:0030312 p=6.0E−02 n=3 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=91/344 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction