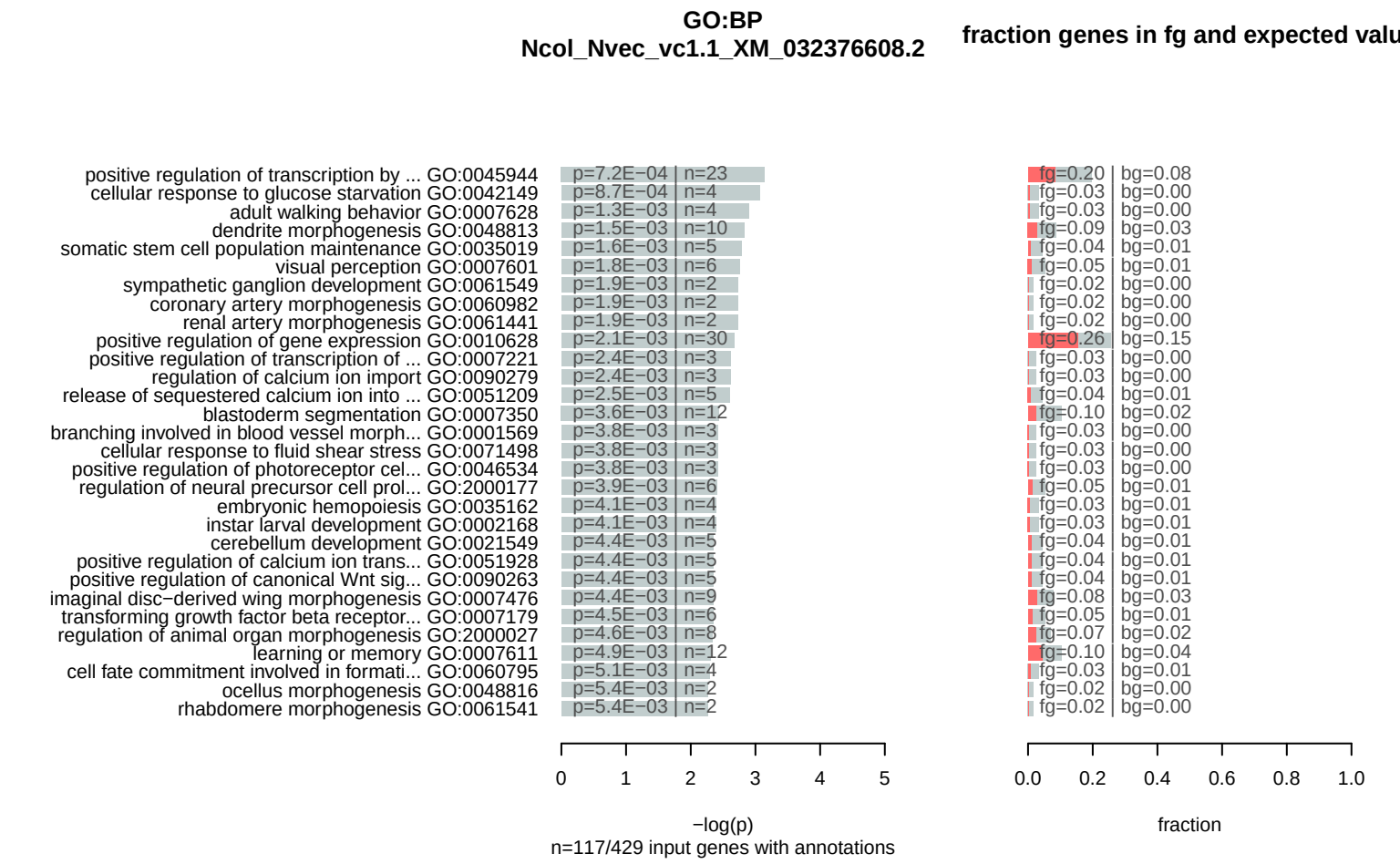
GO:BP
Ncol_Nvec_vc1.1_XM_032376608.2
fraction genes in fg and expected valu
positive regulation of transcription by ... GO:0045944 p=7.2E−04 n=23 fg=0.20 bg=0.08
cellular response to glucose starvation GO:0042149 p=8.7E−04 n=4 fg=0.03 bg=0.00
adult walking behavior GO:0007628 p=1.3E−03 n=4 fg=0.03 bg=0.00
dendrite morphogenesis GO:0048813 p=1.5E−03 n=10 fg=0.09 bg=0.03
somatic stem cell population maintenance GO:0035019 p=1.6E−03 n=5 fg=0.04 bg=0.01
visual perception GO:0007601 p=1.8E−03 n=6 fg=0.05 bg=0.01
sympathetic ganglion development GO:0061549 p=1.9E−03 n=2 fg=0.02 bg=0.00
coronary artery morphogenesis GO:0060982 p=1.9E−03 n=2 fg=0.02 bg=0.00
renal artery morphogenesis GO:0061441 p=1.9E−03 n=2 fg=0.02 bg=0.00
positive regulation of gene expression GO:0010628 p=2.1E−03 n=30 fg=0.26 bg=0.15
positive regulation of transcription of ... GO:0007221 p=2.4E−03 n=3 fg=0.03 bg=0.00
regulation of calcium ion import GO:0090279 p=2.4E−03 n=3 fg=0.03 bg=0.00
release of sequestered calcium ion into ... GO:0051209 p=2.5E−03 n=5 fg=0.04 bg=0.01
blastoderm segmentation GO:0007350 p=3.6E−03 n=12 fg=0.10 bg=0.02
branching involved in blood vessel morph... GO:0001569 p=3.8E−03 n=3 fg=0.03 bg=0.00
cellular response to fluid shear stress GO:0071498 p=3.8E−03 n=3 fg=0.03 bg=0.00
positive regulation of photoreceptor cel... GO:0046534 p=3.8E−03 n=3 fg=0.03 bg=0.00
regulation of neural precursor cell prol... GO:2000177 p=3.9E−03 n=6 fg=0.05 bg=0.01
embryonic hemopoiesis GO:0035162 p=4.1E−03 n=4 fg=0.03 bg=0.01
instar larval development GO:0002168 p=4.1E−03 n=4 fg=0.03 bg=0.01
cerebellum development GO:0021549 p=4.4E−03 n=5 fg=0.04 bg=0.01
positive regulation of calcium ion trans... GO:0051928 p=4.4E−03 n=5 fg=0.04 bg=0.01
positive regulation of canonical Wnt sig... GO:0090263 p=4.4E−03 n=5 fg=0.04 bg=0.01
imaginal disc−derived wing morphogenesis GO:0007476 p=4.4E−03 n=9 fg=0.08 bg=0.03
transforming growth factor beta receptor... GO:0007179 p=4.5E−03 n=6 fg=0.05 bg=0.01
regulation of animal organ morphogenesis GO:2000027 p=4.6E−03 n=8 fg=0.07 bg=0.02
learning or memory GO:0007611 p=4.9E−03 n=12 fg=0.10 bg=0.04
cell fate commitment involved in formati... GO:0060795 p=5.1E−03 n=4 fg=0.03 bg=0.01
ocellus morphogenesis GO:0048816 p=5.4E−03 n=2 fg=0.02 bg=0.00
rhabdomere morphogenesis GO:0061541 p=5.4E−03 n=2 fg=0.02 bg=0.00
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n=117/429 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
transcription coregulator binding GO:0001221 p=4.5E−04 n=4 fg=0.04 bg=0.00
coreceptor activity GO:0015026 p=1.7E−03 n=3 fg=0.03 bg=0.00
calcium−release channel activity GO:0015278 p=2.9E−03 n=3 fg=0.03 bg=0.00
SMAD binding GO:0046332 p=5.0E−03 n=4 fg=0.04 bg=0.01
protein dimerization activity GO:0046983 p=5.5E−03 n=24 fg=0.22 bg=0.13
voltage−gated sodium channel activity GO:0005248 p=1.2E−02 n=2 fg=0.02 bg=0.00
voltage−gated cation channel activity GO:0022843 p=1.6E−02 n=4 fg=0.04 bg=0.01
DNA−binding transcription factor activit... GO:0003700 p=1.9E−02 n=14 fg=0.13 bg=0.07
transcription coactivator binding GO:0001223 p=1.9E−02 n=2 fg=0.02 bg=0.00
actin monomer binding GO:0003785 p=1.9E−02 n=2 fg=0.02 bg=0.00
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transcription regulator activity GO:0140110 p=2.4E−02 n=18 fg=0.17 bg=0.10
Wnt−protein binding GO:0017147 p=2.8E−02 n=2 fg=0.02 bg=0.00
sodium channel activity GO:0005272 p=2.8E−02 n=2 fg=0.02 bg=0.00
cysteine−type endopeptidase regulator ac... GO:0043028 p=2.8E−02 n=2 fg=0.02 bg=0.00
mitogen−activated protein kinase kinase ... GO:0031434 p=2.8E−02 n=2 fg=0.02 bg=0.00
GTPase activator activity GO:0005096 p=3.3E−02 n=6 fg=0.06 bg=0.02
protein kinase binding GO:0019901 p=3.5E−02 n=13 fg=0.12 bg=0.07
adrenergic receptor binding GO:0031690 p=3.8E−02 n=2 fg=0.02 bg=0.00
ion gated channel activity GO:0022839 p=4.1E−02 n=6 fg=0.06 bg=0.02
voltage−gated channel activity GO:0022832 p=4.1E−02 n=4 fg=0.04 bg=0.01
voltage−gated ion channel activity GO:0005244 p=4.1E−02 n=4 fg=0.04 bg=0.01
cadmium ion binding GO:0046870 p=4.6E−02 n=1 fg=0.01 bg=0.00
DNA topoisomerase type II (double strand... GO:0072586 p=4.6E−02 n=1 fg=0.01 bg=0.00
DNA topoisomerase type II (double strand... GO:0072587 p=4.6E−02 n=1 fg=0.01 bg=0.00
opsin binding GO:0002046 p=4.6E−02 n=1 fg=0.01 bg=0.00
anaphase−promoting complex binding GO:0010997 p=4.6E−02 n=1 fg=0.01 bg=0.00
myosin II binding GO:0045159 p=4.6E−02 n=1 fg=0.01 bg=0.00
semaphorin receptor activity GO:0017154 p=4.6E−02 n=1 fg=0.01 bg=0.00
short−branched−chain−acyl−CoA dehydrogen... GO:0016937 p=4.6E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=109/429 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032376608.2
fraction genes in fg and expected valu
beta−catenin−TCF complex GO:1990907 p=5.3E−03 n=2 fg=0.02 bg=0.00
phagophore assembly site membrane GO:0034045 p=5.3E−03 n=2 fg=0.02 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=1.7E−02 n=2 fg=0.02 bg=0.00
perinuclear endoplasmic reticulum GO:0097038 p=1.7E−02 n=2 fg=0.02 bg=0.00
kinetochore microtubule GO:0005828 p=1.7E−02 n=2 fg=0.02 bg=0.00
sensory dendrite GO:0071683 p=1.7E−02 n=2 fg=0.02 bg=0.00
Golgi cis cisterna GO:0000137 p=1.7E−02 n=2 fg=0.02 bg=0.00
chromatin GO:0000785 p=2.0E−02 n=11 fg=0.09 bg=0.05
tight junction GO:0070160 p=2.9E−02 n=3 fg=0.03 bg=0.01
Scrib−APC−beta−catenin complex GO:0034750 p=4.3E−02 n=1 fg=0.01 bg=0.00
catenin−TCF7L2 complex GO:0071664 p=4.3E−02 n=1 fg=0.01 bg=0.00
condensin complex GO:0000796 p=4.3E−02 n=1 fg=0.01 bg=0.00
apoptosome GO:0043293 p=4.3E−02 n=1 fg=0.01 bg=0.00
smooth septate junction GO:0005920 p=4.3E−02 n=1 fg=0.01 bg=0.00
semaphorin receptor complex GO:0002116 p=4.3E−02 n=1 fg=0.01 bg=0.00
fascia adherens GO:0005916 p=4.3E−02 n=1 fg=0.01 bg=0.00
polycystin complex GO:0002133 p=4.3E−02 n=1 fg=0.01 bg=0.00
axonemal basal plate GO:0097541 p=4.3E−02 n=1 fg=0.01 bg=0.00
beta−catenin−TCF7L2 complex GO:0070369 p=4.3E−02 n=1 fg=0.01 bg=0.00
transport vesicle GO:0030133 p=4.4E−02 n=8 fg=0.07 bg=0.03
exocytic vesicle GO:0070382 p=5.1E−02 n=6 fg=0.05 bg=0.02
MLL1 complex GO:0071339 p=5.4E−02 n=2 fg=0.02 bg=0.00
melanosome GO:0042470 p=5.4E−02 n=2 fg=0.02 bg=0.00
calcium channel complex GO:0034704 p=5.4E−02 n=2 fg=0.02 bg=0.00
cell projection membrane GO:0031253 p=6.3E−02 n=7 fg=0.06 bg=0.03
pigment granule GO:0048770 p=6.6E−02 n=2 fg=0.02 bg=0.00
supramolecular polymer GO:0099081 p=7.2E−02 n=10 fg=0.09 bg=0.05
supramolecular fiber GO:0099512 p=7.2E−02 n=10 fg=0.09 bg=0.05
endoplasmic reticulum−Golgi intermediate... GO:0005793 p=7.3E−02 n=3 fg=0.03 bg=0.01
supramolecular complex GO:0099080 p=7.6E−02 n=14 fg=0.12 bg=0.08
0 1 2 3 4 5
−log(p)
n=116/429 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction