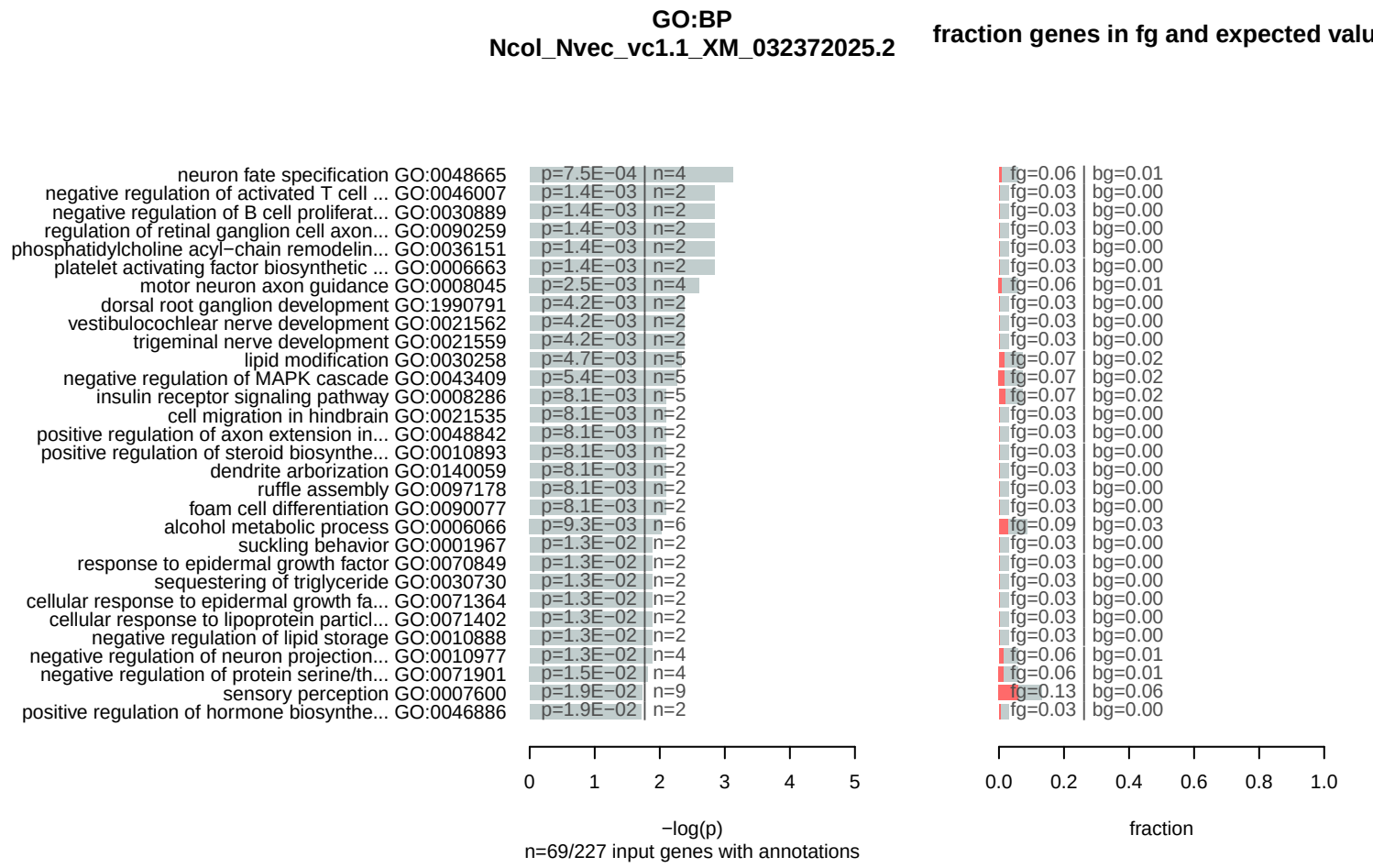
GO:BP
Ncol_Nvec_vc1.1_XM_032372025.2
fraction genes in fg and expected valu
neuron fate specification GO:0048665 p=7.5E−04 n=4 fg=0.06 bg=0.01
negative regulation of activated T cell ... GO:0046007 p=1.4E−03 n=2 fg=0.03 bg=0.00
negative regulation of B cell proliferat... GO:0030889 p=1.4E−03 n=2 fg=0.03 bg=0.00
regulation of retinal ganglion cell axon... GO:0090259 p=1.4E−03 n=2 fg=0.03 bg=0.00
phosphatidylcholine acyl−chain remodelin... GO:0036151 p=1.4E−03 n=2 fg=0.03 bg=0.00
platelet activating factor biosynthetic ... GO:0006663 p=1.4E−03 n=2 fg=0.03 bg=0.00
motor neuron axon guidance GO:0008045 p=2.5E−03 n=4 fg=0.06 bg=0.01
dorsal root ganglion development GO:1990791 p=4.2E−03 n=2 fg=0.03 bg=0.00
vestibulocochlear nerve development GO:0021562 p=4.2E−03 n=2 fg=0.03 bg=0.00
trigeminal nerve development GO:0021559 p=4.2E−03 n=2 fg=0.03 bg=0.00
lipid modification GO:0030258 p=4.7E−03 n=5 fg=0.07 bg=0.02
negative regulation of MAPK cascade GO:0043409 p=5.4E−03 n=5 fg=0.07 bg=0.02
insulin receptor signaling pathway GO:0008286 p=8.1E−03 n=5 fg=0.07 bg=0.02
cell migration in hindbrain GO:0021535 p=8.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of axon extension in... GO:0048842 p=8.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of steroid biosynthe... GO:0010893 p=8.1E−03 n=2 fg=0.03 bg=0.00
dendrite arborization GO:0140059 p=8.1E−03 n=2 fg=0.03 bg=0.00
ruffle assembly GO:0097178 p=8.1E−03 n=2 fg=0.03 bg=0.00
foam cell differentiation GO:0090077 p=8.1E−03 n=2 fg=0.03 bg=0.00
alcohol metabolic process GO:0006066 p=9.3E−03 n=6 fg=0.09 bg=0.03
suckling behavior GO:0001967 p=1.3E−02 n=2 fg=0.03 bg=0.00
response to epidermal growth factor GO:0070849 p=1.3E−02 n=2 fg=0.03 bg=0.00
sequestering of triglyceride GO:0030730 p=1.3E−02 n=2 fg=0.03 bg=0.00
cellular response to epidermal growth fa... GO:0071364 p=1.3E−02 n=2 fg=0.03 bg=0.00
cellular response to lipoprotein particl... GO:0071402 p=1.3E−02 n=2 fg=0.03 bg=0.00
negative regulation of lipid storage GO:0010888 p=1.3E−02 n=2 fg=0.03 bg=0.00
negative regulation of neuron projection... GO:0010977 p=1.3E−02 n=4 fg=0.06 bg=0.01
negative regulation of protein serine/th... GO:0071901 p=1.5E−02 n=4 fg=0.06 bg=0.01
sensory perception GO:0007600 p=1.9E−02 n=9 fg=0.13 bg=0.06
positive regulation of hormone biosynthe... GO:0046886 p=1.9E−02 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=69/227 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032372025.2
fraction genes in fg and expected valu
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=1.3E−03 n=2 fg=0.03 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=1.3E−03 n=2 fg=0.03 bg=0.00
phosphatidylinositol−3,4,5−trisphosphate... GO:0034485 p=1.3E−03 n=2 fg=0.03 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=1.3E−03 n=2 fg=0.03 bg=0.00
inositol−polyphosphate 5−phosphatase act... GO:0004445 p=1.3E−03 n=2 fg=0.03 bg=0.00
inositol−1,3,4,5−tetrakisphosphate 5−pho... GO:0052659 p=3.8E−03 n=2 fg=0.03 bg=0.00
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=3.8E−03 n=2 fg=0.03 bg=0.00
potassium channel regulator activity GO:0015459 p=6.2E−03 n=3 fg=0.05 bg=0.01
transmitter−gated ion channel activity GO:0022824 p=1.2E−02 n=2 fg=0.03 bg=0.00
transmitter−gated channel activity GO:0022835 p=1.2E−02 n=2 fg=0.03 bg=0.00
ubiquitin−like protein ligase activity GO:0061659 p=1.5E−02 n=6 fg=0.10 bg=0.04
ubiquitin protein ligase activity GO:0061630 p=1.5E−02 n=6 fg=0.10 bg=0.04
ubiquitin−protein transferase activity GO:0004842 p=1.6E−02 n=8 fg=0.14 bg=0.06
cholesterol binding GO:0015485 p=1.8E−02 n=2 fg=0.03 bg=0.00
potassium channel inhibitor activity GO:0019870 p=1.8E−02 n=2 fg=0.03 bg=0.00
ubiquitin−like protein transferase activ... GO:0019787 p=1.9E−02 n=8 fg=0.14 bg=0.06
sterol binding GO:0032934 p=2.4E−02 n=2 fg=0.03 bg=0.00
steroid binding GO:0005496 p=3.2E−02 n=2 fg=0.03 bg=0.00
NEDD8 conjugating enzyme activity GO:0061654 p=3.6E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.6E−02 n=1 fg=0.02 bg=0.00
semaphorin receptor activity GO:0017154 p=3.6E−02 n=1 fg=0.02 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=3.6E−02 n=1 fg=0.02 bg=0.00
phorbol ester receptor activity GO:0001565 p=3.6E−02 n=1 fg=0.02 bg=0.00
dolichyl−phosphate beta−glucosyltransfer... GO:0004581 p=3.6E−02 n=1 fg=0.02 bg=0.00
platelet−derived growth factor receptor ... GO:0005161 p=3.6E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0052890 p=3.6E−02 n=1 fg=0.02 bg=0.00
vascular endothelial growth factor bindi... GO:0038085 p=3.6E−02 n=1 fg=0.02 bg=0.00
butyryl−CoA dehydrogenase activity GO:0004085 p=3.6E−02 n=1 fg=0.02 bg=0.00
MDM2/MDM4 family protein binding GO:0097371 p=3.6E−02 n=1 fg=0.02 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=3.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=58/227 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032372025.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=3.6E−03 n=3 fg=0.04 bg=0.01
endoplasmic reticulum membrane GO:0005789 p=4.5E−03 n=12 fg=0.18 bg=0.08
lipid droplet GO:0005811 p=4.6E−03 n=4 fg=0.06 bg=0.01
exocytic vesicle GO:0070382 p=1.5E−02 n=6 fg=0.09 bg=0.03
plasma membrane proton−transporting V−ty... GO:0033181 p=1.9E−02 n=2 fg=0.03 bg=0.00
mitochondrial nucleoid GO:0042645 p=1.9E−02 n=2 fg=0.03 bg=0.00
nucleoid GO:0009295 p=1.9E−02 n=2 fg=0.03 bg=0.00
postsynaptic membrane GO:0045211 p=2.4E−02 n=4 fg=0.06 bg=0.02
cytoplasm GO:0005737 p=2.4E−02 n=62 fg=0.91 bg=0.80
vacuolar proton−transporting V−type ATPa... GO:0016471 p=2.6E−02 n=2 fg=0.03 bg=0.00
transport vesicle membrane GO:0030658 p=2.7E−02 n=4 fg=0.06 bg=0.02
dendritic shaft GO:0043198 p=2.8E−02 n=3 fg=0.04 bg=0.01
presynapse GO:0098793 p=2.9E−02 n=8 fg=0.12 bg=0.05
synaptic vesicle GO:0008021 p=3.2E−02 n=5 fg=0.07 bg=0.03
cell leading edge GO:0031252 p=3.3E−02 n=6 fg=0.09 bg=0.04
proton−transporting V−type ATPase comple... GO:0033176 p=3.4E−02 n=2 fg=0.03 bg=0.00
cytoplasmic microtubule GO:0005881 p=3.4E−02 n=2 fg=0.03 bg=0.00
proton−transporting two−sector ATPase co... GO:0016469 p=3.4E−02 n=2 fg=0.03 bg=0.00
exocytic vesicle membrane GO:0099501 p=3.7E−02 n=3 fg=0.04 bg=0.01
cell surface GO:0009986 p=3.7E−02 n=6 fg=0.09 bg=0.04
isocitrate dehydrogenase complex (NAD+) GO:0045242 p=3.8E−02 n=1 fg=0.01 bg=0.00
death−inducing signaling complex GO:0031264 p=3.8E−02 n=1 fg=0.01 bg=0.00
9+2 non−motile cilium GO:0097732 p=3.8E−02 n=1 fg=0.01 bg=0.00
axonemal microtubule GO:0005879 p=3.8E−02 n=1 fg=0.01 bg=0.00
mitochondrial DNA−directed RNA polymeras... GO:0034245 p=3.8E−02 n=1 fg=0.01 bg=0.00
kinocilium GO:0060091 p=3.8E−02 n=1 fg=0.01 bg=0.00
semaphorin receptor complex GO:0002116 p=3.8E−02 n=1 fg=0.01 bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0005962 p=3.8E−02 n=1 fg=0.01 bg=0.00
mitochondrial protein−containing complex GO:0098798 p=4.7E−02 n=4 fg=0.06 bg=0.02
leading edge membrane GO:0031256 p=6.5E−02 n=3 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=68/227 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction