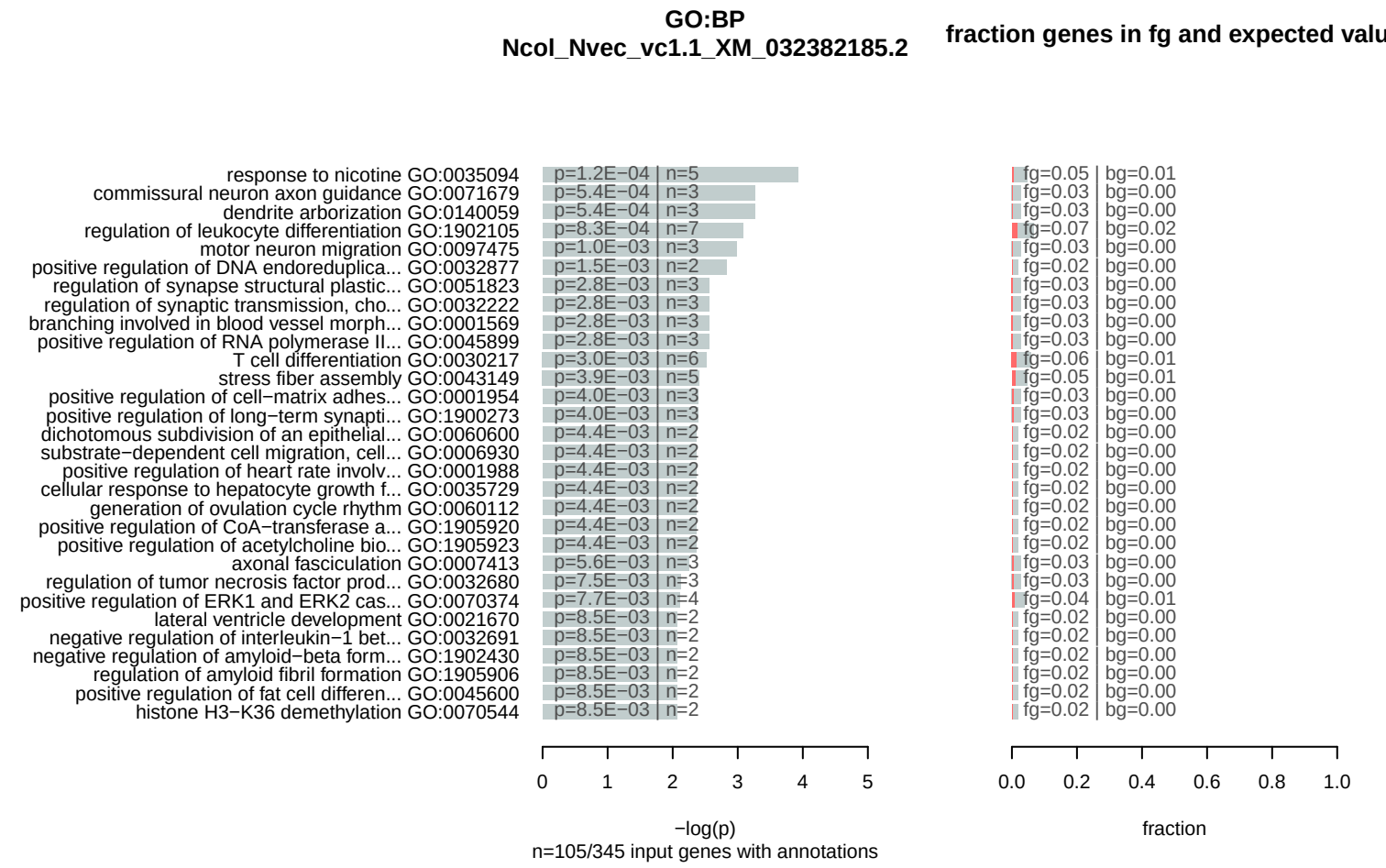
GO:BP
Ncol_Nvec_vc1.1_XM_032382185.2
fraction genes in fg and expected valu
response to nicotine GO:0035094 p=1.2E−04 n=5 fg=0.05 bg=0.01
commissural neuron axon guidance GO:0071679 p=5.4E−04 n=3 fg=0.03 bg=0.00
dendrite arborization GO:0140059 p=5.4E−04 n=3 fg=0.03 bg=0.00
regulation of leukocyte differentiation GO:1902105 p=8.3E−04 n=7 fg=0.07 bg=0.02
motor neuron migration GO:0097475 p=1.0E−03 n=3 fg=0.03 bg=0.00
positive regulation of DNA endoreduplica... GO:0032877 p=1.5E−03 n=2 fg=0.02 bg=0.00
regulation of synapse structural plastic... GO:0051823 p=2.8E−03 n=3 fg=0.03 bg=0.00
regulation of synaptic transmission, cho... GO:0032222 p=2.8E−03 n=3 fg=0.03 bg=0.00
branching involved in blood vessel morph... GO:0001569 p=2.8E−03 n=3 fg=0.03 bg=0.00
positive regulation of RNA polymerase II... GO:0045899 p=2.8E−03 n=3 fg=0.03 bg=0.00
T cell differentiation GO:0030217 p=3.0E−03 n=6 fg=0.06 bg=0.01
stress fiber assembly GO:0043149 p=3.9E−03 n=5 fg=0.05 bg=0.01
positive regulation of cell−matrix adhes... GO:0001954 p=4.0E−03 n=3 fg=0.03 bg=0.00
positive regulation of long−term synapti... GO:1900273 p=4.0E−03 n=3 fg=0.03 bg=0.00
dichotomous subdivision of an epithelial... GO:0060600 p=4.4E−03 n=2 fg=0.02 bg=0.00
substrate−dependent cell migration, cell... GO:0006930 p=4.4E−03 n=2 fg=0.02 bg=0.00
positive regulation of heart rate involv... GO:0001988 p=4.4E−03 n=2 fg=0.02 bg=0.00
cellular response to hepatocyte growth f... GO:0035729 p=4.4E−03 n=2 fg=0.02 bg=0.00
generation of ovulation cycle rhythm GO:0060112 p=4.4E−03 n=2 fg=0.02 bg=0.00
positive regulation of CoA−transferase a... GO:1905920 p=4.4E−03 n=2 fg=0.02 bg=0.00
positive regulation of acetylcholine bio... GO:1905923 p=4.4E−03 n=2 fg=0.02 bg=0.00
axonal fasciculation GO:0007413 p=5.6E−03 n=3 fg=0.03 bg=0.00
regulation of tumor necrosis factor prod... GO:0032680 p=7.5E−03 n=3 fg=0.03 bg=0.00
positive regulation of ERK1 and ERK2 cas... GO:0070374 p=7.7E−03 n=4 fg=0.04 bg=0.01
lateral ventricle development GO:0021670 p=8.5E−03 n=2 fg=0.02 bg=0.00
negative regulation of interleukin−1 bet... GO:0032691 p=8.5E−03 n=2 fg=0.02 bg=0.00
negative regulation of amyloid−beta form... GO:1902430 p=8.5E−03 n=2 fg=0.02 bg=0.00
regulation of amyloid fibril formation GO:1905906 p=8.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of fat cell differen... GO:0045600 p=8.5E−03 n=2 fg=0.02 bg=0.00
histone H3−K36 demethylation GO:0070544 p=8.5E−03 n=2 fg=0.02 bg=0.00
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−log(p)
n=105/345 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032382185.2
fraction genes in fg and expected valu
ammonium ion binding GO:0070405 p=1.3E−03 n=4 fg=0.04 bg=0.01
acetylcholine−gated cation−selective cha... GO:0022848 p=4.6E−03 n=2 fg=0.02 bg=0.00
acetylcholine receptor activity GO:0015464 p=4.6E−03 n=2 fg=0.02 bg=0.00
acetylcholine binding GO:0042166 p=4.6E−03 n=2 fg=0.02 bg=0.00
histone H3−methyl−lysine−36 demethylase ... GO:0051864 p=8.9E−03 n=2 fg=0.02 bg=0.00
cytochrome−c oxidase activity GO:0004129 p=8.9E−03 n=2 fg=0.02 bg=0.00
protein−disulfide reductase activity GO:0015035 p=1.0E−02 n=3 fg=0.03 bg=0.01
transcription coactivator binding GO:0001223 p=1.4E−02 n=2 fg=0.02 bg=0.00
satellite DNA binding GO:0003696 p=1.4E−02 n=2 fg=0.02 bg=0.00
histone H3−methyl−lysine−4 demethylase a... GO:0032453 p=1.4E−02 n=2 fg=0.02 bg=0.00
toxic substance binding GO:0015643 p=1.4E−02 n=2 fg=0.02 bg=0.00
chaperone binding GO:0051087 p=1.6E−02 n=5 fg=0.05 bg=0.02
disulfide oxidoreductase activity GO:0015036 p=1.6E−02 n=3 fg=0.03 bg=0.01
nuclear receptor activity GO:0004879 p=2.9E−02 n=2 fg=0.02 bg=0.00
chloride channel regulator activity GO:0017081 p=2.9E−02 n=2 fg=0.02 bg=0.00
adenylate cyclase binding GO:0008179 p=2.9E−02 n=2 fg=0.02 bg=0.00
dopamine receptor binding GO:0050780 p=2.9E−02 n=2 fg=0.02 bg=0.00
phosphatidylcholine binding GO:0031210 p=2.9E−02 n=2 fg=0.02 bg=0.00
ligand−activated transcription factor ac... GO:0098531 p=2.9E−02 n=2 fg=0.02 bg=0.00
molecular carrier activity GO:0140104 p=3.7E−02 n=2 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=4.0E−02 n=1 fg=0.01 bg=0.00
siRNA binding GO:0035197 p=4.0E−02 n=1 fg=0.01 bg=0.00
vascular endothelial growth factor bindi... GO:0038085 p=4.0E−02 n=1 fg=0.01 bg=0.00
misfolded RNA binding GO:0034336 p=4.0E−02 n=1 fg=0.01 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=4.0E−02 n=1 fg=0.01 bg=0.00
double−stranded methylated DNA binding GO:0010385 p=4.0E−02 n=1 fg=0.01 bg=0.00
ACP phosphopantetheine attachment site b... GO:0044620 p=4.0E−02 n=1 fg=0.01 bg=0.00
phosphopantetheine binding GO:0031177 p=4.0E−02 n=1 fg=0.01 bg=0.00
glucose−6−phosphate dehydrogenase activi... GO:0004345 p=4.0E−02 n=1 fg=0.01 bg=0.00
D5 dopamine receptor binding GO:0031752 p=4.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=94/345 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032382185.2
fraction genes in fg and expected valu
dendritic spine neck GO:0044326 p=1.6E−03 n=2 fg=0.02 bg=0.00
acetylcholine−gated channel complex GO:0005892 p=4.6E−03 n=2 fg=0.02 bg=0.00
Fanconi anaemia nuclear complex GO:0043240 p=4.6E−03 n=2 fg=0.02 bg=0.00
neuron projection membrane GO:0032589 p=7.1E−03 n=4 fg=0.04 bg=0.01
PcG protein complex GO:0031519 p=1.3E−02 n=3 fg=0.03 bg=0.00
presynaptic periactive zone GO:0036062 p=1.5E−02 n=2 fg=0.02 bg=0.00
protein phosphatase type 1 complex GO:0000164 p=1.5E−02 n=2 fg=0.02 bg=0.00
growth cone GO:0030426 p=1.5E−02 n=6 fg=0.06 bg=0.02
site of polarized growth GO:0030427 p=1.9E−02 n=6 fg=0.06 bg=0.02
external side of plasma membrane GO:0009897 p=2.1E−02 n=4 fg=0.04 bg=0.01
sperm midpiece GO:0097225 p=2.1E−02 n=2 fg=0.02 bg=0.00
protein serine/threonine phosphatase com... GO:0008287 p=2.4E−02 n=3 fg=0.03 bg=0.01
side of membrane GO:0098552 p=2.7E−02 n=8 fg=0.07 bg=0.03
chaperone complex GO:0101031 p=2.9E−02 n=2 fg=0.02 bg=0.00
axolemma GO:0030673 p=2.9E−02 n=2 fg=0.02 bg=0.00
phosphatase complex GO:1903293 p=3.3E−02 n=3 fg=0.03 bg=0.01
dendrite membrane GO:0032590 p=3.8E−02 n=2 fg=0.02 bg=0.00
cytoplasmic side of dendritic spine plas... GO:1990780 p=4.0E−02 n=1 fg=0.01 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=4.0E−02 n=1 fg=0.01 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=4.0E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=4.0E−02 n=1 fg=0.01 bg=0.00
FANCM−MHF complex GO:0071821 p=4.0E−02 n=1 fg=0.01 bg=0.00
cyclin D2−CDK4 complex GO:0097129 p=4.0E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=4.0E−02 n=1 fg=0.01 bg=0.00
cyclin D2−CDK6 complex GO:0097132 p=4.0E−02 n=1 fg=0.01 bg=0.00
TSC1−TSC2 complex GO:0033596 p=4.0E−02 n=1 fg=0.01 bg=0.00
UTP−C complex GO:0034456 p=4.0E−02 n=1 fg=0.01 bg=0.00
semaphorin receptor complex GO:0002116 p=4.0E−02 n=1 fg=0.01 bg=0.00
tRNA methyltransferase complex GO:0043527 p=4.0E−02 n=1 fg=0.01 bg=0.00
CURI complex GO:0032545 p=4.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=108/345 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction