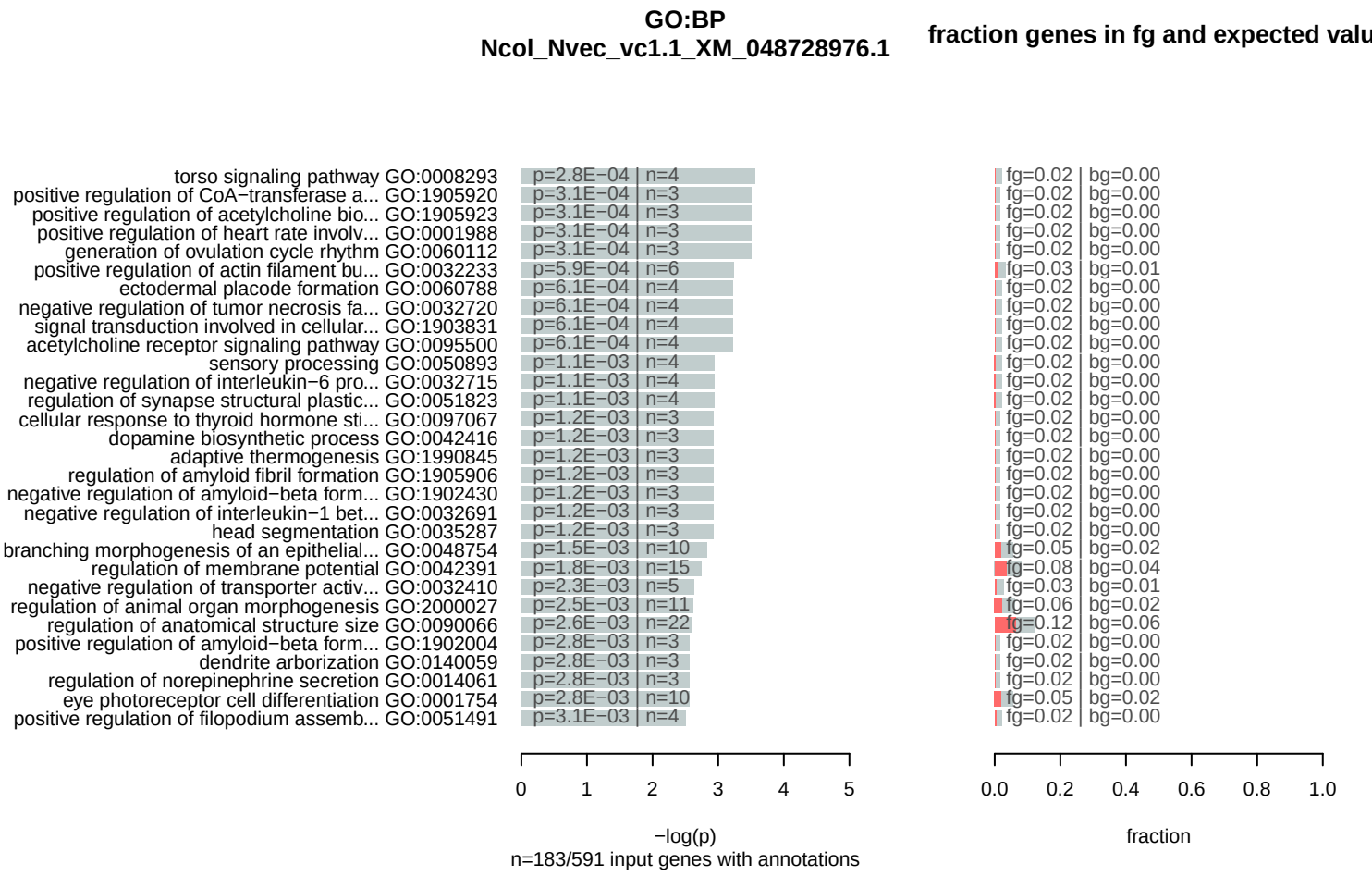
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fraction genes in fg and expected valu
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positive regulation of CoA−transferase a... GO:1905920 p=3.1E−04 n=3 fg=0.02 bg=0.00
positive regulation of acetylcholine bio... GO:1905923 p=3.1E−04 n=3 fg=0.02 bg=0.00
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generation of ovulation cycle rhythm GO:0060112 p=3.1E−04 n=3 fg=0.02 bg=0.00
positive regulation of actin filament bu... GO:0032233 p=5.9E−04 n=6 fg=0.03 bg=0.01
ectodermal placode formation GO:0060788 p=6.1E−04 n=4 fg=0.02 bg=0.00
negative regulation of tumor necrosis fa... GO:0032720 p=6.1E−04 n=4 fg=0.02 bg=0.00
signal transduction involved in cellular... GO:1903831 p=6.1E−04 n=4 fg=0.02 bg=0.00
acetylcholine receptor signaling pathway GO:0095500 p=6.1E−04 n=4 fg=0.02 bg=0.00
sensory processing GO:0050893 p=1.1E−03 n=4 fg=0.02 bg=0.00
negative regulation of interleukin−6 pro... GO:0032715 p=1.1E−03 n=4 fg=0.02 bg=0.00
regulation of synapse structural plastic... GO:0051823 p=1.1E−03 n=4 fg=0.02 bg=0.00
cellular response to thyroid hormone sti... GO:0097067 p=1.2E−03 n=3 fg=0.02 bg=0.00
dopamine biosynthetic process GO:0042416 p=1.2E−03 n=3 fg=0.02 bg=0.00
adaptive thermogenesis GO:1990845 p=1.2E−03 n=3 fg=0.02 bg=0.00
regulation of amyloid fibril formation GO:1905906 p=1.2E−03 n=3 fg=0.02 bg=0.00
negative regulation of amyloid−beta form... GO:1902430 p=1.2E−03 n=3 fg=0.02 bg=0.00
negative regulation of interleukin−1 bet... GO:0032691 p=1.2E−03 n=3 fg=0.02 bg=0.00
head segmentation GO:0035287 p=1.2E−03 n=3 fg=0.02 bg=0.00
branching morphogenesis of an epithelial... GO:0048754 p=1.5E−03 n=10 fg=0.05 bg=0.02
regulation of membrane potential GO:0042391 p=1.8E−03 n=15 fg=0.08 bg=0.04
negative regulation of transporter activ... GO:0032410 p=2.3E−03 n=5 fg=0.03 bg=0.01
regulation of animal organ morphogenesis GO:2000027 p=2.5E−03 n=11 fg=0.06 bg=0.02
regulation of anatomical structure size GO:0090066 p=2.6E−03 n=22 fg=0.12 bg=0.06
positive regulation of amyloid−beta form... GO:1902004 p=2.8E−03 n=3 fg=0.02 bg=0.00
dendrite arborization GO:0140059 p=2.8E−03 n=3 fg=0.02 bg=0.00
regulation of norepinephrine secretion GO:0014061 p=2.8E−03 n=3 fg=0.02 bg=0.00
eye photoreceptor cell differentiation GO:0001754 p=2.8E−03 n=10 fg=0.05 bg=0.02
positive regulation of filopodium assemb... GO:0051491 p=3.1E−03 n=4 fg=0.02 bg=0.00
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n=183/591 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048728976.1
fraction genes in fg and expected valu
acetylcholine binding GO:0042166 p=3.5E−04 n=3 fg=0.02 bg=0.00
acetylcholine−gated cation−selective cha... GO:0022848 p=3.5E−04 n=3 fg=0.02 bg=0.00
acetylcholine receptor activity GO:0015464 p=3.5E−04 n=3 fg=0.02 bg=0.00
cAMP binding GO:0030552 p=1.3E−03 n=3 fg=0.02 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=1.3E−03 n=3 fg=0.02 bg=0.00
ammonium ion binding GO:0070405 p=1.4E−03 n=5 fg=0.03 bg=0.01
ATPase binding GO:0051117 p=2.6E−03 n=7 fg=0.04 bg=0.01
toxic substance binding GO:0015643 p=3.2E−03 n=3 fg=0.02 bg=0.00
protein domain specific binding GO:0019904 p=4.5E−03 n=24 fg=0.14 bg=0.08
beta−2 adrenergic receptor binding GO:0031698 p=5.0E−03 n=2 fg=0.01 bg=0.00
eukaryotic initiation factor 4E binding GO:0008190 p=5.0E−03 n=2 fg=0.01 bg=0.00
malic enzyme activity GO:0004470 p=5.0E−03 n=2 fg=0.01 bg=0.00
D3 dopamine receptor binding GO:0031750 p=5.0E−03 n=2 fg=0.01 bg=0.00
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protein disulfide isomerase activity GO:0003756 p=6.0E−03 n=3 fg=0.02 bg=0.00
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signaling receptor binding GO:0005102 p=7.3E−03 n=30 fg=0.18 bg=0.10
phospholipid binding GO:0005543 p=7.9E−03 n=13 fg=0.08 bg=0.04
voltage−gated chloride channel activity GO:0005247 p=9.9E−03 n=3 fg=0.02 bg=0.00
adenylate cyclase binding GO:0008179 p=9.9E−03 n=3 fg=0.02 bg=0.00
chloride channel regulator activity GO:0017081 p=9.9E−03 n=3 fg=0.02 bg=0.00
phosphatidylinositol bisphosphate bindin... GO:1902936 p=1.4E−02 n=6 fg=0.04 bg=0.01
D2 dopamine receptor binding GO:0031749 p=1.4E−02 n=2 fg=0.01 bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=1.4E−02 n=2 fg=0.01 bg=0.00
S100 protein binding GO:0044548 p=1.4E−02 n=2 fg=0.01 bg=0.00
U2 snRNA binding GO:0030620 p=1.4E−02 n=2 fg=0.01 bg=0.00
cAMP−dependent protein kinase regulator ... GO:0008603 p=1.4E−02 n=2 fg=0.01 bg=0.00
snRNA binding GO:0017069 p=1.5E−02 n=3 fg=0.02 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=1.5E−02 n=3 fg=0.02 bg=0.00
ion gated channel activity GO:0022839 p=1.5E−02 n=9 fg=0.05 bg=0.02
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−log(p)
n=168/591 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048728976.1
fraction genes in fg and expected valu
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dendritic shaft GO:0043198 p=2.6E−03 n=6 fg=0.03 bg=0.01
apical plasma membrane GO:0016324 p=3.5E−03 n=14 fg=0.08 bg=0.03
extrinsic component of plasma membrane GO:0019897 p=3.7E−03 n=7 fg=0.04 bg=0.01
extracellular vesicle GO:1903561 p=4.2E−03 n=6 fg=0.03 bg=0.01
DNA polymerase III complex GO:0009360 p=4.5E−03 n=2 fg=0.01 bg=0.00
neuronal cell body GO:0043025 p=4.7E−03 n=20 fg=0.11 bg=0.06
cell leading edge GO:0031252 p=5.1E−03 n=16 fg=0.09 bg=0.04
presynaptic membrane GO:0042734 p=5.4E−03 n=7 fg=0.04 bg=0.01
perinuclear region of cytoplasm GO:0048471 p=5.4E−03 n=21 fg=0.12 bg=0.06
growth cone GO:0030426 p=6.1E−03 n=9 fg=0.05 bg=0.02
actin−based cell projection GO:0098858 p=6.1E−03 n=9 fg=0.05 bg=0.02
dendritic spine GO:0043197 p=6.9E−03 n=9 fg=0.05 bg=0.02
side of membrane GO:0098552 p=7.0E−03 n=13 fg=0.07 bg=0.03
extracellular space GO:0005615 p=7.8E−03 n=12 fg=0.07 bg=0.03
membrane raft GO:0045121 p=8.6E−03 n=11 fg=0.06 bg=0.03
axolemma GO:0030673 p=8.6E−03 n=3 fg=0.02 bg=0.00
lysosomal lumen GO:0043202 p=8.9E−03 n=5 fg=0.03 bg=0.01
extrinsic component of cytoplasmic side ... GO:0031234 p=1.1E−02 n=5 fg=0.03 bg=0.01
stereocilium GO:0032420 p=1.2E−02 n=4 fg=0.02 bg=0.01
stereocilium bundle GO:0032421 p=1.2E−02 n=4 fg=0.02 bg=0.01
cAMP−dependent protein kinase complex GO:0005952 p=1.3E−02 n=2 fg=0.01 bg=0.00
muscle cell projection GO:0036194 p=1.3E−02 n=2 fg=0.01 bg=0.00
muscle cell projection membrane GO:0036195 p=1.3E−02 n=2 fg=0.01 bg=0.00
actin cap GO:0030478 p=1.3E−02 n=2 fg=0.01 bg=0.00
plasma membrane raft GO:0044853 p=1.3E−02 n=6 fg=0.03 bg=0.01
filopodium GO:0030175 p=1.3E−02 n=5 fg=0.03 bg=0.01
postsynaptic membrane GO:0045211 p=1.4E−02 n=7 fg=0.04 bg=0.01
extracellular exosome GO:0070062 p=1.6E−02 n=5 fg=0.03 bg=0.01
Cul3−RING ubiquitin ligase complex GO:0031463 p=1.9E−02 n=3 fg=0.02 bg=0.00
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−log(p)
n=182/591 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction