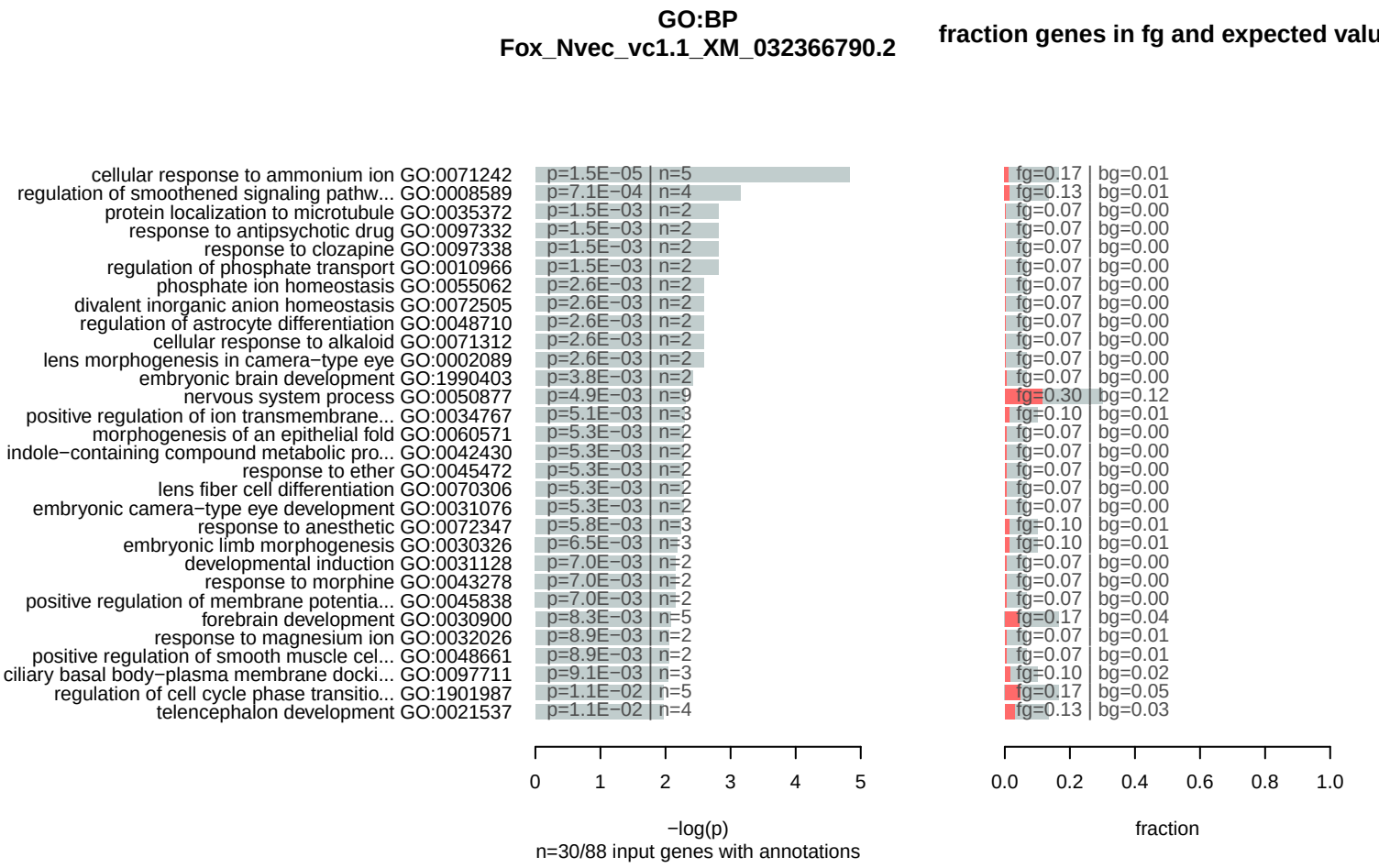
GO:BP
Fox_Nvec_vc1.1_XM_032366790.2
fraction genes in fg and expected valu
cellular response to ammonium ion GO:0071242 p=1.5E−05 n=5 fg=0.17 bg=0.01
regulation of smoothened signaling pathw... GO:0008589 p=7.1E−04 n=4 fg=0.13 bg=0.01
protein localization to microtubule GO:0035372 p=1.5E−03 n=2 fg=0.07 bg=0.00
response to antipsychotic drug GO:0097332 p=1.5E−03 n=2 fg=0.07 bg=0.00
response to clozapine GO:0097338 p=1.5E−03 n=2 fg=0.07 bg=0.00
regulation of phosphate transport GO:0010966 p=1.5E−03 n=2 fg=0.07 bg=0.00
phosphate ion homeostasis GO:0055062 p=2.6E−03 n=2 fg=0.07 bg=0.00
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regulation of astrocyte differentiation GO:0048710 p=2.6E−03 n=2 fg=0.07 bg=0.00
cellular response to alkaloid GO:0071312 p=2.6E−03 n=2 fg=0.07 bg=0.00
lens morphogenesis in camera−type eye GO:0002089 p=2.6E−03 n=2 fg=0.07 bg=0.00
embryonic brain development GO:1990403 p=3.8E−03 n=2 fg=0.07 bg=0.00
nervous system process GO:0050877 p=4.9E−03 n=9 fg=0.30 bg=0.12
positive regulation of ion transmembrane... GO:0034767 p=5.1E−03 n=3 fg=0.10 bg=0.01
morphogenesis of an epithelial fold GO:0060571 p=5.3E−03 n=2 fg=0.07 bg=0.00
indole−containing compound metabolic pro... GO:0042430 p=5.3E−03 n=2 fg=0.07 bg=0.00
response to ether GO:0045472 p=5.3E−03 n=2 fg=0.07 bg=0.00
lens fiber cell differentiation GO:0070306 p=5.3E−03 n=2 fg=0.07 bg=0.00
embryonic camera−type eye development GO:0031076 p=5.3E−03 n=2 fg=0.07 bg=0.00
response to anesthetic GO:0072347 p=5.8E−03 n=3 fg=0.10 bg=0.01
embryonic limb morphogenesis GO:0030326 p=6.5E−03 n=3 fg=0.10 bg=0.01
developmental induction GO:0031128 p=7.0E−03 n=2 fg=0.07 bg=0.00
response to morphine GO:0043278 p=7.0E−03 n=2 fg=0.07 bg=0.00
positive regulation of membrane potentia... GO:0045838 p=7.0E−03 n=2 fg=0.07 bg=0.00
forebrain development GO:0030900 p=8.3E−03 n=5 fg=0.17 bg=0.04
response to magnesium ion GO:0032026 p=8.9E−03 n=2 fg=0.07 bg=0.01
positive regulation of smooth muscle cel... GO:0048661 p=8.9E−03 n=2 fg=0.07 bg=0.01
ciliary basal body−plasma membrane docki... GO:0097711 p=9.1E−03 n=3 fg=0.10 bg=0.02
regulation of cell cycle phase transitio... GO:1901987 p=1.1E−02 n=5 fg=0.17 bg=0.05
telencephalon development GO:0021537 p=1.1E−02 n=4 fg=0.13 bg=0.03
0 1 2 3 4 5
−log(p)
n=30/88 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032366790.2
fraction genes in fg and expected valu
scaffold protein binding GO:0097110 p=9.9E−04 n=3 fg=0.14 bg=0.01
dopamine receptor binding GO:0050780 p=2.4E−03 n=2 fg=0.10 bg=0.00
adrenergic receptor binding GO:0031690 p=3.4E−03 n=2 fg=0.10 bg=0.00
enzyme binding GO:0019899 p=4.8E−03 n=11 fg=0.52 bg=0.24
signaling receptor binding GO:0005102 p=5.3E−03 n=9 fg=0.43 bg=0.10
protein domain specific binding GO:0019904 p=1.1E−02 n=6 fg=0.29 bg=0.09
catalytic activity, acting on a protein GO:0140096 p=1.3E−02 n=9 fg=0.43 bg=0.20
phosphate ion binding GO:0042301 p=1.3E−02 n=1 fg=0.05 bg=0.00
CD4 receptor binding GO:0042609 p=1.3E−02 n=1 fg=0.05 bg=0.00
beta−adrenergic receptor kinase activity GO:0047696 p=1.3E−02 n=1 fg=0.05 bg=0.00
sodium:phosphate symporter activity GO:0005436 p=1.3E−02 n=1 fg=0.05 bg=0.00
endothelial differentiation G protein−co... GO:0031753 p=1.3E−02 n=1 fg=0.05 bg=0.00
Edg−2 lysophosphatidic acid receptor bin... GO:0031755 p=1.3E−02 n=1 fg=0.05 bg=0.00
rhodopsin kinase activity GO:0050254 p=1.3E−02 n=1 fg=0.05 bg=0.00
G protein−coupled receptor kinase activi... GO:0004703 p=1.3E−02 n=1 fg=0.05 bg=0.00
opioid receptor binding GO:0031628 p=1.3E−02 n=1 fg=0.05 bg=0.00
fatty acid alpha−hydroxylase activity GO:0080132 p=1.3E−02 n=1 fg=0.05 bg=0.00
delta−type opioid receptor binding GO:0031850 p=1.3E−02 n=1 fg=0.05 bg=0.00
kappa−type opioid receptor binding GO:0031851 p=1.3E−02 n=1 fg=0.05 bg=0.00
protein homodimerization activity GO:0042803 p=1.3E−02 n=6 fg=0.29 bg=0.10
kinesin binding GO:0019894 p=1.4E−02 n=2 fg=0.10 bg=0.01
protein−containing complex binding GO:0044877 p=1.9E−02 n=6 fg=0.29 bg=0.11
protein kinase activity GO:0004672 p=2.1E−02 n=4 fg=0.19 bg=0.05
alpha−2A adrenergic receptor binding GO:0031694 p=2.6E−02 n=1 fg=0.05 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=2.6E−02 n=1 fg=0.05 bg=0.00
transcription corepressor binding GO:0001222 p=2.6E−02 n=1 fg=0.05 bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=2.6E−02 n=1 fg=0.05 bg=0.00
cAMP−dependent protein kinase regulator ... GO:0008603 p=2.6E−02 n=1 fg=0.05 bg=0.00
phosphate ion transmembrane transporter ... GO:0015114 p=2.6E−02 n=1 fg=0.05 bg=0.00
nucleosomal DNA binding GO:0031492 p=2.6E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=21/88 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032366790.2
fraction genes in fg and expected valu
dendritic shaft GO:0043198 p=1.4E−04 n=4 fg=0.14 bg=0.01
dendritic spine GO:0043197 p=3.3E−04 n=5 fg=0.17 bg=0.02
membrane raft GO:0045121 p=1.2E−03 n=5 fg=0.17 bg=0.03
perinuclear region of cytoplasm GO:0048471 p=3.8E−03 n=7 fg=0.24 bg=0.07
intracellular non−membrane−bounded organ... GO:0043232 p=7.4E−03 n=17 fg=0.59 bg=0.30
ciliary basal body GO:0036064 p=8.4E−03 n=3 fg=0.10 bg=0.01
dendritic spine neck GO:0044326 p=1.6E−02 n=1 fg=0.03 bg=0.00
dendritic spine head GO:0044327 p=1.6E−02 n=1 fg=0.03 bg=0.00
UBC13−UEV1A complex GO:0035370 p=1.6E−02 n=1 fg=0.03 bg=0.00
cytoplasmic side of dendritic spine plas... GO:1990780 p=1.6E−02 n=1 fg=0.03 bg=0.00
Ski complex GO:0055087 p=1.6E−02 n=1 fg=0.03 bg=0.00
RCAF complex GO:0035059 p=1.6E−02 n=1 fg=0.03 bg=0.00
asymmetric synapse GO:0032279 p=3.0E−02 n=3 fg=0.10 bg=0.02
neuron to neuron synapse GO:0098984 p=3.2E−02 n=3 fg=0.10 bg=0.02
extrinsic component of Golgi membrane GO:0090498 p=3.2E−02 n=1 fg=0.03 bg=0.00
plasma membrane raft GO:0044853 p=4.3E−02 n=2 fg=0.07 bg=0.01
ubiquitin conjugating enzyme complex GO:0031371 p=4.7E−02 n=1 fg=0.03 bg=0.00
NuRD complex GO:0016581 p=4.7E−02 n=1 fg=0.03 bg=0.00
mitochondrial respiratory chain complex ... GO:0005751 p=4.7E−02 n=1 fg=0.03 bg=0.00
dendritic spine membrane GO:0032591 p=4.7E−02 n=1 fg=0.03 bg=0.00
growth cone lamellipodium GO:1990761 p=4.7E−02 n=1 fg=0.03 bg=0.00
CHD−type complex GO:0090545 p=4.7E−02 n=1 fg=0.03 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=4.7E−02 n=1 fg=0.03 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=4.7E−02 n=1 fg=0.03 bg=0.00
respiratory chain complex IV GO:0045277 p=4.7E−02 n=1 fg=0.03 bg=0.00
intraciliary transport particle GO:0030990 p=4.7E−02 n=1 fg=0.03 bg=0.00
intraciliary transport particle A GO:0030991 p=4.7E−02 n=1 fg=0.03 bg=0.00
neuronal cell body GO:0043025 p=4.8E−02 n=5 fg=0.17 bg=0.07
ciliary transition zone GO:0035869 p=5.1E−02 n=2 fg=0.07 bg=0.01
presynaptic membrane GO:0042734 p=5.9E−02 n=2 fg=0.07 bg=0.01
0 1 2 3 4 5
−log(p)
n=29/88 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction