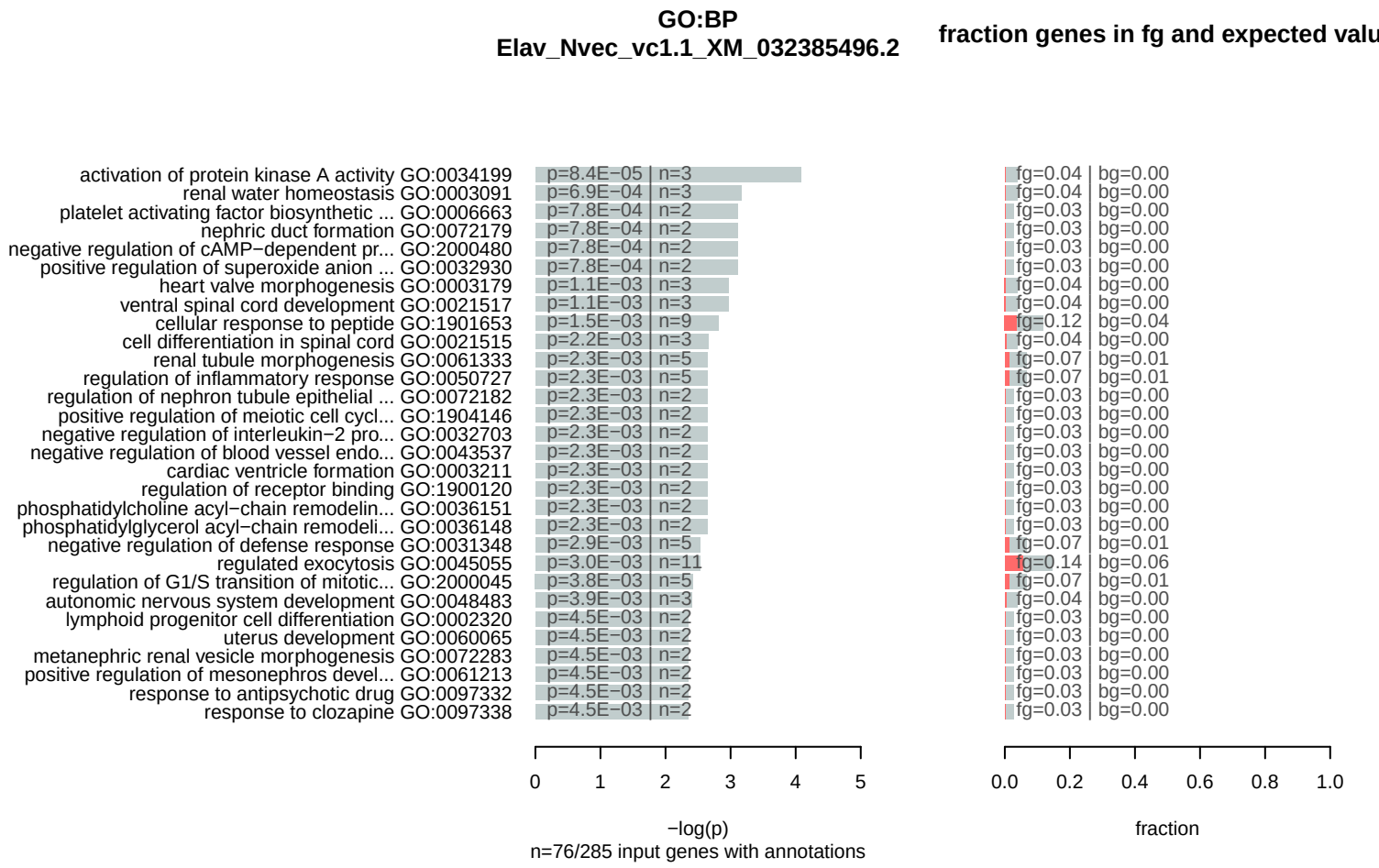
GO:BP
Elav_Nvec_vc1.1_XM_032385496.2
fraction genes in fg and expected valu
activation of protein kinase A activity GO:0034199 p=8.4E−05 n=3 fg=0.04 bg=0.00
renal water homeostasis GO:0003091 p=6.9E−04 n=3 fg=0.04 bg=0.00
platelet activating factor biosynthetic ... GO:0006663 p=7.8E−04 n=2 fg=0.03 bg=0.00
nephric duct formation GO:0072179 p=7.8E−04 n=2 fg=0.03 bg=0.00
negative regulation of cAMP−dependent pr... GO:2000480 p=7.8E−04 n=2 fg=0.03 bg=0.00
positive regulation of superoxide anion ... GO:0032930 p=7.8E−04 n=2 fg=0.03 bg=0.00
heart valve morphogenesis GO:0003179 p=1.1E−03 n=3 fg=0.04 bg=0.00
ventral spinal cord development GO:0021517 p=1.1E−03 n=3 fg=0.04 bg=0.00
cellular response to peptide GO:1901653 p=1.5E−03 n=9 fg=0.12 bg=0.04
cell differentiation in spinal cord GO:0021515 p=2.2E−03 n=3 fg=0.04 bg=0.00
renal tubule morphogenesis GO:0061333 p=2.3E−03 n=5 fg=0.07 bg=0.01
regulation of inflammatory response GO:0050727 p=2.3E−03 n=5 fg=0.07 bg=0.01
regulation of nephron tubule epithelial ... GO:0072182 p=2.3E−03 n=2 fg=0.03 bg=0.00
positive regulation of meiotic cell cycl... GO:1904146 p=2.3E−03 n=2 fg=0.03 bg=0.00
negative regulation of interleukin−2 pro... GO:0032703 p=2.3E−03 n=2 fg=0.03 bg=0.00
negative regulation of blood vessel endo... GO:0043537 p=2.3E−03 n=2 fg=0.03 bg=0.00
cardiac ventricle formation GO:0003211 p=2.3E−03 n=2 fg=0.03 bg=0.00
regulation of receptor binding GO:1900120 p=2.3E−03 n=2 fg=0.03 bg=0.00
phosphatidylcholine acyl−chain remodelin... GO:0036151 p=2.3E−03 n=2 fg=0.03 bg=0.00
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=2.3E−03 n=2 fg=0.03 bg=0.00
negative regulation of defense response GO:0031348 p=2.9E−03 n=5 fg=0.07 bg=0.01
regulated exocytosis GO:0045055 p=3.0E−03 n=11 fg=0.14 bg=0.06
regulation of G1/S transition of mitotic... GO:2000045 p=3.8E−03 n=5 fg=0.07 bg=0.01
autonomic nervous system development GO:0048483 p=3.9E−03 n=3 fg=0.04 bg=0.00
lymphoid progenitor cell differentiation GO:0002320 p=4.5E−03 n=2 fg=0.03 bg=0.00
uterus development GO:0060065 p=4.5E−03 n=2 fg=0.03 bg=0.00
metanephric renal vesicle morphogenesis GO:0072283 p=4.5E−03 n=2 fg=0.03 bg=0.00
positive regulation of mesonephros devel... GO:0061213 p=4.5E−03 n=2 fg=0.03 bg=0.00
response to antipsychotic drug GO:0097332 p=4.5E−03 n=2 fg=0.03 bg=0.00
response to clozapine GO:0097338 p=4.5E−03 n=2 fg=0.03 bg=0.00
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−log(p)
n=76/285 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032385496.2
fraction genes in fg and expected valu
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=7.4E−04 n=2 fg=0.03 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=7.4E−04 n=2 fg=0.03 bg=0.00
purine ribonucleotide binding GO:0032555 p=1.9E−03 n=13 fg=0.20 bg=0.07
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=2.2E−03 n=2 fg=0.03 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=2.2E−03 n=2 fg=0.03 bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=2.2E−03 n=2 fg=0.03 bg=0.00
purine ribonucleoside triphosphate bindi... GO:0035639 p=4.1E−03 n=10 fg=0.15 bg=0.06
cAMP binding GO:0030552 p=4.3E−03 n=2 fg=0.03 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=4.3E−03 n=2 fg=0.03 bg=0.00
peptide hormone binding GO:0017046 p=4.3E−03 n=2 fg=0.03 bg=0.00
ephrin receptor binding GO:0046875 p=7.0E−03 n=2 fg=0.03 bg=0.00
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=1.0E−02 n=2 fg=0.03 bg=0.00
HMG box domain binding GO:0071837 p=1.4E−02 n=2 fg=0.03 bg=0.00
acylglycerol O−acyltransferase activity GO:0016411 p=1.4E−02 n=2 fg=0.03 bg=0.00
outward rectifier potassium channel acti... GO:0015271 p=1.9E−02 n=2 fg=0.03 bg=0.00
voltage−gated cation channel activity GO:0022843 p=2.1E−02 n=3 fg=0.05 bg=0.01
metalloendopeptidase activity GO:0004222 p=2.4E−02 n=2 fg=0.03 bg=0.00
monosaccharide binding GO:0048029 p=2.4E−02 n=2 fg=0.03 bg=0.00
cytokine receptor binding GO:0005126 p=2.4E−02 n=3 fg=0.05 bg=0.01
heparan sulfate binding GO:1904399 p=2.7E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.7E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−arginine−2 demethylase... GO:0033746 p=2.7E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−arginine−3 demethylase... GO:0033749 p=2.7E−02 n=1 fg=0.02 bg=0.00
Roundabout binding GO:0048495 p=2.7E−02 n=1 fg=0.02 bg=0.00
calcitonin family binding GO:0097644 p=2.7E−02 n=1 fg=0.02 bg=0.00
peptidyl−lysine 5−dioxygenase activity GO:0070815 p=2.7E−02 n=1 fg=0.02 bg=0.00
amylin binding GO:0097645 p=2.7E−02 n=1 fg=0.02 bg=0.00
BH4 domain binding GO:0051435 p=2.7E−02 n=1 fg=0.02 bg=0.00
neuropilin binding GO:0038191 p=2.7E−02 n=1 fg=0.02 bg=0.00
beta−endorphin binding GO:0031626 p=2.7E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=65/285 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032385496.2
fraction genes in fg and expected valu
dendritic shaft GO:0043198 p=3.0E−04 n=5 fg=0.06 bg=0.01
germinal vesicle GO:0042585 p=7.2E−04 n=3 fg=0.04 bg=0.00
stress fiber GO:0001725 p=2.3E−03 n=3 fg=0.04 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=2.4E−03 n=2 fg=0.03 bg=0.00
dendritic spine GO:0043197 p=3.2E−03 n=6 fg=0.08 bg=0.02
RNA polymerase II transcription represso... GO:0090571 p=4.6E−03 n=2 fg=0.03 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=4.6E−03 n=2 fg=0.03 bg=0.00
T−tubule GO:0030315 p=5.2E−03 n=3 fg=0.04 bg=0.00
cell periphery GO:0071944 p=9.6E−03 n=31 fg=0.40 bg=0.25
plasma membrane GO:0005886 p=1.2E−02 n=29 fg=0.38 bg=0.23
secretory granule membrane GO:0030667 p=1.4E−02 n=5 fg=0.06 bg=0.02
myofibril GO:0030016 p=2.0E−02 n=5 fg=0.06 bg=0.02
azurophil granule membrane GO:0035577 p=2.5E−02 n=2 fg=0.03 bg=0.00
host cell nuclear part GO:0044094 p=2.9E−02 n=1 fg=0.01 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=2.9E−02 n=1 fg=0.01 bg=0.00
amyloid−beta complex GO:0106003 p=2.9E−02 n=1 fg=0.01 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=2.9E−02 n=1 fg=0.01 bg=0.00
host cell part GO:0033643 p=2.9E−02 n=1 fg=0.01 bg=0.00
host intracellular part GO:0033646 p=2.9E−02 n=1 fg=0.01 bg=0.00
host intracellular organelle GO:0033647 p=2.9E−02 n=1 fg=0.01 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=2.9E−02 n=1 fg=0.01 bg=0.00
host cell nucleus GO:0042025 p=2.9E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=2.9E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=2.9E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=2.9E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=2.9E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=2.9E−02 n=1 fg=0.01 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=2.9E−02 n=1 fg=0.01 bg=0.00
high−density lipoprotein particle GO:0034364 p=2.9E−02 n=1 fg=0.01 bg=0.00
acrosomal membrane GO:0002080 p=2.9E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=77/285 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction