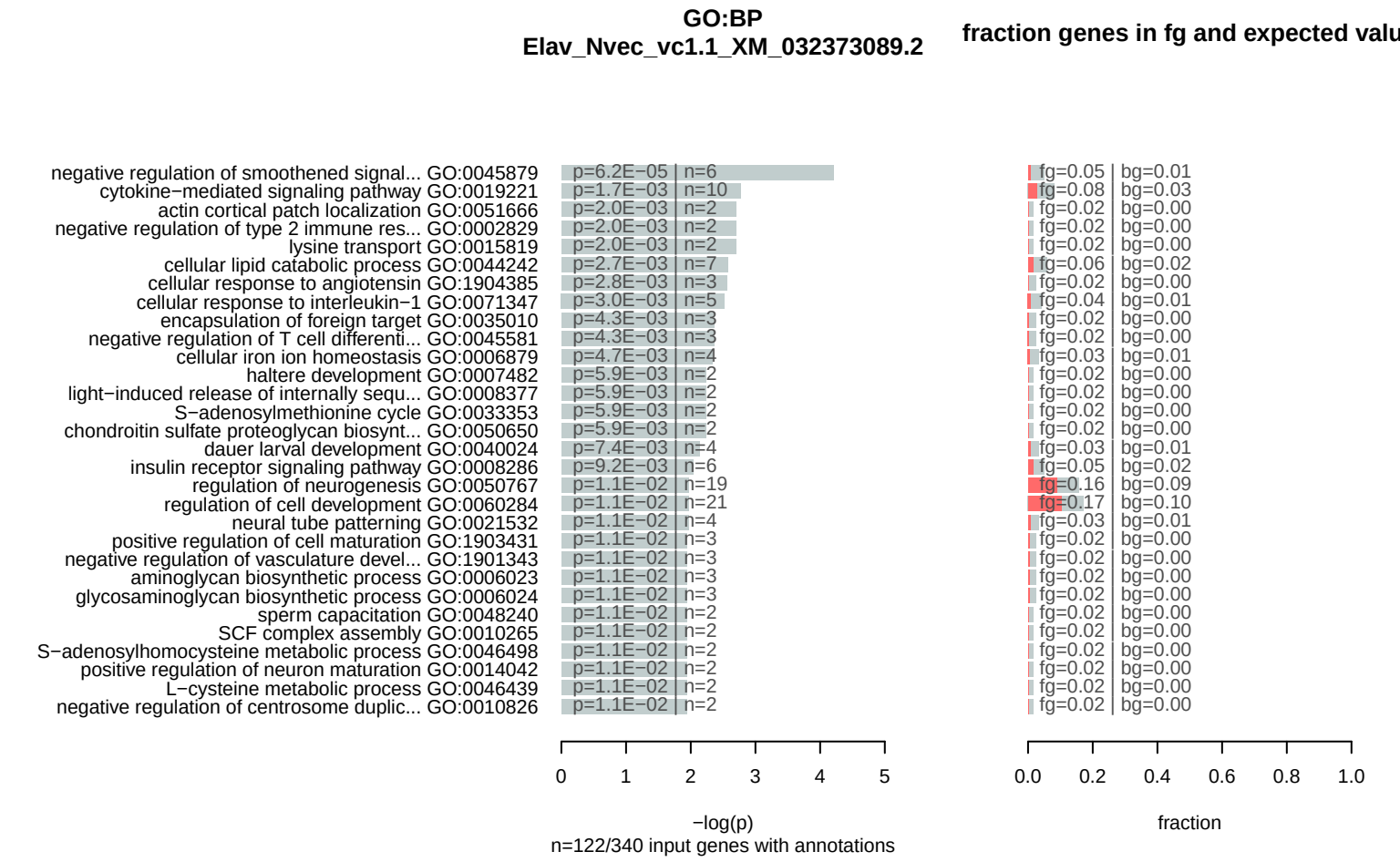
GO:BP
Elav_Nvec_vc1.1_XM_032373089.2
fraction genes in fg and expected valu
negative regulation of smoothened signal... GO:0045879 p=6.2E−05 n=6 fg=0.05 bg=0.01
cytokine−mediated signaling pathway GO:0019221 p=1.7E−03 n=10 fg=0.08 bg=0.03
actin cortical patch localization GO:0051666 p=2.0E−03 n=2 fg=0.02 bg=0.00
negative regulation of type 2 immune res... GO:0002829 p=2.0E−03 n=2 fg=0.02 bg=0.00
lysine transport GO:0015819 p=2.0E−03 n=2 fg=0.02 bg=0.00
cellular lipid catabolic process GO:0044242 p=2.7E−03 n=7 fg=0.06 bg=0.02
cellular response to angiotensin GO:1904385 p=2.8E−03 n=3 fg=0.02 bg=0.00
cellular response to interleukin−1 GO:0071347 p=3.0E−03 n=5 fg=0.04 bg=0.01
encapsulation of foreign target GO:0035010 p=4.3E−03 n=3 fg=0.02 bg=0.00
negative regulation of T cell differenti... GO:0045581 p=4.3E−03 n=3 fg=0.02 bg=0.00
cellular iron ion homeostasis GO:0006879 p=4.7E−03 n=4 fg=0.03 bg=0.01
haltere development GO:0007482 p=5.9E−03 n=2 fg=0.02 bg=0.00
light−induced release of internally sequ... GO:0008377 p=5.9E−03 n=2 fg=0.02 bg=0.00
S−adenosylmethionine cycle GO:0033353 p=5.9E−03 n=2 fg=0.02 bg=0.00
chondroitin sulfate proteoglycan biosynt... GO:0050650 p=5.9E−03 n=2 fg=0.02 bg=0.00
dauer larval development GO:0040024 p=7.4E−03 n=4 fg=0.03 bg=0.01
insulin receptor signaling pathway GO:0008286 p=9.2E−03 n=6 fg=0.05 bg=0.02
regulation of neurogenesis GO:0050767 p=1.1E−02 n=19 fg=0.16 bg=0.09
regulation of cell development GO:0060284 p=1.1E−02 n=21 fg=0.17 bg=0.10
neural tube patterning GO:0021532 p=1.1E−02 n=4 fg=0.03 bg=0.01
positive regulation of cell maturation GO:1903431 p=1.1E−02 n=3 fg=0.02 bg=0.00
negative regulation of vasculature devel... GO:1901343 p=1.1E−02 n=3 fg=0.02 bg=0.00
aminoglycan biosynthetic process GO:0006023 p=1.1E−02 n=3 fg=0.02 bg=0.00
glycosaminoglycan biosynthetic process GO:0006024 p=1.1E−02 n=3 fg=0.02 bg=0.00
sperm capacitation GO:0048240 p=1.1E−02 n=2 fg=0.02 bg=0.00
SCF complex assembly GO:0010265 p=1.1E−02 n=2 fg=0.02 bg=0.00
S−adenosylhomocysteine metabolic process GO:0046498 p=1.1E−02 n=2 fg=0.02 bg=0.00
positive regulation of neuron maturation GO:0014042 p=1.1E−02 n=2 fg=0.02 bg=0.00
L−cysteine metabolic process GO:0046439 p=1.1E−02 n=2 fg=0.02 bg=0.00
negative regulation of centrosome duplic... GO:0010826 p=1.1E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=122/340 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032373089.2
fraction genes in fg and expected valu
phosphotransferase activity, carboxyl gr... GO:0016774 p=1.9E−03 n=2 fg=0.02 bg=0.00
UDP−galactose:beta−N−acetylglucosamine b... GO:0008499 p=2.5E−03 n=3 fg=0.03 bg=0.00
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=5.5E−03 n=3 fg=0.03 bg=0.00
phosphatase regulator activity GO:0019208 p=6.4E−03 n=4 fg=0.04 bg=0.01
phosphatase activator activity GO:0019211 p=1.1E−02 n=2 fg=0.02 bg=0.00
protein phosphatase activator activity GO:0072542 p=1.1E−02 n=2 fg=0.02 bg=0.00
nucleobase−containing compound transmemb... GO:0015932 p=1.3E−02 n=3 fg=0.03 bg=0.01
protein phosphatase regulator activity GO:0019888 p=2.5E−02 n=3 fg=0.03 bg=0.01
peptide antigen binding GO:0042605 p=2.5E−02 n=2 fg=0.02 bg=0.00
glucuronosyltransferase activity GO:0015020 p=2.5E−02 n=2 fg=0.02 bg=0.00
L−cystine transmembrane transporter acti... GO:0015184 p=2.5E−02 n=2 fg=0.02 bg=0.00
sulfur amino acid transmembrane transpor... GO:0000099 p=3.4E−02 n=2 fg=0.02 bg=0.00
G protein−coupled receptor activity GO:0004930 p=4.0E−02 n=5 fg=0.05 bg=0.02
CoA carboxylase activity GO:0016421 p=4.3E−02 n=1 fg=0.01 bg=0.00
glutamate−5−semialdehyde dehydrogenase a... GO:0004350 p=4.3E−02 n=1 fg=0.01 bg=0.00
phosphatidylinositol 3−kinase catalytic ... GO:0036313 p=4.3E−02 n=1 fg=0.01 bg=0.00
purine−specific nucleoside:sodium sympor... GO:0015390 p=4.3E−02 n=1 fg=0.01 bg=0.00
nucleobase:cation symporter activity GO:0015391 p=4.3E−02 n=1 fg=0.01 bg=0.00
growth hormone−releasing hormone recepto... GO:0016520 p=4.3E−02 n=1 fg=0.01 bg=0.00
myosin head/neck binding GO:0032028 p=4.3E−02 n=1 fg=0.01 bg=0.00
pyrimidine nucleobase transmembrane tran... GO:0005350 p=4.3E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=4.3E−02 n=1 fg=0.01 bg=0.00
N−acetylgalactosaminyl−proteoglycan 3−be... GO:0050510 p=4.3E−02 n=1 fg=0.01 bg=0.00
RNA guanylyltransferase activity GO:0008192 p=4.3E−02 n=1 fg=0.01 bg=0.00
tRNA guanylyltransferase activity GO:0008193 p=4.3E−02 n=1 fg=0.01 bg=0.00
purine nucleoside transmembrane transpor... GO:0015211 p=4.3E−02 n=1 fg=0.01 bg=0.00
P−type calcium transporter activity invo... GO:0086039 p=4.3E−02 n=1 fg=0.01 bg=0.00
glutamate 5−kinase activity GO:0004349 p=4.3E−02 n=1 fg=0.01 bg=0.00
pyrimidine− and adenine−specific:sodium ... GO:0015389 p=4.3E−02 n=1 fg=0.01 bg=0.00
pseudophosphatase activity GO:0001691 p=4.3E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=103/340 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032373089.2
fraction genes in fg and expected valu
rough endoplasmic reticulum GO:0005791 p=2.5E−03 n=5 fg=0.04 bg=0.01
integral component of membrane GO:0016021 p=3.9E−03 n=29 fg=0.24 bg=0.14
mitochondria−associated endoplasmic reti... GO:0044233 p=6.0E−03 n=2 fg=0.02 bg=0.00
ciliary membrane GO:0060170 p=6.2E−03 n=4 fg=0.03 bg=0.01
endoplasmic reticulum subcompartment GO:0098827 p=8.8E−03 n=17 fg=0.14 bg=0.07
inaD signaling complex GO:0016027 p=1.2E−02 n=2 fg=0.02 bg=0.00
lumenal side of endoplasmic reticulum me... GO:0098553 p=1.2E−02 n=2 fg=0.02 bg=0.00
integral component of lumenal side of en... GO:0071556 p=1.2E−02 n=2 fg=0.02 bg=0.00
endoplasmic reticulum membrane GO:0005789 p=1.5E−02 n=16 fg=0.13 bg=0.07
nuclear outer membrane−endoplasmic retic... GO:0042175 p=1.8E−02 n=16 fg=0.13 bg=0.07
fungal−type vacuole GO:0000324 p=1.9E−02 n=2 fg=0.02 bg=0.00
fungal−type vacuole membrane GO:0000329 p=1.9E−02 n=2 fg=0.02 bg=0.00
lumenal side of membrane GO:0098576 p=1.9E−02 n=2 fg=0.02 bg=0.00
cell tip GO:0051286 p=2.7E−02 n=2 fg=0.02 bg=0.00
transcription elongation factor complex GO:0008023 p=2.8E−02 n=3 fg=0.02 bg=0.01
Golgi medial cisterna GO:0005797 p=2.8E−02 n=3 fg=0.02 bg=0.01
cation channel complex GO:0034703 p=2.8E−02 n=4 fg=0.03 bg=0.01
organelle membrane GO:0031090 p=2.9E−02 n=41 fg=0.33 bg=0.24
Golgi apparatus GO:0005794 p=3.2E−02 n=21 fg=0.17 bg=0.11
integral component of endoplasmic reticu... GO:0030176 p=3.4E−02 n=6 fg=0.05 bg=0.02
storage vacuole GO:0000322 p=3.7E−02 n=2 fg=0.02 bg=0.00
cell pole GO:0060187 p=3.7E−02 n=2 fg=0.02 bg=0.00
secondary lysosome GO:0005767 p=3.7E−02 n=2 fg=0.02 bg=0.00
autophagosome GO:0005776 p=4.0E−02 n=4 fg=0.03 bg=0.01
intrinsic component of endoplasmic retic... GO:0031227 p=4.3E−02 n=6 fg=0.05 bg=0.02
ion channel complex GO:0034702 p=4.5E−02 n=4 fg=0.03 bg=0.01
rhabdomere microvillus GO:0035996 p=4.6E−02 n=1 fg=0.01 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=4.6E−02 n=1 fg=0.01 bg=0.00
Shu complex GO:0097196 p=4.6E−02 n=1 fg=0.01 bg=0.00
apical cytoplasm GO:0090651 p=4.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=123/340 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction