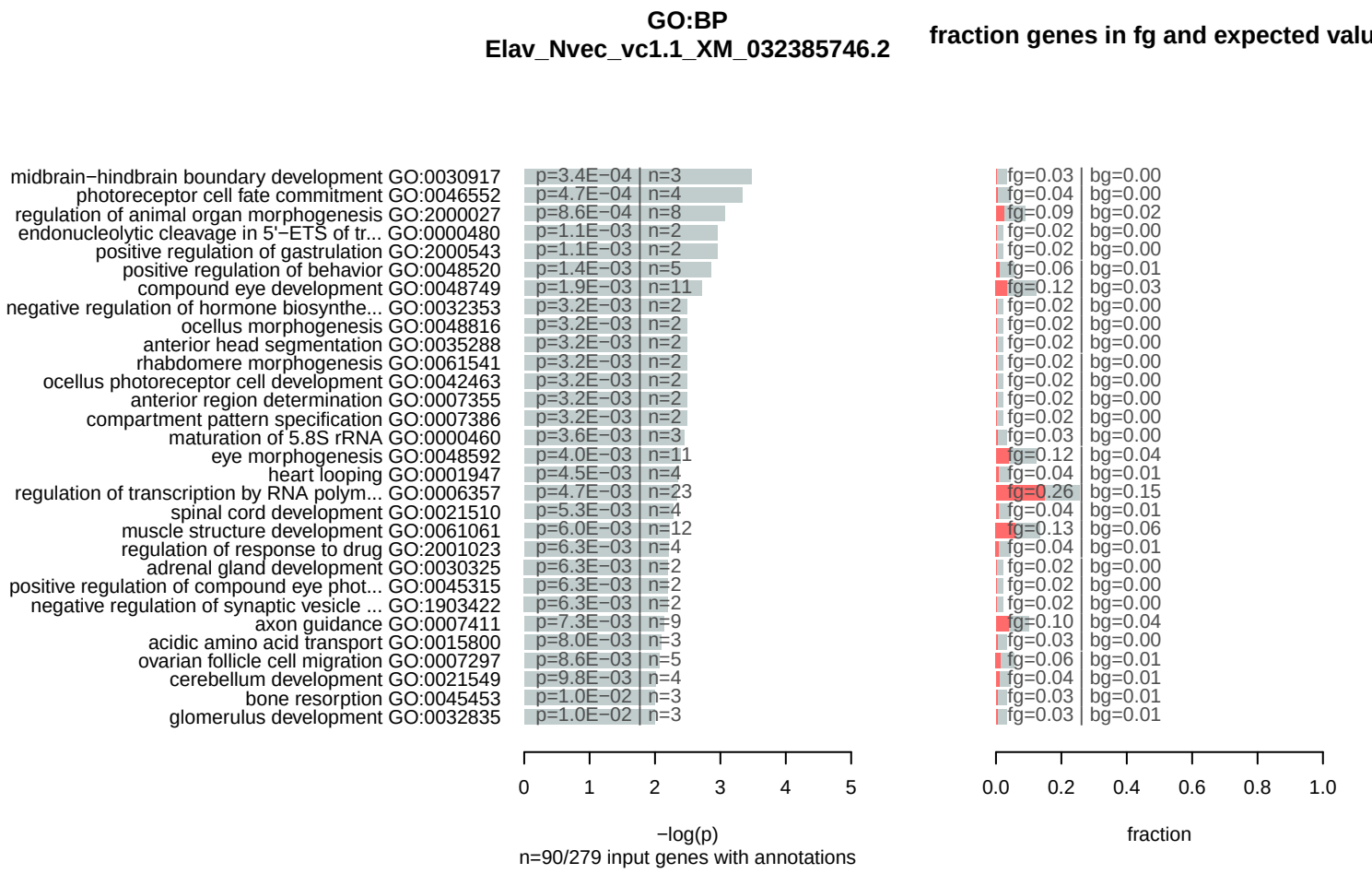
GO:BP
Elav_Nvec_vc1.1_XM_032385746.2
fraction genes in fg and expected valu
midbrain−hindbrain boundary development GO:0030917 p=3.4E−04 n=3 fg=0.03 bg=0.00
photoreceptor cell fate commitment GO:0046552 p=4.7E−04 n=4 fg=0.04 bg=0.00
regulation of animal organ morphogenesis GO:2000027 p=8.6E−04 n=8 fg=0.09 bg=0.02
endonucleolytic cleavage in 5'−ETS of tr... GO:0000480 p=1.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of gastrulation GO:2000543 p=1.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of behavior GO:0048520 p=1.4E−03 n=5 fg=0.06 bg=0.01
compound eye development GO:0048749 p=1.9E−03 n=11 fg=0.12 bg=0.03
negative regulation of hormone biosynthe... GO:0032353 p=3.2E−03 n=2 fg=0.02 bg=0.00
ocellus morphogenesis GO:0048816 p=3.2E−03 n=2 fg=0.02 bg=0.00
anterior head segmentation GO:0035288 p=3.2E−03 n=2 fg=0.02 bg=0.00
rhabdomere morphogenesis GO:0061541 p=3.2E−03 n=2 fg=0.02 bg=0.00
ocellus photoreceptor cell development GO:0042463 p=3.2E−03 n=2 fg=0.02 bg=0.00
anterior region determination GO:0007355 p=3.2E−03 n=2 fg=0.02 bg=0.00
compartment pattern specification GO:0007386 p=3.2E−03 n=2 fg=0.02 bg=0.00
maturation of 5.8S rRNA GO:0000460 p=3.6E−03 n=3 fg=0.03 bg=0.00
eye morphogenesis GO:0048592 p=4.0E−03 n=11 fg=0.12 bg=0.04
heart looping GO:0001947 p=4.5E−03 n=4 fg=0.04 bg=0.01
regulation of transcription by RNA polym... GO:0006357 p=4.7E−03 n=23 fg=0.26 bg=0.15
spinal cord development GO:0021510 p=5.3E−03 n=4 fg=0.04 bg=0.01
muscle structure development GO:0061061 p=6.0E−03 n=12 fg=0.13 bg=0.06
regulation of response to drug GO:2001023 p=6.3E−03 n=4 fg=0.04 bg=0.01
adrenal gland development GO:0030325 p=6.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of compound eye phot... GO:0045315 p=6.3E−03 n=2 fg=0.02 bg=0.00
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axon guidance GO:0007411 p=7.3E−03 n=9 fg=0.10 bg=0.04
acidic amino acid transport GO:0015800 p=8.0E−03 n=3 fg=0.03 bg=0.00
ovarian follicle cell migration GO:0007297 p=8.6E−03 n=5 fg=0.06 bg=0.01
cerebellum development GO:0021549 p=9.8E−03 n=4 fg=0.04 bg=0.01
bone resorption GO:0045453 p=1.0E−02 n=3 fg=0.03 bg=0.01
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−log(p)
n=90/279 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032385746.2
fraction genes in fg and expected valu
DNA−binding transcription activator acti... GO:0001228 p=2.5E−03 n=8 fg=0.10 bg=0.03
11−cis retinal binding GO:0005502 p=3.1E−03 n=2 fg=0.03 bg=0.00
profilin binding GO:0005522 p=6.2E−03 n=2 fg=0.03 bg=0.00
ephrin receptor binding GO:0046875 p=1.0E−02 n=2 fg=0.03 bg=0.00
proteoglycan binding GO:0043394 p=1.5E−02 n=2 fg=0.03 bg=0.00
steroid hydroxylase activity GO:0008395 p=3.3E−02 n=1 fg=0.01 bg=0.00
1−alpha,25−dihydroxyvitamin D3 24−hydrox... GO:0030342 p=3.3E−02 n=1 fg=0.01 bg=0.00
vitamin D3 25−hydroxylase activity GO:0030343 p=3.3E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.3E−02 n=1 fg=0.01 bg=0.00
heteroduplex DNA loop binding GO:0000404 p=3.3E−02 n=1 fg=0.01 bg=0.00
double−strand/single−strand DNA junction... GO:0000406 p=3.3E−02 n=1 fg=0.01 bg=0.00
glyceraldehyde−3−phosphate dehydrogenase... GO:0004365 p=3.3E−02 n=1 fg=0.01 bg=0.00
cholesterol 26−hydroxylase activity GO:0031073 p=3.3E−02 n=1 fg=0.01 bg=0.00
25−hydroxycholecalciferol−24−hydroxylase... GO:0008403 p=3.3E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on paire... GO:0016709 p=3.3E−02 n=1 fg=0.01 bg=0.00
all−trans−retinol binding GO:1904768 p=3.3E−02 n=1 fg=0.01 bg=0.00
all−trans retinol 3,4−desaturase activit... GO:0061896 p=3.3E−02 n=1 fg=0.01 bg=0.00
all−trans retinal 3,4−desaturase activit... GO:0061897 p=3.3E−02 n=1 fg=0.01 bg=0.00
all−trans retinoic acid 3,4−desaturase a... GO:0061898 p=3.3E−02 n=1 fg=0.01 bg=0.00
11−cis−retinal 3,4−desaturase activity GO:0061899 p=3.3E−02 n=1 fg=0.01 bg=0.00
biotin−protein ligase activity GO:0018271 p=3.3E−02 n=1 fg=0.01 bg=0.00
4−hydroxyphenylpyruvate dioxygenase acti... GO:0003868 p=3.3E−02 n=1 fg=0.01 bg=0.00
activin receptor activity, type I GO:0016361 p=3.3E−02 n=1 fg=0.01 bg=0.00
tricarboxylate secondary active transmem... GO:0005371 p=3.3E−02 n=1 fg=0.01 bg=0.00
biotin−[propionyl−CoA−carboxylase (ATP−h... GO:0004080 p=3.3E−02 n=1 fg=0.01 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=3.3E−02 n=1 fg=0.01 bg=0.00
all−trans retinal binding GO:0005503 p=3.3E−02 n=1 fg=0.01 bg=0.00
biotin binding GO:0009374 p=3.3E−02 n=1 fg=0.01 bg=0.00
AMP deaminase activity GO:0003876 p=3.3E−02 n=1 fg=0.01 bg=0.00
DNA insertion or deletion binding GO:0032135 p=3.3E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=78/279 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032385746.2
fraction genes in fg and expected valu
nuclear lamina GO:0005652 p=2.6E−03 n=3 fg=0.03 bg=0.00
stress fiber GO:0001725 p=3.6E−03 n=3 fg=0.03 bg=0.00
filopodium tip GO:0032433 p=1.5E−02 n=2 fg=0.02 bg=0.00
secretory granule GO:0030141 p=1.7E−02 n=10 fg=0.11 bg=0.05
excitatory synapse GO:0060076 p=2.1E−02 n=2 fg=0.02 bg=0.00
tertiary granule membrane GO:0070821 p=2.7E−02 n=2 fg=0.02 bg=0.00
preribosome, large subunit precursor GO:0030687 p=2.7E−02 n=2 fg=0.02 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=3.3E−02 n=1 fg=0.01 bg=0.00
microvesicle GO:1990742 p=3.3E−02 n=1 fg=0.01 bg=0.00
MutSbeta complex GO:0032302 p=3.3E−02 n=1 fg=0.01 bg=0.00
apical cytoplasm GO:0090651 p=3.3E−02 n=1 fg=0.01 bg=0.00
dense core granule membrane GO:0032127 p=3.3E−02 n=1 fg=0.01 bg=0.00
dendritic growth cone GO:0044294 p=3.3E−02 n=1 fg=0.01 bg=0.00
steroid hormone aporeceptor complex GO:0005831 p=3.3E−02 n=1 fg=0.01 bg=0.00
ESCRT−0 complex GO:0033565 p=3.3E−02 n=1 fg=0.01 bg=0.00
Sec61 translocon complex GO:0005784 p=3.3E−02 n=1 fg=0.01 bg=0.00
lamin filament GO:0005638 p=3.3E−02 n=1 fg=0.01 bg=0.00
translocon complex GO:0071256 p=3.3E−02 n=1 fg=0.01 bg=0.00
focal adhesion GO:0005925 p=3.9E−02 n=3 fg=0.03 bg=0.01
supramolecular polymer GO:0099081 p=4.0E−02 n=9 fg=0.10 bg=0.05
supramolecular fiber GO:0099512 p=4.0E−02 n=9 fg=0.10 bg=0.05
integrator complex GO:0032039 p=4.2E−02 n=2 fg=0.02 bg=0.00
adherens junction GO:0005912 p=4.2E−02 n=5 fg=0.06 bg=0.02
secretory vesicle GO:0099503 p=4.5E−02 n=11 fg=0.12 bg=0.07
tertiary granule GO:0070820 p=4.9E−02 n=3 fg=0.03 bg=0.01
ficolin−1−rich granule GO:0101002 p=5.3E−02 n=4 fg=0.04 bg=0.02
nucleus GO:0005634 p=5.5E−02 n=54 fg=0.60 bg=0.50
cell−substrate junction GO:0030055 p=5.9E−02 n=3 fg=0.03 bg=0.01
apical part of cell GO:0045177 p=6.5E−02 n=8 fg=0.09 bg=0.05
activin receptor complex GO:0048179 p=6.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=90/279 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction