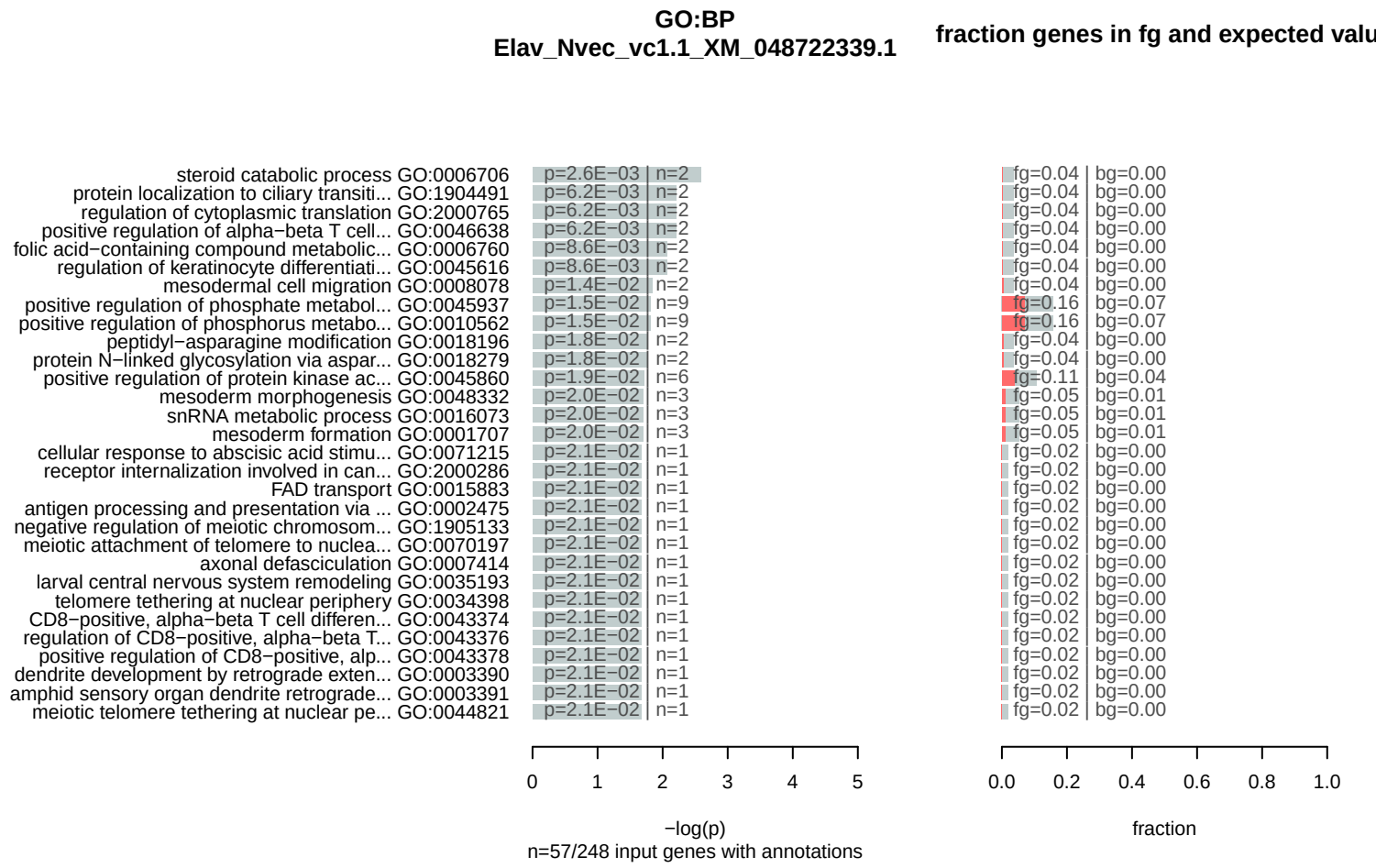
GO:BP
Elav_Nvec_vc1.1_XM_048722339.1
fraction genes in fg and expected valu
steroid catabolic process GO:0006706 p=2.6E−03 n=2 fg=0.04 bg=0.00
protein localization to ciliary transiti... GO:1904491 p=6.2E−03 n=2 fg=0.04 bg=0.00
regulation of cytoplasmic translation GO:2000765 p=6.2E−03 n=2 fg=0.04 bg=0.00
positive regulation of alpha−beta T cell... GO:0046638 p=6.2E−03 n=2 fg=0.04 bg=0.00
folic acid−containing compound metabolic... GO:0006760 p=8.6E−03 n=2 fg=0.04 bg=0.00
regulation of keratinocyte differentiati... GO:0045616 p=8.6E−03 n=2 fg=0.04 bg=0.00
mesodermal cell migration GO:0008078 p=1.4E−02 n=2 fg=0.04 bg=0.00
positive regulation of phosphate metabol... GO:0045937 p=1.5E−02 n=9 fg=0.16 bg=0.07
positive regulation of phosphorus metabo... GO:0010562 p=1.5E−02 n=9 fg=0.16 bg=0.07
peptidyl−asparagine modification GO:0018196 p=1.8E−02 n=2 fg=0.04 bg=0.00
protein N−linked glycosylation via aspar... GO:0018279 p=1.8E−02 n=2 fg=0.04 bg=0.00
positive regulation of protein kinase ac... GO:0045860 p=1.9E−02 n=6 fg=0.11 bg=0.04
mesoderm morphogenesis GO:0048332 p=2.0E−02 n=3 fg=0.05 bg=0.01
snRNA metabolic process GO:0016073 p=2.0E−02 n=3 fg=0.05 bg=0.01
mesoderm formation GO:0001707 p=2.0E−02 n=3 fg=0.05 bg=0.01
cellular response to abscisic acid stimu... GO:0071215 p=2.1E−02 n=1 fg=0.02 bg=0.00
receptor internalization involved in can... GO:2000286 p=2.1E−02 n=1 fg=0.02 bg=0.00
FAD transport GO:0015883 p=2.1E−02 n=1 fg=0.02 bg=0.00
antigen processing and presentation via ... GO:0002475 p=2.1E−02 n=1 fg=0.02 bg=0.00
negative regulation of meiotic chromosom... GO:1905133 p=2.1E−02 n=1 fg=0.02 bg=0.00
meiotic attachment of telomere to nuclea... GO:0070197 p=2.1E−02 n=1 fg=0.02 bg=0.00
axonal defasciculation GO:0007414 p=2.1E−02 n=1 fg=0.02 bg=0.00
larval central nervous system remodeling GO:0035193 p=2.1E−02 n=1 fg=0.02 bg=0.00
telomere tethering at nuclear periphery GO:0034398 p=2.1E−02 n=1 fg=0.02 bg=0.00
CD8−positive, alpha−beta T cell differen... GO:0043374 p=2.1E−02 n=1 fg=0.02 bg=0.00
regulation of CD8−positive, alpha−beta T... GO:0043376 p=2.1E−02 n=1 fg=0.02 bg=0.00
positive regulation of CD8−positive, alp... GO:0043378 p=2.1E−02 n=1 fg=0.02 bg=0.00
dendrite development by retrograde exten... GO:0003390 p=2.1E−02 n=1 fg=0.02 bg=0.00
amphid sensory organ dendrite retrograde... GO:0003391 p=2.1E−02 n=1 fg=0.02 bg=0.00
meiotic telomere tethering at nuclear pe... GO:0044821 p=2.1E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=57/248 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048722339.1
fraction genes in fg and expected valu
all−trans retinol 3,4−desaturase activit... GO:0061896 p=2.2E−02 n=1 fg=0.02 bg=0.00
all−trans retinal 3,4−desaturase activit... GO:0061897 p=2.2E−02 n=1 fg=0.02 bg=0.00
all−trans retinoic acid 3,4−desaturase a... GO:0061898 p=2.2E−02 n=1 fg=0.02 bg=0.00
11−cis−retinal 3,4−desaturase activity GO:0061899 p=2.2E−02 n=1 fg=0.02 bg=0.00
3−phosphoinositide−dependent protein kin... GO:0004676 p=2.2E−02 n=1 fg=0.02 bg=0.00
all−trans−retinol binding GO:1904768 p=2.2E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0046997 p=2.2E−02 n=1 fg=0.02 bg=0.00
dimethylglycine dehydrogenase activity GO:0047865 p=2.2E−02 n=1 fg=0.02 bg=0.00
calcidiol 1−monooxygenase activity GO:0004498 p=2.2E−02 n=1 fg=0.02 bg=0.00
25−hydroxycholecalciferol−24−hydroxylase... GO:0008403 p=2.2E−02 n=1 fg=0.02 bg=0.00
retinol binding GO:0019841 p=2.2E−02 n=1 fg=0.02 bg=0.00
steroid hydroxylase activity GO:0008395 p=2.2E−02 n=1 fg=0.02 bg=0.00
neuregulin binding GO:0038132 p=2.2E−02 n=1 fg=0.02 bg=0.00
vitamin D 24−hydroxylase activity GO:0070576 p=2.2E−02 n=1 fg=0.02 bg=0.00
insulin−like growth factor I binding GO:0031994 p=2.2E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on paire... GO:0016709 p=2.2E−02 n=1 fg=0.02 bg=0.00
vitamin D 25−hydroxylase activity GO:0070643 p=2.2E−02 n=1 fg=0.02 bg=0.00
alpha−1,6−mannosylglycoprotein 2−beta−N−... GO:0008455 p=2.2E−02 n=1 fg=0.02 bg=0.00
poly(G) binding GO:0034046 p=2.2E−02 n=1 fg=0.02 bg=0.00
hedgehog receptor activity GO:0008158 p=2.2E−02 n=1 fg=0.02 bg=0.00
1−alpha,25−dihydroxyvitamin D3 24−hydrox... GO:0030342 p=2.2E−02 n=1 fg=0.02 bg=0.00
vitamin D3 25−hydroxylase activity GO:0030343 p=2.2E−02 n=1 fg=0.02 bg=0.00
steryl−sulfatase activity GO:0004773 p=2.2E−02 n=1 fg=0.02 bg=0.00
cholesterol 26−hydroxylase activity GO:0031073 p=2.2E−02 n=1 fg=0.02 bg=0.00
dolichyl−phosphate beta−glucosyltransfer... GO:0004581 p=2.2E−02 n=1 fg=0.02 bg=0.00
all−trans retinal binding GO:0005503 p=2.2E−02 n=1 fg=0.02 bg=0.00
FAD transmembrane transporter activity GO:0015230 p=2.2E−02 n=1 fg=0.02 bg=0.00
translation factor activity, RNA binding GO:0008135 p=2.2E−02 n=3 fg=0.06 bg=0.01
translation regulator activity, nucleic ... GO:0090079 p=2.7E−02 n=3 fg=0.06 bg=0.01
translation regulator activity GO:0045182 p=4.0E−02 n=3 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=52/248 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048722339.1
fraction genes in fg and expected valu
centrosome GO:0005813 p=8.2E−03 n=8 fg=0.14 bg=0.05
polytene chromosome interband GO:0005705 p=1.8E−02 n=2 fg=0.04 bg=0.00
integrin alpha3−beta1 complex GO:0034667 p=2.1E−02 n=1 fg=0.02 bg=0.00
eukaryotic translation initiation factor... GO:0071540 p=2.1E−02 n=1 fg=0.02 bg=0.00
integrin alpha6−beta4 complex GO:0034676 p=2.1E−02 n=1 fg=0.02 bg=0.00
integrin alpha7−beta1 complex GO:0034677 p=2.1E−02 n=1 fg=0.02 bg=0.00
core−binding factor complex GO:0016513 p=2.1E−02 n=1 fg=0.02 bg=0.00
AP−3 adaptor complex GO:0030123 p=2.1E−02 n=1 fg=0.02 bg=0.00
organelle envelope GO:0031967 p=3.3E−02 n=11 fg=0.19 bg=0.11
envelope GO:0031975 p=3.3E−02 n=11 fg=0.19 bg=0.11
box H/ACA RNP complex GO:0072588 p=4.2E−02 n=1 fg=0.02 bg=0.00
box H/ACA scaRNP complex GO:0072589 p=4.2E−02 n=1 fg=0.02 bg=0.00
box H/ACA telomerase RNP complex GO:0090661 p=4.2E−02 n=1 fg=0.02 bg=0.00
DRM complex GO:0070176 p=4.2E−02 n=1 fg=0.02 bg=0.00
TORC2 complex GO:0031932 p=4.2E−02 n=1 fg=0.02 bg=0.00
NELF complex GO:0032021 p=4.2E−02 n=1 fg=0.02 bg=0.00
box H/ACA snoRNP complex GO:0031429 p=4.2E−02 n=1 fg=0.02 bg=0.00
RSF complex GO:0031213 p=4.2E−02 n=1 fg=0.02 bg=0.00
U2AF complex GO:0089701 p=4.2E−02 n=1 fg=0.02 bg=0.00
nuclear envelope GO:0005635 p=4.3E−02 n=6 fg=0.11 bg=0.05
intracellular anatomical structure GO:0005622 p=4.7E−02 n=57 fg=1.00 bg=0.94
transcription repressor complex GO:0017053 p=5.4E−02 n=2 fg=0.04 bg=0.01
ciliary basal body GO:0036064 p=5.7E−02 n=3 fg=0.05 bg=0.02
TORC1 complex GO:0031931 p=6.2E−02 n=1 fg=0.02 bg=0.00
hemidesmosome GO:0030056 p=6.2E−02 n=1 fg=0.02 bg=0.00
integral component of cytoplasmic side o... GO:0071458 p=6.2E−02 n=1 fg=0.02 bg=0.00
intrinsic component of nuclear inner mem... GO:0031229 p=6.2E−02 n=1 fg=0.02 bg=0.00
multi−eIF complex GO:0043614 p=6.2E−02 n=1 fg=0.02 bg=0.00
TOR complex GO:0038201 p=6.2E−02 n=1 fg=0.02 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=6.2E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=57/248 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction