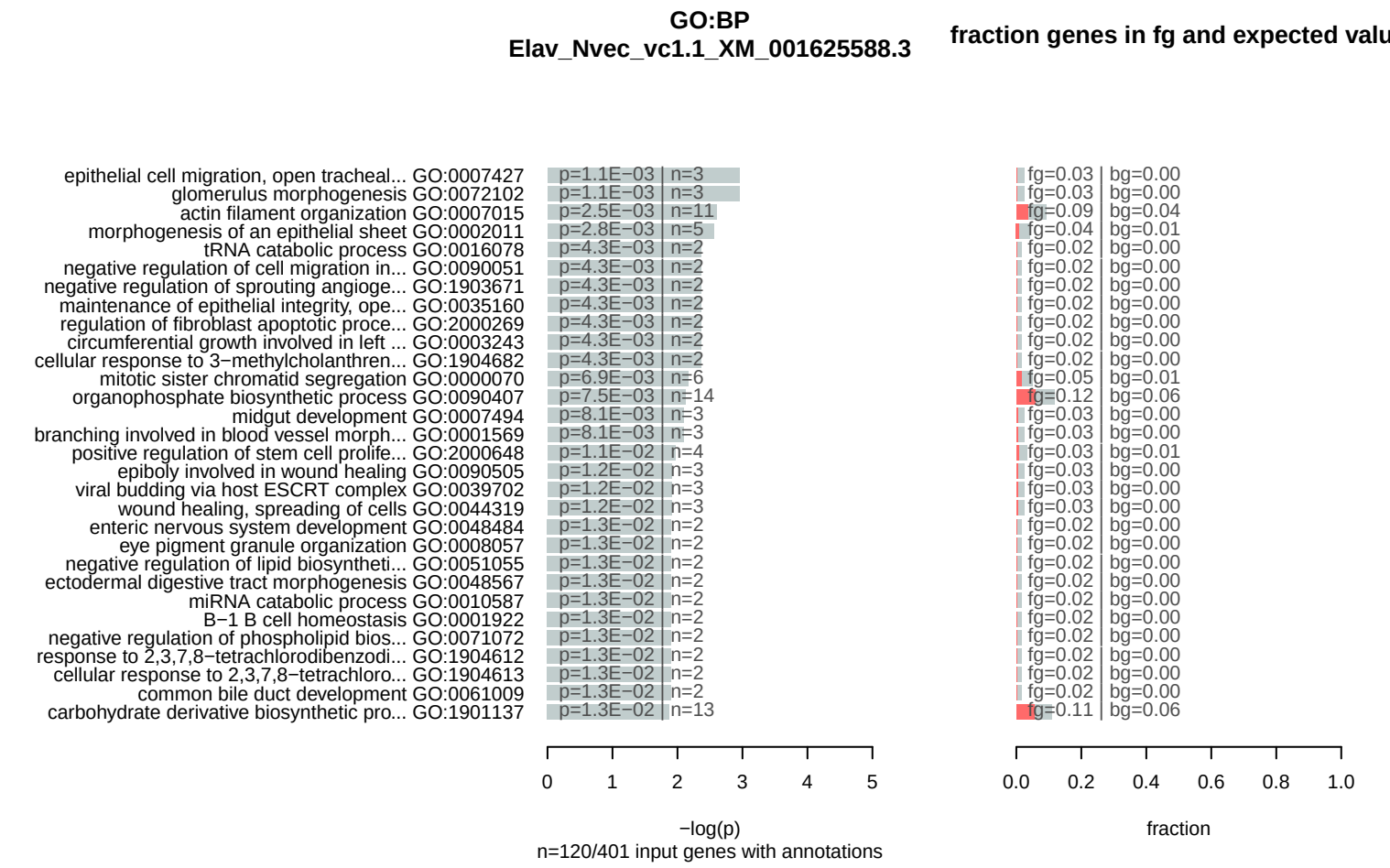
GO:BP
Elav_Nvec_vc1.1_XM_001625588.3
fraction genes in fg and expected valu
epithelial cell migration, open tracheal... GO:0007427 p=1.1E−03 n=3 fg=0.03 bg=0.00
glomerulus morphogenesis GO:0072102 p=1.1E−03 n=3 fg=0.03 bg=0.00
actin filament organization GO:0007015 p=2.5E−03 n=11 fg=0.09 bg=0.04
morphogenesis of an epithelial sheet GO:0002011 p=2.8E−03 n=5 fg=0.04 bg=0.01
tRNA catabolic process GO:0016078 p=4.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of cell migration in... GO:0090051 p=4.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of sprouting angioge... GO:1903671 p=4.3E−03 n=2 fg=0.02 bg=0.00
maintenance of epithelial integrity, ope... GO:0035160 p=4.3E−03 n=2 fg=0.02 bg=0.00
regulation of fibroblast apoptotic proce... GO:2000269 p=4.3E−03 n=2 fg=0.02 bg=0.00
circumferential growth involved in left ... GO:0003243 p=4.3E−03 n=2 fg=0.02 bg=0.00
cellular response to 3−methylcholanthren... GO:1904682 p=4.3E−03 n=2 fg=0.02 bg=0.00
mitotic sister chromatid segregation GO:0000070 p=6.9E−03 n=6 fg=0.05 bg=0.01
organophosphate biosynthetic process GO:0090407 p=7.5E−03 n=14 fg=0.12 bg=0.06
midgut development GO:0007494 p=8.1E−03 n=3 fg=0.03 bg=0.00
branching involved in blood vessel morph... GO:0001569 p=8.1E−03 n=3 fg=0.03 bg=0.00
positive regulation of stem cell prolife... GO:2000648 p=1.1E−02 n=4 fg=0.03 bg=0.01
epiboly involved in wound healing GO:0090505 p=1.2E−02 n=3 fg=0.03 bg=0.00
viral budding via host ESCRT complex GO:0039702 p=1.2E−02 n=3 fg=0.03 bg=0.00
wound healing, spreading of cells GO:0044319 p=1.2E−02 n=3 fg=0.03 bg=0.00
enteric nervous system development GO:0048484 p=1.3E−02 n=2 fg=0.02 bg=0.00
eye pigment granule organization GO:0008057 p=1.3E−02 n=2 fg=0.02 bg=0.00
negative regulation of lipid biosyntheti... GO:0051055 p=1.3E−02 n=2 fg=0.02 bg=0.00
ectodermal digestive tract morphogenesis GO:0048567 p=1.3E−02 n=2 fg=0.02 bg=0.00
miRNA catabolic process GO:0010587 p=1.3E−02 n=2 fg=0.02 bg=0.00
B−1 B cell homeostasis GO:0001922 p=1.3E−02 n=2 fg=0.02 bg=0.00
negative regulation of phospholipid bios... GO:0071072 p=1.3E−02 n=2 fg=0.02 bg=0.00
response to 2,3,7,8−tetrachlorodibenzodi... GO:1904612 p=1.3E−02 n=2 fg=0.02 bg=0.00
cellular response to 2,3,7,8−tetrachloro... GO:1904613 p=1.3E−02 n=2 fg=0.02 bg=0.00
common bile duct development GO:0061009 p=1.3E−02 n=2 fg=0.02 bg=0.00
carbohydrate derivative biosynthetic pro... GO:1901137 p=1.3E−02 n=13 fg=0.11 bg=0.06
0 1 2 3 4 5
−log(p)
n=120/401 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001625588.3
fraction genes in fg and expected valu
carbon−nitrogen ligase activity, with gl... GO:0016884 p=4.4E−03 n=2 fg=0.02 bg=0.00
TFIID−class transcription factor complex... GO:0001094 p=1.3E−02 n=2 fg=0.02 bg=0.00
basal transcription machinery binding GO:0001098 p=1.8E−02 n=3 fg=0.03 bg=0.01
basal RNA polymerase II transcription ma... GO:0001099 p=1.8E−02 n=3 fg=0.03 bg=0.01
transcription coregulator binding GO:0001221 p=1.8E−02 n=3 fg=0.03 bg=0.01
E−box binding GO:0070888 p=1.8E−02 n=3 fg=0.03 bg=0.01
RNA polymerase II general transcription ... GO:0001091 p=2.4E−02 n=2 fg=0.02 bg=0.00
nuclear receptor activity GO:0004879 p=2.4E−02 n=2 fg=0.02 bg=0.00
actin monomer binding GO:0003785 p=2.4E−02 n=2 fg=0.02 bg=0.00
ligand−activated transcription factor ac... GO:0098531 p=2.4E−02 n=2 fg=0.02 bg=0.00
poly(U) RNA binding GO:0008266 p=3.8E−02 n=2 fg=0.02 bg=0.00
transcription coactivator binding GO:0001223 p=3.8E−02 n=2 fg=0.02 bg=0.00
cyclic nucleotide binding GO:0030551 p=3.8E−02 n=2 fg=0.02 bg=0.00
integrin binding GO:0005178 p=4.1E−02 n=3 fg=0.03 bg=0.01
collagen binding GO:0005518 p=5.5E−02 n=2 fg=0.02 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=5.5E−02 n=2 fg=0.02 bg=0.00
aryl hydrocarbon receptor binding GO:0017162 p=5.5E−02 n=2 fg=0.02 bg=0.00
ribonuclease activity GO:0004540 p=6.1E−02 n=3 fg=0.03 bg=0.01
kinesin binding GO:0019894 p=6.1E−02 n=3 fg=0.03 bg=0.01
transcription cis−regulatory region bind... GO:0000976 p=6.6E−02 n=10 fg=0.09 bg=0.06
4−hydroxy−2−oxoglutarate aldolase activi... GO:0008700 p=6.7E−02 n=1 fg=0.01 bg=0.00
insulin−like growth factor I binding GO:0031994 p=6.7E−02 n=1 fg=0.01 bg=0.00
protein−arginine omega−N monomethyltrans... GO:0035241 p=6.7E−02 n=1 fg=0.01 bg=0.00
protein−arginine omega−N symmetric methy... GO:0035243 p=6.7E−02 n=1 fg=0.01 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=6.7E−02 n=1 fg=0.01 bg=0.00
growth hormone−releasing hormone recepto... GO:0016520 p=6.7E−02 n=1 fg=0.01 bg=0.00
glutaminase activity GO:0004359 p=6.7E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=6.7E−02 n=1 fg=0.01 bg=0.00
SUMO binding GO:0032183 p=6.7E−02 n=1 fg=0.01 bg=0.00
heparanase activity GO:0030305 p=6.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=106/401 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001625588.3
fraction genes in fg and expected valu
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=4.2E−03 n=2 fg=0.02 bg=0.00
actin cytoskeleton GO:0015629 p=8.8E−03 n=9 fg=0.08 bg=0.03
nuclear aryl hydrocarbon receptor comple... GO:0034753 p=1.2E−02 n=2 fg=0.02 bg=0.00
ruffle membrane GO:0032587 p=2.3E−02 n=3 fg=0.03 bg=0.01
intercellular canaliculus GO:0046581 p=2.3E−02 n=2 fg=0.02 bg=0.00
ruffle GO:0001726 p=2.6E−02 n=4 fg=0.03 bg=0.01
lipid droplet GO:0005811 p=3.1E−02 n=4 fg=0.03 bg=0.01
methyltransferase complex GO:0034708 p=3.1E−02 n=4 fg=0.03 bg=0.01
cell pole GO:0060187 p=3.7E−02 n=2 fg=0.02 bg=0.00
transcription elongation factor complex GO:0008023 p=3.9E−02 n=3 fg=0.03 bg=0.01
centriole GO:0005814 p=4.3E−02 n=4 fg=0.03 bg=0.01
excitatory synapse GO:0060076 p=5.3E−02 n=2 fg=0.02 bg=0.00
integrin alpha3−beta1 complex GO:0034667 p=6.5E−02 n=1 fg=0.01 bg=0.00
cell cortex of cell tip GO:0051285 p=6.5E−02 n=1 fg=0.01 bg=0.00
integrin alpha6−beta4 complex GO:0034676 p=6.5E−02 n=1 fg=0.01 bg=0.00
integrin alpha7−beta1 complex GO:0034677 p=6.5E−02 n=1 fg=0.01 bg=0.00
ribonuclease MRP complex GO:0000172 p=6.5E−02 n=1 fg=0.01 bg=0.00
exosome (RNase complex) GO:0000178 p=6.5E−02 n=1 fg=0.01 bg=0.00
chromaffin granule GO:0042583 p=6.5E−02 n=1 fg=0.01 bg=0.00
chromaffin granule membrane GO:0042584 p=6.5E−02 n=1 fg=0.01 bg=0.00
nucleolar ribonuclease P complex GO:0005655 p=6.5E−02 n=1 fg=0.01 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=6.5E−02 n=1 fg=0.01 bg=0.00
CORVET complex GO:0033263 p=6.5E−02 n=1 fg=0.01 bg=0.00
exoribonuclease complex GO:1905354 p=6.5E−02 n=1 fg=0.01 bg=0.00
methylosome GO:0034709 p=6.5E−02 n=1 fg=0.01 bg=0.00
PET complex GO:1990923 p=6.5E−02 n=1 fg=0.01 bg=0.00
sno(s)RNA−containing ribonucleoprotein c... GO:0005732 p=6.5E−02 n=1 fg=0.01 bg=0.00
CCAAT−binding factor complex GO:0016602 p=6.5E−02 n=1 fg=0.01 bg=0.00
vesicle coat GO:0030120 p=7.1E−02 n=2 fg=0.02 bg=0.00
AP−type membrane coat adaptor complex GO:0030119 p=7.1E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=118/401 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction