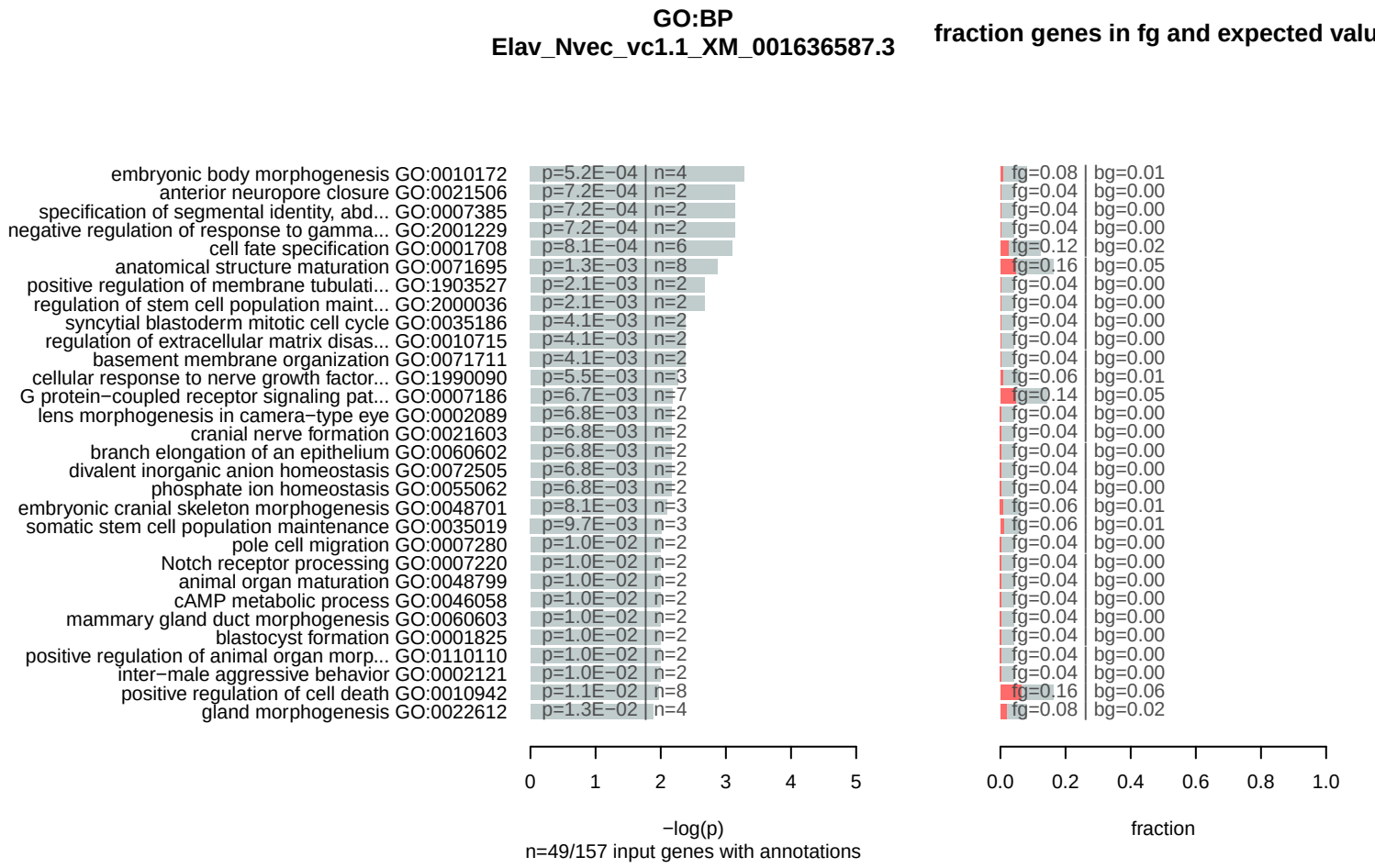
GO:BP
Elav_Nvec_vc1.1_XM_001636587.3
fraction genes in fg and expected valu
embryonic body morphogenesis GO:0010172 p=5.2E−04 n=4 fg=0.08 bg=0.01
anterior neuropore closure GO:0021506 p=7.2E−04 n=2 fg=0.04 bg=0.00
specification of segmental identity, abd... GO:0007385 p=7.2E−04 n=2 fg=0.04 bg=0.00
negative regulation of response to gamma... GO:2001229 p=7.2E−04 n=2 fg=0.04 bg=0.00
cell fate specification GO:0001708 p=8.1E−04 n=6 fg=0.12 bg=0.02
anatomical structure maturation GO:0071695 p=1.3E−03 n=8 fg=0.16 bg=0.05
positive regulation of membrane tubulati... GO:1903527 p=2.1E−03 n=2 fg=0.04 bg=0.00
regulation of stem cell population maint... GO:2000036 p=2.1E−03 n=2 fg=0.04 bg=0.00
syncytial blastoderm mitotic cell cycle GO:0035186 p=4.1E−03 n=2 fg=0.04 bg=0.00
regulation of extracellular matrix disas... GO:0010715 p=4.1E−03 n=2 fg=0.04 bg=0.00
basement membrane organization GO:0071711 p=4.1E−03 n=2 fg=0.04 bg=0.00
cellular response to nerve growth factor... GO:1990090 p=5.5E−03 n=3 fg=0.06 bg=0.01
G protein−coupled receptor signaling pat... GO:0007186 p=6.7E−03 n=7 fg=0.14 bg=0.05
lens morphogenesis in camera−type eye GO:0002089 p=6.8E−03 n=2 fg=0.04 bg=0.00
cranial nerve formation GO:0021603 p=6.8E−03 n=2 fg=0.04 bg=0.00
branch elongation of an epithelium GO:0060602 p=6.8E−03 n=2 fg=0.04 bg=0.00
divalent inorganic anion homeostasis GO:0072505 p=6.8E−03 n=2 fg=0.04 bg=0.00
phosphate ion homeostasis GO:0055062 p=6.8E−03 n=2 fg=0.04 bg=0.00
embryonic cranial skeleton morphogenesis GO:0048701 p=8.1E−03 n=3 fg=0.06 bg=0.01
somatic stem cell population maintenance GO:0035019 p=9.7E−03 n=3 fg=0.06 bg=0.01
pole cell migration GO:0007280 p=1.0E−02 n=2 fg=0.04 bg=0.00
Notch receptor processing GO:0007220 p=1.0E−02 n=2 fg=0.04 bg=0.00
animal organ maturation GO:0048799 p=1.0E−02 n=2 fg=0.04 bg=0.00
cAMP metabolic process GO:0046058 p=1.0E−02 n=2 fg=0.04 bg=0.00
mammary gland duct morphogenesis GO:0060603 p=1.0E−02 n=2 fg=0.04 bg=0.00
blastocyst formation GO:0001825 p=1.0E−02 n=2 fg=0.04 bg=0.00
positive regulation of animal organ morp... GO:0110110 p=1.0E−02 n=2 fg=0.04 bg=0.00
inter−male aggressive behavior GO:0002121 p=1.0E−02 n=2 fg=0.04 bg=0.00
positive regulation of cell death GO:0010942 p=1.1E−02 n=8 fg=0.16 bg=0.06
gland morphogenesis GO:0022612 p=1.3E−02 n=4 fg=0.08 bg=0.02
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−log(p)
n=49/157 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001636587.3
fraction genes in fg and expected valu
poly(U) RNA binding GO:0008266 p=6.2E−03 n=2 fg=0.05 bg=0.00
cysteine−type endopeptidase regulator ac... GO:0043028 p=6.2E−03 n=2 fg=0.05 bg=0.00
G−protein alpha−subunit binding GO:0001965 p=9.1E−03 n=2 fg=0.05 bg=0.00
enzyme activator activity GO:0008047 p=1.3E−02 n=6 fg=0.15 bg=0.05
methylation−dependent protein binding GO:0140034 p=1.6E−02 n=2 fg=0.05 bg=0.01
methylated histone binding GO:0035064 p=1.6E−02 n=2 fg=0.05 bg=0.01
D−glucose transmembrane transporter acti... GO:0055056 p=2.6E−02 n=1 fg=0.02 bg=0.00
rRNA primary transcript binding GO:0042134 p=2.6E−02 n=1 fg=0.02 bg=0.00
sugar transmembrane transporter activity GO:0051119 p=2.6E−02 n=1 fg=0.02 bg=0.00
carbohydrate:cation symporter activity GO:0005402 p=2.6E−02 n=1 fg=0.02 bg=0.00
carbohydrate transmembrane transporter a... GO:0015144 p=2.6E−02 n=1 fg=0.02 bg=0.00
monosaccharide transmembrane transporter... GO:0015145 p=2.6E−02 n=1 fg=0.02 bg=0.00
hexose transmembrane transporter activit... GO:0015149 p=2.6E−02 n=1 fg=0.02 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=2.6E−02 n=1 fg=0.02 bg=0.00
dystroglycan binding GO:0002162 p=2.6E−02 n=1 fg=0.02 bg=0.00
beta−1 adrenergic receptor binding GO:0031697 p=2.6E−02 n=1 fg=0.02 bg=0.00
polypeptide N−acetylgalactosaminyltransf... GO:0004653 p=2.6E−02 n=1 fg=0.02 bg=0.00
endoribonuclease activity, producing 3'−... GO:0016892 p=2.6E−02 n=1 fg=0.02 bg=0.00
endonuclease activity, active with eithe... GO:0016894 p=2.6E−02 n=1 fg=0.02 bg=0.00
carbohydrate:proton symporter activity GO:0005351 p=2.6E−02 n=1 fg=0.02 bg=0.00
glucose transmembrane transporter activi... GO:0005355 p=2.6E−02 n=1 fg=0.02 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=2.6E−02 n=1 fg=0.02 bg=0.00
riboflavin transmembrane transporter act... GO:0032217 p=2.6E−02 n=1 fg=0.02 bg=0.00
kinetochore binding GO:0043515 p=2.6E−02 n=1 fg=0.02 bg=0.00
protein kinase binding GO:0019901 p=3.0E−02 n=7 fg=0.17 bg=0.08
peptidase regulator activity GO:0061134 p=3.1E−02 n=2 fg=0.05 bg=0.01
kinase binding GO:0019900 p=3.8E−02 n=7 fg=0.17 bg=0.08
ribonuclease activity GO:0004540 p=4.8E−02 n=2 fg=0.05 bg=0.01
protein tyrosine kinase binding GO:1990782 p=4.8E−02 n=2 fg=0.05 bg=0.01
actin binding GO:0003779 p=5.1E−02 n=3 fg=0.07 bg=0.02
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−log(p)
n=41/157 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001636587.3
fraction genes in fg and expected valu
intercalary heterochromatin GO:0005725 p=2.0E−03 n=2 fg=0.04 bg=0.00
PRC1 complex GO:0035102 p=2.0E−03 n=2 fg=0.04 bg=0.00
mitochondrial large ribosomal subunit GO:0005762 p=4.0E−03 n=2 fg=0.04 bg=0.00
cell periphery GO:0071944 p=9.1E−03 n=22 fg=0.46 bg=0.29
excitatory synapse GO:0060076 p=9.7E−03 n=2 fg=0.04 bg=0.00
Golgi apparatus subcompartment GO:0098791 p=1.3E−02 n=9 fg=0.19 bg=0.08
Golgi cisterna membrane GO:0032580 p=1.3E−02 n=2 fg=0.04 bg=0.00
COPI−coated vesicle GO:0030137 p=1.3E−02 n=2 fg=0.04 bg=0.00
Golgi apparatus GO:0005794 p=1.9E−02 n=12 fg=0.25 bg=0.13
chromaffin granule GO:0042583 p=2.6E−02 n=1 fg=0.02 bg=0.00
chromaffin granule membrane GO:0042584 p=2.6E−02 n=1 fg=0.02 bg=0.00
centrosomal corona GO:0031592 p=2.6E−02 n=1 fg=0.02 bg=0.00
RNA polymerase III transcription regulat... GO:0090576 p=2.6E−02 n=1 fg=0.02 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=2.6E−02 n=1 fg=0.02 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=2.6E−02 n=1 fg=0.02 bg=0.00
exoribonuclease complex GO:1905354 p=2.6E−02 n=1 fg=0.02 bg=0.00
hippocampal mossy fiber to CA3 synapse GO:0098686 p=2.6E−02 n=1 fg=0.02 bg=0.00
exosome (RNase complex) GO:0000178 p=2.6E−02 n=1 fg=0.02 bg=0.00
transcription factor TFIIIC complex GO:0000127 p=2.6E−02 n=1 fg=0.02 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=2.6E−02 n=1 fg=0.02 bg=0.00
apoptosome GO:0043293 p=2.6E−02 n=1 fg=0.02 bg=0.00
lumenal side of Golgi membrane GO:0098547 p=2.6E−02 n=1 fg=0.02 bg=0.00
cortical microtubule GO:0055028 p=2.6E−02 n=1 fg=0.02 bg=0.00
tRNA−intron endonuclease complex GO:0000214 p=2.6E−02 n=1 fg=0.02 bg=0.00
nuclear outer membrane GO:0005640 p=2.6E−02 n=1 fg=0.02 bg=0.00
AP−3 adaptor complex GO:0030123 p=2.6E−02 n=1 fg=0.02 bg=0.00
cortical microtubule plus−end GO:1903754 p=2.6E−02 n=1 fg=0.02 bg=0.00
centrosome GO:0005813 p=3.2E−02 n=6 fg=0.12 bg=0.05
organelle subcompartment GO:0031984 p=3.3E−02 n=12 fg=0.25 bg=0.14
plasma membrane region GO:0098590 p=3.8E−02 n=9 fg=0.19 bg=0.10
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−log(p)
n=48/157 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction