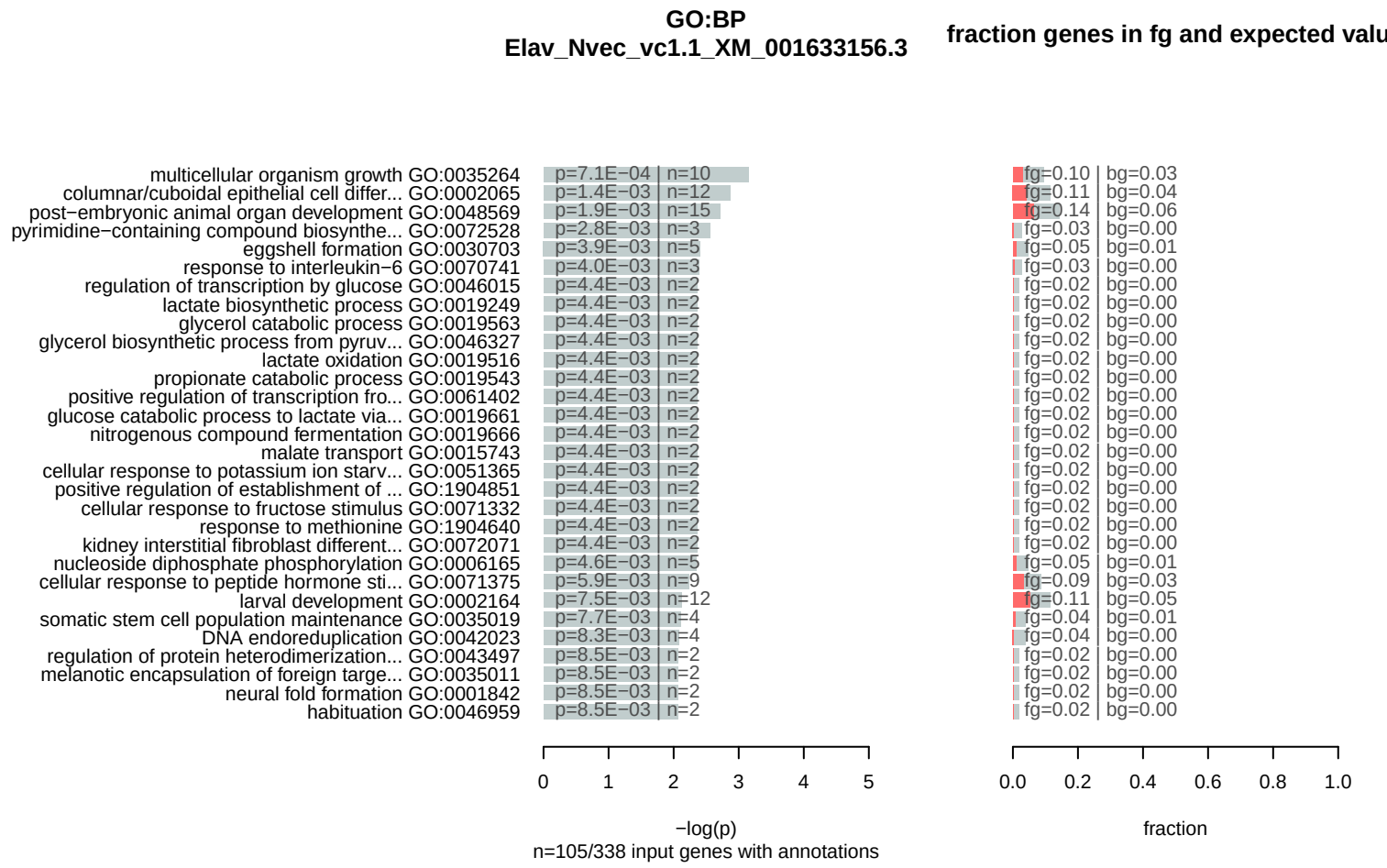
GO:BP
Elav_Nvec_vc1.1_XM_001633156.3
fraction genes in fg and expected valu
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columnar/cuboidal epithelial cell differ... GO:0002065 p=1.4E−03 n=12 fg=0.11 bg=0.04
post−embryonic animal organ development GO:0048569 p=1.9E−03 n=15 fg=0.14 bg=0.06
pyrimidine−containing compound biosynthe... GO:0072528 p=2.8E−03 n=3 fg=0.03 bg=0.00
eggshell formation GO:0030703 p=3.9E−03 n=5 fg=0.05 bg=0.01
response to interleukin−6 GO:0070741 p=4.0E−03 n=3 fg=0.03 bg=0.00
regulation of transcription by glucose GO:0046015 p=4.4E−03 n=2 fg=0.02 bg=0.00
lactate biosynthetic process GO:0019249 p=4.4E−03 n=2 fg=0.02 bg=0.00
glycerol catabolic process GO:0019563 p=4.4E−03 n=2 fg=0.02 bg=0.00
glycerol biosynthetic process from pyruv... GO:0046327 p=4.4E−03 n=2 fg=0.02 bg=0.00
lactate oxidation GO:0019516 p=4.4E−03 n=2 fg=0.02 bg=0.00
propionate catabolic process GO:0019543 p=4.4E−03 n=2 fg=0.02 bg=0.00
positive regulation of transcription fro... GO:0061402 p=4.4E−03 n=2 fg=0.02 bg=0.00
glucose catabolic process to lactate via... GO:0019661 p=4.4E−03 n=2 fg=0.02 bg=0.00
nitrogenous compound fermentation GO:0019666 p=4.4E−03 n=2 fg=0.02 bg=0.00
malate transport GO:0015743 p=4.4E−03 n=2 fg=0.02 bg=0.00
cellular response to potassium ion starv... GO:0051365 p=4.4E−03 n=2 fg=0.02 bg=0.00
positive regulation of establishment of ... GO:1904851 p=4.4E−03 n=2 fg=0.02 bg=0.00
cellular response to fructose stimulus GO:0071332 p=4.4E−03 n=2 fg=0.02 bg=0.00
response to methionine GO:1904640 p=4.4E−03 n=2 fg=0.02 bg=0.00
kidney interstitial fibroblast different... GO:0072071 p=4.4E−03 n=2 fg=0.02 bg=0.00
nucleoside diphosphate phosphorylation GO:0006165 p=4.6E−03 n=5 fg=0.05 bg=0.01
cellular response to peptide hormone sti... GO:0071375 p=5.9E−03 n=9 fg=0.09 bg=0.03
larval development GO:0002164 p=7.5E−03 n=12 fg=0.11 bg=0.05
somatic stem cell population maintenance GO:0035019 p=7.7E−03 n=4 fg=0.04 bg=0.01
DNA endoreduplication GO:0042023 p=8.3E−03 n=4 fg=0.04 bg=0.00
regulation of protein heterodimerization... GO:0043497 p=8.5E−03 n=2 fg=0.02 bg=0.00
melanotic encapsulation of foreign targe... GO:0035011 p=8.5E−03 n=2 fg=0.02 bg=0.00
neural fold formation GO:0001842 p=8.5E−03 n=2 fg=0.02 bg=0.00
habituation GO:0046959 p=8.5E−03 n=2 fg=0.02 bg=0.00
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−log(p)
n=105/338 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_001633156.3
fraction genes in fg and expected valu
nucleoside diphosphate kinase activity GO:0004550 p=5.4E−04 n=3 fg=0.03 bg=0.00
glycerol−3−phosphate O−acyltransferase a... GO:0004366 p=1.5E−03 n=2 fg=0.02 bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016814 p=1.8E−03 n=3 fg=0.03 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=4.4E−03 n=2 fg=0.02 bg=0.00
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=4.4E−03 n=2 fg=0.02 bg=0.00
inosine kinase activity GO:0008906 p=4.4E−03 n=2 fg=0.02 bg=0.00
DNA binding domain binding GO:0050692 p=8.5E−03 n=2 fg=0.02 bg=0.00
lactate dehydrogenase activity GO:0004457 p=8.5E−03 n=2 fg=0.02 bg=0.00
deaminase activity GO:0019239 p=1.4E−02 n=2 fg=0.02 bg=0.00
epinephrine binding GO:0051379 p=1.4E−02 n=2 fg=0.02 bg=0.00
catecholamine binding GO:1901338 p=1.4E−02 n=2 fg=0.02 bg=0.00
solute:cation symporter activity GO:0015294 p=2.6E−02 n=3 fg=0.03 bg=0.01
protein folding chaperone GO:0044183 p=2.8E−02 n=2 fg=0.02 bg=0.00
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core promoter sequence−specific DNA bind... GO:0001046 p=3.0E−02 n=3 fg=0.03 bg=0.01
alkanesulfonate transmembrane transporte... GO:0042959 p=3.9E−02 n=1 fg=0.01 bg=0.00
amino acid:sodium symporter activity GO:0005283 p=3.9E−02 n=1 fg=0.01 bg=0.00
protein N−acetylglucosaminyltransferase ... GO:0016262 p=3.9E−02 n=1 fg=0.01 bg=0.00
deoxycytidine deaminase activity GO:0047844 p=3.9E−02 n=1 fg=0.01 bg=0.00
purine−specific nucleoside:sodium sympor... GO:0015390 p=3.9E−02 n=1 fg=0.01 bg=0.00
nucleobase:cation symporter activity GO:0015391 p=3.9E−02 n=1 fg=0.01 bg=0.00
taurine transmembrane transporter activi... GO:0005368 p=3.9E−02 n=1 fg=0.01 bg=0.00
taurine:sodium symporter activity GO:0005369 p=3.9E−02 n=1 fg=0.01 bg=0.00
pyrimidine nucleobase transmembrane tran... GO:0005350 p=3.9E−02 n=1 fg=0.01 bg=0.00
CTP synthase activity GO:0003883 p=3.9E−02 n=1 fg=0.01 bg=0.00
sphingolipid transporter activity GO:0046624 p=3.9E−02 n=1 fg=0.01 bg=0.00
purine nucleoside transmembrane transpor... GO:0015211 p=3.9E−02 n=1 fg=0.01 bg=0.00
glucose−6−phosphate dehydrogenase activi... GO:0004345 p=3.9E−02 n=1 fg=0.01 bg=0.00
pyrimidine− and adenine−specific:sodium ... GO:0015389 p=3.9E−02 n=1 fg=0.01 bg=0.00
high−affinity glutamate transmembrane tr... GO:0005314 p=3.9E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=92/338 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001633156.3
fraction genes in fg and expected valu
zona pellucida receptor complex GO:0002199 p=4.2E−03 n=2 fg=0.02 bg=0.00
chaperonin−containing T−complex GO:0005832 p=1.3E−02 n=2 fg=0.02 bg=0.00
chaperone complex GO:0101031 p=2.7E−02 n=2 fg=0.02 bg=0.00
proteasome regulatory particle, base sub... GO:0008540 p=2.7E−02 n=2 fg=0.02 bg=0.00
sperm cytoplasmic droplet GO:0097598 p=3.8E−02 n=1 fg=0.01 bg=0.00
actin rod GO:0031002 p=3.8E−02 n=1 fg=0.01 bg=0.00
plasmodesma GO:0009506 p=3.8E−02 n=1 fg=0.01 bg=0.00
chloroplast GO:0009507 p=3.8E−02 n=1 fg=0.01 bg=0.00
kinocilium GO:0060091 p=3.8E−02 n=1 fg=0.01 bg=0.00
spectrosome GO:0045170 p=3.8E−02 n=1 fg=0.01 bg=0.00
symplast GO:0055044 p=3.8E−02 n=1 fg=0.01 bg=0.00
cyclin E1−CDK2 complex GO:0097134 p=3.8E−02 n=1 fg=0.01 bg=0.00
cyclin E2−CDK2 complex GO:0097135 p=3.8E−02 n=1 fg=0.01 bg=0.00
proteasome storage granule GO:0034515 p=3.8E−02 n=1 fg=0.01 bg=0.00
apoplast GO:0048046 p=3.8E−02 n=1 fg=0.01 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=3.8E−02 n=1 fg=0.01 bg=0.00
spectrin GO:0008091 p=3.8E−02 n=1 fg=0.01 bg=0.00
lamin filament GO:0005638 p=3.8E−02 n=1 fg=0.01 bg=0.00
cofilin−actin rod GO:0090732 p=3.8E−02 n=1 fg=0.01 bg=0.00
cytoophidium GO:0097268 p=3.8E−02 n=1 fg=0.01 bg=0.00
9+2 non−motile cilium GO:0097732 p=3.8E−02 n=1 fg=0.01 bg=0.00
plastid GO:0009536 p=3.8E−02 n=1 fg=0.01 bg=0.00
fusome GO:0045169 p=4.4E−02 n=2 fg=0.02 bg=0.00
mitotic spindle GO:0072686 p=5.5E−02 n=4 fg=0.04 bg=0.01
proteasome regulatory particle GO:0005838 p=7.4E−02 n=2 fg=0.02 bg=0.00
proteasome accessory complex GO:0022624 p=7.4E−02 n=2 fg=0.02 bg=0.00
extrinsic component of mitochondrial inn... GO:0031314 p=7.5E−02 n=1 fg=0.01 bg=0.00
female germline ring canal GO:0035324 p=7.5E−02 n=1 fg=0.01 bg=0.00
nuclear stress granule GO:0097165 p=7.5E−02 n=1 fg=0.01 bg=0.00
GAIT complex GO:0097452 p=7.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=103/338 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction