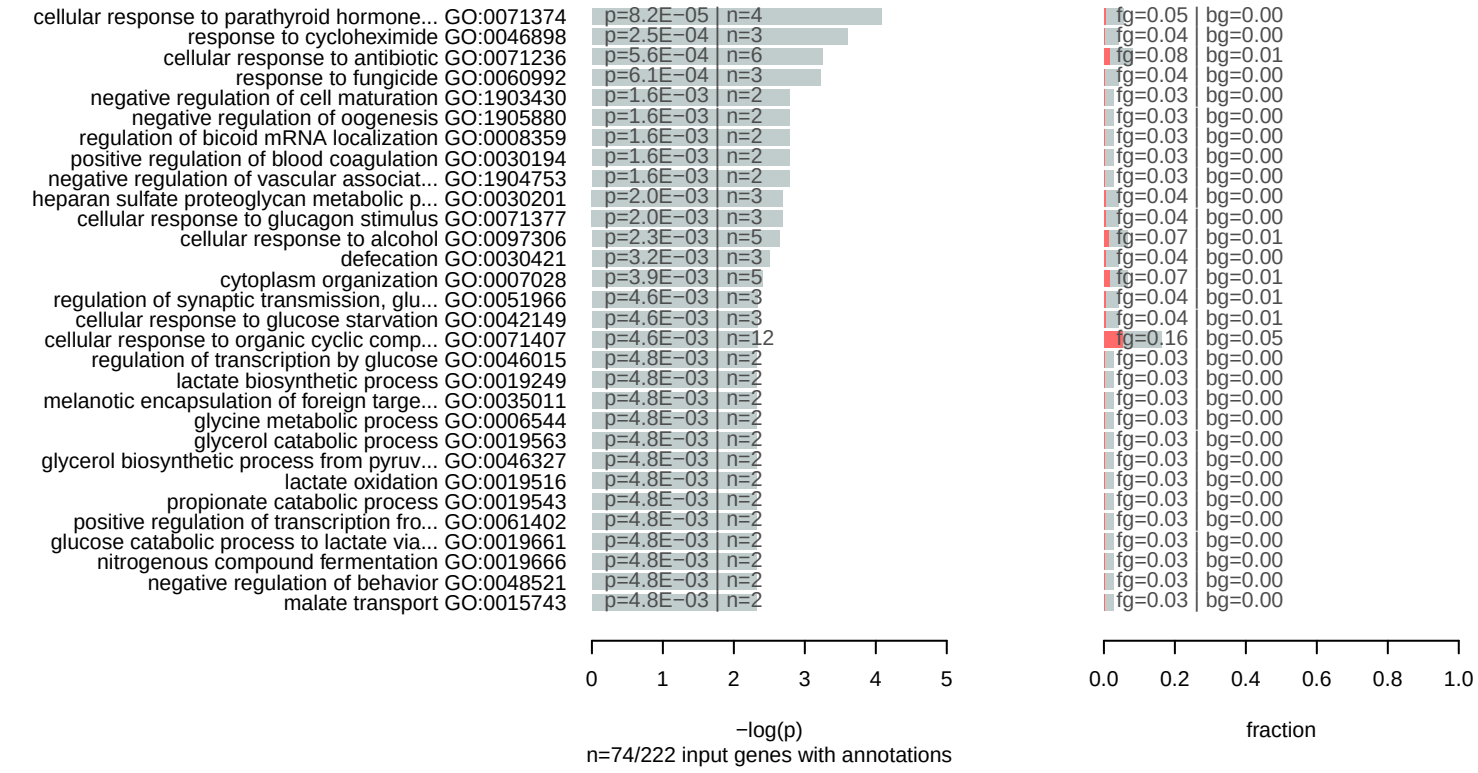
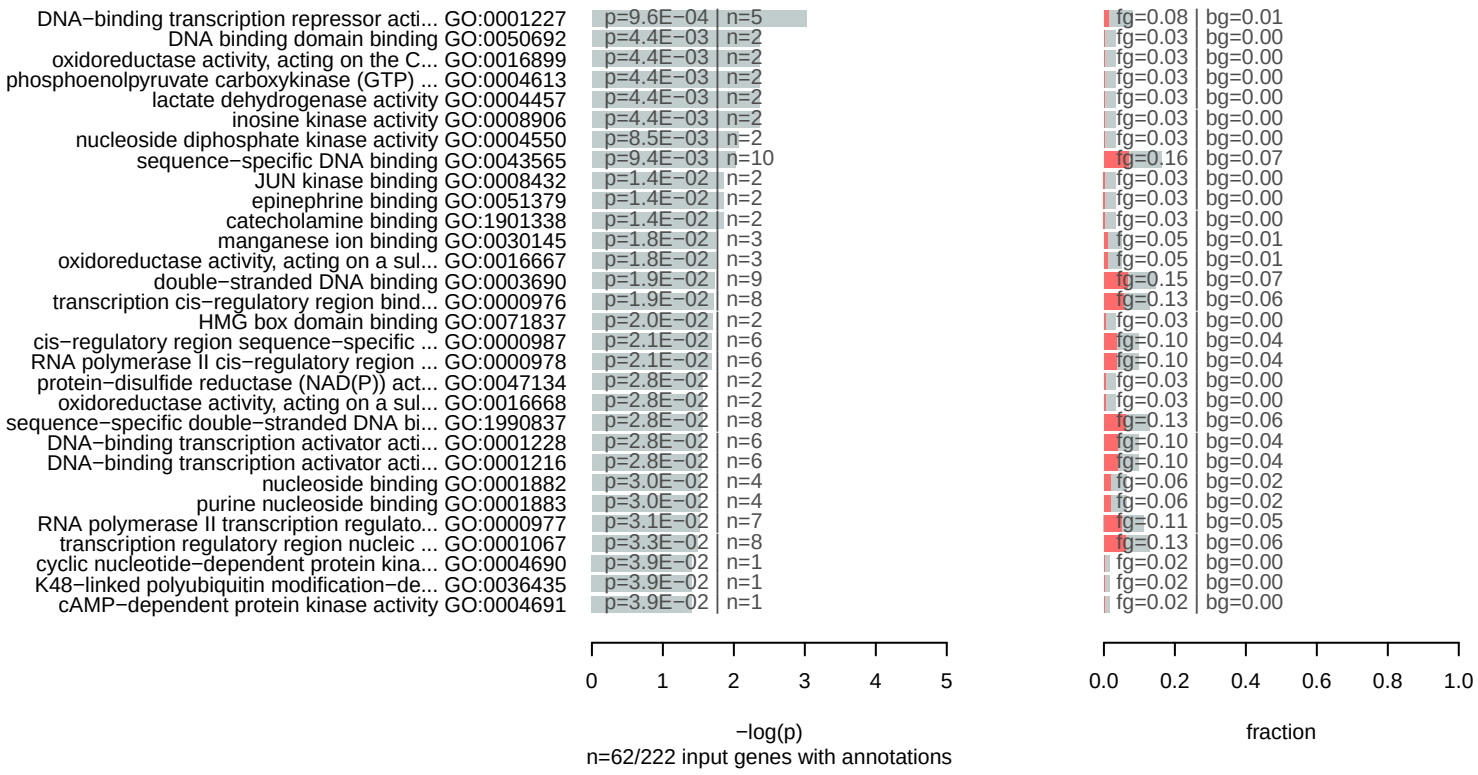

GO:BP
Elav_Nvec_vc1.1_XM_001634460.3
fraction genes in fg and expected valu
cellular response to parathyroid hormone... GO:0071374 p=8.2E−05 n=4 fg=0.05 bg=0.00
response to cycloheximide GO:0046898 p=2.5E−04 n=3 fg=0.04 bg=0.00
cellular response to antibiotic GO:0071236 p=5.6E−04 n=6 fg=0.08 bg=0.01
response to fungicide GO:0060992 p=6.1E−04 n=3 fg=0.04 bg=0.00
negative regulation of cell maturation GO:1903430 p=1.6E−03 n=2 fg=0.03 bg=0.00
negative regulation of oogenesis GO:1905880 p=1.6E−03 n=2 fg=0.03 bg=0.00
regulation of bicoid mRNA localization GO:0008359 p=1.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of blood coagulation GO:0030194 p=1.6E−03 n=2 fg=0.03 bg=0.00
negative regulation of vascular associat... GO:1904753 p=1.6E−03 n=2 fg=0.03 bg=0.00
heparan sulfate proteoglycan metabolic p... GO:0030201 p=2.0E−03 n=3 fg=0.04 bg=0.00
cellular response to glucagon stimulus GO:0071377 p=2.0E−03 n=3 fg=0.04 bg=0.00
cellular response to alcohol GO:0097306 p=2.3E−03 n=5 fg=0.07 bg=0.01
defecation GO:0030421 p=3.2E−03 n=3 fg=0.04 bg=0.00
cytoplasm organization GO:0007028 p=3.9E−03 n=5 fg=0.07 bg=0.01
regulation of synaptic transmission, glu... GO:0051966 p=4.6E−03 n=3 fg=0.04 bg=0.01
cellular response to glucose starvation GO:0042149 p=4.6E−03 n=3 fg=0.04 bg=0.01
cellular response to organic cyclic comp... GO:0071407 p=4.6E−03 n=12 fg=0.16 bg=0.05
regulation of transcription by glucose GO:0046015 p=4.8E−03 n=2 fg=0.03 bg=0.00
lactate biosynthetic process GO:0019249 p=4.8E−03 n=2 fg=0.03 bg=0.00
melanotic encapsulation of foreign targe... GO:0035011 p=4.8E−03 n=2 fg=0.03 bg=0.00
glycine metabolic process GO:0006544 p=4.8E−03 n=2 fg=0.03 bg=0.00
glycerol catabolic process GO:0019563 p=4.8E−03 n=2 fg=0.03 bg=0.00
glycerol biosynthetic process from pyruv... GO:0046327 p=4.8E−03 n=2 fg=0.03 bg=0.00
lactate oxidation GO:0019516 p=4.8E−03 n=2 fg=0.03 bg=0.00
propionate catabolic process GO:0019543 p=4.8E−03 n=2 fg=0.03 bg=0.00
positive regulation of transcription fro... GO:0061402 p=4.8E−03 n=2 fg=0.03 bg=0.00
glucose catabolic process to lactate via... GO:0019661 p=4.8E−03 n=2 fg=0.03 bg=0.00
nitrogenous compound fermentation GO:0019666 p=4.8E−03 n=2 fg=0.03 bg=0.00
negative regulation of behavior GO:0048521 p=4.8E−03 n=2 fg=0.03 bg=0.00
malate transport GO:0015743 p=4.8E−03 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=74/222 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
Elav_Nvec_vc1.1_XM_001634460.3
fraction genes in fg and expected valu
DNA−binding transcription repressor acti... GO:0001227 p=9.6E−04 n=5 fg=0.08 bg=0.01
DNA binding domain binding GO:0050692 p=4.4E−03 n=2 fg=0.03 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=4.4E−03 n=2 fg=0.03 bg=0.00
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=4.4E−03 n=2 fg=0.03 bg=0.00
lactate dehydrogenase activity GO:0004457 p=4.4E−03 n=2 fg=0.03 bg=0.00
inosine kinase activity GO:0008906 p=4.4E−03 n=2 fg=0.03 bg=0.00
nucleoside diphosphate kinase activity GO:0004550 p=8.5E−03 n=2 fg=0.03 bg=0.00
sequence−specific DNA binding GO:0043565 p=9.4E−03 n=10 fg=0.16 bg=0.07
JUN kinase binding GO:0008432 p=1.4E−02 n=2 fg=0.03 bg=0.00
epinephrine binding GO:0051379 p=1.4E−02 n=2 fg=0.03 bg=0.00
catecholamine binding GO:1901338 p=1.4E−02 n=2 fg=0.03 bg=0.00
manganese ion binding GO:0030145 p=1.8E−02 n=3 fg=0.05 bg=0.01
oxidoreductase activity, acting on a sul... GO:0016667 p=1.8E−02 n=3 fg=0.05 bg=0.01
double−stranded DNA binding GO:0003690 p=1.9E−02 n=9 fg=0.15 bg=0.07
transcription cis−regulatory region bind... GO:0000976 p=1.9E−02 n=8 fg=0.13 bg=0.06
HMG box domain binding GO:0071837 p=2.0E−02 n=2 fg=0.03 bg=0.00
cis−regulatory region sequence−specific ... GO:0000987 p=2.1E−02 n=6 fg=0.10 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=2.1E−02 n=6 fg=0.10 bg=0.04
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=2.8E−02 n=2 fg=0.03 bg=0.00
oxidoreductase activity, acting on a sul... GO:0016668 p=2.8E−02 n=2 fg=0.03 bg=0.00
sequence−specific double−stranded DNA bi... GO:1990837 p=2.8E−02 n=8 fg=0.13 bg=0.06
DNA−binding transcription activator acti... GO:0001228 p=2.8E−02 n=6 fg=0.10 bg=0.04
DNA−binding transcription activator acti... GO:0001216 p=2.8E−02 n=6 fg=0.10 bg=0.04
nucleoside binding GO:0001882 p=3.0E−02 n=4 fg=0.06 bg=0.02
purine nucleoside binding GO:0001883 p=3.0E−02 n=4 fg=0.06 bg=0.02
RNA polymerase II transcription regulato... GO:0000977 p=3.1E−02 n=7 fg=0.11 bg=0.05
transcription regulatory region nucleic ... GO:0001067 p=3.3E−02 n=8 fg=0.13 bg=0.06
cyclic nucleotide−dependent protein kina... GO:0004690 p=3.9E−02 n=1 fg=0.02 bg=0.00
K48−linked polyubiquitin modification−de... GO:0036435 p=3.9E−02 n=1 fg=0.02 bg=0.00
cAMP−dependent protein kinase activity GO:0004691 p=3.9E−02 n=1 fg=0.02 bg=0.00
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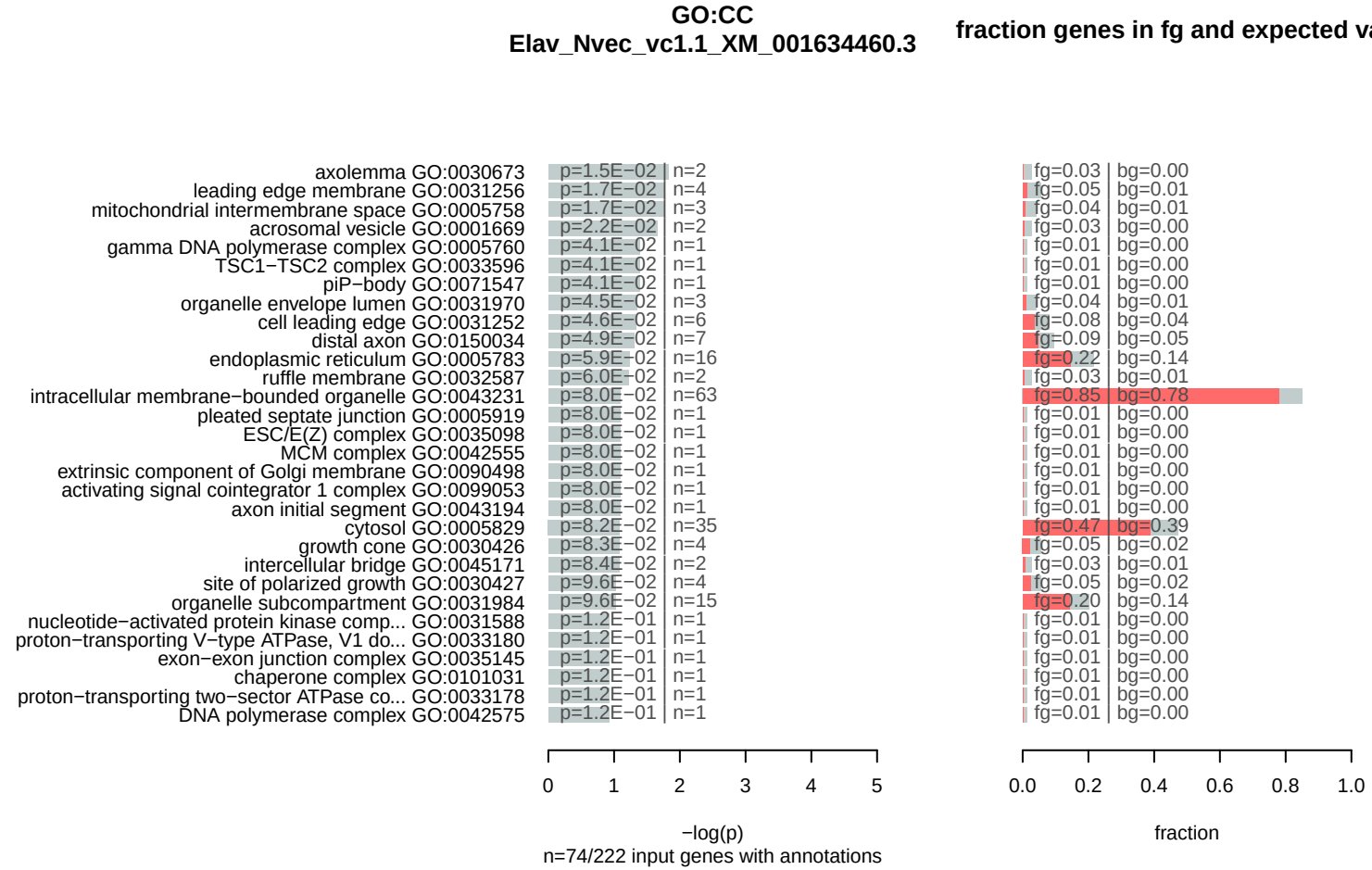
−log(p)
n=62/222 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Elav_Nvec_vc1.1_XM_001634460.3
fraction genes in fg and expected valu
axolemma GO:0030673 p=1.5E−02 n=2 fg=0.03 bg=0.00
leading edge membrane GO:0031256 p=1.7E−02 n=4 fg=0.05 bg=0.01
mitochondrial intermembrane space GO:0005758 p=1.7E−02 n=3 fg=0.04 bg=0.01
acrosomal vesicle GO:0001669 p=2.2E−02 n=2 fg=0.03 bg=0.00
gamma DNA polymerase complex GO:0005760 p=4.1E−02 n=1 fg=0.01 bg=0.00
TSC1−TSC2 complex GO:0033596 p=4.1E−02 n=1 fg=0.01 bg=0.00
piP−body GO:0071547 p=4.1E−02 n=1 fg=0.01 bg=0.00
organelle envelope lumen GO:0031970 p=4.5E−02 n=3 fg=0.04 bg=0.01
cell leading edge GO:0031252 p=4.6E−02 n=6 fg=0.08 bg=0.04
distal axon GO:0150034 p=4.9E−02 n=7 fg=0.09 bg=0.05
endoplasmic reticulum GO:0005783 p=5.9E−02 n=16 fg=0.22 bg=0.14
ruffle membrane GO:0032587 p=6.0E−02 n=2 fg=0.03 bg=0.01
intracellular membrane−bounded organelle GO:0043231 p=8.0E−02 n=63 fg=0.85 bg=0.78
pleated septate junction GO:0005919 p=8.0E−02 n=1 fg=0.01 bg=0.00
ESC/E(Z) complex GO:0035098 p=8.0E−02 n=1 fg=0.01 bg=0.00
MCM complex GO:0042555 p=8.0E−02 n=1 fg=0.01 bg=0.00
extrinsic component of Golgi membrane GO:0090498 p=8.0E−02 n=1 fg=0.01 bg=0.00
activating signal cointegrator 1 complex GO:0099053 p=8.0E−02 n=1 fg=0.01 bg=0.00
axon initial segment GO:0043194 p=8.0E−02 n=1 fg=0.01 bg=0.00
cytosol GO:0005829 p=8.2E−02 n=35 fg=0.47 bg=0.39
growth cone GO:0030426 p=8.3E−02 n=4 fg=0.05 bg=0.02
intercellular bridge GO:0045171 p=8.4E−02 n=2 fg=0.03 bg=0.01
site of polarized growth GO:0030427 p=9.6E−02 n=4 fg=0.05 bg=0.02
organelle subcompartment GO:0031984 p=9.6E−02 n=15 fg=0.20 bg=0.14
nucleotide−activated protein kinase comp... GO:0031588 p=1.2E−01 n=1 fg=0.01 bg=0.00
proton−transporting V−type ATPase, V1 do... GO:0033180 p=1.2E−01 n=1 fg=0.01 bg=0.00
exon−exon junction complex GO:0035145 p=1.2E−01 n=1 fg=0.01 bg=0.00
chaperone complex GO:0101031 p=1.2E−01 n=1 fg=0.01 bg=0.00
proton−transporting two−sector ATPase co... GO:0033178 p=1.2E−01 n=1 fg=0.01 bg=0.00
DNA polymerase complex GO:0042575 p=1.2E−01 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=74/222 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction