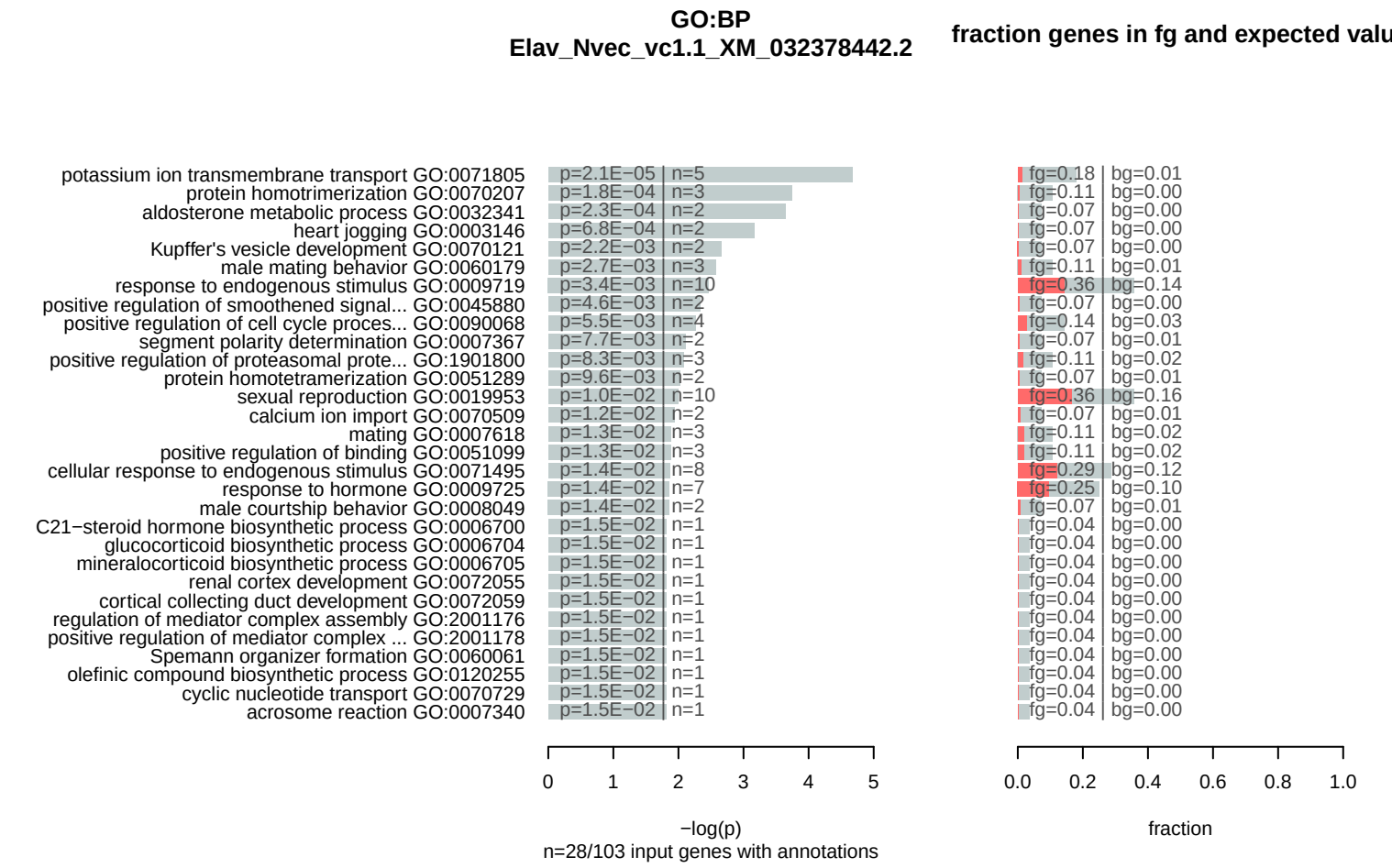
GO:BP
Elav_Nvec_vc1.1_XM_032378442.2
fraction genes in fg and expected valu
potassium ion transmembrane transport GO:0071805 p=2.1E−05 n=5 fg=0.18 bg=0.01
protein homotrimerization GO:0070207 p=1.8E−04 n=3 fg=0.11 bg=0.00
aldosterone metabolic process GO:0032341 p=2.3E−04 n=2 fg=0.07 bg=0.00
heart jogging GO:0003146 p=6.8E−04 n=2 fg=0.07 bg=0.00
Kupffer's vesicle development GO:0070121 p=2.2E−03 n=2 fg=0.07 bg=0.00
male mating behavior GO:0060179 p=2.7E−03 n=3 fg=0.11 bg=0.01
response to endogenous stimulus GO:0009719 p=3.4E−03 n=10 fg=0.36 bg=0.14
positive regulation of smoothened signal... GO:0045880 p=4.6E−03 n=2 fg=0.07 bg=0.00
positive regulation of cell cycle proces... GO:0090068 p=5.5E−03 n=4 fg=0.14 bg=0.03
segment polarity determination GO:0007367 p=7.7E−03 n=2 fg=0.07 bg=0.01
positive regulation of proteasomal prote... GO:1901800 p=8.3E−03 n=3 fg=0.11 bg=0.02
protein homotetramerization GO:0051289 p=9.6E−03 n=2 fg=0.07 bg=0.01
sexual reproduction GO:0019953 p=1.0E−02 n=10 fg=0.36 bg=0.16
calcium ion import GO:0070509 p=1.2E−02 n=2 fg=0.07 bg=0.01
mating GO:0007618 p=1.3E−02 n=3 fg=0.11 bg=0.02
positive regulation of binding GO:0051099 p=1.3E−02 n=3 fg=0.11 bg=0.02
cellular response to endogenous stimulus GO:0071495 p=1.4E−02 n=8 fg=0.29 bg=0.12
response to hormone GO:0009725 p=1.4E−02 n=7 fg=0.25 bg=0.10
male courtship behavior GO:0008049 p=1.4E−02 n=2 fg=0.07 bg=0.01
C21−steroid hormone biosynthetic process GO:0006700 p=1.5E−02 n=1 fg=0.04 bg=0.00
glucocorticoid biosynthetic process GO:0006704 p=1.5E−02 n=1 fg=0.04 bg=0.00
mineralocorticoid biosynthetic process GO:0006705 p=1.5E−02 n=1 fg=0.04 bg=0.00
renal cortex development GO:0072055 p=1.5E−02 n=1 fg=0.04 bg=0.00
cortical collecting duct development GO:0072059 p=1.5E−02 n=1 fg=0.04 bg=0.00
regulation of mediator complex assembly GO:2001176 p=1.5E−02 n=1 fg=0.04 bg=0.00
positive regulation of mediator complex ... GO:2001178 p=1.5E−02 n=1 fg=0.04 bg=0.00
Spemann organizer formation GO:0060061 p=1.5E−02 n=1 fg=0.04 bg=0.00
olefinic compound biosynthetic process GO:0120255 p=1.5E−02 n=1 fg=0.04 bg=0.00
cyclic nucleotide transport GO:0070729 p=1.5E−02 n=1 fg=0.04 bg=0.00
acrosome reaction GO:0007340 p=1.5E−02 n=1 fg=0.04 bg=0.00
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−log(p)
n=28/103 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032378442.2
fraction genes in fg and expected valu
calcium−activated potassium channel acti... GO:0015269 p=5.4E−06 n=3 fg=0.10 bg=0.00
voltage−gated potassium channel activity GO:0005249 p=8.3E−04 n=4 fg=0.14 bg=0.01
voltage−gated sodium channel activity GO:0005248 p=1.9E−03 n=2 fg=0.07 bg=0.00
translation factor activity, RNA binding GO:0008135 p=2.6E−03 n=3 fg=0.10 bg=0.01
outward rectifier potassium channel acti... GO:0015271 p=6.4E−03 n=2 fg=0.07 bg=0.00
voltage−gated calcium channel activity GO:0005245 p=8.4E−03 n=2 fg=0.07 bg=0.01
translation initiation factor activity GO:0003743 p=1.6E−02 n=2 fg=0.07 bg=0.01
ecdysis−triggering hormone receptor acti... GO:0042654 p=1.8E−02 n=1 fg=0.03 bg=0.00
cytosine C−5 DNA demethylase activity GO:0051747 p=1.8E−02 n=1 fg=0.03 bg=0.00
nucleobase transmembrane transporter act... GO:0015205 p=1.8E−02 n=1 fg=0.03 bg=0.00
guanine transmembrane transporter activi... GO:0015208 p=1.8E−02 n=1 fg=0.03 bg=0.00
purine nucleobase transmembrane transpor... GO:0005345 p=1.8E−02 n=1 fg=0.03 bg=0.00
amine transmembrane transporter activity GO:0005275 p=1.8E−02 n=1 fg=0.03 bg=0.00
large conductance calcium−activated pota... GO:0060072 p=1.8E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=1.8E−02 n=1 fg=0.03 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=1.8E−02 n=1 fg=0.03 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=1.8E−02 n=1 fg=0.03 bg=0.00
guanine nucleotide transmembrane transpo... GO:0001409 p=1.8E−02 n=1 fg=0.03 bg=0.00
HLH domain binding GO:0043398 p=1.8E−02 n=1 fg=0.03 bg=0.00
ABC−type 3',5'−cyclic GMP transmembrane ... GO:1905948 p=1.8E−02 n=1 fg=0.03 bg=0.00
muscle alpha−actinin binding GO:0051371 p=1.8E−02 n=1 fg=0.03 bg=0.00
voltage−gated calcium channel activity i... GO:0086056 p=1.8E−02 n=1 fg=0.03 bg=0.00
voltage−gated calcium channel activity i... GO:0086059 p=1.8E−02 n=1 fg=0.03 bg=0.00
DNA demethylase activity GO:0035514 p=1.8E−02 n=1 fg=0.03 bg=0.00
cyclic GMP−AMP synthase activity GO:0140699 p=1.8E−02 n=1 fg=0.03 bg=0.00
RNA−3'−phosphate cyclase activity GO:0003963 p=1.8E−02 n=1 fg=0.03 bg=0.00
2',3'−cyclic GMP−AMP synthase activity GO:0061501 p=1.8E−02 n=1 fg=0.03 bg=0.00
ABC−type guanine transporter activity GO:0008558 p=1.8E−02 n=1 fg=0.03 bg=0.00
RNA polymerase II−specific DNA−binding t... GO:0061629 p=3.0E−02 n=3 fg=0.10 bg=0.02
core promoter sequence−specific DNA bind... GO:0001046 p=3.3E−02 n=2 fg=0.07 bg=0.01
0 1 2 3 4 5
−log(p)
n=29/103 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032378442.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=2.6E−04 n=3 fg=0.11 bg=0.01
plasma membrane raft GO:0044853 p=3.7E−03 n=3 fg=0.11 bg=0.01
calcium channel complex GO:0034704 p=4.6E−03 n=2 fg=0.07 bg=0.00
eukaryotic translation initiation factor... GO:0071540 p=1.5E−02 n=1 fg=0.04 bg=0.00
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polycystin complex GO:0002133 p=1.5E−02 n=1 fg=0.04 bg=0.00
integral component of pigment granule me... GO:0090740 p=1.5E−02 n=1 fg=0.04 bg=0.00
pigment granule membrane GO:0090741 p=1.5E−02 n=1 fg=0.04 bg=0.00
caveola GO:0005901 p=2.4E−02 n=2 fg=0.07 bg=0.01
mitotic spindle GO:0072686 p=2.7E−02 n=2 fg=0.07 bg=0.01
eukaryotic translation initiation factor... GO:0005850 p=3.1E−02 n=1 fg=0.04 bg=0.00
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multi−eIF complex GO:0043614 p=3.1E−02 n=1 fg=0.04 bg=0.00
nuclear stress granule GO:0097165 p=3.1E−02 n=1 fg=0.04 bg=0.00
Hedgehog signaling complex GO:0035301 p=3.1E−02 n=1 fg=0.04 bg=0.00
basolateral plasma membrane GO:0016323 p=3.4E−02 n=3 fg=0.11 bg=0.03
basal plasma membrane GO:0009925 p=3.4E−02 n=3 fg=0.11 bg=0.03
sarcolemma GO:0042383 p=4.0E−02 n=2 fg=0.07 bg=0.01
ribonucleoprotein complex GO:1990904 p=4.1E−02 n=5 fg=0.18 bg=0.07
dendrite GO:0030425 p=4.6E−02 n=5 fg=0.18 bg=0.07
dendritic tree GO:0097447 p=4.6E−02 n=5 fg=0.18 bg=0.07
nucleotide−activated protein kinase comp... GO:0031588 p=4.6E−02 n=1 fg=0.04 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=4.6E−02 n=1 fg=0.04 bg=0.00
integral component of cytoplasmic side o... GO:0071458 p=4.6E−02 n=1 fg=0.04 bg=0.00
perinuclear region of cytoplasm GO:0048471 p=4.8E−02 n=5 fg=0.18 bg=0.07
basal part of cell GO:0045178 p=5.1E−02 n=3 fg=0.11 bg=0.03
nucleus GO:0005634 p=5.5E−02 n=18 fg=0.64 bg=0.48
basal cortex GO:0045180 p=6.1E−02 n=1 fg=0.04 bg=0.00
integral component of lumenal side of en... GO:0071556 p=6.1E−02 n=1 fg=0.04 bg=0.00
germinal vesicle GO:0042585 p=6.1E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=28/103 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction