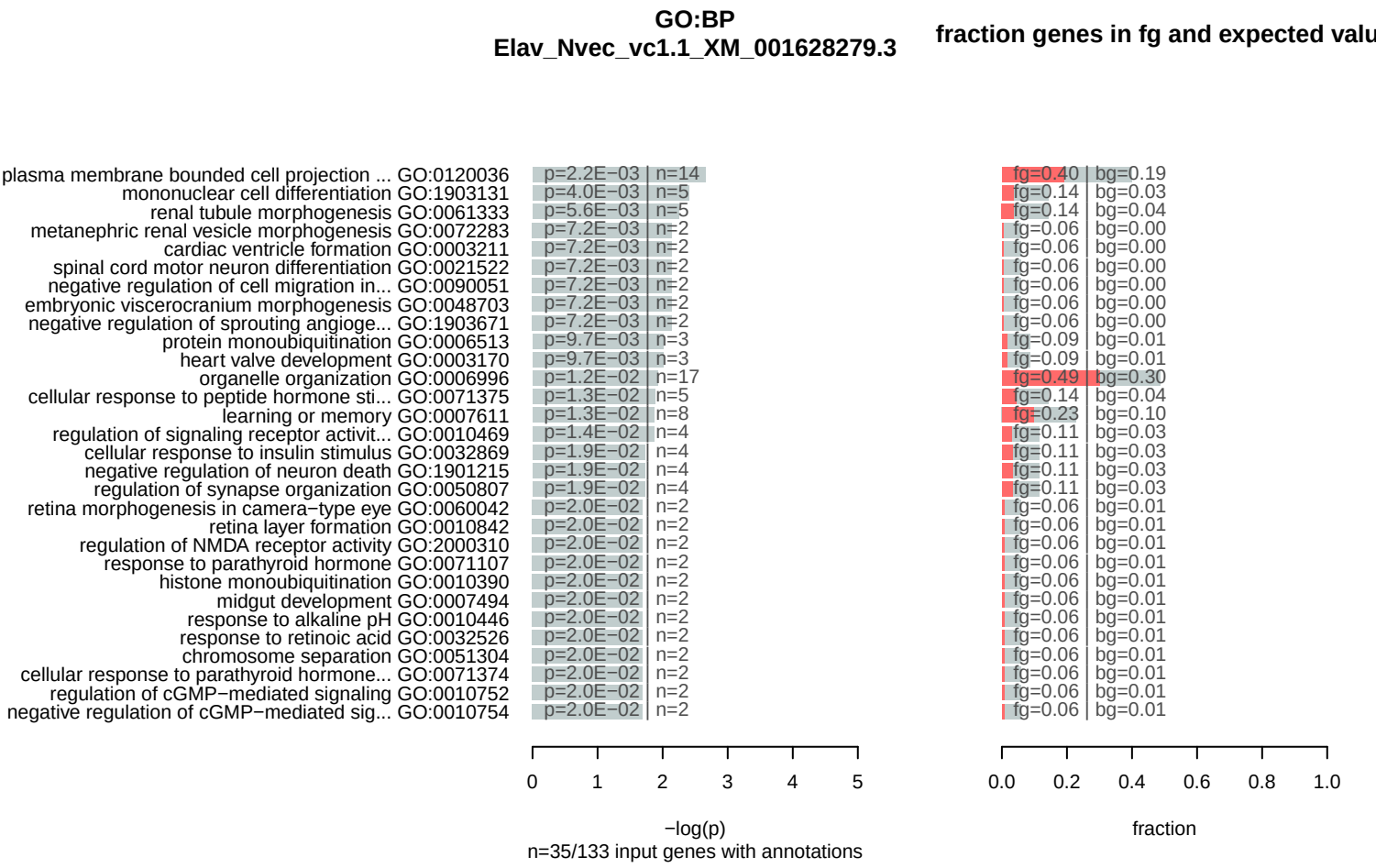
GO:BP
Elav_Nvec_vc1.1_XM_001628279.3
fraction genes in fg and expected valu
plasma membrane bounded cell projection ... GO:0120036 p=2.2E−03 n=14 fg=0.40 bg=0.19
mononuclear cell differentiation GO:1903131 p=4.0E−03 n=5 fg=0.14 bg=0.03
renal tubule morphogenesis GO:0061333 p=5.6E−03 n=5 fg=0.14 bg=0.04
metanephric renal vesicle morphogenesis GO:0072283 p=7.2E−03 n=2 fg=0.06 bg=0.00
cardiac ventricle formation GO:0003211 p=7.2E−03 n=2 fg=0.06 bg=0.00
spinal cord motor neuron differentiation GO:0021522 p=7.2E−03 n=2 fg=0.06 bg=0.00
negative regulation of cell migration in... GO:0090051 p=7.2E−03 n=2 fg=0.06 bg=0.00
embryonic viscerocranium morphogenesis GO:0048703 p=7.2E−03 n=2 fg=0.06 bg=0.00
negative regulation of sprouting angioge... GO:1903671 p=7.2E−03 n=2 fg=0.06 bg=0.00
protein monoubiquitination GO:0006513 p=9.7E−03 n=3 fg=0.09 bg=0.01
heart valve development GO:0003170 p=9.7E−03 n=3 fg=0.09 bg=0.01
organelle organization GO:0006996 p=1.2E−02 n=17 fg=0.49 bg=0.30
cellular response to peptide hormone sti... GO:0071375 p=1.3E−02 n=5 fg=0.14 bg=0.04
learning or memory GO:0007611 p=1.3E−02 n=8 fg=0.23 bg=0.10
regulation of signaling receptor activit... GO:0010469 p=1.4E−02 n=4 fg=0.11 bg=0.03
cellular response to insulin stimulus GO:0032869 p=1.9E−02 n=4 fg=0.11 bg=0.03
negative regulation of neuron death GO:1901215 p=1.9E−02 n=4 fg=0.11 bg=0.03
regulation of synapse organization GO:0050807 p=1.9E−02 n=4 fg=0.11 bg=0.03
retina morphogenesis in camera−type eye GO:0060042 p=2.0E−02 n=2 fg=0.06 bg=0.01
retina layer formation GO:0010842 p=2.0E−02 n=2 fg=0.06 bg=0.01
regulation of NMDA receptor activity GO:2000310 p=2.0E−02 n=2 fg=0.06 bg=0.01
response to parathyroid hormone GO:0071107 p=2.0E−02 n=2 fg=0.06 bg=0.01
histone monoubiquitination GO:0010390 p=2.0E−02 n=2 fg=0.06 bg=0.01
midgut development GO:0007494 p=2.0E−02 n=2 fg=0.06 bg=0.01
response to alkaline pH GO:0010446 p=2.0E−02 n=2 fg=0.06 bg=0.01
response to retinoic acid GO:0032526 p=2.0E−02 n=2 fg=0.06 bg=0.01
chromosome separation GO:0051304 p=2.0E−02 n=2 fg=0.06 bg=0.01
cellular response to parathyroid hormone... GO:0071374 p=2.0E−02 n=2 fg=0.06 bg=0.01
regulation of cGMP−mediated signaling GO:0010752 p=2.0E−02 n=2 fg=0.06 bg=0.01
negative regulation of cGMP−mediated sig... GO:0010754 p=2.0E−02 n=2 fg=0.06 bg=0.01
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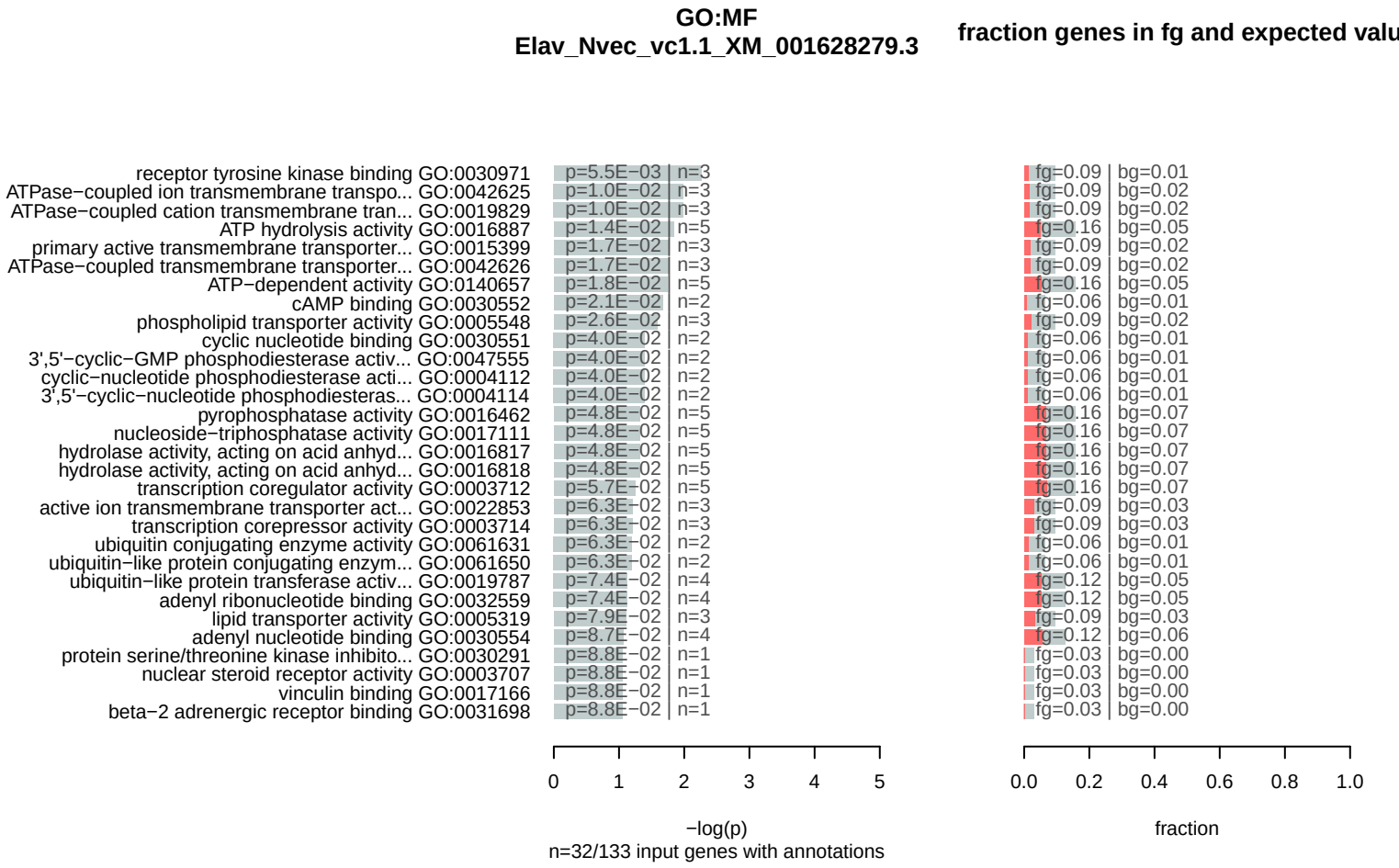
−log(p)
n=35/133 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
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fraction genes in fg and expected valu
receptor tyrosine kinase binding GO:0030971 p=5.5E−03 n=3 fg=0.09 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=1.0E−02 n=3 fg=0.09 bg=0.02
ATPase−coupled cation transmembrane tran... GO:0019829 p=1.0E−02 n=3 fg=0.09 bg=0.02
ATP hydrolysis activity GO:0016887 p=1.4E−02 n=5 fg=0.16 bg=0.05
primary active transmembrane transporter... GO:0015399 p=1.7E−02 n=3 fg=0.09 bg=0.02
ATPase−coupled transmembrane transporter... GO:0042626 p=1.7E−02 n=3 fg=0.09 bg=0.02
ATP−dependent activity GO:0140657 p=1.8E−02 n=5 fg=0.16 bg=0.05
cAMP binding GO:0030552 p=2.1E−02 n=2 fg=0.06 bg=0.01
phospholipid transporter activity GO:0005548 p=2.6E−02 n=3 fg=0.09 bg=0.02
cyclic nucleotide binding GO:0030551 p=4.0E−02 n=2 fg=0.06 bg=0.01
3',5'−cyclic−GMP phosphodiesterase activ... GO:0047555 p=4.0E−02 n=2 fg=0.06 bg=0.01
cyclic−nucleotide phosphodiesterase acti... GO:0004112 p=4.0E−02 n=2 fg=0.06 bg=0.01
3',5'−cyclic−nucleotide phosphodiesteras... GO:0004114 p=4.0E−02 n=2 fg=0.06 bg=0.01
pyrophosphatase activity GO:0016462 p=4.8E−02 n=5 fg=0.16 bg=0.07
nucleoside−triphosphatase activity GO:0017111 p=4.8E−02 n=5 fg=0.16 bg=0.07
hydrolase activity, acting on acid anhyd... GO:0016817 p=4.8E−02 n=5 fg=0.16 bg=0.07
hydrolase activity, acting on acid anhyd... GO:0016818 p=4.8E−02 n=5 fg=0.16 bg=0.07
transcription coregulator activity GO:0003712 p=5.7E−02 n=5 fg=0.16 bg=0.07
active ion transmembrane transporter act... GO:0022853 p=6.3E−02 n=3 fg=0.09 bg=0.03
transcription corepressor activity GO:0003714 p=6.3E−02 n=3 fg=0.09 bg=0.03
ubiquitin conjugating enzyme activity GO:0061631 p=6.3E−02 n=2 fg=0.06 bg=0.01
ubiquitin−like protein conjugating enzym... GO:0061650 p=6.3E−02 n=2 fg=0.06 bg=0.01
ubiquitin−like protein transferase activ... GO:0019787 p=7.4E−02 n=4 fg=0.12 bg=0.05
adenyl ribonucleotide binding GO:0032559 p=7.4E−02 n=4 fg=0.12 bg=0.05
lipid transporter activity GO:0005319 p=7.9E−02 n=3 fg=0.09 bg=0.03
adenyl nucleotide binding GO:0030554 p=8.7E−02 n=4 fg=0.12 bg=0.06
protein serine/threonine kinase inhibito... GO:0030291 p=8.8E−02 n=1 fg=0.03 bg=0.00
nuclear steroid receptor activity GO:0003707 p=8.8E−02 n=1 fg=0.03 bg=0.00
vinculin binding GO:0017166 p=8.8E−02 n=1 fg=0.03 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=8.8E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=32/133 input genes with annotations
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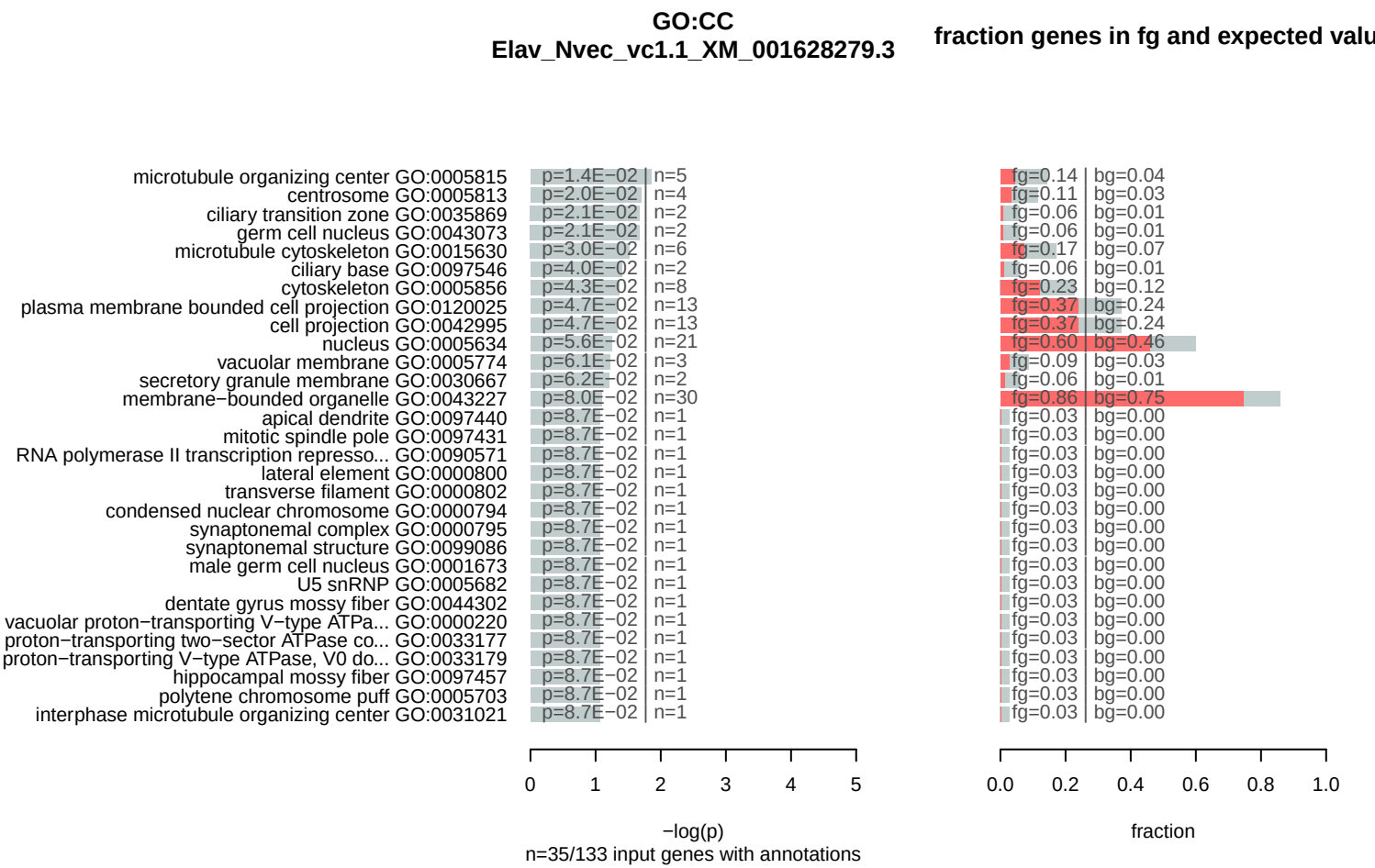
fraction


GO:CC
Elav_Nvec_vc1.1_XM_001628279.3
fraction genes in fg and expected valu
microtubule organizing center GO:0005815 p=1.4E−02 n=5 fg=0.14 bg=0.04
centrosome GO:0005813 p=2.0E−02 n=4 fg=0.11 bg=0.03
ciliary transition zone GO:0035869 p=2.1E−02 n=2 fg=0.06 bg=0.01
germ cell nucleus GO:0043073 p=2.1E−02 n=2 fg=0.06 bg=0.01
microtubule cytoskeleton GO:0015630 p=3.0E−02 n=6 fg=0.17 bg=0.07
ciliary base GO:0097546 p=4.0E−02 n=2 fg=0.06 bg=0.01
cytoskeleton GO:0005856 p=4.3E−02 n=8 fg=0.23 bg=0.12
plasma membrane bounded cell projection GO:0120025 p=4.7E−02 n=13 fg=0.37 bg=0.24
cell projection GO:0042995 p=4.7E−02 n=13 fg=0.37 bg=0.24
nucleus GO:0005634 p=5.6E−02 n=21 fg=0.60 bg=0.46
vacuolar membrane GO:0005774 p=6.1E−02 n=3 fg=0.09 bg=0.03
secretory granule membrane GO:0030667 p=6.2E−02 n=2 fg=0.06 bg=0.01
membrane−bounded organelle GO:0043227 p=8.0E−02 n=30 fg=0.86 bg=0.75
apical dendrite GO:0097440 p=8.7E−02 n=1 fg=0.03 bg=0.00
mitotic spindle pole GO:0097431 p=8.7E−02 n=1 fg=0.03 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=8.7E−02 n=1 fg=0.03 bg=0.00
lateral element GO:0000800 p=8.7E−02 n=1 fg=0.03 bg=0.00
transverse filament GO:0000802 p=8.7E−02 n=1 fg=0.03 bg=0.00
condensed nuclear chromosome GO:0000794 p=8.7E−02 n=1 fg=0.03 bg=0.00
synaptonemal complex GO:0000795 p=8.7E−02 n=1 fg=0.03 bg=0.00
synaptonemal structure GO:0099086 p=8.7E−02 n=1 fg=0.03 bg=0.00
male germ cell nucleus GO:0001673 p=8.7E−02 n=1 fg=0.03 bg=0.00
U5 snRNP GO:0005682 p=8.7E−02 n=1 fg=0.03 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=8.7E−02 n=1 fg=0.03 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000220 p=8.7E−02 n=1 fg=0.03 bg=0.00
proton−transporting two−sector ATPase co... GO:0033177 p=8.7E−02 n=1 fg=0.03 bg=0.00
proton−transporting V−type ATPase, V0 do... GO:0033179 p=8.7E−02 n=1 fg=0.03 bg=0.00
hippocampal mossy fiber GO:0097457 p=8.7E−02 n=1 fg=0.03 bg=0.00
polytene chromosome puff GO:0005703 p=8.7E−02 n=1 fg=0.03 bg=0.00
interphase microtubule organizing center GO:0031021 p=8.7E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=35/133 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction