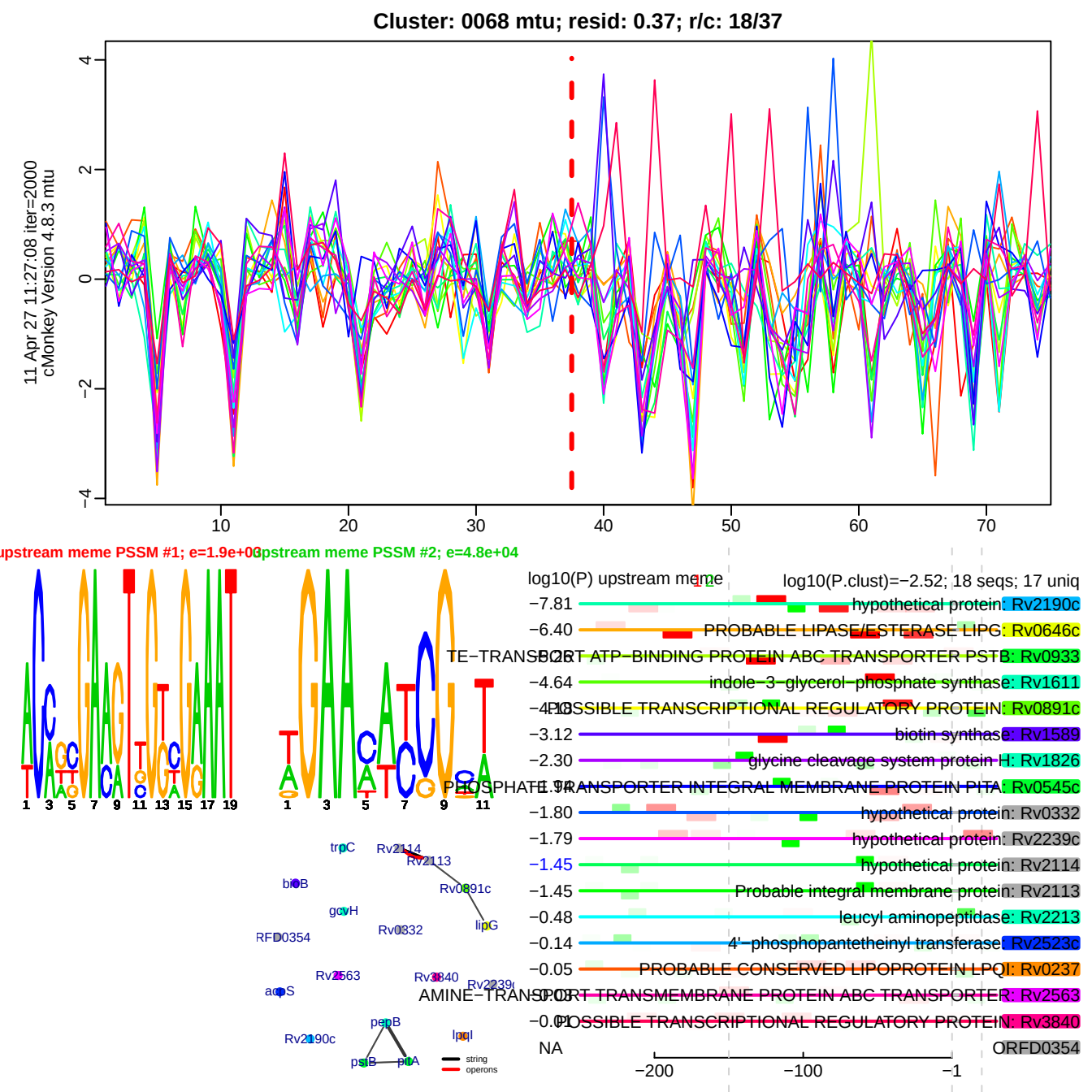
Cluster: 0068 mtu; resid: 0.37; r/c: 18/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=1.9e+03
upstream meme PSSM #2; e=4.8e+04
log10(P) upstream meme
log10(P.clust)=−2.52; 18 seqs; 17 uniq
−7.81 hypothetical protein: Rv2190c
−6.40 PROBABLE LIPASE/ESTERASE LIPG: Rv0646c
−5.26 TE−TRANSPORT ATP−BINDING PROTEIN ABC TRANSPORTER PSTB: Rv0933
−4.64 indole−3−glycerol−phosphate synthase: Rv1611
−4.13 POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv0891c
−3.12 biotin synthase: Rv1589
−2.30 glycine cleavage system protein H: Rv1826
−1.94 PHOSPHATE TRANSPORTER INTEGRAL MEMBRANE PROTEIN PITA: Rv0545c
−1.80 hypothetical protein: Rv0332
−1.79 hypothetical protein: Rv2239c
−1.45 hypothetical protein: Rv2114
−1.45 Probable integral membrane protein: Rv2113
−0.48 leucyl aminopeptidase: Rv2213
−0.14 4'−phosphopantetheinyl transferase: Rv2523c
−0.05 PROBABLE CONSERVED LIPOPROTEIN LPQI: Rv0237
−0.03 AMINE−TRANSPORT TRANSMEMBRANE PROTEIN ABC TRANSPORTER: Rv2563
−0.01 POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv3840
NA ORFD0354
−200 −100 −1
trpC
Rv2114
Rv2113
bioB
Rv0891c
gcvH
lipG
RFD0354
Rv0332
Rv2563
Rv3840
Rv2239c
aspS
pepB
Rv2190c
lpqI
pstB
pitA
string
operons