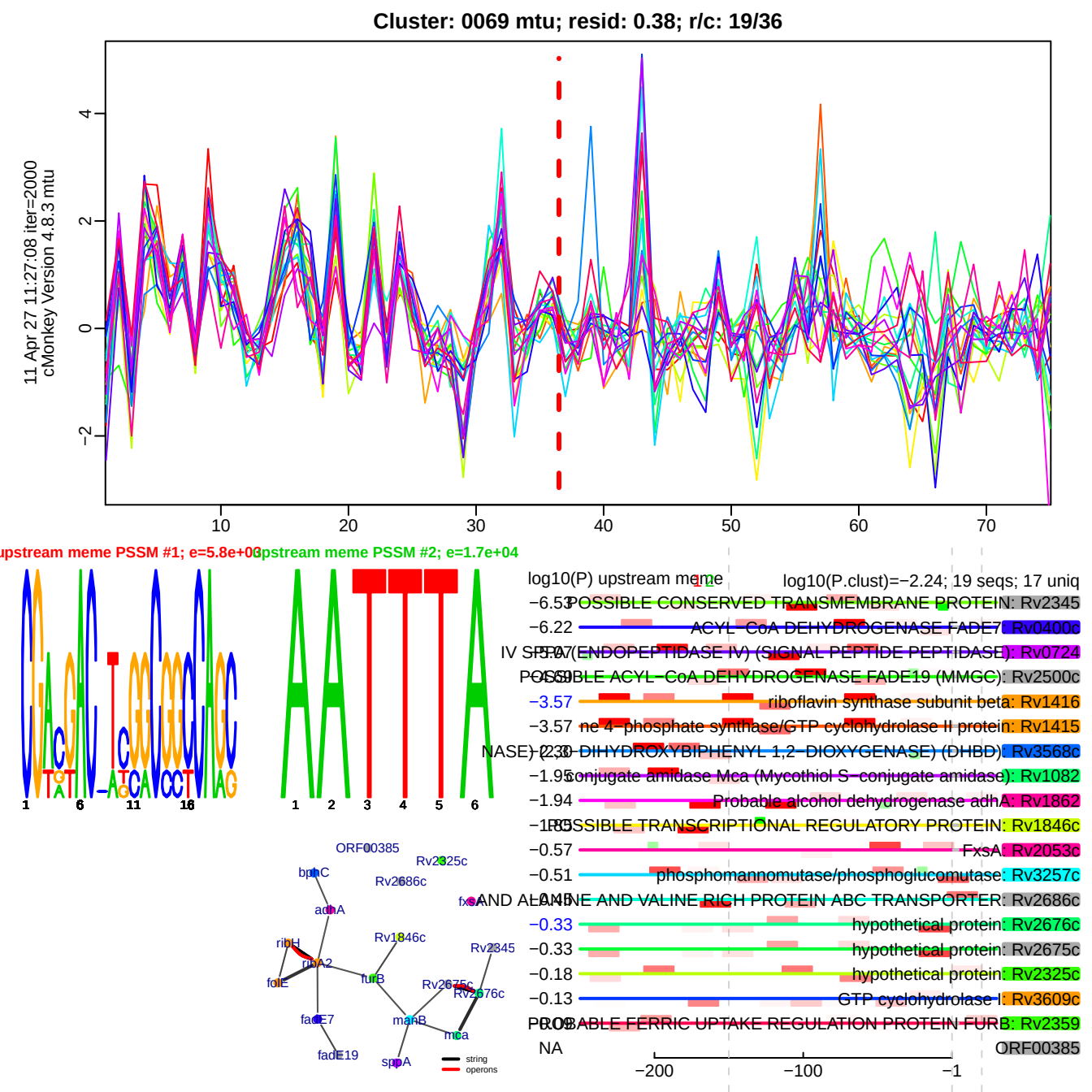
Cluster: 0069 mtu; resid: 0.38; r/c: 19/36
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=5.8e+03
upstream meme PSSM #2; e=1.7e+04
log10(P) upstream meme
log10(P.clust)=−2.24; 19 seqs; 17 uniq
−6.53 POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN: Rv2345
−6.22 ACYL−CoA DEHYDROGENASE FADE7: Rv0400c
−5.47 IV SPASE (ENDOPEPTIDASE IV) (SIGNAL PEPTIDE PEPTIDASE): Rv0724
−5.59 POSSIBLE ACYL−CoA DEHYDROGENASE FADE19 (MMGC): Rv2500c
−3.57 riboflavin synthase subunit beta: Rv1416
−3.57 ne 4−phosphate synthase/GTP cyclohydrolase II protein: Rv1415
−2.30 NASE) (2,3−DIHYDROXYBIPHENYL 1,2−DIOXYGENASE) (DHBD): Rv3568c
−1.95 conjugate amidase Mca (Mycothiol S−conjugate amidase): Rv1082
−1.94 Probable alcohol dehydrogenase adhA: Rv1862
−1.85 POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv1846c
−0.57 FxsA: Rv2053c
−0.51 phosphomannomutase/phosphoglucomutase: Rv3257c
−0.45 AND ALANINE AND VALINE RICH PROTEIN ABC TRANSPORTER: Rv2686c
−0.33 hypothetical protein: Rv2676c
−0.33 hypothetical protein: Rv2675c
−0.18 hypothetical protein: Rv2325c
−0.13 GTP cyclohydrolase I: Rv3609c
0.09 PROBABLE FERRIC UPTAKE REGULATION PROTEIN FURB: Rv2359
NA ORF00385
−200
−100
−1
ORF00385
Rv2325c
bpoC
Rv2686c
fxsA
adhA
Rv1846c
ribH
ribA2
Rv2345
folE
furB
Rv2675c
Rv2676c
fadE7
mabB
mca
fadE19
sppA
string
operons