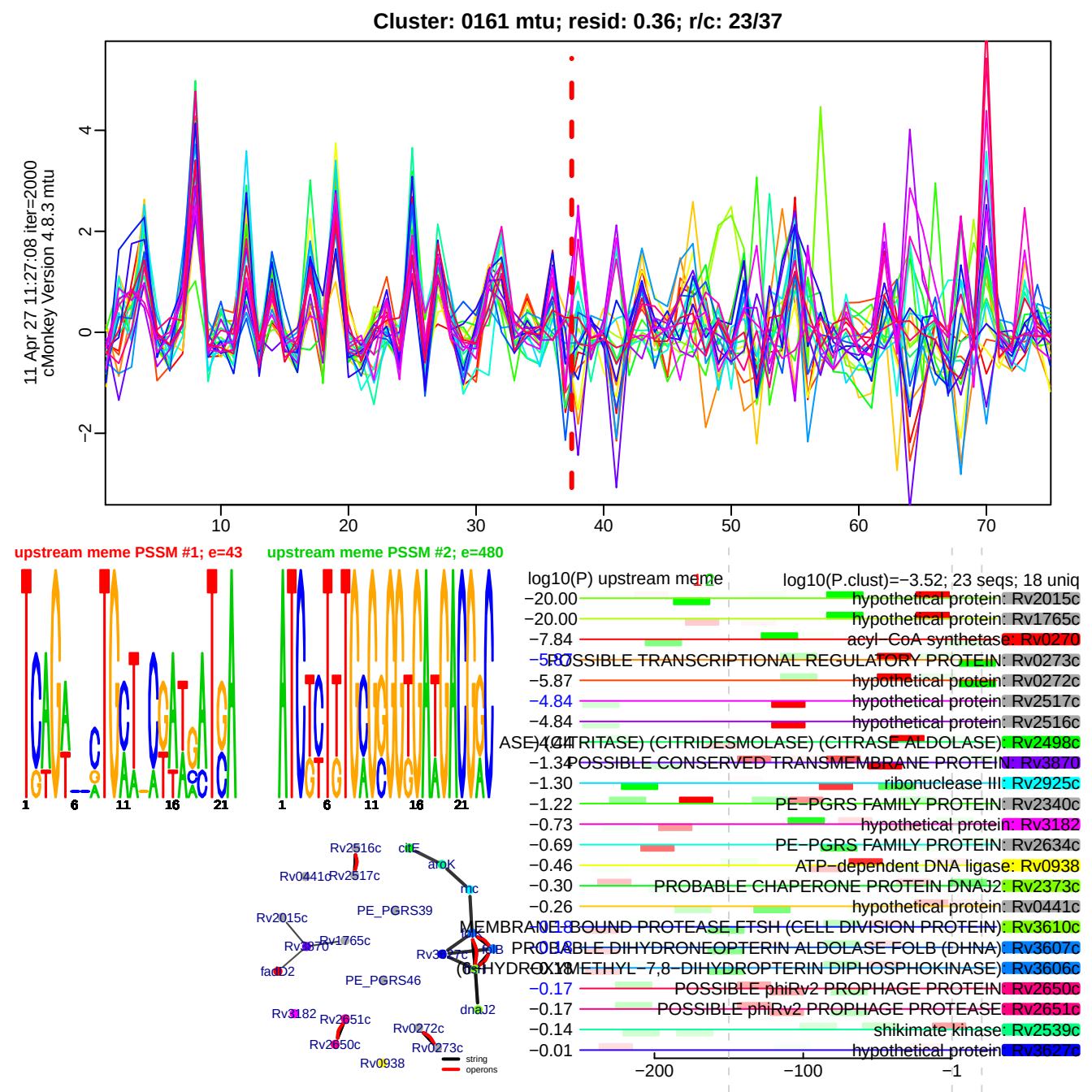
Cluster: 0161 mtu; resid: 0.36; r/c: 23/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=43
upstream meme PSSM #2; e=480
log10(P) upstream meme
log10(P.clust)=−3.52; 23 seqs; 18 uniq
−20.00 hypothetical protein: Rv2015c
−20.00 hypothetical protein: Rv1765c
−7.84 acyl−CoA synthetase: Rv0270
−5.87 POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv0273c
−5.87 hypothetical protein: Rv0272c
−4.84 hypothetical protein: Rv2517c
−4.84 hypothetical protein: Rv2516c
−4.44 ASE) (CITRITASE) (CITRIDESMOLASE) (CITRASE ALDOLASE): Rv2498c
−1.34 POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN: Rv3870
−1.30 ribonuclease III: Rv2925c
−1.22 PE−PGRS FAMILY PROTEIN: Rv2340c
−0.73 hypothetical protein: Rv3182
−0.69 PE−PGRS FAMILY PROTEIN: Rv2634c
−0.46 ATP−dependent DNA ligase: Rv0938
−0.30 PROBABLE CHAPERONE PROTEIN DNAJ2: Rv2373c
−0.26 hypothetical protein: Rv0441c
−0.18 MEMBRANE−BOUND PROTEASE FTSH (CELL DIVISION PROTEIN): Rv3610c
−0.18 PROBABLE DIHYDRONEOPTERIN ALDOLASE FOLB (DHNA): Rv3607c
−0.18 (6−HYDROXYMETHYL−7,8−DIHYDROPTERIN DIPHOSPHOKINASE): Rv3606c
−0.17 POSSIBLE phiRv2 PROPHAGE PROTEIN: Rv2650c
−0.17 POSSIBLE phiRv2 PROPHAGE PROTEASE: Rv2651c
−0.14 shikimate kinase: Rv2539c
−0.01 hypothetical protein: Rv3627c
Rv2516c
cinE
aroK
Rv0441c
Rv2517c
mc
PE_PGRS39
Rv2015c
Rv3870
Rv1765c
Rv3627c
RIB
fadD2
PE_PGRS46
Rv3182
Rv2651c
dnaJ2
Rv0272c
Rv2650c
Rv0273c
Rv0938
string
operons