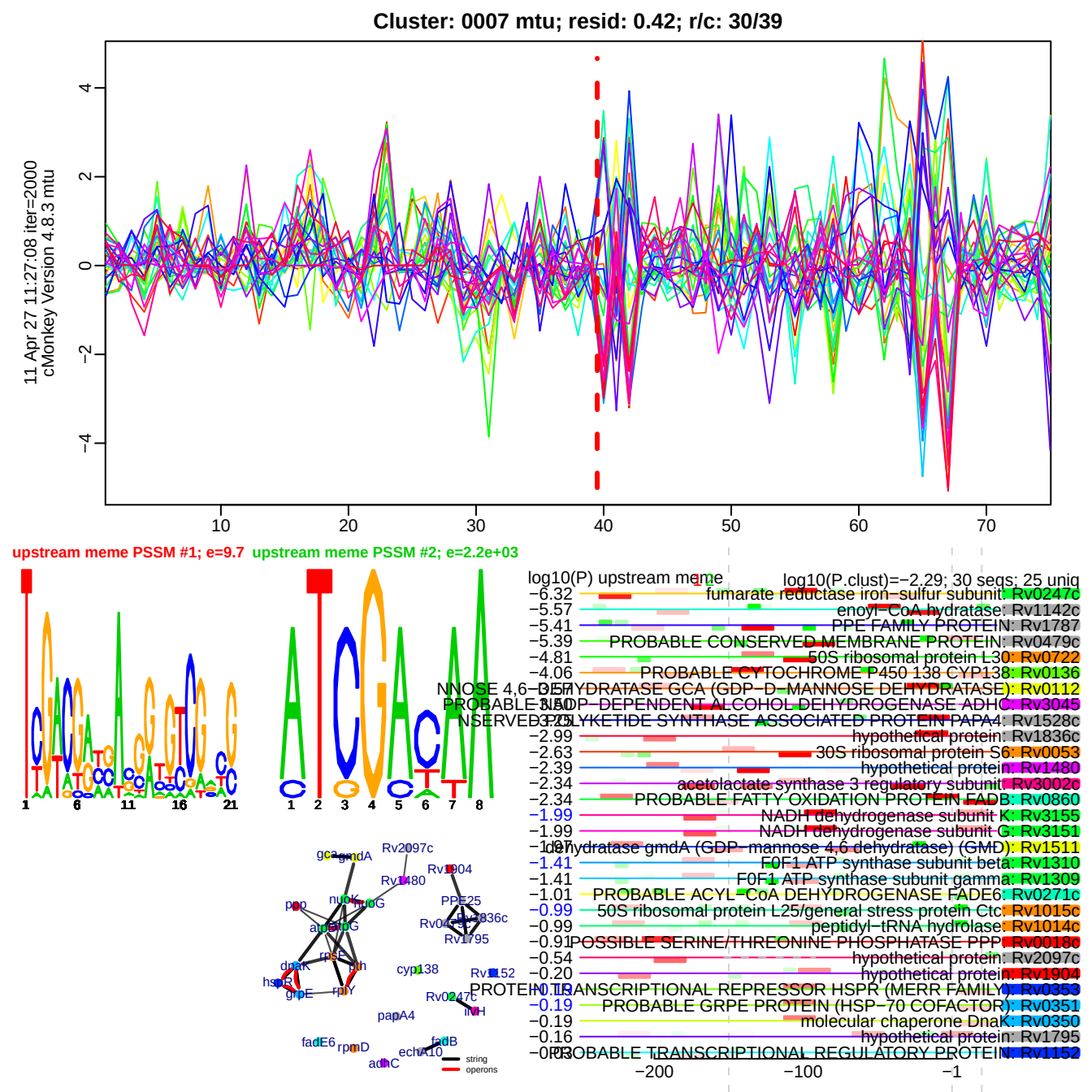
Cluster: 0007 mtu; resid: 0.42; r/c: 30/39
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=9.7
upstream meme PSSM #2; e=2.2e+03
log10(P) upstream meme
log10(P.clust)=−2.29; 30 seqs; 25 uniq
−6.32 fumarate reductase iron−sulfur subunit: Rv0247c
−5.57 enoyl−CoA hydratase: Rv1142c
−5.41 PPE FAMILY PROTEIN: Rv1787
−5.39 PROBABLE CONSERVED MEMBRANE PROTEIN: Rv0479c
−4.81 50S ribosomal protein L30: Rv0722
−4.06 PROBABLE CYTOCHROME P450 138 CYP138: Rv0136
−3.57 DEHYDRATASE GCA (GDP−D−MANNOSE DEHYDRATASE): Rv0112
−3.50 NADP−DEPENDENT ALCOHOL DEHYDROGENASE ADHC: Rv3045
−3.25 POLYKETIDE SYNTHASE ASSOCIATED PROTEIN PAPA4: Rv1528c
−2.99 hypothetical protein: Rv1836c
−2.63 30S ribosomal protein S6: Rv0053
−2.39 hypothetical protein: Rv1480
−2.34 acetolactate synthase 3 regulatory subunit: Rv3002c
−2.34 PROBABLE FATTY OXIDATION PROTEIN FADB: Rv0860
−1.99 NADH dehydrogenase subunit K: Rv3155
−1.99 NADH dehydrogenase subunit G: Rv3151
−1.97 dehydratase gmdA (GDP−mannose 4,6 dehydratase) (GMD): Rv1511
−1.41 F0F1 ATP synthase subunit beta: Rv1310
−1.41 F0F1 ATP synthase subunit gamma: Rv1309
−1.01 PROBABLE ACYL−CoA DEHYDROGENASE FADE6: Rv0271c
−0.99 50S ribosomal protein L25/general stress protein Ctc: Rv1015c
−0.99 peptidyl−tRNA hydrolase: Rv1014c
−0.91 POSSIBLE SERINE/THREONINE PHOSPHATASE PPP: Rv0018c
−0.54 hypothetical protein: Rv2097c
−0.20 hypothetical protein: Rv1904
−0.19 PROTEIN TRANSCRIPTIONAL REPRESSOR HSPR (MERR FAMILY): Rv0353
−0.19 PROBABLE GRPE PROTEIN (HSP−70 COFACTOR): Rv0351
−0.19 molecular chaperone DnaK: Rv0350
−0.16 hypothetical protein: Rv1795
−0.03 PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv1152
−200
−100
−1
string
operons