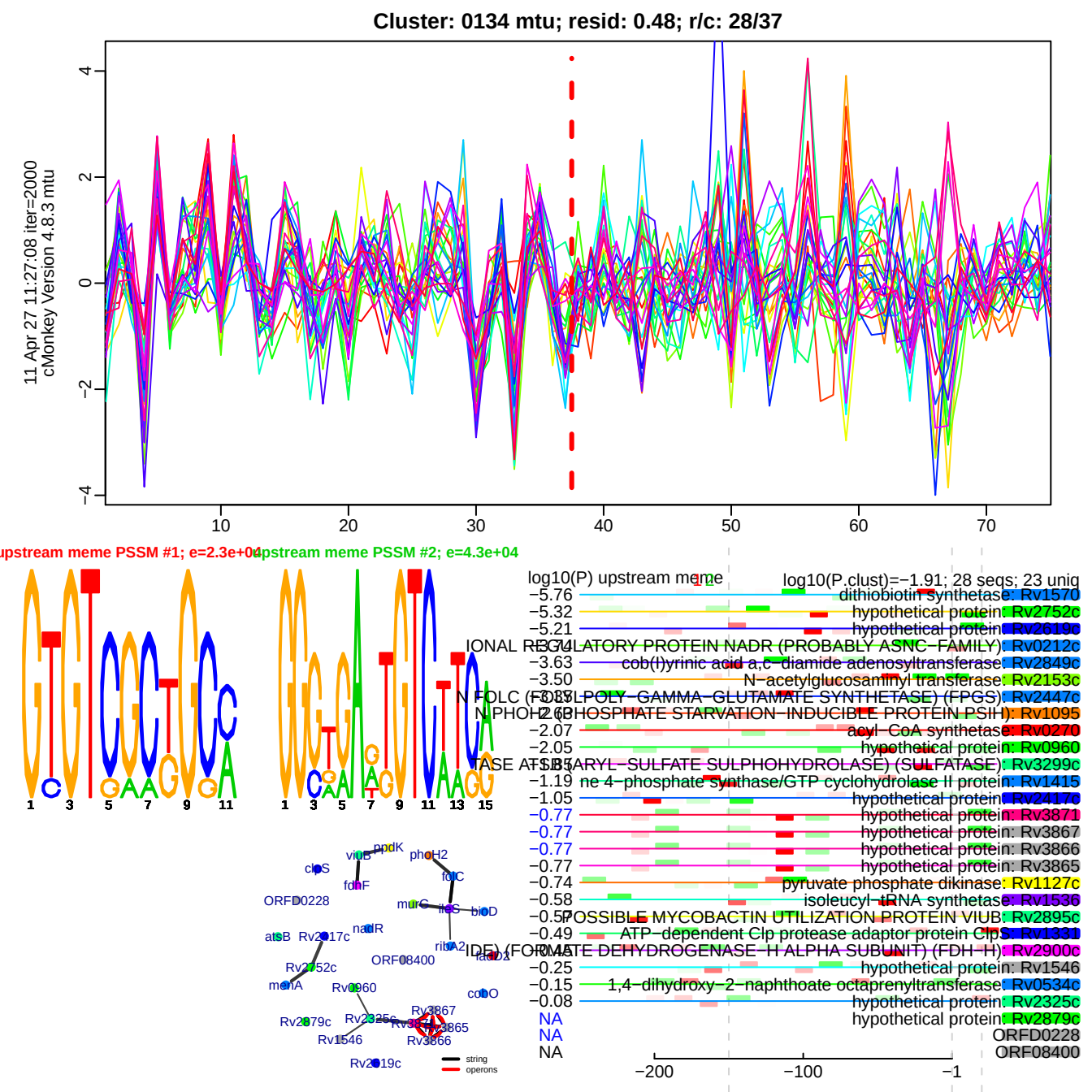
Cluster: 0134 mtu; resid: 0.48; r/c: 28/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=2.3e+04
upstream meme PSSM #2; e=4.3e+04
log10(P) upstream meme
log10(P.clust)=−1.91; 28 seqs; 23 uniq
−5.76 dithiobiotin synthetase: Rv1570
−5.32 hypothetical protein: Rv2752c
−5.21 hypothetical protein: Rv2619c
−3.74 IONAL REGULATORY PROTEIN NADR (PROBABLY ASNC−FAMILY): Rv0212c
−3.63 cob(I)yrinic acid a,c−diamide adenosyltransferase: Rv2849c
−3.50 N−acetylglucosaminyl transferase: Rv2153c
−3.35 N FOLC (FOLYL−POLY−GAMMA−GLUTAMATE SYNTHETASE) (FPGS): Rv2447c
−2.68 N PHOH2 (PHOSPHATE STARVATION−INDUCIBLE PROTEIN PSIH): Rv1095
−2.07 acyl−CoA synthetase: Rv0270
−2.05 hypothetical protein: Rv0960
−1.85 TASE ATS5 (ARYL−SULFATE SULPHOHYDROLASE) (SULFATASE): Rv3299c
−1.19 ne 4−phosphate synthase/GTP cyclohydrolase II protein: Rv1415
−1.05 hypothetical protein: Rv2417c
−0.77 hypothetical protein: Rv3871
−0.77 hypothetical protein: Rv3867
−0.77 hypothetical protein: Rv3866
−0.77 hypothetical protein: Rv3865
−0.74 pyruvate phosphate dikinase: Rv1127c
−0.58 isoleucyl−tRNA synthetase: Rv1536
−0.57 POSSIBLE MYCOBACTIN UTILIZATION PROTEIN VIUB: Rv2895c
−0.49 ATP−dependent Clp protease adaptor protein ClpS: Rv1331
−0.45 IDE) (FORMATE DEHYDROGENASE−H ALPHA SUBUNIT) (FDH−H): Rv2900c
−0.25 hypothetical protein: Rv1546
−0.15 1,4−dihydroxy−2−naphthoate octaprenyltransferase: Rv0534c
−0.08 hypothetical protein: Rv2325c
NA hypothetical protein: Rv2879c
NA ORFD0228
NA ORFD08400
−200
−100
−1
string
operons