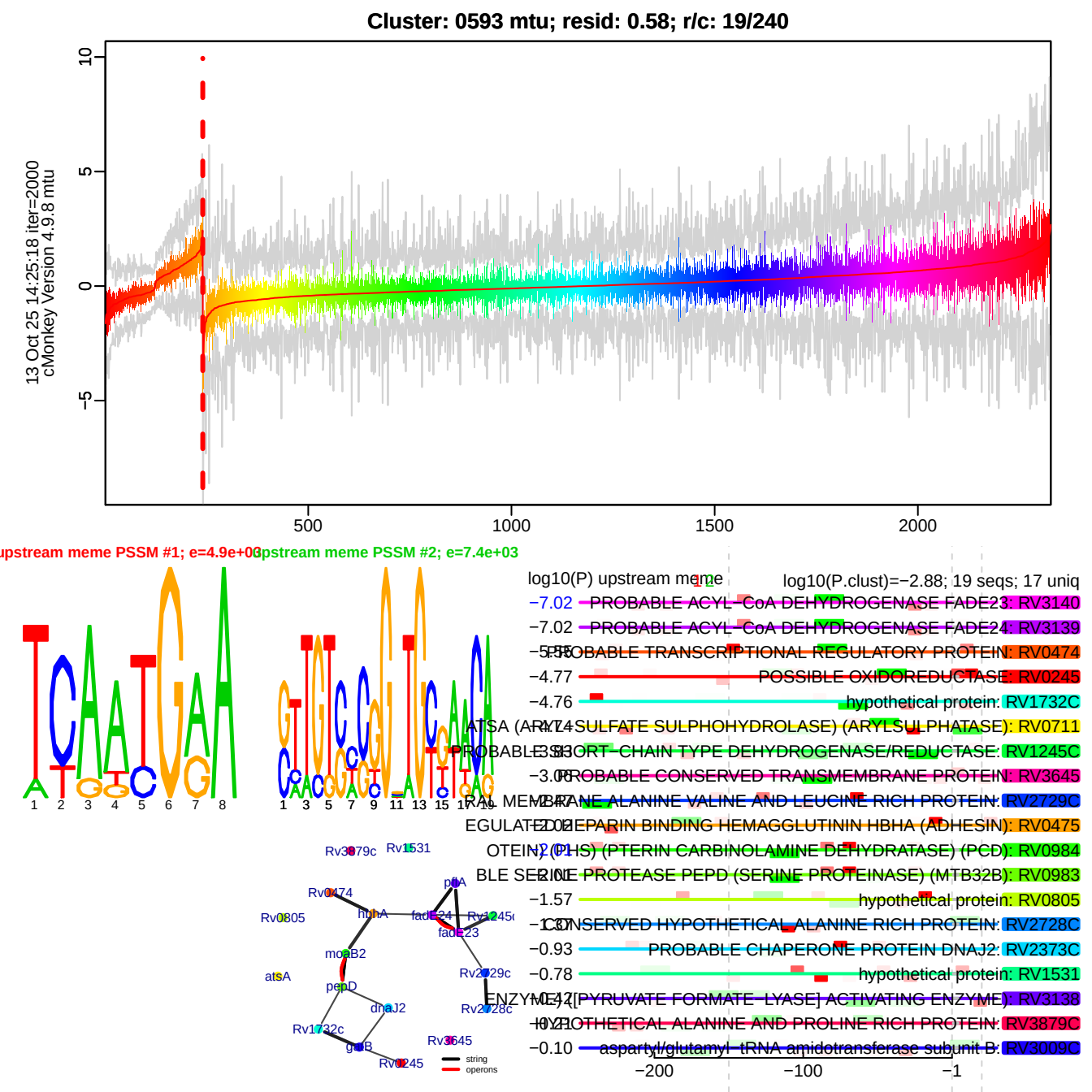

Cluster: 0593 mtu; resid: 0.58; r/c: 19/240
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu
10
5
0
−5
500
1000
1500
2000
upstream meme PSSM #1; e=4.9e+03
upstream meme PSSM #2; e=7.4e+03
1 2 3 4 5 6 7 8
1 3 5 7 9 11 13 15 17 19
log10(P) upstream meme
log10(P.clust)=−2.88; 19 seqs; 17 uniq
−7.02 PROBABLE ACYL−CoA DEHYDROGENASE FADE23: RV3140
−7.02 PROBABLE ACYL−CoA DEHYDROGENASE FADE24: RV3139
−5.55 PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN: RV0474
−4.77 POSSIBLE OXIDOREDUCTASE: RV0245
−4.76 hypothetical protein: RV1732C
−4.74 ATSA (ARYLSULFATE SULPHOHYDROLASE) (ARYLSULPHATASE): RV0711
−3.83 PROBABLE SHORT−CHAIN TYPE DEHYDROGENASE/REDUCTASE: RV1245C
−3.08 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: RV3645
−2.47 RAL MEMBRANE ALANINE VALINE AND LEUCINE RICH PROTEIN: RV2729C
−2.02 EGULATED EPARIN BINDING HEMAGGLUTININ HBHA (ADHESIN): RV0475
−2.01 OTEIN (PHS) (PTERIN CARBINOLAMINE DEHYDRATASE) (PCD): RV0984
−2.01 BLE SERINE PROTEASE PEPD (SERINE PROTEINASE) (MTB32B): RV0983
−1.57 hypothetical protein: RV0805
−1.37 CONSERVED HYPOTHETICAL ALANINE RICH PROTEIN: RV2728C
−0.93 PROBABLE CHAPERONE PROTEIN DNAJ2: RV2373C
−0.78 hypothetical protein: RV1531
−0.42 ENZYME [PYRUVATE FORMATE−LYASE] ACTIVATING ENZYME): RV3138
−0.21 HYPOTHETICAL ALANINE AND PROLINE RICH PROTEIN: RV3879C
−0.10 aspartyl/glutamyl−tRNA amidotransferase subunit B: RV3009C
−200
−100
−1
Rv3879c
Rv1531
Rv0474
Rv0805
hbhA
fadE24
Rv1245c
fadE23
moaB2
atsA
pepD
Rv2729c
dnaJ2
Rv2728c
Rv1732c
gatB
Rv3645
Rv0245
string
operons