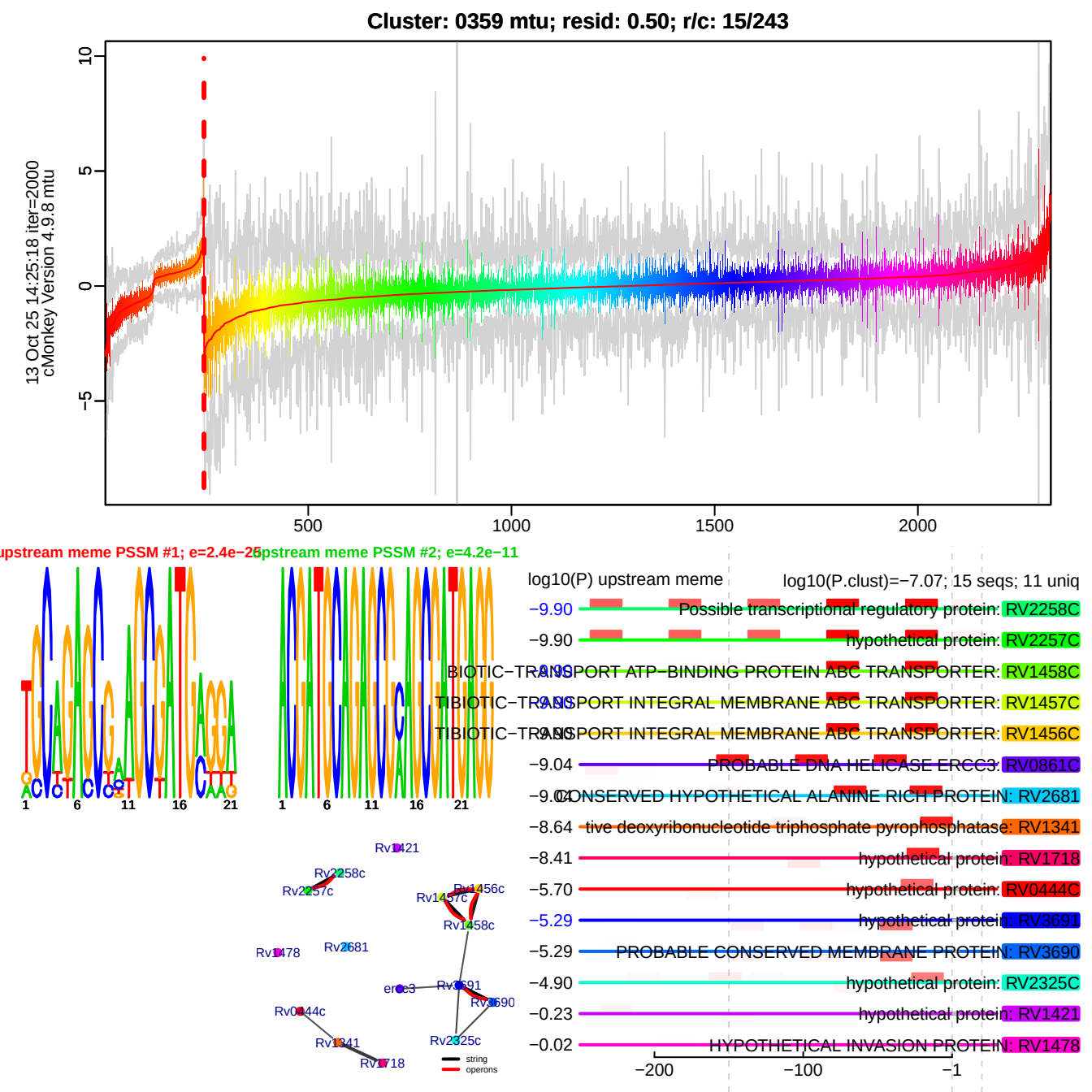
Cluster: 0359 mtu; resid: 0.50; r/c: 15/243
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu
upstream meme PSSM #1; e=2.4e−25
upstream meme PSSM #2; e=4.2e−11
log10(P) upstream meme
log10(P.clust)=−7.07; 15 seqs; 11 uniq
−9.90 Possible transcriptional regulatory protein: RV2258C
−9.90 hypothetical protein: RV2257C
−9.90 BIOTIC−TRANSPORT ATP−BINDING PROTEIN ABC TRANSPORTER: RV1458C
−9.90 TIBIOTIC−TRANSPORT INTEGRAL MEMBRANE ABC TRANSPORTER: RV1457C
−9.90 TIBIOTIC−TRANSPORT INTEGRAL MEMBRANE ABC TRANSPORTER: RV1456C
−9.04 PROBABLE DNA HELICASE ERCC3: RV0861C
−9.04 CONSERVED HYPOTHETICAL ALANINE RICH PROTEIN: RV2681
−8.64 tive deoxyribonucleotide triphosphatase: RV1341
−8.41 hypothetical protein: RV1718
−5.70 hypothetical protein: RV0444C
−5.29 hypothetical protein: RV3691
−5.29 PROBABLE CONSERVED MEMBRANE PROTEIN: RV3690
−4.90 hypothetical protein: RV2325C
−0.23 hypothetical protein: RV1421
−0.02 HYPOTHETICAL INVASION PROTEIN: RV1478
−200
−100
−1
Rv1421
Rv2258c
Rv2257c
Rv1456c
Rv1457c
Rv1458c
Rv1478
Rv2681
erc3
Rv3691
Rv3690
Rv0444c
Rv1341
Rv1718
Rv2325c
string
operons