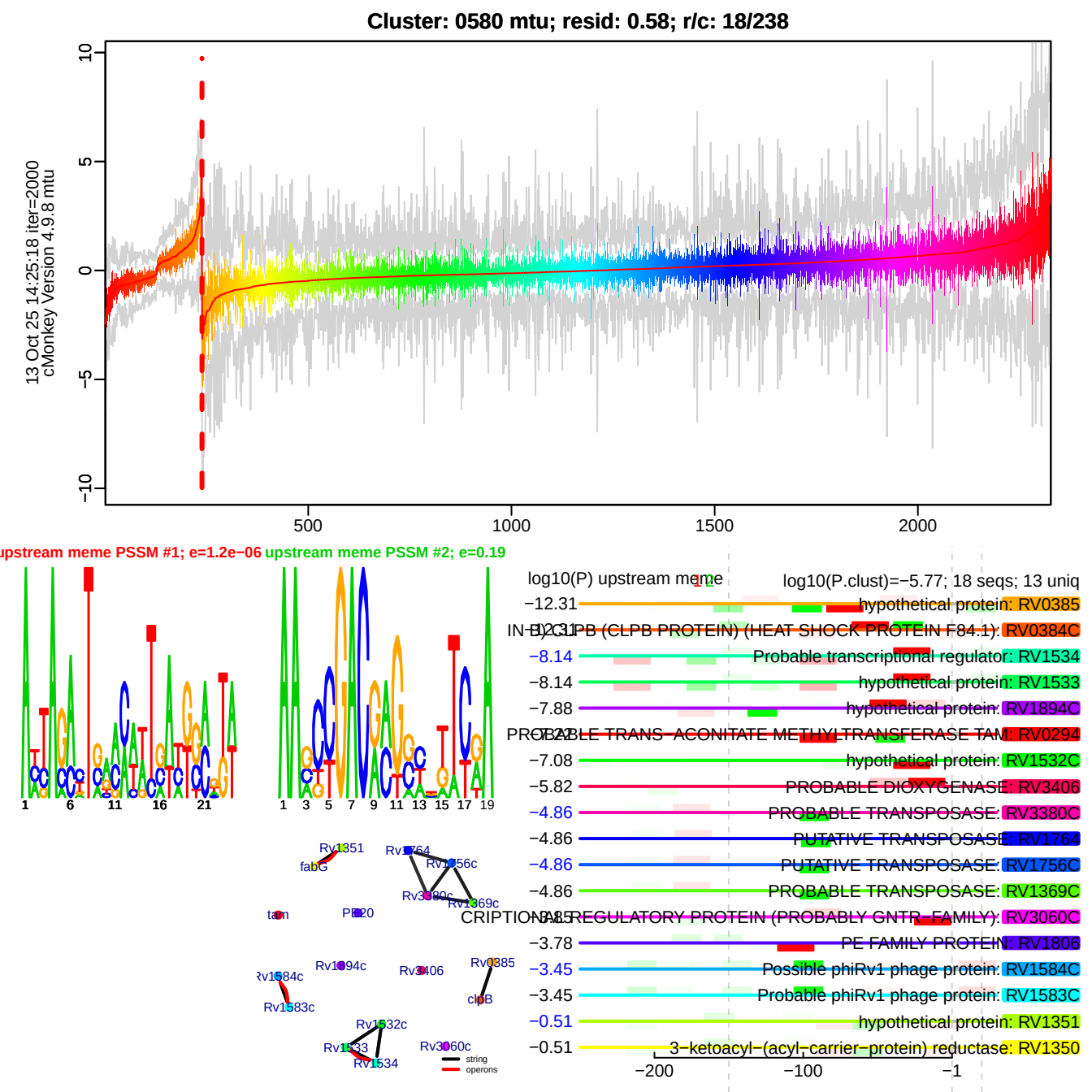
Cluster: 0580 mtu; resid: 0.58; r/c: 18/238
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu
upstream meme PSSM #1; e=1.2e−06
upstream meme PSSM #2; e=0.19
log10(P) upstream meme
log10(P.clust)=−5.77; 18 seqs; 13 uniq
−12.31 hypothetical protein: RV0385
−12.31 CLPB (CLPB PROTEIN) (HEAT SHOCK PROTEIN F84.1): RV0384C
−8.14 Probable transcriptional regulator: RV1534
−8.14 hypothetical protein: RV1533
−7.88 hypothetical protein: RV1894C
−7.22 PROBABLE TRANS−ACONITATE METHYLTRANSFERASE TAM: RV0294
−7.08 hypothetical protein: RV1532C
−5.82 PROBABLE DIOXYGENASE: RV3406
−4.86 PROBABLE TRANSPOSASE: RV3380C
−4.86 PUTATIVE TRANSPOSASE: RV1764
−4.86 PUTATIVE TRANSPOSASE: RV1756C
−4.86 PROBABLE TRANSPOSASE: RV1369C
−4.85 TRANSCRIPTIONAL REGULATORY PROTEIN (PROBABLY GNTR−FAMILY): RV3060C
−3.78 PE FAMILY PROTEIN: RV1806
−3.45 Possible phiRv1 phage protein: RV1584C
−3.45 Probable phiRv1 phage protein: RV1583C
−0.51 hypothetical protein: RV1351
−0.51 3−ketoacyl−(acyl−carrier−protein) reductase: RV1350
−200
−100
−1
string
operons