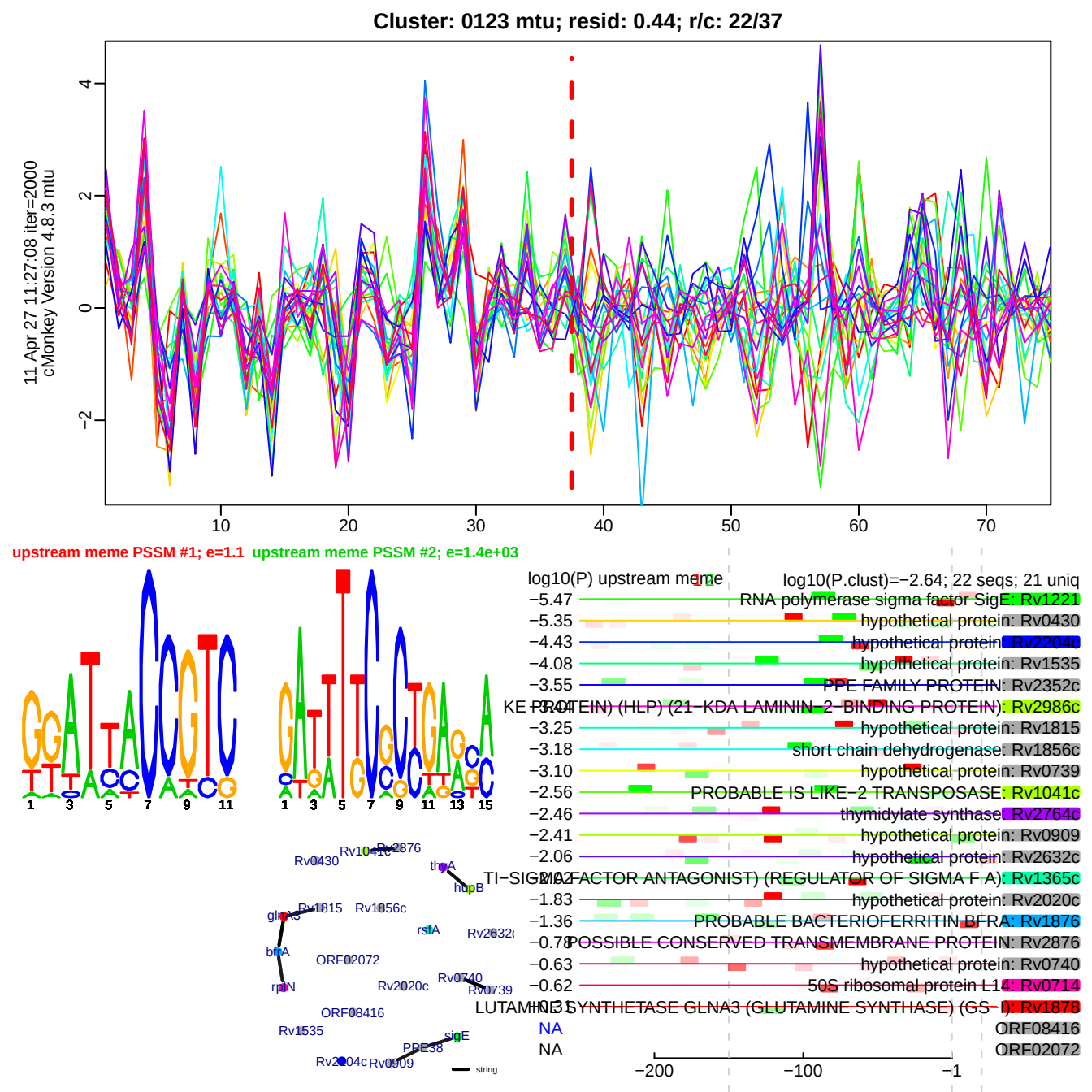
Cluster: 0123 mtu; resid: 0.44; r/c: 22/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=1.1
upstream meme PSSM #2; e=1.4e+03
log10(P) upstream meme
log10(P.clust)=−2.64; 22 seqs; 21 uniq
−5.47 RNA polymerase sigma factor SigE: Rv1221
−5.35 hypothetical protein: Rv0430
−4.43 hypothetical protein: Rv2204c
−4.08 hypothetical protein: Rv1535
−3.55 PPE FAMILY PROTEIN: Rv2352c
−3.44 KE PROTEIN) (HLP) (21−KDA LAMININ−2−BINDING PROTEIN): Rv2986c
−3.25 hypothetical protein: Rv1815
−3.18 short chain dehydrogenase: Rv1856c
−3.10 hypothetical protein: Rv0739
−2.56 PROBABLE IS LIKE−2 TRANSPOSASE: Rv1041c
−2.46 thymidylate synthase: Rv2764c
−2.41 hypothetical protein: Rv0909
−2.06 hypothetical protein: Rv2632c
−2.02 TI−SIGMA FACTOR ANTAGONIST) (REGULATOR OF SIGMA F A): Rv1365c
−1.83 hypothetical protein: Rv2020c
−1.36 PROBABLE BACTERIOFERRITIN BFRA: Rv1876
−0.78 POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN: Rv2876
−0.63 hypothetical protein: Rv0740
−0.62 50S ribosomal protein L14: Rv0714
−0.31 LUTAMINE SYNTHETASE GLNA3 (GLUTAMINE SYNTHASE) (GS−I): Rv1878
NA ORF08416
NA ORF02072
−200
−100
−1
Rv0430
Rv1041c
Rv2876
thyA
hupB
glnA3
Rv1815
Rv1856c
rsfA
Rv2632c
bfrA
ORF02072
rplN
Rv2020c
Rv0740
Rv0739
ORF08416
Rv1535
sigE
PPE38
Rv2204c
Rv0909
string