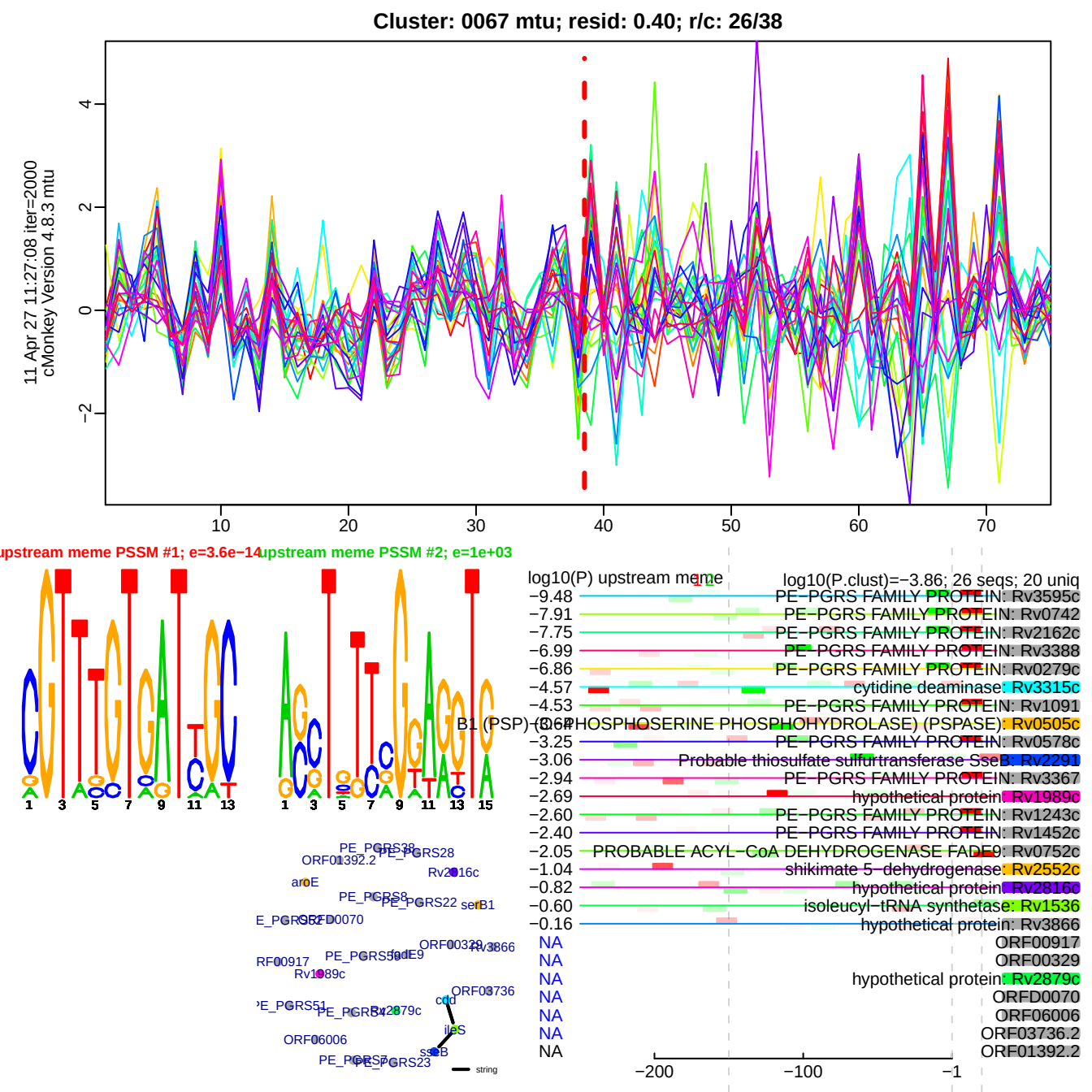
Cluster: 0067 mtu; resid: 0.40; r/c: 26/38
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=3.6e−14
upstream meme PSSM #2; e=1e+03
log10(P) upstream meme
log10(P.clust)=−3.86; 26 seqs; 20 uniq
−9.48 PE−PGRS FAMILY PROTEIN: Rv3595c
−7.91 PE−PGRS FAMILY PROTEIN: Rv0742
−7.75 PE−PGRS FAMILY PROTEIN: Rv2162c
−6.99 PE−PGRS FAMILY PROTEIN: Rv3388
−6.86 PE−PGRS FAMILY PROTEIN: Rv0279c
−4.57 cytidine deaminase: Rv3315c
−4.53 PE−PGRS FAMILY PROTEIN: Rv1091
−4.49 B1 (PSP)-(O-PHOSPHOSERINE PHOSPHOHYDROLASE) (PSPASE): Rv0505c
−3.25 PE−PGRS FAMILY PROTEIN: Rv0578c
−3.06 Probable thiosulfate sulfurtransferase SseB: Rv2291
−2.94 PE−PGRS FAMILY PROTEIN: Rv3367
−2.69 hypothetical protein: Rv1989c
−2.60 PE−PGRS FAMILY PROTEIN: Rv1243c
−2.40 PE−PGRS FAMILY PROTEIN: Rv1452c
−2.05 PROBABLE ACYL−CoA DEHYDROGENASE FADE9: Rv0752c
−1.04 shikimate 5−dehydrogenase: Rv2552c
−0.82 hypothetical protein: Rv2816c
−0.60 isoleucyl−tRNA synthetase: Rv1536
−0.16 hypothetical protein: Rv3866
NA ORF00917
NA ORF00329
NA hypothetical protein: Rv2879c
NA ORFD0070
NA ORF06006
NA ORF03736.2
NA ORF01392.2
−200
−100
−1
string