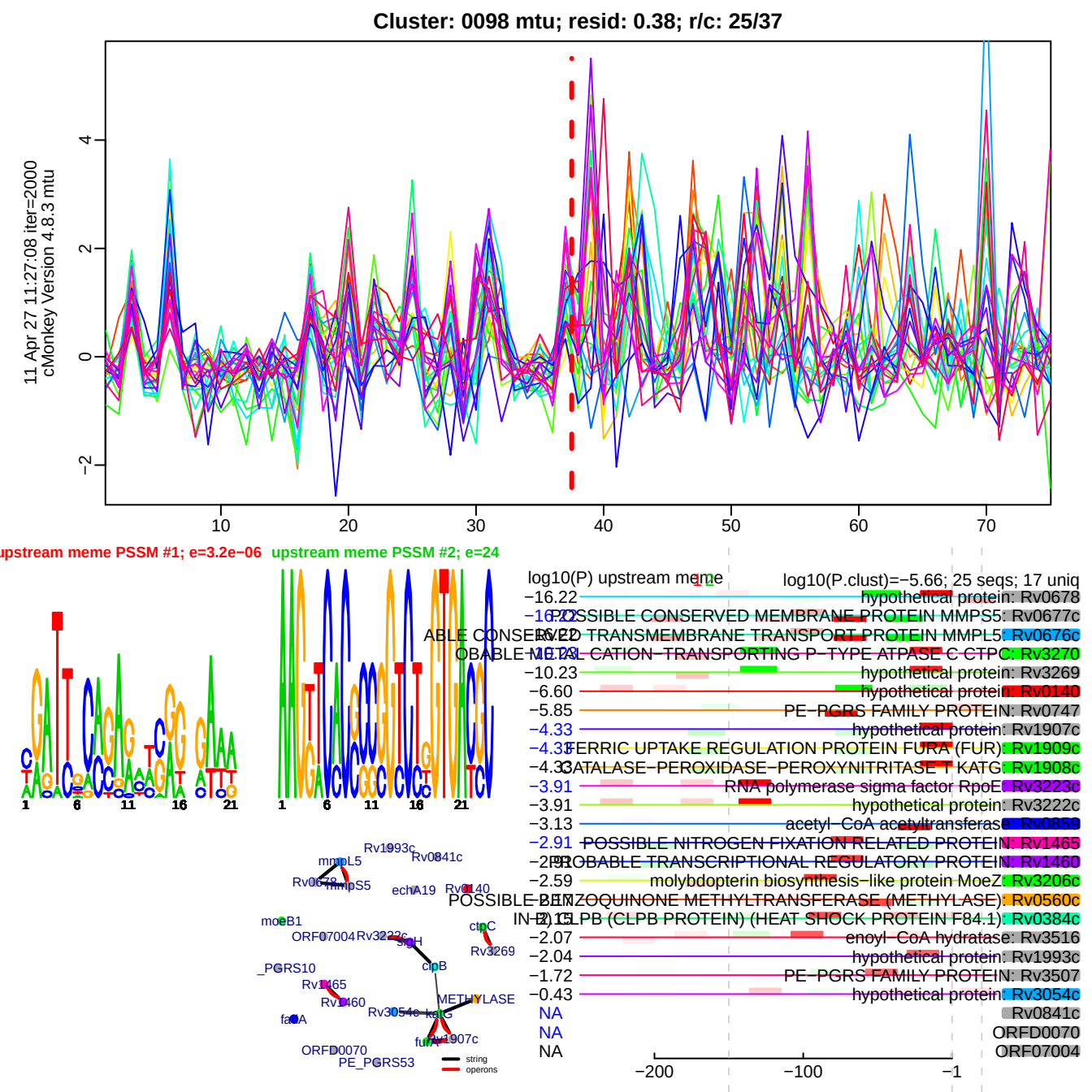
Cluster: 0098 mtu; resid: 0.38; r/c: 25/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=3.2e−06
upstream meme PSSM #2; e=24
log10(P) upstream meme
log10(P.clust)=−5.66; 25 seqs; 17 uniq
−16.22 hypothetical protein: Rv0678
−16.22 POSSIBLE CONSERVED MEMBRANE PROTEIN MMPS5: Rv0677c
−16.22 PROBABLE TRANSMEMBRANE TRANSPORT PROTEIN MMPL5: Rv0676c
−10.23 hypothetical protein: Rv3269
−6.60 hypothetical protein: Rv0140
−5.85 PE−PGRS FAMILY PROTEIN: Rv0747
−4.33 hypothetical protein: Rv1907c
−4.33 FERRIC UPTAKE REGULATION PROTEIN FURA (FUR): Rv1909c
−4.33 CATALASE−PEROXIDASE−PEROXYNITRITASE T KATG: Rv1908c
−3.91 RNA polymerase sigma factor RpoE: Rv3223c
−3.91 hypothetical protein: Rv3222c
−3.13 acetyl−CoA acetyltransferase: Rv0859
−2.91 POSSIBLE NITROGEN FIXATION RELATED PROTEIN: Rv1465
−2.59 molybdopterin biosynthesis−like protein MoeZ: Rv3206c
−2.07 enoyl−CoA hydratase: Rv3516
−2.04 hypothetical protein: Rv1993c
−1.72 PE−PGRS FAMILY PROTEIN: Rv3507
−0.43 hypothetical protein: Rv3054c
Rv0841c
ORFD0070
ORF07004
−200
−100
−1
Rv1993c
mmpL5
Rv0841c
Rv0678
mmpS5
echA19
Rv0140
moeB1
ORF07004
Rv3222c
sigH
ctpC
Rv3269
_PGRS10
clpB
Rv1465
Rv1460
METHYLASE
Rv3054c
katG
fadA
furA
Rv1907c
ORFD0070
PE_PGRS53
string
operons