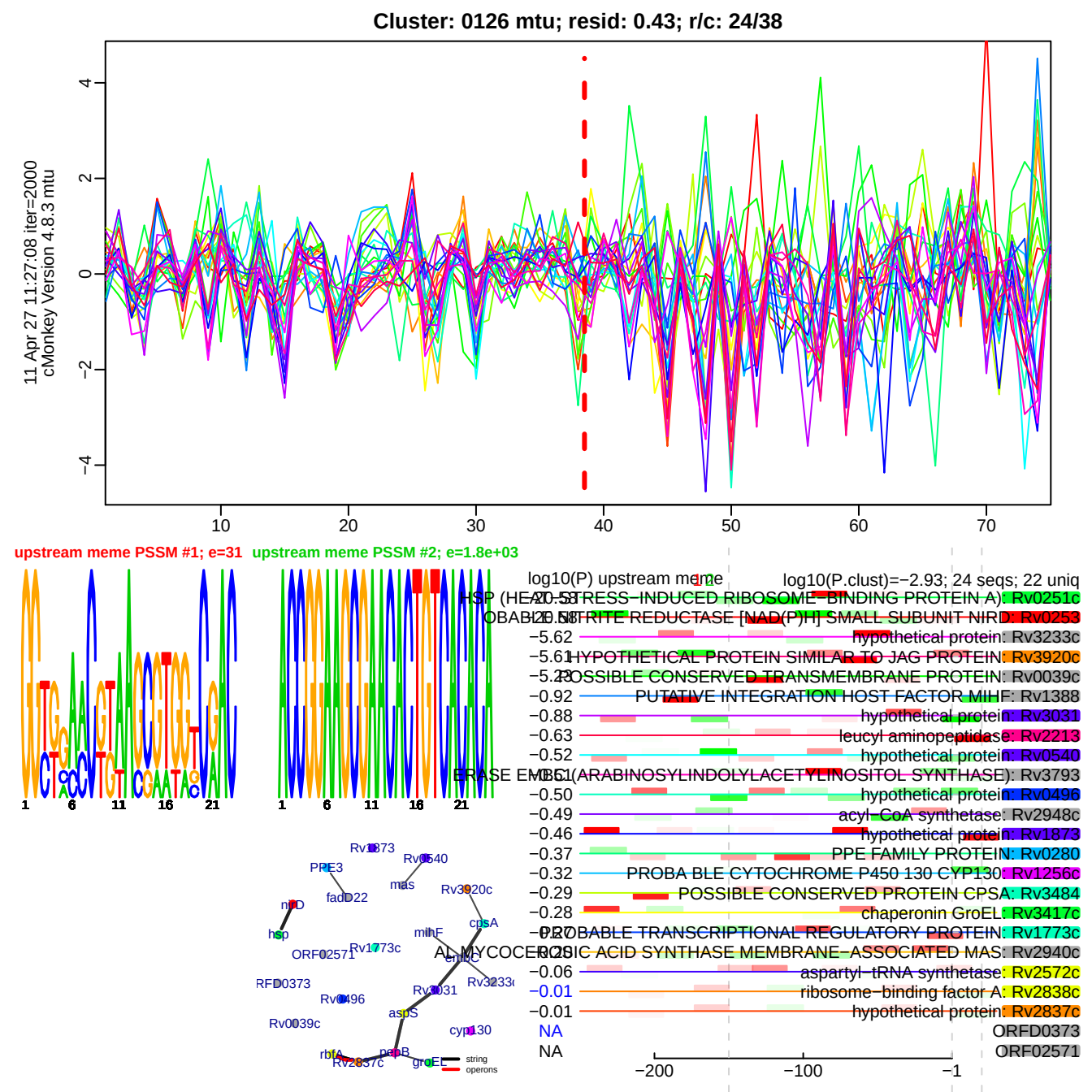
Cluster: 0126 mtu; resid: 0.43; r/c: 24/38
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=31
upstream meme PSSM #2; e=1.8e+03
log10(P) upstream meme
log10(P.clust)=−2.93; 24 seqs; 22 uniq
−5.62 hypothetical protein: Rv3233c
−5.61 HYPOTHETICAL PROTEIN SIMILAR TO JAG PROTEIN: Rv3920c
−5.23 POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN: Rv0039c
−0.92 PUTATIVE INTEGRATION HOST FACTOR MIHF: Rv1388
−0.88 hypothetical protein: Rv3031
−0.63 leucyl aminopeptidase: Rv2213
−0.52 hypothetical protein: Rv0540
−0.50 hypothetical protein: Rv0496
−0.49 acyl−CoA synthetase: Rv2948c
−0.46 hypothetical protein: Rv1873
−0.37 PPE FAMILY PROTEIN: Rv0280
−0.32 PROBA BLE CYTOCHROME P450 130 CYP130: Rv1256c
−0.29 POSSIBLE CONSERVED PROTEIN CPSA: Rv3484
−0.28 chaperonin GroEL: Rv3417c
−0.27 OBABLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv1773c
−0.26 AL MYCOCEROSIC ACID SYNTHASE MEMBRANE−ASSOCIATED MAS: Rv2940c
−0.06 aspartyl−tRNA synthetase: Rv2572c
−0.01 ribosome−binding factor A: Rv2838c
−0.01 hypothetical protein: Rv2837c
NA ORFD0373
NA ORF02571
−200
−100
−1
Rv1873
Rv0640
PPE3
mas
fadD22
Rv3920c
hsp
mihF
cpsA
ORF02571
Rv1773c
cmtC
RFD0373
Rv3233c
Rv3031
Rv0496
asnS
Rv0039c
cyp130
rbfA
pepB
Rv2837c
groEL
string
operons