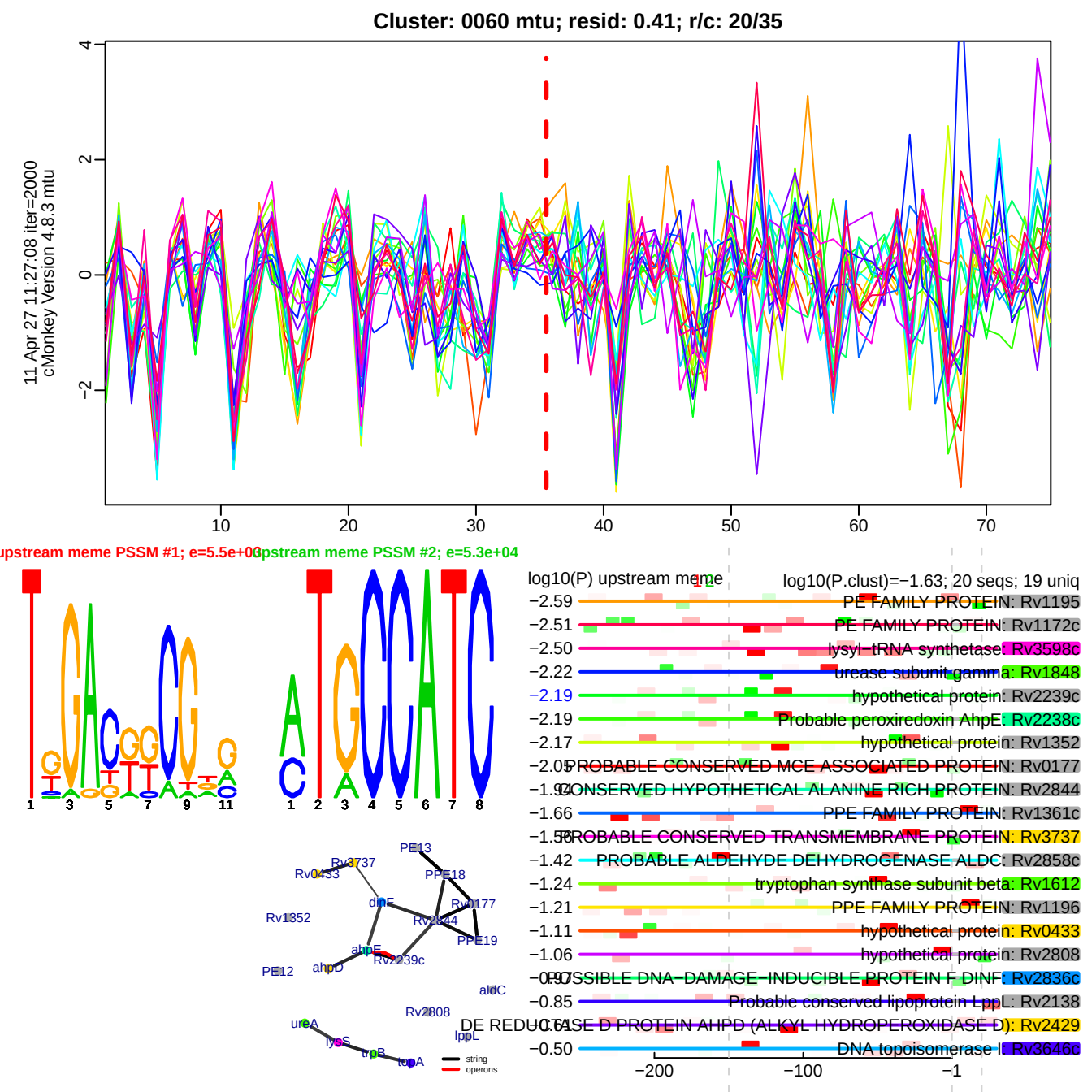
Cluster: 0060 mtu; resid: 0.41; r/c: 20/35
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=5.5e+06
upstream meme PSSM #2; e=5.3e+04
log10(P) upstream meme
log10(P.clust)=−1.63; 20 seqs; 19 uniq
−2.59 PE FAMILY PROTEIN: Rv1195
−2.51 PE FAMILY PROTEIN: Rv1172c
−2.50 lysyl−tRNA synthetase: Rv3598c
−2.22 urease subunit gamma: Rv1848
−2.19 hypothetical protein: Rv2239c
−2.19 Probable peroxiredoxin AhpE: Rv2238c
−2.17 hypothetical protein: Rv1352
−2.05 PROBABLE CONSERVED MCE ASSOCIATED PROTEIN: Rv0177
−1.94 CONSERVED HYPOTHETICAL ALANINE RICH PROTEIN: Rv2844
−1.66 PPE FAMILY PROTEIN: Rv1361c
−1.58 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: Rv3737
−1.42 PROBABLE ALDEHYDE DEHYDROGENASE ALDC: Rv2858c
−1.24 tryptophan synthase subunit beta: Rv1612
−1.21 PPE FAMILY PROTEIN: Rv1196
−1.11 hypothetical protein: Rv0433
−1.06 hypothetical protein: Rv2808
−0.97 POSSIBLE DNA−DAMAGE−INDUCIBLE PROTEIN F DINF: Rv2836c
−0.85 Probable conserved lipoprotein LppL: Rv2138
−0.61 DE REDUCTASE D PROTEIN AHPD (ALKYL HYDROPEROXIDASE D): Rv2429
−0.50 DNA topoisomerase I: Rv3646c
PE13
Rv3737
Rv0433
PPE18
dinF
Rv0177
Rv1852
Rv2844
PPE19
ahpE
Rv2239c
PE12
ahpD
aldC
Rv2808
ureA
lppL
lysS
trpB
topA
string
operons