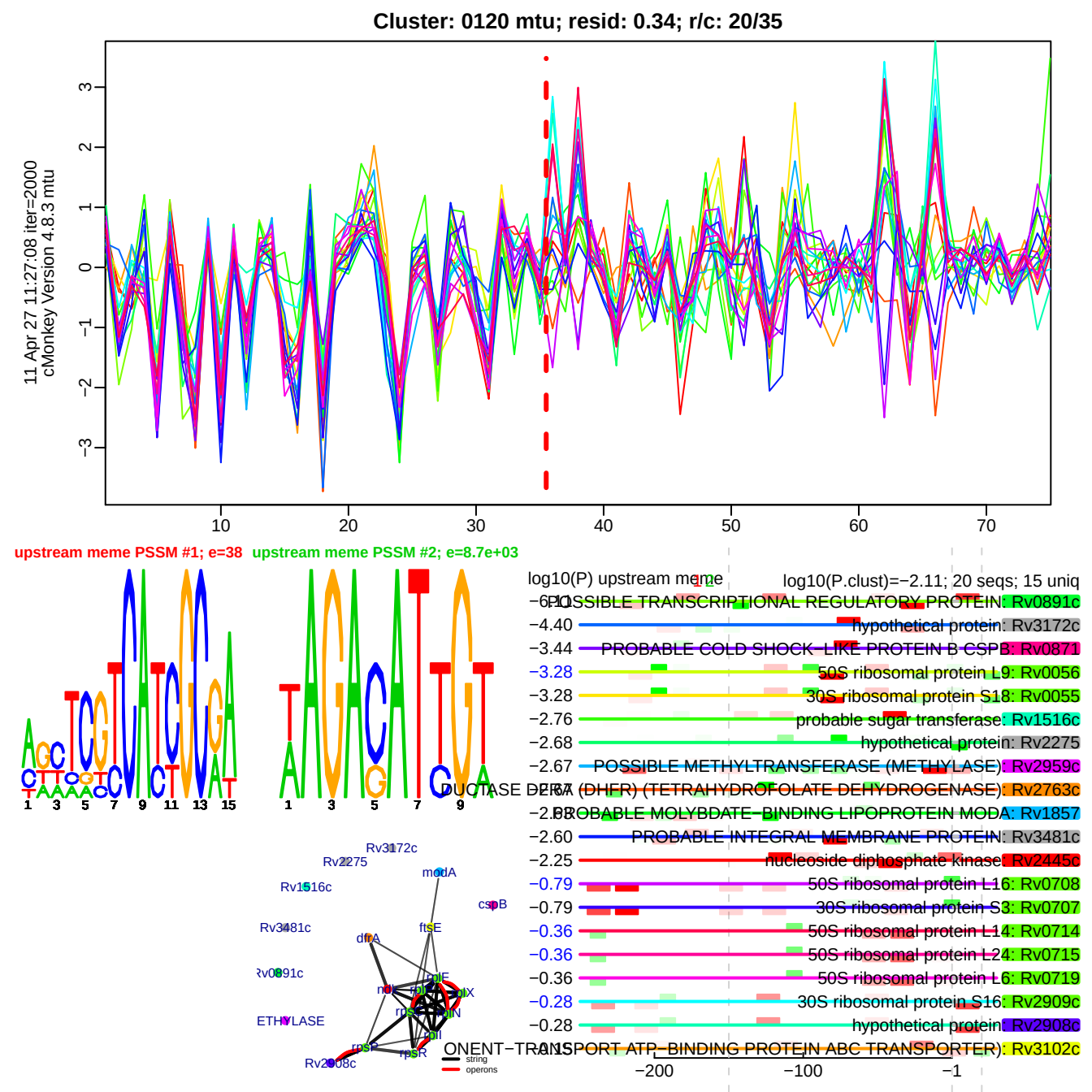
Cluster: 0120 mtu; resid: 0.34; r/c: 20/35
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=38
upstream meme PSSM #2; e=8.7e+03
log10(P) upstream meme
log10(P.clust)=−2.11; 20 seqs; 15 uniq
−6.10 POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv0891c
−4.40 hypothetical protein: Rv3172c
−3.44 PROBABLE COLD SHOCK-LIKE PROTEIN B CSPB: Rv0871
−3.28 50S ribosomal protein L9: Rv0056
−3.28 30S ribosomal protein S18: Rv0055
−2.76 probable sugar transferase: Rv1516c
−2.68 hypothetical protein: Rv2275
−2.67 POSSIBLE METHYLTRANSFERASE (METHYLASE): Rv2959c
−2.67 DUCTASE DEFA (DHFR) (TETRAHYDROFOLATE DEHYDROGENASE): Rv2763c
−2.58 PROBABLE MOLYBDATE-BINDING LIPOPROTEIN MODA: Rv1857
−2.60 PROBABLE INTEGRAL MEMBRANE PROTEIN: Rv3481c
−2.25 nucleoside diphosphate kinase: Rv2445c
−0.79 50S ribosomal protein L16: Rv0708
−0.79 30S ribosomal protein S3: Rv0707
−0.36 50S ribosomal protein L14: Rv0714
−0.36 50S ribosomal protein L24: Rv0715
−0.36 50S ribosomal protein L6: Rv0719
−0.28 30S ribosomal protein S16: Rv2909c
−0.28 hypothetical protein: Rv2908c
−0.15 ONENT-TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER): Rv3102c
−200
−100
−1
Rv3172c
Rv2275
modA
Rv1516c
cspB
Rv3481c
ftsE
dfrA
Rv0891c
ETHYLASE
Rv2908c
rpsR
string
operons