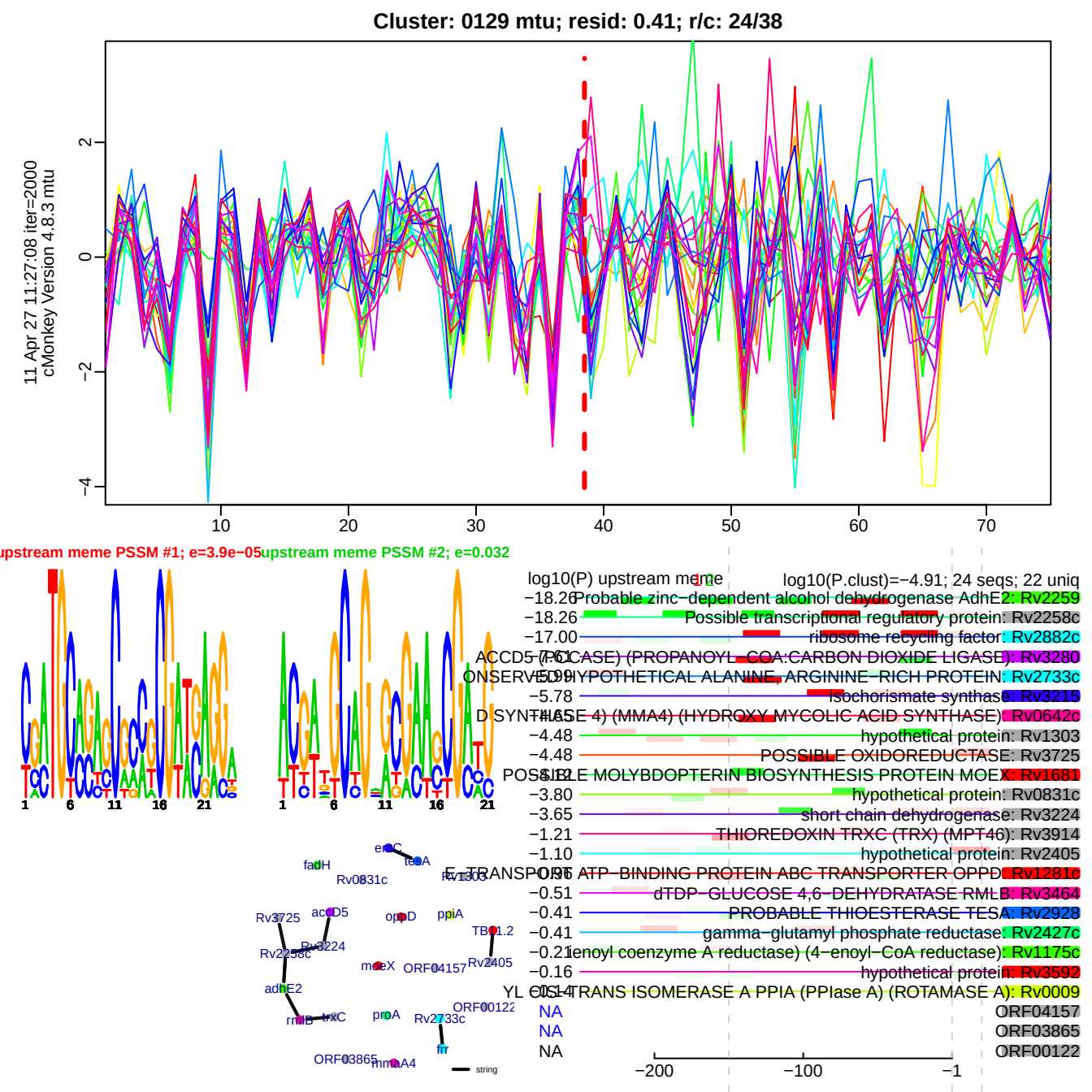
Cluster: 0129 mtu; resid: 0.41; r/c: 24/38
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=3.9e−05
upstream meme PSSM #2; e=0.032
log10(P) upstream meme
log10(P.clust)=−4.91; 24 seqs; 22 uniq
−18.26 Probable zinc−dependent alcohol dehydrogenase AdhE2: Rv2259
−18.26 Possible transcriptional regulatory protein: Rv2258c
−17.00 ribosome recycling factor: Rv2882c
ACCD5 (PCCASE) (PROPANOYL−COA:CARBON DIOXIDE LIGASE): Rv3280
ONSERVED HYPOTHETICAL ALANINE, ARGININE−RICH PROTEIN: Rv2733c
−5.78 isochorismate synthase: Rv3215
D SYNTHASE 4) (MMA4) (HYDROXY MYCOLIC ACID SYNTHASE): Rv0642c
−4.48 hypothetical protein: Rv1303
−4.48 POSSIBLE OXIDOREDUCTASE: Rv3725
POSSIBLE MOLYBDOPTERIN BIOSYNTHESIS PROTEIN MOEX: Rv1681
−3.80 hypothetical protein: Rv0831c
−3.65 short chain dehydrogenase: Rv3224
−1.21 THIOREDOXIN TRXC (TRX) (MPT46): Rv3914
−1.10 hypothetical protein: Rv2405
E TRANSPORT ATP−BINDING PROTEIN ABC TRANSPORTER OPPD: Rv1281c
−0.51 dTDP−GLUCOSE 4,6−DEHYDRATASE RMLB: Rv3464
−0.41 PROBABLE THIOESTERASE TESA: Rv2928
−0.41 gamma−glutamyl phosphate reductase: Rv2427c
−0.21 enoyl coenzyme A reductase) (4−enoyl−CoA reductase): Rv1175c
−0.16 hypothetical protein: Rv3592
YL CIS-TRANS ISOMERASE A PPIA (PPIase A) (ROTAMASE A): Rv0009
NA ORF04157
NA ORF03865
NA ORF00122
−200
−100
−1
fadH
Rv0831c
Rv1303
Rv3725
accD5
oppD
ppiA
TB01.2
Rv3224
Rv2405
moeX
ORF04157
adhE2
rmlB
trxC
proA
Rv2733c
ORF00122
frr
ORF03865
rnmA4
string