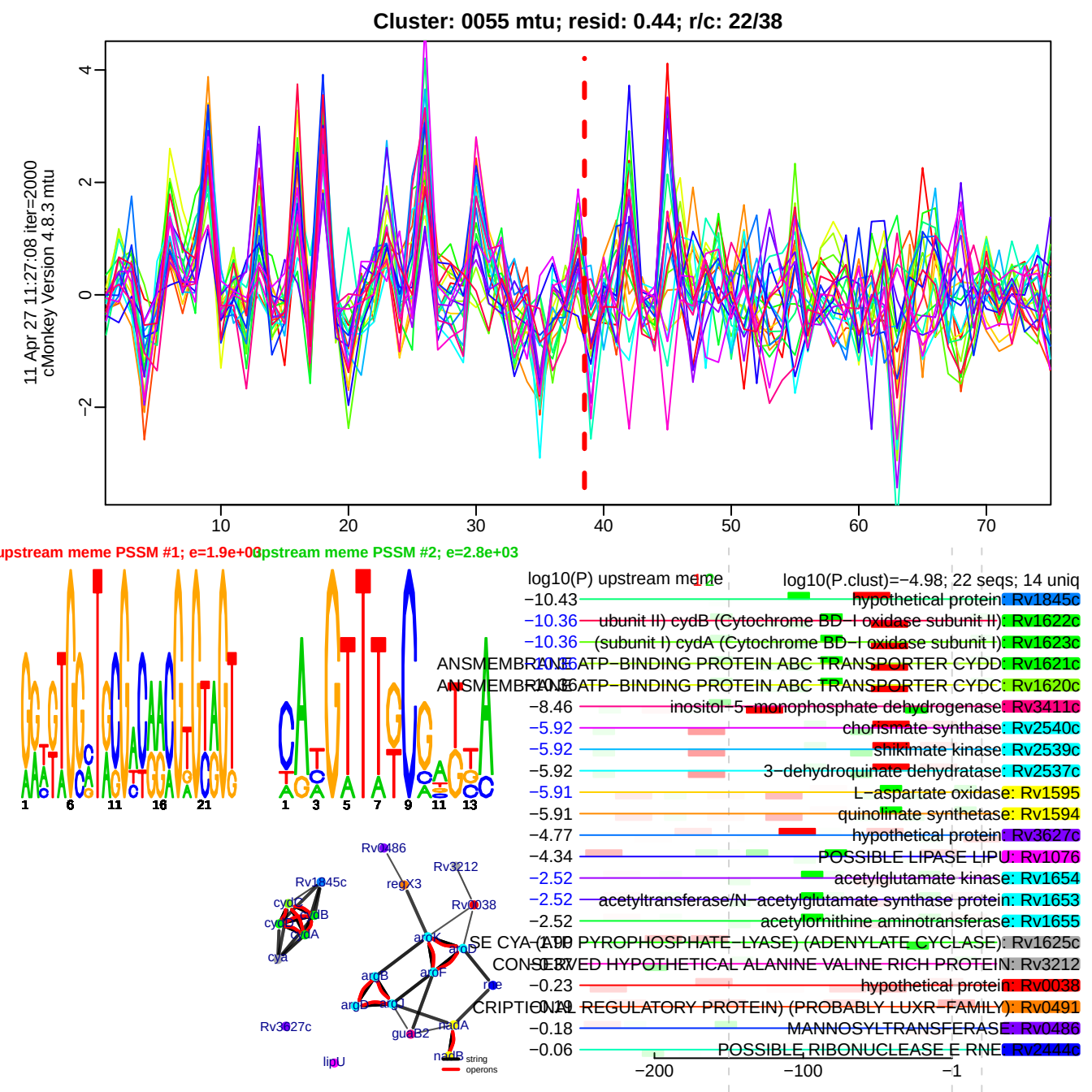
Cluster: 0055 mtu; resid: 0.44; r/c: 22/38
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=1.9e+03
upstream meme PSSM #2; e=2.8e+03
log10(P) upstream meme
log10(P.clust)=−4.98; 22 seqs; 14 uniq
−10.43 hypothetical protein: Rv1845c
−10.36 ubunit II) cydB (Cytochrome BD−I oxidase subunit II): Rv1622c
−10.36 (subunit I) cydA (Cytochrome BD−I oxidase subunit I): Rv1623c
−10.36 ANSMEMBRANE ATP−BINDING PROTEIN ABC TRANSPORTER CYDD: Rv1621c
−10.36 ANSMEMBRANE ATP−BINDING PROTEIN ABC TRANSPORTER CYDC: Rv1620c
−8.46 inositol−5−monophosphate dehydrogenase: Rv3411c
−5.92 chorismate synthase: Rv2540c
−5.92 shikimate kinase: Rv2539c
−5.92 3−dehydroquinate dehydratase: Rv2537c
−5.91 L−aspartate oxidase: Rv1595
−5.91 quinolinate synthetase: Rv1594
−4.77 hypothetical protein: Rv3627c
−4.34 POSSIBLE LIPASE LIPU: Rv1076
−2.52 acetylglutamate kinase: Rv1654
−2.52 acetyltransferase/N−acetylglutamate synthase protein: Rv1653
−2.52 acetylornithine aminotransferase: Rv1655
−1.99 PYROPHOSPHATE−LYASE) (ADENYLATE CYCLASE): Rv1625c
−1.37 CONSERVED HYPOTHETICAL ALANINE VALINE RICH PROTEIN: Rv3212
−0.23 hypothetical protein: Rv0038
−0.19 CRIPTIONAL REGULATORY PROTEIN) (PROBABLY LUXR−FAMILY): Rv0491
−0.18 MANNOSYLTRANSFERASE: Rv0486
−0.06 POSSIBLE RIBONUCLEASE E RNE: Rv2444c
−200
−100
−1
Rv0486
Rv3212
Rv1845c
regX3
Rv0038
cydD
cydB
cydA
cya
argC
argD
argB
argF
rne
argG
argH
Rv3627c
guaB2
nadA
nadB
lipU
string
operons