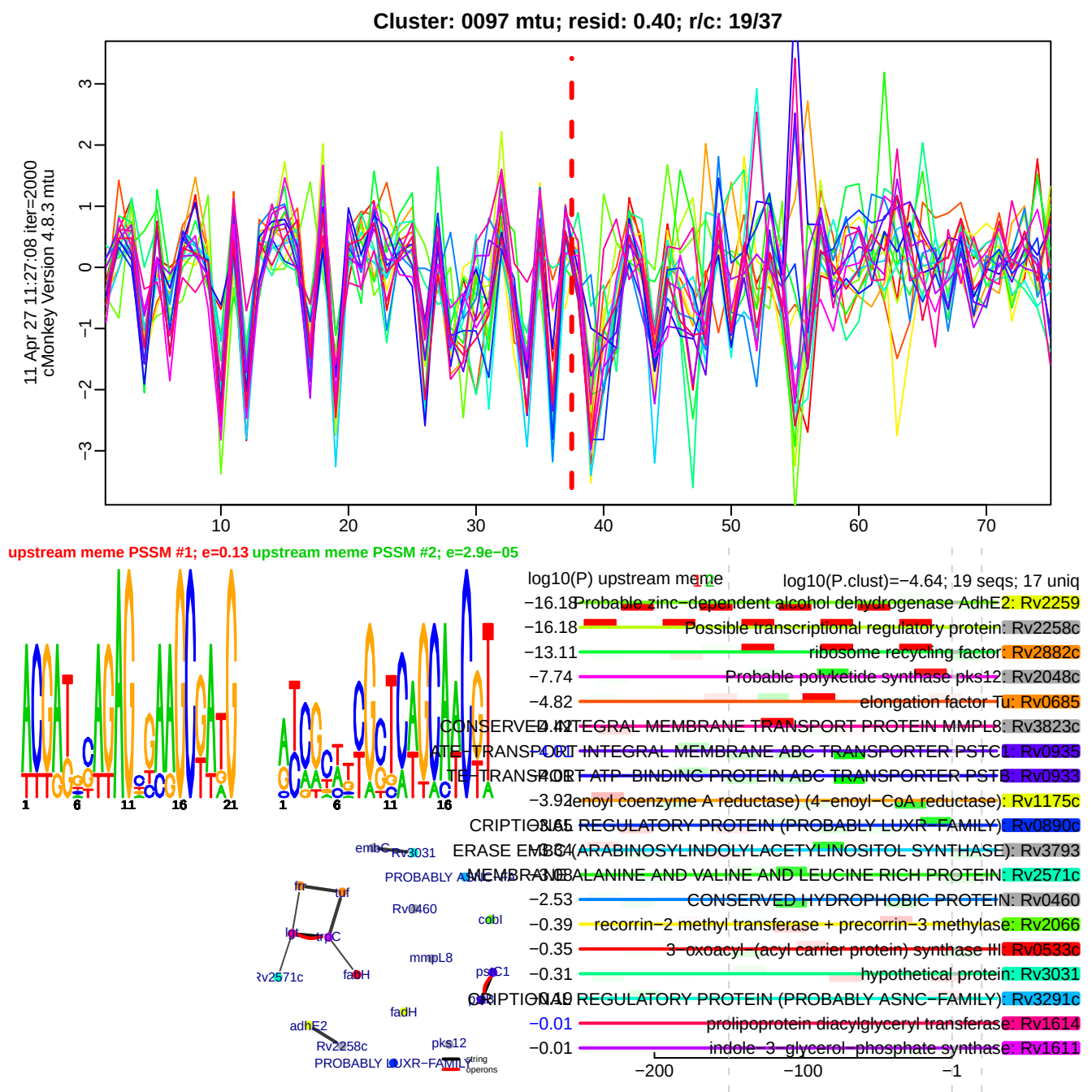
Cluster: 0097 mtu; resid: 0.40; r/c: 19/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=0.13
upstream meme PSSM #2; e=2.9e−05
log10(P) upstream meme
log10(P.clust)=−4.64; 19 seqs; 17 uniq
−16.18 Probable zinc−dependent alcohol dehydrogenase AdhE2: Rv2259
−16.18 Possible transcriptional regulatory protein: Rv2258c
−13.11 ribosome recycling factor: Rv2882c
−7.74 Probable polyketide synthase pks12: Rv2048c
−4.82 elongation factor Tu: Rv0685
−4.42 CONSERVED INTEGRAL MEMBRANE TRANSPORT PROTEIN MMPL8: Rv3823c
−4.01 ATP−TRANSPORT INTEGRAL MEMBRANE ABC TRANSPORTER PSTC1: Rv0935
−3.92 TP−TRANSPORT ATP−BINDING PROTEIN ABC TRANSPORTER PSTB: Rv0933
−3.92 enoyl coenzyme A reductase) (4−enoyl−CoA reductase): Rv1175c
−3.45 CRIPTIONAL REGULATORY PROTEIN (PROBABLY LUXR−FAMILY): Rv0890c
−3.34 ERASE EMBC (ARABINOSYLINDOLYLACETYLINOSITOL SYNTHASE): Rv3793
−3.08 MEMBRANE GLYCINE−ALANINE AND VALINE AND LEUCINE RICH PROTEIN: Rv2571c
−2.53 CONSERVED HYDROPHOBIC PROTEIN: Rv0460
−0.39 recorrin−2 methyl transferase + precorrin−3 methylase: Rv2066
−0.35 3−oxoacyl−(acyl carrier protein) synthase III: Rv0533c
−0.31 hypothetical protein: Rv3031
−0.19 CRIPTIONAL REGULATORY PROTEIN (PROBABLY ASNC−FAMILY): Rv3291c
−0.01 prolipoprotein diacylglyceryl transferase: Rv1614
−0.01 indole−3−glycerol−phosphate synthase: Rv1611
−200
−100
−1
embC
Rv3031
PROBABLY ABC−TYPE
frr
tuf
Rv0460
cobI
lpt
trpC
mmpL8
Rv2571c
fadH
pstC1
fadH
adhE2
Rv2258c
pks12
PROBABLY LUXR−FAMILY
string
operons