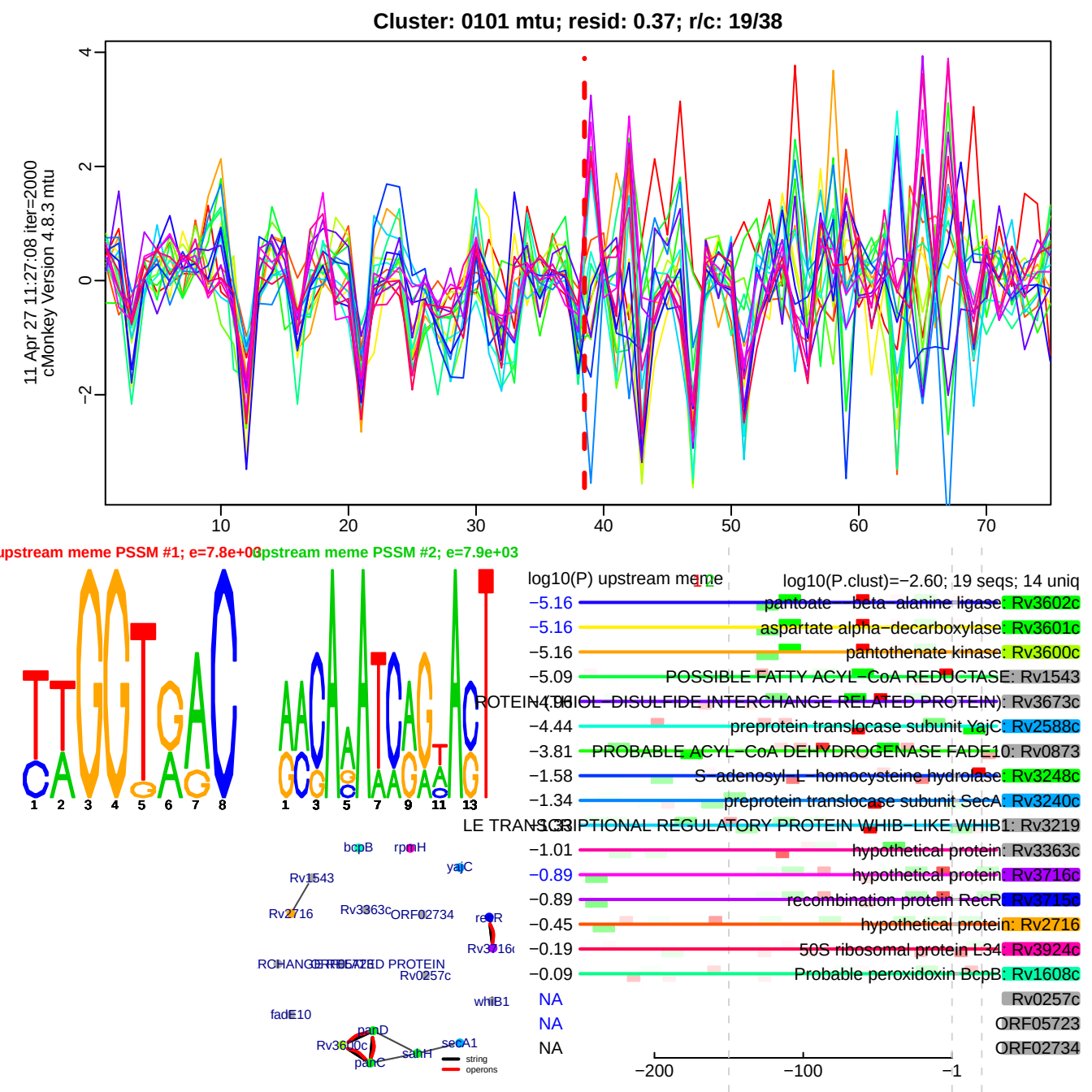
Cluster: 0101 mtu; resid: 0.37; r/c: 19/38
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=7.8e+03
upstream meme PSSM #2; e=7.9e+03
log10(P) upstream meme
log10(P.clust)=−2.60; 19 seqs; 14 uniq
−5.16 pantoate−beta−alanine ligase: Rv3602c
−5.16 aspartate alpha−decarboxylase: Rv3601c
−5.16 pantothenate kinase: Rv3600c
−5.09 POSSIBLE FATTY ACYL−CoA REDUCTASE: Rv1543
ROTEIN 4 (THIOL−DISULFIDE INTERCHANGE RELATED PROTEIN): Rv3673c
−4.44 preprotein translocase subunit YajC: Rv2588c
−3.81 PROBABLE ACYL−CoA DEHYDROGENASE FADE10: Rv0873
−1.58 S−adenosyl−L−homocysteine hydrolase: Rv3248c
−1.34 preprotein translocase subunit SecA: Rv3240c
LE TRANSCRIPTIONAL REGULATORY PROTEIN WHIB−LIKE WHIB1: Rv3219
−1.01 hypothetical protein: Rv3363c
−0.89 hypothetical protein: Rv3716c
−0.89 recombination protein RecR: Rv3715c
−0.45 hypothetical protein: Rv2716
−0.19 50S ribosomal protein L34: Rv3924c
−0.09 Probable peroxidoxin BcpB: Rv1608c
NA Rv0257c
NA ORF05723
NA ORF02734
−200
−100
−1
bcpB
rpmH
yajC
Rv1543
Rv2716
Rv3363c
ORF02734
recR
Rv0257c
whiB1
fadE10
panD
Rv3600c
secA1
sahH
panC
string
operons