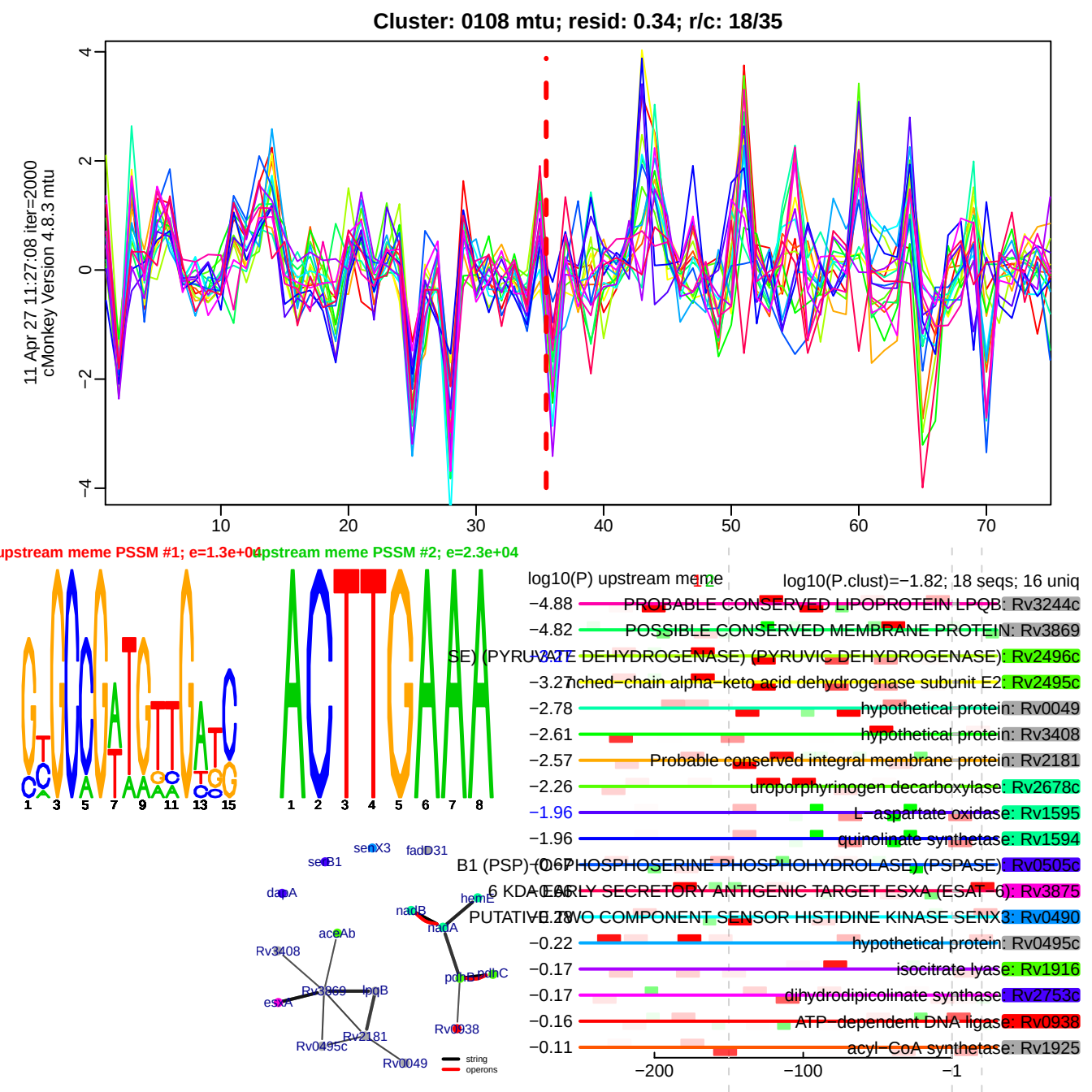
Cluster: 0108 mtu; resid: 0.34; r/c: 18/35
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=1.3e+04
upstream meme PSSM #2; e=2.3e+04
log10(P) upstream meme
log10(P.clust)=−1.82; 18 seqs; 16 uniq
−4.88 PROBABLE CONSERVED LIPOPROTEIN LPQB: Rv3244c
−4.82 POSSIBLE CONSERVED MEMBRANE PROTEIN: Rv3869
SE) (PYRUVIC DEHYDROGENASE) (PYRUVIC DEHYDROGENASE): Rv2496c
−3.27 nched−chain alpha−keto acid dehydrogenase subunit E2: Rv2495c
−2.78 hypothetical protein: Rv0049
−2.61 hypothetical protein: Rv3408
−2.57 Probable conserved integral membrane protein: Rv2181
−2.26 uroporphyrinogen decarboxylase: Rv2678c
−1.96 L−aspartate oxidase: Rv1595
−1.96 quinolinate synthetase: Rv1594
B1 (PSP) (O−PHOSPHOSERINE PHOSPHOHYDROLASE) (PSPASE): Rv0505c
6 KDA EARLY SECRETORY ANTIGENIC TARGET ESXA (ESAT−6): Rv3875
PUTATIVE TWO COMPONENT SENSOR HISTIDINE KINASE SENX3: Rv0490
−0.22 hypothetical protein: Rv0495c
−0.17 isocitrate lyase: Rv1916
−0.17 dihydrodipicolinate synthase: Rv2753c
−0.16 ATP−dependent DNA ligase: Rv0938
−0.11 acyl−CoA synthetase: Rv1925
senX3
fadD31
senB1
dapA
hemE
nadB
nadA
aceAb
Rv3408
pdhB
pdhC
esxA
Rv3869
lpqB
Rv0938
Rv2181
Rv0495c
Rv0049
string
operons