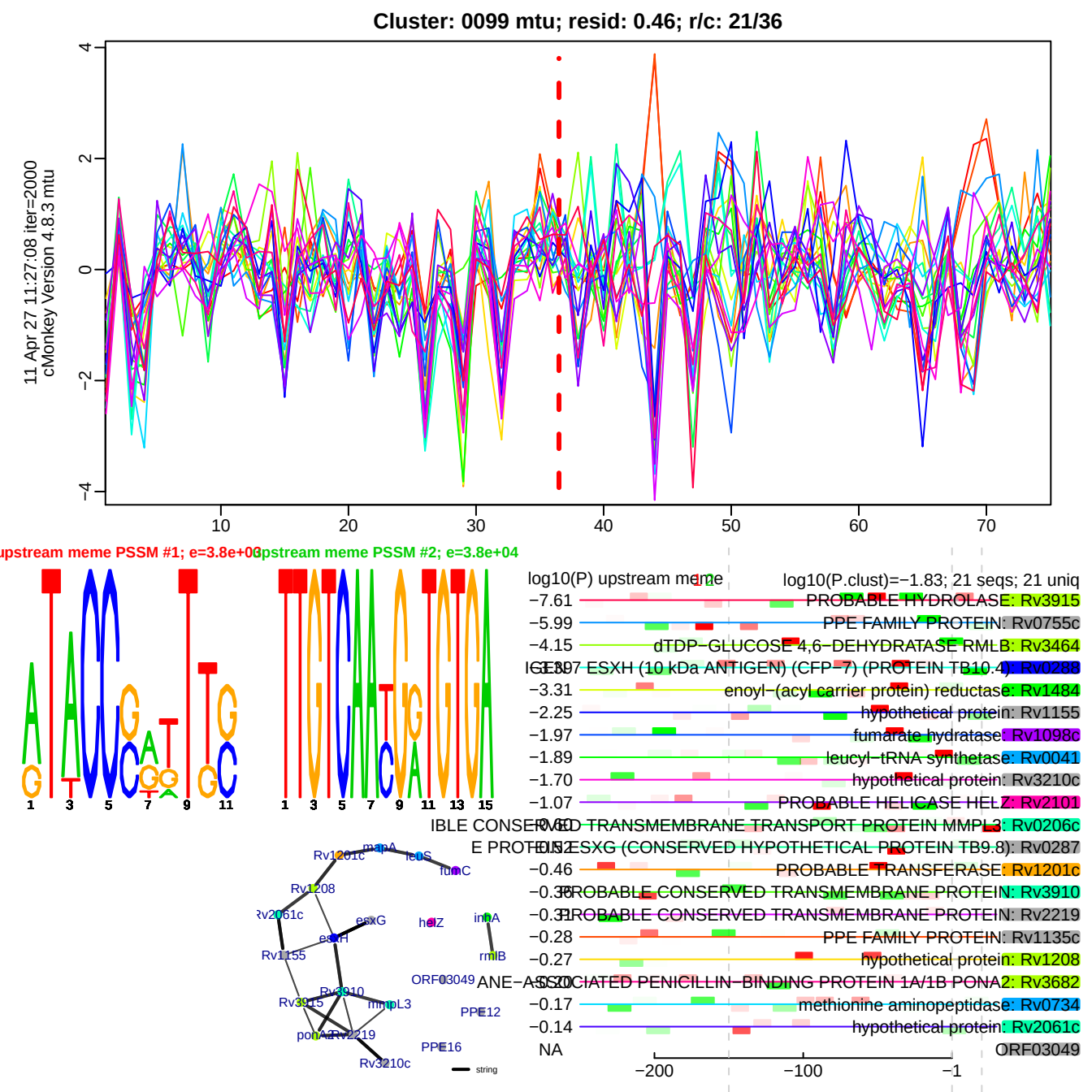
Cluster: 0099 mtu; resid: 0.46; r/c: 21/36
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=3.8e+03
upstream meme PSSM #2; e=3.8e+04
log10(P) upstream meme
log10(P.clust)=−1.83; 21 seqs; 21 uniq
−7.61 PROBABLE HYDROLASE: Rv3915
−5.99 PPE FAMILY PROTEIN: Rv0755c
−4.15 dTDP−GLUCOSE 4,6−DEHYDRATASE RMLB: Rv3464
−3.97 ESXH (10 kDa ANTIGEN) (CFP−7) (PROTEIN TB10.4): Rv0288
−3.31 enoyl−(acyl carrier protein) reductase: Rv1484
−2.25 hypothetical protein: Rv1155
−1.97 fumarate hydratase: Rv1098c
−1.89 leucyl−tRNA synthetase: Rv0041
−1.70 hypothetical protein: Rv3210c
−1.07 PROBABLE HELICASE HELZ: Rv2101
−0.46 PROBABLE TRANSFERASE: Rv1201c
−0.36 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: Rv3910
−0.31 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: Rv2219
−0.28 PPE FAMILY PROTEIN: Rv1135c
−0.27 hypothetical protein: Rv1208
−0.20 ANE−ASSOCIATED PENICILLIN−BINDING PROTEIN 1A/1B PONA2: Rv3682
−0.17 methionine aminopeptidase: Rv0734
−0.14 hypothetical protein: Rv2061c
NA ORF03049
−200
−100
−1
Rv1201c
mapA
leuS
fumC
Rv1208
Rv2061c
esxG
esxH
helZ
infA
Rv1155
rmlB
ORF03049
Rv3910
Rv3915
mmpL3
PPE12
ponA2
Rv2219
PPE16
Rv3210c
string