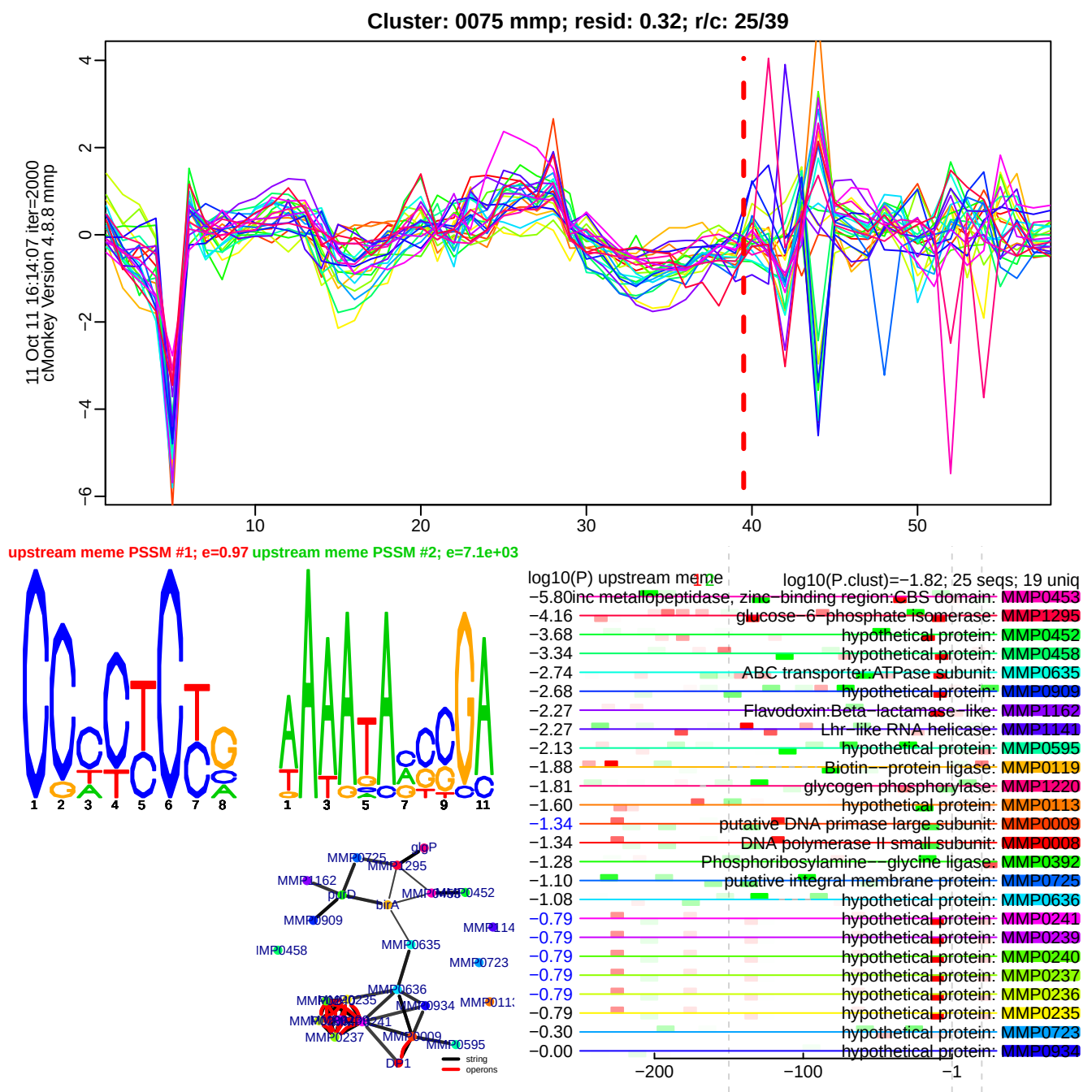
Cluster: 0075 mmp; resid: 0.32; r/c: 25/39
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
upstream meme PSSM #1; e=0.97
upstream meme PSSM #2; e=7.1e+03
log10(P) upstream meme
log10(P.clust)=−1.82; 25 seqs; 19 uniq
−5.80 inc metallopeptidase, zinc−binding region:CBS domain: MMP0453
−4.16 glucose−6−phosphate isomerase: MMP1295
−3.68 hypothetical protein: MMP0452
−3.34 hypothetical protein: MMP0458
−2.74 ABC transporter:ATPase subunit: MMP0635
−2.68 hypothetical protein: MMP0909
−2.27 Flavodoxin:Beta−lactamase−like: MMP1162
−2.27 Lhr−like RNA helicase: MMP1141
−2.13 hypothetical protein: MMP0595
−1.88 Biotin−−protein ligase: MMP0119
−1.81 glycogen phosphorylase: MMP1220
−1.60 hypothetical protein: MMP0113
−1.34 putative DNA primase large subunit: MMP0009
−1.34 DNA polymerase II small subunit: MMP0008
−1.28 Phosphoribosylamine−−glycine ligase: MMP0392
−1.10 putative integral membrane protein: MMP0725
−1.08 hypothetical protein: MMP0636
−0.79 hypothetical protein: MMP0241
−0.79 hypothetical protein: MMP0239
−0.79 hypothetical protein: MMP0240
−0.79 hypothetical protein: MMP0237
−0.79 hypothetical protein: MMP0236
−0.79 hypothetical protein: MMP0235
−0.30 hypothetical protein: MMP0723
−0.00 hypothetical protein: MMP0934
−200
−100
−1
string
operons