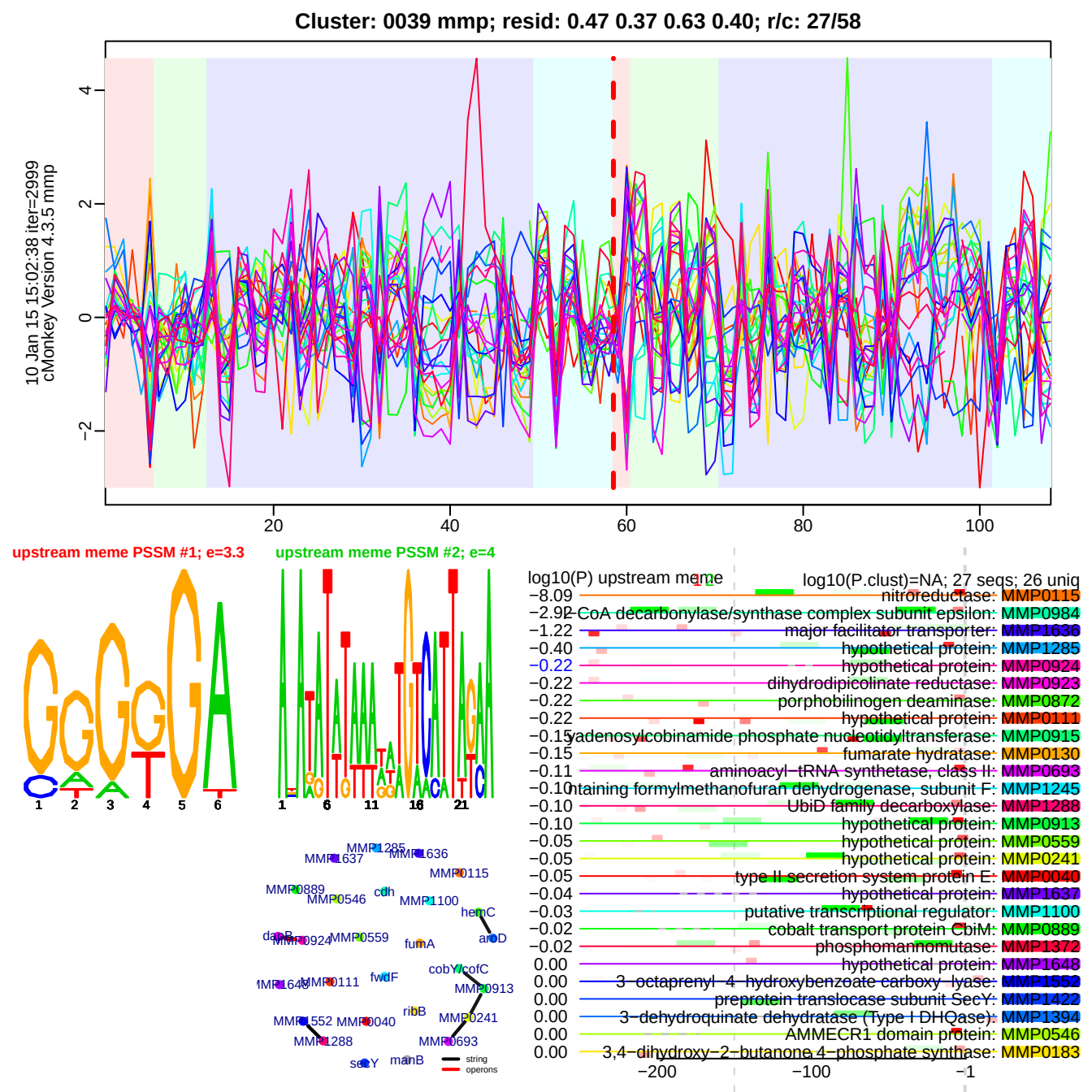
Cluster: 0039 mmp; resid: 0.47 0.37 0.63 0.40; r/c: 27/58
10 Jan 15 15:02:38 iter=2999
cMonkey Version 4.3.5 mmp
upstream meme PSSM #1; e=3.3
upstream meme PSSM #2; e=4
log10(P) upstream meme
log10(P.clust)=NA; 27 seqs; 26 uniq
−8.09 nitroreductase: MMP0115
−2.92 2-CoA decarbonylase/synthase complex subunit epsilon: MMP0984
−1.22 major facilitator transporter: MMP1636
−0.40 hypothetical protein: MMP1285
−0.22 hypothetical protein: MMP0924
−0.22 dihydrodipicolinate reductase: MMP0923
−0.22 porphobilinogen deaminase: MMP0872
−0.22 hypothetical protein: MMP0111
−0.15 adenosylcobinamide phosphate nucleotidyltransferase: MMP0915
−0.15 fumarate hydratase: MMP0130
−0.11 aminoacyl−tRNA synthetase, class II: MMP0693
−0.10 containing formylmethanofuran dehydrogenase, subunit F: MMP1245
−0.10 UbiD family decarboxylase: MMP1288
−0.10 hypothetical protein: MMP0913
−0.05 hypothetical protein: MMP0559
−0.05 hypothetical protein: MMP0241
−0.05 type II secretion system protein E: MMP0040
−0.04 hypothetical protein: MMP1637
−0.03 putative transcriptional regulator: MMP1100
−0.02 cobalt transport protein CbiM: MMP0889
−0.02 phosphomannomutase: MMP1372
0.00 hypothetical protein: MMP1648
0.00 3−octaprenyl−4−hydroxybenzoate carboxy−lyase: MMP1552
0.00 preprotein translocase subunit SecY: MMP1422
0.00 3−dehydroquinate dehydratase (Type I DHQase): MMP1394
0.00 AMMECR1 domain protein: MMP0546
0.00 3,4−dihydroxy−2−butanone 4−phosphate synthase: MMP0183
−200
−100
−1
MMP1285
MMP1636
MMP1637
MMP0115
MMP0889
MMP0546
cdh
MMP1100
hemC
MMP0924
MMP0559
fumA
aroD
cobY
cofC
MMP1648
MMP0111
fwdF
MMP0913
ribB
MMP1552
MMP0040
MMP0241
MMP1288
MMP0693
secY
manB
string
operons