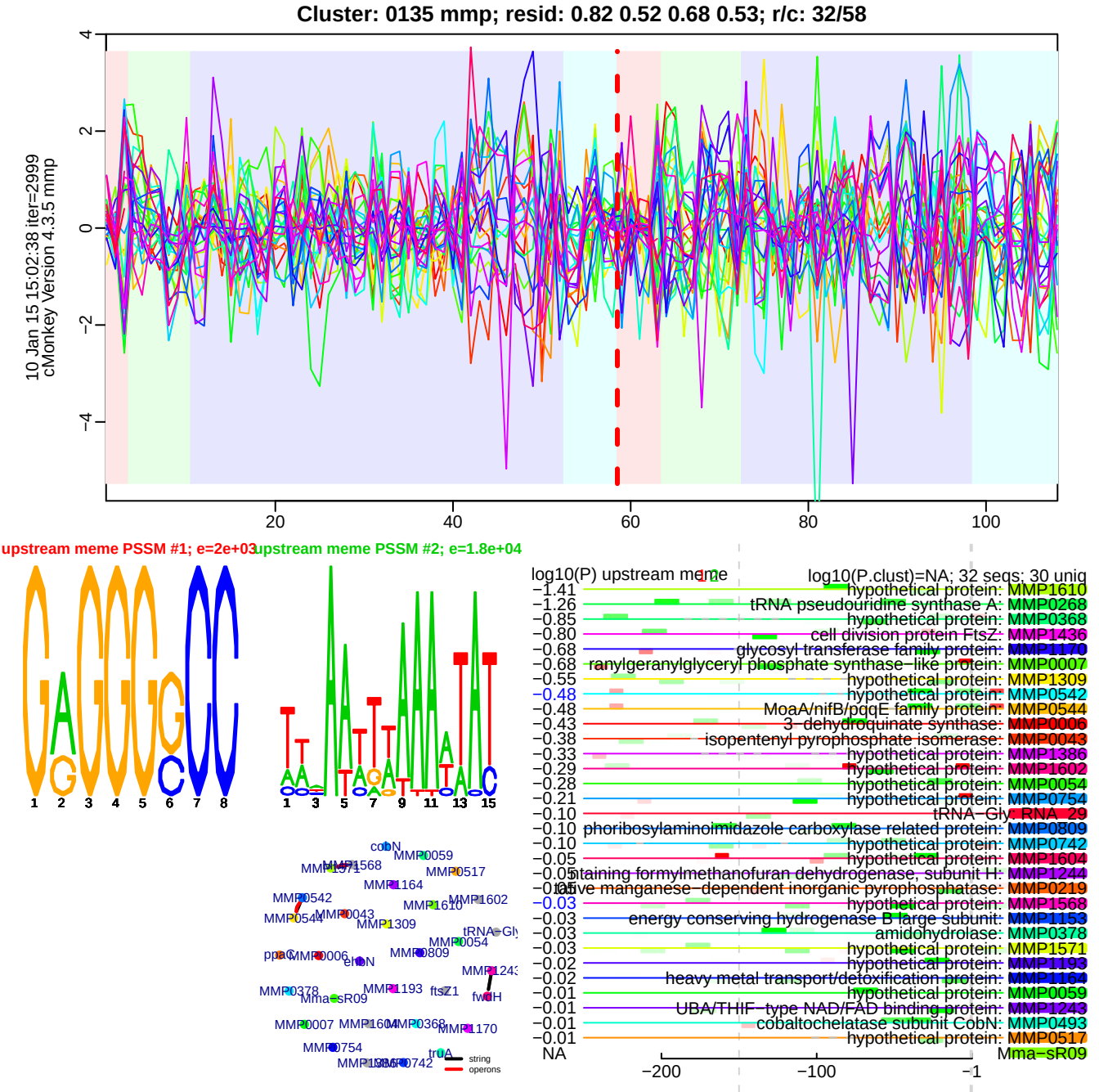
Cluster: 0135 mmp; resid: 0.82 0.52 0.68 0.53; r/c: 32/58
10 Jan 15 15:02:38 iter=2999
cMonkey Version 4.3.5 mmp
upstream meme PSSM #1; e=2e+03
upstream meme PSSM #2; e=1.8e+04
log10(P) upstream meme
log10(P.clust)=NA; 32 seqs; 30 uniq
−1.41 hypothetical protein: MMP1610
−1.26 tRNA pseudouridine synthase A: MMP0268
−0.85 hypothetical protein: MMP0368
−0.80 cell division protein FtsZ: MMP1436
−0.68 glycosyl transferase family protein: MMP1170
−0.68 ranylgeranylglyceryl phosphate synthase−like protein: MMP0007
−0.55 hypothetical protein: MMP1309
−0.48 hypothetical protein: MMP0542
−0.48 MoaA/nifB/pqqE family protein: MMP0544
−0.43 3−dehydroquinate synthase: MMP0006
−0.38 isopentenyl pyrophosphate isomerase: MMP0043
−0.33 hypothetical protein: MMP1386
−0.29 hypothetical protein: MMP1602
−0.28 hypothetical protein: MMP0054
−0.21 hypothetical protein: MMP0754
−0.10 tRNA−Gly, RNA_29
−0.10 phoribosylaminoimidazole carboxylase related protein: MMP0809
−0.10 hypothetical protein: MMP0742
−0.05 hypothetical protein: MMP1604
−0.05 staining formylmethanofuran dehydrogenase, subunit H: MMP1244
−0.04 ative manganese−dependent inorganic pyrophosphatase: MMP0219
−0.03 hypothetical protein: MMP1568
−0.03 energy conserving hydrogenase B large subunit: MMP1153
−0.03 amidohydrolase: MMP0378
−0.03 hypothetical protein: MMP1571
−0.02 hypothetical protein: MMP1193
−0.02 heavy metal transport/detoxification protein: MMP1164
−0.01 hypothetical protein: MMP0059
−0.01 UBA/THIF−type NAD/FAD binding protein: MMP1243
−0.01 cobaltochelatase subunit CobN: MMP0493
−0.01 hypothetical protein: MMP0517
NA Mma−sR09
−200 −100 −1
cobN
MMP0059
MMP1568
MMP1571
MMP0517
MMP1164
MMP0542
MMP1602
MMP1610
MMP0544
MMP0043
MMP1309
tRNA−Gly
MMP0054
ppaC
MMP0006
MMP0809
ehbN
MMP1243
MMP0378
MMP1193
ftsZ1
Mma−sR09
fwdH
MMP0007
MMP1604
MMP0368
MMP1170
MMP0754
truA
MMP1386
MMP0742
string
operons