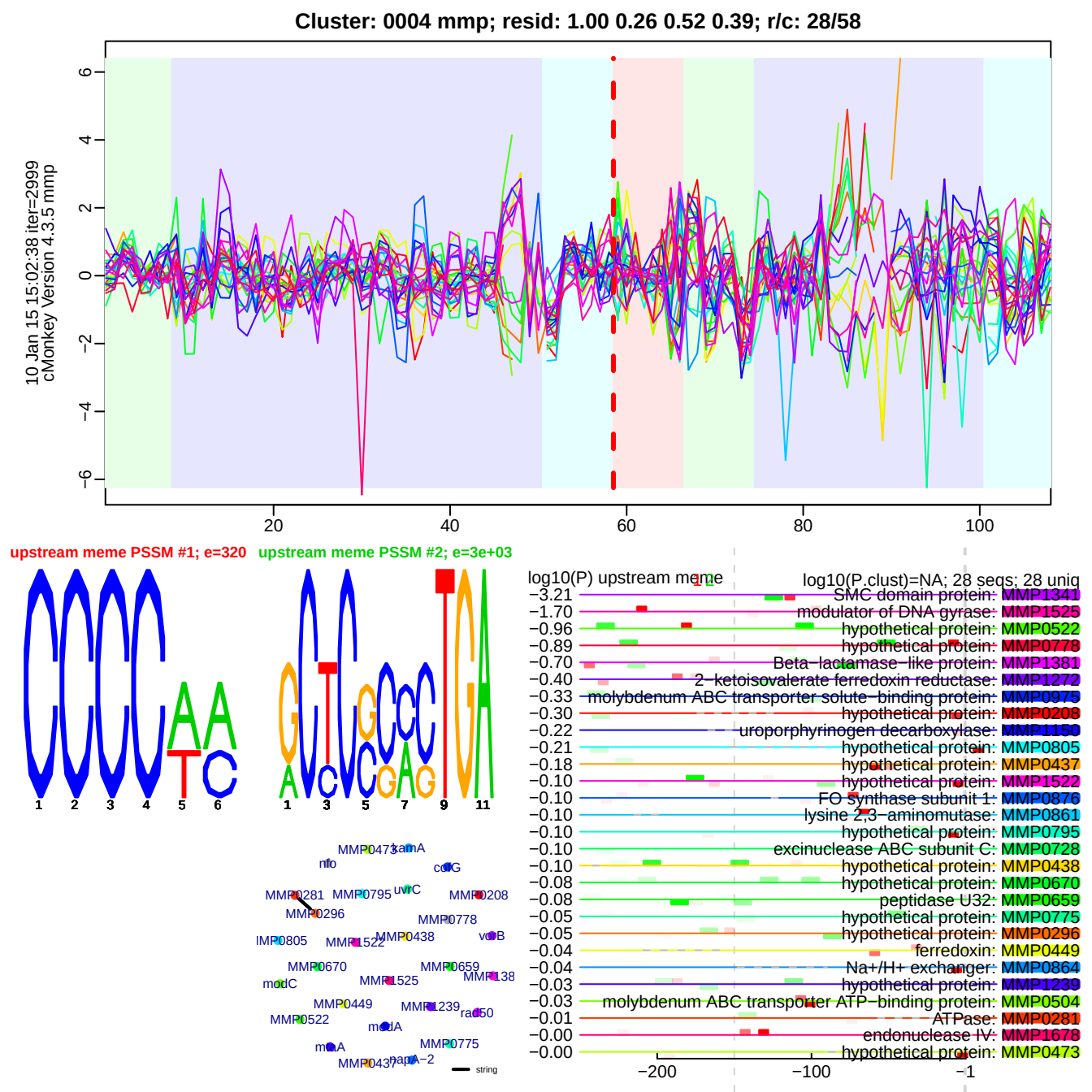
Cluster: 0004 mmp; resid: 1.00 0.26 0.52 0.39; r/c: 28/58
10 Jan 15 15:02:38 iter=2999
cMonkey Version 4.3.5 mmp
upstream meme PSSM #1; e=320
upstream meme PSSM #2; e=3e+03
log10(P) upstream meme
log10(P.clust)=NA; 28 seqs; 28 uniq
−3.21 SMC domain protein: MMP1341
−1.70 modulator of DNA gyrase: MMP1525
−0.96 hypothetical protein: MMP0522
−0.89 hypothetical protein: MMP0778
−0.70 Beta−lactamase−like protein: MMP1381
−0.40 2−ketoisovalerate ferredoxin reductase: MMP1272
−0.33 molybdenum ABC transporter solute−binding protein: MMP0975
−0.30 hypothetical protein: MMP0208
−0.22 uroporphyrinogen decarboxylase: MMP1150
−0.21 hypothetical protein: MMP0805
−0.18 hypothetical protein: MMP0437
−0.10 hypothetical protein: MMP1522
−0.10 FO Synthase subunit 1: MMP0876
−0.10 lysine 2,3−aminomutase: MMP0861
−0.10 hypothetical protein: MMP0795
−0.10 excinuclease ABC subunit C: MMP0728
−0.10 hypothetical protein: MMP0438
−0.08 hypothetical protein: MMP0670
−0.08 peptidase U32: MMP0659
−0.05 hypothetical protein: MMP0775
−0.05 hypothetical protein: MMP0296
−0.04 ferredoxin: MMP0449
−0.04 Na+/H+ exchanger: MMP0864
−0.03 hypothetical protein: MMP1239
−0.03 molybdenum ABC transporter ATP−binding protein: MMP0504
−0.01 ATPase: MMP0281
−0.00 endonuclease IV: MMP1678
−0.00 hypothetical protein: MMP0473
−200
−100
−1
MMP0473
kamA
nfo
cobG
MMP0281
MMP0795
uvrC
MMP0208
MMP0296
MMP0778
MMP0805
MMP1522
MMP0438
valB
MMP0670
MMP0659
modC
MMP1525
MMP1138
MMP0449
MMP1239
radC
MMP0522
modA
MMP0775
MMP0437
papA−2
string