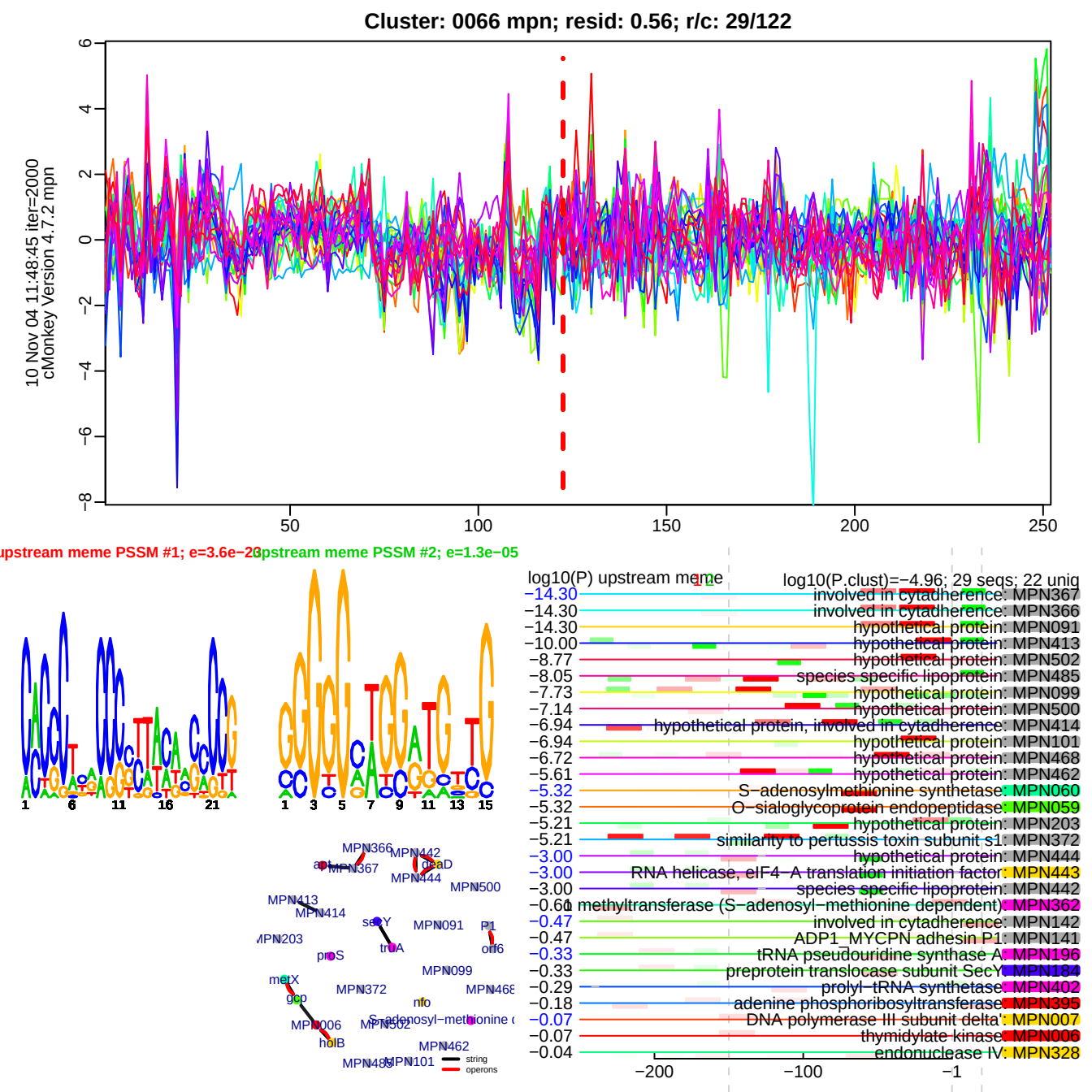
Cluster: 0066 mpn; resid: 0.56; r/c: 29/122
10 Nov 04 11:48:45 iter=2000
cMonkey Version 4.7.2 mpn
upstream meme PSSM #1; e=3.6e−26
upstream meme PSSM #2; e=1.3e−05
log10(P) upstream meme
log10(P.clust)=−4.96; 29 seqs; 22 uniq
−14.30 involved in cytadherence: MPN367
−14.30 involved in cytadherence: MPN366
−14.30 hypothetical protein: MPN091
−10.00 hypothetical protein: MPN413
−8.77 hypothetical protein: MPN502
−8.05 species specific lipoprotein: MPN485
−7.73 hypothetical protein: MPN099
−7.14 hypothetical protein: MPN500
−6.94 hypothetical protein, involved in cytadherence: MPN414
−6.94 hypothetical protein: MPN101
−6.72 hypothetical protein: MPN468
−5.61 hypothetical protein: MPN462
−5.32 S−adenosylmethionine synthetase: MPN060
−5.32 O−sialoglycoprotein endopeptidase: MPN059
−5.21 hypothetical protein: MPN203
−5.21 similarity to pertussis toxin subunit s1: MPN372
−3.00 hypothetical protein: MPN444
−3.00 RNA helicase, eIF4−A translation initiation factor: MPN443
−3.00 species specific lipoprotein: MPN442
−0.60 methyltransferase (S−adenosyl−methionine dependent): MPN362
−0.47 involved in cytadherence: MPN142
−0.47 ADP1_MYCPN adhesin P1: MPN141
−0.33 tRNA pseudouridine synthase A: MPN196
−0.33 preprotein translocase subunit SecY: MPN184
−0.29 prolyl−tRNA synthetase: MPN402
−0.18 adenine phosphoribosyltransferase: MPN395
−0.07 DNA polymerase III subunit delta': MPN007
−0.07 thymidylate kinase: MPN006
−0.04 endonuclease IV: MPN328
−200
−100
−1
MPN366
MPN367
MPN442
dnaD
MPN444
MPN500
MPN413
MPN414
secY
MPN091
P1
MPN203
truA
orf6
proS
MPN099
metX
MPN372
MPN468
gcp
nfo
MPN006
MPN502
holB
MPN462
MPN485
MPN101
string
operons