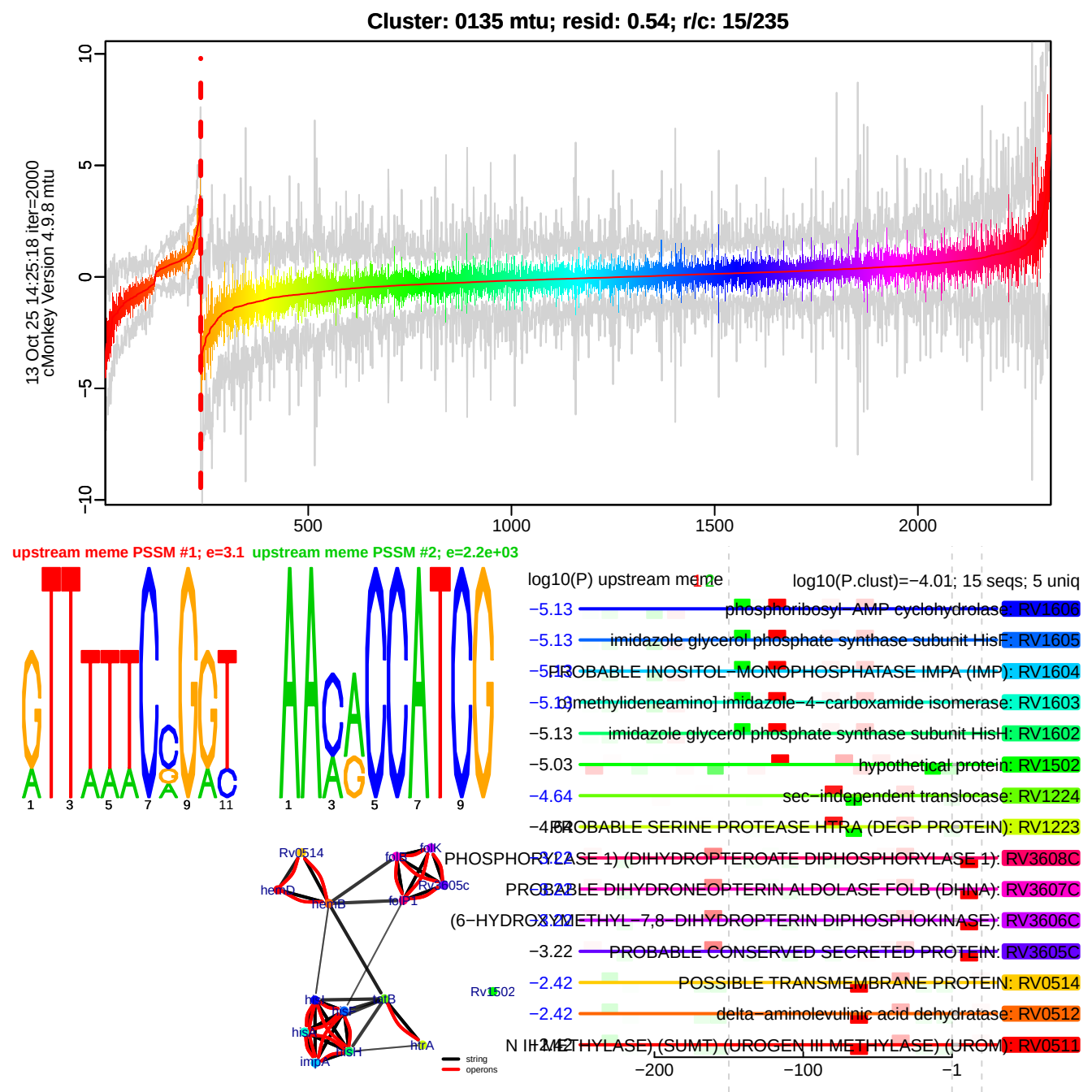

Cluster: 0135 mtu; resid: 0.54; r/c: 15/235
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu
10
5
0
−5
−10
500
1000
1500
2000
upstream meme PSSM #1; e=3.1
upstream meme PSSM #2; e=2.2e+03
1
3
5
7
9
11
log10(P) upstream meme
log10(P.clust)=−4.01; 15 seqs; 5 uniq
−5.13 phosphoribosyl−AMP cyclohydrolase: RV1606
−5.13 imidazole glycerol phosphate synthase subunit HisF: RV1605
−5.13 PROBABLE INOSITOL−MONOPHOSPHATASE IMPA (IMP): RV1604
−5.13 [(methylideneamino] imidazole−4−carboxamide isomerase: RV1603
−5.13 imidazole glycerol phosphate synthase subunit HisH: RV1602
−5.03 hypothetical protein: RV1502
−4.64 sec−independent translocase: RV1224
−4.64 PROBABLE SERINE PROTEASE HTRA (DEGP PROTEIN): RV1223
−3.22 PHOSPHORYLASE 1) (DIHYDROPTEROATE DIPHOSPHORYLASE 1): RV3608C
−3.22 PROBABLE DIHYDRONEOPTERIN ALDOLASE FOLB (DHNA): RV3607C
−3.22 (6−HYDROXYMETHYL−7,8−DIHYDROPTERIN DIPHOSPHOKINASE): RV3606C
−3.22 PROBABLE CONSERVED SECRETED PROTEIN: RV3605C
−2.42 POSSIBLE TRANSMEMBRANE PROTEIN: RV0514
−2.42 delta−aminolevulinic acid dehydratase: RV0512
−2.42 N III METHYLASE) (SUMT) (UROGEN III METHYLASE) (UROM): RV0511
−200
−100
−1
Rv0514
folB
folK
hemD
hemB
folP1
Rv3605c
Rv1502
hisI
hisF
hisB
hisH
hisA
impA
htrA
string
operons