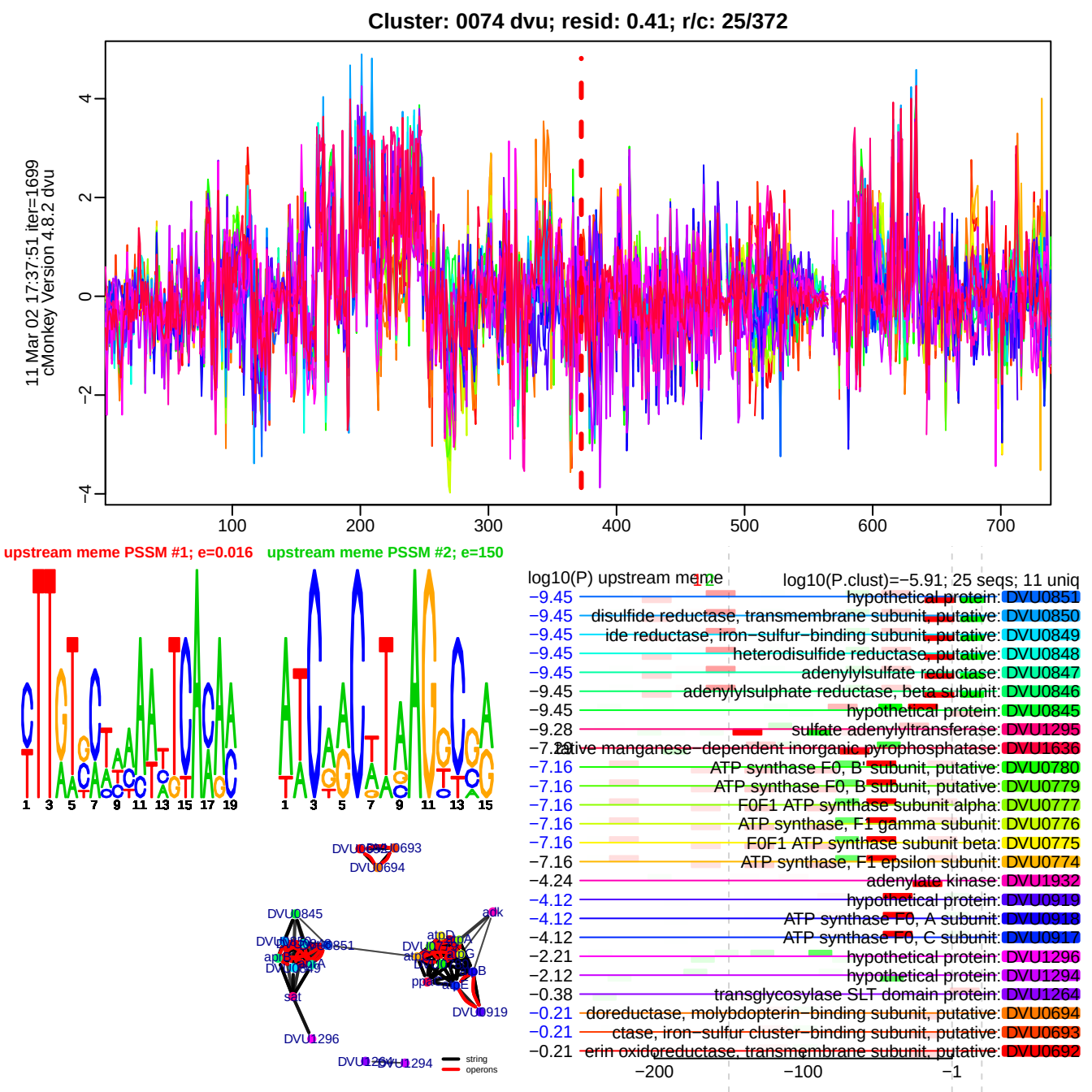
Cluster: 0074 dvu; resid: 0.41; r/c: 25/372
11 Mar 02 17:37:51 iter=1699
cMonkey Version 4.8.2 dvu
upstream meme PSSM #1; e=0.016
upstream meme PSSM #2; e=150
log10(P) upstream meme
log10(P.clust)=−5.91; 25 seqs; 11 uniq
−9.45 hypothetical protein: DVU0851
−9.45 disulfide reductase, transmembrane subunit, putative: DVU0850
−9.45 ide reductase, iron−sulfur−binding subunit, putative: DVU0849
−9.45 heterodisulfide reductase, putative: DVU0848
−9.45 adenylylsulfate reductase: DVU0847
−9.45 adenylylsulphate reductase, beta subunit: DVU0846
−9.45 hypothetical protein: DVU0845
−9.28 sulfate adenylyltransferase: DVU1295
−7.28 ative manganese−dependent inorganic pyrophosphatase: DVU1636
−7.16 ATP synthase F0, B' subunit, putative: DVU0780
−7.16 ATP synthase F0, B subunit, putative: DVU0779
−7.16 F0F1 ATP synthase subunit alpha: DVU0777
−7.16 ATP synthase, F1 gamma subunit: DVU0776
−7.16 F0F1 ATP synthase subunit beta: DVU0775
−7.16 ATP synthase, F1 epsilon subunit: DVU0774
−4.24 adenylate kinase: DVU1932
−4.12 hypothetical protein: DVU0919
−4.12 ATP synthase F0, A subunit: DVU0918
−4.12 ATP synthase F0, C subunit: DVU0917
−2.21 hypothetical protein: DVU1296
−2.12 hypothetical protein: DVU1294
−0.38 transglycosylase SLT domain protein: DVU1264
−0.21 doreductase, molybdopterin−binding subunit, putative: DVU0694
−0.21 ctase, iron−sulfur cluster−binding subunit, putative: DVU0693
−0.21 erin oxidoreductase, transmembrane subunit, putative: DVU0692
−200
−100
−1
DVU0693
DVU0694
DVU0845
DVU0851
DVU0849
DVU1296
DVU1294
DVU0919
string
operons