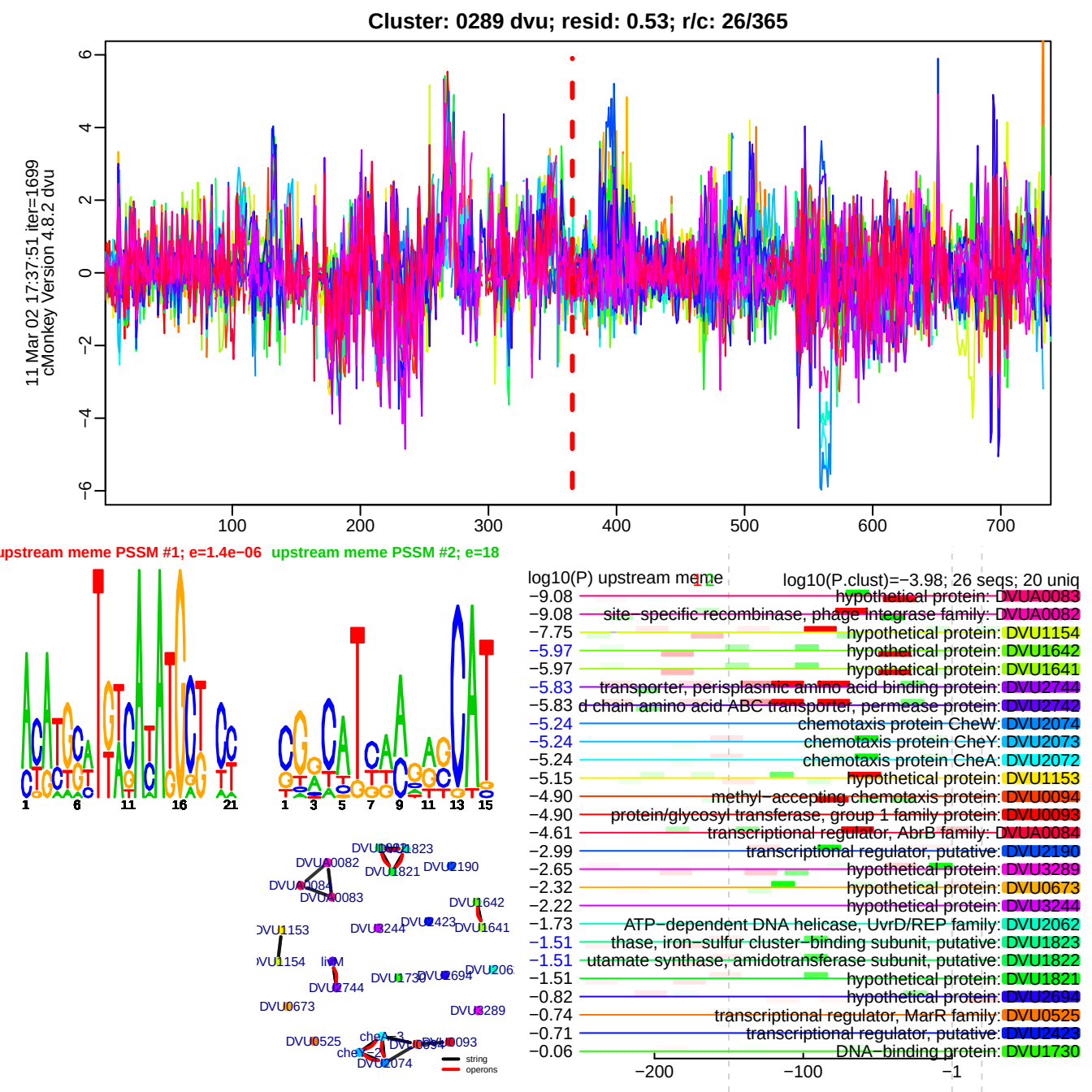
Cluster: 0289 dvu; resid: 0.53; r/c: 26/365
11 Mar 02 17:37:51 iter=1699
cMonkey Version 4.8.2 dvu
upstream meme PSSM #1; e=1.4e−06
upstream meme PSSM #2; e=18
log10(P) upstream meme
log10(P.clust)=−3.98; 26 seqs; 20 uniq
−9.08 hypothetical protein: DVUA0083
−9.08 site−specific recombinase, phage integrase family: DVUA0082
−7.75 hypothetical protein: DVU1154
−5.97 hypothetical protein: DVU1642
−5.97 hypothetical protein: DVU1641
−5.83 transporter, periplasmic amino acid binding protein: DVU2744
−5.83 d chain amino acid ABC transporter, permease protein: DVU2742
−5.24 chemotaxis protein CheW: DVU2074
−5.24 chemotaxis protein CheY: DVU2073
−5.24 chemotaxis protein CheA: DVU2072
−5.15 hypothetical protein: DVU1153
−4.90 methyl−accepting chemotaxis protein: DVU0094
−4.90 protein/glycosyl transferase, group 1 family protein: DVU0093
−4.61 transcriptional regulator, AbrB family: DVUA0084
−2.99 transcriptional regulator, putative: DVU2190
−2.65 hypothetical protein: DVU3289
−2.32 hypothetical protein: DVU0673
−2.22 hypothetical protein: DVU3244
−1.73 ATP−dependent DNA helicase, UvrD/REP family: DVU2062
−1.51 thase, iron−sulfur cluster−binding subunit, putative: DVU1823
−1.51 utamate synthase, amidotransferase subunit, putative: DVU1822
−1.51 hypothetical protein: DVU1821
−0.82 hypothetical protein: DVU2694
−0.74 transcriptional regulator, MarR family: DVU0525
−0.71 transcriptional regulator, putative: DVU2423
−0.06 DNA−binding protein: DVU1730
−200
−100
−1
string
operons