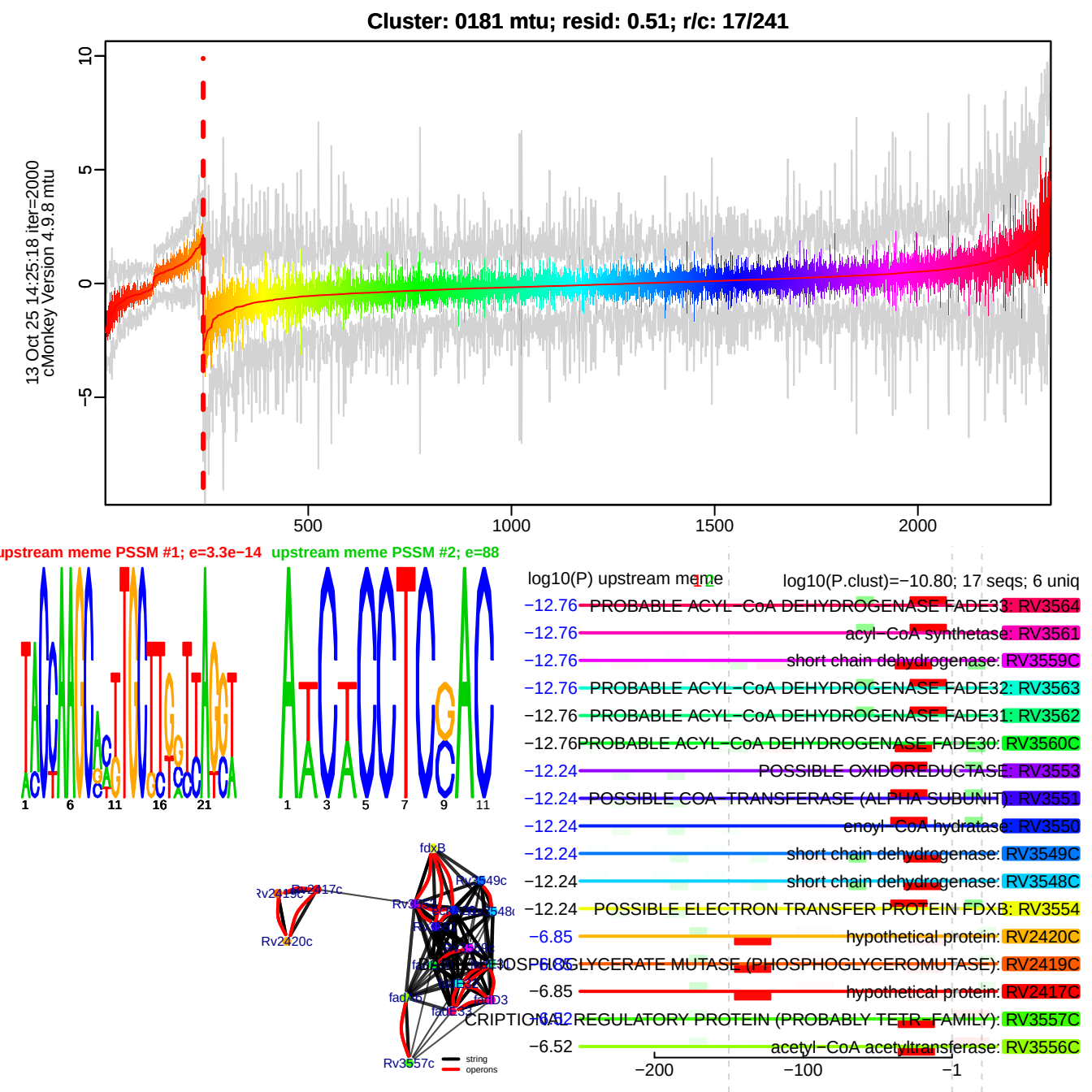
Cluster: 0181 mtu; resid: 0.51; r/c: 17/241
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu
upstream meme PSSM #1; e=3.3e−14
upstream meme PSSM #2; e=88
log10(P) upstream meme
log10(P.clust)=−10.80; 17 seqs; 6 uniq
−12.76 PROBABLE ACYL−CoA DEHYDROGENASE FADE33: RV3564
−12.76 acyl−CoA synthetase: RV3561
−12.76 short chain dehydrogenase: RV3559C
−12.76 PROBABLE ACYL−CoA DEHYDROGENASE FADE32: RV3563
−12.76 PROBABLE ACYL−CoA DEHYDROGENASE FADE31: RV3562
−12.76 PROBABLE ACYL−CoA DEHYDROGENASE FADE30: RV3560C
−12.24 POSSIBLE OXIDOREDUCTASE: RV3553
−12.24 POSSIBLE COA−TRANSFERASE (ALPHA SUBUNIT): RV3551
−12.24 enoyl−CoA hydratase: RV3550
−12.24 short chain dehydrogenase: RV3549C
−12.24 short chain dehydrogenase: RV3548C
−12.24 POSSIBLE ELECTRON TRANSFER PROTEIN FDXB: RV3554
−6.85 hypothetical protein: RV2420C
−6.85 PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE): RV2419C
−6.85 hypothetical protein: RV2417C
−6.52 TRANSCRIPTIONAL REGULATORY PROTEIN (PROBABLY TETR−FAMILY): RV3557C
−6.52 acetyl−CoA acetyltransferase: RV3556C
fdxB
Rv2420c
Rv3557c
string
operons