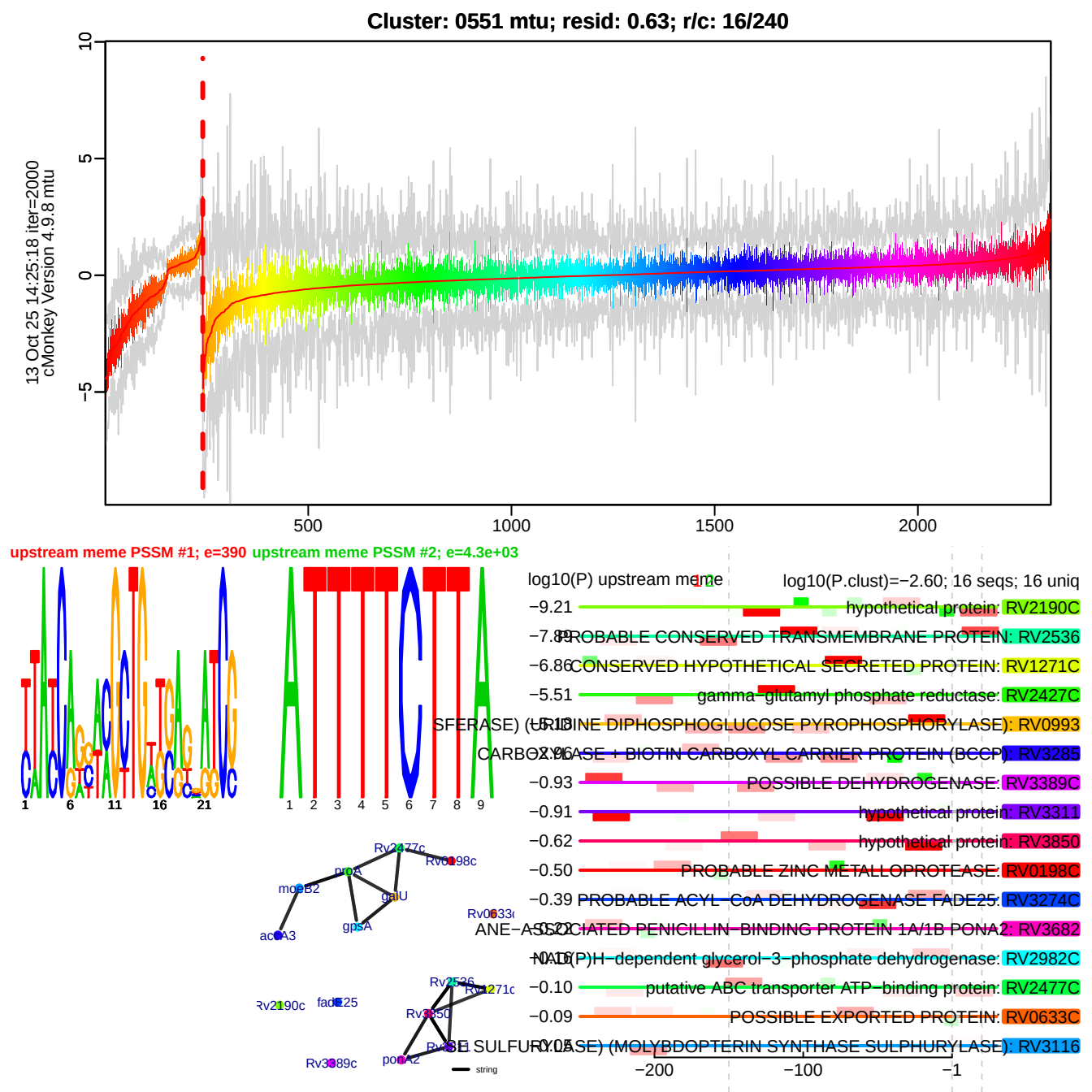
Cluster: 0551 mtu; resid: 0.63; r/c: 16/240
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu
upstream meme PSSM #1; e=390
upstream meme PSSM #2; e=4.3e+03
log10(P) upstream meme
log10(P.clust)=−2.60; 16 seqs; 16 uniq
−9.21 hypothetical protein: RV2190C
−7.89 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: RV2536
−6.86 CONSERVED HYPOTHETICAL SECRETED PROTEIN: RV1271C
−5.51 gamma−glutamyl phosphate reductase: RV2427C
−5.13 SFERASE) (TRIBINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE): RV0993
−2.96 CARBOXYLASE + BIOTIN CARBOXYL CARRIER PROTEIN (BCCP): RV3285
−0.93 POSSIBLE DEHYDROGENASE: RV3389C
−0.91 hypothetical protein: RV3311
−0.62 hypothetical protein: RV3850
−0.50 PROBABLE ZINC METALLOPROTEASE: RV0198C
−0.39 PROBABLE ACYL−CoA DEHYDROGENASE FADE25: RV3274C
−0.22 ANE−ASSOCIATED PENICILLIN−BINDING PROTEIN 1A/1B PONA2: RV3682
−0.16 (P)H−dependent glycerol−3−phosphate dehydrogenase: RV2982C
−0.10 putative ABC transporter ATP−binding protein: RV2477C
−0.09 POSSIBLE EXPORTED PROTEIN: RV0633C
−0.05 SE SULFURYLASE) (MOLYBDOPTERIN SYNTHASE SULPHURYLASE): RV3116
−200
−100
−1
moeB2
galU
gpsA
acnA3
fadE25
ponA2
string