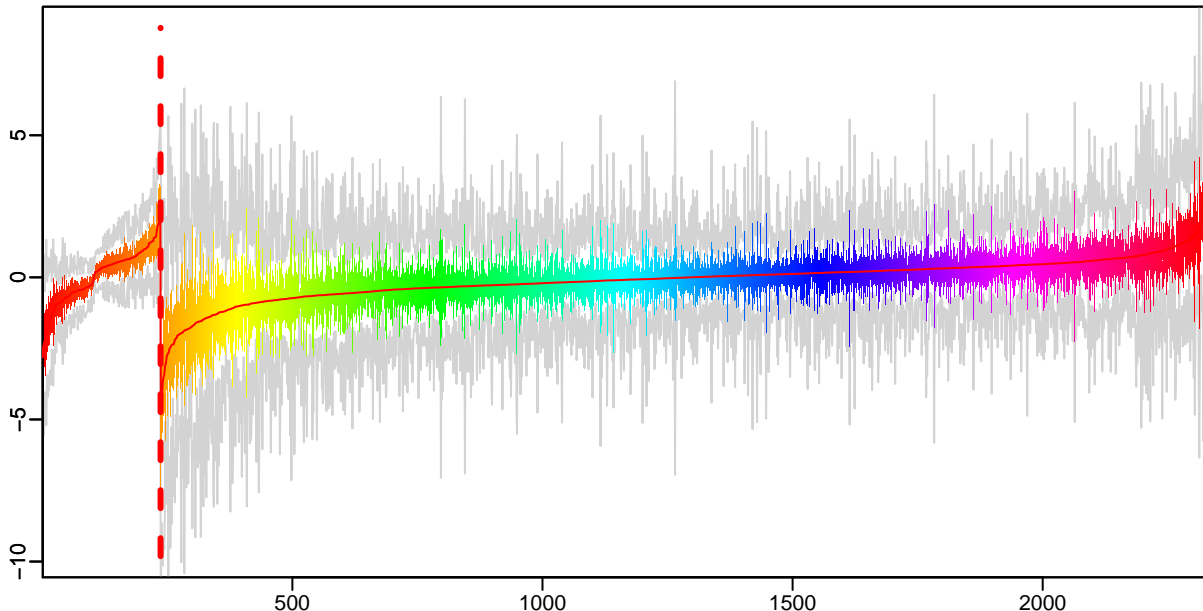
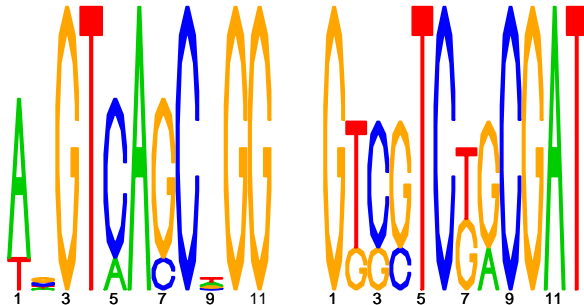


Cluster: 0251 mtu; resid: 0.46; r/c: 8/236

13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu



upstream meme PSSM #1; e=780 upstream meme PSSM #2; e=7.2e+03



log10(P) upstream meme

log10(P.clust)=-3.64; 8 seqs; 7 uniq

-5.61onal GMP synthase/glutamine amidotransferase protein: RV3396C

-5.25PROBABLE SERINE ACETYLTRANSFERASE CYSE (SAT): RV2335

DRYLA2E A (O-ACETYL SERINE (THIOL)-LYASE A) (CSASE A): RV2334

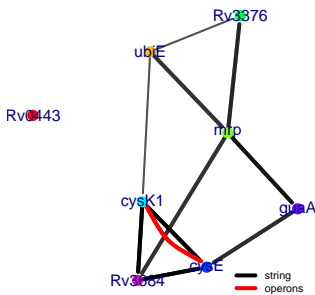
-3.93hypothetical protein: RV3376

-2.75ubiquinone/menaquinone biosynthesis methyltransferase: RV0558

-2.43hypothetical protein: RV0443

-2.42PROBABLE LYASE: RV3684

-1.43PROBABLE MRP-RELATED PROTEIN MRP: RV1229C



-200 -100 -1