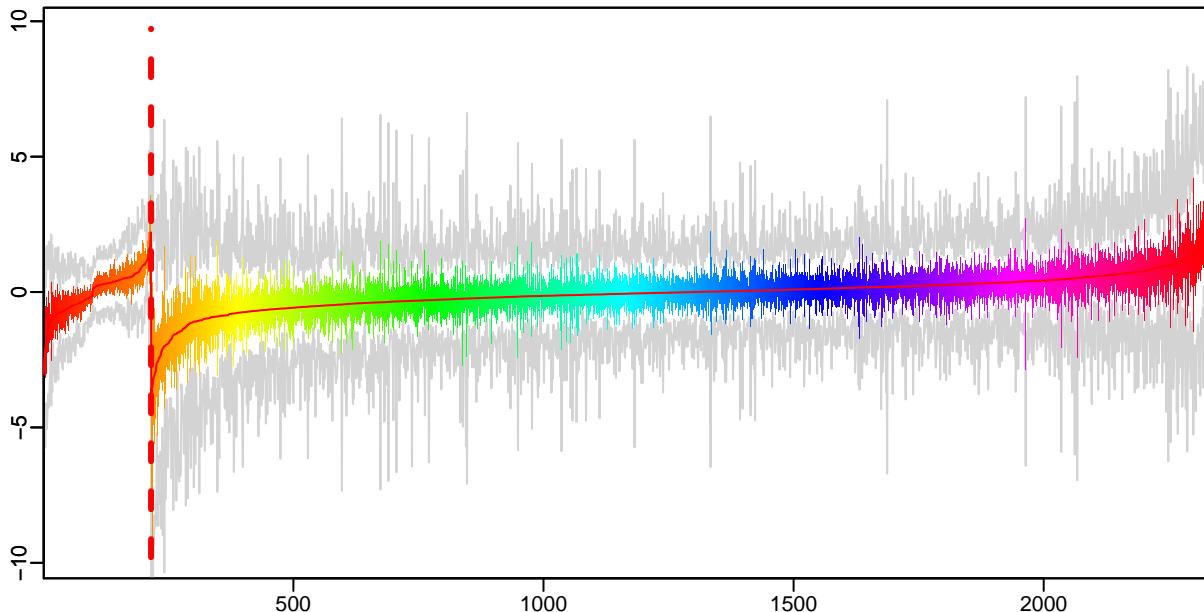
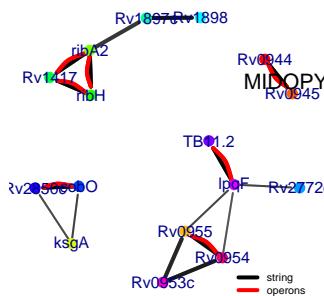
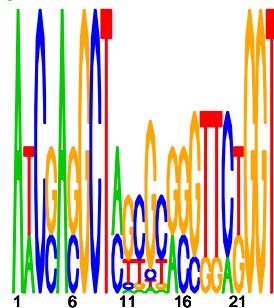
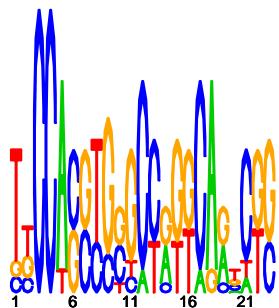


Cluster: 0145 mtu; resid: 0.56; r/c: 16/215

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



upstream meme PSSM #1; e=0.00077 upstream meme PSSM #2; e=0.16



log10(P) upstream meme log10(P.clust)=-6.97; 16 seqs; 10 uniq

- 14.14 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: RV0954
- 14.13 POSSIBLE OXIDOREDUCTASE: RV0953C
- PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN: RV0955
- 12.97 hypothetical protein: RV1898
- 12.97 D-tyrosyl-tRNA deacylase: RV1897C
- 8.00 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: RV2772C
- 4.23 dimethyladenosine transferase: RV1010
- 3.99 PROBABLE CONSERVED LIPOPROTEIN LPQF: RV3593
- 3.99 hypothetical protein: RV3592
- 3.75 short chain dehydrogenase: RV0945
- MIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY)-DNA GLYCOSYLASE: RV0944
- 3.31 POSSIBLE CONSERVED MEMBRANE PROTEIN: RV1417
- 3.31 riboflavin synthase subunit beta: RV1416
- 3.31 ne 4-phosphate synthase/GTP cyclohydrolase II protein: RV1415
- 2.76 POSSIBLE MAGNESIUM CHELATASE: RV2850C
- 2.76 cob(II)yrinic acid a,c-diamide adenosyltransferase: RV2849C