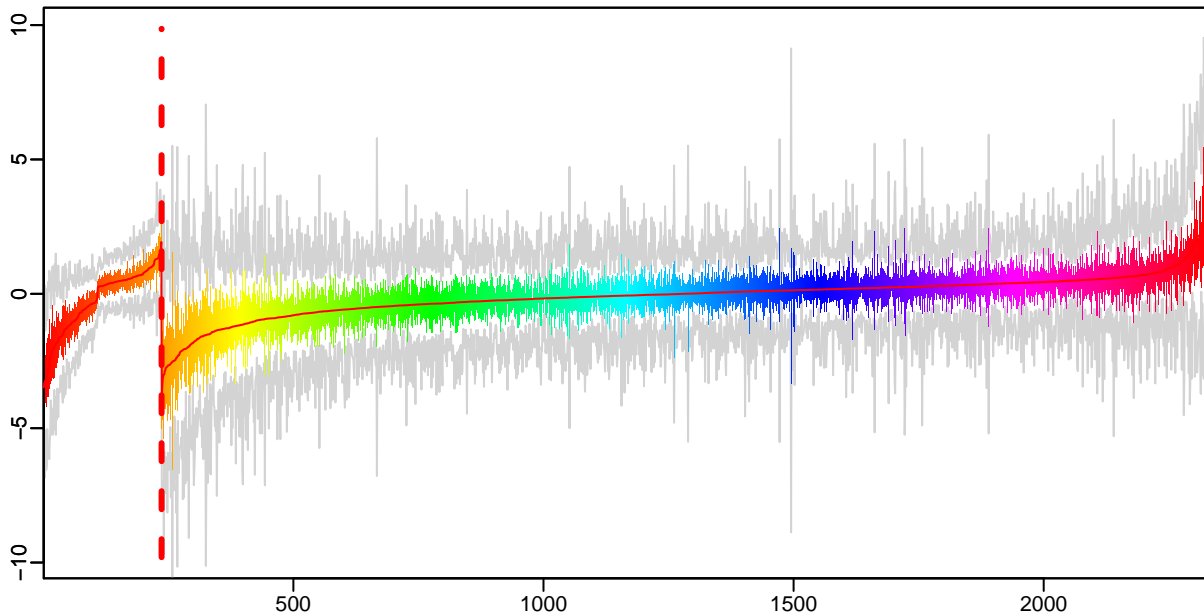
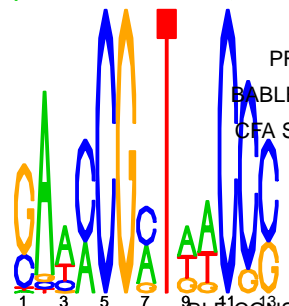
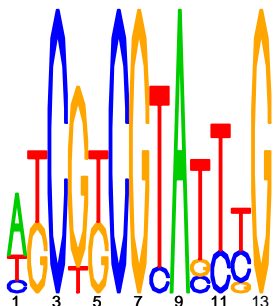


Cluster: 0287 mtu; resid: 0.56; r/c: 16/236

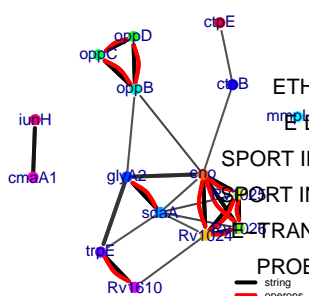
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu



upstream meme PSSM #1; e=0.0046 upstream meme PSSM #2; e=4.3



- log10(P) upstream meme log10(P.clust)=-5.11; 16 seqs; 9 uniq
- PROBABLE CATION-TRANSPORTER P-TYPE ATPASE B CTPB: RV0103C
 - PROBABLE NUCLEOSIDE HYDROLASE I/INH (PURINE NUCLEOSIDASE): RV3393C
 - CFA SYNTHETASE (CYCLOPROPANE MYCOLIC ACID SYNTHASE 1): RV3392C
 - 5.85 hypothetical protein: RV1026
 - 5.85 hypothetical protein: RV1025
 - 5.85 POSSIBLE CONSERVED MEMBRANE PROTEIN: RV1024
 - 5.85 phosphopyruvate hydratase: RV1023
 - 5.41 POSSIBLE CONSERVED MEMBRANE PROTEIN: RV1610
 - 5.41 anthranilate synthase component I: RV1609
 - ETHYLTRANSFERASE GLY2 (SERINE METHYLASE 2) (SHMT 2): RV0070C
 - ALDEHYDE DEHYDRATASE SDAA (L-SERINE DEAMINASE) (SDH) (L-SD): RV0069C
 - SPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER OPPB: RV1283C
 - SPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER OPPC: RV1282C
 - TRANSPORTER 3 ATP-BINDING PROTEIN ABC TRANSPORTER OPPD: RV1281C
 - PROBABLE METAL CATION TRANSPORTER ATPASE P-TYPE CTPB: RV0908



— string
— operons

-200 -100 -1