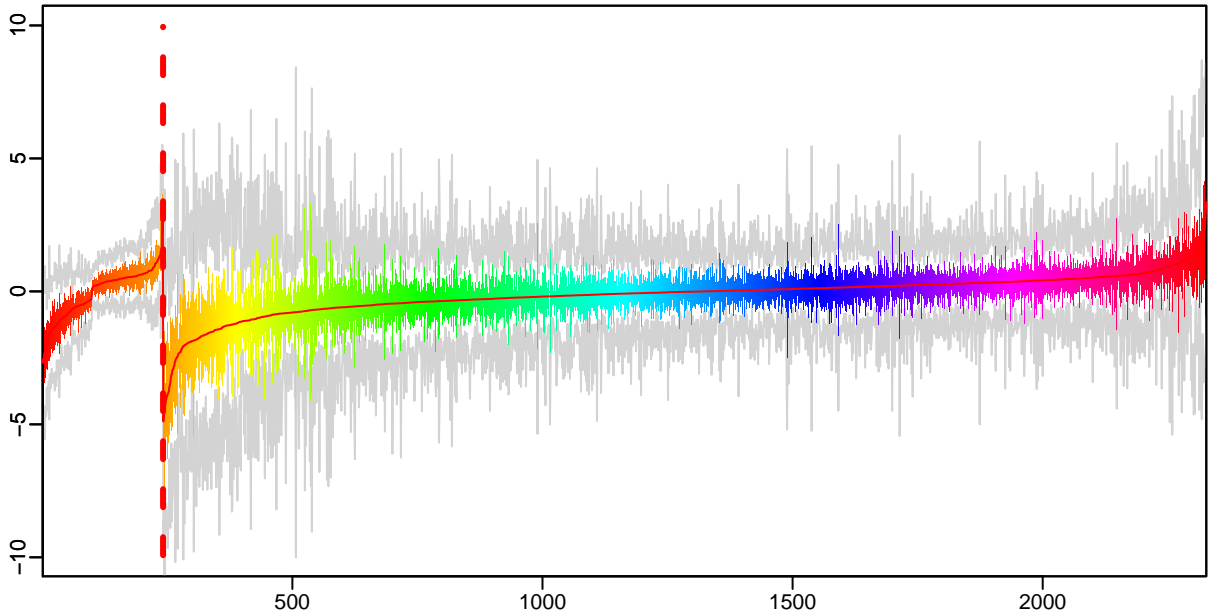
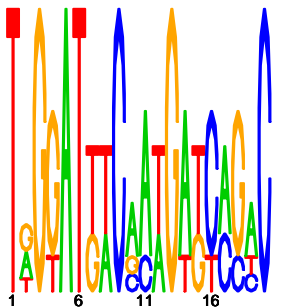


Cluster: 0480 mtu; resid: 0.52; r/c: 16/241

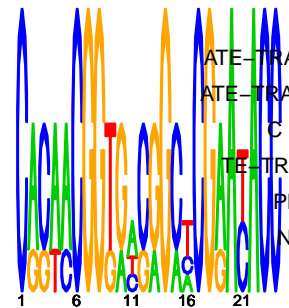
13 Oct 25 14:25:18 iter=2000  
cMonkey Version 4.9.8 mtu



upstream meme PSSM #1; e=0.3



upstream meme PSSM #2; e=53



log10(P) upstream meme

log10(P.clust)=-9.78; 16 seqs; 11 uniq

ATE-TRANSPORT INTEGRAL MEMBRANE ABC TRANSPORTER PSTA2: RV0936

ATE-TRANSPORT INTEGRAL MEMBRANE ABC TRANSPORTER PSTC1: RV0935

C PHOSPHATE-BINDING LIPOPROTEIN PSTS1 (PBP-1) (PSTS1): RV0934

TE-TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER PSTB: RV0933

PHOSPHATE-BINDING LIPOPROTEIN PSTS2 (PBP-2) (PSTS2): RV0932C

NE-PROTEIN KINASE D PKND (PROTEIN KINASE D) (STPK-D): RV0931C

-7.06 ————— hypothetical protein: RV1558

-6.26 ————— threonine dehydratase: RV1559

-5.30 ————— MOLECULAR WEIGHT PROTEIN ANTIGEN 6 (CFP-6): RV3004

-5.17 ————— POSSIBLE THIOREDOXIN: RV1324

ABLE ARSENIC TRANSPORT INTEGRAL MEMBRANE PROTEIN ARSB1: RV2685

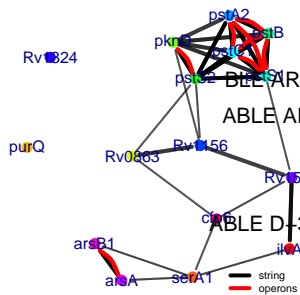
ABLE ARSENIC TRANSPORT INTEGRAL MEMBRANE PROTEIN ARSA: RV2684

-0.66 ————— hypothetical protein: RV0863

-0.37 ————— hypothetical protein: RV1156

ABLE D-3-PHOSPHOGLYCERATE DEHYDROGENASE SERA1 (PGDH): RV2996C

-0.10 ————— phosphoribosylformylglycinamide synthase subunit I: RV0788



-200 -100 -1