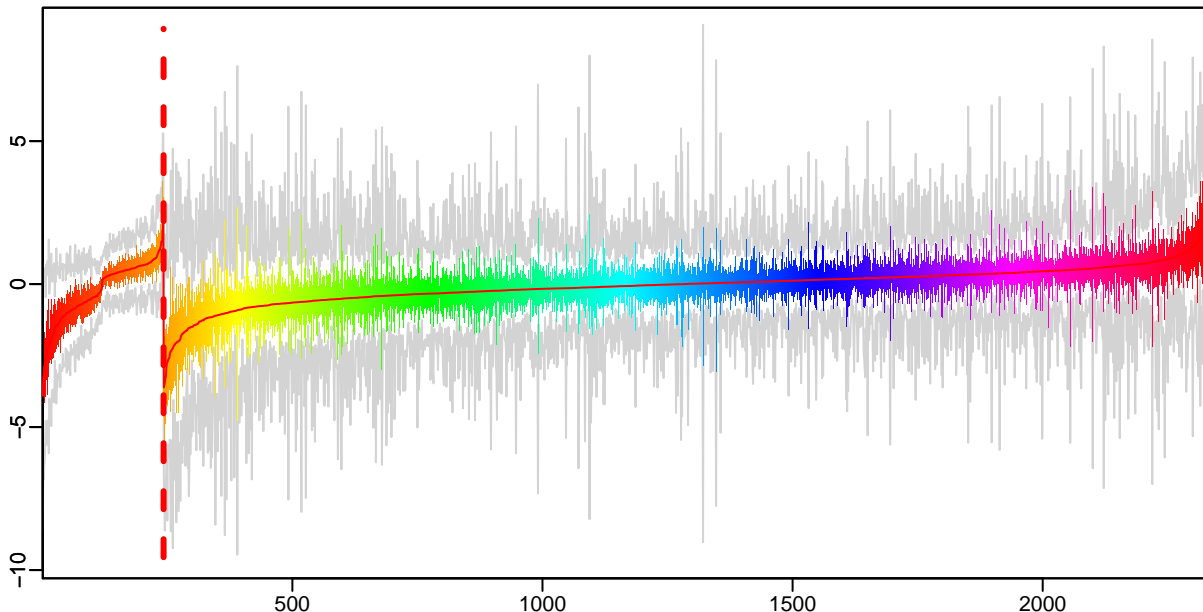
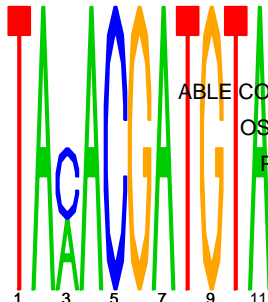
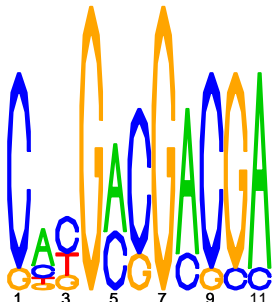


Cluster: 0456 mtu; resid: 0.56; r/c: 16/242

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

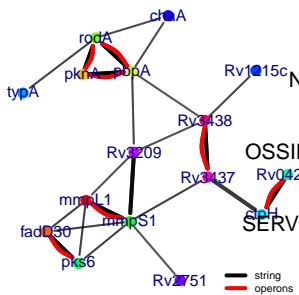


upstream meme PSSM #1; e=190 upstream meme PSSM #2; e=9.4e+03



log10(P) upstream meme log10(P.clust)=-3.02; 16 seqs; 10 uniq

- PROBABLE CONSERVED MEMBRANE PROTEIN MMPS1: RV0403C
- PROBABLE CONSERVED TRANSMEMBRANE TRANSPORT PROTEIN MMPL1: RV0402C
- PROBABLE CONSERVED PHOSPHORYLATED PROTEIN (GTP-BINDING PROTEIN): RV1165
- PROBABLE MEMBRANE BOUND POLYKETIDE SYNTHASE PKS6: RV0405
- 5.13 acyl-CoA synthetase: RV0404
- 2.73 hypothetical protein: RV3438
- 2.73 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: RV3437
- 2.29 hypothetical protein: RV2751
- 2.18 PROBABLE CELL DIVISION PROTEIN RODA: RV0017C
- 2.18 PROBABLE PENICILLIN-BINDING PROTEIN PBPA: RV0016C
- PROBABLE PROTEIN KINASE A PKNA (PROTEIN KINASE A) (STPK A): RV0015C
- 2.11 hypothetical protein: RV1215C
- PROBABLE METAL CATION TRANSPORTING P-TYPE ATPASE CTPH: RV0425C
- 1.70 hypothetical protein: RV0424C
- PROBABLE CONSERVED HYPOTHETICAL THREONIN AND PROLINE RICH PROTEIN: RV3209
- 1.29 probable ionic transporter integral membrane protein chaA: RV1807



-200 -100 -1