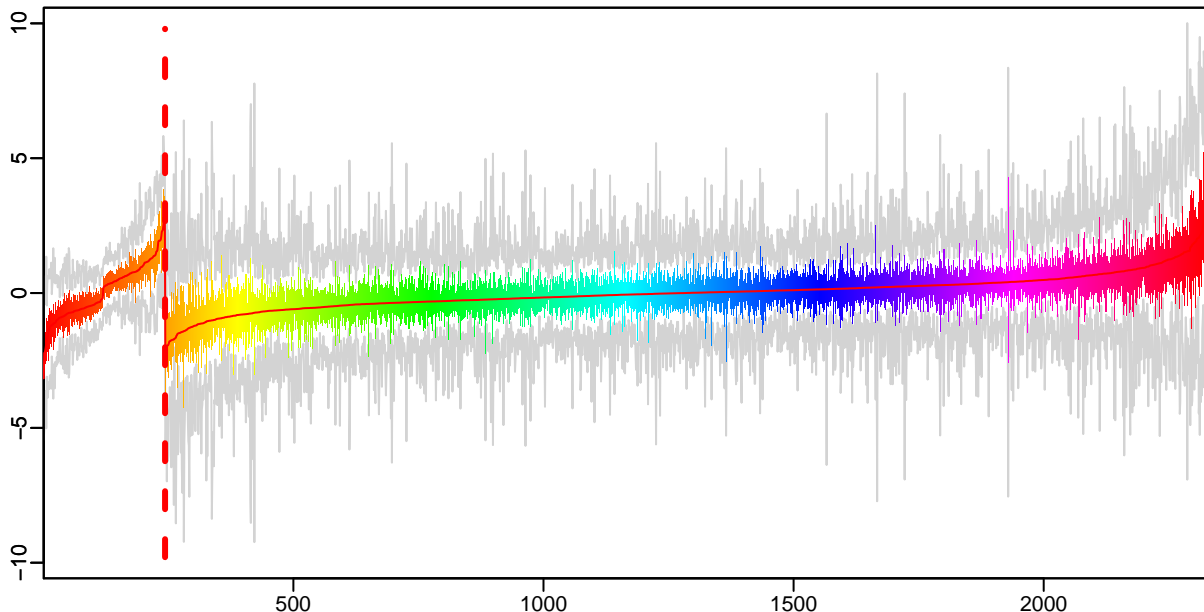


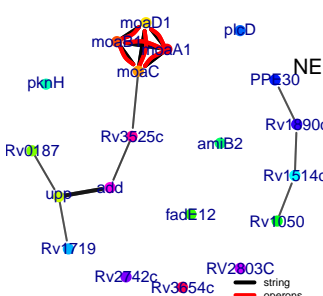
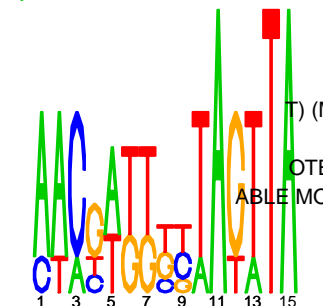
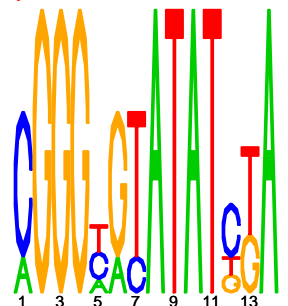
Cluster: 0535 mtu; resid: 0.57; r/c: 20/243

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



upstream meme PSSM #1; e=11

upstream meme PSSM #2; e=3e+03



- log10(P) upstream meme log10(P.clust)=-3.35; 20 seqs; 16 uniq
- 9.77 POSSIBLE SIDEROPHORE-BINDING PROTEIN: RV3525C
 - 7.08 uracil phosphoribosyltransferase: RV3309C
 - 5.71 molybdenum cofactor biosynthesis protein C: RV3111C
 - 4.00 MOLYBDENUM COFACTOR CONVERTING FACTOR, SUBUNIT 1: RV3112C
 - 3.95 OSTEIN5(PHS) (PTERIN CARBINOLAMINE DEHYDRATASE) (PCD): RV3110C
 - 3.95 PROBABLE MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN A MOA: RV3109C
 - 3.95 CONSERVED HYPOTHETICAL ARGININE RICH PROTEIN: RV2742C
 - 3.95 PROBABLE O-METHYLTRANSFERASE: RV0187
 - 3.76 hypothetical protein: RV3654C
 - 3.66 PROBABLE OXIDOREDUCTASE: RV1050
 - 2.52 adenosine deaminase: RV3313C
 - 1.18 amidase: RV1263
 - 0.32 NE-PROTEIN KINASE H PKNH (PROTEIN KINASE H) (STPK H): RV1266C
 - 0.32 hypothetical protein: RV1514C
 - 0.18 PPE FAMILY PROTEIN: RV1802C
 - 0.04 PROBABLE ACYL-CoA DEHYDROGENASE FAD12: RV0972C
 - 0.01 hypothetical protein: RV1890C
 - 0.00 PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN: RV1719
 - NA
 - NA PROBABLE PHOSPHOLIPASE C 4 (FRAGMENT) PLCD: RV1755C