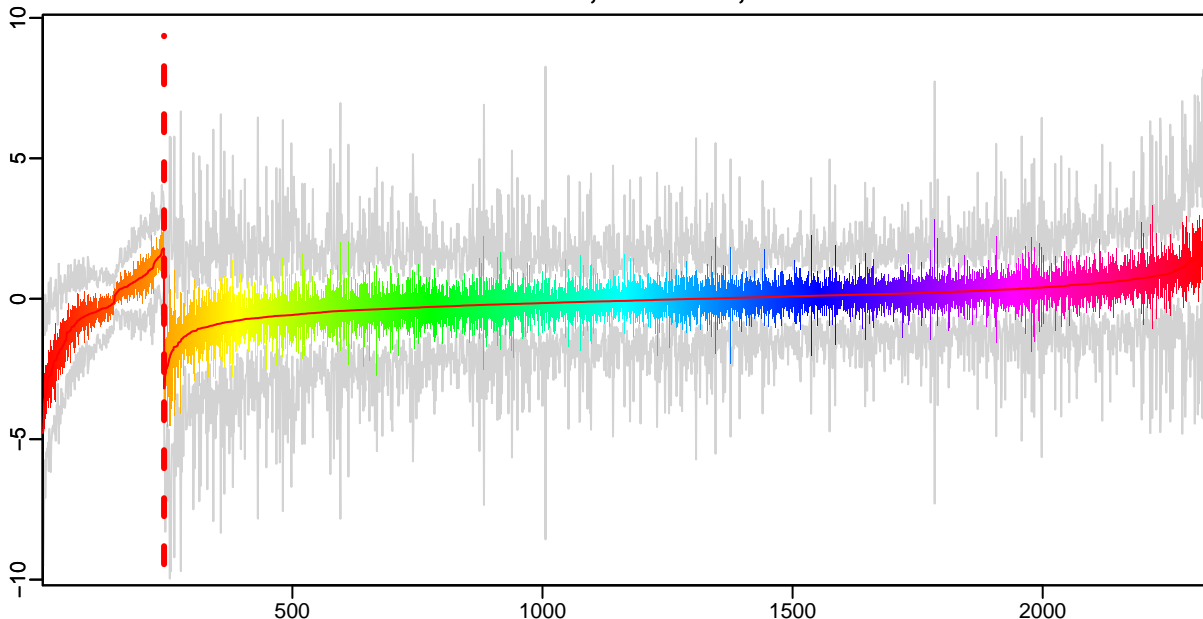
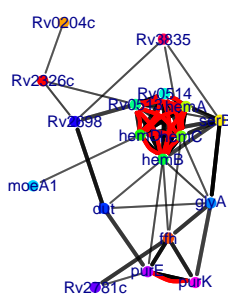
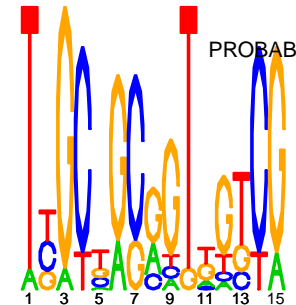
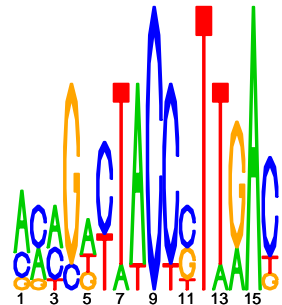


Cluster: 0581 mtu; resid: 0.61; r/c: 19/243

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



upstream meme PSSM #1; e=0.0065 upstream meme PSSM #2; e=120



- log10(P) upstream meme log10(P.clust)=-4.61; 19 seqs; 13 uniq
- PROBABLE CONSERVED ALANINE RICH TRANSMEMBRANE PROTEIN: RV2698
 - 7.96 deoxyuridine 5'-triphosphate nucleotidylase: RV2697C
 - 5.75 POSSIBLE TRANSMEMBRANE PROTEIN: RV0514
 - 5.75 POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN: RV0513
 - 5.75 delta-aminolevulinic acid dehydratase: RV0512
 - N III METHYLASE) (SUMT) (UROGEN III METHYLASE) (UROM): RV0511
 - 5.75 porphobilinogen deaminase: RV0510
 - 5.75 glutamyl-tRNA reductase: RV0509
 - 5.47 PROBABLE CONSERVED MEMBRANE PROTEIN: RV3835
 - B1 (PSP) (PHOSPHOSERINE PHOSPHOHYDROLASE) (PSPASE): RV0505C
 - 4.71 serine hydroxymethyltransferase: RV1093
 - TICLE PROTEIN FFH (FIFTY-FOUR HOMOLOG) (SPP PROTEIN): RV2916C
 - 3.46 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: RV0204C
 - BLE TRANSMEMBRANE ATP-BINDING PROTEIN ABC TRANSPORTER: RV2326C
 - sigJ -2.92 RNA polymerase sigma factor SigJ: RV3328C
 - 2.81 POSSIBLE ALANINE RICH OXIDOREDUCTASE: RV2781C
 - PROBABLE MOLYBDOPTERIN BIOSYNTHESIS PROTEIN MOEA 1: RV0994
 - 1.64 phorbosylaminoimidazole carboxylase ATPase subunit: RV3276C
 - 1.64 oribosylaminoimidazole carboxylase catalytic subunit: RV3275C
- 200 -100 -1