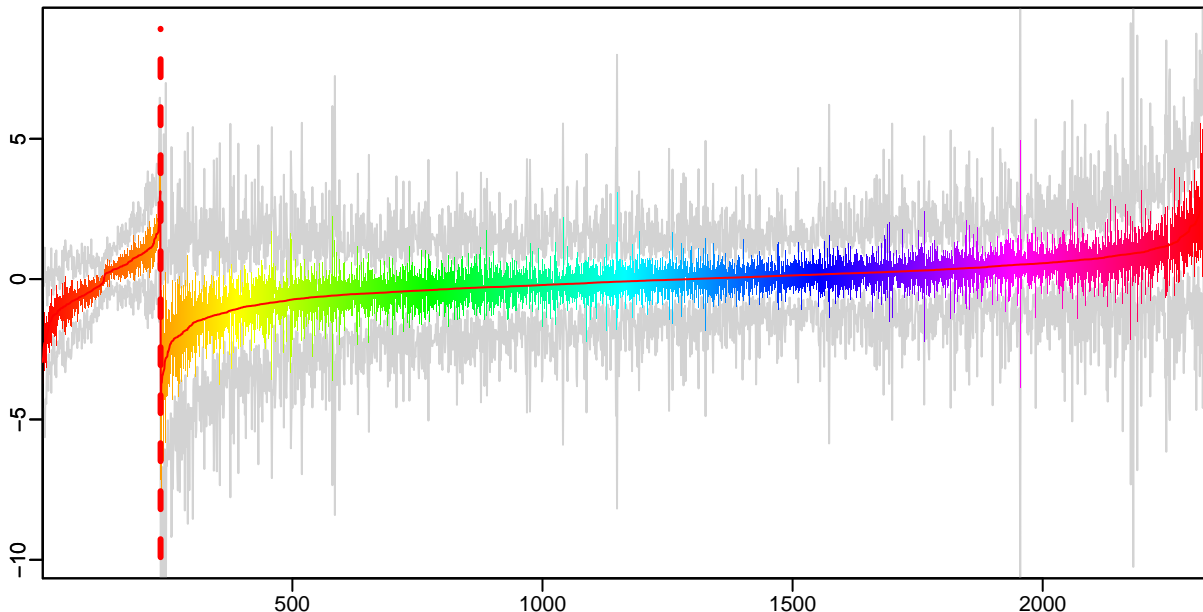
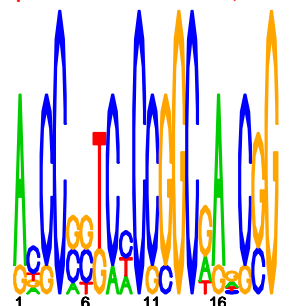


Cluster: 0533 mtu; resid: 0.51; r/c: 9/236

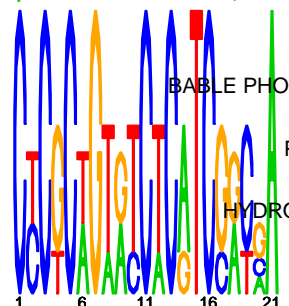
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu



upstream meme PSSM #1; e=12



upstream meme PSSM #2; e=60



log10(P) upstream meme log10(P.clust)=-9.92; 9 seqs; 7 uniq

PROBABLE PHOSPHOMANNOMUTASE PMMB (PHOSPHOMANNOSE MUTASE): RV3308

PROBABLE AMIDOHYDROLASE AMIB1 (AMINOHYDROLASE): RV3306C

HYDROLASE OSMIA1 (N-ACYL-L-AMINO ACID AMINOHYDROLASE): RV3305C

-15.05 purine nucleoside phosphorylase: RV3307

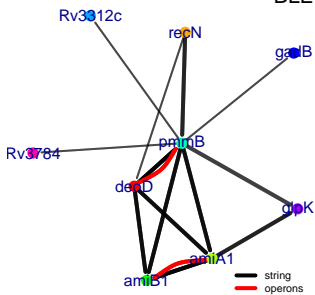
BLE DNA REPAIR PROTEIN REC N (RECOMBINATION PROTEIN N): RV1696

-8.00 POSSIBLE dTDP-GLUCOSE 4,6-DEHYDRATASE: RV3784

-4.14 PROBABLE GLUTAMATE DECARBOXYLASE GADB: RV3432C

-3.79 glycerol kinase: RV3696C

-3.24 hypothetical protein: RV3312C



-200 -100 -1