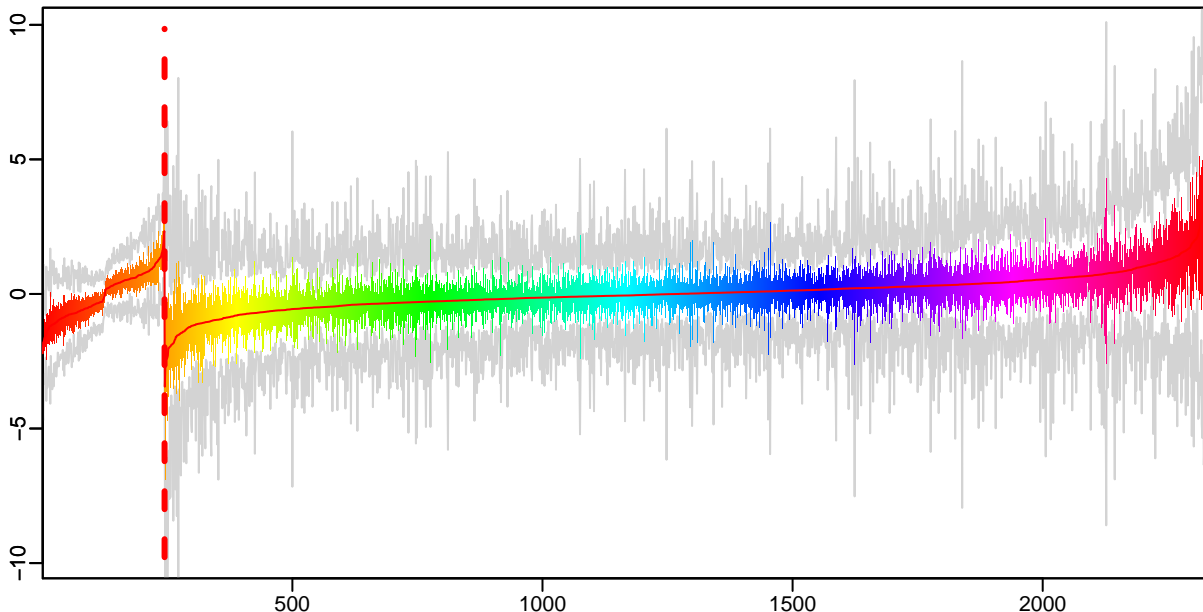


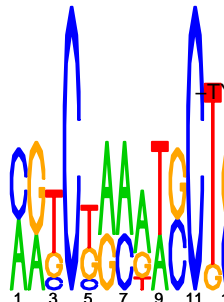
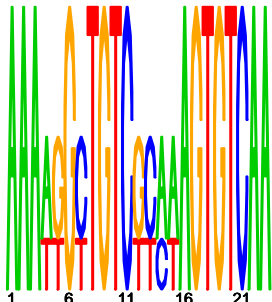
Cluster: 0245 mtu; resid: 0.51; r/c: 16/244

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



upstream meme PSSM #1; e=0.15

upstream meme PSSM #2; e=240



log10(P) upstream meme log10(P.clust)=-8.14; 16 seqs; 9 uniq

NG TRANSCRIPTIONAL REGULATOR VIRS (ARAG/XYLS FAMILY): RV3082C

TYPE ALCOHOL DEHYDROGENASE ADHD (ALDEHYDE REDUCTASE): RV3086

PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE: RV3085

-15.13 PROBABLE ACETYL-HYDROLASE/ESTERASE LIPR: RV3084

-15.13 PROBABLE MONOOXYGENASE (HYDROXYLASE): RV3083

-11.00 POSSIBLE OXIDOREDUCTASE: RV3742C

-11.00 POSSIBLE OXIDOREDUCTASE: RV3741C

-11.00 hypothetical protein: RV3740C

OXIDOREDUCTASE BISC (BDS reductase) (BSO reductase): RV1442

TY-ACID COA LIGASE FADD13 (FATTY-ACYL-CoA SYNTHETASE): RV3089

-2.99 hypothetical protein: RV3088

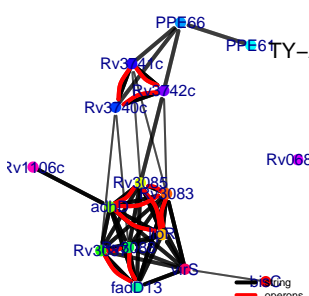
-2.99 hypothetical protein: RV3087

Rv0889c: -2.85 PPE FAMILY PROTEIN: RV3532

-2.40 hypothetical protein: RV0689C

-1.96 PROBABLE CHOLESTEROL DEHYDROGENASE: RV1106C

-0.34 PPE FAMILY PROTEIN: RV3738C



-200 -100 -1