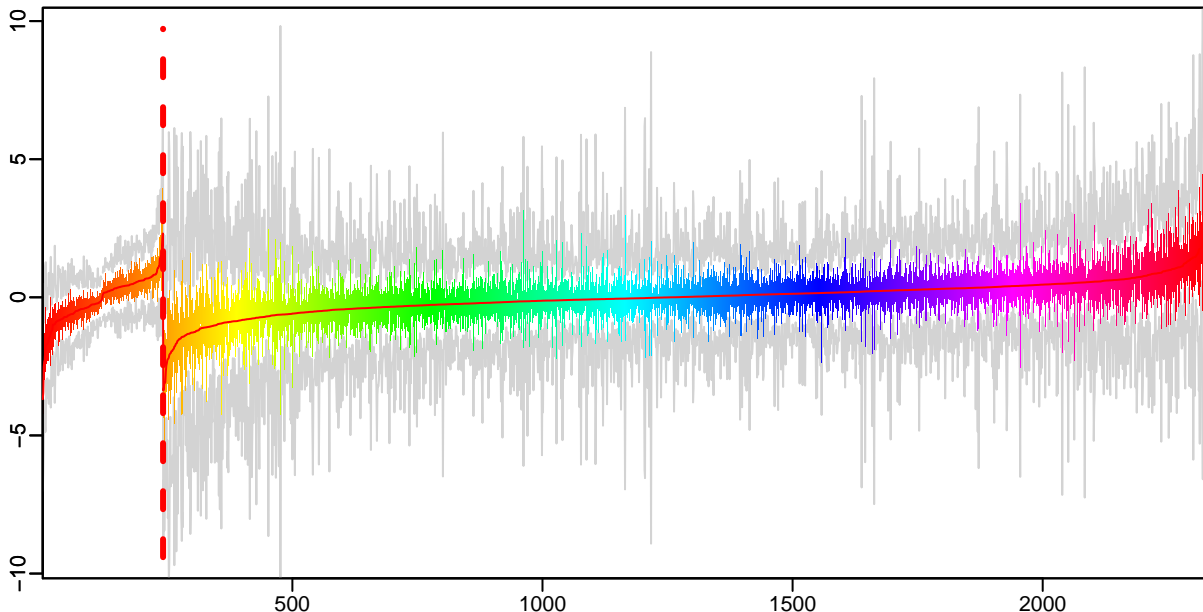


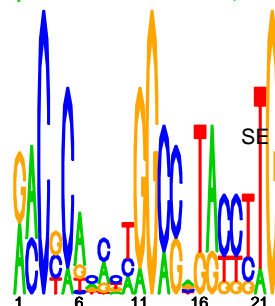
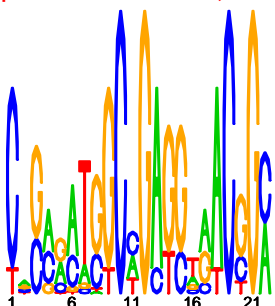
Cluster: 0102 mtu; resid: 0.50; r/c: 10/241

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



upstream meme PSSM #1; e=0.26

upstream meme PSSM #2; e=81



log10(P) upstream meme log10(P.clust)=-8.05; 10 seqs; 9 uniq

-10.10 probable two-component system transcriptional regulator: RV1626

SE CYA (ATP PYROPHOSPHATE LYASE), (ADENYLATE CYCLASE): RV1625C

-10.10 Probable conserved membrane protein: RV1624C

-8.54 hypothetical protein: RV2740

-8.54 POSSIBLE ALANINE RICH TRANSFERASE: RV2739C

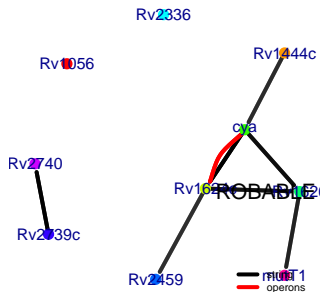
-7.97 hypothetical protein: RV1056

-7.64 POSSIBLE HYDROLASE MUTT1: RV2985

-7.62 hypothetical protein: RV2336

PROBABLE CONSERVED INTEGRAL MEMBRANE TRANSPORT PROTEIN: RV2459

-2.89 hypothetical protein: RV1444C



-200 -100 -1