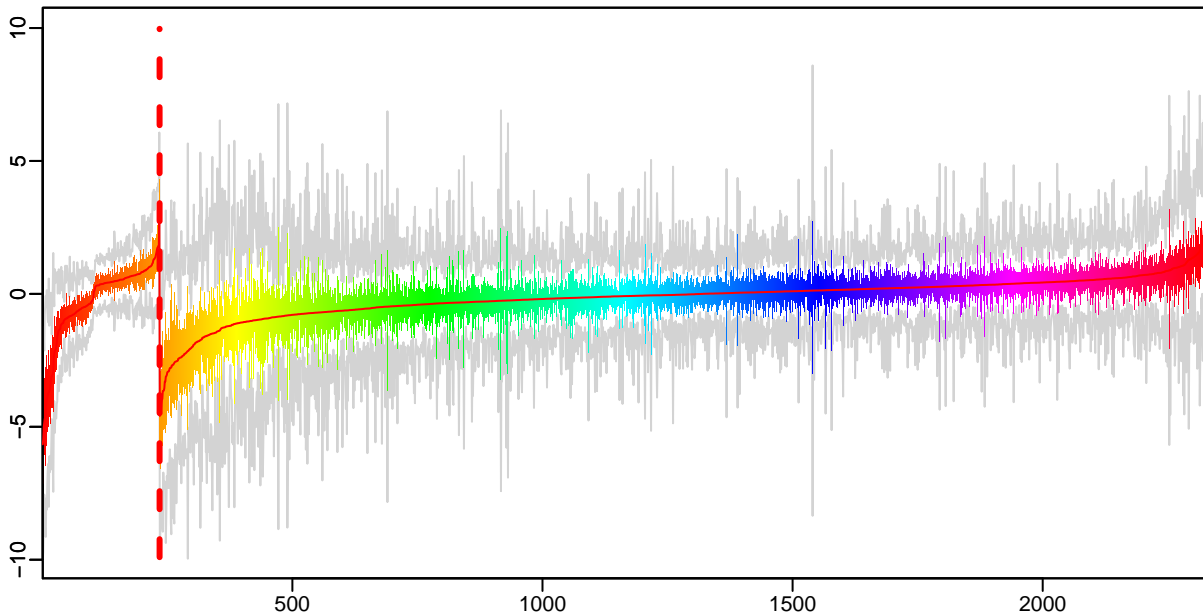
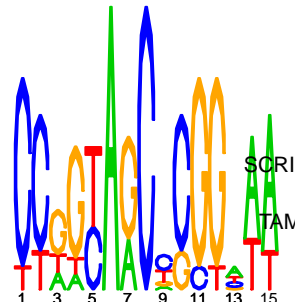
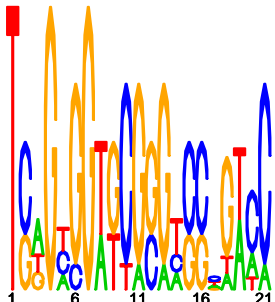


Cluster: 0030 mtu; resid: 0.60; r/c: 20/234

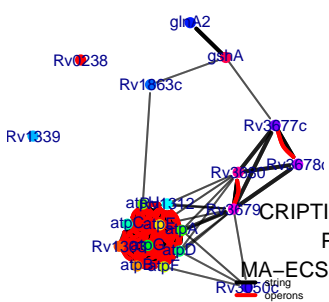
13 Oct 25 14:25:18 iter=2000  
cMonkey Version 4.9.8 mtu



upstream meme PSSM #1; e=0.052 upstream meme PSSM #2; e=0.81



- log10(P) upstream meme      log10(P.clust)=-6.63; 20 seqs; 9 uniq
- 10.56 PROBABLE ANION TRANSPORTER ATPASE: RV3680
  - 10.56 PROBABLE ANION TRANSPORTER ATPASE: RV3679
  - 10.56 hypothetical protein: RV3678C
  - 10.56 POSSIBLE HYDROLASE: RV3677C
  - SCRIPTONAL REGULATORY PROTEIN (PROBABLY TETR-FAMILY): RV0238
  - 6.70 hypothetical protein: RV1339
  - TAMINES SYNTHETASE GLNA2 (GLUTAMINE SYNTHASE) (GS-II): RV2222C
  - 5.84 CONSERVED HYPOTHETICAL SECRETED PROTEIN: RV1312
  - 5.84 F0F1 ATP synthase subunit epsilon: RV1311
  - 5.84 F0F1 ATP synthase subunit beta: RV1310
  - 5.84 F0F1 ATP synthase subunit gamma: RV1309
  - 5.84 F0F1 ATP synthase subunit alpha: RV1308
  - 5.84 PROBABLE ATP SYNTHASE DELTA CHAIN ATPH: RV1307
  - 5.84 F0F1 ATP synthase subunit B: RV1306
  - 5.84 F0F1 ATP synthase subunit C: RV1305
  - 5.84 F0F1 ATP synthase subunit A: RV1304
  - 5.84 hypothetical protein: RV1303



- SCRIPTONAL REGULATORY PROTEIN (PROBABLY ASNC-FAMILY): RV3050C
- PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN: RV1863C
- MA-ECS) (378) (GAMMA-GLUTAMYL-L-CYSTEINE SYNTHETASE): RV3704C

-200      -100      -1