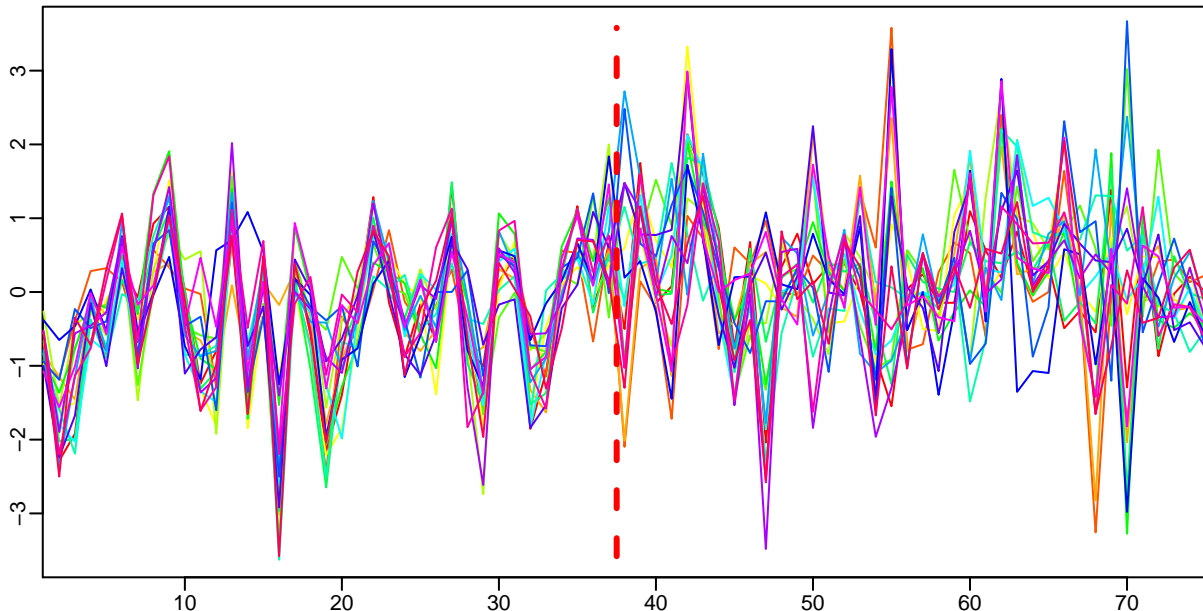


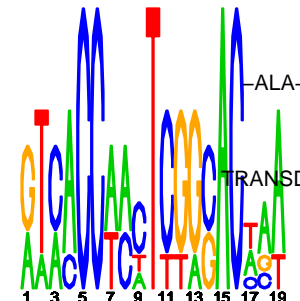
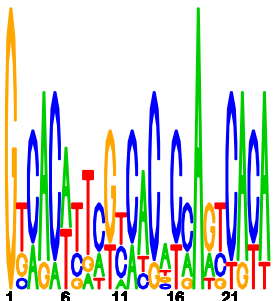
Cluster: 0090 mtu; resid: 0.35; r/c: 18/37

11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu

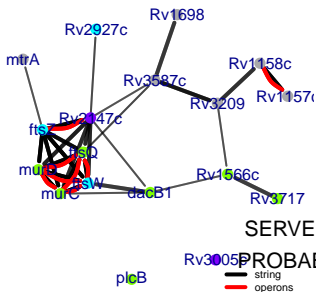


upstream meme PSSM #1; e=1.4

upstream meme PSSM #2; e=530



- log10(P) upstream meme
- log10(P.clust)=-4.45; 18 seqs; 13 uniq
- 12.08 Possible inv protein: Rv1566c
 - 9.49 ALA-D-ALA CARBOXYPEPTIDASE (D-AMINO ACID HYDROLASE): Rv3330
 - 6.43 hypothetical protein: Rv3005c
 - 6.43 hypothetical protein: Rv1698
 - TRANSDUCTION TRANSCRIPTIONAL REGULATORY PROTEIN, MTR: Rv3246c
 - 5.06 hypothetical protein: Rv2927c
 - 4.88 cell division protein FtsZ: Rv2150c
 - 4.88 hypothetical protein: Rv2147c
 - 4.88 hypothetical protein: Rv3717
 - CONSERVED HYPOTHETICAL ALA-, PRO-RICH PROTEIN: Rv1157c
 - CONSERVED HYPOTHETICAL ALA-, PRO-RICH PROTEIN: Rv1158c
 - 1.13 POSSIBLE CELL DIVISION PROTEIN FTSQ: Rv2151c
 - 1.13 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase: Rv2155c
 - 1.13 FtsW-like protein FtsW: Rv2154c
 - 1.13 UDP-N-acetylmuramate-L-alanine ligase: Rv2152c
 - 0.76 PROBABLE CONSERVED MEMBRANE PROTEIN: Rv3587c
 - SERVED HYPOTHETICAL THREONIN AND PROLINE RICH PROTEIN: Rv3209
 - PROBABLE MEMBRANE-ASSOCIATED PHOSPHOLIPASE C-2 PLCB: Rv2350c



-200 -100 -1