Supplementary material to E. Paquet, G. Rey, and F. Naef (PLoS Computational Biology).

Fig. S2

converged model ($p_1=2^{-11}$, $p_2=2^{-4}$)
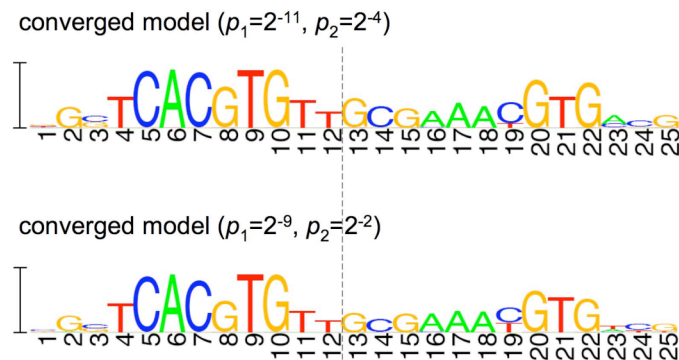

converged model ($p_1=2^{-9}$, $p_2=2^{-2}$)

Figure S2. Models obtained with different transitions probabilities p_1 and p_2.
Top: model from Fig. 2A ($p_1=2^{-11}$, $p_2=2^{-4}$). The converged model uses approximately 15 high scoring instances of the E1 box and 6 for the E2 box in the training sequences (Methods). Bottom: ($p_1=2^{-9}$, $p_2=2^{-2}$), here the converged model uses 24 high scoring instances of E1 box and 10 for the E2 box. Both models are given at http://circaclock.epfl.ch/Models. Dashed line indicates the separation between E1 and E2.