Figure S1: The distribution of promoter elements among the master list genes based on the ChIP-seq data of TFs (E-box: CLOCK, BMAL1, NPAS2; D-box: E4BP4; RRE: REV-ERBα, β, RORα).

Figure S2: The distribution of total scores for each gene in the 1000 gene-long master list (in green) compared against the empirical distribution of total scores based on the randomized shuffling procedure described in the Method section.