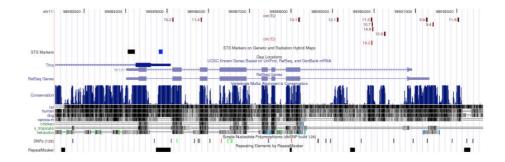
Supplementary material to E. Paquet, G. Rey, and F. Naef (PLoS Computational Biology).

Fig. S7A

Rev-erblpha



1^{rst} intron

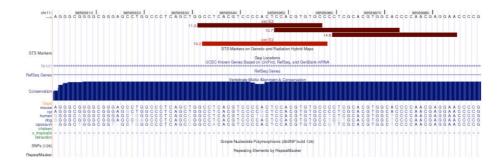
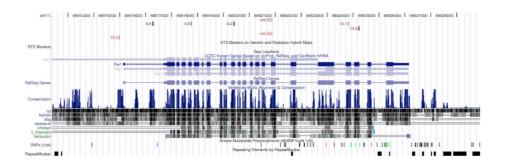


Fig. S7B

Per1

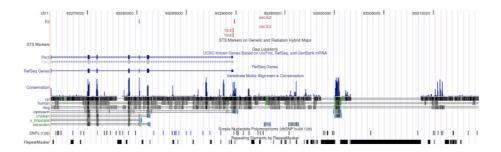


promoter



Fig. S7C





promoter

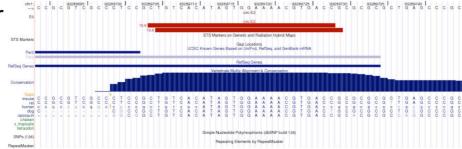
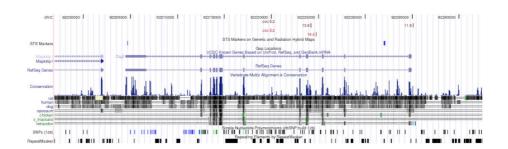


Fig. S7D

Cry2

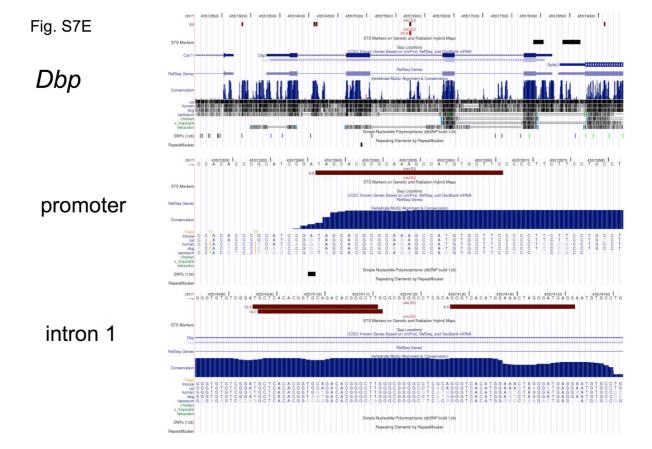


promoter



intron 3





Dbp intron 2

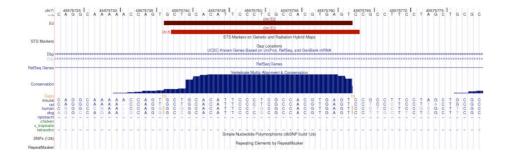
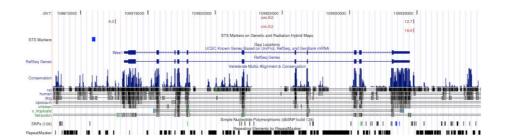
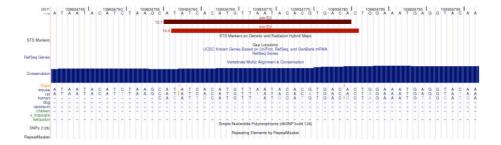


Fig. S7F



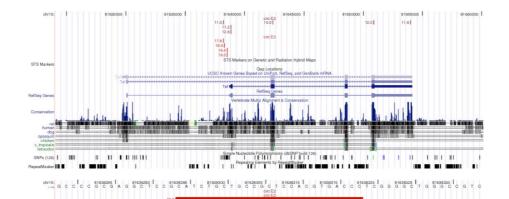


3' end





Tef



promoter

Fig. Seq. Garces

Weredouse Multip Alignment & Conservation

Weredouse Alignment & Conservation

Weredouse Alignment & Conservation

Weredouse Alignment & Conservation

Weredouse Alignment & Conser

promoter



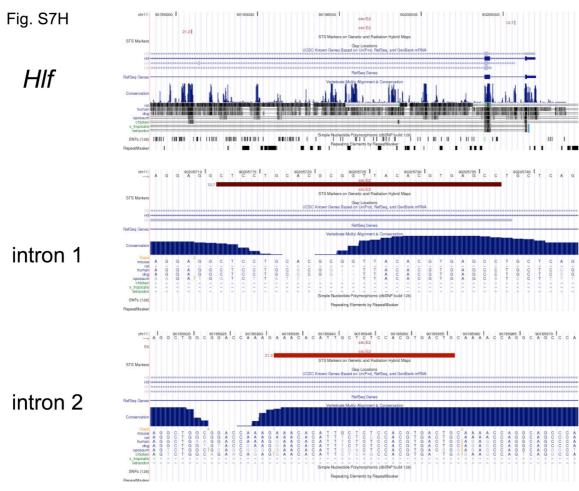
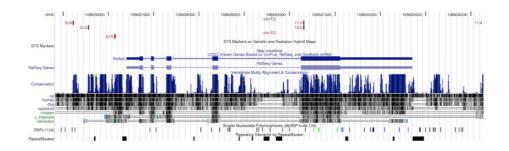


Fig. S7I

Bhlhb2



promoter

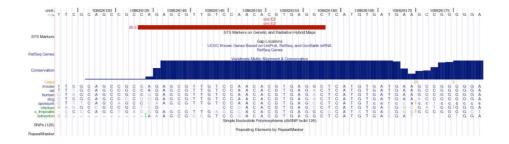


Figure S7. Position of E1-E2 enhancers in circadian mouse genes.

Plots are from the UCSC genome browser with our hit file (available as mouse-scan_conserved.bed) uploaded as a custom track. Hits with score between 9-15 bits are shown in dark red and hits above 15 bits in bright red. For each gene we show a large-scale overview and zoomed views that emphasize the conservation profiles. Since the E1-E2 sequence is nearly palindromic, we often find hits that are doubled but offset by one base (e.g. the Per2 gene, panel C). Alignments are from the UCSC mm8 genome version.