**Figure S1**: Quantification of Bmal1 protein levels in TRE-Rev-erbα/LAP-tTA transgenic mice. Upper panel: RT-TaqMan qPCR was performed for Bmal1 mRNA employing the cDNAs used for the data presented in figure 2. Integration of the qPCR signals revealed a decrease of four fold for Bmal1 mRNA in mice overexpressing HA-REV-ERBα.

Lower panel: densitometry analysis of the Western signals shown in Figure 1C. Since the BMAL1 protein does not show a significant circadian variation in abundance, all 6 time points of the –Dox (left) and +Dox (right) have been averaged and the standard deviation is represented by the error bar. This analysis suggests that BMAL1 protein expression is downregulated about 12 fold by HA-REV-ERBα overexpression.