Supplementary Figures

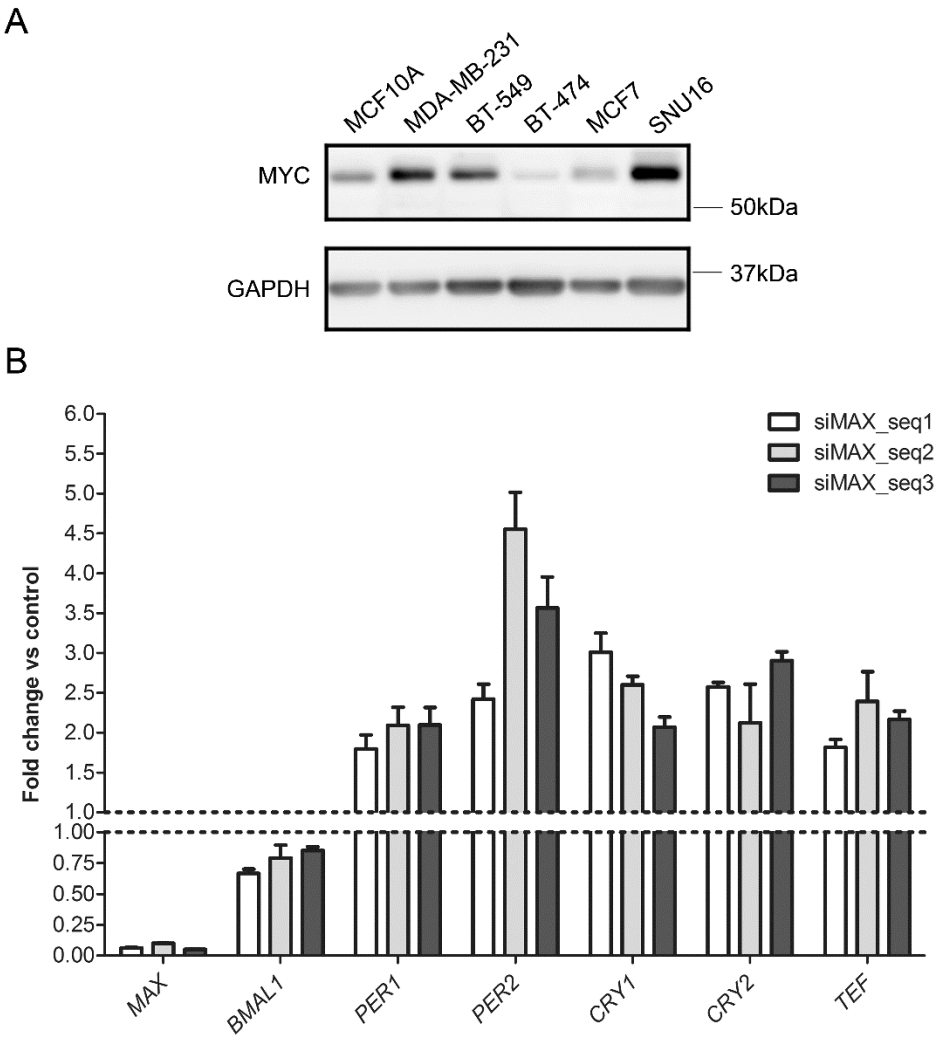

Figure S1. (*A*) Expression of MYC protein in triple negative (MDA-MB-231, BT-549) and non-triple negative (BT-474, MCF7) breast cancer cell lines. Epithelial MCF10A was used as a representative non-cancerous epithelial cell line while stomach SNU16 was used as a representative MYC overexpressing cancer cell line. (*B*) Specificity of MAX silencing on the expression of clock core genes. Expression of the inidicated clock genes in MDA-MB-231 cells upon knockdown of MAX with three diverse and non-redundant siRNA sequences. A non-coding siRNA was used as control. Relative expression was determined by qRT-PCR using *GAPDH* for normalization. Values of control cells were set to 1. Shown as mean fold change versus control + SEM, n = 3.

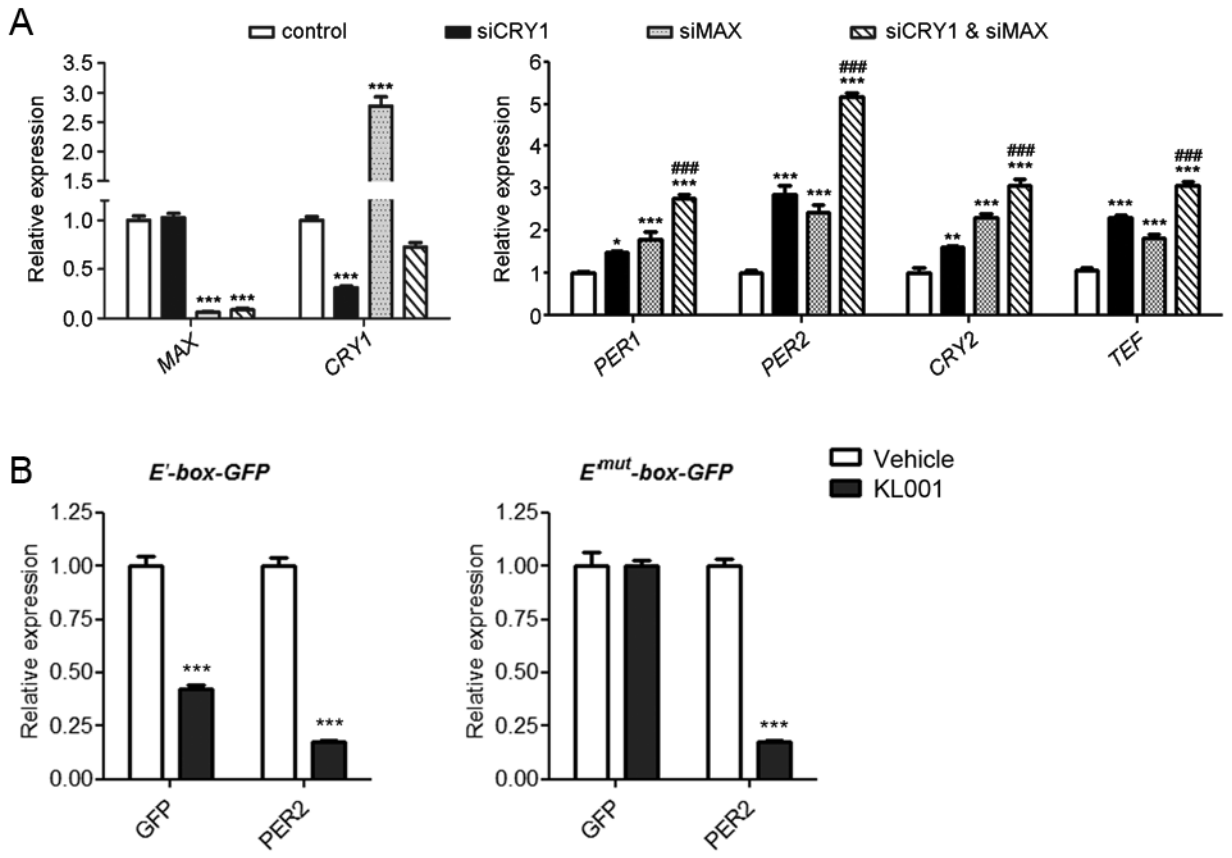

Figure S2. (*A*) Expression of clock genes (*PER1*, *PER2*, *CRY2*, and *TEF*) in MDA-MB-231 cells with knocked down *CRY1* (siCRY1), *MAX* (siMAX), and both *CRY1* and *MAX* (siCRY1&siMAX). A non-coding siRNA was used as control. Relative expression was determined by qRT-PCR using *GAPDH* for normalization. Values of control cells were set to 1. Shown as mean ± SEM, n ≥ 3. *P < 0.05. **P < 0.01 and ***P < 0.001, two-way ANOVA with Bonferroni post hoc test, silencing versus control. $^{###}$P < 0.001, siCRY1&siMAX versus siCRY1. (*B)* Repression of *PER2*-promoter driven *GFP* by a CRY agonist, KL001 (5 µM), in reporter MDA-MB-231 cell lines bearing either a wild type (*E'-box-GFP*) or a mutated (*E'^{mut}-box-GFP*) PER2 promoter sequence. Expression of the endogenous *PER2* was used as a control of the responsiveness of the cells to KL001. Two-way ANOVA with Bonferroni post hoc test comparing KL001 versus vehicle. **P < 0.01 and ***P < 0.001.

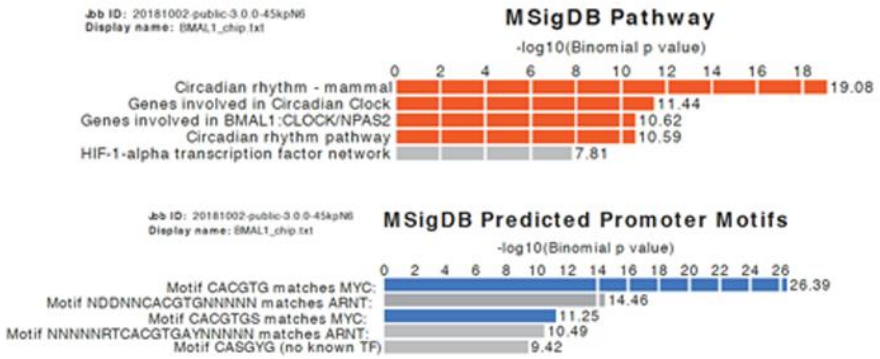

Figure S3 Ontological annotation of BMAL1 bound regions by Genomic Regions Enrichment of Annotations Tool (GREAT) (http://great.stanford.edu/public/html/). A significant enrichment for circadian regulated genes and E-box motifs is shown.