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SUPPLEMENTARY INFORMATION

MicroRNA-185 oscillation controls circadian amplitude of mouse CRYPTOCHROME1 via translational regulation

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Supplementary Figure Legends

Supplementary Figure S1. CRY1 expression is regulated by the microRNA machinery.

(A) Renilla luciferase reporter fused to mCry1 3'UTR was transfected with control siRNA (Con_si) or Ago2 specific siRNA to NIH 3T3 cells by microporation. After a 24-h incubation, cells were subjected to luciferase assays. The activity of RLUC was normalized to that of FLUC, and the activity of Con-si was set to 1. (B) The knock-down of Ago2 expression observed in panel A was confirmed by real-time PCR. Ago2 or Actb mRNA levels were quantified, and Ago2 mRNA levels normalized to those of Actb mRNA. The results are expressed as the mean \pm SEM of 3 independent experiments.

Supplementary Figure S2. miR-185 overexpression does not repress the translation of control system proteins.

(A) NIH 3T3 cells were co-transfected by microporation with the RL control vector that does not contain any 3'UTR sequence and control or miR-185 expressing plasmids, and then incubated for 24 h. The luciferase activities of RLUC and FLUC were quantified, and RLUC activity normalized to that of FLUC. (B) NIH 3T3 cells were transfected with the RL control vector along with pre-miR-con or pre-miR-185. Luciferase assays were then carried out, and the ratio of RLUC over FLUC was calculated. Results shown are the mean \pm SEM of 3 separate experiments.

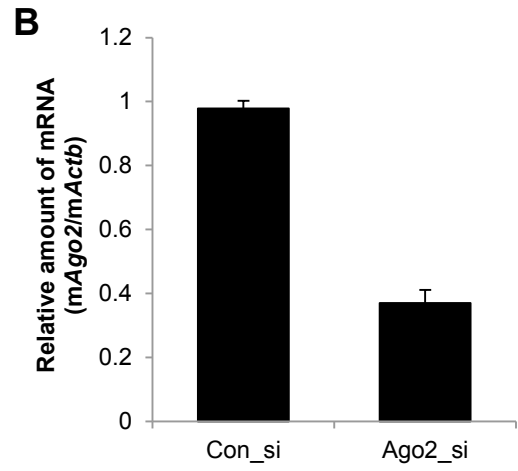
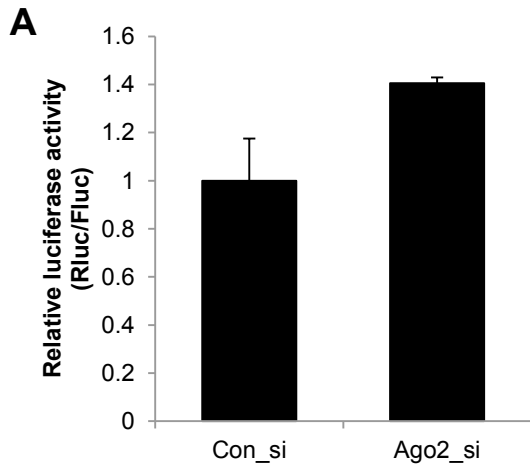
Supplementary Figure S3. Inhibition of miR-185 increase amplitude of mCRY1 expression.

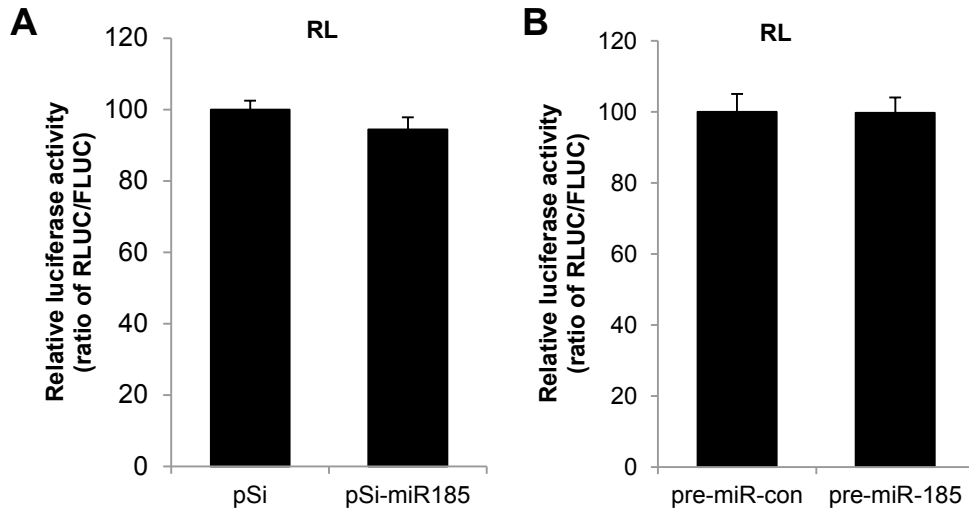
(A) NIH 3T3 cells were treated with water, or transfected with anti-miR-con or anti-miR-185. After 12h incubation, dexamethasone was treated and cells were harvested at every 4 h; then

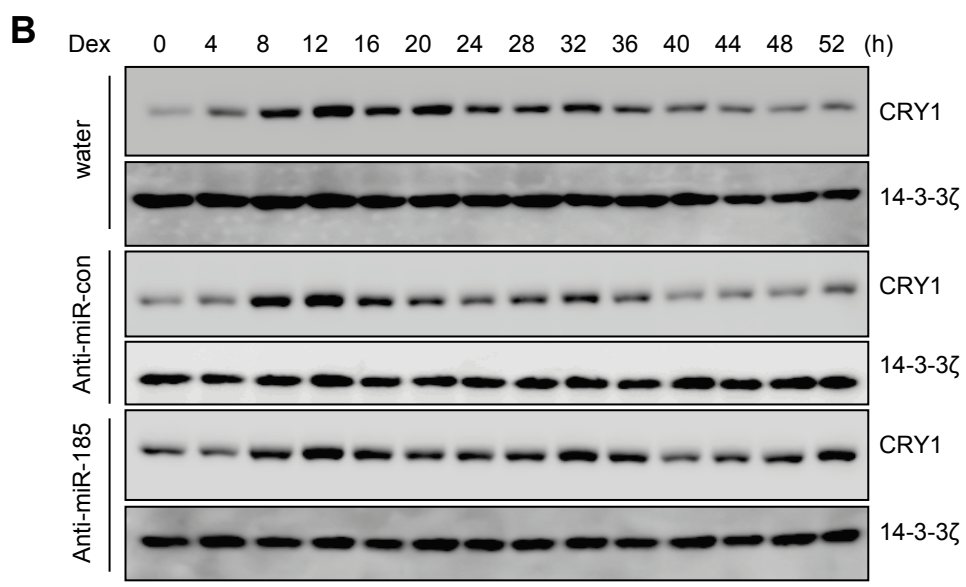
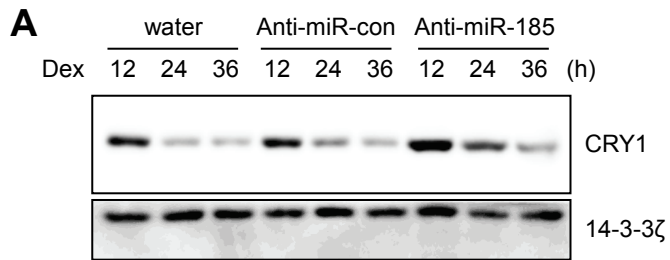
immunoblotting was performed in a single SDS-PAGE gel to check the amplitude. (B) With same extracts of panel A, immunoblotting was performed with indicated antibodies.

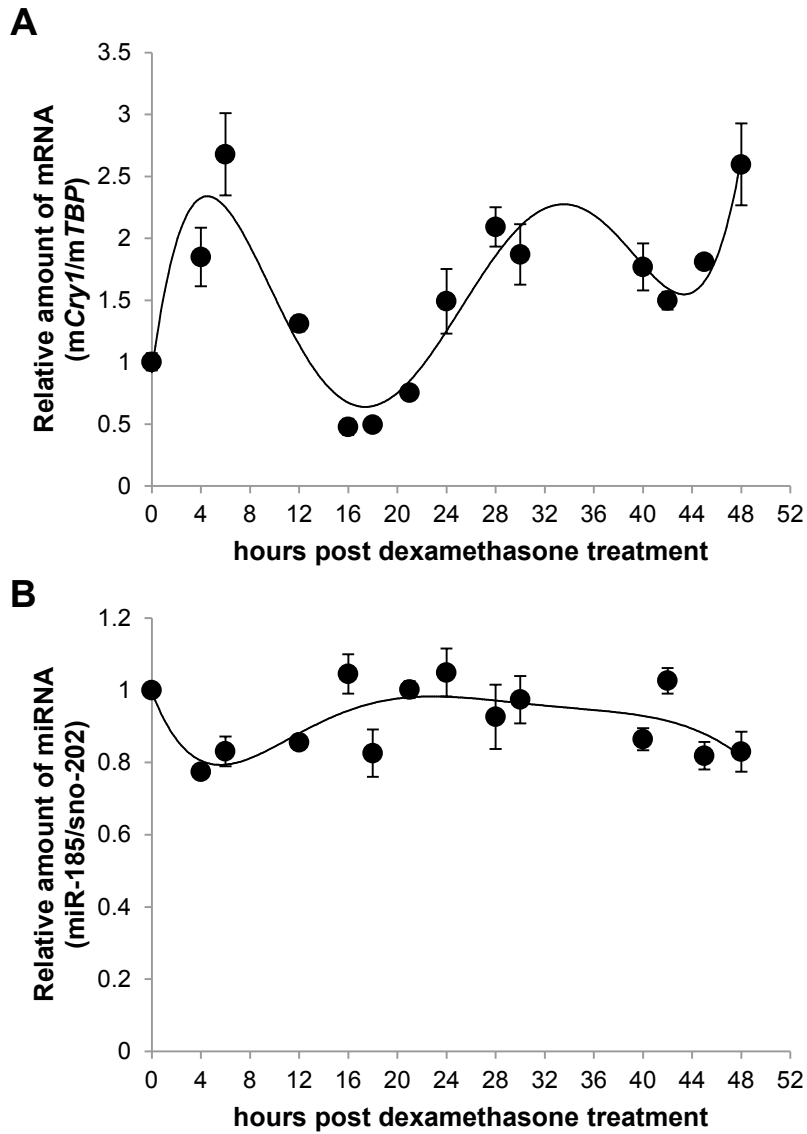
Supplementary Figure S4. miR-185 expression profile. (A) To determine the expression profile of miR-185, the synchronization of NIH 3T3 cells were confirmed by measuring *mCry1* levels. NIH 3T3 cells were treated with 100 nM dexamethasone for 2 h before being harvested at the indicated times. Total RNA (1 μ g) from each time point was subjected to real-time PCR with specific oligonucleotides for *mCry1* and *mTbp*, as a normalizing control. (B) miR-185 and small nucleolar RNA-202 (sno-202) levels were quantified by real-time PCR in the same extracts shown in panel A, and miR-185 levels normalized to sno-202 levels. The normalized activity of the 0 h time point was set to 1. All results shown are representative of the mean \pm SEM of 3 independent experiments.

Supplementary Table S1. Sequences of real-time PCR primers









	Sequence (5' to 3')
mCry1 (forward)	CCTTGAAAAGCCTGGGAAAT
mCry1 (reverse)	TCCGCTGCGTCTATATCCTC
mTbp (forward)	CAGCCTTCCACCTTATGCTC
mTbp (reverse)	TTGCTGCTGCTGTCTTTGTT
Rluc (forward)	GTAACGCTGCCTCCAGCTAC
Rluc (reverse)	CCAAGCGGTGAGGTACTIONTGT
Fluc (forward)	TTCGCTAAGAGCACCTGAT
Fluc (reverse)	GTAATCAGAATGGCGCTGGT
mAgo2 (forward)	AAGTCGGACAGGAGCAGAAA
mAgo2 (reverse)	GAAACTTGCACTTCGCATCA
mDicer (forward)	CTCGTCAACTCTGCAAACCA
mDicer (reverse)	CAGTCAAGGCGACATAGCAA
mDrosha (forward)	AACAGTTCAACCCCGAAGTG
mDrosha (reverse)	CTCTGAGCCAGCTTCTGCTT
mActb (forward)	TGTTACCAACTGGGACGACA
mActb (reverse)	GGGGTGTGAAGGTCTCAA