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| **Supplementary Table 1**. Location of circadian gene CpG islands included in this study |
| **Gene** | **CpG Island Location** | **Number of probes within island** | **Gene Region Feature Category\*** |
| *PER3* island 1 | chr1:7843460-7843693 | 2 | TSS 1500 |
| *PER3* island 2 | chr1:7843915-7845104 | 9 | TSS 1500 |
| *PER3* island 3 | chr1:7887198-7887476 | 4 | Body |
| *BMAL1* | chr11:13298796-13300735 | 9 | 5’ UTR |
| *CRY2* | chr11:45868742-45869413 | 8 | 1st Exon |
| *CRY1* | chr12:107486612-107487811 | 11 | 1st Exon; 5’ UTR |
| *RORA* island 1 | chr15:60883298-60885350 | 16 | Body |
| *RORA* island 2 | chr15:61519621-61520031 | 2 | Body |
| *RORA* island 3 | chr15:61520423-61521716 | 10 | Body; TSS 200 |
| *NR1D1* island 1 | chr17:38255274-38255896 | 4 | Body |
| *NR1D1* island 2 | chr17:38256635-38257082 | 7 | TSS 200 |
| *PER1* | chr17:8054550-8055835 | 5 | 5’ UTR |
| *PER2* | chr2:239196923-239197900 | 6 | TSS 1500 |
| *NR1D2* | chr3:23986693-23988021 | 10 | TSS 200 |
| *CLOCK* | chr4:56411993-56413357 | 13 | TSS 1500 |
| *RORB* | chr9:77112712-77113583 | 2 | 1st Exon |

\*Feature(s) that each CpG island occurs in are estimated from UCSC refGene. TSS=transcription start site; UTR=untranslated region.

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| **Supplementary Table 2**. Spearman Correlations between DNA methylation in CpG islands and RNAseq gene expression |
|  | Spearman correlation with corresponding gene expression |
| *PER1* | 0.0633 |
| *PER2* | -0.1321 |
| *PER3* island 1 | -0.1062 |
| *PER3* island 2 | 0.0581 |
| *PER3* island 3 | 0.0549 |
| *CRY2* | 0.0732 |
| *BMAL1* | 0.1934 |
| *CLOCK* | 0.062 |
| *RORA* island 1 | 0.068 |
| *RORA* island 2 | -0.0581 |
| *RORA* island 3 | 0.3597\* |
| *RORB* | -0.1218 |
| *NR1D1* island 1 | -0.0014 |
| *NR1D1* island 2 | 0.1447 |
| *NR1D2* | 0.2715 |

\*Statistically significant at P<0.05