Supplementary Table 1. Logistic regression analysis of *CLOCK* and *CRY2* methylation levels in day workers and long-term shiftworkers.

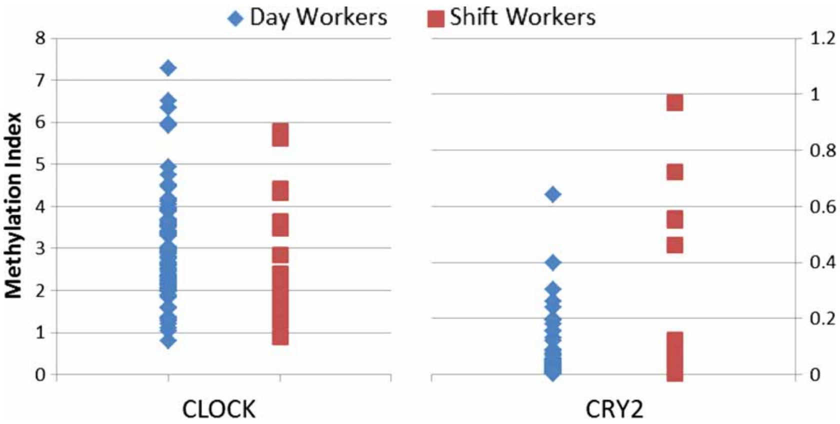
Methylation Tertile	Day Workers*	Shift Workers†	Unadjusted OR (95% CI)	Unadjusted P-Value	Multivariate OR (95% CI)‡	Multivariate P-Value‡
CLOCK						
Low	33 (34%)	**11** (58%)	Ref	-	Ref.	-
Mid	33 (34%)	2(11%)	**.18 (.04-.88)**	**.0347**	**.18 (.04-.87)**	**.0333**
High	32 (33%)	6 (32%)	.56 (.19-1,70)	.3084	.56(.18-1.70)	.3032
Mid/High	65 (66%)	8 (42%)	.37(.14-1.01)	.0514	**.36 (.13-1.00)**	**.0499**
CRY2						
High	25 (33%)	**11** (61%)	Ref	-	Ref	
Mid	25 (33%)	2(11%)	**.18 (.04-.91)**	**.0374**	**.18 (.04-.92)**	**.0388**
Low	25 (33%)	5 (28%)	.46(.14-1.50)	.1954	.46(.14-1.53)	.2033
Mid/Low	50 (67%)	7 (39%)	**.32 (.11-.92)**	**.0346**	**.32 (.11-.93)**	**.0359**

*0 yrs lifetime shiftwork; †10 yrs or more lifetime shiftwork; ‡Adjusted for age and total folate intake.
Note: samples from 23 workers and 1 shiftworker failed to reproducibly amplify one or more CRY2 methylation reactions.

Supplementary Table 2. Top five networks identified as significantly associated with differentially methylated genes by the IPA software.

ID	Top functions	*P*-value
1	DNA Replication, Recombination, and Repair, Cellular Compromise, Gene Expression	$1.0E^{-19}$
2	Protein Synthesis, Neurological Disease, Cellular Growth and Proliferation	$1.0E^{-19}$
3	DNA Replication, Recombination, and Repair, Gene Expression, Behavior	$1.0E^{-17}$
4	Gene Expression, Embryonic Development, Organismal Development	$1.0E^{-17}$
5	Drug Metabolism, Endocrine System Development and function, Lipid Metabolism	$1.0E^{-16}$

Supplementary Figure 1. Scatter plot of methylation indices for *CLOCK* and *CRY2* in day and long-term shiftworkers.



Supplementary Figue 2. Methylation measurement of *CLOCK, CRY2, ERCC3*, and *GTF2H2* by methylation-specific qPCR. These data showed good agreement in the magnitude of changes observed by both qPCR and the Illumina Infinium Methylation Assay. Primers of methylation-specific PCR for *CLOCK* and *CRY2* can be found in our previous publications (see Methods for references) and for *GTF2H2* and *ERCC3* are: GTF2H2: M.Left: 5'-TTTTGTGAATTTTAGTTGGAATATC-3', M.Right: 5'-CGCCTAACTAACCAAACGAC-3', U.Left: 5' TTTTGTGAATTTTAGTTGGAATATT-3'U.Right: 5'-CCACCTAACTAACCAAACAAC-3', ERCC3: M.Left: 5'- AGTAGGAGTTTT-TAGGGTTTTTTTC-3', M.Right: 5'- GCTCTACCTCGAAACTACTCCG -3', U.Left: 5'- GGAGTTTTTAGGGTTTTTTTT-3', U.Right: 5'- CCACTC-TACCTCAAAACTACTCCA-3'.