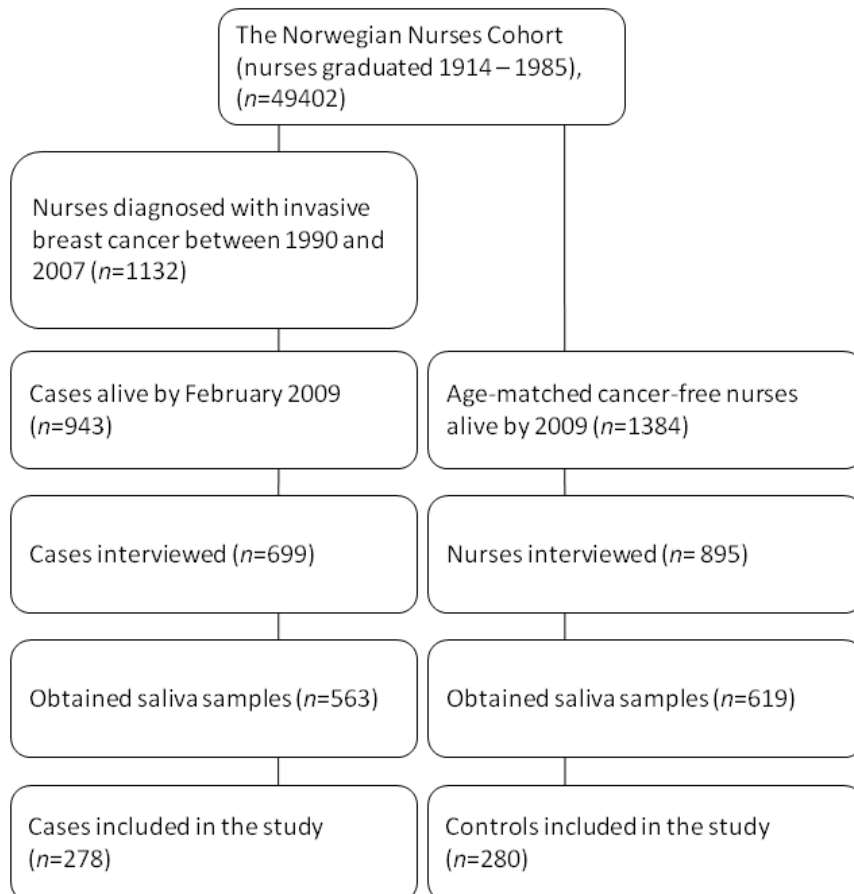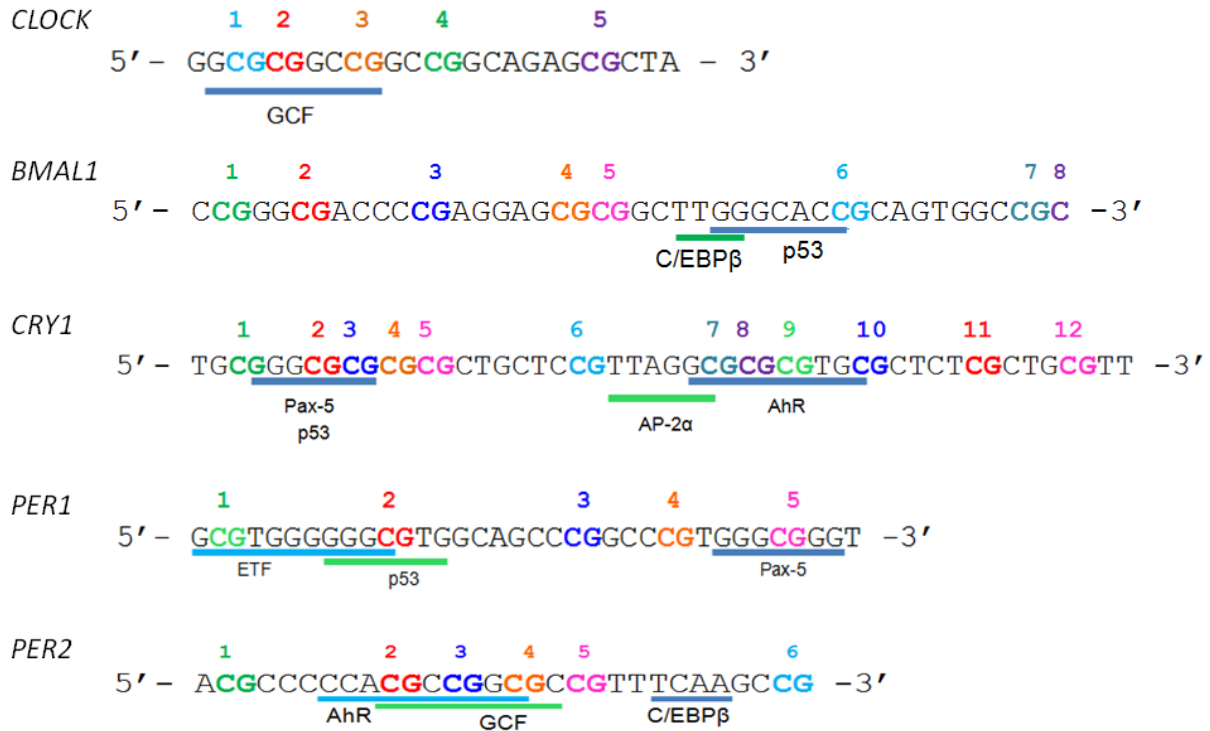# Supplementary Figures and Tables

Supplementary Figure 1. Flow chart illustrating the study design.

Supplementary Figure 2. Analysis of transcription factor binding in the target CpG site for each of the genes was performed using PROMO and the TRANSFAC database. Transcription factors with DM ≤5% are included in the illustration.

CLOCK
        1 2   3   4   5
5'- GGCGCGGCCGGCCGGCAGAGCGCTA - 3'
        GCF

BMAL1
      1   2   3   4 5   6   7 8
5'- CCGGGCGACCCCGAGGAGCGCGGCTTGGGCACCGCAGTGGCCGC -3'
                                C/EBPβ   p53

CRY1
        1   2 3 4 5   6   7 8 9   10   11   12
5'- TGCGGGCGCGCGCGCTGCTCCGTTAGGCGCGCGTGCGCTCTCGCTGCGTT -3'
        Pax-5   AP-2α   AhR
        p53

PER1
      1   2   3   4   5
5'- GCGTGGGGGGCGTGGCAGCCCGGCCCGTGGGCGGGT -3'
    ETF   p53   Pax-5

PER2
    1   2 3   4 5   6
5'- ACGCCCCCACGCCGGCGCCGTTTCAAGCCG -3'
      AhR   GCF   C/EBPβ

Supplementary Table 1. Selected core circadian genes and settings used for analysis.

Gene ID	Location	Forward Primer	Reverse Primer	Sequencing primer
CLOCK	4:55547169 - 55547193	TTTTTGGGTAGAAATTTGGTTTTGTAG	TCTAACCTCTAAATCCCTCATCC	GTTTGGTAGGGTGGAG
BMAL1	11:13277344-13277387	AGTAGGAGGGAGAGAGGGAGTTA	CCCCTACCCTCTCCCTTTC	ATTTAGAGAAGAGGGATAT
CRY1	12:107093928-107093977	GGTTTTTTGTGAGGGAAGGTTTAGT	ACCCCCCCCCCTTACCCTCTA	GGGATGAGGGGAGTT
PER1	17:8156372-8156407	Predesigned: Hs_PER1_02_PM PyroMark CpG assay (PM00182616)		
PER2	2:238288480-238288509	TTATTTTTTATTTGGGATAGGGTTAAGGG	AAAATTCCTTAAACTACTAAACTCC	GGATAGGGTTAAGGGTA

Supplementary Table 2. Overview of selected SNPs in core circadian genes.

Gene	SNP ID	Position/ SNP type	Base or AA change	MAF/GMAF	H-W wq. (X2, P-value)	Genotyping rate (controls/cases)
CLOCK	rs1048004	4q12/tagging	C/A	0.26/0.22	0.51, 0.47	96.8/97.5
	rs11133373	4q12/tagging	C/G	0.36/0.34	0.019, 0.89	95.3/94.1
	rs11133376	4q12/tagging	T/C	0.35/0.29	0.14, 0.70	96.5/97.7
	rs13102385	4q12/tagging	C/T	0.35/0.40	0.38, 0.54	91.7/89.1
	rs17776421	4q12/tagging	G/A	0.36/0.43	0.12, 0.72	97.1/96.8
	rs1801260	4q12/tagging	A/G	0.26/0.22	0.83, 0.36	95.3/95.3
	rs3749474a	4q12/tagging	C/T	0.40/0.39	4,59, 0.032	96.1/96.2
	rs7698022	4q12/tagging	A/C	0.26/0.22	0.26, 0.63	90.7/90.1
BMAL1	rs2278749	11p15/tagging	C/T	0.19/0.15	4.73, 0.03	92.3/93.9
	rs2290035	11p15/tagging	T/A	0.43/0.40	0.09, 0.76	94.1/95
	rs7126303	11p15/tagging	T/C	0.44/0.41	0.001, 0.99	92.1/92.8
	rs969485	11p15/ tagging	A/G	0.25/0.40	0.04, 0.83	89.7/89.5
CRY1	rs12315175	12q23-24.1/tagging	T/C	0.16/0.23	4.84, 0.03	90.0/91.8
	rs3809235	12q23-24.1/5'UTR	T/C	0.45/0.45	0.31, 0.51	96.1/95.2
PER1	rs2253820	17p13.1-p12/tagging	G/A	0.14/0.14	0.54, 0.46	93.8/91.8
	rs2289591	17p13.1-p12/tagging	G/T	0.25/0.12	0.24, 0.62	89.9/91
	rs885747	17p13.1-p12/tagging	C/G	0.43/0.35	0.35, 0.55	97.1/97.3
PER2	rs11695472	2q37.3/tagging	A/C	0.26/0.16	0.77, 0.36	96.6/96.2
	rs7602358	2q37.3/tagging	T/G	0.19/0.16	0.45, 0.50	87.9/88.2