Supplementary Tables

Supplementary Table 1. SNP annotation, Odds Ratios (OR) and P-values corresponding to main effect of 178 common variants in genes that regulate circadian rhythm on breast cancer susceptibility (incident and prevalent cases), adjusted for matching factors (n_{cases}=609, $n_{controls}$=1216). ORs and p-values are also presented for an analysis of the main effect of each SNP within strata of exposure to rotating shift-work (<24 vs. ≥24 cumulative months of rotating shift-work). P-values are reported for both the independent effect of the interaction term and the joint effect of genotype and the interaction term. Analyses stratified by or adjusted for shift-work exposure were restricted to incident cases and their matched controls (n_{cases}=438, $n_{controls}$=880). Multiple-testing-adjusted p-values (P-perm) were obtained using the max(T) permutation procedure in PLINK (10,000 permutations)) within covariate defined clusters.

SNP	**Allele**	**MAF**	**Gene**	**Location**	**Main Effect Analysis**			**<24mo Shift-work**			**≥24mo Shift-work**			**Joint Test**	**Interaction Term**
					OR (CI)	**P-value**	**P-perm**	**OR (CI)**	**P-value**	**P-perm**	**OR (CI)**	**P-value**	**P-perm**	**P-value**	**P-value**
rs707455	G > A	0.422	PER3	upstream	1.08 (0.94, 1.25)	0.2672	1.0000	1.13 (0.91, 1.41)	0.2730	1.0000	1.06 (0.82, 1.36)	0.6751	1.0000	0.5106	0.6102
rs697672	A > G	0.14	PER3	upstream	0.90 (0.74, 1.10)	0.3191	1.0000	0.85 (0.62, 1.17)	0.3193	1.0000	0.99 (0.69, 1.42)	0.9632	1.0000	0.5744	0.5069

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interac-tion Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs1044245	G > A	0.15	PER3	upstream	1.02 (0.84, 1.25)	0.8221	1.0000	1.11 (0.82, 1.51)	0.4867	1.0000	1.04 (0.72, 1.50)	0.8551	1.0000	0.7626	0.6888
rs697673	G > A	0.22	PER3	upstream	0.94 (0.79, 1.11)	0.4767	1.0000	0.81 (0.62, 1.05)	0.1141	1.0000	1.01 (0.74, 1.37)	0.9631	1.0000	0.2829	0.2955
rs228729	G > A	0.34	PER3	intron	1.02 (0.87, 1.18)	0.8389	1.0000	1.00 (0.79, 1.27)	0.9818	1.0000	0.97 (0.74, 1.27)	0.7991	1.0000	0.9992	0.7577
rs228644	G > A	0.40	PER3	intron	1.01 (0.88, 1.17)	0.8477	1.0000	0.86 (0.69, 1.08)	0.1866	1.0000	1.17 (0.91, 1.52)	0.2188	1.0000	0.4471	0.0844
rs11121029	G > A	0.23	PER3	intron	1.07 (0.90, 1.26)	0.4407	1.0000	1.09 (0.85, 1.41)	0.4977	1.0000	1.12 (0.82, 1.53)	0.4612	1.0000	0.7811	0.9265
rs17374292	G > A	0.14	PER3	intron	1.13 (0.94, 1.37)	0.1983	1.0000	1.16 (0.86, 1.58)	0.3364	1.0000	1.30 (0.93, 1.81)	0.1278	1.0000	0.6435	0.5991
rs697690	A > G	0.32	PER3	intron	1.07 (0.92, 1.24)	0.4131	1.0000	1.17 (0.92, 1.47)	0.1980	1.0000	1.05 (0.80, 1.37)	0.7195	1.0000	0.4322	0.5591
rs2640909	A > G	0.31	PER3	coding	0.88 (0.75, 1.02)	0.0974	1.0000	0.83 (0.65, 1.05)	0.1197	1.0000	0.92 (0.69, 1.23)	0.5696	1.0000	0.2850	0.5010
rs1773138	G > A	0.18	PER3	intron	1.00 (0.83, 1.20)	0.9843	1.0000	1.16 (0.88, 1.53)	0.2945	1.0000	0.83 (0.60, 1.16)	0.2756	0.9998	0.5698	0.1221
rs228651	G > A	0.37	PER3	downstream	1.03 (0.89, 1.19)	0.7084	1.0000	0.93 (0.75, 1.17)	0.5370	1.0000	1.29 (1.00, 1.66)	0.0545	1.0000	0.8403	0.0697
rs228648	A > G	0.45	PER3	downstream	0.99 (0.86, 1.14)	0.9000	1.0000	1.15 (0.93, 1.42)	0.2118	1.0000	0.85 (0.66, 1.10)	0.2105	1.0000	0.4779	0.0927
rs11686712	G > A	0.43	NPAS2	flanking_5UTR	1.00 (0.87, 1.16)	0.9542	1.0000	0.97 (0.78, 1.21)	0.8046	1.0000	0.93 (0.71, 1.22)	0.5946	1.0000	0.9524	0.8357
rs3888170	A > G	0.20	NPAS2	intron	1.15 (0.96, 1.36)	0.1209	1.0000	1.14 (0.87, 1.49)	0.3355	1.0000	1.23 (0.90, 1.67)	0.1914	1.0000	0.6144	0.7849
rs3849381	A > G	0.31	NPAS2	intron	1.05 (0.90, 1.22)	0.5461	1.0000	0.91 (0.72, 1.15)	0.4146	1.0000	1.08 (0.81, 1.44)	0.6050	1.0000	0.6980	0.3631
rs10165970	G > A	0.16	NPAS2	intron	1.05 (0.86, 1.27)	0.6561	1.0000	1.24 (0.93, 1.66)	0.1505	1.0000	0.77 (0.53, 1.12)	0.1685	0.9998	0.3417	0.0460

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interaction Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs11691732	G > C	0.26	NPAS2	intron	1.00 (0.85, 1.18)	0.9986	1.0000	1.17 (0.92, 1.50)	0.2001	1.0000	0.86 (0.64, 1.17)	0.3521	1.0000	0.4491	0.1273
rs10206927	G > C	0.26	NPAS2	intron	1.00 (0.85, 1.17)	0.9606	1.0000	1.16 (0.91, 1.48)	0.2368	1.0000	0.87 (0.64, 1.18)	0.3808	1.0000	0.4998	0.1529
rs965519	A > G	0.17	NPAS2	intron	0.97 (0.80, 1.17)	0.7121	1.0000	1.02 (0.77, 1.37)	0.8810	1.0000	0.81 (0.56, 1.17)	0.2565	1.0000	0.9797	0.2996
rs7598826	A > G	0.44	NPAS2	intron	0.93 (0.80, 1.07)	0.3016	1.0000	1.02 (0.82, 1.27)	0.8818	1.0000	0.83 (0.63, 1.09)	0.1706	1.0000	0.9852	0.2436
rs930309	A > T	0.24	NPAS2	intron	1.05 (0.89, 1.23)	0.5822	1.0000	1.20 (0.93, 1.55)	0.1553	1.0000	0.95 (0.70, 1.28)	0.7235	1.0000	0.3786	0.2367
rs12472321	A > G	0.30	NPAS2	intron	0.98 (0.84, 1.15)	0.8062	1.0000	1.08 (0.85, 1.37)	0.5377	1.0000	0.97 (0.73, 1.29)	0.8322	1.0000	0.8395	0.6056
rs2871389	A > G	0.30	NPAS2	intron	0.99 (0.85, 1.15)	0.8591	1.0000	1.09 (0.86, 1.38)	0.4816	1.0000	0.99 (0.74, 1.31)	0.9330	1.0000	0.7925	0.6360
rs6740935	G > A	0.38	NPAS2	intron	0.93 (0.81, 1.08)	0.3486	1.0000	0.98 (0.79, 1.22)	0.8755	1.0000	0.87 (0.66, 1.15)	0.3174	1.0000	0.9882	0.5261
rs12712083	A > G	0.45	NPAS2	intron	0.94 (0.82, 1.08)	0.4147	1.0000	0.98 (0.79, 1.20)	0.8151	1.0000	0.93 (0.72, 1.20)	0.5756	1.0000	0.9803	0.8033
rs1369481	G > A	0.29	NPAS2	intron	1.05 (0.90, 1.23)	0.5175	1.0000	1.15 (0.91, 1.46)	0.2440	1.0000	0.91 (0.68, 1.22)	0.5360	1.0000	0.5268	0.2362
rs17654772	G > A	0.25	NPAS2	intron	1.02 (0.86, 1.20)	0.8506	1.0000	0.86 (0.67, 1.11)	0.2427	1.0000	1.19 (0.89, 1.60)	0.2461	1.0000	0.5101	0.1172
rs4851377	A > G	0.46	NPAS2	intron	1.01 (0.88, 1.16)	0.9178	1.0000	1.09 (0.88, 1.36)	0.4180	1.0000	0.93 (0.72, 1.21)	0.6074	1.0000	0.6947	0.3639
rs920085	G > A	0.28	NPAS2	intron	1.01 (0.86, 1.18)	0.9046	1.0000	1.11 (0.88, 1.41)	0.3671	1.0000	0.93 (0.69, 1.24)	0.6208	1.0000	0.6309	0.3167
rs13394520	A > G	0.41	NPAS2	intron	1.01 (0.88, 1.16)	0.8874	1.0000	0.90 (0.73, 1.11)	0.3244	1.0000	1.14 (0.88, 1.46)	0.3257	1.0000	0.6035	0.1646
rs356656	C > G	0.17	NPAS2	intron	0.99 (0.82, 1.19)	0.9029	1.0000	0.98 (0.74, 1.30)	0.8896	1.0000	1.01 (0.71, 1.43)	0.9797	1.0000	0.9910	0.8775

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interaction Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs11894671	C > A	0.23	NPAS2	intron	1.02 (0.86, 1.20)	0.8582	1.0000	0.86 (0.66, 1.12)	0.2677	1.0000	1.16 (0.86, 1.56)	0.3199	1.0000	0.5346	0.1514
rs356643	A > G	0.46	NPAS2	intron	1.02 (0.89, 1.17)	0.7837	1.0000	1.05 (0.85, 1.29)	0.6793	1.0000	1.00 (0.78, 1.29)	0.9963	1.0000	0.9039	0.7943
rs6725296	G > A	0.19	NPAS2	intron	1.01 (0.84, 1.21)	0.9101	1.0000	1.14 (0.87, 1.50)	0.3449	1.0000	0.85 (0.60, 1.21)	0.3684	1.0000	0.6070	0.1824
rs13026599	A > G	0.18	NPAS2	intron	0.99 (0.83, 1.18)	0.8965	1.0000	0.92 (0.69, 1.22)	0.5491	1.0000	1.02 (0.74, 1.42)	0.8964	1.0000	0.8281	0.5909
rs17717414	A > G	0.19	NPAS2	intron	1.02 (0.85, 1.21)	0.8632	1.0000	1.10 (0.84, 1.45)	0.4733	1.0000	0.82 (0.58, 1.16)	0.2607	1.0000	0.7646	0.2046
rs3754674	G > C	0.40	NPAS2	intron	0.95 (0.82, 1.09)	0.4491	1.0000	0.96 (0.77, 1.21)	0.7546	1.0000	0.94 (0.72, 1.22)	0.6273	1.0000	0.9639	0.8141
rs13025524	G > A	0.33	NPAS2	intron	0.91 (0.78, 1.06)	0.2174	0.9971	0.99 (0.79, 1.25)	0.9562	1.0000	0.88 (0.67, 1.16)	0.3719	1.0000	1.0000	0.4562
rs11688832	C > A	0.22	NPAS2	intron	0.97 (0.82, 1.15)	0.7428	1.0000	1.03 (0.80, 1.32)	0.8261	1.0000	0.91 (0.66, 1.25)	0.5549	1.0000	0.9722	0.5837
rs3768984	A > C	0.25	NPAS2	intron	0.99 (0.85, 1.16)	0.9372	1.0000	0.94 (0.73, 1.21)	0.6070	1.0000	1.03 (0.77, 1.36)	0.8480	1.0000	0.8661	0.6091
rs17025005	G > A	0.18	NPAS2	intron	0.91 (0.76, 1.09)	0.3206	1.0000	1.06 (0.80, 1.40)	0.6983	1.0000	0.88 (0.64, 1.22)	0.4536	1.0000	0.9217	0.3910
rs7605570	G > A	0.39	NPAS2	intron	0.88 (0.76, 1.01)	0.0707	0.9963	0.72 (0.57, 0.90)	0.0050	0.5975	1.01 (0.78, 1.31)	0.9210	1.0000	0.0209	0.0547
rs12712085	G > A	0.42	NPAS2	intron	0.87 (0.75, 1.00)	0.0497	0.9969	0.69 (0.55, 0.87)	0.0016	0.3523	1.05 (0.81, 1.35)	0.7205	1.0000	0.0073	0.0187
rs3820787	G > A	0.35	NPAS2	intron	0.90 (0.78, 1.04)	0.1612	1.0000	0.69 (0.54, 0.87)	0.0016	0.4428	1.04 (0.80, 1.35)	0.7506	1.0000	0.0071	0.0164
rs10191450	G > A	0.37	NPAS2	intron	1.12 (0.97, 1.29)	0.1202	1.0000	1.37 (1.09, 1.71)	0.0062	0.9992	0.89 (0.68, 1.16)	0.3822	1.0000	0.0239	0.0148
rs4851390	A > G	0.19	NPAS2	intron	1.03 (0.87, 1.22)	0.7379	1.0000	1.05 (0.81, 1.36)	0.7173	1.0000	1.05 (0.76, 1.44)	0.7843	1.0000	0.9503	0.9705

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interac-tion Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs882272	G > A	0.42	NPAS2	intron	1.12 (0.97, 1.28)	0.1244	1.0000	1.38 (1.10, 1.72)	0.0055	0.7185	0.93 (0.72, 1.20)	0.5626	1.0000	0.0200	0.0260
rs17020663	G > C	0.13	NPAS2	intron	0.98 (0.80, 1.21)	0.8769	1.0000	1.10 (0.80, 1.50)	0.5669	1.0000	0.92 (0.63, 1.35)	0.6631	1.0000	0.8392	0.4462
rs6747755	G > A	0.22	NPAS2	intron	0.97 (0.82, 1.15)	0.7454	1.0000	1.12 (0.87, 1.45)	0.3664	1.0000	0.79 (0.57, 1.09)	0.1528	1.0000	0.6655	0.0745
rs7581886	A > G	0.14	NPAS2	intron	0.84 (0.68, 1.04)	0.1082	0.9935	0.65 (0.46, 0.91)	0.0127	0.7628	1.17 (0.80, 1.71)	0.4109	1.0000	0.0448	0.0210
rs4851392	G > A	0.28	NPAS2	intron	0.87 (0.75, 1.02)	0.0852	0.9987	0.65 (0.51, 0.84)	0.0009	0.0029	1.13 (0.85, 1.48)	0.4007	1.0000	0.0044	0.0040
rs1562313	G > A	0.19	NPAS2	coding	1.04 (0.87, 1.24)	0.6566	1.0000	1.22 (0.94, 1.60)	0.1409	1.0000	0.98 (0.71, 1.36)	0.8967	1.0000	0.3356	0.2934
rs2305160	G > A	0.34	NPAS2	coding	0.90 (0.78, 1.04)	0.1592	1.0000	0.65 (0.51, 0.82)	0.0003	0.0029	1.19 (0.93, 1.54)	0.1734	1.0000	0.0014	0.0005
rs2305159	A > C	0.28	NPAS2	intron	1.03 (0.88, 1.19)	0.7452	1.0000	1.12 (0.89, 1.41)	0.3267	1.0000	0.93 (0.70, 1.24)	0.6229	1.0000	0.6145	0.2949
rs6719533	A > G	0.46	NPAS2	intron	1.04 (0.90, 1.19)	0.6247	1.0000	1.16 (0.93, 1.45)	0.1841	1.0000	0.84 (0.65, 1.07)	0.1600	1.0000	0.3699	0.0441
rs3754678	G > A	0.38	NPAS2	intron	0.99 (0.86, 1.14)	0.8798	1.0000	1.03 (0.82, 1.28)	0.8231	1.0000	0.99 (0.76, 1.29)	0.9325	1.0000	0.9769	0.8226
rs3768993	G > A	0.48	NPAS2	intron	0.92 (0.80, 1.06)	0.2512	0.9996	0.87 (0.70, 1.07)	0.1847	0.9998	1.08 (0.83, 1.41)	0.5745	1.0000	0.4197	0.2169
rs11123857	A > G	0.28	NPAS2	intron	1.18 (1.02, 1.38)	0.0307	0.9988	1.17 (0.92, 1.49)	0.1923	1.0000	0.94 (0.70, 1.25)	0.6552	1.0000	0.4848	0.3007
rs1867861	G > C	0.47	NPAS2	intron	0.95 (0.83, 1.09)	0.4784	1.0000	0.90 (0.73, 1.11)	0.3059	1.0000	1.12 (0.85, 1.46)	0.4207	1.0000	0.6063	0.2171
rs9223	G > A	0.32	NPAS2	coding	1.00 (0.86, 1.16)	0.9916	1.0000	0.93 (0.74, 1.17)	0.5400	1.0000	1.14 (0.86, 1.51)	0.3508	1.0000	0.8224	0.2817
rs935401	A > T	0.45	NPAS2	flanking_3UTR	1.09 (0.95, 1.25)	0.2330	1.0000	1.01 (0.82, 1.26)	0.8967	1.0000	1.06 (0.82, 1.38)	0.6605	1.0000	0.9949	0.7972

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					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs1374324	G > A	0.33	NPAS2	flanking_3UTR	0.93 (0.80, 1.07)	0.3127	1.0000	0.95 (0.76, 1.18)	0.6336	1.0000	1.00 (0.75, 1.32)	0.9746	1.0000	0.8987	0.8135
rs13417456	A > G	0.22	NPAS2	flanking_3UTR	0.96 (0.82, 1.14)	0.6682	1.0000	1.05 (0.82, 1.35)	0.6948	1.0000	0.91 (0.67, 1.24)	0.5595	1.0000	0.9206	0.5023
rs6735304	G > A	0.35	NPAS2	downstream	1.07 (0.93, 1.23)	0.3690	1.0000	1.16 (0.94, 1.45)	0.1689	1.0000	0.88 (0.68, 1.15)	0.3545	1.0000	0.3839	0.1284
rs2278724	C > G	0.20	NPAS2	downstream	0.92 (0.77, 1.10)	0.3410	1.0000	0.80 (0.60, 1.05)	0.1094	0.9197	0.92 (0.67, 1.28)	0.6400	1.0000	0.2841	0.4954
rs13397106	G > A	0.20	SERPINE2	intron	1.09 (0.92, 1.30)	0.3040	1.0000	1.09 (0.84, 1.42)	0.5238	1.0000	1.17 (0.85, 1.62)	0.3241	1.0000	0.8382	0.6997
rs2305174	G > A	0.16	PER2	upstream	0.95 (0.78, 1.14)	0.5658	1.0000	1.02 (0.76, 1.36)	0.9133	1.0000	0.88 (0.63, 1.23)	0.4447	1.0000	0.9978	0.5172
rs7584376	C > A	0.32	PER2	upstream	1.04 (0.90, 1.20)	0.6136	1.0000	1.01 (0.80, 1.29)	0.9155	1.0000	0.99 (0.76, 1.29)	0.9226	1.0000	0.9924	0.9186
rs11696058	G > A	0.32	PER2	upstream	1.04 (0.90, 1.20)	0.6152	1.0000	0.95 (0.75, 1.21)	0.6779	1.0000	0.98 (0.75, 1.28)	0.8876	1.0000	0.9202	0.8207
rs11894535	G > A	0.22	PER2	intron	0.95 (0.80, 1.12)	0.5291	1.0000	0.90 (0.69, 1.17)	0.4243	1.0000	0.87 (0.65, 1.17)	0.3533	1.0000	0.7122	0.9134
rs2304674	A > G	0.28	PER2	intron	0.98 (0.84, 1.14)	0.7806	1.0000	0.98 (0.77, 1.26)	0.8960	1.0000	0.92 (0.70, 1.22)	0.5714	1.0000	0.9833	0.7691
rs10462023	G > A	0.36	PER2	intron	1.01 (0.87, 1.17)	0.8800	1.0000	0.96 (0.77, 1.20)	0.7327	1.0000	1.04 (0.79, 1.37)	0.7574	1.0000	0.9317	0.6370
rs4663302	G > A	0.34	PER2	flanking_5UTR	1.00 (0.86, 1.16)	0.9968	1.0000	1.06 (0.84, 1.32)	0.6386	1.0000	0.96 (0.73, 1.26)	0.7457	1.0000	0.8603	0.5573
rs7681432	G > A	0.28	CLOCK	upstream	0.90 (0.77, 1.04)	0.1635	0.9996	0.85 (0.67, 1.07)	0.1691	1.0000	0.99 (0.75, 1.31)	0.9472	1.0000	0.3993	0.4122
rs4864539	A > G	0.34	CLOCK	upstream	0.99 (0.85, 1.14)	0.8545	1.0000	1.01 (0.81, 1.27)	0.9108	1.0000	0.99 (0.76, 1.30)	0.9482	1.0000	0.9953	0.9052
rs4864540	G > A	0.30	CLOCK	upstream	0.97 (0.83, 1.13)	0.7064	1.0000	1.04 (0.82, 1.32)	0.7333	1.0000	0.96 (0.73, 1.26)	0.7763	1.0000	0.9567	0.6863

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interac-tion Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs17776421	G > A	0.39	CLOCK	upstream	0.96 (0.83, 1.11)	0.5710	1.0000	0.95 (0.76, 1.18)	0.6493	1.0000	1.05 (0.81, 1.38)	0.7034	1.0000	0.8951	0.5116
rs6837871	G > A	0.22	CLOCK	upstream	1.04 (0.88, 1.22)	0.6789	1.0000	1.06 (0.82, 1.37)	0.6782	1.0000	1.01 (0.75, 1.36)	0.9369	1.0000	0.9288	0.8735
rs11133373	C > G	0.32	CLOCK	upstream	1.10 (0.95, 1.27)	0.2056	1.0000	1.13 (0.90, 1.41)	0.2990	1.0000	1.27 (0.97, 1.66)	0.0770	1.0000	0.5630	0.5336
rs11133375	G > A	0.49	CLOCK	upstream	1.09 (0.95, 1.24)	0.2205	0.9999	1.09 (0.88, 1.34)	0.4381	1.0000	0.83 (0.65, 1.06)	0.1341	0.9891	0.7412	0.5172
rs501679	A > G	0.34	CLOCK	upstream	0.91 (0.79, 1.05)	0.1930	1.0000	0.93 (0.74, 1.17)	0.5532	1.0000	0.89 (0.69, 1.15)	0.3727	1.0000	0.8343	0.8191
rs819270	G > A	0.30	CLOCK	upstream	0.97 (0.84, 1.12)	0.6889	1.0000	0.96 (0.76, 1.21)	0.7107	1.0000	0.91 (0.70, 1.19)	0.4955	1.0000	0.9391	0.7814
rs4864984	G > A	0.19	CLOCK	upstream	0.83 (0.69, 0.99)	0.0366	0.7422	0.86 (0.66, 1.13)	0.2890	1.0000	0.72 (0.51, 1.02)	0.0652	0.9405	0.5660	0.4390
rs11945371	C > A	0.32	CLOCK	upstream	1.15 (1.00, 1.34)	0.0535	0.9036	1.10 (0.88, 1.38)	0.4181	1.0000	1.21 (0.93, 1.57)	0.1532	1.0000	0.7112	0.6192
rs11943456	A > G	0.47	CLOCK	upstream	1.17 (1.02, 1.34)	0.0259	0.8102	1.11 (0.89, 1.37)	0.3571	1.0000	0.80 (0.63, 1.02)	0.0750	0.9548	0.6572	0.4656
rs17776975	G > A	0.28	CLOCK	upstream	0.94 (0.81, 1.09)	0.4380	1.0000	0.94 (0.75, 1.19)	0.6013	1.0000	0.91 (0.69, 1.19)	0.4853	1.0000	0.8750	0.8625
rs1801260	A > G	0.28	CLOCK	3UTR	0.94 (0.81, 1.09)	0.4381	1.0000	0.95 (0.76, 1.20)	0.6914	1.0000	0.89 (0.68, 1.16)	0.3850	1.0000	0.9273	0.6889
rs9791094	A > G	0.46	FLJ41309	flanking_3UTR	0.98 (0.85, 1.12)	0.7390	1.0000	0.91 (0.73, 1.13)	0.3966	1.0000	1.09 (0.84, 1.41)	0.5301	1.0000	0.7156	0.2966
rs10045427	A > C	0.30	CSNK1A1	flanking_3UTR	1.03 (0.88, 1.19)	0.7212	1.0000	0.98 (0.78, 1.23)	0.8830	1.0000	0.98 (0.74, 1.30)	0.8833	1.0000	0.9822	0.9814
rs6886243	A > G	0.25	CSNK1A1	intron	0.96 (0.82, 1.12)	0.5957	1.0000	0.96 (0.74, 1.23)	0.7252	1.0000	1.14 (0.86, 1.52)	0.3694	1.0000	0.9474	0.4226
rs2077482	A > T	0.28	CSNK1A1	intron	0.99 (0.85, 1.15)	0.8928	1.0000	0.93 (0.74, 1.18)	0.5453	1.0000	0.91 (0.68, 1.21)	0.4967	1.0000	0.8230	0.9133

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interaction Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs1947582	G > A	0.48	CSNK1A1	intron	0.96 (0.83, 1.10)	0.5294	1.0000	0.94 (0.76, 1.18)	0.6157	1.0000	0.98 (0.76, 1.27)	0.8809	1.0000	0.8952	0.9175
rs7712431	A > G	0.17	CSNK1A1	intron	1.07 (0.89, 1.29)	0.4616	1.0000	1.07 (0.80, 1.43)	0.6474	1.0000	0.96 (0.69, 1.36)	0.8375	1.0000	0.9130	0.6691
rs10058728	T > A	0.45	CSNK1A1	intron	1.07 (0.93, 1.23)	0.3341	1.0000	1.12 (0.90, 1.39)	0.3070	1.0000	1.04 (0.80, 1.34)	0.7823	1.0000	0.6106	0.7331
rs12201804	G > A	0.15	LOC643954	flanking_3UTR	0.90 (0.74, 1.09)	0.2628	1.0000	1.08 (0.80, 1.45)	0.6393	1.0000	0.78 (0.54, 1.12)	0.1760	1.0000	0.8934	0.1901
rs7809903	C > G	0.43	NXPH1	flanking_3UTR	1.06 (0.92, 1.22)	0.4280	1.0000	1.15 (0.92, 1.43)	0.2152	1.0000	1.02 (0.78, 1.33)	0.8772	1.0000	0.4980	0.5077
rs2188253	G > A	0.30	LOC645680	flanking_5UTR	1.01 (0.86, 1.17)	0.9385	1.0000	1.05 (0.83, 1.33)	0.6922	1.0000	0.97 (0.74, 1.28)	0.8418	1.0000	0.9346	0.6631
rs7823976	A > G	0.48	NAT1	flanking_5UTR	0.99 (0.86, 1.14)	0.8871	1.0000	0.96 (0.78, 1.19)	0.7023	1.0000	0.99 (0.76, 1.28)	0.9258	1.0000	0.9388	0.9290
rs6586710	A > T	0.30	NAT1	flanking_5UTR	1.02 (0.88, 1.19)	0.7968	1.0000	0.94 (0.74, 1.18)	0.5696	1.0000	1.05 (0.79, 1.40)	0.7351	1.0000	0.8315	0.4849
rs4921877	A > T	0.26	NAT1	flanking_5UTR	0.94 (0.81, 1.10)	0.4706	1.0000	0.88 (0.69, 1.12)	0.2956	1.0000	0.88 (0.66, 1.18)	0.3923	1.0000	0.5457	0.9161
rs10888150	G > A	0.42	NAT1	flanking_5UTR	1.02 (0.89, 1.18)	0.7464	1.0000	1.01 (0.81, 1.25)	0.9425	1.0000	0.99 (0.76, 1.29)	0.9364	1.0000	0.9976	0.9690
rs6586712	A > C	0.35	NAT1	flanking_5UTR	0.98 (0.85, 1.13)	0.7772	1.0000	0.94 (0.75, 1.18)	0.5940	1.0000	0.90 (0.69, 1.18)	0.4336	1.0000	0.8607	0.8353
rs4921581	G > A	0.32	NAT1	intron	1.11 (0.95, 1.28)	0.1811	1.0000	1.19 (0.95, 1.50)	0.1296	0.9676	1.10 (0.85, 1.44)	0.4624	1.0000	0.3022	0.6733
rs2172426	A > G	0.46	NAT2	upstream	1.03 (0.90, 1.18)	0.6934	1.0000	1.09 (0.88, 1.36)	0.4151	1.0000	1.09 (0.85, 1.40)	0.4807	1.0000	0.6979	0.9800
rs1495750	G > A	0.45	NAT2	upstream	1.00 (0.87, 1.15)	0.9939	1.0000	0.94 (0.76, 1.16)	0.5678	1.0000	1.17 (0.91, 1.50)	0.2224	1.0000	0.8614	0.2032
rs17595174	C > A	0.34	NAT2	upstream	0.97 (0.84, 1.12)	0.7061	1.0000	0.97 (0.78, 1.22)	0.8059	1.0000	0.81 (0.62, 1.05)	0.1109	1.0000	0.9711	0.3031

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interaction Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs7016785	A > G	0.33	NAT2	upstream	1.01 (0.88, 1.17)	0.8886	1.0000	0.95 (0.76, 1.20)	0.6763	1.0000	1.03 (0.79, 1.34)	0.8373	1.0000	0.9266	0.7008
rs4646246	A > G	0.17	NAT2	flanking_5UTR	0.97 (0.81, 1.16)	0.7299	1.0000	0.85 (0.63, 1.15)	0.2936	1.0000	1.25 (0.92, 1.69)	0.1494	1.0000	0.5724	0.0770
rs7011792	C > G	0.40	NAT2	intron	0.97 (0.85, 1.12)	0.7240	1.0000	0.96 (0.77, 1.20)	0.7058	1.0000	0.80 (0.62, 1.04)	0.0960	0.9997	0.9289	0.3108
rs1961456	A > G	0.30	NAT2	intron	0.97 (0.84, 1.14)	0.7397	1.0000	0.98 (0.77, 1.24)	0.8496	1.0000	1.14 (0.86, 1.50)	0.3566	1.0000	0.9770	0.4027
rs1801280	A > G	0.44	NAT2	coding	1.00 (0.87, 1.14)	0.9442	1.0000	1.03 (0.83, 1.28)	0.7987	1.0000	0.86 (0.67, 1.11)	0.2354	1.0000	0.9694	0.2744
rs721399	A > G	0.29	NAT2	flanking_3UTR	0.92 (0.79, 1.08)	0.2975	1.0000	0.91 (0.71, 1.16)	0.4351	1.0000	1.04 (0.79, 1.37)	0.7790	1.0000	0.7376	0.4616
rs4646257	G > A	0.18	NAT2	flanking_3UTR	0.89 (0.74, 1.07)	0.2156	0.9998	0.80 (0.59, 1.08)	0.1439	0.9941	1.12 (0.82, 1.51)	0.4791	1.0000	0.3437	0.1321
rs12676857	A > G	0.15	NAT2	flanking_3UTR	0.89 (0.73, 1.09)	0.2451	1.0000	0.74 (0.53, 1.04)	0.0794	0.9451	1.21 (0.87, 1.66)	0.2531	1.0000	0.2119	0.0395
rs2410562	A > G	0.41	NAT2	flanking_3UTR	1.06 (0.92, 1.22)	0.4038	1.0000	1.13 (0.91, 1.41)	0.2751	1.0000	1.02 (0.79, 1.31)	0.9041	1.0000	0.5476	0.5429
rs10828243	G > A	0.25	LOC729243	flanking_3UTR	1.13 (0.96, 1.32)	0.1394	0.9996	1.13 (0.88, 1.44)	0.3380	1.0000	1.04 (0.78, 1.39)	0.8029	1.0000	0.6631	0.7338
rs7942486	A > C	0.44	ARNTL	flanking_5UTR	0.95 (0.82, 1.09)	0.4551	1.0000	0.90 (0.72, 1.12)	0.3425	1.0000	1.00 (0.78, 1.29)	0.9778	1.0000	0.6145	0.5116
rs11022742	A > G	0.27	ARNTL	flanking_5UTR	1.00 (0.85, 1.17)	0.9753	1.0000	1.01 (0.79, 1.28)	0.9474	1.0000	1.17 (0.88, 1.56)	0.2741	1.0000	0.9995	0.4292
rs7950226	G > A	0.46	ARNTL	intron	1.03 (0.90, 1.19)	0.6437	1.0000	0.92 (0.74, 1.15)	0.4712	1.0000	1.07 (0.83, 1.38)	0.5995	1.0000	0.7761	0.3788
rs10766074	A > G	0.17	ARNTL	intron	0.94 (0.78, 1.13)	0.4819	1.0000	0.97 (0.73, 1.30)	0.8505	1.0000	0.98 (0.70, 1.38)	0.9263	1.0000	0.9743	0.9883
rs4757144	A > G	0.41	ARNTL	intron	0.92 (0.80, 1.06)	0.2490	1.0000	0.88 (0.71, 1.10)	0.2544	1.0000	0.94 (0.73, 1.21)	0.6157	1.0000	0.5118	0.7050

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interac-tion Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs11022765	C > A	0.25	ARNTL	intron	0.97 (0.82, 1.13)	0.6731	1.0000	1.07 (0.83, 1.37)	0.5907	1.0000	1.01 (0.75, 1.34)	0.9720	1.0000	0.8727	0.7342
rs6486121	A > G	0.37	ARNTL	intron	1.00 (0.86, 1.15)	0.9549	1.0000	1.19 (0.95, 1.49)	0.1359	1.0000	0.90 (0.68, 1.18)	0.4327	1.0000	0.3466	0.1263
rs10832027	A > G	0.32	ARNTL	intron	0.96 (0.82, 1.11)	0.5655	1.0000	1.07 (0.84, 1.35)	0.5951	1.0000	0.98 (0.75, 1.29)	0.8986	1.0000	0.8793	0.6516
rs1562438	G > A	0.28	ARNTL	intron	1.06 (0.91, 1.24)	0.4624	1.0000	1.15 (0.90, 1.46)	0.2713	1.0000	1.12 (0.85, 1.49)	0.4209	1.0000	0.5456	0.9187
rs12421530	C > G	0.39	ARNTL	intron	0.98 (0.85, 1.13)	0.7673	1.0000	1.10 (0.88, 1.38)	0.4003	1.0000	0.85 (0.64, 1.12)	0.2356	1.0000	0.7098	0.1493
rs3789327	A > G	0.46	ARNTL	intron	0.99 (0.86, 1.14)	0.8563	1.0000	1.02 (0.82, 1.27)	0.8785	1.0000	0.87 (0.67, 1.12)	0.2698	1.0000	0.9830	0.3401
rs11022778	A > C	0.32	ARNTL	intron	1.04 (0.89, 1.21)	0.6264	1.0000	0.88 (0.70, 1.11)	0.2908	1.0000	1.07 (0.82, 1.40)	0.6293	1.0000	0.6015	0.3194
rs969485	A > G	0.30	ARNTL	intron	1.16 (0.99, 1.35)	0.0590	0.9944	1.19 (0.94, 1.51)	0.1532	1.0000	1.19 (0.90, 1.57)	0.2280	1.0000	0.3560	0.9400
rs1044432	A > T	0.16	ARNTL	downstream	0.84 (0.69, 1.01)	0.0643	1.0000	0.85 (0.64, 1.14)	0.2859	1.0000	0.88 (0.62, 1.25)	0.4878	1.0000	0.5643	0.8736
rs17452383	A > G	0.13	ARNTL	downstream	1.07 (0.87, 1.30)	0.5336	1.0000	1.01 (0.74, 1.37)	0.9548	1.0000	1.13 (0.78, 1.63)	0.5330	1.0000	0.9960	0.6959
rs10832032	C > A	0.44	ARNTL	downstream	1.01 (0.87, 1.16)	0.9347	1.0000	1.00 (0.80, 1.24)	0.9653	1.0000	1.06 (0.82, 1.37)	0.6417	1.0000	0.9996	0.7339
rs211135	C > A	0.44	TPH1	upstream	0.99 (0.86, 1.14)	0.9103	1.0000	1.11 (0.89, 1.39)	0.3349	1.0000	0.96 (0.75, 1.24)	0.7727	1.0000	0.6542	0.3724
rs1800532	C > A	0.38	TPH1	intron	1.04 (0.90, 1.19)	0.6248	1.0000	0.85 (0.68, 1.07)	0.1686	0.9988	1.13 (0.88, 1.46)	0.3482	1.0000	0.4052	0.0999
rs11024449	G > A	0.24	TPH1	intron	0.95 (0.81, 1.12)	0.5624	1.0000	0.95 (0.74, 1.22)	0.6647	1.0000	1.11 (0.83, 1.48)	0.4893	1.0000	0.9035	0.4505
rs591556	G > A	0.17	TPH1	intron	0.94 (0.78, 1.13)	0.5206	1.0000	1.16 (0.88, 1.53)	0.2897	1.0000	0.75 (0.53, 1.07)	0.1098	0.9786	0.5813	0.0541

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interac-tion Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs623580	T > A	0.35	TPH1	flanking_5UTR	0.99 (0.86, 1.14)	0.8870	1.0000	1.21 (0.97, 1.51)	0.0992	1.0000	0.81 (0.62, 1.06)	0.1210	0.9994	0.2612	0.0246
rs1079785	G > A	0.43	TPH1	flanking_5UTR	0.99 (0.86, 1.14)	0.8763	1.0000	1.02 (0.81, 1.27)	0.8905	1.0000	1.01 (0.78, 1.31)	0.9468	1.0000	0.9937	0.9474
rs6485646	A > G	0.49	CRY2	flanking_5UTR	1.03 (0.90, 1.18)	0.6808	1.0000	0.97 (0.78, 1.20)	0.7785	1.0000	0.81 (0.63, 1.05)	0.1048	1.0000	0.9658	0.1428
rs1401417	C > G	0.23	CRY2	intron	0.94 (0.80, 1.12)	0.5121	1.0000	1.02 (0.79, 1.31)	0.9061	1.0000	0.69 (0.50, 0.95)	0.0249	0.4082	0.9961	0.0611
rs11038699	A > G	0.28	CRY2	intron	1.03 (0.88, 1.20)	0.7425	1.0000	1.13 (0.89, 1.43)	0.3252	1.0000	0.75 (0.56, 1.00)	0.0532	0.9099	0.6355	0.0338
rs10838527	A > G	0.08	CRY2	3UTR	0.89 (0.69, 1.15)	0.3738	1.0000	1.06 (0.73, 1.56)	0.7473	1.0000	0.74 (0.45, 1.19)	0.2149	1.0000	0.9493	0.2409
rs2292910	C > A	0.34	CRY2	3UTR	1.09 (0.94, 1.26)	0.2751	1.0000	1.08 (0.86, 1.36)	0.4953	1.0000	0.89 (0.68, 1.17)	0.3959	1.0000	0.8142	0.2643
rs3824872	C > A	0.21	CRY2	flanking_3UTR	1.03 (0.87, 1.22)	0.7158	1.0000	0.96 (0.74, 1.24)	0.7292	1.0000	1.07 (0.79, 1.44)	0.6671	1.0000	0.9456	0.6142
rs7118472	G > A	0.06	TMEM135	flanking_3UTR	1.03 (0.78, 1.36)	0.8322	1.0000	1.16 (0.75, 1.79)	0.5055	1.0000	0.93 (0.55, 1.58)	0.7992	1.0000	0.8147	0.5582
rs11235185	C > A	0.08	TMEM135	flanking_3UTR	0.94 (0.74, 1.22)	0.6579	1.0000	0.72 (0.47, 1.11)	0.1415	1.0000	0.71 (0.43, 1.17)	0.1781	1.0000	0.3583	0.9308
rs10748185	G > A	0.49	TPH2	intron	1.02 (0.88, 1.17)	0.8009	1.0000	1.03 (0.83, 1.29)	0.7763	1.0000	1.09 (0.84, 1.40)	0.5201	1.0000	0.9562	0.7547
rs11179000	A > T	0.22	TPH2	intron	0.87 (0.73, 1.03)	0.0932	1.0000	0.78 (0.60, 1.02)	0.0738	0.9962	0.75 (0.55, 1.03)	0.0744	1.0000	0.2037	0.7945
rs17110477	A > T	0.24	TPH2	intron	0.88 (0.74, 1.04)	0.1218	1.0000	0.74 (0.57, 0.97)	0.0320	0.9790	0.81 (0.60, 1.09)	0.1653	1.0000	0.1086	0.7335
rs1386492	A > G	0.18	TPH2	intron	1.09 (0.91, 1.30)	0.3678	1.0000	1.24 (0.93, 1.64)	0.1439	1.0000	1.01 (0.75, 1.38)	0.9321	1.0000	0.3463	0.3456
rs4760750	C > A	0.41	TPH2	intron	0.96 (0.84, 1.11)	0.6210	1.0000	0.88 (0.70, 1.11)	0.2712	1.0000	0.93 (0.71, 1.20)	0.5671	1.0000	0.5528	0.7766

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interaction Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs1352250	G > A	0.43	TPH2	intron	0.97 (0.84, 1.11)	0.6301	1.0000	0.89 (0.71, 1.12)	0.3135	1.0000	0.93 (0.72, 1.21)	0.5909	1.0000	0.5927	0.7900
rs11179050	A > G	0.40	TPH2	intron	0.96 (0.83, 1.10)	0.5482	1.0000	0.83 (0.66, 1.04)	0.1070	1.0000	1.12 (0.87, 1.43)	0.3959	1.0000	0.2425	0.0766
rs1487275	A > C	0.29	TPH2	intron	1.01 (0.87, 1.18)	0.8565	1.0000	0.97 (0.76, 1.25)	0.8399	1.0000	1.04 (0.79, 1.37)	0.7805	1.0000	0.9676	0.6826
rs1386482	C > A	0.37	TPH2	intron	1.01 (0.88, 1.17)	0.8541	1.0000	0.92 (0.73, 1.16)	0.4763	1.0000	1.10 (0.85, 1.42)	0.4689	1.0000	0.7499	0.2873
rs1872824	G > A	0.36	TPH2	flanking_3UTR	1.08 (0.93, 1.24)	0.3217	1.0000	1.03 (0.82, 1.29)	0.8018	1.0000	1.03 (0.80, 1.32)	0.8312	1.0000	0.9732	0.9789
rs11113179	G > A	0.08	CRY1	intron	0.94 (0.73, 1.21)	0.6268	1.0000	0.92 (0.62, 1.36)	0.6820	1.0000	0.71 (0.44, 1.15)	0.1601	1.0000	0.9214	0.3922
rs10746085	A > G	0.38	CRY1	intron	1.00 (0.87, 1.16)	0.9805	1.0000	0.93 (0.74, 1.16)	0.5188	1.0000	1.04 (0.80, 1.34)	0.7962	1.0000	0.8077	0.4785
rs10778533	C > A	0.18	CRY1	flanking_5UTR	1.03 (0.87, 1.23)	0.7233	1.0000	1.01 (0.77, 1.33)	0.9499	1.0000	1.00 (0.73, 1.38)	0.9930	1.0000	0.9998	0.9384
rs12315175	A > G	0.23	CRY1	flanking_5UTR	1.06 (0.91, 1.25)	0.4527	1.0000	1.04 (0.81, 1.33)	0.7613	1.0000	1.17 (0.87, 1.57)	0.3022	1.0000	0.9443	0.6045
rs10778534	A > G	0.36	CRY1	flanking_5UTR	1.05 (0.91, 1.21)	0.5052	1.0000	1.07 (0.86, 1.33)	0.5719	1.0000	0.99 (0.76, 1.29)	0.9544	1.0000	0.8446	0.6575
rs11113193	G > A	0.19	CRY1	flanking_5UTR	0.92 (0.77, 1.10)	0.3699	1.0000	0.99 (0.74, 1.31)	0.9239	1.0000	0.97 (0.70, 1.34)	0.8433	1.0000	0.9939	0.8890
rs11074634	G > A	0.26	RBBP6	flanking_3UTR	1.27 (1.09, 1.49)	0.0025	0.4114	1.30 (1.01, 1.67)	0.0387	0.9802	1.26 (0.94, 1.69)	0.1154	1.0000	0.1102	0.8829
rs1442849	G > A	0.26	PER1	upstream	1.10 (0.94, 1.29)	0.2423	1.0000	1.06 (0.83, 1.36)	0.6513	1.0000	1.29 (0.97, 1.72)	0.0792	1.0000	0.8751	0.3050
rs3027279	A > C	0.41	PER1	upstream	1.05 (0.91, 1.20)	0.5295	1.0000	1.09 (0.88, 1.37)	0.4268	1.0000	1.06 (0.83, 1.37)	0.6352	1.0000	0.7015	0.8672
rs9914077	A > G	0.42	PER1	flanking_3UTR	1.11 (0.96, 1.28)	0.1517	0.9998	1.22 (0.99, 1.51)	0.0685	0.9994	0.93 (0.71, 1.21)	0.5744	1.0000	0.2117	0.1396

SNP	Allele	MAF	Gene	Location	Main Effect Analysis			<24mo Shift-work			≥24mo Shift-work			Joint Test	Interaction Term
					OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	OR (CI)	P-value	P-perm	P-value	P-value
rs2253820	G > A	0.16	PER1	coding	0.94 (0.78, 1.14)	0.5455	1.0000	0.98 (0.73, 1.32)	0.9035	1.0000	1.03 (0.73, 1.43)	0.8865	1.0000	0.9907	0.8113
rs3027188	G > C	0.14	PER1	intron	1.01 (0.83, 1.22)	0.9620	1.0000	1.03 (0.77, 1.39)	0.8456	1.0000	1.07 (0.76, 1.51)	0.6976	1.0000	0.9793	0.8527
rs2278637	A > C	0.33	PER1	downstream	0.90 (0.77, 1.04)	0.1584	0.9749	0.91 (0.72, 1.15)	0.4143	1.0000	0.80 (0.61, 1.06)	0.1183	0.9922	0.7468	0.4478
rs7224199	C > A	0.48	SLC6A4	flanking_3UTR	0.90 (0.78, 1.03)	0.1257	1.0000	1.01 (0.81, 1.26)	0.9368	1.0000	0.89 (0.70, 1.14)	0.3569	1.0000	0.9948	0.4627
rs3813034	A > C	0.47	SLC6A4	flanking_3UTR	0.91 (0.79, 1.05)	0.1852	1.0000	0.98 (0.79, 1.22)	0.8540	1.0000	0.95 (0.74, 1.21)	0.6669	1.0000	0.9889	0.8409
rs140701	G > A	0.43	SLC6A4	intron	0.93 (0.81, 1.07)	0.3129	1.0000	0.98 (0.79, 1.23)	0.8745	1.0000	0.97 (0.75, 1.24)	0.7819	1.0000	0.9905	0.8946
rs8076005	A > G	0.20	SLC6A4	intron	0.97 (0.82, 1.16)	0.7612	1.0000	0.95 (0.73, 1.24)	0.6888	1.0000	0.92 (0.67, 1.26)	0.5978	1.0000	0.9096	0.9016
rs2066713	G > A	0.36	SLC6A4	intron	1.09 (0.95, 1.26)	0.2184	1.0000	1.04 (0.83, 1.30)	0.7433	1.0000	1.14 (0.88, 1.47)	0.3324	1.0000	0.9434	0.6198
rs7214991	A > G	0.37	SLC6A4	downstream	0.98 (0.85, 1.13)	0.7815	1.0000	0.88 (0.71, 1.10)	0.2627	1.0000	1.04 (0.81, 1.34)	0.7464	1.0000	0.5214	0.2901
rs7223304	A > G	0.35	AANAT	upstream	1.05 (0.90, 1.21)	0.5331	1.0000	0.97 (0.77, 1.22)	0.8079	1.0000	1.28 (0.98, 1.66)	0.0698	1.0000	0.9460	0.1299
rs11077821	G > A	0.14	AANAT	upstream	1.06 (0.87, 1.29)	0.5865	1.0000	1.01 (0.74, 1.37)	0.9742	1.0000	1.26 (0.90, 1.77)	0.1831	1.0000	0.9984	0.3532

Supplementary Table 2. Analyses presented in Supplementary Table 1 are repeated in CGEMS data for 19 common variants identified in Supplementary Table 1 as having a p-value <0.05 in interaction or permutation analyses in NHSII. All women were post-menopausal at blood draw and followed for incident breast cancer. Analyses are adjusted for matching factors (Main effect analyses: n_{cases}=896, $n_{controls}$=886; Analyses involving shift-work: n_{cases}=882, $n_{controls}$=863).

SNP	Allele	MAF	Chr	Coordinate	Gene	Location	Main Effect Analysis		<24mo Shift-work		≥24mo Shift-work		Joint Test	Interaction Term
							OR	P-value	OR	P-value	OR	P-value	P-value	P-value
rs10165970	G > A	0.151	2	100823421	NPAS2	intron	1.17 (0.98, 1.39)	0.0906	1.10 (0.87, 1.38)	0.4316	1.33 (0.98, 1.79)	0.0635	0.1552	0.3154
rs7605570	G > A	0.393	2	100925336	NPAS2	intron	0.95 (0.83, 1.10)	0.5084	0.91 (0.76, 1.09)	0.2887	1.05 (0.84, 1.31)	0.6576	0.5499	0.3272
rs12712085	G > A	0.433	2	100931583	NPAS2	intron	0.93 (0.81, 1.06)	0.2827	0.87 (0.73, 1.04)	0.1277	1.05 (0.85, 1.31)	0.6343	0.3107	0.2134
rs3820787	G > A	0.34	2	100932666	NPAS2	intron	1.02 (0.89, 1.18)	0.7374	0.97 (0.81, 1.17)	0.7785	1.19 (0.94, 1.50)	0.1488	0.3574	0.2064
rs10191450	G > A	0.36	2	100937167	NPAS2	intron	1.16 (1.01, 1.33)	0.0368	1.08 (0.90, 1.29)	0.3977	1.24 (0.99, 1.56)	0.0634	0.1149	0.3111
rs882272	G > A	0.419	2	100942631	NPAS2	intron	1.15 (1.01, 1.32)	0.0354	1.15 (0.97, 1.37)	0.1115	1.11 (0.89, 1.38)	0.3622	0.1776	0.8444
rs7581886	A > G	0.144	2	100947678	NPAS2	intron	1.09 (0.90, 1.32)	0.3830	1.00 (0.79, 1.27)	0.9933	1.26 (0.91, 1.75)	0.1603	0.3083	0.2310
rs4851392	G > A	0.275	2	100948408	NPAS2	intron	1.09 (0.93, 1.26)	0.2815	1.02 (0.84, 1.25)	0.8207	1.25 (0.97, 1.60)	0.0826	0.2367	0.2404
rs2305160	G > A	0.341	2	100957736	NPAS2	coding	1.01 (0.87, 1.16)	0.9184	0.99 (0.82, 1.19)	0.9244	1.07 (0.84, 1.36)	0.5731	0.8871	0.6732
rs6719533	A > G	0.463	2	100965519	NPAS2	intron	1.09 (0.95, 1.25)	0.2019	1.02 (0.86, 1.21)	0.8452	1.28 (1.01, 1.61)	0.0375	0.1222	0.1347
rs11123857	A > G	0.283	2	100970244	NPAS2	intron	1.01 (0.88, 1.18)	0.8485	1.05 (0.87, 1.26)	0.6278	0.98 (0.76, 1.26)	0.8577	0.8992	0.7205
rs4864984	G > A	0.212	4	55935044	CLOCK	upstream	0.94 (0.80, 1.11)	0.4467	0.94 (0.76, 1.16)	0.5723	0.88 (0.67, 1.15)	0.3415	0.5504	0.7419
rs11943456	A > G	0.456	4	55971091	CLOCK	upstream	1.04 (0.91, 1.19)	0.5653	1.02 (0.86, 1.21)	0.7871	1.06 (0.85, 1.33)	0.5913	0.8495	0.8040
rs12676857	A > G	0.145	8	18310852	NAT2	flanking_ 3UTR	1.01 (0.83, 1.22)	0.9332	0.96 (0.75, 1.22)	0.7236	1.07 (0.77, 1.47)	0.6989	0.8006	0.5073
rs623580	T > A	0.328	11	18020553	TPH1	flanking_ 5UTR	1.10 (0.95, 1.26)	0.1931	1.09 (0.92, 1.30)	0.3301	1.06 (0.84, 1.35)	0.6221	0.5921	0.8195
rs1401417	C > G	0.226	11	45836686	CRY2	intron	1.06 (0.91, 1.25)	0.4512	1.17 (0.95, 1.44)	0.1319	0.94 (0.72, 1.22)	0.6264	0.2847	0.2006
rs11038699	A > G	0.264	11	45853653	CRY2	intron	1.08 (0.93, 1.26)	0.3161	1.14 (0.94, 1.39)	0.1833	1.02 (0.79, 1.31)	0.9059	0.4083	0.4978
rs17110477	A > T	0.249	12	70630130	TPH2	intron	1.06 (0.91, 1.24)	0.4537	0.94 (0.77, 1.15)	0.5658	1.24 (0.96, 1.62)	0.1046	0.1553	0.0700
rs11074634	G > A	0.287	16	24516709	RBBP6	flanking_ 3UTR	0.89 (0.77, 1.03)	0.1297	1.03 (0.85, 1.25)	0.7667	0.70 (0.55, 0.88)	0.0025	0.0071	0.0080