Additional Supporting Information for Ciarleglio et al.:
"Genetic Differences in Human Circadian Clock Genes Among Worldwide Populations"

Table S1. Further information about the SNPs studied in this report.

Genes	Location	Genomic size (bp)	Chromosomal position	SNPs	Flanking Sequence	Ensembl Genomic Reference Sequence	Ensembl Coding Reference Sequence	Primers (forward and reverse, 5'-3')	Reference
Arntl	11p15.2	109 487	13286395	ss95215854	catg**t**ttaa	ENSG00000133794		GTGGTGAGAAATGGTCAC	n/a
								CATGCTAACAATGCTCAG	n/a
			13288144	ss95215855	CCCA**A**GCTT	ENSG00000133794	ENST00000256172	GTCCAATGGATTTAAAGGAC	n/a
								CTGGTAACCTCCACAGA	n/a
			13335041	ss95215856	cact**g**tgtc	ENSG00000133794	ENST00000256172	CAGACAAAGATGACCCTC	n/a
								CCTTGGTGTTCTGTATATTC	n/a
Arntl2	12p11.23	87 478	27374970	rs5797225	gttg**ttg**ttgt			CCTGGCTTCTGTGTTATTTA	n/a
								GTCCTTTTAGCATTCTGCT	n/a
			27375106	rs7137588	cgtg**g**ttcc			ATCTAAGTGGCTTTAGGG	n/a
			27375125	rs11048972	atgg**a**caaa			TCATTGCTAAGTACTCAGG	n/a
			27375128	ss95215857	acaa**a**ggag	ENSG00000029153			
			27375878	rs10548381	ttct**cta**ctaa			CATCTCTGAACTTCTGTTTC	n/a
								CTTGGCTTTCCAGACAAG	n/a
			27420486	rs4964059	ctct**a**tcaa			GGAGAATGGTTCATGTAGAC	n/a
			27420525	ss95215858	gata**t**ttta	ENSG00000029153	ENST00000261178	ACTCACCATGTACCATCTC	n/a
			27464992	ss95215859	aaat**a**tttc	ENSG00000029153	ENST00000261178	CTTCCTGTCACAGGGATG	n/a
								GCCAAAACAATATGTAAG	n/a
Clock	4q12	114 337	55996126	rs1801260	GGCA**T**AGCC			TCCAGCAGTTTCATGAGATGC	Katzenberg et al. (1998)
			55996140	ss95215860	TGAC**A**GTGT	ENSG00000134852	ENST00000381325	GAGGTCATTTCATAGCTGAGC	n/a
Per2	2q37.3	44 406	238830546	ss95215861	tatg**g**gcac	ENSG00000132326	ENST00000254657	GGCACTTGGGTGTCGGTTTCTC	Shiino et al. (2003)
			238830402	rs2304669	TGGC**A**CTGC			CCCCTATCGGGCTATGGTGGA	
			238830383	c.1984A>G	AGAG**A**GTGT	ENSG00000132326	ENST00000254657		
			238830376	ss95215862	GTGG**C**GTCG	ENSG00000132326	ENST00000254657		
			238830375	rs2304670	TGGC**G**TCGC				
			238830372	rs2304671	CGTC**G**CTCA				
			238830273	ss95215863	gaga**g**cagt	ENSG00000132326	ENST00000254657		
Per3	1p36.23	60 853	7792555	rs35426314	GAGC**G**TGTC			ATGATTCTAGATGAGCTCTGCGGTGG	Ebisawa et al. (2001)
			7792635	rs228669	CCAG**T**GGGC			GAACCGAGGTAGTACAGAAAACACGATG	
			7809991	rs35733104	CTTA**C**CTCG			ACCTCGAGCCCGACCTTCCCACCTG	
			7810060	c.2460A>G	CTGC**A**CCGG	AB047532	ENST00000361923	CAAAAACGATGGCGACAACAGAGGACA	
			7810080	rs228696	GGGC**T**GCCC				
			7810086	rs35899625	CCCT**T**GTCC				
			7810166	rs228697	CCCC**C**CTGT				
			7810192	rs17031614	CATC**G**TTTT				
			del(3031-3084nt)	AB047536				GAAGATTAAAGTGTCTTTTCATGTGCCCTTAC	Ebisawa et al. (2001)
								AATGTCTGGCATTGGAGTTTGAAACATTAG	
			7819720	rs10462021	TCTC**A**TGGG			CGGGAAAAGAACCCTGTGTCTTATTCAG	Ebisawa et al. (2001)
								CTACCTGGCCAAAATACATGAGTATATGAC	
AANAT	17q25.1	2 549	71974704	rs3760138	GTGT**G**AGCT			CTCTGCAGGGGGTCAAAAG	
			71974983	rs4238989	TGGG**C**TTGT			CATCTCTAATCCCTGCTCTGTCAC	

SNPs in Table S1 are identified by either rs or ss number with the exception of two SNPs, one in *Per2* (c.1984A>G) and the other in *Per3* (c.2460A>G), which were labelled by the convention described in: den Dunnen JT and Antonarakis SE (2000) Mutation nomenclature extensions and suggestions to describe complex mutations: a discussion. Hum Mutat 5: 7-12.

Table S2. Allele frequencies studied in all populations with deviations from Hardy/Weinberg Equilibrium (HWE).

Gene	Allele	African American	European American	Ghanaian African	Han Chinese	Papua New Guinea
Arntl						
ss95215854	T	1.00	0.99	0.93	1.00	1.00
ss95215855	A	1.00	0.97	1.00	1.00	1.00
ss95215856	G	0.98	0.99	0.98	0.99	0.96
Arntl2						
rs5797225	GTT (7)	0.01	-	-	-	-
	GTT (8)	0.49	0.71	0.51	0.48	0.71
	GTT (9)	0.50	0.29	0.46	0.51	0.28
	GTT (10)	-	-	0.03	0.01	0.01
rs7137588	G	0.86	0.73	0.87	0.93	0.75
rs11048972	A	0.98	0.94	0.87	0.98	1.00
ss95215857	A	1.00	0.96^{+}	1.00	1.00	1.00
rs10548381	+/CTA	0.93^{+}	0.90	0.98	0.98	0.99
rs4964059	A	0.91	0.67	0.88	0.43	0.43^{*}
ss95215858	T	0.99	1.00	1.00	1.00	1.00
ss95215859	A	1.00	1.00	1.00	1.00	1.00
Clock						
rs1801260	T	0.86	0.74^{*}	0.83	0.92	0.83
ss95215860	A	1.00	1.00	1.00	1.00	0.96

Per2						
rs2304669	A	0.97	0.87	0.99	0.94	0.94
c.1984A>G	A	1.00	1.00	1.00	1.00	1.00
ss95215862	C	N/A	1.00	N/A	N/A	N/A
rs2304670	G	0.90	0.93	0.87	0.94	1.00
rs2304671	G	0.96	0.93	0.96	0.89	1.00
Per3						
rs35426314	G	1.00	1.00	1.00	1.00	1.00
rs228669	C	0.96[+]	0.97	0.99	0.99	1.00
rs35733104	C	1.00	1.00	1.00	1.00	1.00
c.2460A>G	A	1.00	1.00	1.00	1.00	1.00
rs228696	C	0.95[*]	0.97	0.98	1.00	1.00
rs228697	C	0.98	0.99	1.00	0.95	0.83
rs17031614	G	1.00	1.00	1.00	1.00	1.00
AB047536	4-repeat	0.59	0.66	0.64	0.81[+]	0.41
rs10462021	A	0.93	0.83	0.96	1.00	0.98
AANAT						
rs4238989	G	0.74	0.53	0.87	0.53	0.51

[*] indicates deviation from HWE at $p < 0.05$

[+] indicates deviation from HWE at $p < 0.01$

N/A indicates that the marker was not genotyped for that population.

Table S3: Allele Frequency Differences (p values listed)

Marker	AA vs EA	AA vs GA	AA vs HC	AA vs PNG	EA vs GA	EA vs HC	EA vs PNG	GA vs HC	GA vs PNG	HC vs PNG
Arntl										
ss95215854	1	0.012	N/A	N/A	0.001	1	0.579	0.038	<0.001	N/A
ss95215855	0.098	N/A	N/A	N/A	0.094	0.092	0.014	N/A	N/A	N/A
ss95215856	0.271	0.618	0.241	0.708	0.068	0.606	0.004	0.246	0.458	0.242
Arntl2										
rs5797225	<0.001	0.263	0.97	0.001	<0.001	<0.001	0.168	0.442	0.003	0.001
rs7137588	0.004	0.682	0.107	0.045	0.001	<0.001	0.526	0.238	0.018	0.001
rs11048972	0.117	0.01	0.623	0.172	0.033	0.062	<0.001	0.001	<0.001	0.163
ss95215857	0.041	N/A	N/A	N/A	0.04	0.041	0.003	N/A	N/A	N/A
rs10548381	0.588	0.085	0.095	0.036	0.007	0.007	0.001	0.617	0.648	0.638
rs4964059	<0.001	0.486	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	0.884
ss95215858	0.103	1	1	0.418	N/A	N/A	N/A	N/A	N/A	N/A
ss95215859	1	N/A	N/A	N/A	1	1	0.131	N/A	N/A	N/A
Clock										
rs1801260	0.006	0.687	0.164	0.566	0.034	<0.001	0.012	0.128	0.86	0.078
ss95215860	1	N/A	N/A	0.074	1	1	<0.001	N/A	0.072	0.073
Per2										
rs2304669	0.001	0.351	0.175	0.217	<0.001	0.064	0.02	0.12	0.033	0.781
c.1984A>G	1	N/A	N/A	N/A	1	1	0.138	N/A	N/A	N/A
rs2304670	0.221	0.508	0.423	<0.001	0.062	0.688	<0.001	0.126	<0.001	0.005
rs2304671	0.307	0.721	0.105	0.031	0.385	0.125	<0.001	0.111	0.027	<0.001

Per3										
rs228669	0.534	0.061	0.203	0.035	0.36	0.33	0.037	1	0.431	0.428
c.2460A>G	0.19	N/A	N/A	N/A	0.195	0.202	1	N/A	N/A	N/A
rs228696	0.196	0.27	0.03	0.014	1	0.159	0.057	0.234	0.177	N/A
rs228697	0.079	0.498	0.462	<0.001	0.579	0.007	<0.001	0.06	<0.001	0.01
rs17031614	1	N/A	N/A	N/A	1	1	0.129	N/A	N/A	N/A
AB047536	0.291	0.517	0.001	0.016	0.743	0.002	<0.001	0.004	0.001	<0.001
rs10462021	0.008	0.534	0.01	0.172	<0.001	<0.001	<0.001	0.118	0.243	0.268
AANAT										
rs4238989	0.001	0.02	0.003	0.002	<0.001	0.902	0.664	<0.001	<0.001	0.674

AA = African American, EA = European American, GA = Ghanaian African, HC = Han Chinese, PNG = Papua New Guinea
N/A indicates test was not performed because marker was fixed for the same allele in all populations.

Table S4: Genotype Frequency Differences (p values listed)

Marker	AA vs EA	AA vs GA	AA vs HC	AA vs PNG	EA vs GA	EA vs HC	EA vs PNG	GA vs HC	GA vs PNG	HC vs PNG
Arntl										
ss95215854	1	0.017	N/A	N/A	<0.001	0.426	0.241	0.026	<0.001	N/A
ss95215855	0.058	N/A	N/A	N/A	0.154	0.166	0.012	N/A	N/A	N/A
ss95215856	0.259	1	0.602	0.455	0.245	0.605	0.019	0.58	0.451	0.232
Arntl2										
rs5797225	<0.001	0.665	0.903	0.001	<0.001	<0.001	0.083	0.864	0.004	0.001
rs7137588	0.009	0.893	0.251	0.182	0.004	<0.001	0.362	0.391	0.146	0.003
rs11048972	0.1	0.014	1	0.165	0.017	0.062	<0.001	0.009	<0.001	0.169
ss95215857	0.134	N/A	N/A	N/A	0.153	0.148	0.063	N/A	N/A	N/A
rs10548381	0.031	0.55	0.364	0.198	0.04	0.027	0.003	1	0.641	1
rs4964059	<0.001	0.596	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	0.607
ss95215858	0.102	1	1	N/A	N/A	N/A	N/A	N/A	N/A	N/A
ss95215859	1	N/A	N/A	N/A	1	1	0.127	N/A	N/A	N/A
Clock										
rs1801260	0.035	0.334	0.45	0.169	0.046	<0.001	0.011	0.015	0.839	0.011
ss95215860	0.197	N/A	N/A	0.418	0.199	0.194	<0.001	N/A	0.071	0.071
Per2										
rs2304669	0.01	0.614	0.469	0.354	0.001	0.199	0.073	0.116	0.03	1
c.1984A>G	1	N/A	N/A	N/A	1	1	0.132	N/A	N/A	N/A
rs2304670	0.238	0.786	0.603	<0.001	0.077	0.864	<0.001	0.206	<0.001	0.005
rs2304671	0.488	1	0.087	0.028	0.499	0.182	<0.001	0.098	0.026	<0.001

Per3										
rs228669	0.121	0.622	1	0.074	0.344	0.326	0.012	1	0.463	0.412
c.2460A>G	0.193	N/A	N/A	N/A	0.188	0.205	0.245	N/A	N/A	N/A
rs228696	0.113	1	0.115	0.032	0.717	0.065	0.093	0.245	0.18	N/A
rs228697	0.073	0.526	0.419	0.002	1	0.001	<0.001	0.054	<0.001	0.042
rs17031614	1	N/A	N/A	N/A	1	1	0.127	N/A	N/A	N/A
AB047536	0.38	0.386	<0.001	0.044	0.521	<0.001	<0.001	0.015	0.003	<0.001
rs10462021	0.013	0.841	0.019	0.309	0.002	<0.001	<0.001	0.122	0.449	0.258
AANAT										
rs4238989	0.006	0.125	0.02	0.009	<0.001	0.926	0.835	<0.001	<0.001	0.734

AA = African American, EA = European American, GA = Ghanaian African, HC = Han Chinese, PNG = Papua New Guinea
N/A indicates that the marker was fixed for the same allele in both populations.

Table S5. Haplotype frequencies

Haplotype	African American	European American	Ghanaian African	Han Chinese	Papua New Guinea
Arntl					
T-G	0.98	0.98	0.92	0.99	0.96
G-G	N/A	0.01	0.06	N/A	N/A
Arntl2					
8-G-A-+-A	0.47	0.56	0.49	0.38	0.39
8-G-A-+-C	N/A	<0.01	N/A	0.03	0.07
8-C-A-+-C	0.02	0.11	N/A	0.04	0.22
9-G-A-+-A	0.34	0.07	0.36	0.02	0.02
9-G-A-+-C	0.02	0.05	0.02	0.48	0.26
9-C-A-+-C	0.04	0.06	N/A	0.01	0.01
9-C-G---C	0.01	0.05	N/A	<0.01	N/A
Per2					
A-A-G	0.1	0.07	0.11	0.05	N/A
A-G-A	0.04	0.07	0.03	0.1	N/A
A-G-G	0.82	0.73	0.83	0.78	0.94
G-G-G	0.03	0.13	0.01	0.06	0.06
Per3					
C-C-C-4-A	0.52	0.48	0.59	0.76	0.29
C-C-C-4-G	0.07	0.16	0.04	N/A	0.02
C-C-G-4-A	0.02	0.01	N/A	0.05	0.1
C-C-C-5-A	0.33	0.3	0.34	0.18	0.52
C-C-G-5-A	N/A	N/A	N/A	<0.01	0.06

Order of SNPs for each haplotype is as follows:

Arntl: (ss95215854/ss95215856)
Arntl2: (rs5797225/rs7137588/rs11048972/rs10548381/rs4964059)

Per2: (rs2304669/rs2304670/rs2304671)
Per3: (rs228669/rs228696/rs228697/AB047536/rs10462021)
N/A indicates that the haplotype was not present in that population.

Table S6: Haplotype Trend Regression (p values listed)

Haplotype	AA vs EA	AA vs GA	AA vs HC	AA vs PNG	EA vs GA	EA vs HC	EA vs PNG	GA vs HC	GA vs PNG	HC vs PNG
Arntl (2 SNPs)	0.84	0.044	0.309	0.474	0.001	0.714	0.099	0.062	0.171	0.123
*Arntl*2 (5 SNPs)	<0.001	0.795	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
Per2 (3 SNPs)	0.04	0.876	0.099	0.006	0.006	0.105	<0.001	0.024	0.011	<0.001
Per3 (5 SNPs)	0.07	0.27	0.006	<0.001	0.005	<0.001	<0.001	0.061	<0.001	<0.001

AA = African American, EA = European American, GA = Ghanaian African, HC = Han Chinese, PNG = Papua New Guinea

Order of SNPs for each haplotype is as follows:
Arntl: ss95215854/ss95215856
Arntl2: rs5797225/rs7137588/rs11048972/rs10548381/rs4964059
Per2: rs2304669/rs2304670/rs2304671
Per3: rs228669/rs228696/rs228697/AB047536/rs10462021

Table S7: FST values (theta P) for the five populations together and for the PNG sub-populations.

	F_{ST}	F_{ST} (PNG only)
Arntl		
ss95215854	0.043	N/A
ss95215855	0.013	N/A
ss95215856	0.005	0
Arntl2		
rs5797225	0.057	0.067
rs7137588	0.042	0.113
rs11048972	0.028	N/A
ss95215857	0.020	N/A
rs10548381	0.025	0
rs4964059	0.139	0.186
ss95215858	0.012	N/A
ss95215859	0	N/A
Clock		
rs1801260	0.034	0
ss95215860	0.035	0.093
Per2		
rs2304669	0.031	0.061
c.1984A>G	0	N/A
rs2304670	0.020	N/A
rs2304671	0.017	N/A
Per3		
rs228669	0.005	N/A
c.2460A>G	0	N/A
rs228696	0.008	N/A
rs228697	0.139	0.008
rs17031614	0	N/A
AB047536	0.059	0.059
rs10462021	0.072	0.041
AANAT		
rs4238989	0.084	0

N/A indicates test was not performed because marker was fixed for the same allele in all populations.

Table S8: Allele frequencies for all polymorphisms in the Papua New Guinea (PNG) sub-populations with deviations from Hardy/Weinberg Equilibrium (HWE).

Gene	Allele	Eastern Highlands	Nasioi	Coastal
Arntl				
ss95215854	T	1.00	1.00	1.00
ss95215855	A	1.00	1.00	1.00
ss95215856	G	0.93	0.98	0.98
Arntl2				
rs5797225	GTT (7)	-	-	-
	GTT (8)	0.83	0.74	0.57^{+}
	GTT (9)	0.17	0.24	0.43
	GTT (10)	-	0.02	-
rs7137588	G	0.57	0.89	0.78
rs11048972	A	1.00	1.00	1.00
ss95215857	A	1.00	1.00	1.00
rs10548381	+	1.00	0.98	0.98
rs4964059	C	0.57	0.35	0.80
ss95215858	T	1.00	1.00	1.00
ss95215859	A	1.00	1.00	1.00
Clock				
rs1801260	T	0.88	0.85	0.77
ss95215860	A	1.00	1.00	0.89
Per2				
rs2304669	A	0.95	1.00	0.86
c.1984A>G	A	1.00	1.00	1.00
rs2304670	G	1.00	1.00	1.00
rs2304671	G	1.00	1.00	1.00
Per3				
rs35426314	G	1.00	1.00	1.00
rs228669	C	1.00	1.00	1.00
rs35733104	C	1.00	1.00	1.00
c.2460A>G	A	1.00	1.00	1.00
rs228696	C	1.00	1.00	1.00
rs228697	C	0.76	0.89	0.84^{+}
rs17031614	G	1.00	1.00	1.00
AB047536	5-repeat	0.74	0.46	0.57
rs10462021	A	1.00	0.93	1.00
AANAT				
rs4238989	G	0.55	0.48	0.50

* indicates deviation from HWE at $p < 0.05$; $^{+}$ indicates deviation from HWE at $p < 0.01$

Eastern Highlands = Gimi and Goroka
Nasioi = Bouganville
Coastal = Sepik and Madang

Table S9: F_{ST} values for clock gene SNPs among the PNG populations.

	EH vs NA	EH vs Coastal	NA vs Coastal
Arntl			
ss95215856	0.005	0	0
Arntl2			
rs5797225	0	0.136	0.052
rs7137588	0.216	0.077	0.021
rs10548381	0	0	0
rs4964059	0.075	0.099	0.337
Clock			
rs1801260	0	0.017	0
ss95215860	N/A	0.090	0.096
Per2			
rs2304669	0.031	0.019	0.119
Per3			
rs228697	0.036	0	0
AB047536	0.132	0.039	0.002
rs10462021	0.041	N/A	0.041
AANAT			
rs4238989	0	0	0

EH = Eastern Highlands (Gimi and Goroka)
NA = Nasioi, Bouganville
Coastal = Sepik, Madang

N/A indicates test was not performed because marker was fixed for the same allele in all populations.

Table S10: FST values (theta P) for all pair-wise combinations of populations.

	AA vs EA	AA vs GA	AA vs HC	AA vs PNG	EA vs GA	EA vs HC	EA vs PNG	GA vs HC	GA vs PNG	HC vs PNG
Arntl										
ss95215854	0	0.06	N/A	N/A	0.11	0	0	0.049	0.074	N/A
ss95215855	0.012	N/A	N/A	N/A	0.011	0.011	0.013	N/A	N/A	N/A
ss95215856	0	0	0	0	0.001	0	0.027	0	0	0.007
Arntl2										
rs5797225	0.092	0	0	0.086	0.068	0.101	0	0	0.062	0.095
rs7137588	0.041	0	0.012	0.027	0.048	0.094	0	0.006	0.035	0.091
rs11048972	0.01	0.069	0	0.017	0.025	0.011	0.034	0.07	0.143	0.016
ss95215857	0.017	N/A	N/A	N/A	0.017	0.017	0.02	N/A	N/A	N/A
rs10548381	0	0.02	0.021	0.037	0.029	0.029	0.037	0	0	0
rs4964059	0.115	0	0.404	0.389	0.094	0.11	0.112	0.366	0.354	0
ss95215858	0.043	0	0	0.004	N/A	N/A	N/A	N/A	N/A	N/A
ss95215859	0	N/A	N/A	N/A	0	0	0	N/A	N/A	N/A
Clock										
rs1801260	0.036	0	0.003	0	0.018	0.076	0.02	0.021	0	0.021
ss95215860	0	N/A	N/A	0.024	0	0	0.078	N/A	0.024	0.024
Per2										
rs2304669	0.039	0	0	0.001	0.058	0.015	0.017	0.025	0.023	0
c.1984A>G	0	N/A	N/A	N/A	0	0	0	N/A	N/A	N/A
ss95215862	1	N/A	N/A	N/A	1	1	1	N/A	N/A	N/A
rs2304670	0.001	0	0.001	0.112	0.018	0	0.04	0.018	0.15	0.064
rs2304671	0.001	0	0.026	0.04	0	0.007	0.039	0.022	0.045	0.124

Per3										
rs228669	0	0.009	0.008	0.04	0.001	0.001	0.013	0	0.003	0.003
c.2460A>G	0	N/A	N/A	N/A	0	0	0	N/A	N/A	N/A
rs228696	0.006	0.002	0.042	0.051	0	0.009	0.011	0.012	0.016	N/A
rs228697	0	0.01	0.003	0.1	0	0.056	0.313	0.041	0.139	0.053
rs17031614	0	N/A	N/A	N/A	0	0	0	N/A	N/A	N/A
AB047536	0.002	0	0.102	0.05	0	0.048	0.108	0.066	0.083	0.27
rs10462021	0.032	0	0.063	0.017	0.057	0.101	0.078	0.032	0	0.011
AANAT										
rs4238989	0.075	0.044	0.076	0.094	0.206	0	0	0.23	0.246	0

AA = African American, EA = European American, GA = Ghanaian African, HC = Han Chinese, PNG = Papua New Guinea
N/A indicates test was not performed because marker was fixed for the same allele in all populations.

Figure S1. Histogram plots of *Arntl and Arntl2* SNPs. Labels: AA = African American, EA = European Americans, HC = Han Chinese, GA = Ghana Africans, and PNG = Papua New Guineans; gray is the common allele, black is the less common polymorphism. For rs36008253, the number of TTG repeats is depicted as: solid gray = 7, black = 8, gray scalloping = 9, and cross-hatching = 10.

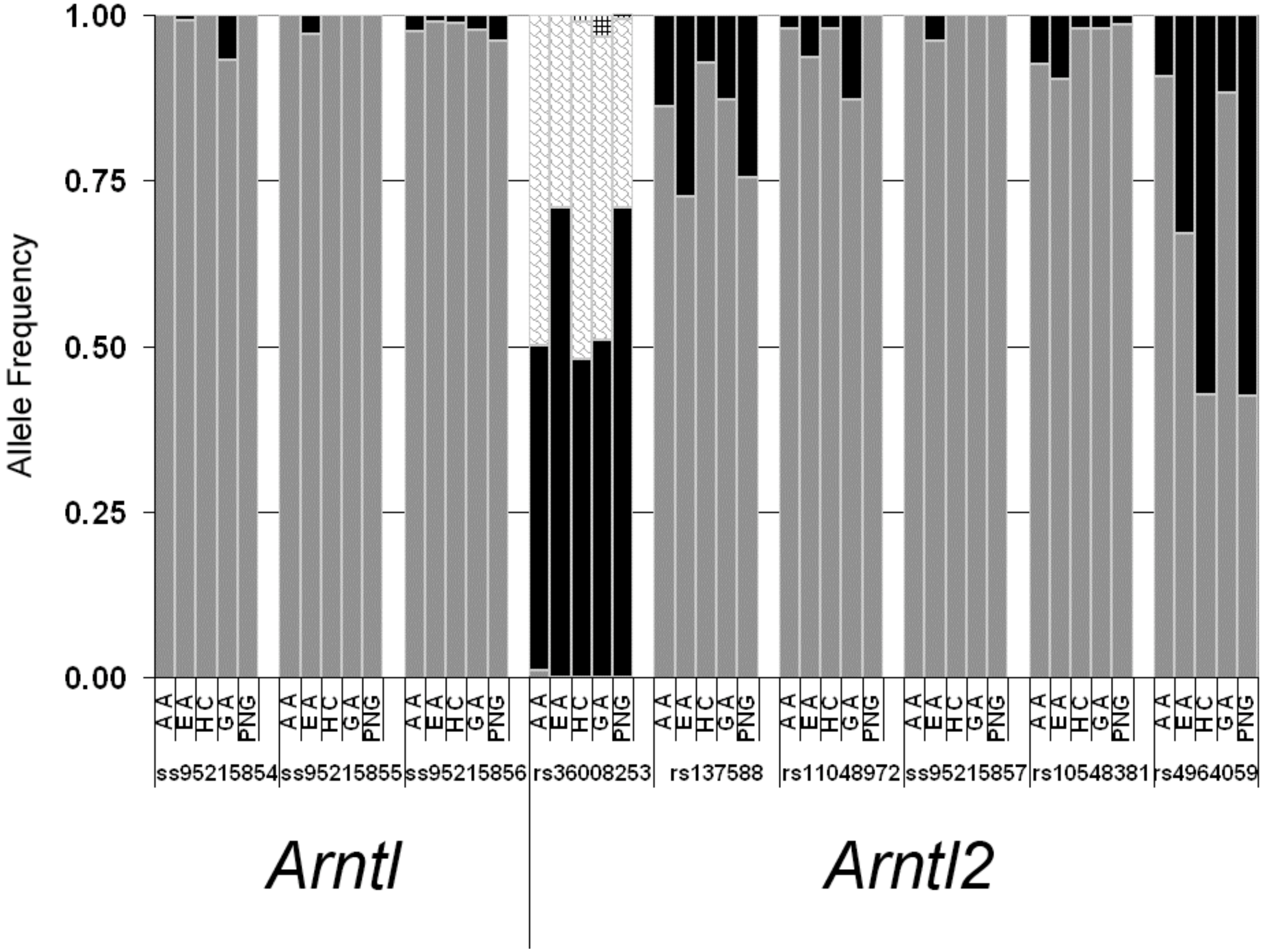

Figure S2. histogram plots of SNPs in *hClock* (rs1801260; panel A) and *hAANAT* (rs4238989; panel B). Labels: AA = African American, EA = European Americans, HC = Han Chinese, GA = Ghana Africans, and PNG = Papua New Guineans.