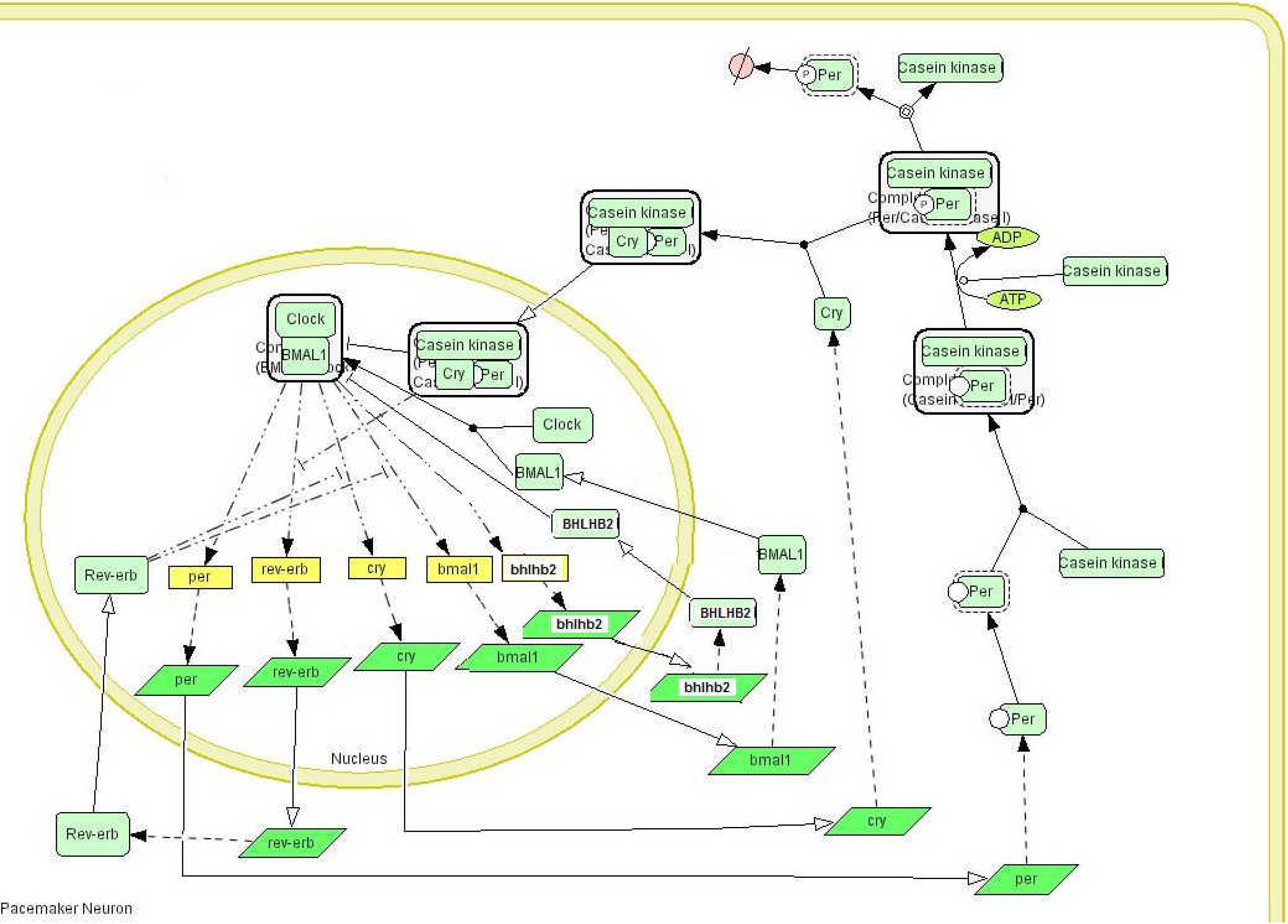
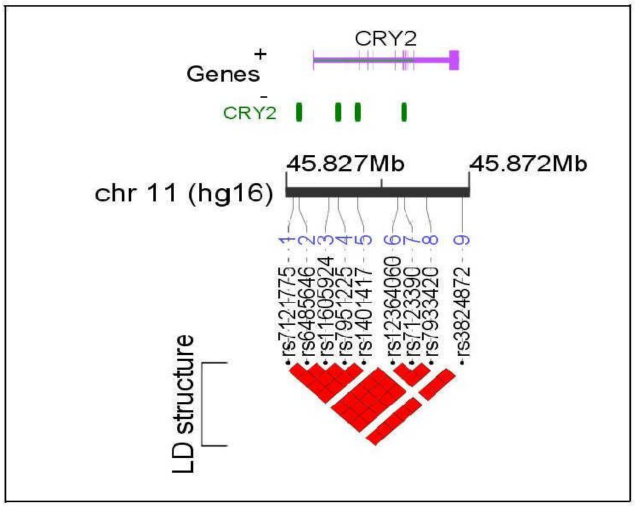
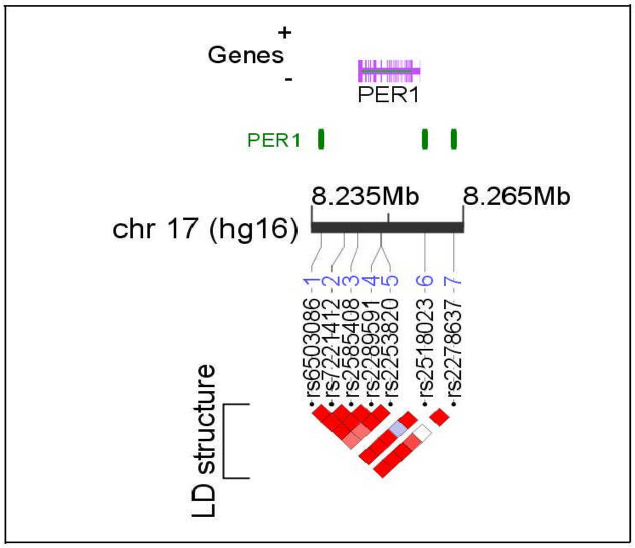
Type of file: figure
Label: 10
Filename: Suppl Figure I.JPG

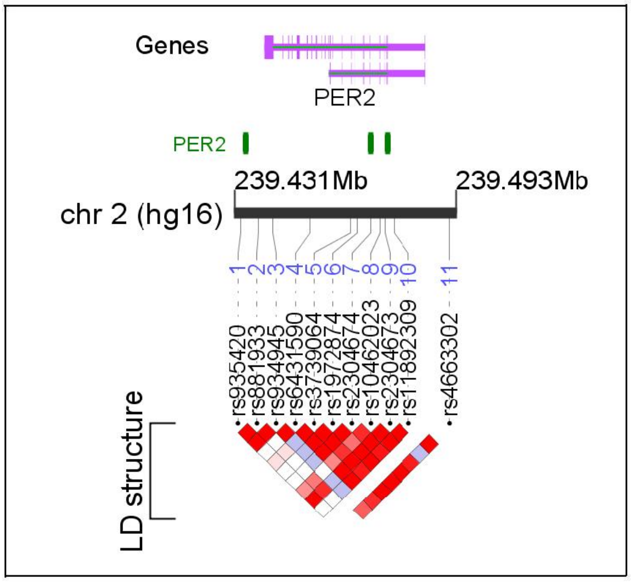

Per
P
Casein kinase I
Casein kinase I
Compl
(Per/Ca ase I)
P
Per
ADP
Casein kinase I
ATP
Casein kinase I
(Pe
Cas
Cry
Per
Cry
Casein kinase I
Compl
(Casein /Per)
Per
Clock
Cor
(BM ock
BMAL1
Casein kinase I
(Pe
Ca
Cry
Per
Clock
BMAL1
BHLHB2
BMAL1
Casein kinase I
Per
Rev-erb
per
rev-erb
cry
bmal1
bhlhb2
bhlhb2
BHLHB2
per
rev-erb
cry
bmal1
bhlhb2
Per
bmal1
Nucleus
cry
Rev-erb
rev-erb
per
Pacemaker Neuron

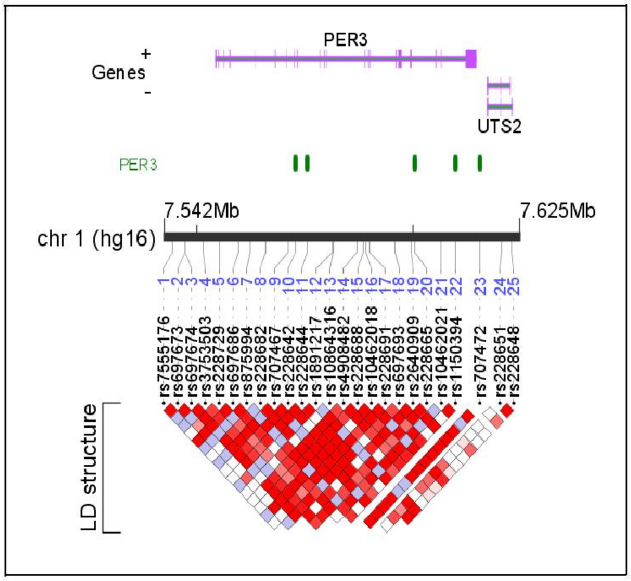
Type of file: figure
Label: 11
Filename: Supplementary Figure II LD plots.doc

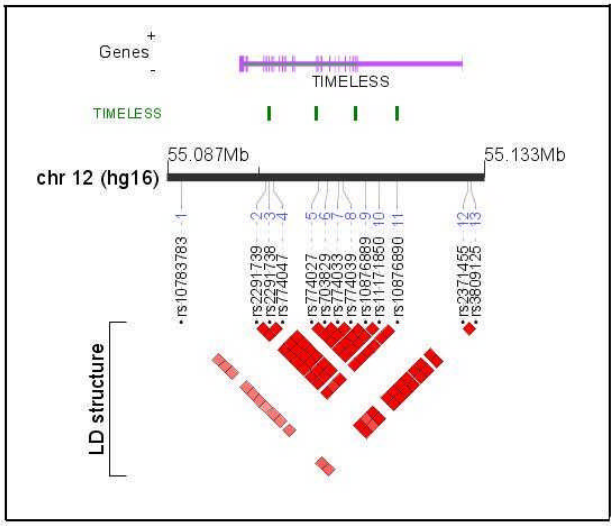
Supplementary Figure II. Linkage Disequilibrium (LD) Plot at Each Circadian Gene Region. The LD structure was constructed using the genotype data of the 30 Centre d'Etude du Polymorphisme Humain (CEPH) trios in the International HapMap Project. The horizontal black line depicts the genomic region. The single nucleotide polymorphisms (SNPs) tested in this study and the structure of each gene, with vertical lines indicating exons, are shown above the chromosome bar in green and in lavender, respectively. SNPs with minor allele frequency ≥ 0.1 in the gene region are shown below the black chromosome line. A linkage disequilibrium plot is shown in the bottom part of the figure based on the measure D': each square represents the magnitude of linkage disequilibrium for a single pair of SNPs, with red color indicating linkage disequilibrium that is strong (D' > 0.8) and statistically significant (logarithm of odds >2.0), and white indicating D' < 0.5. This figure was prepared using the program LocusView 2.0 (T. Petryshen, A. Kirby, M. Ainscow, unpublished software; http://www.broad.mit.edu/mpg/locusview). Genomic positions are in accordance with the National Center for Biotechnology Information build 34 hg16 of the human genome assembly.

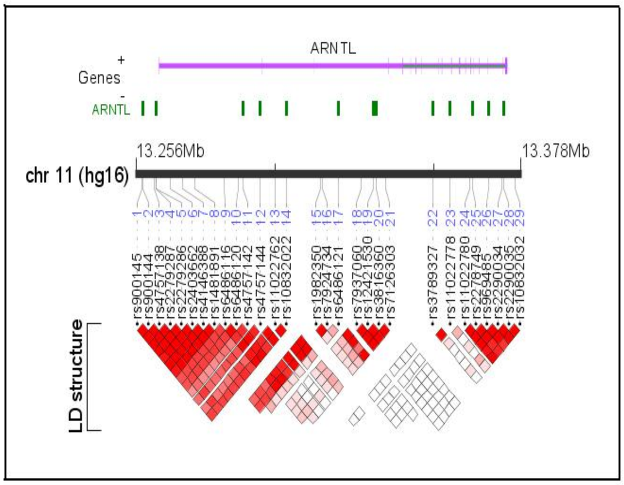

CRY2
Genes
+
-
CRY2
45.827Mb
45.872Mb
chr 11 (hg16)
1
2
3
4
5
6
7
8
9
rs7121775
rs6485646
rs11605924
rs7951225
rs1401417
rs12364060
rs7123390
rs7933420
rs3824872
LD structure

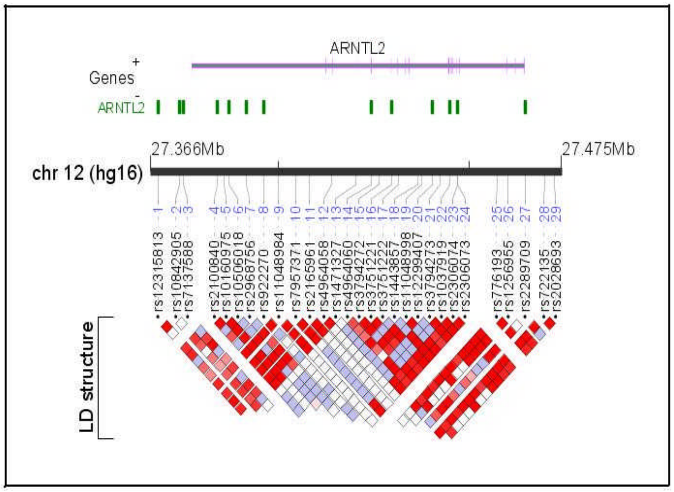

+
Genes
-
PER1
PER1
8.235Mb
8.265Mb
chr 17 (hg16)
1
2
3
4
5
6
7
rs6503086
rs7221412
rs2585408
rs2289591
rs2253820
rs2518023
rs2278637
LD structure

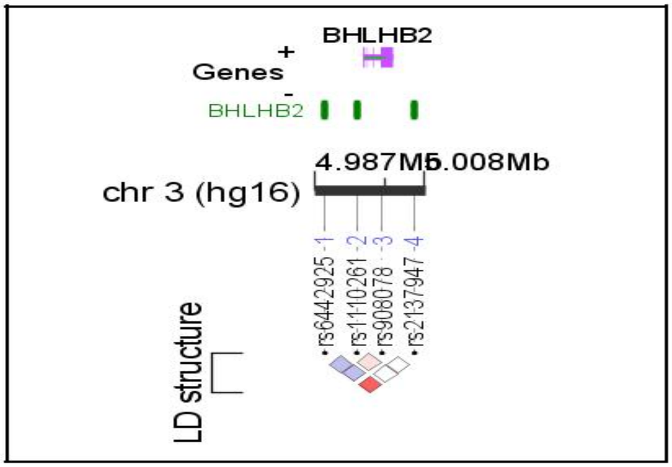

Genes
PER2
PER2
239.431Mb
239.493Mb
chr 2 (hg16)
1
2
3
4
5
6
7
8
9
10
11
rs935420
rs881933
rs934945
rs6431590
rs3739064
rs1972874
rs2304674
rs10462023
rs2304673
rs11892309
rs4663302
LD structure

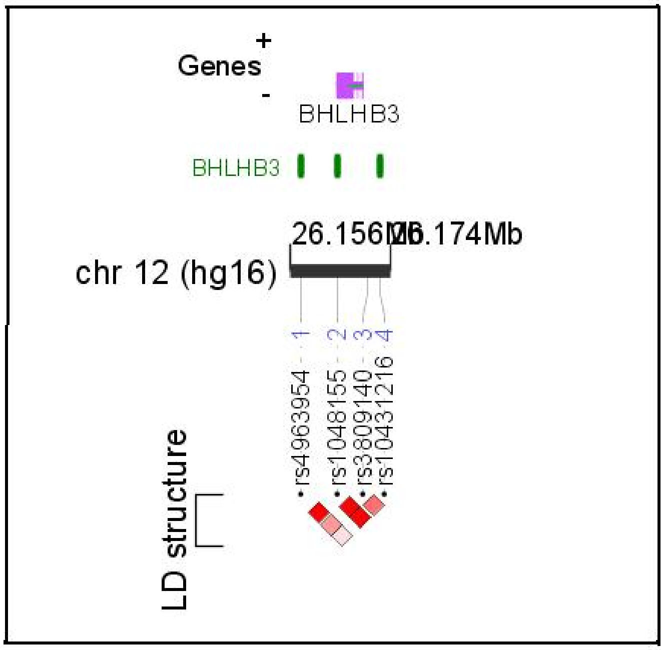

PER3
Genes
+
-
UTS2
PER3
7.542Mb
7.625Mb
chr 1 (hg16)
rs7555176
rs697673
rs697674
rs3753503
rs228729
rs697686
rs875994
rs228682
rs707467
rs228642
rs228644
rs1891217
rs10864316
rs4908482
rs228688
rs10462018
rs228691
rs697693
rs2640909
rs228665
rs10462021
rs1150394
rs707472
rs228651
rs228648
LD structure

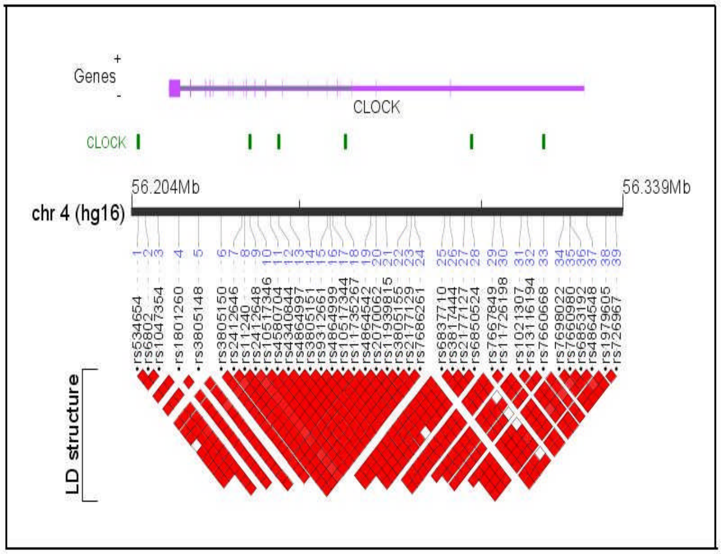

Genes
+
-
TIMELESS
TIMELESS
55.087Mb
55.133Mb
chr 12 (hg16)
rs10783783
rs2291739
rs2291738
rs774047
rs774027
rs703829
rs774033
rs774039
rs10876889
rs11171850
rs10876890
rs2371455
rs3809125
LD structure

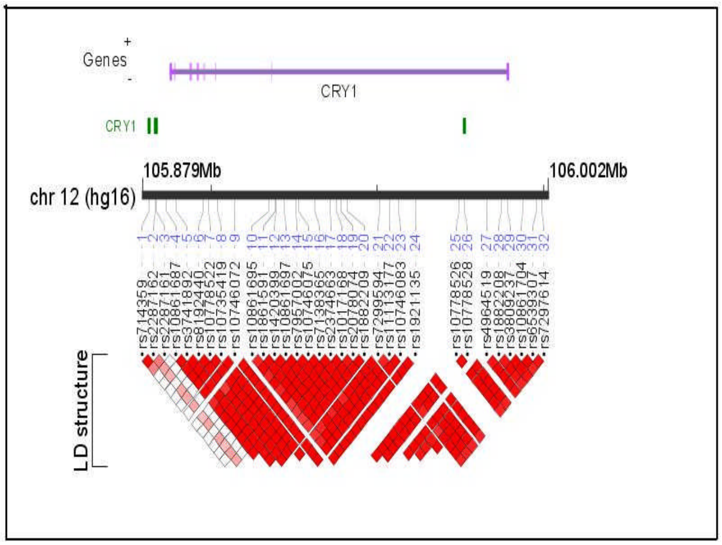

ARNTL
Genes
+
-
ARNTL
13.256Mb
13.378Mb
chr 11 (hg16)
rs900145
rs900144
rs4757138
rs2279287
rs2279286
rs2403662
rs4146388
rs1481891
rs6486116
rs6486120
rs4757142
rs4757144
rs11022762
rs10832022
rs1982350
rs7924734
rs6486121
rs7937060
rs12421530
rs3816360
rs7126303
rs3789327
rs11022778
rs11022780
rs2278749
rs969485
rs2290034
rs2290035
rs10832032
LD structure

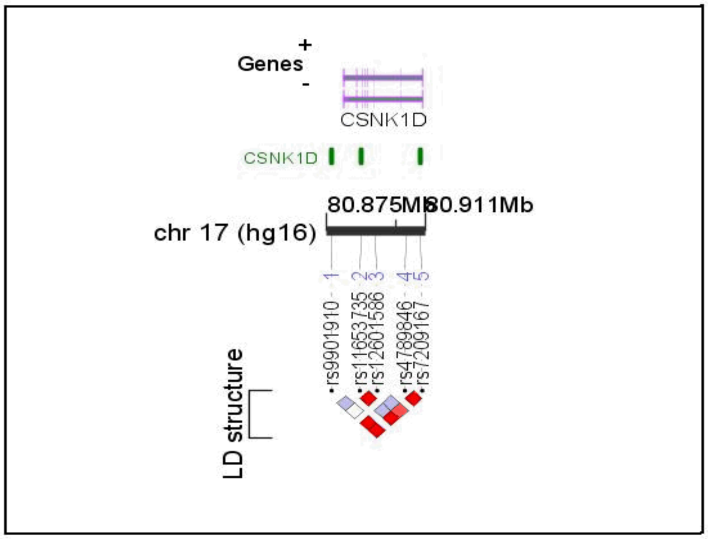

ARNTL2
Genes
+
-
ARNTL2
27.366Mb
27.475Mb
chr 12 (hg16)
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29
rs12315813
rs10842905
rs7137588
rs2100840
rs10160975
rs10506018
rs2968756
rs922270
rs11048984
rs7957371
rs2165961
rs4964058
rs1471327
rs4964060
rs3794272
rs3751221
rs3751222
rs1443857
rs11048998
rs12299407
rs3794273
rs1037919
rs2306074
rs2306073
rs776193
rs1256955
rs2289709
rs722135
rs2028693
LD structure

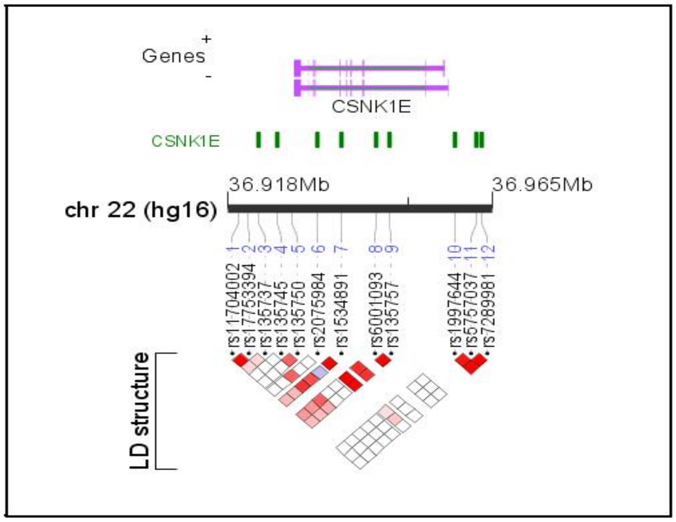

BHLHB2
Genes
+
-
BHLHB2
4.987Mb
5.008Mb
chr 3 (hg16)
1 2 3 4
rs6442925
rs1110261
rs908078
rs2137947
LD structure

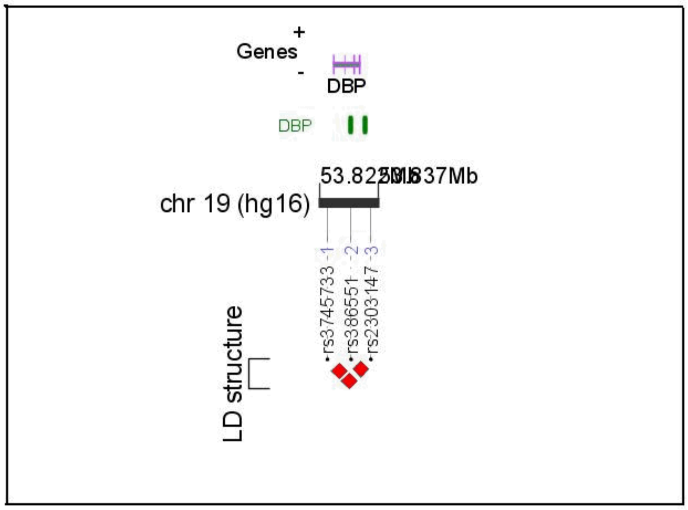

Genes
+
-
BHLHB3
BHLHB3
26.156Mb
26.174Mb
chr 12 (hg16)
1 2 3 4
rs4963954
rs1048155
rs3809140
rs10431216
LD structure

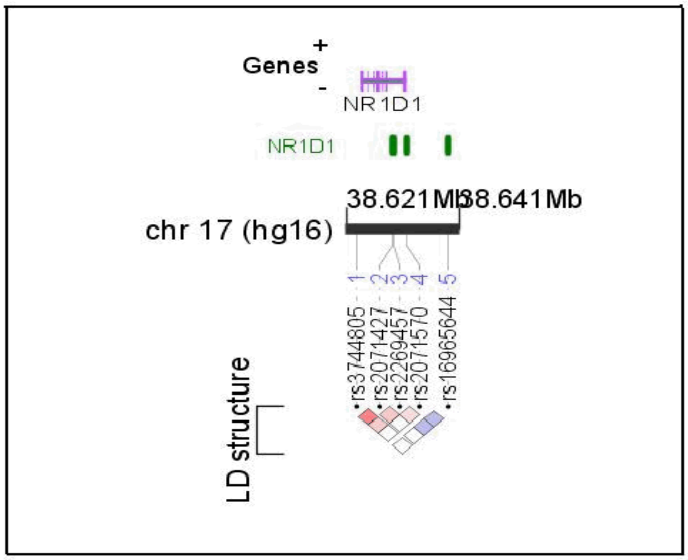

Genes
+
-
CLOCK
CLOCK
chr 4 (hg16)
56.204Mb
56.339Mb
1 rs534654
2 rs6802
3 rs1047354
4 rs1801260
5 rs3805148
6 rs3805150
7 rs2412646
8 rs11240
9 rs2412648
10 rs10517346
11 rs4580704
12 rs4340844
13 rs4864997
14 rs3805151
15 rs9312661
16 rs4864999
17 rs10517344
18 rs11735267
19 rs4864542
20 rs2070062
21 rs11939815
22 rs3805155
23 rs2177129
24 rs7686261
25 rs6837710
26 rs3817444
27 rs2177127
28 rs6850524
29 rs7667849
30 rs11726198
31 rs1021307
32 rs13116194
33 rs7660668
34 rs7698022
35 rs7660980
36 rs6853192
37 rs4864548
38 rs1979605
39 rs726967
LD structure


Genes
+
-
CRY1
CRY1
chr 12 (hg16)
105.879Mb
106.002Mb
1 rs714359
2 rs2287162
3 rs2287161
4 rs10861687
5 rs3741892
6 rs8192440
7 rs10778522
8 rs10735419
9 rs10746072
10 rs10861695
11 rs1861591
12 rs1420399
13 rs10861697
14 rs7957002
15 rs10746075
16 rs7138365
17 rs2374663
18 rs1017168
19 rs2078074
20 rs1882209
21 rs7299594
22 rs11113177
23 rs10746083
24 rs1921135
25 rs10778526
26 rs10778528
27 rs4964519
28 rs1882208
29 rs3809237
30 rs10861704
31 rs6539307
32 rs7297614
LD structure


Genes
+
-
CSNK1D
CSNK1D
chr 17 (hg16)
80.875Mb
80.911Mb
1 rs9901910
2 rs11653735
3 rs12601586
4 rs4789846
5 rs7209167
LD structure


Genes
+
-
CSNK1E
CSNK1E
36.918Mb
36.965Mb
chr 22 (hg16)
1 2 3 4 5 6 7 8 9 10 11 12
rs11704002
rs17753394
rs135737
rs135745
rs135750
rs2075984
rs1534891
rs6001093
rs135757
rs1997644
rs5757037
rs7289981
LD structure


Genes
+
-
DBP
DBP
53.825Mb
53.837Mb
chr 19 (hg16)
1 2 3
rs3745733
rs386551
rs2303147
LD structure


Genes
+
-
NR1D1
NR1D1
38.621Mb
38.641Mb
chr 17 (hg16)
1 2 3 4 5
rs3744805
rs2071427
rs2269457
rs2071570
rs16965644
LD structure

Type of file:	table
Label:	5
Filename:	Suppl Table I Altered Expression data in Stanley samples.doc

Supplementary Table I. Altered Expression of Circadian Genes in the Stanley Foundation Brain Collections of Bipolar Disorder

	Consortium collection[a]	Array collection[b]	Combined analysis
ARNTL	NS	-1.087 (p = 0.0319)[c]	-1.107 (p = 0.0038)
ARNTL2	NS	NS	-1.05 (p = 0.018)
BHLHB2	NS	-1.196 (p = 0.0004)	-1.186 (p = 0.00016)
NPAS2	-1.097 (p = 0.0399)	NS	-1.05 (p = 0.0116)
CLOCK	NS	-1.047 (p = 0.0432)	NS
CRY2	NS	+1.066 (p = 0.0137)	NS

Data are presented as fold changes and *p*-values for difference between patients and controls. [a] The Neuropathology Consortium collection includes 15 patients with bipolar disorder (BP) and 15 unaffected controls. [b] The Stanley Array Collection includes 35 patients with BP and 35 unaffected controls. [c] Fold changes (+ and - indicate increased and decreased gene expression, respectively) have been adjusted for potential confounding variables such as postmortem interval, brain pH, age at death, sex, and severity of substance and/or alcohol abuse. Within each of 12 microarray studies, the probes including that for circadian genes are analyzed individually for association with BP. This produces a fold change and confidence interval for each probe/disease in each study. For each unique gene, these fold changes and confidence intervals are aggregated across probes and studies, giving a mean and confidence interval reflecting all of the study/probe specific data for that gene. The gene's consensus fold change is a weighted mean of the individual fold changes (weights = 1/SE_i), and the *p*-value is based on the t-statistic for the weighted fold change and combined standard error of the fold change. This cross study analysis is performed within the Array collection studies, within the Consortium collection studies, and across all studies (combined analysis).NS, not significant. Other circadian genes tested in our study do not show significant abnormal expression in Stanley bipolar disorder brain samples. For more information, please visit the website of the Stanley Medical Research Institute Online Genomics Database at https://www.stanleygenomics.org/. Unpublished data with permission from Drs Fuller Torrey and Michael Elashoff and the Stanley Medical Research Institute.

Type of file: table
Label: 6
Filename: Suppl Table II Results of sib_tdt of 19 SNPs in sample i.doc

Supplementary Table II. Results of sib_tdt Analyses of 19 SNPs of 5 Circadian Genes in CNG and NIMH Waves 1-2 Bipolar Disorder Families (Sample I)

Gene	SNP	Proportion allele 1 is transmitted	T	NT	TDT *P*-value*
CRY2	rs6485646	0.47	60	69	0.25
CRY2	rs7951225	0.55	47	38	0.07
CRY2	rs1401417	0.46	37	44	0.94
CRY2	rs7123390	0.51	44	43	1.00
PER1	rs6503086	0.53	52	47	0.79
PER1	rs2518023	0.62	23	14	0.51
PER1	rs2278637	0.53	46	40	0.39
PER2	rs10201361	0.33	2	4	1.00
PER2	rs2304674	0.55	48	40	0.49
PER2	rs2304672	0.58	18	13	0.38
PER3	rs228642	0.43	46	60	0.70
PER3	rs228644	0.56	60	47	0.55
PER3	rs228665	0.44	41	53	0.51
PER3	rs1150394	0.54	50	42	1.00
PER3	rs707472	0.62	43	26	0.25
TIMELESS	rs2291738[a]	0.48	43	59	1.00
TIMELESS	rs774026[a]	0.48	38	46	1.00
TIMELESS	rs2279665[a]	0.46	40	52	0.39
TIMELESS	rs10876890[a]	0.52	60	49	0.29

[a] rs2291738 and rs10876890 were found to be associated with insomnia during mania episode in bipolar disorder patients in CNG and waves 1-2 samples, then were genotyped in CHIP and waves 3-4 samples. SNPs rs774026 and rs2279665 were genotyped in CHIP, CNG, and NIMH waves 1-4 samples, as these two SNPs showed suggestive evidence of association with bipolar disorder (Mansour HA et al. *Genes Brain Behav.* 2006; 5:150-157). T and NT: numbers of allele1 transmitted and non-transmitted from heterozygous parents to affected offspring.

Type of file:	table
Label:	7
Filename:	Suppl Table III Haplotype Analysis in sample I.doc

Supplementary Table III. Haplotype Analysis of 19 SNPs in 5 Circadian Genes in the CNG and NIMH waves 1-2 samples (Sample I)

Haplotype	Frequency	*p*-value	q-value[a]
Block-1-Markers:rs228642,rs228644-11	0.03	0.12	0.84
Block-1-Markers:rs228642,rs228644-12	0.39	0.83	1.00
Block-1-Markers:rs228642,rs228644-21	0.42	0.44	0.84
Block-1-Markers:rs228642,rs228644-22	0.16	0.19	0.84
Block-2-Markers:rs228665,rs1150394,rs707472-111	0.33	0.67	0.96
Block-2-Markers:rs228665,rs1150394,rs707472-121	0.15	0.46	0.84
Block-2-Markers:rs228665,rs1150394,rs707472-122	0.15	0.44	0.84
Block-2-Markers:rs228665,rs1150394,rs707472-221	0.35	0.3	0.84
Block-3-Markers:rs6503086,rs2518023,rs2278637-112	0.38	0.99	1.00
Block-3-Markers:rs6503086,rs2518023,rs2278637-211	0.28	0.25	0.84
Block-3-Markers:rs6503086,rs2518023,rs2278637-212	0.23	0.33	0.84
Block-3-Markers:rs6503086,rs2518023,rs2278637-221	0.08	0.66	0.96
Block-4-Markers:rs6485646,rs7951225,rs1401417,rs7123390-1212	0.52	0.24	0.84
Block-4-Markers:rs6485646,rs7951225,rs1401417,rs7123390-2112	0.25	0.013	0.53
Block-4-Markers:rs6485646,rs7951225,rs1401417,rs7123390-2211	0.03	0.51	0.84
Block-4-Markers:rs6485646,rs7951225,rs1401417,rs7123390-2221	0.2	0.48	0.84
Block-5-Markers:rs774026,rs2279665,rs10876890-222[b]	0.01	0.13	0.60
Block-5-Markers:rs774026,rs2279665,rs10876890-111[b]	0.02	0.16	0.60
Block-5-Markers:rs774026,rs2279665,rs10876890-212[b]	0.05	0.18	0.60
Block-5-Markers:rs774026,rs2279665,rs10876890-121[b]	0.05	0.65	1.00
Block-5-Markers:rs774026,rs2279665,rs10876890-221[b]	0.42	0.78	1.00
Block-5-Markers:rs774026,rs2279665,rs10876890-112[b]	0.45	0.97	1.00
Block-6-Markers:rs10201361,rs2304674,rs2304672-212	0.72	0.49	0.84
Block-6-Markers:rs10201361,rs2304674,rs2304672-221	0.08	0.44	0.84
Block-6-Markers:rs10201361,rs2304674,rs2304672-222	0.18	0.99	1.00

[a] q values by false discovery rate (FDR) analysis. [b] rs2291738 and rs10876890 in *TIMELESS* were found to be associated with insomnia during mania episode in bipolar disorder patients in CNG and waves 1-2 samples, then were genotyped in CHIP and waves 3-4 samples. SNPs rs774026 and rs2279665 in *TIMELESS* were genotyped in CHIP, CNG, and NIMH waves 1-4 samples, as these two SNPs showed suggestive association evidence with bipolar disorder by Nimgaonkar's group (Mansour HA et al. Genes Brain Behav. 2006; 5:150-157). Thus, haplotype association data in *TIMELESS* (block 5) was based genotypes in CHIP, CNG, and NIMH waves 1-4 samples.

Type of file:	table
Label:	8
Filename:	Suppl Table IV sib_tdt results of 62 SNPs in sample ii.doc

Supplementary Table IV. Results of sib_tdt Analyses of 62 SNPs at 10 Circadian Genes in CNG, NIMH Waves 1-4, and CHIP Bipolar Disorder Families (Sample II)

Gene	SNP	Proportion allele 1 is transmitted	T	NT	TDT *p*-value*
ARNTL	rs900144	0.45	124	152	1
ARNTL	rs2279286	0.44	104	134	0.85
ARNTL	rs4146388	< 5 transmissions	0	0	1
ARNTL	rs4757142	0.44	114	148	0.94
ARNTL	rs4757144	0.46	125	149	0.91
ARNTL	rs10832022	0.44	93	117	0.59
ARNTL	rs6486121	0.48	131	143	0.71
ARNTL	rs12421530	0.49	134	141	1
ARNTL	rs3816360	0.50	135	135	0.62
ARNTL	rs3789327	0.50	132	132	0.82
ARNTL	rs11022778	0.51	127	121	0.81
ARNTL	rs2278749	0.48	83	90	0.96
ARNTL	rs969485	0.51	120	113	0.6
ARNTL	rs2290035	0.52	154	142	0.63
ARNTL2	rs12315813	0.51	97	93	1
ARNTL2	rs10842905	0.49	124	130	0.83
ARNTL2	rs7137588	0.50	129	131	0.83
ARNTL2	rs2100840	0.48	63	67	0.59
ARNTL2	rs10506018	0.52	77	72	0.56
ARNTL2	rs2968756	0.55	85	70	0.29
ARNTL2	rs922270	0.43	54	71	0.21
ARNTL2	rs4964060	0.48	127	137	0.3
ARNTL2	rs3751221	0.50	69	70	0.52
ARNTL2	rs12299407	0.43	43	56	0.3
ARNTL2	rs1037919	0.46	75	90	0.099
ARNTL2	rs2306074	0.52	125	116	0.65
ARNTL2	rs2289709	0.50	57	56	0.77
BHLHB2	rs6442925	0.61	90	57	0.062
BHLHB2	rs1110261	0.49	87	92	0.83
BHLHB2	rs908078	0.50	75	76	0.5
BHLHB2	rs2137947	0.44	76	95	0.21
BHLHB3	rs4963954	0.52	144	137	0.36
BHLHB3	rs1048155	0.50	157	160	0.88
BHLHB3	rs10431216	0.53	106	94	1
CLOCK	rs534654	0.40	82	122	0.0097
CLOCK	rs2412648	0.46	113	133	0.12
CLOCK	rs4340844	0.44	119	154	0.015
CLOCK	rs11735267	0.55	159	127	0.059

Gene	SNP	Proportion allele 1 is transmitted	T	NT	TDT *p*-value*
CLOCK	rs6850524	0.43	126	168	0.012
CLOCK	rs7660668	0.51	116	113	0.59
CRY1	rs714359	0.48	100	107	0.45
CRY1	rs2287162	0.49	113	116	0.47
CRY1	rs2287161	0.52	159	144	0.55
CRY1	rs10778528	0.51	144	141	0.73
CSNK1D	rs9901910	0.50	77	76	0.8
CSNK1D	rs11653735	0.54	91	77	0.87
CSNK1D	rs7209167	0.53	150	134	0.64
CSNK1E	rs135737	0.47	97	108	0.79
CSNK1E	rs135745	0.48	142	151	0.72
CSNK1E	rs2075984	0.54	159	134	0.35
CSNK1E	rs1534891	0.40	50	75	0.84
CSNK1E	rs6001093	0.53	92	82	0.82
CSNK1E	rs135757	0.44	94	121	0.95
CSNK1E	rs1997644	0.51	148	142	1
CSNK1E	rs5757037	0.51	134	129	0.6
CSNK1E	rs7289981	0.48	58	63	0.94
DBP	rs386551	0.51	111	108	0.51
DBP	rs3848543	0.45	65	78	0.71
NR1D1	rs2071427	0.49	118	123	0.52
NR1D1	rs2269457	0.55	121	98	0.72
NR1D1	rs2071570	0.44	92	118	1
NR1D1	rs16965644	0.47	67	74	0.93

*Nominally significant *p*-values are highlighted in red. T and NT: numbers of allele1 transmitted and non-transmitted from heterozygous parents to affected offspring.

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Supplementary Table V. Haplotype Analysis of 62 SNPs in 10 Circadian Genes in CNG, NIMH Waves 1-4 and CHIP Samples (Sample II)

Haplotype	Frequency	*p*-value	q-value[a]
Block-1-Markers:rs534654,rs2412648,rs4340844,rs11735267,rs6850524,rs7660668-111211	0.19	**0.034**	0.8
Block-1-Markers:rs534654,rs2412648,rs4340844,rs11735267,rs6850524,rs7660668-211112	0.04	**0.025**	0.79
Block-1-Markers:rs534654,rs2412648,rs4340844,rs11735267,rs6850524,rs7660668-211122	0.22	0.81	1
Block-1-Markers:rs534654,rs2412648,rs4340844,rs11735267,rs6850524,rs7660668-211211	0.15	0.94	1
Block-1-Markers:rs534654,rs2412648,rs4340844,rs11735267,rs6850524,rs7660668-212121	0.07	**0.028**	0.79
Block-1-Markers:rs534654,rs2412648,rs4340844,rs11735267,rs6850524,rs7660668-222121	0.31	0.069	0.97
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-11111	0.53	0.56	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-11121	0.01	0.23	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-11211	0.01	0.062	0.97
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-11221	0.01	0.23	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-11222	0.01	0.77	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-12111	0.01	0.14	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-21111	0.01	0.23	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-21211	0.01	0.58	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-21221	0.13	0.9	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-21222	0.01	0.079	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-22111	0.02	0.39	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-22122	0.01	0.85	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-22221	0.03	0.27	1
Block-2-Markers:rs900144,rs2279286,rs4757142,rs4757144,rs10832022-22222	0.19	0.7	1
Block-3-Markers:rs6486121,rs12421530,rs3816360-111	0.01	0.27	1
Block-3-Markers:rs6486121,rs12421530,rs3816360-112	0.6	0.99	1
Block-3-Markers:rs6486121,rs12421530,rs3816360-121	0.04	0.4	1
Block-3-Markers:rs6486121,rs12421530,rs3816360-212	0.01	0.99	1
Block-3-Markers:rs6486121,rs12421530,rs3816360-221	0.29	0.42	1
Block-3-Markers:rs6486121,rs12421530,rs3816360-222	0.05	0.26	1
Block-4-Markers:rs3789327,rs11022778-11	0.54	0.63	1
Block-4-Markers:rs3789327,rs11022778-21	0.13	0.33	1
Block-4-Markers:rs3789327,rs11022778-22	0.33	0.74	1
Block-5-Markers:rs2278749,rs969485,rs2290035-111	0.01	0.74	1
Block-5-Markers:rs2278749,rs969485,rs2290035-112	0.16	0.84	1
Block-5-Markers:rs2278749,rs969485,rs2290035-211	0.51	0.66	1
Block-5-Markers:rs2278749,rs969485,rs2290035-222	0.32	0.68	1
Block-6-Markers:rs4963954,rs1048155-11	0.55	0.62	1
Block-6-Markers:rs4963954,rs1048155-12	0.12	0.15	1
Block-6-Markers:rs4963954,rs1048155-22	0.33	0.6	1
Block-7-Markers:rs12315813,rs10842905,rs7137588,rs2100840,rs10506018-12111	0.11	0.37	1
Block-7-Markers:rs12315813,rs10842905,rs7137588,rs2100840,rs10506018-12221	0.09	0.6	1
Block-7-Markers:rs12315813,rs10842905,rs7137588,rs2100840,rs10506018-21121	0.54	0.41	1
Block-7-Markers:rs12315813,rs10842905,rs7137588,rs2100840,rs10506018-21222	0.16	0.53	1
Block-7-Markers:rs12315813,rs10842905,rs7137588,rs2100840,rs10506018-22121	0.01	0.71	1
Block-7-Markers:rs12315813,rs10842905,rs7137588,rs2100840,rs10506018-22221	0.1	1	1

Block-8-Markers:rs2968756,rs922270-11	0.73	1	1
Block-8-Markers:rs2968756,rs922270-12	0.14	0.29	1
Block-8-Markers:rs2968756,rs922270-21	0.14	0.36	1
Block-9-Markers:rs4964060,rs3751221,rs12299407,rs1037919,rs2306074,rs2289709-111122	0.15	0.1	1
Block-9-Markers:rs4964060,rs3751221,rs12299407,rs1037919,rs2306074,rs2289709-111212	0.07	0.31	1
Block-9-Markers:rs4964060,rs3751221,rs12299407,rs1037919,rs2306074,rs2289709-121221	0.04	1	1
Block-9-Markers:rs4964060,rs3751221,rs12299407,rs1037919,rs2306074,rs2289709-122221	0.06	0.49	1
Block-9-Markers:rs4964060,rs3751221,rs12299407,rs1037919,rs2306074,rs2289709-122222	0.04	0.25	1
Block-9-Markers:rs4964060,rs3751221,rs12299407,rs1037919,rs2306074,rs2289709-211212	0.6	0.38	1
Block-10-Markers:rs714359,rs2287162-11	0.01	0.32	1
Block-10-Markers:rs714359,rs2287162-12	0.2	0.47	1
Block-10-Markers:rs714359,rs2287162-21	0.73	0.34	1
Block-10-Markers:rs714359,rs2287162-22	0.06	0.86	1
Block-11-Markers:rs2269457,rs2071570,rs16965644-111	0.08	0.4	1
Block-11-Markers:rs2269457,rs2071570,rs16965644-121	0.55	0.63	1
Block-11-Markers:rs2269457,rs2071570,rs16965644-122	0.14	0.75	1
Block-11-Markers:rs2269457,rs2071570,rs16965644-211	0.14	0.79	1
Block-11-Markers:rs2269457,rs2071570,rs16965644-221	0.1	0.44	1
Block-12-Markers:rs9901910,rs11653735,rs7209167-111	0.18	0.8	1
Block-12-Markers:rs9901910,rs11653735,rs7209167-121	0.26	0.62	1
Block-12-Markers:rs9901910,rs11653735,rs7209167-122	0.41	0.79	1
Block-12-Markers:rs9901910,rs11653735,rs7209167-222	0.15	1	1
Block-13-Markers:rs386551,rs3848543-12	0.73	0.55	1
Block-13-Markers:rs386551,rs3848543-21	0.14	0.75	1
Block-13-Markers:rs386551,rs3848543-22	0.13	0.28	1
Block-14-Markers:rs135745,rs2075984,rs1534891-112	0.22	0.45	1
Block-14-Markers:rs135745,rs2075984,rs1534891-121	0.1	0.97	1
Block-14-Markers:rs135745,rs2075984,rs1534891-122	0.13	0.43	1
Block-14-Markers:rs135745,rs2075984,rs1534891-212	0.27	0.31	1
Block-14-Markers:rs135745,rs2075984,rs1534891-221	0.01	0.3	1
Block-14-Markers:rs135745,rs2075984,rs1534891-222	0.26	0.26	1
Block-15-Markers:rs6001093,rs135757-11	0.06	0.26	1
Block-15-Markers:rs6001093,rs135757-12	0.75	1	1
Block-15-Markers:rs6001093,rs135757-21	0.19	0.56	1
Block-16-Markers:rs1997644,rs5757037,rs7289981-121	0.12	0.69	1
Block-16-Markers:rs1997644,rs5757037,rs7289981-122	0.41	0.58	1
Block-16-Markers:rs1997644,rs5757037,rs7289981-212	0.38	0.87	1
Block-16-Markers:rs1997644,rs5757037,rs7289981-222	0.09	0.45	1

[a] q-values by false discovery rate (FDR) analysis. *p*-values < 0.05 are shown in bold type.