Table S1. Number of half-sibs families and individuals used in the three experiments carried out on growth cessation. For each experiment and population the first number refers to the number of families and the second to the total number of individuals.

Population name	Abbreviation	Growth Chamber 1	Growth Chamber 2	Greenhouse
Koshurnikovo	KOS-54	11/31	5/40	0/0
Sheberta	SHE-54	0/0	6/45	0/0
Baironovka	BAI-56	0/0	0/0	0/0
Krasnoyarsk	KRQ-56	8/17	0/0	11/167
Enyseysk	ENI-58	2/7	0/0	19/416
Yartsevo	YAR-60	6/17	0/0	8/153
Bor	BOR-61	17/70	0/0	20/422
Turukhansk	TYR-66	9/21	0/0	15/133
Igarka	IGA-67	0/0	5/36	0/0

Table S2. Population genetic summary data for the loci used in this study. The top nine are candidate loci and the rest of the list are control loci named according to [1]

Loci	Length	n	S	θ_π	θ_w	Tajima's D
Po*GI*	2668	92	32	0.00216	0.00220	-0.015
Po*CCA1*	3534	83	81	0.00383	0.00392	-0.31
Po*PhyN*	3167	72	20	0.00089	0.00102	-0.11
Po*PhyO*	2187	76	6	0.00026	0.00051	-0.61
Po*PhyP*	1459	85	9	0.00113	0.00108	0.18
Po*PRR3*	1448	93	28	0.00079	0.00272	-1.79
Po*PRR7*	2634	86	56	0.00146	0.00209	-0.98
Po*FTL2*	1373	83	35	0.00156	0.00285	-0.91
Po*MFTL1*	2081	91	99	0.00736	0.0066	0.21
Sequence 8	652	77	32	0.00984	0.00999	-0.05
Sequence 12	539	95	10	0.00132	0.00362	-1.63
Sequence 14	429	96	3	0.00073	0.00136	-0.84
Sequence 18	821	90	2	0.00026	0.00048	-0.73
Sequence 22	683	95	11	0.00157	0.00314	-1.32
Sequence 24	723	94	11	0.00245	0.00297	-0.46
Sequence 28	1141	82	19	0.00111	0.00335	-1.97
Sequence 31	649	95	10	0.00334	0.00301	0.28
Sequence 32	726	95	9	0.00092	0.00242	-1.56
Sequence 33	803	92	20	0.00402	0.00489	-0.52
Sequence 37	629	96	16	0.00272	0.00495	-1.27
Sequence 49	535	93	9	0.00193	0.00330	-1.05
Sequence 56	572	93	21	0.00832	0.00719	0.46
Sequence 58	600	95	23	0.00964	0.00748	0.86
Sequence 59	740	95	9	0.00316	0.00237	0.84
Sequence 60	434	96	2	0.00032	0.00090	-1.00
Sequence 62	744	96	23	0.00689	0.00602	0.43
Sequence 68	601	92	16	0.00574	0.00523	0.28
Sequence 69	708	95	6	0.00098	0.00165	-0.92
Sequence 70	929	95	28	0.00446	0.00588	-0.73
Sequence 77	507	95	17	0.00478	0.00654	-0.77
Sequence 87	633	90	6	0.00127	0.00187	-0.73
Sequence 88	599	95	26	0.00743	0.00847	-0.37
Sequence 89	642	95	8	0.00225	0.00243	-0.18
Sequence 92	740	91	16	0.00317	0.00425	-0.72
Sequence 99	557	82	5	0.00179	0.00180	-0.02
Sequence 100	459	90	0	0	0	*n.a.*

Table S3. Summary statistics for the seven populations analyzed with 14 SSRs

Population	n	Allelic richness	H_e	F_{IS}	F_{IS} corrected[1]
Koshurnikovo	10	2.52	0.65	0.20	0
Krasnoyarsk	21	2.56	0.66	0.24	0
Yeniseysk	26	2.61	0.66	0.15	0
Yartsevo	17	2.53	0.65	0.16	0
Bor	19	2.43	0.61	0.14	0
Turukhansk	16	2.65	0.69	0.18	0
Igarka	4	2.62	0.73	0.27	0

1: F_{IS} corrected by INEST [2]

Table S4. Model probabilities (bold) and Bayes factors between the three models where Bayes factors are calculated as the ratio of the marginal likelihood of the two models under comparison: $p(y|M_1)/p(y|M_0)$

	SNM	BOT	EXP
SNM	**0.365**	0.878	1.650
BOT	1.139	**0.414**	1.857
EXP	0.606	0.539	**0.222**

Table S5. Enrichment ratios of candidate to control SNPs (LD groups)

	90%	95%	97.5%	99%
LinReg	1.1(0.7)[1]	1.1(0.7)	1.7(0.9)	0.8(0.8)
BAYENV	1.2(0.9)	1.7*(1.3)	0.8(0.9)	1.5(1.7)
F_{ST}	0.9(0.7)	0.9(0.8)	1.1(0.8)	1(1)
LinReg & BAYENV	1.3(0.9)	1.1(1)	1(0.8)	1(1)
BAYENV & F_{ST}	1.8(1.4)	2.8(2.3)	1.3(1.5)	3/0(3/0)
LinReg & BAYENV & F_{ST}	1.2(1.3)	2/0(1/0)	2/0(1/0)	*n.a.*

[1] Numbers in parentheses indicate the ratios calculated using LD groups.
*: Fisher's exact test p-value < 0.05.

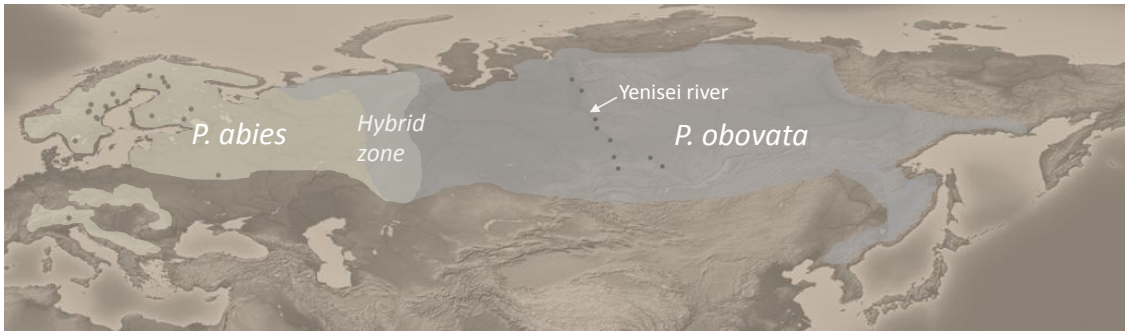

Figure S1. Location of the populations used in this study. The distributions of *P. abies* and *P. obovata* and their hybrid zone are also shown. The distribution of *P. abies* is based on the Euforgen map (EUFORGEN 2009, www.euforgen.org) and that of *P. obovata* is taken from [3]. The approximate location of the hybrid zone was inferred by genotyping 99 populations at 13 nuclear SSR loci and three cpSSR loci (Y. Tsuda, T. Källman, M. Lascoux, L. Parducci, D. Politov, V. Semerikov, J.H. Sønstebø, C. Sperisen, M.M. Tollefsrud, M. Väliranta, G.G. Vendramin, in preparation) and from [4] and [5]. The dots within the *P. abies* range indicates the populations used in [6].

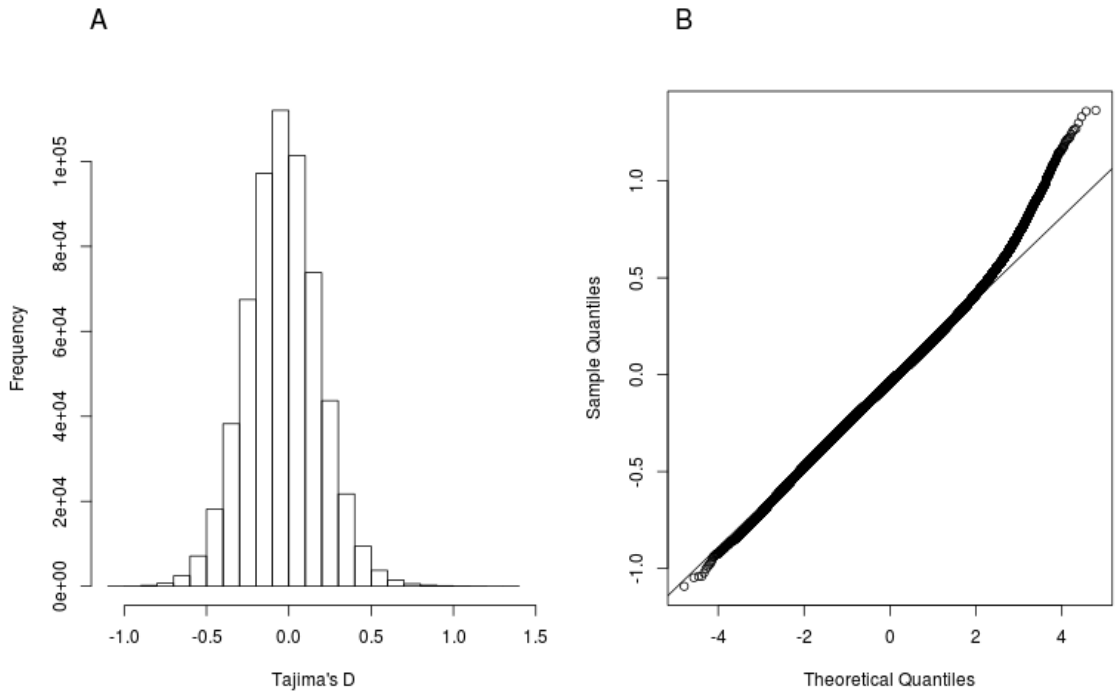

Figure S2. A histogram of Tajima's D values under a standard neutral model (A) and a Q-Q plot of Tajima's D plotted against a standard normal distribution (B).

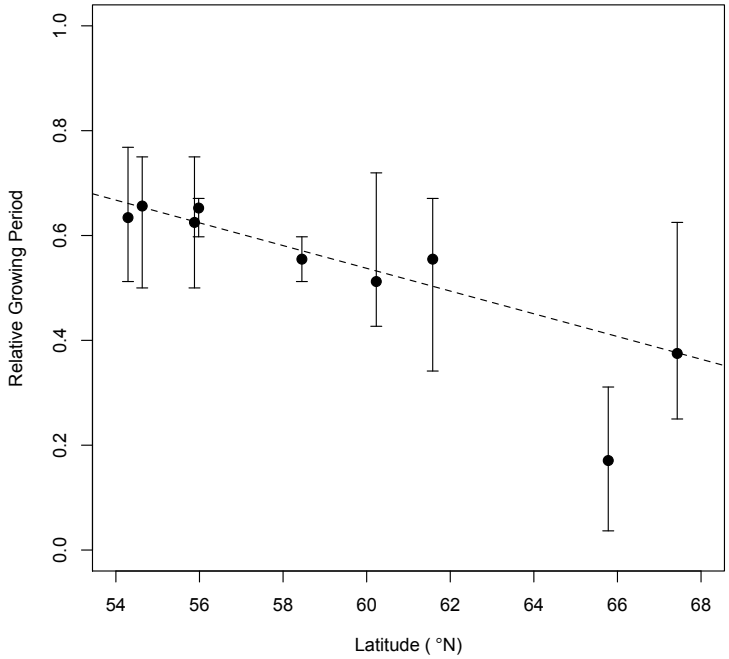

Figure S3. Average number of growing days for populations along the Yenisei river from south to north. Vertical bars represent the standard deviation for each measurement. Data from all nine populations were used here. Photoperiodic treatments started with one week of constant light, followed by one week at 22-h light / 2-h dark, and so on. The dark period was extended by 1.5 hours each week until a photoperiod of 14.5 light / 9.5-h dark was reached. To aid visualization and present the results on the same scale across the two experiments the observed number of growing days was transformed into relative growing period, which is the observed growth relative to the maximum growth period of each experiment ($df = 83$, $r^2 = 0.5904$, p-value $= 3.45E-07$).

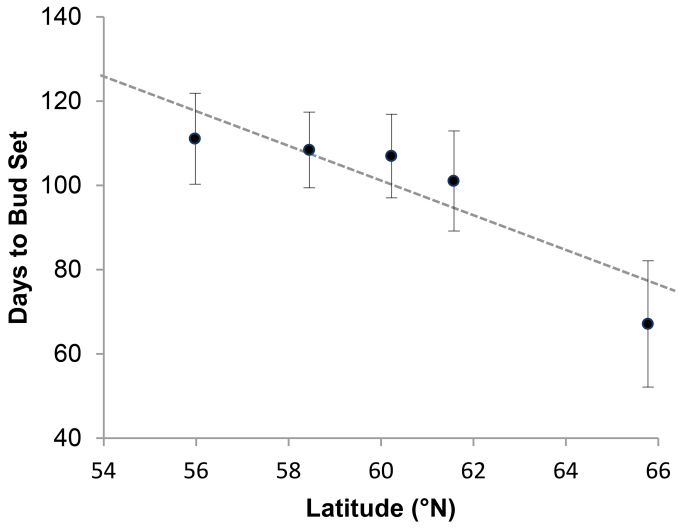

Figure S4. Average days to bud set for five populations along the Yenisei River, included in the greenhouse experiment at Haapastensyrjä in Southern Finland (60.62°N, 24.43°E). Vertical bars represent the standard deviation for each measurement. Time to bud set was observed weekly. The dotted line is a regression line (p-value < 0.001, $r^2 = 0.432$, $df = 1288$)
.

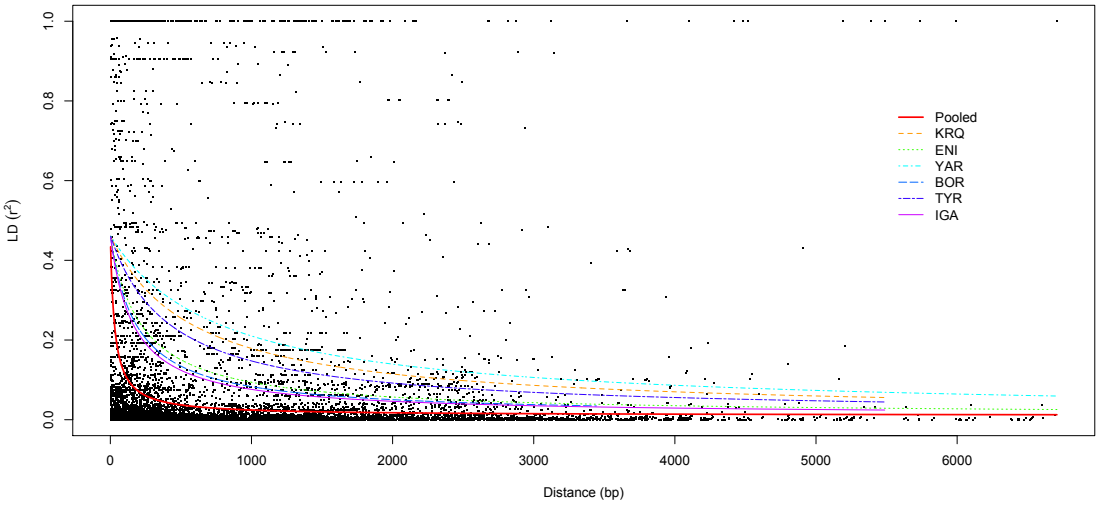

Figure S5. LD decay within each locus in *P. obovata*. Data from all populations were pooled and the curve represents the correlation of r^2 with distance.

Figure S6. Pairwise LD blocks in *P. obovata*. Data from all populations were pooled and the red triangle shows the LD blocks of candidate genes.

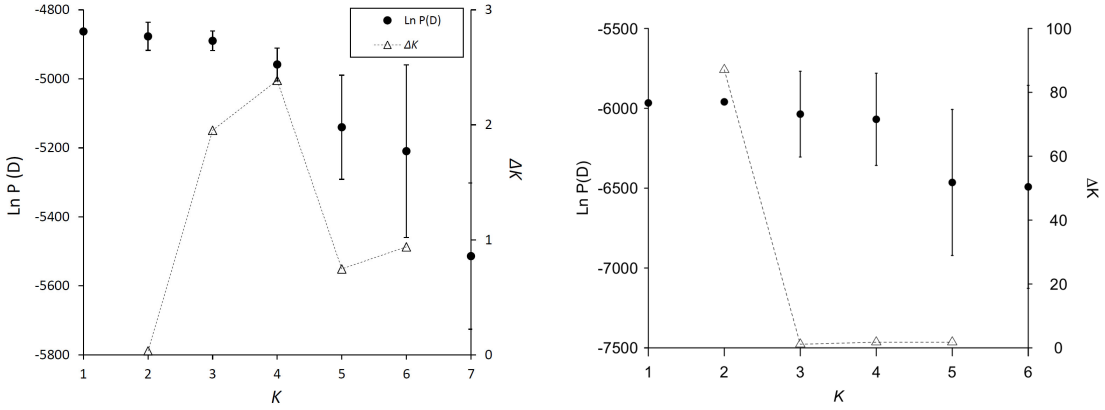

Figure S7. $LnP(D)$ **and** ΔK **for SSRs (left) and SNPs (right)**

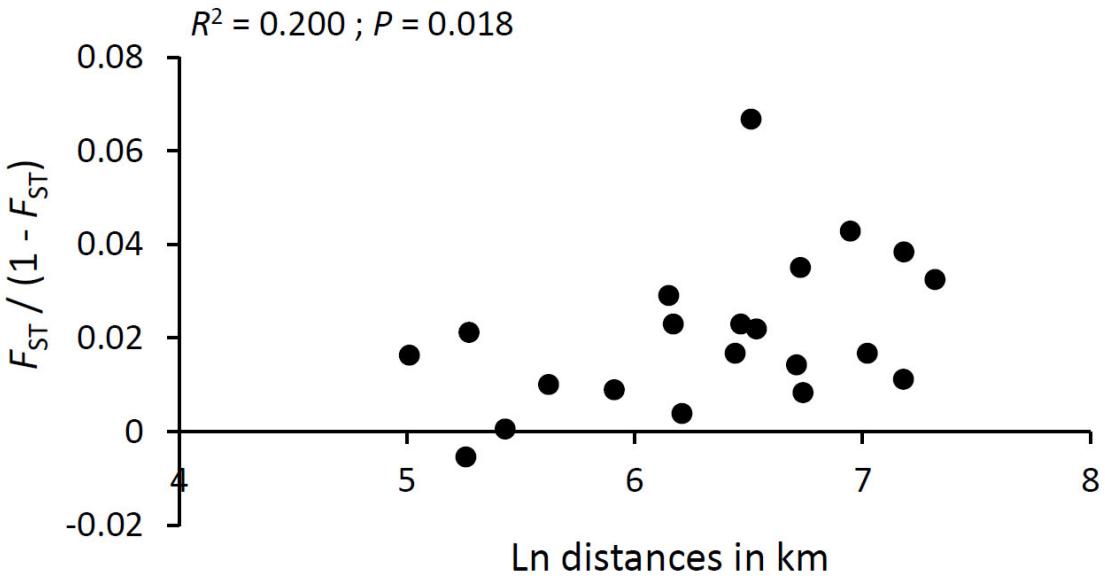

Figure S8. Isolation–by–distance estimated from the 14 SSRs loci

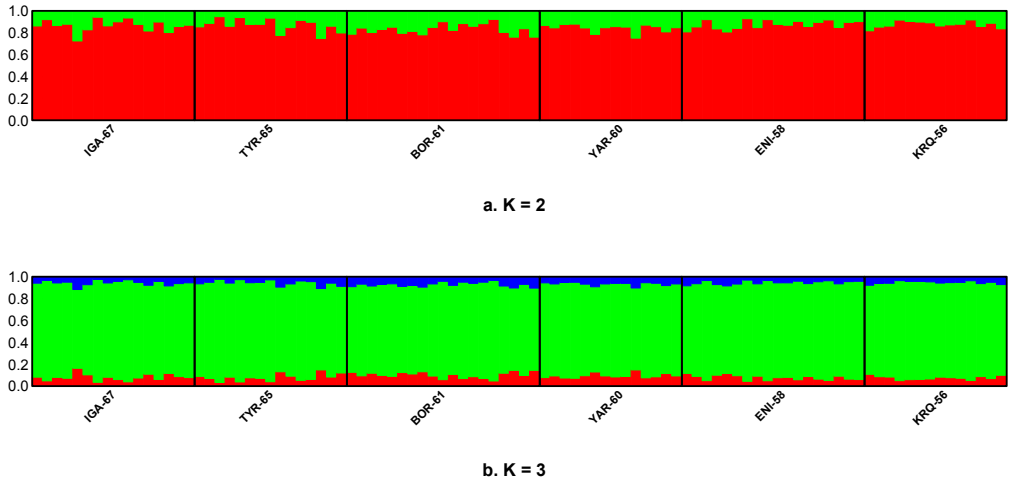

Figure S9. Clustering analysis conducted in STRUCTURE using 240 independent SNPs. For each dataset, $K = 1$ to $K = 6$ were tested. K=2 and K=3 are presented to illustrate the lack of population genetic structure.

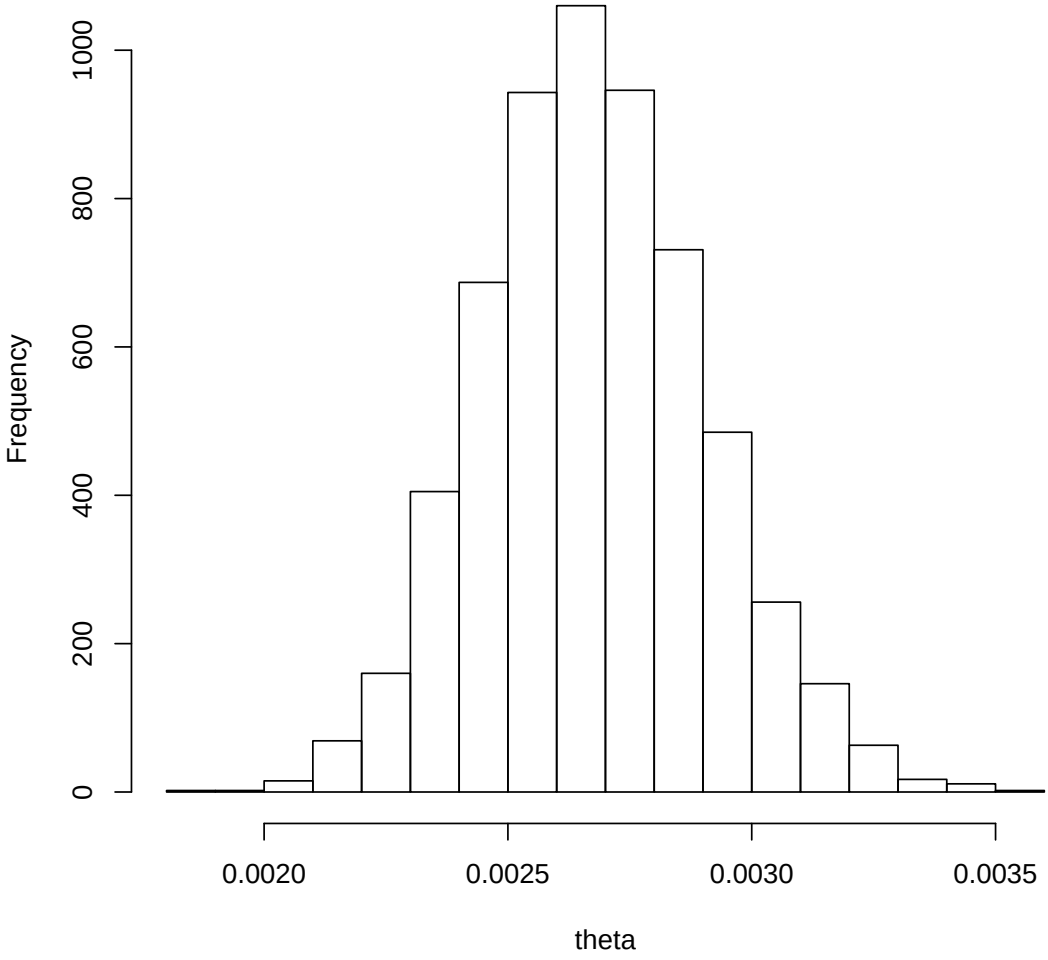

Figure S10. Posterior distribution for SNM model of θ inferred from silent sites.

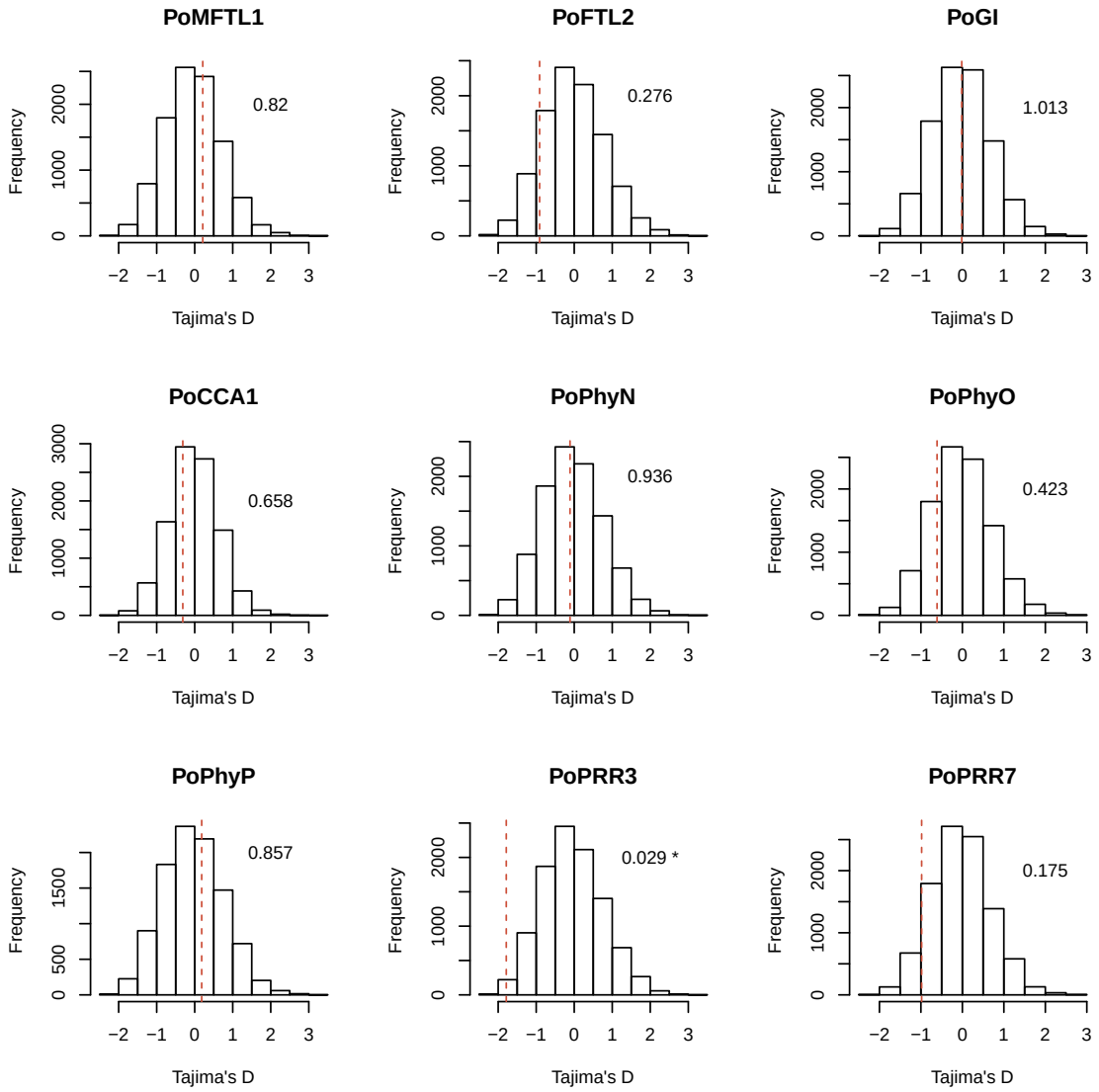

Figure S11. Posterior predictive distributions of Tajima's D for the SNM model inferred from silent sites with the red lines indicating the observed statistics calculated for all sites. p-values indicate whether the loci deviate significantly (*) from the posterior predictive simulations.

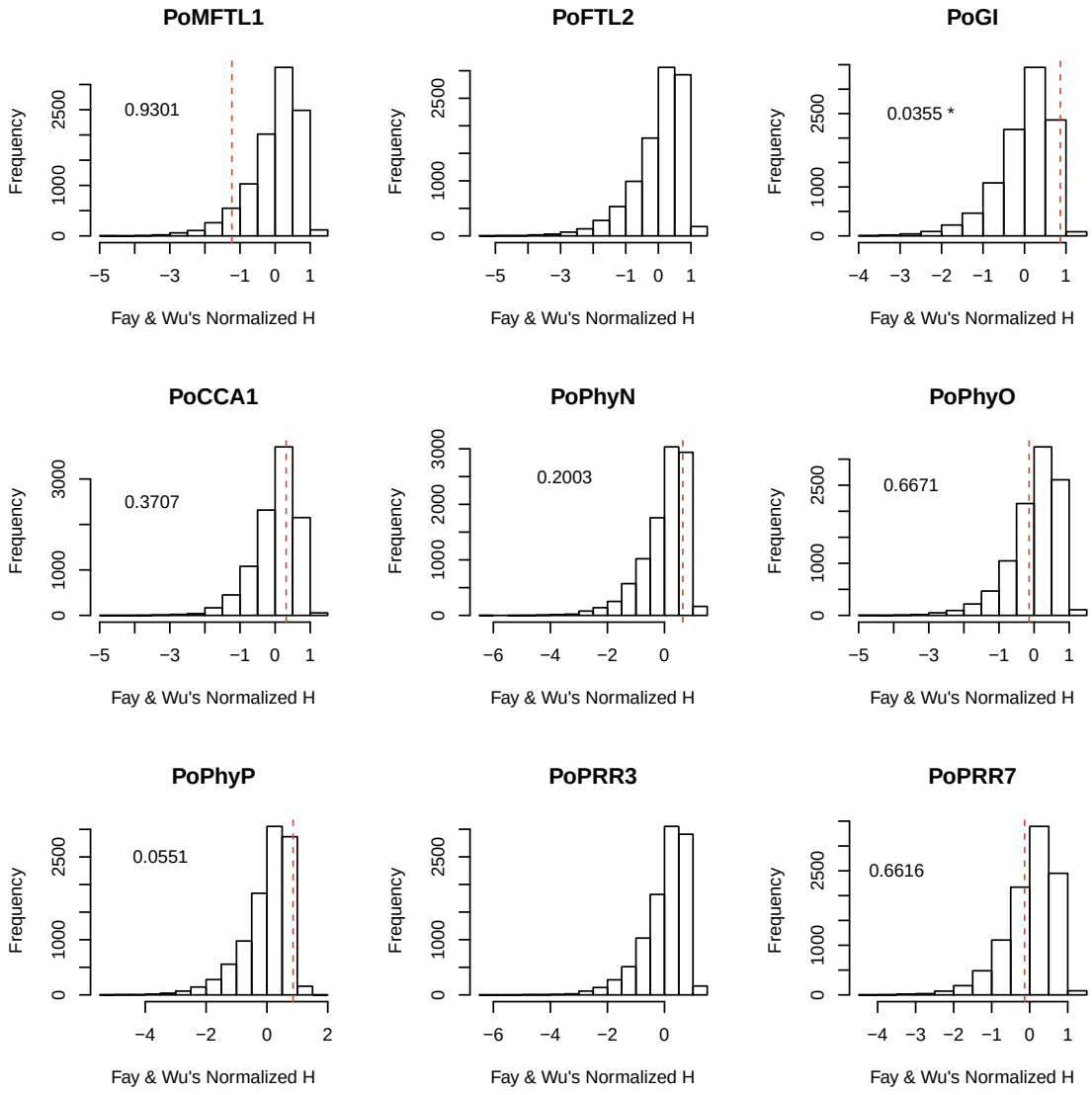

Figure S12. Posterior predictive distributions of Fay and Wu's H for SNM model inferred from silent sites. Red lines are observed statistics calculated for all sites.There are no observed values for Po*FTL2* and Po*PPR3* due to the lack of outgroup.

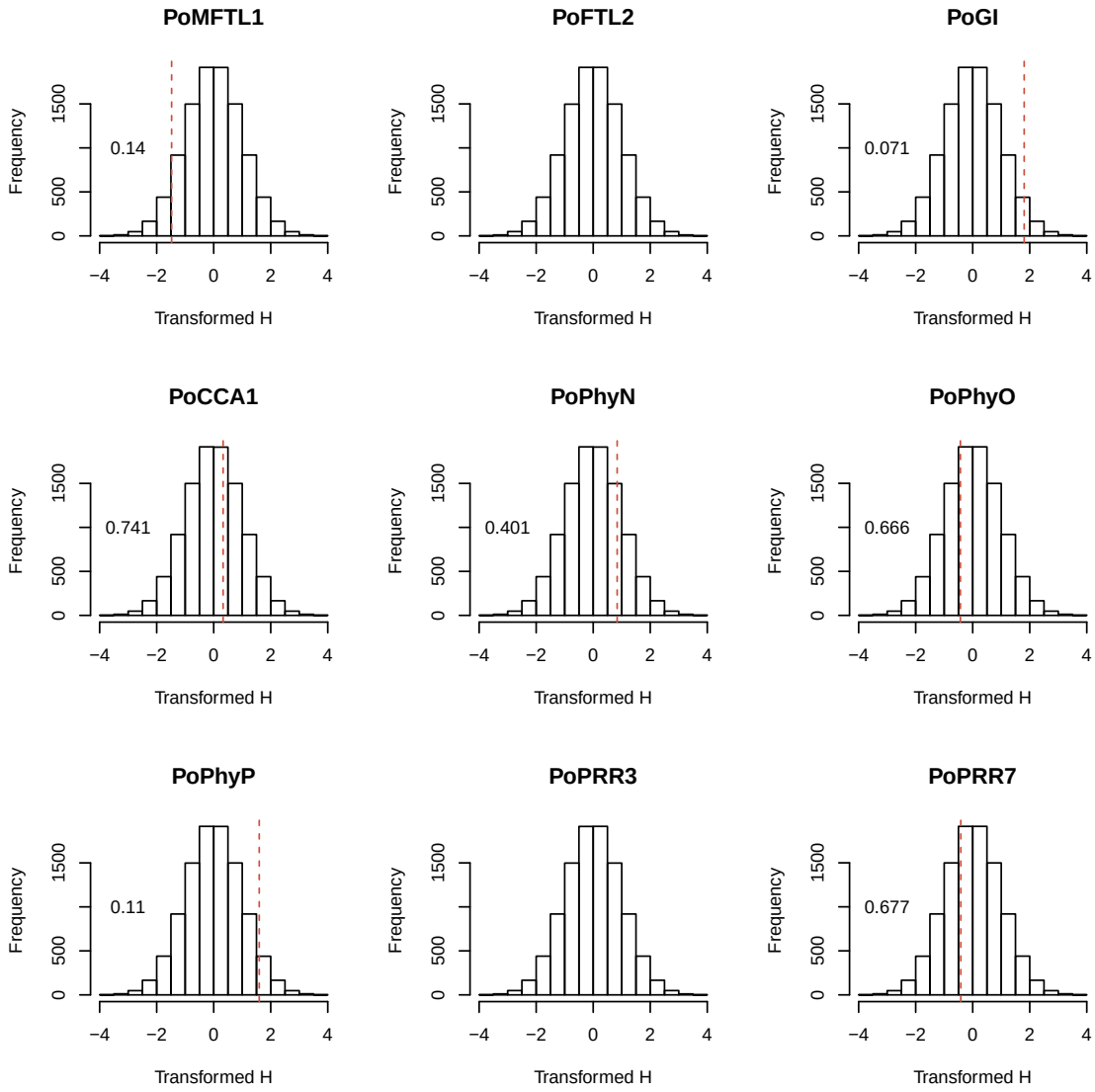

Figure S13. Rank transformed posterior predictive distributions of Fay and Wu's H for SNM model inferred from silent sites. Red lines are observed statistics calculated for all sites. There are no observed values for Po*FTL2* and Po*PPR3* due to the lack of outgroup. p-values indicate whether the loci deviate significantly (*) from the posterior predictive simulations.

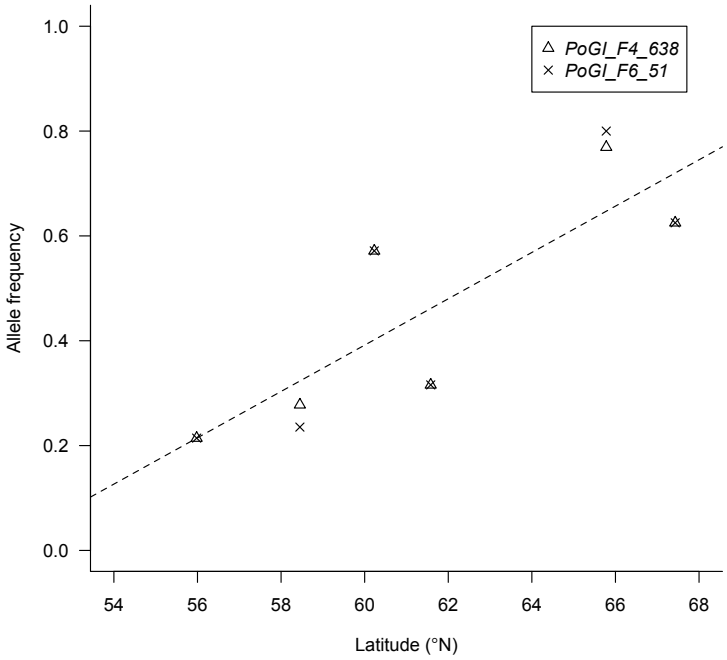

Figure S14. An example of clinal variation in the circadian clock gene Po*GI*. Linear regression of transformed minor allele frequency on latitude at the non-synonymous LD group of PoGI_{F4_638} (linear regression p-value = 0.038, adjusted $R^2 = 0.62$)

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File S1

Outliers detected with different approaches

Available for download as an Excel file at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.163063/-/DC1