Table S9 Fit of the SNM and Ersöz *et al.* (2010) model to all and the trimmed data. Note that loci with less than four alleles and less than two SNPs were excluded from both analyses. Means and variances are weighted by the sample coverage class in each case.

	All (l = 3,360)			Trimmed[a] (l = 3,133)		
Statistic	Obs	*P* (SNM)	*P* (TEM)	Obs	*P* (SNM)	*P* (TEM)
Mean						
θ_π	0.0045	0.995	0.359	0.0047	0.997	0.415
D	-0.487	< 0.001	0.077	-0.467	< 0.001	0.092
Z_{nS}	0.305	> 0.999	0.098	0.298	> 0.999	0.115
Variance						
θ_π	2.28e-05	0.887	0.087	2.26e-05	0.874	0.068
D	0.918	0.997	0.003	0.912	0.001	0.001
Z_{nS}	0.080	> 0.999	0.104	0.079	0.089	0.089

Abbreviations: *D*, Tajima's *D*; l, number of loci or amplicons; Obs, observed value; SNM, standard neutral model; θ_π, nucleotide diversity from the average number of pairwise differences; TEM, three epoch model from Ersöz *et al.* (2010); Z_{nS}, Kelly's statistic representing the average pairwise linkage disequilibrium (LD) among SNPs within an amplicon.

[a] Trimmed data refer to data where samples west of the Mississippi River were excluded. This caused some amplicons to be dropped. The reason for excluding these samples is that the model of Ersöz *et al.* (2010) was fit to data derived from samples exclusively collected from the eastern portion of the range of loblolly pine.